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ViBioM 2026



Save the date for ViBioM 2026 on 18–20 May in Vilnius, Lithuania!
Find all updates and details at the [ViBioM 2026 website!](#)



Deadlines:

Talk submission (abstracts): closed
Poster submission (title only): 17 April 2026
Registration: 30 April 2026

Satellite Event 17 May 2026, 09:00 - 18:00:

Everyone is welcome to join this hybrid event - You do NOT have to attend ViBioM to participate the hackathon!

17 May 2026 | Vilnius, Lithuania + online

Virus Bioinformatics + nf-core Hybrid Collaborative Hackathon

Propose a project!



Calling all collaborative hackers!



Registration opens
April 2026

A satellite event of EVBC ViBioM 2026

Selected Publications by EVBC Members

All publications on PubMed

Diseases and Therapies

This review discusses the paradox of treating Epstein–Barr virus–linked multiple sclerosis with broad immunosuppression, highlighting how such strategies may impair antiviral immune surveillance. It calls for EBV targeted therapeutic approaches to better address the underlying virus contribution to MS. (Open Forum Infect Dis: [10.1093/ofid/ofag097](#))

This study shows that phage–antibiotic synergy can restore β -lactam efficacy against multidrug-resistant *Klebsiella quasipneumoniae* biofilms while reducing resistance emergence. It highlights the potential of combining bacteriophages with antibiotics as a strategy to combat antimicrobial resistance. (J Biomed Sci: [10.1186/s12929-026-01218-1](#))

This preprint describes a systems level exposome model in which climate driven microplastic exposures intersect with Epstein–Barr virus–related host pathways relevant to Alzheimer’s disease and multiple sclerosis. It identifies shared molecular targets across immune, hormonal, and oxidative signalling networks that may influence female biased disease susceptibility. (Preprint Res Sq: [10.21203/rs.3.rs-8928857/v1](#))

Virus Evolution

This article explores the evolution of insect endogenous retroviruses, showing how gain and loss of envelope genes drive transitions between infectious and non-infectious states. It highlights how these elements occupy distinct cellular niches and co-evolve with host defence mechanisms. (EMBO J: [10.1038/s44318-025-00472-7](#))

This study explores the evolutionary origins of virus HSP70 proteins, showing multiple independent acquisitions across RNA and DNA viruses. It reveals distinct evolutionary patterns and supports horizontal gene transfer as a key mechanism shaping their diversity. (J Gen Virol: [10.1099/jgv.0.002242](#))

Methods

This review examines methodological approaches for detecting picobirnaviruses and inferring their host range, highlighting limitations in PCR and metagenomic strategies. It underscores the uncertainty surrounding their biological roles and emphasises the need for improved frameworks to resolve their ecological significance. (Crit Rev Microbiol: [10.1080/1040841X.2025.2560918](#))

This article describes the development and implementation of open access Nextstrain and Nextclade resources for Lassa virus that support live phylogenetic and phylogeographic tracking as well as rapid mutation detection and lineage assignment. The work highlights how near real time genomic surveillance can improve outbreak response and public health decision making in endemic and export case settings, while underscoring persistent barriers to data sharing and timeliness in many West African regions. (Emerg Microbes Infect: [10.1080/22221751.2026.2640699](#))

This review synthesises target cell limited ordinary differential equation models of SARS CoV 2 replication and their use in quantifying antiviral drug efficacies in vitro, emphasising how these models improve mechanistic understanding of virus dynamics and treatment effects. It also identifies key limitations, including data sparsity and structural identifiability issues, that must be addressed to make model based predictions more robust and comparable across studies. (Npj Viruses: [10.1038/s44298-026-00183-8](#))

- 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.

European Conference on Computational Biology (ECCB 2026)

31 August to 4 September 2026 | Geneva, Switzerland

Europe's leading event in computational biology. The theme in 2026 will be "Biodiversity, AI and Health: computational biology to address the challenges of our time".

Submission deadline for highlight talks and posters: **20 April 2026**

Early registration deadline: **31 March 2026**

Regular registration deadline: **30 June 2026**

34th Conference on Intelligent Systems for Molecular Biology (ISMB 2026)

12-16 July 2026 | Washington, DC, United States

ISCB's flagship conference returns to Washington, DC – the very city where ISCB and ISMB began in 1993 – to celebrate over 30 years of advancing computational biology.

Early registration deadline: **31 March 2026**

Abstract deadline: **9 April 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.

Early registration deadline: **15 April 2026**

Late registration deadline: **22 May 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**

Vacancies

 [Find a job](#)

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

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

More info will follow in April. If you are interested in one or more of these positions, please reach out to maria.fabisch@uni-jena.de.

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:

Pascal Mutz, National Institutes of Health, USA

8 April 2026 | 4 pm CET

[online](#)

Illuminating covalently closed circular RNAs from metatranscriptomics: from Obelisks to novel entities

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 talk:

Michael Lässig, University of Cologne, Germany

30 April 2026 | 4 pm CET

[online](#)

(Title TBA)

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