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For more frequent updates, please follow us on Twitter [EVirusBioinfC](https://twitter.com/EVirusBioinfC).

Selected Publications by EVBC Members

 [All publications on Pubmed](#)

MpoxRadar is an interactive dashboard that enables global tracking of mutation profiles and variants of the mpox virus (MPXV), providing customizable filtering options, an interactive world map, and data downloads, making it a practical tool for genomic surveillance of MPXV. (NAR: [10.1093/nar/gkad325](https://doi.org/10.1093/nar/gkad325))

Reconstructing the last eukaryotic common ancestor (LECA) virome suggests that the LECA virome originated from a small set of bacterial viruses rather than archaeal viruses, likely due to the bacterial origin of eukaryotic membranes and the occurrence of endosymbiotic events during eukaryogenesis. (Nat Microbiol: [10.1038/s41564-023-01378-y](https://doi.org/10.1038/s41564-023-01378-y))

Ancient gene transfer between cressdnaviruses and avipoxviruses reveals a virus-to-virus horizontal transfer, with avipoxviruses acquiring Rep genes from the previously unknown viral family Draupnirviridae. (PNAS: [10.1073/pnas.2303844120](https://doi.org/10.1073/pnas.2303844120))

DNA metagenomics and genomics to identify endogenous viral elements of a non-retroviral +ssRNA virus (dinoRNAV) in coral reef ecosystems, highlighting the prevalence of dinoRNAV EVEs in dinoflagellate genomes, particularly in association with Symbiodiniaceae, and suggesting their potential role in nested symbioses and implications for reef health and disease. (Commun Biol: [10.1038/s42003-023-04917-9](https://doi.org/10.1038/s42003-023-04917-9))

Reannotation of the murine cytomegalovirus (MCMV) genome reveals complex gene expression patterns with hundreds of viral transcripts and open reading frames (ORFs), including small ORFs, and identification of novel gene products and regulatory elements, contributing to our understanding of MCMV. (PLoS Pathog: [10.1371/journal.ppat.1010992](https://doi.org/10.1371/journal.ppat.1010992))

Comprehensive screen of fungal transcriptomes identified over 2,500 ambiviral sequences, revealing a diverse range of unknown ambiviruses with a strong presence in the phylum Basidiomycota, highlighting their evolutionary significance, while no evidence of ambiviruses was found in human microbiomes. (Front Microbiol: [10.3389/fmicb.2023.1144003](https://doi.org/10.3389/fmicb.2023.1144003))

Novel method for accurately detecting gene breakpoints in nucleotide sequences of mitochondrial genomes, even in the presence of high substitution rates and sequence inconsistencies, using a position-annotated de-Brujin graph and a heuristic algorithm that searches for bulges associated with breakpoint locations. (BMC Bioinformatics: [10.1186/s12859-023-05371-4](https://doi.org/10.1186/s12859-023-05371-4))

The International Committee on Taxonomy of Viruses (ICTV) approved and ratified changes to virus taxonomy and taxon nomenclature, including renaming existing species and classifying gene transfer agents as viriforms, resulting in the creation of one class, seven orders, 31 families, 214 genera, and 858 species. (Arch Virol: [10.1007/s00705-023-05797-4](https://doi.org/10.1007/s00705-023-05797-4))

RNA fluorescence in situ hybridization flow cytometry (RNA FISH-Flow) protocol utilizing fluorescently labeled DNA probes to detect RNA viruses within infected cells, allowing high-throughput analysis of infection dynamics at the single cell level. (STAR Protoc: [10.1016/j.xpro.2023.102291](https://doi.org/10.1016/j.xpro.2023.102291))

Reviews / Commentaries / Editorials / ...

This review discusses how the study of ancient viruses, made possible by advancements in genomic analysis of ancient nucleic acids, has provided insights into past epidemics, the evolution of viral families, the role of viruses in human evolution, and their impact on major events in human history. (Annu Rev Virol: [10.1146/annurev-virology-111821-123859](https://doi.org/10.1146/annurev-virology-111821-123859))

Complexity of the gut virome, its potential impact on human health, the factors that influence its composition, the role of bacteriophages, the disruption of the virome in disease states, the restoration of gut functionality through fecal microbiome transfer, challenges in studying the virome including "viral dark matter," and various strategies and tools used to investigate and understand the gut virome. (Front Microbiol: [10.3389/fmicb.2023.963173](https://doi.org/10.3389/fmicb.2023.963173))

Factors that contribute to differences in amino acid usage across evolution and within genomes, highlighting the influence of the standard genetic code, species-relatedness, GC content, and intragenomic variations in mammalian species. (J Mol Evol: [10.1007/s00239-023-10120-5](https://doi.org/10.1007/s00239-023-10120-5))

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, or have now been published. Tools developed by EVBC members are marked .


