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Upcoming Events

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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 .

40th German Conference on Bioinformatics (GCB)

22-25 September 2026 | Saarbrücken, Germany

Annual international meeting for the bioinformatics community with inspiring talks, engaging poster sessions, and opportunities to connect.
Registration: **10 September 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.
Registration deadline: **15 October 2026**

3rd RNA Horizons Conference

16-18 September 2026 | Munich, Germany

This event unites leading researchers to explore the latest RNA therapeutic advancements, from established modalities to emerging areas like ASOs and RNA structure-based therapies. Discussions will encompass key trends: pipeline diversification, enhanced RNA modalities, AI integration, and improved delivery technologies.

Early registration deadline: **31 August 2026**

Viral EcoGenomics and Applications (VEGA) 2026 Symposium

18-19 November 2026 | Berkeley, CA, USA

A space for the viral ecogenomics community working in a broad range of environmental and host-associated ecosystems, along with molecular and computational techniques. 3 Sessions: "Functional characterization of novel viral diversity", "Molecular mechanisms of virus-host interactions", "Utilizing phages to manipulate microbiomes".

Early registration deadline: **18 September 2026**

Talk abstract submission deadline: **16 October 2026**

Poster abstract submission deadline: **30 October 2026**

FEMS MICRO 2027

5-8 July 2027 | Ljubljana, Slovenia

Europe's premier Congress and Exhibition for microbial research and collaboration under the theme 'Growing microbial futures'.

Session proposal submission deadline: **30 September 2026**

EVBC Workshops

Workshop Requests

Help shape future EVBC workshops! What topics/tools/challenges in virus bioinformatics should we address? Which workshops would you like to join?

Please let us know: [Submit a workshop request](#).

Selected Publications by EVBC Members

 [All publications on PubMed](#)

Bacteriophages

 Using scalable RB-TnSeq genetic screens, the study identifies 42 bacterial genes associated with infection by 25 diverse Klebsiella phages, revealing both conserved and phage-specific host requirements across phage genera and families. The findings provide a resource for linking phage genomic diversity to host interaction mechanisms, with potential applications in predicting phage host range and designing rational phage cocktails. (PLoS Genet: [10.1371/journal.pgen.1012233](#))

 Phage-encoded transcription factors and sigma factors represent an understudied mechanism of virocell reprogramming that complements auxiliary metabolic genes by reshaping host transcriptional networks and cellular functions. This review summarises genomic, experimental and computational advances that could enable systematic investigation of these factors and reveal their impacts on microbial ecology and ecosystem processes. (Trends Microbiol.: [10.1016/j.tim.2026.05.019](#))

 This educational guide presents 10 practical tips for classifying unknown bacteriophages, combining genome quality assessment, taxonomic tools, database searches, similarity metrics, phylogenetics, structural analysis, host range and ecological information. It advocates a pragmatic and evidence-based approach in which multiple methods are compared, classifications are manually verified and taxonomic assignments are refined as new phage diversity is discovered. (PLoS Comput Biol: [10.1371/journal.pcbi.1014403](#))

 Groundwater viromes from three rural hand pumps in Egypt were analysed, recovering 9,534 virus contigs dominated by highly novel tailed double-stranded DNA bacteriophages and revealing strongly site-specific community structures. Predicted virus-host associations and auxiliary metabolic genes linked to amino acid, cofactor, vitamin and energy metabolism suggest that groundwater phages may regulate microbial communities and contribute to subsurface metabolic processes. (Microb Ecol: [10.1007/s00248-026-02818-y](#))

Virus Proteins

 This new publication defines structural and antigenic boundaries across Henipavirus and Parahenipavirus glycoproteins using a globally representative panel, biochemical analyses, animal immunisation, cryo-electron microscopy and crystallography. The findings reveal determinants of fusion-protein prefusion stability and cross-reactive epitopes within both genera, providing a foundation for broadly reactive countermeasures against henipaviruses. (Nat Commun: [10.1038/s41467-026-74212-8](#))

 The authors adapt AlphaFold2-Multimer to enrich predictions of both prefusion and postfusion conformations of class I virus fusion proteins, with template selection playing a central role in directing the predicted structural state. The approach supports accurate modelling for structure-based epitope prediction and vaccine design, while showing that low pLDDT values may not exclude valid alternative conformations. (PLoS One: [10.1371/journal.pone.0351662](#))

Virus mRNA

 Using nanopore direct RNA sequencing, the authors show that mRNAs from diverse alpha-, beta- and gammaherpesviruses consistently possess longer poly(A) tails than host mRNAs, suggesting a shared mechanism that may promote virus gene expression. Comparisons with coronavirus, poxvirus and adenovirus RNAs demonstrate that extended poly(A) tails are not a universal virus strategy and that tail-length regulation varies between viruses and individual transcripts. (PLoS Pathog: [10.1371/journal.ppat.1014341](#))

Plant Virus Mimicry

 The study examines the use of virus-mimicking artificial positive controls for epidemiological surveillance, emphasising reliable detection and interpretation of virus infections. Its approach highlights how validated laboratory workflows can improve monitoring, support epidemiological assessment and inform public-health responses. (J Virol Methods: [10.1016/j.jviromet.2026.115434](#))

