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Selected Publications by EVBC Members

[All publications on Pubmed](#)

Tools:

- pyCapsid analyzes protein shell dynamics and mechanical units in high-resolution structures, especially virus capsids, providing insights through collective vibrations and disassembly-associated regions. (Bioinformatics: [10.1093/bioinformatics/btad761](https://doi.org/10.1093/bioinformatics/btad761))
- MuDoGeR facilitates the recovery of prokaryotic, eukaryotic, and viral genomes from metagenomes, with demonstrated applicability for both individual-isolated genomes and high-throughput metagenomic datasets. (Mol Ecol Resour: [10.1111/1755-0998.13904](https://doi.org/10.1111/1755-0998.13904))
- Hybracter is a fast and scalable method for reconstructing near-perfect complete bacterial genomes by employing a long-read first assembly approach, outperforming existing automated hybrid assembly tools in accuracy and speed, even matching hybrid methods in recovering small plasmids, crucial for identifying medically significant antimicrobial resistance genes. (bioRxiv: [10.1101/2023.12.12.571215](https://doi.org/10.1101/2023.12.12.571215))

Evolution:

- Host immune pressure, particularly the RNAi response, shapes *Drosophila C* virus evolution in fruit flies, resulting in increased replication efficiency, virulence, and parallel mutations in the VP3 capsid protein, indicating a reproducible yet unpredictable process with a restrictive impact on viral sequence space exploration. (Virus Evol: [10.1093/ve/vead074](https://doi.org/10.1093/ve/vead074))
- Influence of GC content on the frequencies of synonymous triplets in DNA sequences, specifically focusing on stop codons, revealing a bias for triplets corresponding to stop codons near the 5'- and 3'-splice sites in introns across various clades, with an overall maximum Shannon information at 43.3% GC content. (Sci Rep: [10.1038/s41598-023-49626-9](https://doi.org/10.1038/s41598-023-49626-9))
- Leishmania braziliensis* populations in rainforests have low-prevalence single viral lineages, while more dispersed hybrid parasites show increased viral prevalence, diversity, and spread, suggesting that gene flow and hybridization may impact the frequency of parasite-virus symbioses and influence leishmaniasis epidemiology in the region. (Nat Commun: [10.1038/s41467-023-44085-2](https://doi.org/10.1038/s41467-023-44085-2))
- Investigating Polintons, virus-like self-synthesizing transposons in eukaryotic genomes, across nematode genomes, reveals ancient and recent integrations, and identifies a unique group with a distinct DNA polymerase B, suggesting interphylum horizontal gene transfers among cohabiting hosts. (Mol Biol Evol: [10.1093/molbev/msad274](https://doi.org/10.1093/molbev/msad274))
- Discovery of seven potentially complete bornavirus genomes in fish samples, including novel species, and identification of *Wuhan* sharpbelly bornavirus in grass carp cell lines, a Murray-Darling carp bornavirus in a goldfish, and a unique little skate bornavirus with an unusual genomic architecture. (Virus Evol: [10.1093/ve/vead062](https://doi.org/10.1093/ve/vead062))
- Investigating soil viruses and their interactions with host microbes across different depth intervals, finding varying adaptation patterns but suggesting the potential of soil viruses to influence hosts in recycling plant-derived carbon, highlighting the need to explore soil viral functions at various depths in ecosystems. (mBio: [10.1128/mbio.02246-23](https://doi.org/10.1128/mbio.02246-23))

Virology:

- Molecular tool for investigating Influenza D virus (IDV): Fluorescent reporter Influenza D virus (IDV), applicable for antiviral drug discovery and monitoring viral replication, identifies compounds that influence IDV infection. (Viruses: [10.3390/v15122444](https://doi.org/10.3390/v15122444))
- Newly identified sea bass toti-like virus (SBTLV) in Mediterranean aquaculture linked to abnormal mortality in larval stages. (Viruses: [10.3390/v15122423](https://doi.org/10.3390/v15122423))

- Despite the common hypothesis suggesting bats as reservoirs for zoonotic viruses due to their unique antiviral interferon system, functional studies on key components like RIG-I show that bat RIG-Is from two suborders are similar to human RIG-I in various aspects, challenging the idea that the bat IFN system alone is responsible for their role as zoonotic virus reservoirs. (J Virol: [10.1128/jvi.00205-23](https://doi.org/10.1128/jvi.00205-23))

