EVBC Newsletter

Volume 100 • February 2026

European
VIRUS BIOINFORMATICS
Center

Send us your news to evbc@uni-jena.de.
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Welcome to the 100th EVBC Newsletter!

Dear friends, dear colleagues,

One hundred newsletters!

When we sent out the first one, back in the early days of the European Virus Bioinformatics Center (EVBC), we could not know what would unfold. We only knew that our field needed a home – a place where virologists, bioinformaticians, data scientists, and clinicians could find each other across borders and disciplines.

Since then, month after month, this newsletter has been a quiet thread stitching our community together.

In its pages we have shared new tools and databases, fresh ideas and hard-won insights. We have announced meetings and celebrated the International Virus Bioinformatics Meetings. We have highlighted workshops, webinars, training opportunities, and job openings. We have welcomed new members, new collaborations, and new energy. When the world was shaken by emerging viruses and global uncertainty, this space became even more important – a steady channel for reliable information and scientific exchange.

What moves me most is not the number 100.

It is the people behind it:

The researchers who submit announcements at midnight before a deadline. The early-career scientists who find their first postdoc position through a link in these pages. The colleagues who meet at an EVBC event and begin a collaboration that would not otherwise exist. The generosity of those who share code, data, and time. And the many readers – some we know and many we don't – who open this newsletter each month and remain part of this growing network.

EVBC has become more than an organization. It is a community built on openness, rigor, and mutual support. A place where virus bioinformatics has a voice – and, more importantly, many voices.

Thank you for being part of this journey. Whether you have been with us since the beginning or joined only recently, you have helped shape what these last 100 newsletters represent.

Let us continue connecting, supporting one another, and pushing the field forward – together.

With sincere gratitude,

Manja Marz
Managing Director of the EVBC

EVBC Special Issues

Special issue list

Special Issue "Virus Bioinformatics 2025"
MDPI grants a discount of 20 % for submissions from ViBioM 2025 attendees and EVBC members!
Submission deadline: extended to 31 March 2026!

ViBioM 2026

Save the date for ViBioM 2026 on 18–20 May in Vilnius, Lithuania!

Stay tuned for all updates and details about abstract submission and registration on the ViBioM 2026 website!

Abstract submission for talks:	6 March 2026
Title submission for posters:	17 April 2026
Registration:	open within the next two weeks until 30 April 2026

Join us also for the **Satellite event on Sunday 17 May:**
2026 Virus Bioinformatics and nf-core Community Hackathon
- Towards building open-source virus bioinformatics workflows and standards -
Time: Sunday, 17 May 2026, 09:00 - 18:00
Type: Hybrid event (online and in-person)
Organized by the VirJenDB (NFDI4Microbiota) and the global nf-core community. You do NOT have to attend ViBioM to participate in the hackathon, everyone is welcome!

Vacancies

Find a job

Assistant Professor - Virology
The Department of Molecular Genetics in the Temerty Faculty of Medicine at the University of Toronto (St. George campus) invites applications for a full-time tenure stream position in the area of Virology. The appointment will be at the rank of Assistant Professor, with an anticipated start date of January 1, 2027.
Application deadline: 16 March 2026

PhD - Computational Infection Genomics
The Computational Virology group (Prof. Dr. Chris Lauber) at the TWINCORE Centre for Experimental and Clinical Infection Research in Hannover, a joint institution of the Helmholtz Centre for Infection Research (HZI) and Hannover Medical School (MHH), is seeking a highly motivated PhD student with a strong computational background. The project aims to develop genetic risk scores for severe course of infection with the respiratory syncytial virus (RSV) to enable individualized risk stratification, prevention, and therapy. The work is part of the RESIST Cluster of Excellence at Hannover Medical School and involves close collaboration with clinical and experimental groups.
Application deadline: 22 March 2026

Selected Publications by EVBC Members

All publications on PubMed

Phages

🔓 This study demonstrates that bacteriophages and phage inducible chromosomal islands mobilize chromosomal antiphage defense systems via lateral transduction, enabling efficient horizontal transfer of immune genes between bacteria. The process diversifies defense repertoires and profoundly impacts bacterial evolution and pathogen population dynamics. (Sci Adv: **10.1126/sciadv.adx5749**)

Nanopore Sequencing

🔓 ⊞ This interdisciplinary review provides practical and statistically supported guidance for optimising nanopore sequencing workflows, spanning experimental protocols and advanced computational analysis. It offers comprehensive recommendations to maximise data quality and biological insight from long-read sequencing technologies. (Nucleic Acids Res.: **10.1093/nar/gkag023**)

