EVBC Newsletter

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Announcements

⚙ EVBC back on track

Welcome back to our monthly newsletter following a short interruption in October due to moving of our faculty into a new building! Thank you for your patience and continued engagement - We are delighted to share the latest updates and activities from across our consortium again.
We're also pleased to share that our EVBC website is online again! Over the past weeks, we experienced technical interruptions and unexpected downtime due to the relocation of our faculty. We sincerely apologize for any inconvenience this may have caused.

⚙ Viruses Young Investigator Award

The journal *Viruses* will be awarding two prizes to early career investigators demonstrating excellence in virology. Nomination deadline is 31 December 2025. Find more information here.

Tools and Resources

🔧 Virus tools website

Tools developed by EVBC members are marked ⚙.

⚙ **ViralBottleneck**: An R package implementing six methods to estimate viral transmission bottlenecks from deep sequencing data, demonstrating method-dependent variability in bottleneck size estimates using simulated datasets.

⚙ **TRAMbio**: A Python package for graph-based rigidity analysis of macromolecules using the pebble game algorithm, enabling efficient identification of rigid components and conformational dynamics in large molecular structures.

⚙ **Viro3D**: Is a comprehensive database of over 85,000 predicted virus protein structures, enabling functional annotation, evolutionary analysis, and structure-informed investigation of viral proteins across the human and animal virosphere.

⚙ **HIPSTR**: Summary tree method in TreeAnnotator X that reconstructs highest independent posterior subtrees, yielding clades with higher support than maximum clade credibility trees and offering improved performance for Bayesian phylogenetic analyses.

⚙ **CLASV**: A Python-based Random Forest tool for rapid and accurate Lassa virus lineage assignment from nucleotide sequences, facilitating outbreak tracking and epidemiological analyses.

⚙ **VirTrack**: A computational framework integrating EBV–host protein interactions with MS clinical type–specific transcriptomes, revealing that EBV exerts dynamic, stage-dependent effects on host pathways, strongly modulating immunity in early MS and driving selective cellular remodeling in progressive MS.

Selected Publications by EVBC Members

📰 All publications on PubMed

RNA

🔓 This work presents a comprehensive structural survey revealing multiple backbone topology variants of GNRA tetraloop-like RNA motifs, demonstrating their versatility in diverse nucleic acid contexts and roles in intermolecular interactions. (Sci Rep: **10.1038/s41598-025-21072-9**)

🔓 This study identifies and characterizes 3,560 previously unrecognized RNA virus-derived RdRp and endogenous viral element sequences from major protein databases, revealing extensive hidden viral diversity and providing improved taxonomic annotations and guidance for constructing accurate negative control datasets. (Virus Evol: **10.1093/ve/veaf074**)

This study demonstrates that host-derived Z-RNAs generated through virus-induced disruption of transcription termination, rather than viral RNAs, are the primary activators of ZBP1-mediated cell death during HSV-1 and influenza A infection. (Nature: **10.1038/s41586-025-09705-5**)

PLANT viruses

🔓 This metagenomic survey of commercial tomato crops across multiple continents identified 43 eukaryotic viral species, characterized the low genetic diversity of major prevalent viruses such as PepMV, ToBRFV, and STV, and evaluated their potential roles in symptom development. (Viruses: **10.3390/v17101334**)

🔓 This study reveals that wild and globally traded ornamental aquatic plants harbor diverse known and novel plant viruses, including regulated crop pathogens, underscoring the biosecurity risks associated with the international aquatic plant trade. (Environ Microbiome: **10.1186/s40793-025-00783-6**)

Taxonomy, phylogeography

🔓 This study analyzes RdRP and related genomic features of flaviviruses and flavi-like viruses, leading to a reorganization of their taxonomy into three families and twelve genera that better reflect their evolutionary relationships, genome structures, and host ranges. (Nat Microbiol: **10.1038/s41564-025-02134-0**)

