# EVBC Newsletter

Volume 96 • September 2025

European
VIRUS BIOINFORMATICS
Center

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## Upcoming Events

Subscribe to Calendar

### 27th Annual Conference of the European Society for Clinical Virology (ESCV)

**17-20 September 2025 | Thessaloniki, Greece**

The ESCV conference will be covering all topics of clinical virology, enabling delegates to exchange knowledge with world-class experts, network with colleagues, and vividly discuss the latest advances on "traditional" and emerging viruses with the global virology community.

Registration deadline: 10 September 2025

### Aging and Microbiome Conference 2025

**28-29 October 2025 | Jena, Germany**

This conference will bring together leading researchers to explore the interactions between aging and microbiomes, highlighting cutting-edge research and opportunities for interdisciplinary collaboration.

Late registration deadline: 14 September 2025

### Future Virology 2025 Conference (3rd Global Virology Congress)

**25-26 September 2025 | Berlin, Germany**

A review of innovative therapeutic approaches to combat various viral diseases. A discussion of current status and future developments in antiviral drug discovery.

Abstract submission and registration: Still open

### 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: 12 October 2025
Early bird registration deadline: 5 January 2026

### 15th International dsRNA Virus Symposium

**3-7 November 2025 | Porto, Portugal**

This Symposium with Vaccine Satellite is the foremost international meeting for virologists and medical professionals interested in viruses that harbor a double-stranded RNA viral genome.

Registration deadline: Still open

## Selected Publications by EVBC Members

All publications on PubMed

### Virus Infection Research

🔓 Using ex vivo human precision-cut lung slices, this study demonstrates that Raman spectroscopy can non-invasively characterize alveolar macrophage phenotypic changes in response to SARS-CoV-2 infection and distinguish infected from uninfected cells with 83% accuracy (Clin Transl Med: **10.1002/ctm2.70453**)

🔓 HIV-phyloTSI is a Random Forest regression model that combines within-host diversity (MAF) and divergence (LRTT) from deep HIV-1 sequence data to provide continuous time-since-infection estimates up to nine years with MAE <12 months overall and <5 months for infections ≤1 year, performing consistently across major subtypes (BMC Bioinformatics: **10.1186/s12859-025-06189-y**)

🔓 Using the MiFi platform, the authors design and curate 40-nt electronic probes targeting three hop viruses and two viroids, validate probe specificity via BLAST and variant mapping, and demonstrate sensitive, specific detection from unassembled HTS datasets in both in silico and in vitro assays (PhytoFrontiers: **10.1094/PHYTOFR-09-24-0106-FI**)

🔓 Quantifying bovine leukemia virus proviral load in plasma cfDNA versus whole blood via qPCR demonstrated perfect sensitivity and specificity for diagnosing enzootic bovine leukosis (EBL) and shows that cfDNA originates predominantly from tumor-cell integration sites, highlighting its potential as a robust biomarker for EBL diagnosis (Microbiol Immunol: **10.1111/1348-0421.13231**)

### Omics Analyses

⊞ The authors caution against over-interpreting viral "auxiliary metabolic genes" detected by automated annotations, outlining common pitfalls and proposing an expanded concept - auxiliary viral genes (AVGs) - with an eco-evolutionary framework and best-practice guidance for stronger biological claims (Nat Microbiol: **10.1038/s41564-025-02095-4**)

🔓 A novel tiling amplicon panel targeting HA, NA and M segments for H1N1 and H3N2 applies high-coverage sequencing to Swiss wastewater samples (2022 to 2024) to recover influenza A lineages and clinically relevant mutations, showing concordance between wastewater-derived lineage abundance and clinical surveillance and enabling detection of vaccine- and drug-target mutations (Water Res: **10.1016/j.watres.2025.124453**)

🔓 Using high-throughput sequencing of double-stranded RNA from pooled leaf samples across major German hop growing regions (2021–2023), the study detected four hop viruses (HpLV, HpMV, ApMV, ArMV) and two viroids (HLVd, CBCVd), found CBCVd restricted to Hallertau, and demonstrated HTS utility for plant pathogen surveillance and disease-management planning (PLoS One: **10.1371/journal.pone.0329289**)

### Virus Phylogeny

🔓⊞ The review highlights advancements in reconstructing deep viral evolutionary history using Bayesian models with time-dependent substitution rates and introduces structural phylogenetics as a promising approach when sequence homology is saturated (J Virol: **10.1128/jvi.00292-25**)

🔓 A One Health seven-year study in the Netherlands maps emergence and co-circulation of Usutu and West Nile viruses using integrated ecological, serological and genomic surveillance - revealing enzootic USUV Africa-3, sporadic Europe-3 introductions, and early WNV lineage-2 establishment that preceded human cases (Nat Commun: **10.1038/s41467-025-63122-w**)

### RNA structure modeling

🔓 ⊞ This review surveys recent computational advances for modeling flexible RNA 3D structures and RNA–protein complexes, emphasizing approaches that capture conformational heterogeneity and integrate experimental restraints to better represent biologically relevant states (Curr Opin Struct Biol: **10.1016/j.sbi.2025.103137**)

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*🔓 – open access* *χ – preprints* *⊞ – reviews, meta analyses* *🔧 – tools*

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# EVBC Newsletter

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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

## Tools and Resources — Virus tools website

Tools developed by EVBC members are marked ⚙.

⚙ **Jaeger:** A novel deep-learning method for rapid and accurate identification of bacteriophage genome fragments in metagenomic assemblies, demonstrating high sensitivity (0.87) and precision (0.92) and processing datasets 20× faster than contemporary tools, recovering over five million phage contigs from >16,000 MGnify assemblies.

⚙ **ganon2:** An upgraded, highly scalable metagenomic classifier that supports fast, incremental reference indexing and accurate taxonomic binning/profiling of sequencing reads against massive and frequently updated databases.

⚙ **CLEAN:** This tool offers a targeted approach for decontaminating sequencing data, enhancing the accuracy of viral genome analyses by removing unwanted sequences.

## 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 talk:**

**Chronotyping the Ocean Virome: Fine-Scale Temporal Clustering Reveals Viral Ecological and Evolutionary Patterns**
**Luis Bolaños Avellaneda**, Exeter University, UK
**10 September 2025 | 4 pm CEST** 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:**

**SIRIUS and beyond: Turning tandem mass spectra into metabolite structure information**
**Sebastian Böcker**, Friedrich Schiller University Jena, Germany
**30 October 2025 | 4 pm CET** online

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

## 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!