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Selected Publications by EVBC Members

[All publications on Pubmed](#)

Three families of Asgard archaeal viruses identified in metagenome-assembled genomes from deep-sea sediments of the basin off the Shimokita Peninsula. (Nat Microbiol: [10.1038/s41564-022-01144-6](https://doi.org/10.1038/s41564-022-01144-6))

High-resolution description of the HIV-1 epidemic in Oryol Oblast, Russia. (Virus Evol: [10.1093/ve/veac044](https://doi.org/10.1093/ve/veac044))

Accommodating sampling location uncertainty in continuous phylogeography: when genomic sequences are associated with a geographic area of sampling instead of precise coordinates. (Virus Evol: [10.1093/ve/veac041](https://doi.org/10.1093/ve/veac041))

Evolutionary traits of Tick-borne encephalitis virus: Pervasive non-coding RNA structure conservation and molecular epidemiology. (Virus Evol: [10.1093/ve/veac051](https://doi.org/10.1093/ve/veac051))

Variability in host defenses determines the rates and extent of virus evolution. (Virus Evol: [10.1093/ve/veac059](https://doi.org/10.1093/ve/veac059))

Diversity of novel archaeal viruses infecting methanogens discovered through coupling of stable isotope probing and metagenomics. (Environ Microbiol: [10.1111/1462-2920.16120](https://doi.org/10.1111/1462-2920.16120))

Reviews / Commentaries / Editorials

Monkeypox genomic surveillance will challenge lessons learned from SARS-CoV-2. (Lancet: [10.1016/S0140-6736\(22\)01106-0](https://doi.org/10.1016/S0140-6736(22)01106-0))

A simple functional logic to explain virus macroevolution that appears to define the course of virus evolution. (Cell Host Microbe: [10.1016/j.chom.2022.06.008](https://doi.org/10.1016/j.chom.2022.06.008))

The use of NGS technologies on HIV drug resistance testing will allow unprecedented insights into genomic structures of virus populations. (Curr Opin HIV AIDS: [10.1097/COH.0000000000000737](https://doi.org/10.1097/COH.0000000000000737))

Are pigs overestimated as a source of zoonotic influenza viruses? (Porcine Health Manag: [10.1186/s40813-022-00274-x](https://doi.org/10.1186/s40813-022-00274-x))

Different virus, same mistakes: Why (re-) emerging viruses are one step ahead of us. (Innovation: [10.1016/j.xinn.2022.100273](https://doi.org/10.1016/j.xinn.2022.100273))

Preprints

A vast world of viroid-like circular RNAs revealed by mining metatranscriptomes. (bioRxiv: [10.1101/2022.07.19.500677](https://doi.org/10.1101/2022.07.19.500677))

Replidex uses Naive Bayes classifier to identify three most common phage replication cycles from metagenomics data. (bioRxiv: [10.1101/2022.07.18.500415](https://doi.org/10.1101/2022.07.18.500415))

SARS-CoV-2

[Pubmed](#)

SARS-CoV-2 Omicron is an immune escape variant with an altered cell entry pathway. (Nat Microbiol: [10.1038/s41564-022-01143-7](https://doi.org/10.1038/s41564-022-01143-7))

Early detection and surveillance of SARS-CoV-2 genomic variants in wastewater using COJAC. (Nat Microbiol: [10.1038/s41564-022-01185-x](https://doi.org/10.1038/s41564-022-01185-x))

Neutralization capacity of antibodies elicited through homologous or heterologous infection or vaccination against SARS-CoV-2 VOCs. (Nat Commun: [10.1038/s41467-022-31556-1](https://doi.org/10.1038/s41467-022-31556-1))

Monitoring the evolution of SARS-CoV-2 on a Spanish university campus through wastewater analysis: A pilot project for the reopening strategy. (Sci Total Environ: [10.1016/j.scitotenv.2022.157370](https://doi.org/10.1016/j.scitotenv.2022.157370))

CovRadar: Continuously tracking and filtering SARS-CoV-2 mutations for genomic surveillance. (Bioinformatics: [10.1093/bioinformatics/btac411](https://doi.org/10.1093/bioinformatics/btac411))

