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Selected Publications by EVBC Members

[All publications on Pubmed](#)

Short- and long-range interactions in the HIV-1 5' UTR regulate genome dimerization and packaging. (Nat Struct Mol Biol: [10.1038/s41594-022-00746-2](#))

Archival influenza virus genomes from Europe reveal genomic variability during the 1918 pandemic. (Nat Commun: [10.1038/s41467-022-29614-9](#))

A World of Viruses Nested within Parasites: Unraveling Viral Diversity within Parasitic Flatworms. (Microbiol Spectr: [10.1128/spectrum.00138-22](#))

Virus-Host Interactions and Genetic Diversity of Antarctic Sea Ice Bacteriophages. (mBio: [10.1128/mbio.00651-22](#))

Genome-wide diversity of Zika virus: Exploring spatio-temporal dynamics to guide a new nomenclature proposal. (Virus Evol: [10.1093/ve/veac029](#))

Making genomic surveillance deliver: A lineage classification and nomenclature system to inform rabies elimination. (PLoS Pathog: [10.1371/journal.ppat.1010023](#))

Protection of other planets: spread of host-associated phages studied in extraterrestrial analogue Antarctica to prevent future contamination of celestial bodies with alien biomolecules or life forms. (Viruses: [10.1128/aem.00315-22](#))

Molecular epidemiology screening identified the largest population of confirmed HIV-1 superinfections in the Swiss HIV Cohort Study. (J Infect Dis: [10.1093/infdis/jiac166](#))

Metasearch tool for Defective Viral Genomes with gradient boosting classifier machine learning algorithm to reduce the number of false-positive events. (Viruses: [10.3390/v14051114](#))

Genotype-based adeno-associated virus classification below the species level based on the *rep* gene. (Viruses: [10.3390/v14051038](#))

DcHEV is a novel zoonotic pathogen detected in domestic and imported Dromedary camels. (Sci Rep: [10.1038/s41598-022-11208-6](#))

Monitoring human viral pathogens in treated wastewater: crAssphage is a poor marker for viral occurrence and viral integrity/infectivity. (Front Microbiol: [10.3389/fmicb.2022.836193](#))

Genomic, epidemiological and demographic characteristic of predominately urban transmission of dengue virus serotype 2 in Angola. (PLoS Negl Trop Dis: [10.1371/journal.pntd.0010255](#))

Genetic variability in minor capsid protein (L2 gene) of human papillomavirus type 16. (Med Microbiol Immunol: [10.1007/s00430-022-00739-4](#))

Epidemiology of a major honey bee pathogen, deformed wing virus: potential worldwide replacement of genotype A by genotype B. (Int J Parasitol Parasites Wildl: [10.1016/j.ijppaw.2022.04.013](#))

Rapid high-throughput compatible label-free virus particle quantification method based on time-resolved luminescence. (Anal Bioanal Chem: [10.1007/s00216-022-04104-5](#))

Inference for a spatio-temporal model with partial spatial data: African horse sickness virus in Morocco. (Epidemics: [10.1016/j.epidem.2022.100566](#))

The Virome of Healthy Honey Bee Colonies: Ubiquitous Occurrence of Known and New Viruses in Bee Populations. (mSystems: [10.1128/mSystems.00072-22](#))

Reviews / Commentaries / Editorials

Plant-derived natural compound thapsigargin represents a new prototype of compounds with multimodal host-directed antiviral activity. (Trends Pharmacol Sci: [10.1016/j.tips.2022.04.004](#))

Nanopore-Based Detection of Viral RNA Modifications. (mBio: [10.1128/mbio.03702-21](#))

An overview of dinucleotide and codon usage in all viruses. (Arch Virol: [10.1007/s00705-022-05454-2](#))

Preprints

HIV-phyloTSI: Subtype-independent estimation of time since HIV-1 infection for cross-sectional measures of population incidence using deep sequence data. (medRxiv: [10.1101/2022.05.15.22275117](#))

Tools and Resources

[Virus tools website](#)

DVGfinder: Defective Viral Genome finder

HIV-phyloTSI: Estimate time since infection (TSI) from HIV deep-sequencing data

RABV-GLUE: A Sequence Data Resource for Rabies Virus

Vacancies

[Find a job](#)

Bioinformatics PhD student in 'Virus diversity and evolution in natural plant ecosystems' at the Evolutionary (Meta-)genomics group in the Bioinformatics Group at Wageningen University.

