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## Recent Selected Publications by EVBC Members

Gut Phage Database: phage mining in the cave of wonders. *Signal Transduct Target Ther* [10.1038/s41392-021-00615-2](#)

Analysis of Zika virus capsid-Aedes aegypti mosquito interactome reveals pro-viral host factors critical for establishing infection. *Nat Commun* [10.1038/s41467-021-22966-8](#)

Ecology and molecular targets of hypermutation in the global microbiome. *Nat Commun* [10.1038/s41467-021-23402-7](#)

Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. *Commun Biol* [10.1038/s42003-021-02112-2](#)

Evaluating assembly and variant calling software for strain-resolved analysis of large DNA viruses. *Brief Bioinform* [10.1093/bib/bbaa123](#)

Stability of the human gut virome and effect of gluten-free diet. *Cell Rep* [10.1016/j.celrep.2021.109132](#)

Blood Virosphere in Febrile Tanzanian Children. *Emerg Microbes Infect* [10.1080/22221751.2021.1925161](#)

Viromics of extant insect orders unveil the evolution of the flavi-like superfamily. *Virus Evol* [10.1093/ve/veab030](#)

Phylogeographic analysis of foot-and-mouth disease virus serotype O dispersal and associated drivers in East Africa. *Mol Ecol* [10.1111/mec.15991](#)

ITN-VIROINF: Understanding (Harmful) Virus-Host Interactions by Linking Virology and Bioinformatics. *Viruses* [10.3390/v13050766](#)

DOE JGI Metagenome Workflow. *mSystems* [10.1128/mSystems.00804-20](#)

### Reviews

Extreme dimensions - how big (or small) can tailed phages be? *Nat Rev Microbiol* [10.1038/s41579-021-00574-z](#)

New technologies for developing phage-based tools to manipulate the human microbiome. *Trends Microbiol* [10.1016/j.tim.2021.04.007](#)

A Primer on the Analysis of High-Throughput Sequencing Data for Detection of Plant Viruses. *Microorganisms* [10.3390/microorganisms9040841](#)

Rational Design of Profile Hidden Markov Models for Viral Classification and Discovery. *Exon Publications Bioinformatics* [10.36255/exonpublications.bioinformatics.2021.ch9](#)

### Preprints

Archival influenza virus genomes from Europe reveal genomic and phenotypic variability during the 1918 pandemic. *bioRxiv* [10.1101/2021.05.14.444134](#)

Diversity, taxonomy and evolution of archaeal viruses of the class Caudoviricetes. *bioRxiv* [10.1101/2021.05.26.445827](#)

Benchmark of thirteen bioinformatic pipelines for metagenomic virus diagnostics using datasets from clinical samples. *medRxiv* [10.1101/2021.05.04.21256618](#)

Analysis of viromes and microbiomes from pig fecal samples reveals that phages and prophages are not vectors of antibiotic resistance genes. *bioRxiv* [10.1101/2021.05.20.444921](#)

OnTheFly2.0: a text-mining web application for automated biomedical entity recognition, document annotation, network and functional enrichment analysis. *bioRxiv* [10.1101/2021.05.14.444150](#)

 [EVBC publications website](#)

## Tools and Resources

**DOE JGI Metagenome Workflow:** metagenome data processing.

**E-Finder:** find multigene elements using profile HMMs.

**Gut Phage Database:** large-scale catalog of phage genomes.

**HMM-prospector:** surveying genomic and metagenomic data.

**MinionDB:** profile HMMs from viral protein sequences.

**OnTheFly<sup>2.0</sup>:** text-mining for automated biomedical entity recognition, network and functional enrichment analysis.

**QuasiModo:** Quasispecies Metric determination on omics.

**TABAJARA:** rational design of profile Hidden Markov Models for viral classification and discovery.

 [Virus tools website](#)

## viruses in silico | EVBC Lectures

**Viral reference database as a critical factor for clinical metagenomics: a review using Virosaurus as an example.**

14. June 2021 | 04–05pm CEST

[online](#)

*Dr. Philippe Le Mercier, SIB, Switzerland*

Challenges and pitfalls of viral genomics: why is it complex to represent viral diversity in a viral reference database. There are more than 10 datasets available, all developed from different viewpoints: from simple queries on GenBank to datasets processed using all public sequences. P. Le Mercier will discuss the process used to generate Virosaurus: a database representing all publicly available vertebrate/plant/fungal viral genomes; and the particular case of segmented viruses.

 [Register](#)

## EVBC Special Issues

**Applied Evolutionary Virology and Applications.**

SI in *Life* (guest edited by E. G. Kostaki and D. Paraskevis) addressing COVID-19-related diseases and the healthcare burden, building on information of the pandemic's prevalence and incidence.

Deadline:

[22 October 2021](#)

 [More special issues by EVBC members](#)

## Vacancies

**PostDoc in virus bioinformatics – NIB Slovenia**

Work in a dynamic and internationally active research group using state-of-the-art molecular biology techniques for detection, surveillance and studies of biology, diversity and evolution of viruses (from plant to human pathogens, including SARS-CoV-2).

Application deadline:

[17 June 2021](#)

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