Plant viruses

- HTS of irrigation and surface water sources detected nucleic acids of plant viruses, including novel ones from economically important taxa, suggesting the potential use of a water virome surveillance system for monitoring and detecting plant disease outbreaks. (Water Res: [10.1016/j.watres.2023.120712](https://doi.org/10.1016/j.watres.2023.120712))
- A plant-based method replicating RNA-induced RNA silencing in vitro has been successfully applied to identify antisense oligodeoxynucleotides effective in DNA-induced RNA silencing, demonstrating comparable antiviral activity to small interfering RNAs and suggesting potential applications in crop protection. (Int J Mol Sci: [10.3390/ijms242417153](https://doi.org/10.3390/ijms242417153))
- Diverse and mostly unclassified plant-infecting RNA viruses were identified in water samples from Berlin, revealing 647 novel sequences. (Pathogens: [10.3390/pathogens12121458](https://doi.org/10.3390/pathogens12121458))

SARS-CoV-2:

- Impact of SARS-CoV-2 variants delta and omicron on premature cellular senescence: only omicron variants influence the expression of cell cycle genes, including increased p21 expression, and lead to an upregulated senescence-associated secretory phenotype (SASP), suggesting a substantially different cellular response with implications for premature aging. (Aging: [10.18632/aging.205297](https://doi.org/10.18632/aging.205297))
- Systems bioinformatics approach to show that viruses, including Herpesviridae and hepatitis viruses, influence Alzheimer's Disease processes, emphasizing a complex link between viral infections and AD development, with potential synergistic effects during SARS-CoV-2 infection. (bioRxiv: [10.1101/2023.12.05.570187](https://doi.org/10.1101/2023.12.05.570187))

Microscopy

- Blob-B-Gone is a lightweight framework utilizing geometrical features and k-means++ clustering to computationally identify and remove artifactually immobilized particle accumulations (blobs) in MINIFLUX single-particle tracking measurements. (Front Bioinform: [10.3389/fbinf.2023.1268899](https://doi.org/10.3389/fbinf.2023.1268899))
- Significance of accurate calibration in superresolution microscopy (STED-FCS) for measuring molecular mobility, suggesting simpler methods like acetone cleaning and point scanning are sufficient. (J Microsc: [10.1111/jmi.13250](https://doi.org/10.1111/jmi.13250))

Datamanagement:

- Effective public health actions rely on organized systems, and the proposed Pathogen Data Object Model (DOM) seeks to standardize international databases like INSDC, streamlining submissions and ensuring consistency through a structured approach to sequence and contextual data. (Microb Genom: [10.1099/mgen.0.001145](https://doi.org/10.1099/mgen.0.001145))
- List2Net is a web-based tool to analyze and represent diverse biological entity lists as networks, providing a versatile approach for multi-source data, demonstrated through a case study on Multiple Sclerosis datasets. (Comput Struct Biotechnol J: [10.1016/j.csbj.2023.11.020](https://doi.org/10.1016/j.csbj.2023.11.020))
- ViralZone 2024 now offers enhanced access with contextual popups and interactive SVG images, featuring a new coronavirus-specific resource for SARS-CoV-2 data and additional content on HIV, herpesviruses, and poxviruses. (Nucleic Acids Res: [10.1093/nar/gkad946](https://doi.org/10.1093/nar/gkad946))

Publication shortcuts: If you would like us to add a shortcut to a specific virus (family) or topic, drop us an [email](mailto:evbc@uni-jena.de).

SARS-CoV-2


influenza







HIV

monkeypox

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 .

-  **Blob-B-Gone:** remove blob artifacts from 2D/3D point cloud data as produced by MINFLUX
-  **Hybracter:** automated long-read first bacterial genome assembly pipeline
-  **List2Net:** Linking multiple lists of biological data in a network context
-  **MuDoGeR:** Multi-Domain Genome recovery from metagenomes
-  **pyCapsid:** analysis of viral capsids
-  **ViralZone:** a knowledge resource to understand virus diversity

ViBioM 2024

Stay tuned

ViBioM 2024

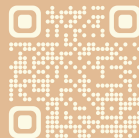
International Virus
Bioinformatics Meeting

28. – 30. May 2024 | Leuven, Belgium



NOW OPEN


Registration is limited to 160 participants
Submission closes on 15 March 2024



evbc.uni-jena.de/vibiom2024

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 .


33rd Annual Meeting of the Society for Virology

25–28 March 2024 | Vienna, Austria

The meeting will cover a broad spectrum of topics in basic, translational, and clinical virology.

Abstract submission deadline:

14 January 2024

 I. Eckerle (plenary speaker)

ONT London Calling

21–24 May 2024 | London, UK

The latest research from scientists using nanopore sequencing in their work.

Abstract submission deadline:

14 January 2024

7th Joint Microbiology & Infection Conference

02–05 June 2024 | Würzburg, Germany

Addresses global challenges, emphasizing Planetary Health, and focuses on key topics such as biotechnology, antimicrobial resistance, climate change, and digital era microbiology.

Abstract submission deadline:

02 February 2024

International Virus Bioinformatics Meeting

28–30 May 2024 | Leuven, Belgium

The pioneering conference bridging the gap between virology and bioinformatics.

Registration / submission opens:

08 January 2024