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Selected Publications by EVBC Members

[All publications on Pubmed](#)

Mirusviricota: New phylum of plankton-infecting herpesviruses, which has chimeric attributes connecting it to both herpesviruses and giant eukaryotic viruses, plays a crucial role in the ecology and evolution of eukaryotic DNA viruses in the oceans. (*Nature*: [10.1038/s41586-023-05962-4](#))

e-RNA is a collection of web-servers for the prediction and visualization of RNA secondary structures and their functional features, including RNA-RNA interactions. (*Nucleic Acids Res*: [10.1093/nar/gkad296](#))

A comparative analysis of ten state-of-the-art phage identification tools was performed to inform their usage in microbiome research, with VIBRANT and VirSorter2 achieving the highest F1 scores and k-mer-based tools performing better than reference similarity tools and gene-based methods. (*Microbiome*: [10.1186/s40168-023-01533-x](#))

LECA virus repertoire reconstructed to understand the biology of the last eukaryotic common ancestor (LECA) and eukaryogenesis: the origin of the LECA virome can be traced back to a small set of bacterial viruses, likely due to the bacterial origin of eukaryotic membranes. (*Nat Microbiol*: [10.1038/s41564-023-01378-y](#))

New targeted single-phage isolation method has been developed to detect and isolate phages of interest and characterize their kinetics in a high-throughput manner, revealing cell-to-cell variations in phage-bacterium interactions. (*Microbiol Spectr*: [10.1128/spectrum.05149-22](#))

A new computational tool called iPhoP has been developed to predict the host taxonomy at the genus rank for a diverse range of viruses infecting bacteria and archaea using metagenome-derived virus genomes, with low false discovery rate and high precision and recall. (*PLoS Biol*: [10.1371/journal.pbio.3002083](#))

PepGM is a probabilistic graphical model for taxonomic assignment of virus proteomic samples, combining standard proteomic database search algorithms with belief propagation to calculate confidence scores for potential taxonomic assignments, with demonstrated strain-level resolution performance. (*Bioinformatics*: [10.1093/bioinformatics/btad289](#))

Publicly available transcriptomic data sets mined to expand the known diversity of RNA viruses by developing 77 family-level Hidden Markov Model profiles for the viral RNA-dependent RNA polymerase and identifying 5,867 contigs encoding RNA virus RdRps or fragments thereof. (*Mol Biol Evol*: [10.1093/molbev/msad060](#))

Pan-viral similarities and virus-specific differences in the life cycle of plus-strand RNA viruses: suppressing host cell mRNA translation may be a key factor for

in vitro replication efficiency, and targeting viral RNA translation may be the most promising drug target for all plus-strand RNA viruses. (*PLoS Comput Biol*: [10.1371/journal.pcbi.1010423](#))

Preprints

COVID-19 genomic sequencing led to unprecedented data sharing and facilitated vaccine development, supported by the European COVID-19 Data Platform and SARS-CoV-2 Data Hubs for systematic analysis and infrastructure setup for future pathogen surveillance. (bioRxiv: [10.1101/2023.04.19.537514](#))

Machine learning models to analyze SARS-CoV-2 genomic data and associated metadata to understand the factors that contributed to the rise and fall of regional infection cases during the COVID-19 pandemic. (bioRxiv: [10.1101/2023.04.07.536037](#))

Phables, a new computational method, uses graph algorithms and flow decomposition techniques to resolve bacteriophage genomes from fragmented viral metagenomic assemblies, and was able to identify over 80% of the bacteriophage genomes with high quality and longer lengths than those identified by existing viral identification tools. (bioRxiv: [10.1101/2023.04.04.535632](#))

The analysis of over 2.5 million prophages from half a million bacterial genome assemblies suggests that the benefits bacteria accrue from the presence of prophages balance the energetics involved in supporting prophages. (bioRxiv: [10.1101/2023.04.20.537752](#))

Prophages play a crucial role in monitoring and protecting host bacteria in almost all microbiomes and can affect bacterial growth and sculpt the microbiome, with their content varying by isolation site, human health, and symptomatic diseases. (bioRxiv: [10.1101/2023.05.04.539508](#))

An independent benchmarking of ten state-of-the-art virus identification tools in thirteen modes on eight paired viral and microbial datasets from three distinct biomes provides guidance for viromics researchers. (bioRxiv: [10.1101/2023.04.26.538077](#))

Magnetic bead-based sample preparation scheme to enable a Raman spectroscopic differentiation of SARS-CoV-2 positive and negative samples, which could be applicable for other virus species with different recognition elements, by calculating correlation coefficients to differentiate between sample types. (Preprints: [10.20944/preprints202304.1111.v1](#))

EvoMIL: a deep learning method that predicts virus-host association at the species level from viral sequence only. (bioRxiv: [10.1101/2023.04.07.536023](#))

Publication shortcuts: If you would like us to add a shortcut to a specific virus (family) or topic, drop us an [email](#).

