EVBC Newsletter
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For more frequent updates, follow us on Bluesky and LinkedIn.

ViBioM 2026

We look forward to the International Virus Bioinformatics Meeting 2026!
Save the date for ViBioM 2026 on 18–20 May in Vilnius, Lithuania!

Stay tuned for updates and details about abstract submission and registration on our website!

Abstract submission for talks: open soon until 6 March 2026
Registration: open from mid February until 30 April 2026

EVBC Special Issues — Special issue list

Special Issue "Virus Bioinformatics 2025"
MDPI grants a discount of 20 % for submissions from ViBioM 2025 attendees and EVBC members!
Submission deadline: extended to 31 March 2026!

Tools and Resources — 🔧 Virus tools website

Tools developed by EVBC members are marked ✹.

✹ **SquiDBase**: A community resource compiling raw microbial nanopore sequencing data with accompanying metadata and processing pipelines to maximise reuse and comparability across studies for a deeper exploration of microbial sequence diversity.
✹ **VirJenDB**: an integrated, FAIR compliant bioinformatics platform aggregating virus sequences and richly curated metadata to facilitate unified analyses across all viruses, including eukaryotic and phage genomes. The database offers advanced search, download and API tools, supporting community driven metadata curation and bioinformatics workflows to advance virus ecology, evolution and comparative research.
✹ **SIMPLICITY**: An agent based, multi scale model that couples within host virus evolution and disease progression with population level transmission dynamics to simulate SARS CoV 2 evolutionary patterns. The model demonstrates how immune escape and infection history drive selective sweeps similar to observed pandemic evolution, providing a flexible framework for exploring host–pathogen interactions and virus adaptation.

Selected Publications by EVBC Members
All publications on PubMed

RNA Secondary Stuctures
🔓 The study shows that glycyl-tRNA synthetase binding to the Mengovirus genome enhances translation, shedding light on specific RNA–protein interactions essential for virus gene expression. The findings provide mechanistic insight into how host factors influence virus translation and may inform future antiviral strategies. (Nucleic Acids Res: **10.1093/nar/gkaf1451**)

🔧 This protocol describes NACDDB and NAIRDB, curated databases of circular dichroism and Fourier transform spectra designed to facilitate structural analysis of nucleic acids using spectroscopic methods. They provide standardised datasets and analytical context to support interpretation of RNA conformational and interaction studies. (Methods Mol Biol: **10.1007/978-1-0716-5084-4**$_4$)

🔓 This article reports the first full-genome multiple sequence alignment for the Pestivirus genus, identifying conserved RNA secondary structures throughout pestivirus genomes, including untranslated regions and coding segments. These findings provide a foundational comparative resource for understanding functional roles of pestivirus RNA elements. (RNA: **10.1261/rna.080732.125**)

RNA Modifications
🔓 This study presents DRAP3R, a modified direct RNA nanopore sequencing and analysis system that captures and characterises pre-mature and novel Pol III transcripts, thereby expanding the RNA Pol III transcriptome and epitranscriptome. Application across cell types reveals previously unconfirmed tRNA genes and other Pol III-derived RNAs, enhancing understanding of Pol III biology and transcript diversity. (Nat. Commun.: **10.1038/s41467-025-68230-1**)

🔓 χ This preprint demonstrates that extended poly(A) tails are a shared feature among herpesvirus mRNAs, suggesting a conserved mechanism of post-transcriptional regulation across the herpesvirus family. The findings provide a foundational observation with implications for understanding virus mRNA stability and translation. (bioRxiv: **10.64898/2025.12.15.694445**)

Phylogeny/History
🔓 Large-scale comparative genomic and phylogenetic analyses of the Geminiviridae family reveal extensive diversity, recombination, and instances of misclassification across genera. The findings inform virus taxonomy and global distribution patterns, enhancing understanding of geminivirus evolution and host–vector dynamics. (PLoS ONE: **10.1371/journal.p.one.0338481**)

🔓 χ The recovery of near-complete RNA virus genomes from Adelie penguin mummies spanning recent to nearly two millennia of age, including picornavirus and rotavirus sequences, demonstrated unexpected preservation of virus RNA in Antarctic conditions and provided a novel framework for direct investigation of long-term RNA virus evolution. (bioRxiv: **10.64898/2025.12.17.693957**)

🔓 This study identifies a recurrent adaptive mutation in the transmembrane 2B protein of an insect picorna like virus during serial passage in a non native Drosophila host. The selected variant enhances replication and virulence across distinct host immune backgrounds, highlighting a role for 2B in cross species virus fitness. (J Virol: **10.1128/jvi.01239 25**)

🔓 This study identifies and characterises 20 transcribed amphibian retroviruses from RNA sequencing data spanning 102 species, revealing novel circulating and endogenous retrovirus lineages across all three amphibian orders. The findings illuminate the breadth of retrovirus diversity in ectothermic hosts and provide insights into the evolutionary history and genomic integration of retroviruses in vertebrate genomes. (Retrovirology: **10.1186/s12977 025 00669 y**)