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

Selected Publications by EVBC Members

 All publications on Pubmed

Evolution / Classification / Discovery

 This review proposes an integrated framework linking genomic sites, protein structure and serology to explain and predict antigenic evolution in viruses such as influenza and SARS-CoV-2. Combining genomic surveillance, phylogenetics, structural analysis, antigenic cartography and machine learning could improve prospective variant assessment and guide the development of vaccines and therapeutics. (J Virol: [10.1128/jvi.01687-25](#))

 The review explores how AI-based protein structure prediction can advance the study of deep virus evolution when rapid sequence change obscures ancient relationships. The authors discuss applications in viral dark-matter discovery, taxonomy of orphan lineages, functional annotation and structural phylogenetics, while highlighting the remaining methodological and interpretive challenges. (Annu Rev Virol: [10.1146/annurev-virology-100424-122154](#))

 The report from the BV-BRC, CDC, NCBI and NIAID Viral Sub-Species Classification Workshop examines the scientific and technological challenges of classifying viruses below the species level and tracking their evolution during outbreaks. The authors advocate interoperable and sustainable systems that combine genomic, antigenic and other phenotypic data with dynamic, non-stigmatising nomenclature to support surveillance, public-health communication and the development of countermeasures. (J Virol: [10.1128/jvi.00210-26](#))

 This review explores how nonstandard virus genome architectures with structural rearrangements influence virus ecology and evolution. It examines their effects on replication, transmission, host interactions and adaptation, and highlights mathematical modelling as a tool for explaining their emergence, persistence and evolutionary consequences. (Curr Opin Virol: [10.1016/j.coviro.2026.101567](#))

 This review traces the development of virus identification from classical experimental and molecular methods to genome-resolved metagenomics, sequence-based artificial intelligence and hybrid computational pipelines, drawing on 502 virome studies published between 2010 and early 2026. The authors identify reference-database bias and viral dark matter as continuing challenges, while highlighting protein-structure comparison and integrated experimental-computational frameworks as promising directions for discovering and classifying the virosphere. (Microb Genom: [10.1099/mgen.0.001785](#))

Tools, Ressources & Methods

 This **protocol** presents an integrated workflow for characterising metagenomic prokaryotic viruses using PharoKka, Phold and Phytany, combining sequence homology, protein structural similarity, genome synteny and protein language models to improve virus genome and protein annotation. The workflow also includes Phold Plot for visualising annotated genomes and provides a scalable approach for exploring the functional potential of poorly characterised virus sequences. (Curr Protoc: [10.1002/cpz1.70405](#))

 The authors **benchmark** sequence-search and alignment tools for detecting CRISPR spacer-protospacer matches, showing that tool choice, distance metric and reporting settings substantially affect recall, runtime and computational resource requirements. For large-scale analyses of host-mobile genetic element interactions, Bowtie1 with up to three mismatches is suggested as a practical option offering a balance of sensitivity, efficiency and consistency. (Bioinformatics: [10.1093/bioinformatics/btag394](#))

 **VirBench** is introduced, a benchmark of 120 virus sequence-retrieval queries, and gget virus, a deterministic framework for reproducible, programmatic access to filtered virus genome data. Integrating gget virus substantially improved the accuracy and stability of tested AI agents while reducing data transfer by more than 98% in a representative SARS-CoV-2 workflow, supporting reliable science and virus genomics. (arXiv: [10.48550/arXiv.2606.06749](#))

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Tools

 [Virus tools website](#)

Tools developed by EVBC members are marked .

 **RdRpCATCH**: this framework integrates multiple profile Hidden Markov model resources for detecting virus RNA-dependent RNA polymerases in (meta)transcriptomic assemblies and provides subsequent taxonomic annotation of detected RNA viruses. By combining complementary pHMM collections in a user-friendly Conda package and web server, the resource addresses fragmentation in existing approaches and facilitates comprehensive RNA virus discovery across diverse sequencing datasets.

 **ConvMut**: an interactive platform that automatically identifies and visualises recurrent mutations, including substitutions, insertions and deletions, across SARS-CoV-2 phylogenies. By revealing convergent evolutionary patterns and mutation hotspots, the tool may support genomic surveillance and guide the development of broadly effective Spike-based vaccines and monoclonal antibodies.

Job Vacancies

 [Find a job](#)

Independent Research Group Leaders (f/m/d) for Computational RNA Biology

The Frankfurt Institute for Advanced Studies (FIAS) and the newly funded Cluster of Excellence SCALE (SubCellular Architecture of Life) offer several positions as Independent Research Group Leaders (f/m/d) for Computational RNA Biology.

Application deadline:

30 August 2026

Postdoctoral Researcher in AI-driven antigen evolution and vaccine design

The new Antigen Evolution & Design Lab of Spyros Lytras is seeking a highly motivated early-career scientist to develop cutting-edge machine learning approaches for understanding and designing pathogen antigens. This is a unique opportunity to help shape a new research program at the intersection of computational biology, protein language models, structural biology, and immunology.

- Work on new AI technologies for decoding antigen protein evolution in a fresh research environment, at the heart of Paris.

Application deadline:

1 September 2026

Postdoctoral Fellow or Bioinformatics Scientist

The Nomburg Lab at AITHYRA in Vienna, Austria, is seeking a motivated Postdoctoral Fellow or Bioinformatics Scientist to join their interdisciplinary team that combines AI, structural biology, and high-throughput molecular virology to decode the virus-host conflict. The Nomburg Lab pairs computational and experimental methods, with a special emphasis on interactions between viruses and cellular immunity.

Application deadline:

15 September 2026

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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.

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