🔓 This study evaluates an adjusted Bayes factor that incorporates relative sample abundance to mitigate sampling bias in discrete phylogeographic analyses, showing improved error balance and providing guidance for its complementary use alongside the standard approach. (Mol Biol Evol: **10.1093/molbev/msaf253**)

Phages; metagenomics

🔓 This study shows that bacteriophage diversity decreases with increasing COPD severity and that disrupted phage–bacteria relationships, including reduced phages of oral anaerobes and virulence factor–carrying phages, reshape respiratory microbial ecology in diseased lungs. (Cell Rep: **10.1016/j.celrep.2025.116413**)

🔓 This study shows that integrating viral metagenomic sequencing with standard diagnostics improves pathogen detection in neuroinflammatory disorders, enabling identification of rare or unexpected viral infections and increasing overall diagnostic accuracy. (Diagn Microbiol Infect Dis: **10.1016/j.diagmicrobio.2025.117140**)

This study reconstructs viromes from hypersaline lakes and reveals complex nested interactions among haloarchaea, their nanosized DPANN symbionts, diverse viruses, and plasmid-derived viral satellites, demonstrating convergent adaptation and extensive gene exchange in these extremophile ecosystems. (Nat Microbiol: **10.1038/s41564-025-02149-7**)

🔓 ⊞ This review highlights how phage-antibiotic synergy can target efflux-mediated resistance in multidrug- and extensively drug-resistant ESKAPEE pathogens, restoring antibiotic susceptibility and offering a promising strategy for precision-based antimicrobial therapy. (mBio: **10.1128/mbio.01822-25**)

🔓 – open access   χ – 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.

Viruses 2026 – New Horizons in Virology

11-13 March 2026 | Barcelona, Spain

This conference aims to bring together international researchers studying various topics related to viral replication, pathogenesis, structure, immunology, epidemiology, public health, and other areas of virology.

Abstract submission deadline:	9 November 2025
Early bird registration deadline:	5 January 2026

Microbiology Society Annual Conference 2026

13-16 April 2026 | Belfast, UK

Includes two Virus Symposia “A virus for all seasons” / “Viral manipulation of the intracellular RNA world”, and sessions such as “AI-enabled Microbiology” or “Phage biology with a view to application”.

Abstract submission deadline:	11 November 2025
Registration:	now open

4th European Congress on Biomedical Science & Engineering

27-28 April 2026 | Berlin, Germany

Theme: “Re-Imagining Biomedical Engineering for a Future World Wellness”. Includes a session on Bioinformatics.

Early bird registration and abstract deadline:	18 November 2025

35th Annual Meeting of the Society of Virology (GfV)

17-20 March 2026 | Heidelberg, Germany

Conference on the latest developments in virology, ranging from basic research to clinical virology and covering novel technologies.

Abstract submission deadline:	4 January 2026
Early bird registration deadline:	start on short notice from mid-Nov

European Conference on Computational Biology (ECCB 2026)

31 August to 4 September 2026 | Geneva, Switzerland

Europe’s leading event in computational biology. The theme in 2026 will be ”Biodiversity, AI and Health: computational biology to address the challenges of our time”.

Submission deadline for **tutorial and workshop proposals**: 5 Jan 2026

1st World Conference on Microbiology, Virology and Infectious Diseases (MVID 2026)

25-27 March 2026 | Kyoto, Japan

Topics include advances in virology research, pathology and microbial genomics, vaccine research and development. There will be a session on “Genomics and Bioinformatics in Infectious Diseases”.