🔓 🔧 Torchtree, a PyTorch based framework, enables flexible development and efficient inference of phylogenetic models using variational Bayes and other gradient based algorithms. This study demonstrates that torchtree can match traditional MCMC inference speeds while facilitating rapid implementation of complex phylogenetic inference methods. (Syst Biol: **10.1093/sysbio/syaf047**)

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

Selected Publications by EVBC Members

All publications on Pubmed

Virology

🔓 This paper demonstrates that inefficient entry of human cytomegalovirus into monocytes contributes to latency establishment, while enhanced entry via expression of entry receptors such as integrin β3 enables productive infection. Differentiation associated increases in virus entry capacity thus shape the balance between latent and lytic infection states in myeloid cells. (Nat. Commun.: **10.1038/s41467 025 68063 y**)

🔓 This study develops a genome wide CRISPR knockout screening strategy using stable virus replicon cell lines to identify host genes essential for replication of multiple RNA viruses, including dengue virus type 2, chikungunya virus and Ebola virus. The replicon based platform reveals both known and novel host factors required for virus replication, offering a scalable approach to dissect virus–host interactions and discover host directed antiviral targets. (Nat. Commun.: **10.1038/s41467 025 65979 3**)

🔓 This study reports that MERS CoV specific antibodies and T cell responses induced by three doses of the MVA MERS S vaccine remain detectable in healthy adults for at least 24 months, with sustained neutralising activity including against spike variants. The findings highlight long term durability of vaccine induced humoral and cellular immunity for this coronavirus vaccine candidate. (Nat. Commun.: **10.1038/s41467 025 68248 5**)

🔓 ⊞ This systematic review examines data driven, model informed decision making studies on COVID 19 interventions, identifying testing/tracing, social distancing, vaccination and infrastructure enhancements as commonly effective strategies. The synthesis emphasises the value of empirical modelling to guide public health decision making and prepares for future infectious disease threats. (BMJ Open: **10.1136/bmjopen 2025 107660**)

Bioinformatics Methods

🔓 ⊞ 🔧 This review article examines the application of artificial intelligence and machine learning approaches to mitotic checkpoint modelling, detailing advances in predictive analytics and mechanistic insights into cell division control. It highlights how AI driven models integrate complex data, including multi omics, to uncover regulatory mechanisms and suggests a roadmap for translating computational insights toward precision medicine. (Brief Bioinform: **10.1093/bib/bbaf729**)

🔓 🔧 ViMOP is a pipeline designed for untargeted virus genome assembly from nanopore sequencing reads that integrates de novo contig assembly, reference matching and consensus generation into a field ready workflow. By emphasising usability and flexibility, it facilitates high quality virus genome reconstruction for clinical and resource limited settings. (Bioinformatics: **10.1093/bioinformatics/btaf687**)

🔓 – 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.

Sixth German Conference on Research Software Engineering (deRSE26)

3-5 March 2026 | Stuttgart, Germany

Early bird registration deadline: 31 January 2026

Microbiology Society Annual Conference 2026

13-16 April 2026 | Belfast, UK

Including Virus Symposia “A virus for all seasons” and “Viral manipulation of the intracellular RNA world” as well as sessions such as “AI-enabled Microbiology” or “Genetics and Genomics”.

Abstract submission: closed

Registration: re-opens at 28 January 2026

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: closed

Early bird registration deadline: 15 February 2026

2026 Ascona Workshop on “Statistical and AI methods for multi-modal multi-scale modeling of biological systems”

28 June to 3 July 2026 | Ascona, Switzerland

This workshop/conference co-organized by EVBC member Niko Beerenwinkel will address critical challenges in integrating and interpreting multi-modal datasets across biological scales.

Pre-registration incl. abstract: 28 February 2026

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 **full manuscripts**: 5 March 2026

Submission deadline for **highlight talks and posters**: 20 April 2026

Viruses of Microbes (VoM) Conference 2026

6-10 July 2026 | Prague, Czech Republic

World’s leading event for research on bacteriophages, archaeal viruses, and viruses of microbial eukaryotes, themed ”Revealing Novel Interactions, Innovations, and Applications” in 2026.

Abstract submission deadline: 31 March 2026

Early bird registration deadline: 31 March 2026

19th Congress of the International Union of Microbiological Societies (IUMS)

4-6 November 2026 | Lisbon, Portugal

Key topics will include microbial genetics, molecular and synthetic biology, gene regulation, proteomics, biotechnology, clinical and medical sciences, industrial applications, and environmental sustainability. Special attention will be paid to how AI can affect any aspect of microbiology. There will be a session on Computational Microbiology.

Abstract submission deadline: 29 April 2026

Early bird registration deadline: 29 July 2026

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European
VIRUS BIOINFORMATICS
Center

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 talk:

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!

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:

Jonas Fuchs, University Hospital Freiburg, Germany
11 February 2026 | 4 pm CET online
How viral evolution is shaped during long-term infections of immunecompromised hosts

Pascal Mutz, National Institutes of Health, United States
8 April 2026 | 4 pm CET online
(Title TBA)

We wish you a happy, healthy, and successful year 2026!