RNA Viruses / Secondary Structures

🔓 This study provides the first full genome multiple sequence alignment representative of all known Pestivirus species and identifies conserved RNA structural elements across the genus. The resources and analyses reported facilitate future pestivirus comparative genomics and RNA biology research. (RNA: **10.1261/rna.080732.125**)

Phylogeny

🔓 The authors re assemble nearly all public SARS CoV 2 raw sequencing data using an amplicon aware workflow to correct systematic errors inherent to tiled amplicon sequencing and inconsistent assembly practices. With these high quality consensus genomes, they provide an improved global phylogeny of 4,471,579 samples, enhancing the accuracy of pandemic scale evolutionary inference. (Nat Methods: **10.1038/s41592-025-02947-1**)

Applications

🔓 This study provides a comprehensive catalogue of bacterial and fungal communities inhabiting groundwaters of the Slovenian Dinaric Karst, an important biodiversity hotspot. By mapping microbiome diversity across aquifer systems, the work lays a foundation for improved understanding of subsurface ecosystem structure and function. (Ecotoxicol Environ Saf: **10.1016/j.ecoenv.2026.119890**)

🔓 This study characterises the diversity of DNA viruses in the atmosphere above sub Antarctic South Georgia, uncovering numerous virus taxa with links to marine environments and extremophile hosts. The findings suggest that location influences airborne viruscommunity composition and that some virus functional homologs may support microbial resilience under challenging conditions. (Front Microbiol: **10.3389/fmicb.2025.1726848**)

🔓 In this multicentre cohort study of 13,611 patients with community acquired pneumonia, diabetic patients had a distinct pathogen profile, elevated inflammatory markers, and higher mortality than non diabetic patients. Enhanced pathogen testing in diabetic CAP cases may inform tailored management strategies. (Infection: **10.1007/s15010-025-02659-w**)

🔓 This study reveals that virus prevalence across multispecies bee communities is determined by the presence of multiple key host species and the structure of their ecological interaction networks. The results highlight the role of host diversity and network architecture in shaping pathogen dynamics in natural pollinator systems. (Ecol Lett: **10.1111/ele.70327**)

🔓 – open access *χ – 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 **full manuscripts**:	5 March 2026
Submission deadline for **highlight talks and posters**:	20 April 2026

Viruses of Microbes (VoM) Conference 2026

6-10 July 2026 | Prague, Czech Republic

World's leading event for research on bacteriophages, archaeal viruses, and viruses of microbial eukaryotes, themed "Revealing Novel Interactions, Innovations, and Applications" in 2026.

Abstract submission deadline:	31 March 2026
Early bird registration deadline:	31 March 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:	1 April 2026
Abstract deadline:	9 April 2026

4th (Inter-) National Conference on Infectious Disease Modeling

20-22 May 2026 | Halle (Saale), Germany

This 4th Annual Meeting of the Modeling Network for Severe Infectious Diseases (MONID) provides the opportunity to exchange ideas with renowned experts in the field of mathematical modeling of severe infectious diseases and related disciplines on the latest findings in these fields. Pre-conference workshop on 19 May 2026.

Abstract submission:	Closed
Registration deadline:	30 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 online registration deadline:	22 May 2026
Poster abstract deadline:	(no details yet)

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

4-6 November 2026 | Lisbon, Portugal

Key topics will include microbial genetics, molecular and synthetic biology, gene regulation, proteomics, biotechnology, clinical and medical sciences, industrial applications, and environmental sustainability. Special attention will be paid to 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

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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:

Sebastian Böcker, Friedrich Schiller University Jena, Germany
26 February 2026 | 4 pm CET online
SIRIUS and beyond: Turning tandem mass spectra into metabolite structure information

Michael Lässig, University of Cologne, Germany
30 April 2026 | 4 pm CET online
(Title TBA)

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 talks:

James Kosmopoulos, Anantharaman Lab, University of Wisconsin-Madison, USA
11 March 2026 | 4 pm CET online
Scalable annotation and curation of auxiliary viral genes with Check-AMG

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

Tools and Resources — Virus tools website

Tools developed by EVBC members are marked ⚙.

⚙ **CRESSENT:** A comprehensive bioinformatics toolkit for systematic ssDNA virus annotation from metagenomic datasets, addressing challenges in diversity, decontamination and classification. The modular design supports scalable analyses including phylogeny, motif detection and structure prediction, enhancing integration of ssDNA viruses into viromics workflows.

⚙ **TEvarSim:** provides an integrated framework for simulating transposable element variants and benchmarking detection tools, improving evaluation of TE genotyping performance. The software facilitates more accurate studies of transposable elements across diverse genomes.

⚙ **LolliPop:** A computational method for estimating SARS-CoV-2 variant abundances from mixed wastewater sequencing data. The approach improves the accuracy and utility of wastewater-based genomic surveillance.

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!

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