Abstract submission deadline:	10 January 2026
Poster abstract deadline:	20 January 2026
Early bird registration deadline:	18 December 2025

Selected Publications by EVBC Members

All publications on Pubmed

Virus methods/tools in wet-lab

🔓 This study demonstrates that dry blood spots can serve as a practical alternative to whole blood for whole-genome sequencing of Lassa virus, despite lower RNA yield, higher Ct values, and reduced sequencing coverage. (Infect Dis Poverty: **10.1186/s40249-025-01362-0**)

🔓 This study introduces CLAE, a high-fidelity Nanopore sequencing strategy that enhances accuracy, read length, and throughput, enabling precise viral variant detection and the recovery of novel RNA virus genomes from environmental and clinical samples. (Adv Sci: **10.1002/advs.202505978**)

🔓 This protocol describes a virus-delivered short RNA (vsRNAi) method using TRV vectors to trigger targeted gene silencing in plants, demonstrated by robust phenotypes such as leaf yellowing and reduced chlorophyll in Nicotiana benthamiana. (STAR Protoc: **10.1016/j.xpro.2025.104094**)

🔓 This protocol presents VECOS, a virus-encoded CRISPR-based system that enables multidimensional analysis of host-virus interactions by using sgRNA abundance within the viral genome as a direct readout of gene-perturbation effects across infection stages. (Nat Protoc: **10.1038/s41596-025-01242-9**)

Potential future techniques for viruses

🔓 This study presents a multiplexed microfluidic platform using angle-resolved light scattering and fluorescence coding to perform rapid, high-throughput phenotypic antibiotic susceptibility testing, achieving accurate results in three hours and significantly reducing incubation time compared to standard methods. (J Adv Res: **10.1016/j.jare.2025.09.047**)

🔓 This study uses high-speed interferometric scattering microscopy to characterize compartmentalized lipid diffusion in living cell membranes, revealing a mixture of diffusion modes and quantifying transient confinement, intracompartmental, and intercompartmental diffusion dynamics. (Chemphyschem: **10.1002/cphc.202400407**)

Mathematical modeling

🔓 This study uses mathematical modeling to show that in Ebola virus outbreaks, trade-offs between diagnostic test accuracy, time-to-isolation, and accessibility can make rapid, lower-accuracy tests more effective than PCR alone in reducing epidemic size. (BMC Infect Dis: **10.1186/s12879-025-11273-y**)

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EVBC Special Issues

Special issue list

Current Special Issues:

Special Issue ”Virus Bioinformatics 2025”

MDPI grants a discount of 20 % for submissions from ViBioM 2025 attendees and EVBC members!

Submission deadline:	31 December 2025

Research Topic “Bridging Gaps in Antiviral Therapy: Innovative Approaches in Drug Discovery and Vaccine Development”

in *Frontiers in Virology*

Call for Papers by Topic Editor and EVBC Member: Arif Ansori

Section “Bioinformatic and Predictive Virology”

in *Frontiers in Virology*

Editorial Board incl. L. Kaderali | M. Marz | F. Erhard | C. C. Friedel | A. Gruber | D. Heider | M. Hölzer | C. Lauber

ECR Viromics Webinar Series

Register

This lecture series features early career researchers studying viruses in complex communities. It is organized together with the Center of Microbiome Science at Ohio State University and the NSF EMERGE Biology Integration Institute. You can register **here** for the ECR Viromics mailing list and receive the access details for every webinar. You can unsubscribe at any time.

Upcoming talks:

Untangle the complexity of the virosphere using single-cell RNA-sequencing
Amir Fromm, Weizmann Institute of Science, Israel
12 November 2025 | 4 pm CET online

Drawing from phage diversity to uncover genomic factors shaping host interaction
Antônio Pedro Camargo, University of São Paulo, Brazil
10 December 2025 | 4 pm CET online

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. You can register **here** for the viruses in silico mailing list and receive the access details for every lecture. You can unsubscribe at any time.

Upcoming talks:

Emma Hodcroft, Swiss Tropical & Public Health Institute, Switzerland
27 November 2025 | 4 pm CET online

Sebastian Böcker, Friedrich Schiller University Jena, Germany
26 February 2026 | 4 pm CET online
SIRIUS and beyond: Turning tandem mass spectra into metabolite structure information

Be part of the Newsletter

✉ Email us

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!