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## Selected Publications by EVBC Members publications on Pubmed All


### RNA Structure & Interaction


 Overview and benchmark of RNA-protein interaction prediction tools that do not require high-throughput data, highlighting their inputs, usability, and outputs for improving RPI research. (Comput Struct Biotechnol J: [10.1016/j.csbj.2024.11.015](https://doi.org/10.1016/j.csbj.2024.11.015))


### Viral Evolution and Phylogenetics


This study examines how the 2009 H1N1 and COVID-19 pandemics disrupted seasonal influenza circulation and evolution in Southeastern Asia (Nat Commun: [10.1038/s41467-025-55840-y](https://doi.org/10.1038/s41467-025-55840-y))

 This study analyzes recombination events among coronavirids, concluding that SARS-CoV-2 likely acquired unique features through recombination with closely related sarbecoviruses (J Virol: [10.1128/jvi.011100-24](https://doi.org/10.1128/jvi.011100-24))


 This study constructs the Orthornavirae structurome to uncover lineage-specific protein domains and explore viral proteomic dark matter. (mBio: [10.1128/mbio.03200-24](https://doi.org/10.1128/mbio.03200-24))

 This study employs continuous phylogeographic inference to analyze the dispersal dynamics of viral lineages, revealing diverse spread patterns influenced by host species and human-mediated movements. (Curr Opin Microbiol: [10.1016/j.mib.2024.102555](https://doi.org/10.1016/j.mib.2024.102555))


 This study investigates the role of Remdesivir's functional groups in its antiviral potency and resistance mechanisms against the SARS-CoV-2 polymerase, offering insights into its multi-faceted mode of action. (Antiviral Res: [10.1016/j.antiviral.2024.105678](https://doi.org/10.1016/j.antiviral.2024.105678))


 This study uses molecular modeling to evaluate the inhibition potential of natural flavonoids against Omicron (B.1.19) mutations in the SARS-CoV-2 spike receptor-binding domain (J Biomol Struct Dyn: [10.1080/07391102.2023.2291165](https://doi.org/10.1080/07391102.2023.2291165))


### Virome and Microbiome Analysis

 This study identifies draft genomes of Pseudomonas phages from bronchoalveolar lavage fluid using a metagenomic pipeline. (Microbiol Resour Anounc: [10.1128/mra.01030-24](https://doi.org/10.1128/mra.01030-24))

 This review highlights the genomic diversity of atypical phages and calls for experimental methods to study their infectivity pathways, with potential biotechnological applications (Curr Opin Microbiol: [10.1016/j.mib.2024.102555](https://doi.org/10.1016/j.mib.2024.102555))

 This review highlights microbial involvement in Alzheimer's disease pathogenesis, emphasizing the gut-brain axis, viral infections, and microbiome-based therapies (Microorganisms: [10.3390/microorganisms13010090](https://doi.org/10.3390/microorganisms13010090))

 This study identifies a novel lineage of anelloviruses with large genomes from dolphins, shedding light on their genomic diversity and evolutionary adaptations. (Microbiome: [10.1038/s41522-024-00320-x](https://doi.org/10.1038/s41522-024-00320-x))

 This study evaluates the effectiveness of different next-generation sequencing technologies for wastewater-based epidemiology, providing insights into public health monitoring. (Environ Sci Technol: [10.1021/acs.est.4c01234](https://doi.org/10.1021/acs.est.4c01234))

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

## viruses *in silico* lecture series

### Donor-Specific Antiviral Immunity Mediated by APOBEC3 enzymes

27. January 2025 | 4 pm CET

online


Diako Ebrahimi, Texas Biomedical Research Institute, USA


## ViBioM 2024

 Register



## 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 .

### ISMB/ECCB conference

20-27 July 2025 | Liverpool, UK

Organized by the International Society for Computational Biology (ISCB), this 33rd annual ISMB meeting, in conjunction with the 24th ECCB, will feature over 500 scientific talks, training workshops, and networking opportunities, both in-person and virtually.

Call for abstract opens:

20 January 2025

### [BC]<sup>2</sup> 2025 | Bioinformatics meets AI: shaping the future of data-driven biology

08-10 September 2025 | Basel, Switzerland

Flagship scientific meeting of the SIB Swiss Institute of Bioinformatics, held every two years, attracting around 500 scientists from academia, industry, and healthcare.

Call for abstracts opens:

07 January 2025


Tutorials & workshops submission deadline:


07 January 2025

## 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 .

 **VILOCA**: Sequencing quality-aware viral haplotype reconstruction and mutation calling for short-read and long-read data

 **Rfam15**: RNA families database in 2025 include viral sequences

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