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 .

 **e-RNA:** A collection of electronic tools to help you find your way in the RNA world

 **iPhoP:** Integrated Phage HOst Prediction

 **PepGM:** Graphical model for taxonomic profiling

 **Phables:** resolve bacteriophage genomes from fragmented viral metagenomic assemblies.

PHAMB: downstream processing of VAMB binning for Viral Elucidation

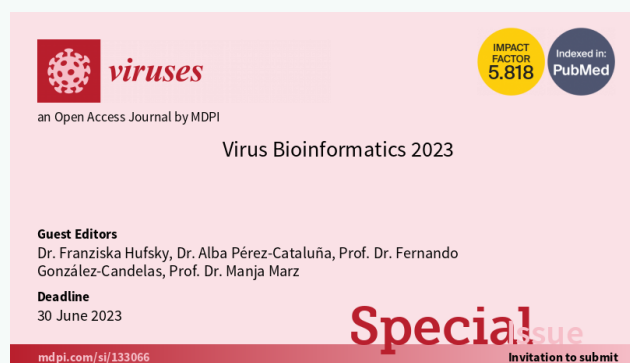
vRhyme: multi-functional tool for binning virus genomes from metagenomes

EVBC Special Issues

 Special issue list

For our special issue **Virus Bioinformatics 2023** running alongside ViBioM 2023, we have vouchers available for EVBC members. Get in contact if you are interested!

Manuscript submission deadline: **30 June 2023**



viruses
an Open Access Journal by MDPI

IMPACT FACTOR 5.818 Indexed in PubMed

Virus Bioinformatics 2023

Guest Editors
Dr. Franziska Hufsky, Dr. Alba Pérez-Cataluña, Prof. Dr. Fernando González-Candelas, Prof. Dr. Manja Marz

Deadline
30 June 2023

Special Issue
Invitation to submit

mdpi.com/si/133066

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.

Due to our annual conference this month, there will be no “viruses *in silico*” lecture.

You can, however, already **register** for our upcoming lectures:

- 19. June 2023 Masayuki Horie, Osaka Metropolitan University, Japan
- 28. August 2023 Dominik Heider, University of Marburg, Germany
- 23. October 2023 Gabriel da Luz Wallau, Bernhard Nocht Institute for Tropical Medicine, Germany

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.

ViBioM 2023

 Register



ViBioM International Virus Bioinformatics Meeting
24–26 May | Valencia, Spain

We are delighted to announce that the **full programme** is now available online!

We are very much looking forward to welcome you in Valencia to hear the newest insights and perspectives in virus bioinformatics. This conference promises to be a dynamic platform for exchanging ideas, and we are confident that it will be a productive and enjoyable experience for all. As a warm welcome, we invite you to join us on Tuesday evening at Tyriss On Tap to meet and greet fellow attendees.

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**.

Eco-evolutionary dynamics of massive, parallel bacteriophage outbreaks in compost communities


10 May 2023 | 04-05 pm CET

online

Jeroen Meijer, *Utrecht University, Netherlands*

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 Conference of the VAAM (Association for General and Applied Microbiology)


10–13 September 2023 | Goettingen, Germany

Abstract submission deadline: **12 May 2023**

20th Smögen Symposium on Virology 2023

24–26 August 2023 | Smögen, Sweden

Abstract submission deadline: **31 July 2023**

 Emma Thomson (keynote speaker)

Vacancies

 Find a job

The group of Prof. Dr. Manja Marz in the Department of RNA Bioinformatics & High-Throughput Analysis at the Friedrich Schiller University Jena is looking for a **PostDoc in Viromics, a PhD student in molecular biology, and a technical assistant in the wetlab**.

The Laboratory for RNA-based Lifeforms (Babaian Lab) at the University of Toronto is seeking a passionate **computational virologist PostDoc** (strong background in either biology/virology OR bioinformatics). You will join the Serratus Consortium to develop the state of the art for the detection and sequence analysis of RNA viruses and virus-like agents. Building upon the first release of the **Serratus** project we will explore the far limits of Earth’s Virome. Briefly, we developed an open-source AWS-cloud backed computing architecture to analyze 5.7 million sequencing datasets (10.2 petabytes) and discover >130,000 novel RNA viruses... in only 11 days.