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Selected Publications by EVBC Members

 [All publications on Pubmed](#)

gutSMASH algorithm identified metabolic gene clusters in microbial genomes, revealing taxonomic metabolic differences and emphasizing the role of pathway-specific gene regulation in understanding microbiome chemistry. (Nat Biotechnol: [10.1038/s41587-023-01675-1](#))

Host protein SND1 identified as a critical factor in SARS-CoV-2 RNA synthesis, with SND1 interacting with the viral RNA and altering NSP9 occupancy, suggesting a role for NSP9 in initiating viral RNA synthesis, revealing a previously unknown cellular protein involvement in viral RNA production. (Cell: [10.1016/j.cell.2023.09.002](#))

Impact of *Helicobacter pylori* infection on lower gastrointestinal bacterial and viral communities in mouse models reveals an increase in temperate phages, potentially linked to colorectal cancer development through interactions with the bacterial community. (Gut Microbes: [10.1080/19490976.2023.2257291](#))

The scTEA-db is a single-cell-based database providing 12,063 previously unannotated terminal exons and their associated transcript isoforms, enabling the exploration of their role in cell identity and function, including in cancer driver genes. (Nucleic Acids Res: [10.1093/nar/gkad878](#))

The study introduced the term "protected environmental DNA" (peDNA) to describe genetic material isolated from size-fractionated samples, highlighting its diverse sources, including viruses, and revealed the significant role of extracellular vesicle-mediated gene transfer in marine environments. (ISME Commun: [10.1038/s43705-023-00317-6](#))

LAMPPrimerBank is a manually curated database of experimentally validated LAMP primers, primarily for respiratory pathogens, providing a user-friendly interface and an open API for easy access to LAMP primer sequences and related information from the literature to aid in prompt diagnosis and specificity in nucleic acid amplification tests. (Infection: [10.1007/s15010-023-02100-0](#))

Gut virome in inflammatory bowel disease patients undergoing biological therapy reveals two virome configurations linked to IBD, that were associated with the therapeutic outcomes, suggesting clinical relevance. (J Crohns Colitis: [10.1093/ecco-jcc/jjad061](#))

In murine obesity models, adipose tissue, particularly near the lungs, supported influenza virus replication, and human adipocytes showed direct influenza virus replication in vitro, suggesting a potential role of adipose tissue in respiratory virus infections, although no active replication of SARS-CoV-2 was observed in adipocytes. (Int J Obes: [10.1038/s41366-023-01362-w](#))

Benchmarking of two virome analysis approaches using synthetic communities, reveals that the dsRNA-based approach is better for complex RNA viromes, while the VANA method is suitable for simpler viromes, with a clear link between virome completeness and sequencing depth. (J Virol: [10.1128/jvi.01300-23](#))

Investigation of soil DNA and RNA viruses uncovers a wide variety of previously unknown viruses, and shows that active viruses in soil change with seasonal environmental conditions, suggesting a "seed-bank" viral community structure that can impact ecosystem biogeochemistry. (Microbiome: [10.1186/s40168-023-01666-z](#))

Recent discoveries in prokaryotes have unveiled a novel mechanism of RNA-guided transposition in mobile genetic elements, connecting them with host defense mechanisms, including the recruitment of CRISPR systems, and suggesting the likelihood of finding more RNA-guided functionalities in mobile genetic elements. (Curr Opin Syst Biol: [10.1016/j.coisb.2023.100473](#))

SARS-CoV-2 HaploGraph platform was developed to visualize the timing and geographical transmission of SARS-CoV-2 haplotypes in Japan using data from the GISAID EpiCoV database, aiding in tracking virus evolution and guiding public health control strategies during the COVID-19 pandemic. (Genes Genet Syst: [10.1266/ggs.23-00085](#))

Reviews / Commentaries / Editorials / ...

