


Send us your news to evbc@uni-jena.de.

For more frequent updates, please follow us on [X](https://www.instagram.com/EVirusBioinfC) [EVirusBioinfC](https://www.facebook.com/EVirusBioinfC).

Selected Publications by EVBC Members

 All

publications on Pubmed

 This paper is a call to action, demanding immediate, tangible steps that harness the power of microbiology and the expertise of researchers and policymakers to safeguard the planet for future generations. (NPJ Biodivers: [10.1038/s44185-024-00066-2](https://doi.org/10.1038/s44185-024-00066-2))

This paper has been published concurrently across multiple journals like an emergency bulletin:

Commun Biol [10.1038/s42003-024-07108-2](https://doi.org/10.1038/s42003-024-07108-2)

mSystems [10.1128/msystems.01416-24](https://doi.org/10.1128/msystems.01416-24)


Nat Commun [10.1038/s41467-024-53680-w](https://doi.org/10.1038/s41467-024-53680-w)

Nat Microbiol [10.1038/s41564-024-01861-0](https://doi.org/10.1038/s41564-024-01861-0)

Nat Rev Microbiol [10.1038/s41579-024-01123-0](https://doi.org/10.1038/s41579-024-01123-0)



NPJ Biodivers [10.1038/s44185-024-00066-2](https://doi.org/10.1038/s44185-024-00066-2)


NPJ Biofilms Microbiomes [10.1038/s41522-024-00591-9](https://doi.org/10.1038/s41522-024-00591-9)



 This review highlights the transformative potential of large language models in bioinformatics, particularly for analyzing complex omics datasets and accelerating discoveries in genomics, proteomics, and drug discovery. (Comput Struct Biotechnol J: [10.1016/j.csbj.2024.09.031](https://doi.org/10.1016/j.csbj.2024.09.031))

RNA Structure & Interaction



 Predictions from 18 modeling groups for 23 RNA structures, highlighting key steps and challenges in improving RNA structure modeling accuracy. (Nat Methods: [10.1038/s41592-024-02543-9](https://doi.org/10.1038/s41592-024-02543-9))

  Overview and benchmark of RNA-protein interaction prediction tools that do not require high-throughput data, highlighting their inputs, usability, and outputs for improving RPI research. (Comput Struct Biotechnol J: [10.1016/j.csbj.2024.11.015](https://doi.org/10.1016/j.csbj.2024.11.015))

 Rfam 15.0 significantly enhances its RNA family database with expanded genomic coverage, improved structural annotations, new data types, and integration features to support RNA research and machine learning. (Nucleic Acids Res: [10.1093/nar/gkae1023](https://doi.org/10.1093/nar/gkae1023))

  Sci-ModoM is a pioneering RNA modification database, offering FAIR data principles and tools for analyzing six million RNA modifications across 156 datasets. (Nucleic Acids Res: [10.1093/nar/gkae972](https://doi.org/10.1093/nar/gkae972))

This study identifies "obelisks," a novel class of heritable RNA elements with viroid-like features prevalent in human microbiomes and ecological niches globally. (Cell: [10.1016/j.cell.2024.09.033](https://doi.org/10.1016/j.cell.2024.09.033))

  This review highlights recent advances in RNA 3D structure prediction, combining AI-driven computational methods and new experimental data, with implications for molecular biology and RNA-targeted drug discovery. (Struct: [10.1016/j.str.2024.08.015](https://doi.org/10.1016/j.str.2024.08.015))

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

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.

SimRNAweb v2.0: Web Server for RNA Folding Simulations and 3D Structure Modeling


19. December 2024 | 4 pm CET

online

Naeim Moafinejad, International Institute of Molecular and Cell Biology, Poland

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 .

Annual Meeting of the Society for Virology (GfV 2025)

04–07 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 extended: **08 December 2024**

ISMB/ECCB conference

20–27 July 2025 | Liverpool, UK

Organized by the International Society for Computational Biology (ISCB), this 33rd annual ISMB meeting, in conjunction with the 24th ECCB, will feature over 500 scientific talks, training workshops, and networking opportunities, both in-person and virtually.

Call for proceedings opens: **05 December 2024**

Tutorial proposals deadline: **19 December 2024**

1st International Symposium on Ancient Pathogen Genomics

12–13 April 2025 | Querétaro, México

The event aims to unite researchers in the field of ancient pathogen genomics, encompassing both ancient DNA and paleovirology studies.

Early bird registration deadline: **01 January 2025**

9th European Congress of Virology

27 – 30 April 2025 | Dubrovnik, Croatia

ECV brings together virologists to discuss advances in virology, including virus research, clinical treatments, public health, and emerging technologies.