DeepHost: Phage host prediction tool with convolutional neural network

HostG: Graph convolutional neural network for host prediction

HostPhinder: Prediction of bacterial host of phages by examining the phage genome sequence

 **multiPHATE2:** Throughput PhATE processing of draft or finished phage genomes with comparative genomics

PHIAF: Prediction of phage-host interactions with GAN-based data augmentation and sequence-based feature fusion

 **VirMatcher:** Prediction of virus-host relationships

WisH: Prediction of prokaryotic host for phage metagenomic sequences

EVBC Special Issues

 [Special issue list](#)

Don't forget to submit to our special issue **Virus Bioinformatics 2023**.

Manuscript submission deadline: **30 June 2023**

New papers published:

Idiotope-Driven T-Cell/B-Cell Collaboration-Based T-Cell Epitope Prediction Using B-Cell Receptor Repertoire Sequences in Infectious Diseases [10.3390/v15051186](https://doi.org/10.3390/v15051186)

Novel Approach for Identification of Basic and Effective Reproduction Numbers Illustrated with COVID-19 [10.3390/v15061352](https://doi.org/10.3390/v15061352)

Special issues edited by EVBC members:

Ecology, Evolution, and Biodiversity of Microbiomes and Viromes From Extreme Environments in *Frontiers in Microbiomes* (edited by **J. Rahlff**)

Manuscript submission deadline: **31 August 2023**

ViBioM 2023

[Register](#)



Thank you to everyone who attended ViBioM this year! It was a blast! I enjoyed very much meeting you and want to thank you for your invaluable feedback on the EVBC services.

We would greatly appreciate it if you could spare a few minutes to complete the [feedback survey](#) for the conference (if you have not already done so). Your input is invaluable in helping us improve future events and ensure that we continue to deliver a high-quality conference. Thank you in advance for your time!

The conference report will be published in our special issue "Virus Bioinformatics 2023" in *Viruses*. Please reach out to us to make sure that all key points and noteworthy mentions are included. If you would also like to submit your work there, the submission deadline is 30 June 2023.

Hope to see you again next year in Leuven!

ECR Viromics Webinar Series

[Register](#)

This lecture for early career researchers studying viruses in complex communities is organized together with the [Center of Microbiome Science](#) at Ohio State University and the [NSF EMERGE Biology Integration Institute](#).

The utility of phylogeny in virus discovery: Host association, taxonomy and disease potential


14 June 2023 | 04-05 pm CET

Erin Harvey, The University of Sydney, Australia

online

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 .

19th International Symposium on Bioinformatics Research and Applications (ISBRA 2023)

09–12 October, 2023 | Wrocław, Poland

Abstract submission deadline: **25 June, 2023**

7th International Symposium on Image-based Systems Biology


21–22 September, 2023 | Jena, Germany

Abstract submission deadline: **30 June, 2023**

20th Smögen Symposium on Virology 2023

24–26 August 2023 | Smögen, Sweden

Abstract submission deadline: **31 July 2023**

 Emma Thomson (keynote speaker)

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.

TBA

19 June 2023 | 10 am CEST

Masayuki Horie, Osaka Metropolitan University, Japan

online

You can also already [register](#) for our upcoming lectures:

- | | |
|-------------------|--|
| 28. August 2023 | Dominik Heider, University of Marburg, Germany |
| 23. October 2023 | Gabriel da Luz Wallau, Bernhard Nocht Institute for Tropical Medicine, Germany |
| 20. November 2023 | Anton Petrov, Riboscope Ltd., UK |

If you are attending the "viruses in silico" lecture regularly and do not want to register every month, you can choose to be permanently registered. You will be added to the mailing list and receive the access details every month. You can unsubscribe at any time.

Vacancies

[Find a job](#)

The group of Prof. Dr. Manja Marz (RNA Bioinformatics & High-Throughput Analysis) at the Friedrich Schiller University Jena is looking for a **PostDoc Computer Scientist**. A Programming Challenge will take place on 23.06.2023, which will be an integral part of the selection process.

Application deadline:

21 June 2023

The Dept. of Molecular Immunology at the Ruhr-University Bochum is looking for a **Postdoc in Bioinformatics** with an interest in the regulation of gene expression influencing immune responses, the development of immune cells, and host-pathogen interactions.

Application deadline:

19 June 2023

The Institute of Novel and Emerging Infectious Diseases of the Friedrich-Loeffler-Institut is seeking to recruit a **Research assistant (Doctoral candidate)** on the topic "Development and implementation of automated bioinformatics pipelines for the rapid detection and characterization of BSL3 and BSL4 viruses by nanopore sequencing". Application deadline:

30 June 2023