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## ViBioM 2026



Thank you for an inspiring ViBioM 2026 in Vilnius!

We had a fantastic time at the International Virus Bioinformatics Meeting, hosted at beautiful Vilnius University with the support of the EVBC from 18 to 20 May. It was a pleasure to bring together 80 participants from around the world, who work at the intersection of virology, bioinformatics, and computational biology. Throughout the conference, attendees shared their latest research on virus metagenomics, phylogeny, protein and RNA biology, and machine learning methods, highlighting methodological advancements and novel biological insights.

Conference Award Winners:

- **Best Poster:** **Aistė Židonytė | Vilnius University** – “*What is facilitating a global virus pandemic in mosquitoes?*”
- **Best Talk:** **Emma Harding | University of Oxford** – “*Exploring historical retroviral transmission patterns in vertebrates using endogenous retroviruses*”

A sincere thank you to all organisers, committee members, and on-site helpers who made this event possible, and to our generous sponsors (Go Vilnius, MDPI Viruses, and FEBS Open Bio) for their support! Beyond the excellent science, it was the genuine sense of community and exchange that made this meeting truly special. We are deeply grateful to everyone who helped create such an inspiring atmosphere.

We are already looking forward to ViBioM 2027 in Jena! Hope to see you again next year!

## ECR Viromics Webinar Series



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 W. Abdelsalam**, Sidra Medicine, Doha, Qatar  
**12 August 2026 | 4 pm CEST** online  
**Understanding the viral composition and the dynamic phage-bacterial interplay in Idiopathic nephrotic syndrome**

## Tools and Resources



[Virus tools website](#)

Tools developed by EVBC members are marked .

✳️ **PHLEGM:** This computational framework combining AlphaFold-Multimer and interface scoring to predict homooligomeric states of bacteriophage proteins at scale. It resolves thousands of virus protein complexes with improved accuracy over sequence-based methods, supported by experimental validation of selected predictions.

✳️ **nf-core/viralmetagenome:** A scalable Nextflow pipeline for automated reconstruction and analysis of eukaryotic virus genomes from metagenomic sequencing data. The workflow integrates assembly, reference selection and consensus refinement to enable robust virus genome recovery for surveillance and outbreak applications.

✳️ **Covvfit:** A framework that uses wastewater sequencing data to model and forecast SARS-CoV-2 variant selection dynamics. It enables inference of variant fitness and temporal shifts in virus populations for epidemiological surveillance.

### Virus resources / catalogues

🕒 This study presents a comprehensive catalogue of all known RNA viruses capable of infecting humans, bringing together standardised information in a single accessible resource. The dataset supports research into virus diversity, evolution and emergence, while providing a valuable tool for surveillance and pandemic preparedness. (Sci Data: [10.1038/s41597-026-07281-5](#))

🕒 New study analyses Lassa virus proteins at the population scale and characterises lineage-specific biophysical properties across hundreds of virus sequences. The authors also generate a comprehensive glycoprotein structure catalogue that provides a valuable resource for understanding virus diversity and supporting vaccine and therapeutic development. (npj Viruses: [10.1038/s44298-026-00196-3](#))

🕒 This study establishes a comprehensive catalogue of bacteriophages inhabiting the gut microbiome of the honey bee, providing a detailed overview of virus diversity and host relationships. It advances understanding of phage-microbe interactions in an ecologically important pollinator and supports future research into microbiome function and bee health. (Nat Commun: [10.1038/s41467-026-72757-2](#))

## Viruses *in silico* lecture series



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 talk:



**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**


## Selected Publications by EVBC Members

 [All publications on PubMed](#)



### Virus phylogeny



  This article introduces a parallelised algorithmic framework for structured coalescent phylogeographic inference, achieving major computational speedups by restructuring likelihood calculations and enabling scalable real-time analysis of large outbreak datasets. The method improves feasibility of high-resolution pathogen surveillance across many regions and integrates into BEAST X and BEAGLE. (PNAS: [10.1073/pnas.2602412123](#))

  This new review synthesises current knowledge on the organisation and evolution of the virosphere, highlighting multiple virus origins, extensive gene sharing, and host-virus coevolution driven by arms races and exaptation. It provides a conceptual framework for understanding virus diversity and high-level virus taxonomy. (CR Biol.: [10.5802/crbio.193](#))