Abstract submission deadline: **05 January 2025**

[BC]² 2025 | Bioinformatics meets AI: shaping the future of data-driven biology

08–10 September 2025 | Basel, Switzerland


Flagship scientific meeting of the SIB Swiss Institute of Bioinformatics, held every two years, attracting around 500 scientists from academia, industry, and healthcare.





Call for abstracts opens: **07 January 2025**

Tutorials & workshops submission deadline: **07 January 2025**

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 .

-  **EEfinder**: Identification of Endogenous Elements present on Eukaryotic Genomes
-  **Sphae**: Phage annotations and predictions
-  **EvoMIL**: Prediction of virus-host association using protein language models and multiple instance learning
-  **Sci-ModoM**: Quantitative database of transcriptome-wide high-throughput RNA modification sites

 evbc@uni-jena.de

 +49-3641-9-46482

 <http://evbc.uni-jena.de/>

 Leutrargaben 1, 07743 Jena


Board of Directors


Martin Beer, Li Deng, Bas E. Dutilh, Philippe Le Mercier, Manja Marz, Volker Thiel

Selected Publications by EVBC Members (part 2)


 [All publications on Pubmed](#)

Viral Evolution and Phylogenetics

 The review discusses the mechanisms of SARS-CoV-2 persistence, the evolution of viral variants, and the potential role of persistent infections in long COVID. (Nat Rev Microbiol: [10.1038/s41579-024-01125-y](#))


 Genomic and epidemiological evidence reveals mammal-to-mammal transmission of H5N1 in southern elephant seals in Argentina, highlighting viral adaptability and potential global risks. (Nat Commun: [10.1038/s41467-024-53766-5](#))

This study introduces Phylogenetic Integrated Velocity models to enhance the accuracy of dispersal velocity estimates for evolving pathogens, demonstrated through analysis of West Nile virus data. (Proc Natl Acad Sci U S A: [10.1073/pnas.2411582121](#))



 This study explores intra-host viral genetic diversity and integration, revealing conserved viral persistence, selective pressures, and non-clonal integration events across human tissues. (Nucleic Acids Res: [10.1093/nar/gkae871](#))

  This study reprocessed global SARS-CoV-2 sequencing data using the novel tool Viridian to create a high-quality phylogeny of over 4.4 million samples, addressing pandemic-wide systematic errors. (bioRxiv: [10.1101/2024.04.29.591666](#))



Virus-Host Interaction


 This study reveals distinct immune signatures in fatal lung COVID-19 cases from a Malawian cohort, highlighting differences in immune responses across populations and suggesting shared and unique treatment targets. (Nat Med:


[10.1038/s41591-024-03354-3](#))

  EvoMIL, a deep learning method combining protein language models and multiple instance learning, improves virus-host association predictions and identifies key viral proteins influencing specificity. (PLoS Comput Biol: [10.1371/journal.pcbi.1012597](#))

  This review highlights the challenges and opportunities in studying atypical phages, emphasizing the need for advanced isolation methods and new model systems to unlock their biotechnological potential. (Curr Opin Microbiol: [10.1016/j.mib.2024.102555](#))

  Sphae is an automated bioinformatics pipeline designed to streamline the identification of therapeutic potential in phage therapy candidates by quickly assessing genomic markers for virulence, antimicrobial resistance, and lysogeny. (bioRxiv: [10.1101/2024.11.18.624194](#))

 This study presents a neuron-derived human model system that supports Hepatitis E virus infection, revealing reduced neurite length and limited innate immune response, which could help elucidate the pathogenesis of HEV-associated neurological disorders. (PNAS: [10.1073/pnas.2411434121](#))

 This study explores the dynamics of defective viral genomes (DVGs) of tomato black ring virus (TBRV) during sequential host-to-host transmission, revealing diverse deletion patterns influenced by host plant combinations. (J Virol: [10.1128/jvi.01244-24](#))

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

News and Announcements

Dearest EVBC Community,

The year is coming to an end and with it my time as the Scientific Coordinator of the EVBC.

For me, it has been an honour to make the EVBC what it is today by working with such talented, passionate and innovative researchers. I have enjoyed watching the community grow and come together, meeting so many of you in person at our annual conference, and I hope to see you again in the future.

I am proud of what we have achieved and I have no doubt that the EVBC will continue to thrive. Together we have built a vibrant community dedicated to scientific excellence in virus bioinformatics. I am delighted to pass the torch to **Paula Istvan**, whose expertise and vision make her the perfect choice to lead our network into the next chapter. Please join me in offering Paula your full support as she takes on this exciting new role.

Thank you all for your cooperation, trust, enthusiasm and inspiration. I look forward to cheering on the continued success of the EVBC.

If you would like to stay in touch, I would be delighted to connect on [LinkedIn](#).

