EVBC Newsletter

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European VIRUS BIOINFORMATICS Center

Send us your news to evbc@uni-jena.de.
For more frequent updates, follow us on Bluesky and LinkedIn.

ViBioM 2026

We are looking forward to welcome you to ViBioM 2026 on 18–20 May in Vilnius, Lithuania!
Find all updates and details at the ViBioM 2026 website!

Deadlines:

Submissions:	closed
Registration:	30 April 2026
Registration Conference Dinner:	30 April 2026
Registration Satellite Hackathon:	22 April to 8 May 2026

Conference Dinner:
The ViBioM conference dinner will take place on Tuesday, 19 May 2026. You can now register here.

Job Market:
During ViBioM 2026, we will again be hosting a job market for participants who are looking for a job or who are hiring. Your job searches and offers will be featured in the breaks and on a job board on-site.

Tools and Resources

🔧 Virus tools website

Tools developed by EVBC members are marked ✹.

✹ **Peptonizer2000:** This framework improves taxonomic confidence in metaproteomics by addressing ambiguity in protein-to-taxon assignments caused by conserved sequences. This enhances the accuracy of microbial community profiling in complex microbiomes.

Selected Publications by EVBC Members

▤ All publications on Pubmed

RdRp-based RNA virus phylogeny
🔓 Structural modelling of RNA-dependent RNA polymerases using AlphaFold enabled reconstruction of deep evolutionary relationships across diverse RNA viruses, even where sequence similarity is limited. The study refines higher-level taxonomy and reveals inconsistencies in current phylum-level classifications. (Mol Biol Evol: **10.1093/molbev/msag088**)

🔓 – open access χ – preprints ▦ – reviews, meta analyses 🔧 – tools

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Plant pathogens
🔓 Metagenomic analysis of *Freesia refracta* plants with necrotic disorder revealed diverse virus sequences, including previously uncharacterised taxa. The findings refine phylogenetic relationships within the Konkoviridae and Yueviridae families, improving understanding of plant virus evolution. (Virol J: **10.1186/s12985-026-03075-8**)

🔓 Characterisation of Italian isolates of Tomato spotted wilt virus identified the emergence of double resistance-breaking strains infecting tomato and pepper crops. The study links resistance-breaking capacity to mutations in the NSm protein, providing insights relevant to disease management and resistance breeding. (Virology: **10.1016/j.virol.2026.110820**)

Phages in stool transplants
🔓 Bacteriophages were shown to mediate extensive genetic exchange within faecal microbiota, particularly in the context of faecal microbiota transplantation. These findings highlight the role of viruses in shaping microbial community structure and influencing therapeutic outcomes. (Cell Host Microbe: **10.1016/j.chom.2026.03.017**)

Human RNAs during virus infection
🔓 Transcriptomic analysis of monkeypox virus infection in human epithelial cells revealed distinct temporal gene expression patterns associated with different stages of replication. The study provides insights into virus–host interactions and identifies potential molecular targets for antiviral intervention. (Emerg Microbes Infect: **10.1080/22221751.2026.2627079**)

🔓 Analysis of the human tRNA pool during infection revealed dynamic regulation and functional specialisation of specific tRNAs and modifying enzymes. These findings demonstrate how virus replication and host cell fitness are shaped by translational control mechanisms and adaptation to host tRNA availability. (Mol Syst Biol: **10.1038/s44320-025-00181-7**)

sgRNA libraries during virus infection
🔧 The VECOS system enables multidimensional analysis of host–virus interactions by encoding sgRNA libraries directly within virus genomes, providing a quantitative readout of gene perturbation effects. This protocol allows stage-specific investigation of infection dynamics and a powerful tool to study mechanisms of virus propagation. (Nat Protoc: **10.1038/s41596-025-01242-9**)

RNA-binding proteins
🔓 RNA binding was identified as an additional regulatory dimension of the type I interferon response, shaping cellular defence mechanisms during infection. The study highlights how RNA–protein interactions influence host–virus dynamics and immune regulation. (Cell Rep: **10.1016/j.celrep.2026.117174**)

ssRNA phages in metatranscriptomes
🔓 χ Screening of metatranscriptomes for ultrastable RNA secondary structures enabled the identification of previously undetected bacteriophages and associated capsid nanomaterials. The study highlights RNA structural features as a powerful tool for uncovering hidden virus diversity and expanding approaches to phage discovery. (bioRxiv: **10.64898/2026.04.05.716407**)