 This study reconstructs the evolutionary history of Jamestown Canyon virus using 658 genomes and shows that mosquito phenology strongly shapes its slow evolution and seasonal transmission dynamics. Phylodynamic analyses reveal long-term circulation in North America and distinct roles of univoltine and multivoltine mosquito vectors in virus persistence and spread. (Curr. Biol.: [10.1016/j.cub.2026.03.076](#))




### Microscopy and spectroscopy

  This study introduces event-triggered MINFLUX microscopy, which combines real-time confocal analysis with adaptive control to enable targeted nanoscale imaging of rare cellular events. The approach improves acquisition efficiency and enables high-resolution study of dynamic membrane processes in live cells. (Nat. Commun.: [10.1038/s41467-026-73176-z](#))



  This protocol presents a microfluidic platform integrated with confocal general polarization fluorescence microscopy to quantify lipid packing in giant unilamellar vesicles using polarity-sensitive dyes. It provides a stepwise workflow for device fabrication, vesicle preparation, trapping, and membrane order analysis in controlled fluidic environments. (STAR Protoc.: [10.1016/j.xpro.2026.104525](#))

This work presents a machine-learning-augmented Raman spectroscopy framework for quantifying components in model vaccine formulations. The approach enhances spectral analysis and improves compositional resolution in complex biological mixtures. (Anal. Chem.: [10.1021/acs.analchem.5c05538](#))

### ncRNAs of viruses

   This work presents computational protocols for viral ncRNA annotation and programmatic data retrieval using Rfam and R2DT, enabling automated genome-wide RNA structure analysis and API-based integration into bioinformatics workflows. It facilitates scalable annotation and visualization of structured RNA elements in virus genomes. (bioRxiv: [10.64898/2026.05.10.724034](#))

### Virus-host interactions

  This review synthesises current knowledge on infection cycles across the phylum Nucleocytoviricota, comparing major giant virus lineages to identify conserved and divergent mechanisms. It provides a unified framework for understanding virus-host interactions and outlines open questions in the cell biology and evolution of these large DNA viruses. (Nat Rev Microbiol: [10.1038/s41579-026-01319-6](#))

 - open access    - preprints    - reviews, meta analyses    - tools

## 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.

### 32nd International Symposium on Hepatitis C Virus, Flaviviruses and Related Viruses (HCV-Flavi 2026)

**14-17 September 2026 | Copenhagen, Denmark**

This meeting brings together researchers in the fields of hepatitis C virus (HCV), orthoflaviviruses, and related viruses, including pesti-, pegi-, and other hepatitis viruses. It highlights major advances in virus replication, immune responses, pathogenesis, and genetics, antiviral therapies and vaccine development.

Early registration deadline:

**14 June 2026**

### 28th Annual Conference of the European Society for Clinical Virology (ESCV 2026)

**16-19 September 2026 | Porto, Portugal**

This meeting showcases research in Clinical Virology (including viral evolution & emergence, viral diseases affecting vulnerable & special populations, HIV and hepatitis, host-virus interactions, antiviral & vaccine strategies, innovative genomic & diagnostic approaches).

Early registration deadline:

**21 June 2026**

Late-breaking abstract submission deadline:

**30 June 2026**

### Viruses of Microbes (VoM) Conference 2026

**6-10 July 2026 | Prague, Czech Republic**

World's leading event for research on viruses of microorganisms, including bacteriophages, archaeal viruses, and viruses of microbial eukaryotes.

Regular registration deadline:

**30 June 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.

Early bird registration:

**5 July 2026**

Poster abstract deadline:

**6 August 2026**

### 45th Annual Meeting of the American Society for Virology (ASV 2026)

**27-30 July 2026 | Minneapolis, United States**

The meeting provides a forum to promote discussion and collaboration among scientists active in all aspects of virology, from basic research to vaccines and antiviral therapeutics.

Regular registration deadline:

**13 July 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.

Late-breaking abstract submission:

**8 July 2026**

Early bird registration deadline:

**29 July 2026**

## Vacancies

 Find a job

### 2 PhDs - VACCINATION-INDUCED B CELL IMMUNITY AGAINST LASSA VIRUS

The Experimental Virology at the University of Basel, led by Prof. Daniel Pinschewer, is looking for two PhD students. The work will be centered around protective B cell immunity against Lassa virus (LASV). LASV is endemic in West Africa and causes several thousand cases of fatal hemorrhagic fever each year but a vaccine for clinical use remains unavailable. Join the community and help shape the future of biomedicine.

### Several positions in the RNA Bioinformatics Group, Friedrich Schiller University Jena, starting in fall of 2026:

- 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

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