The importance of accurate and well-curated metadata in biomedical research, especially genomics data, is highlighted due to its role in ensuring research credibility, reproducibility, and the discovery of new insights, as underscored by an incident involving critical metadata errors in patient data published in high-impact journals. (Comput Struct Biotechnol J: [10.1016/j.csbj.2023.10.006](#))

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 .

gutSMASH: Specialized Primary Metabolite Analysis From Anaerobic Bacteria

LAMPPrimerBank: database of experimentally validated loop-mediated isothermal amplification primers


SARS-CoV-2 HaploGraph: visualization of SARS-CoV-2 haplotype spread

scTEA-db: single cell-based Terminal Exon Annotation - database

VirMake: Snakemake based pipeline for viral metagenic data analysis on paired-end data

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 .

5th Central German Meeting on Bioinformatics (Mittelerde Meeting)

29 February – 01 March 2024 | Jena, Germany

Abstract submission deadline: **10 November 2023**

1st Workshop “Young PI” of the Society of Virology (GfV)

11 – 12 Dezember 2023 | Marburg, Germany

The goal of the working group is to provide knowledge that facilitates the transition from bench to successful leadership of one's own working group. Therefore the Young PI working group organizes meetings and workshops where important tips, tricks and soft skills are imparted. [Register here](#) (limited availability)

Annual Conference of the Microbiology Society 2024

08 – 11 April 2024 | Edinburgh, UK

Abstract submission is now open.

Abstract submission deadline: **11 December 2023**

33rd Annual Meeting of the Society for Virology

25 – 28 March 2024 | Vienna, Austria

If enough bioinformatics tools will be submitted this year, we will possibly get an own virus bioinformatics session.

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.

Visualising RNA secondary structures using R2DT

20. November 2023 | 4 pm CET

online

Anton I. Petrov, Riboscope Ltd., UK

RNA structure is essential for the biological function of many viruses. Key RNA secondary structures, such as HCV IRES or the SARS-CoV-2 5' UTR, are commonly visualised with a specific orientation of structural elements. R2DT software automatically generates consistent and recognizable RNA secondary structure diagrams using a library of templates, allowing visualization of position-specific information and pseudoknots. R2DT is widely used in various biological databases, including RNAcentral and is accessible at <https://r2dt.bio/>.

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

19. December 2023 Dominik Heider, University of Marburg, 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 2024

 [Stay tuned](#)

ViBioM 2024

International Virus
Bioinformatics Meeting

28. – 30. May 2024 | Leuven, Belgium



We are delighted to announce date and venue for the International Virus Bioinformatics Meeting 2024!

ViBioM is the pioneering conference that brings together the most influential scientists bridging the gap between virology and bioinformatics and fostering collaboration and innovation in the study of viruses. We are delighted to invite you to join us for **ViBioM 2024 in Leuven, Belgium**. The meeting will take place at the **Rega Institute, 28.–30. May 2024** and is organized together with Jelle Matthijssens, Philippe Lemey at KU Leuven and Simon Dellicour at Université libre de Bruxelles.

We are pleased to already announce the first keynote speakers:

- **Houriiyah Tegally**, Centre for Epidemic Research and Innovation, South Africa
- **Vera Van Noort**, Leiden University, Netherlands
- **Mart Krupovic**, Institut Pasteur, France

Stay tuned for more updates and registration details.

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](#).

Into the wild and digital: Virus hunting beyond the traditional

08 November 2023 | 04-05 pm CET

online

Mark Paul Selda Rivarez

North Carolina State University, USA / Caraga State University, Philippines

Open to Work

At ViBioM 2023 we announced that we would also like to post your job requests to the EVBC community. So if you are open to work, let us know and we will spread the news!

Looking for a PhD position in molecular medicine/ bioengineering/ biocomputation. After his M.Sc. in Bioinformatics at FSU Jena, and the Molecular Mechanisms of Disease Research Master Programme at Radboud University with a Master's Project at Robert-Koch-Institute, **Maximilian Artl** is looking for a PhD project seeking to combine the power of bioinformatics and biomolecular techniques in an infectious, autoimmune or malignant disease to integrate our mechanistic understanding of pathogenic and healthy molecular pathways to develop novel treatment strategies.