I wish you all a Merry Christmas filled with peace, warmth and time with your loved ones. May the New Year bring you health, happiness and continued success in your personal and professional endeavours.

- All the best, Franziska -



Dearest EVBC Community,

It is with great enthusiasm that I step into the role of Scientific Coordinator for the EVBC.

With a Master's degree in Molecular Biology and a PhD in Biotechnology, I specialize in the integration of advanced bioinformatics tools and workflows to analyze complex datasets. My work focuses on environmental and human microbiome and virome, leveraging biotechnology and computational biology to uncover critical health-related applications. By bridging these fields, I adopt an innovative approach to uncover connections and solutions that propel both environmental and human studies forward. My goal is to drive scientific discovery and enable translational research through cutting-edge, interdisciplinary methodologies.

I look forward to working with you to continue our mission of advancing the field of virus bioinformatics. I am excited to embark on this journey with all of you.


Wishing you a joyous Christmas season filled with peace, warmth, and meaningful time with your loved ones. May the New Year bring you good health, happiness, and continued success in all your personal and professional pursuits.

- All the best, Paula -

Selected Publications by EVBC Members (part 3)

 [All publications on Pubmed](#)

Virus Discovery and Classification

🔗  Efinder, a new tool for identifying and classifying endogenous viral and bacterial elements in eukaryotic genomes, streamlines analysis with six integrated steps and high sensitivity. (Comput Struct Biotechnol J: [10.1016/j.csbj.2024.10.012](#))

🔗 Researchers identified a divergent RNA virus in Plasmodium knowlesi, a zoonotic malaria pathogen, expanding the understanding of ormycovirus diversity and its impact on protozoa. (Virus Evol: [10.1093/ve/veae091](#))

🔗 Researchers screened great ape museum specimens for DNA viruses, uncovering multiple near-complete viral genomes, including hepatitis B virus strains phylogenetically linked to gorillas and chimpanzees. (Sci Rep: [10.1038/s41598-024-80780-w](#))

🔗 This study reveals a highly diverse RNA virome from urban freshwater ecosystems in Berlin, identifying numerous novel and recombinant viruses that contribute to our understanding of virus modularity. (Microorganisms: [10.3390/microorganisms12112361](#))

Epidemiology & Surveillance

🔗 Impact of Scotland's COVID-19 risk-based travel policies on international travel, SARS-CoV-2 case importation, and variant establishment using population-based surveillance data. (BMJ Open: [10.1136/bmjopen-2024-085332](#))

🔗 CrAssphage markers validated as highly effective tools for detecting human-specific faecal contamination in surface water, outperforming traditional bacterial markers and providing insights into water pollution in China. (Environ

Pollut: [10.1016/j.envpol.2024.125403](#))

🔗 This study uses high-throughput sequencing to analyze plant viruses in wastewater and reclaimed water, revealing high levels of viral contamination, including the harmful Tomato Brown Rugose Fruit virus (ToBRFV), underscoring the need for rigorous monitoring from a One Health perspective. (Water Res: [10.1016/j.watres.2024.122827](#))

🔗 The study crowdsourced and sequenced river microbiomes across the U.S., creating the Genome Resolved Open Watersheds database (GROWdb), which profiles microbial genomes, their function, and distribution, offering new insights into river biogeochemistry. (Nature: [10.1038/s41586-024-08240-z](#))

🔗 This study uses mathematical modeling of seroprevalence data to assess the circulation dynamics of Enterovirus A71 and Coxsackievirus A6 in England, revealing that increased reports of CVA6 cases are likely due to increased virus pathogenicity, not changes in surveillance. (PLoS Pathog: [10.1371/journal.ppat.1012703](#))

🔗 Genomic and structural analyses of locally acquired dengue virus infections in Italy reveal insights into viral adaptation and transmission dynamics. (Emerg Microbes Infect: [10.1080/22221751.2024.2420734](#))

🔗 This study benchmarks various next-generation sequencing technologies for SARS-CoV-2 surveillance in wastewater, revealing tradeoffs in cost, timeliness, and accuracy. (Water Res: [10.1016/j.watres.2024.122465](#))

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

ViBioM 2024

 Stay tuned

We are still 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.

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!](#)

Follow us:

 LinkedIn

 Bluesky

 (Twitter)

The EVBC coordination team sends warm wishes to you and your loved ones for a joyful holiday season. May this time bring you moments of happiness, laughter, and meaningful connections with those who matter most.

Many thanks to all of you for your commitment to the EVBC and for advancing the field of virus bioinformatics! Here's to a new year brimming with groundbreaking discoveries, impactful collaborations, and ongoing success in our shared mission.

Wishing you a Merry Christmas, Happy Holidays, and a wonderful New Year!