Application deadline: **6 June 2022**

Junior research group leader on mechanistic modeling of microbial interactions at FSU Jena.

Application deadline: **15 June 2022**

Postdoctoral Fellow in the new BMBF-funded research group in Computational Virology at Ruhr University Bochum.

Application deadline: **30 June 2022**

PostDoc for the integration of bacterial and viral metagenomics datasets in the context of liver diseases at KU Leuven.

Application deadline: **02 August 2022**

Postdoc opportunity at Ohio State to develop and/or apply viral ecogenomic tools in soils, oceans or humans.

Send CV and brief statement of interest to [Matt Sullivan](#).

ViBioM 2022

Conference Report: The International Virus Bioinformatics Meeting 2022 (Viruses: [10.3390/v14050973](#))

viruses *in silico* lecture series

[Register](#)

Identifying and prioritising poorly-characterised viruses with zoonotic potential

27 June 2022 | 04–05 pm CEST

online

Nardus Mollentze, MRC-University of Glasgow CVR, UK

How virus genomes – often the first and only data available for newly-discovered viruses – can be used to identify and prioritise potential human-infecting viruses, and how host phylogeny can be used to optimise surveillance by identifying other potential hosts.

EVBC Workshops

[Register](#)

A practical introduction to software testing in Python

9./10. June 2022 | 9:30am–12:30pm CEST

online

Terry Jones, Charité – Universitätsmedizin Berlin, Germany

ECR Viromics Webinar Series

[Register](#)

Ecology and evolutionary origins of the Global Ocean RNA virome

08 Jun 2022 | 04-05 pm CEST

online

Ahmed Zayed, Ohio State University, USA

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Member Profile: Florian Erhard



Name: Florian Erhard

Position: Professor for Computational Systems Virology, Institute for Virology and Immunobiology, University of Würzburg

Research focus: Herpesviruses, gene regulation in infected cell, cryptic MHC-I epitopes



What do you love about viruses?

Viruses are experts in molecular cell biology and they can teach us about it.

On what topic could you give a 30-minute presentation without any preparation?

Statistical methods and applications of metabolic RNA labeling.

What is your favourite way to spend a day off?

With my family.

What are you currently learning?

To play the 3rd movement of Beethoven's Moonlight Sonata on the piano.

If you could create a new invention, what would it be?

A device that can quantitatively and accurately measure each biomolecule in many single cells over time. Or an iron man suit.

What do people think about you that isn't true?

The more computational persons: That I "only" do applied research to pursue biological questions. The more wet-lab biologists: That my research is focussed "only" on computational approaches.

Which scientific topic (outside of your field of research) do you think should have more scientific attention?

Emerging viruses beyond SARS-CoV-2.

If you were completely free to choose a scientific topic to work on, which would it be?

Viruses :)

If you had the option to advise a younger version of yourself, what would that be?

As a student: Visit more lectures on immunology and cell biology. And buy Amazon stocks.

Member Profile: Dimitri Boeckaerts



Name: Dimitri Boeckaerts

Position: PhD researcher at Ghent University

Research focus: phage-host interactions in a computational context with the goal to develop machine learning models to predict these interactions



What do you love about viruses?

I love the fact that viruses can be so simple, and yet are capable of very complex interactions.

Who is your favourite scientist and why?

Leonardo Da Vinci for his eternal curiosity and perspective on bringing together science and art.

On what topic could you give a 30-minute presentation without any preparation?

Trampolining

What is your favourite way to spend a day off?

Simply enjoying a relaxing Sunday afternoon with good weather and friends or family!

What is the most interesting question or challenge in science that is still unanswered?

Do aliens exist?!

What is the coolest thing about your research?

The coolest thing about my research is that it is situated at the intersection of Bioinformatics, Artificial intelligence and Synthetic biology. Three fields I'm widely interested in.

If you had the option to advise a younger version of yourself, what would that be?

Don't ever be afraid to communicate openly & honestly.