

Send us your news to [evbc@uni-jena.de](mailto:evbc@uni-jena.de).  
For more frequent updates, please follow us on Twitter [EVirusBioinfC](https://twitter.com/EVirusBioinfC).

## Selected Publications by EVBC Members

[All publications on Pubmed](#)

### Prediction tools

③ VirusPredictor, a fast XGBoost-based software designed for accurately predicting viral sequences in human data, achieves high prediction accuracies for different sequence lengths and taxonomic subgroups, making it useful for discovering disease-causing pathogens, particularly viruses without reference genomes. (Bioinformatics: [10.1093/bioinformatics/btae192](https://doi.org/10.1093/bioinformatics/btae192))

### Wet lab protocols

③ FISHToFigure, a user-friendly software tool designed for the automated spatial analysis of mRNA abundance and co-expression in single molecule fluorescence *in situ* hybridisation (smFISH) data, enables researchers to analyze transcript expression in single cells without the need for extensive programming expertise, and demonstrating its effectiveness in investigating mRNA expression patterns in various biological systems. (Sci Rep: [10.1038/s41598-024-58641-3](https://doi.org/10.1038/s41598-024-58641-3))

Next-RSV-SEQ, an experimental and computational pipeline designed for robust, cost-effective whole genome sequencing of respiratory syncytial virus (RSV) from clinical samples, offers scalability, high-quality genome recovery, and suitability for high-throughput sequencing, addressing the urgent need for comprehensive genomic surveillance of RSV. (Virology: [10.1128/jcm.01111-23](https://doi.org/10.1128/jcm.01111-23))

The review covers the advancements in organ-on-chip (OoC) technologies for infectious disease research, highlighting their ability to create physiologically relevant *in vitro* models that mimic human infection processes more accurately than traditional animal and cell culture models, while also addressing their properties, limitations, and potential future applications in microbiology. (Nat Microbiol: [10.1128/jcm.01111-23](https://doi.org/10.1128/jcm.01111-23))

### Drug design

③ Recent advancements in structure-based *de novo* drug design, exploring various computational algorithms such as fragment-based methods, evolutionary algorithms, Metropolis Monte Carlo methods, and deep generative models, while emphasizing efforts to enhance synthetic accessibility and validate proposed frameworks through benchmarking strategies. (J Chem Inf Model: [10.1021/acs.jcim.4c00247](https://doi.org/10.1021/acs.jcim.4c00247))

③ The development of artificial neural networks (ANNs) to predict protein post-translational modifications (PTMs) and their implementation in the computational protein modeling suite Rosetta enables the design and understanding of modified protein sites' impact on stability and function, offering potential applications in protein therapeutics design. (PLoS Comput Biol: [10.1371/journal.pcbi.1011939](https://doi.org/10.1371/journal.pcbi.1011939))

③ The study presents the NMR backbone assignments of siderocalin for the mouse model organism, contributing valuable data for structure-based drug discovery, and reveals secondary structure elements consistent with the conserved fold of the lipocalin family. (Biomol NMR Assign: [10.1007/s12104-024-10171-9](https://doi.org/10.1007/s12104-024-10171-9))

### Virus Evolution

③ Using comprehensive genomic data, the authors investigate the evolutionary mechanisms behind viral host jumps, revealing that humans are both sources

and recipients of viral spillover events, with heightened evolution observed in viral lineages involved in host jumps, and genomic targets of natural selection varying across viral families. (Nat Ecol Evol: [10.1038/s41559-024-02353-4](https://doi.org/10.1038/s41559-024-02353-4))

③ VIPERA is a software for analyzing the evolutionary dynamics of SARS-CoV-2 within individual patients through the integration of intra-patient sequence ancestry evaluation and evolutionary trajectory analysis, validated with control datasets and successfully applied to a new case, unveiling population dynamics and signs of adaptive evolution. (Virus Evol: [10.1093/ve/veae018](https://doi.org/10.1093/ve/veae018))

③ AleRax, a software tool for inferring reconciled gene trees and a shared species tree, addresses uncertainty in gene tree estimation and reconciliation by using a probabilistic model of gene duplication, transfer, and loss, and enables analysis of genome-scale datasets with multiple gene families in parallel. (Bioinformatics: [10.1093/bioinformatics/btae162](https://doi.org/10.1093/bioinformatics/btae162))

### Epidemiology

Genomic surveillance has revealed the complex transmission dynamics and lineage shifts of West Nile virus in Europe, with multiple introductions of lineages 1a and 2 contributing to its spread, leading to a shift in lineage prevalence and autochthonous cases in northerly temperate regions, highlighting the importance of expanded genomic surveillance programs to better understand its epidemiology. (One Health: [10.1016/j.onehlt.2023.100664](https://doi.org/10.1016/j.onehlt.2023.100664))

### Phages

③ Phage therapy against vancomycin-resistant *Enterococcus faecium* strains, belonging to clonal complex 17, was enhanced by isolating and evolving virulent phages through a cocktail approach, resulting in a single evolved phage with an extended host range and potential tail fiber genetic region mutations driving its evolution. (Antimicrob Agents Chemother: [10.1128/aac.01439-23](https://doi.org/10.1128/aac.01439-23))

