

Recent Selected Publications by EVBC Members

Measles Virus and Rinderpest Virus Divergence Dated to the Sixth Century BCE. *Science* [10.1126/science.aba9411](https://doi.org/10.1126/science.aba9411)

Hybrid Gene Origination Creates Human-Virus Chimeric Proteins During Infection. *Cell* [10.1016/j.cell.2020.05.035](https://doi.org/10.1016/j.cell.2020.05.035)

Gradients Do Grow on Trees: A Linear-Time $O(N)$ -dimensional Gradient for Statistical Phylogenetics *Mol Biol Evol* [10.1093/molbev/msaa130](https://doi.org/10.1093/molbev/msaa130)

Identification of Umbre Orthobunyavirus as a Novel Zoonotic Virus Responsible for Lethal Encephalitis in 2 French Patients with Hypogammaglobulinemia. *Clin Infect Dis* [10.1093/cid/ciaa308](https://doi.org/10.1093/cid/ciaa308)

Predicting host taxonomic information from viral genomes: A comparison of feature representations. *PLoS Comput Biol* [10.1371/journal.pcbi.1007894](https://doi.org/10.1371/journal.pcbi.1007894)

Novel enteric viruses in fatal enteritis of grey squirrels. *J Gen Virol* [10.1099/jgv.0.001431](https://doi.org/10.1099/jgv.0.001431)

Reorganizing the Family *Parvoviridae*: A Revised Taxonomy Independent of the Canonical Approach Based on Host Association. *Arch Virol* [10.1007/s00705-020-04632-4](https://doi.org/10.1007/s00705-020-04632-4)

Reviews

Pangenome Graphs *Annu Rev Genomics Hum Genet* [10.1146/annurev-genom-120219-080406](https://doi.org/10.1146/annurev-genom-120219-080406)

Quality Control of Next-Generation Sequencing-Based HIV-1 Drug Resistance Data in Clinical Laboratory Information Systems Framework. *Viruses* [10.3390/v12060645](https://doi.org/10.3390/v12060645)

Hepatitis A Infections From Food. *J Appl Microbiol* [10.1111/jam.14727](https://doi.org/10.1111/jam.14727)

Preprints

Ancient viral genomes reveal introduction of HBV and B19V to Mexico during the transatlantic slave trade. *bioRxiv* [10.1101/2020.06.05.137083](https://doi.org/10.1101/2020.06.05.137083)

V-pipe: a computational pipeline for assessing viral genetic diversity from high-throughput sequencing data. *bioRxiv* [10.1101/2020.06.09.142919](https://doi.org/10.1101/2020.06.09.142919)

We are happy to announce your research in our newsletter. Send your publications to evbc@uni-jena.de. For more frequent updates on publications, please follow us on Twitter [EVirusBioinfC](https://twitter.com/EVirusBioinfC) or check our [publications website](#).

Tools and Resources

We are curating a list of [useful tools in virus bioinformatics](#). Please let us know about the tools you have developed to advance the field.

- **V-Pipe** for automated end-to-end analyses of raw sequencing reads from viral high-throughput sequencing studies.
- **ELM resource** for annotation and detection of eukaryotic linear motifs (ELMs) by providing both a repository of annotated motif data and an exploratory tool for motif prediction.
- The **IUPred2A server** is a biophysics-based prediction to identify intrinsically disordered protein regions (IDRs) and binding sites inside IDRs.
- **Persephone** is a multi-genome browser, that allows to align several virus sequences and see the result of sequence comparison in real time.

News and Announcements

RNA Bioinformatics Lab at FSU Jena is looking for a molecular biology PostDoc experienced in virus research to be heading the wetlab group, and for a science technician. For more details please contact rna@uni-jena.de.

The Max Planck Institute for Evolutionary Anthropology is offering a Post-Doctoral Position in Viral Genomics with a focus on the reconstruction of ancient viral genomes from archaeological contexts. The postdoc will work in the framework of the ERC project CoDisEASE. Please submit your application to the [application portal](#).

AllGenetics is looking for research teams which might be interested in their services. AllGenetics is one of the most highly regarded laboratories for those outsourcing genomics-related projects.

News related to SARS-CoV-2 are covered in our [Special Issue Newsletter](#).