Molecular architecture of Influenza A virions
🔓 χ High-resolution structural and proteomic analysis of Influenza A virus particles revealed detailed organisation of virus components within virions. The study advances understanding of virus assembly and structural architecture, providing a basis for future functional investigations. (bioRxiv: **10.64898/2026.04.02.715802**)

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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.

29th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology (VEME)

6-11 September 2026 | Stellenbosch, South Africa

The program comprises two key modules providing an overview of the current methods used to analyze the vast data generated by modern DNA sequencing technologies: "Phylogeny inference" and "Evolutionary Hypothesis Testing".
Abstract and application deadline: 30 April 2026

19th Congress of the International Union of Microbiological Societies (IUMS)

4-6 November 2026 | Lisbon, Portugal

Key topics include microbial genetics, biotechnology, clinical and medical sciences, with special attention on how AI can affect any aspect of microbiology. There will be a session on Computational Microbiology.
Abstract submission deadline: 29 April 2026
Early bird registration deadline: 29 July 2026

40th German Conference on Bioinformatics (GCB)

22-25 September 2026 | Saarbrücken, Germany

Annual international meeting for the entire bioinformatics community with inspiring talks, engaging poster sessions, and plenty of opportunities to connect.
Presentation abstract deadline: 3 May 2026
Poster abstract deadline: 6 August 2026
Early bird registration: May until 5 July 2026

Metagenomic Virus Discovery Workshop

12-16 October 2026 | Stellenbosch, South Africa

This five day workshop offers lectures on core knowledge components of virus metagenomics and phylogenetics as well as hands-on practical skills in tailoring analysis pipelines and downstream analysis for high impact results taught by global experts in the field.
Application deadline: 15 May 2026

33rd International Dynamics and Evolution of Human Viruses Conference

19–22 May 2026 | British Columbia, Canada

This meeting series was designed to promote discussion between specialists in quantitative and computational approaches in two areas in the field of virology where these are particularly important: Modeling of viral and cellular dynamics and Viral evolution and population genetics.
Registration for virtual participation still possible: 19 May 2026

30th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2026)

26-29 May 2026 | Thessaloniki, Greece

This algorithmic computational biology conferences bridges the areas of computational, mathematical, statistical and biological sciences.
Late registration deadline: 22 May 2026

Vacancies — Find a job

Several positions in the RNA Bioinformatics Group of Manja Marz at Friedrich Schiller University Jena, starting in fall of 2026 (subject to funding approval):

- Junior Research Group leader "Machine Learning Data Integration from Photonics to Genomics"
- Doctoral researcher in bioinformatics (tool development)
- Research software engineer (database development)
- Science communication coordinator
- Scientific coordinator of a Research Training Group
- Scientific coordinator of a Collaborative Research Centre

Find more information here.

ECR Viromics Webinar Series — Register

This lecture series features early career researchers studying viruses in complex communities. It is organized together with the Center of Microbiome Science at Ohio State University and the NSF EMERGE Biology Integration Institute. You can register **here** for the ECR Viromics mailing list and receive the access details for every webinar. You can unsubscribe at any time.

Upcoming talk:

Eman Wehedy Abdelsalam, Sidra Medicine, Qatar
12 August 2026 | 4 pm CEST online
(Title TBA)

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. You can register **here** for the viruses in silico mailing list and receive the access details for every lecture. You can unsubscribe at any time.

Upcoming talks:

Michael Lässig, University of Cologne, Germany
30 April 2026 | 4 pm CEST online
Influenza and SARS-CoV-2: from evolutionary predictions to prospective vaccination

Elliot J. Lefkowitz, The University of Alabama at Birmingham, United States; International Committee on Taxonomy of Viruses
25 June 2026 | 4 pm CEST online
The ICTV at Sixty Years: Classifying the Worldwide Virosphere

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!