③ Bacteriophages, such as VP882, interact with *Vibrio cholerae* through quorum sensing, where the induction of VP882 leads to the binding of phage transcripts to the RNA chaperone Hfq, influencing the regulation of host-encoded small RNAs and phage replication, highlighting a complex interplay between phage and host defense mechanisms. (Cell Host Microbe: [10.1016/j.chom.2024.03.010](https://doi.org/10.1016/j.chom.2024.03.010))


### Viromics / metagenomics

③ Investigation of DNA methylation patterns in a halophilic consortium involving *Haloferax lucertense* SVX82, *Haloferax* sp. SVX81, and *Candidatus Nanohalococcus occultus* SVXNc reveals unique methylation motifs specific to each member and suggesting potential roles in gene regulation and host-symbiont interactions. (Environ Microbiol Rep: [10.1111/1758-2229.13258](https://doi.org/10.1111/1758-2229.13258))

③ The review examines the evolving understanding of the animal virome, emphasizing the impact of factors such as metagenomic sequencing on virus diversity, composition, and evolution, while highlighting ongoing challenges and future research directions, particularly focusing on how evolutionary events in animal history have influenced the diversity and evolution of associated viruses. (Nat Rev Microbiol: [10.1038/s41579-021-00665-x](https://doi.org/10.1038/s41579-021-00665-x))

## Tools and Resources

### Virus tools website

Tools that have been added to our [collection](#) this month have been newly released or updated. Tools developed by EVBC members are marked .

**Cenote-Taker 3:** Identify sequences containing genes specific to viruses and annotate virus sequences, scaling from individual genome sequences to metagenome assemblies.

**DePP:** Depolymerase Predictor – a machine learning tool facilitating phage depolymerase discovery

**VirusPredictor:** XGBoost software to predict virus-related sequences

**FISHtoFigure:** Analysis of differential RNA transcript and cell type abundance in smFISH data

**Next-RSV-SEQ:** Assembly of RSV genome sequences based on short read data

**PTMPrediction:** Predicting and engineering post-translational modifications using Rosetta

**VIPERA:** Snakemake workflow for SARS-CoV-2 viral intra-patient evolution reporting and analysis

**AleRax:** Species tree – gene tree inference and reconciliation from gene tree distributions

## ViBioM 2024

### Stay tuned

## ViBioM 2024

### International Virus Bioinformatics Meeting

28. – 30. May 2024 | Leuven, Belgium



#### Live Stream:

We are pleased to be able to offer a live stream of ViBioM 2024. The live stream is free of charge, but is only open to people who do not work in the industry. You can register for the live stream [here](#). Please note that this will be a live stream only. We will not be able to offer chat or discussion.

#### Schedule:

The full schedule will be available next week.

#### Job Market at ViBioM 2024:

Are you looking for new opportunities or seeking talented individuals to join your team? During ViBioM 2024, we will be hosting a job market for participants who are looking for a job or who are hiring. More information [here](#).

#### Further information:

Please find all further important details for ViBioM 2024 [here!](#)

## EVBC Special Issues

### Special issue list

We are again running a [Special Issue "Virus Bioinformatics 2024"](#) alongside ViBioM 2024. We encourage you to publish your work in this Special Issue and present it at ViBioM 2024. However, this is not an obligation for publication.


Submission deadline:

31 July 2024

**MDPI grants a discount of 20 % for submissions from EVBC members.**

## 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. EVBC members are involved in events marked .

#### International Conference on Research in Computational Molecular Biology (RECOMB)

29 April – 02 May, 2024 | Cambridge, MA, USA

*Conference theme: Theoretical advances in computational biology and their applications in molecular biology and medicine*

Registration open until:

19 April 2024

#### International Conference on Intelligent Systems for Molecular Biology (ISMB)

12–16 July, 2024 | Montreal, Canada

*This annual meeting of the International Society for Computational Biology (ISCB) is the world's largest conference on the latest international developments in bioinformatics and computational biology.*

Abstract Submission deadline:

19 April 2024


#### European Conference on Computational Biology

16–20 September, 2024 | Turku, Finland

*Conference theme: Data and Algorithms for health and science*

Submission deadline Highlight talks & posters:

23 April 2024

 Lars Juhl Jenssen (Scientific committee)

#### 26th Annual Conference of the European Society for Clinical Virology (ESCV 2024)

18–21 September 2024 | Frankfurt/Main, Germany

*The Conference will be dedicated to various aspects of clinical virology and comprise presentations, symposia, discussions, and various workshops.*

Abstract Submission deadline:

06 May 2024

 Christian Drosten, Isabella Eckerle (keynote speakers)


#### German Conference on Bioinformatics (GCB)

30 September – 02 October, 2024 | Bielefeld, Germany

*Conference theme: all areas of bioinformatics*

Abstract Submission deadline:

06 May 2024

 Bas Dutilh, Caroline Friedel (keynote speakers)