Conserved recombination patterns across coronavirus subgenera. (Virus Evol: [10.1093/ve/veac054](https://doi.org/10.1093/ve/veac054))

Upcoming Events

[Subscribe to Calendar](#)

Genomes of Microbiomes

15–16 September 2022 | Birmingham, UK

Registration deadline: **04 August 2022**

EVBC members involved: Evelien Adriaenssens (organising committee, speaker), Manja Marz (speaker)

German Conference on Bioinformatics

06–08 September 2022 | Halle, Germany

Poster submission deadline: **07 August 2022**

EVBC members involved: Ivo Hofacker (keynote speaker), Muriel Ritsch (speaker), Sebastian Krautwurst (speaker)

Intl. Symposium on Bioinformatics Research & Applications

14–17 November 2022 | Haifa, Israel

Submission deadline: **08 August 2022**

VEGA, Viral EcoGenomics & Applications

06–07 October 2022 | Berkeley, USA

Registration and abstract deadline: **31 August 2022**

EVBC members involved: Simon Roux (organizer)

Annual Conference of the European Society for Clinical Virology

07–10 September 2022 | Manchester, UK

Registration deadline: **02 September 2022**

viruses *in silico* lecture series

[Register](#)

RNA phages: more than meets the eye?

22 August 2022 | 06–07 pm CEST / 09–10 am PDT

online

Simon Roux, DOE Joint Genome Institute, USA

Please be aware of the deviating time!

This global RNA virosphere analysis unveiled an unprecedented and so-far-uncharacterized richness of RNA phages, highlighted key environments such as soil and hot spring biofilms where a large portion of this novel RNA phage diversity resides, and indicates that RNA phages must be considered when investigating phage impact on microbiomes.

ECR Viromics Webinar Series

[Register](#)

Viral diversity in the ocean

10 August 2022 | 04-05 pm CEST

online

Elaine Luo, Woods Hole Oceanographic Institution, USA

Tools and Resources

[Virus tools website](#)

COJAC: CoOccurrence adJusted Analysis and Calling.

CovRadar: Tracking and filtering SARS-CoV-2 mutations.

Replidex: Replication Cycle Detector for Phages.

Member Profile: Robert Paxton



Name: Robert Paxton

Position: Professor for general zoology at Martin Luther University Halle-Wittenberg

Research focus: evolution and epidemiology of viruses in bees



Photo by Markus Deutsch, MLU

What do you love about viruses?

Their evolutionary dynamism

Who is your favourite scientist and why?

Charles Darwin, for his wisdom, deep insight and cautious interpretation of the world

On what topic could you give a 30-min talk without preparation?

The decline of bees and the role therein of viruses

What is your favourite way to spend a day off?

Walking in the mountains

What are you currently learning?

Bayesian statistical inference

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

A time machine

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

The one I'm working on right now

What is the coolest thing about your research?

Having the opportunity to interact with lots of interesting folk

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

I'm mad about bees

What was your most surprising scientific finding?

That viral sequences extracted from two different hosts at the same field site were identical i.e. pathogen sharing among diverse host species

What was your biggest achievement / what your biggest failure?

Achievements build one on the other such that each is diminished by the next advance. Not to learn from a failure.

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

AI

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

Write more papers

Member Profile: Arli Aditya Parikesit



Name: Arli Aditya Parikesit

Position: Associate Professor in Bioinformatics Program

Research focus: Structural Bioinformatics and Proteomics



What do you love about viruses?

Viruses are enigmatic. Scientist made many predictive models on them, and almost all of them proven to be incorrect after a while.

Who is your favourite scientist and why?

Rosalind Franklin. She played role also in coal chemistry field development, not only in structural biology.

On what topic could you give a 30-min talk without preparation?

Rational Drug Design

What is your favourite way to spend a day off?

Watching video streaming

What are you currently learning?

Re-learning quantum chemistry, so I can use quantum based modeling

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

Useful bioinformatics software in quantum computer

What is the coolest thing about your research?

Unpredictable outcomes are always possible

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

Some people said that Bioinformatics is useless, I find that extremely offensive. Ofcourse it is beneficial for many things. They think that freaky statement did not offend me, but actually it is.

What was your most surprising scientific finding?

Some people knew it, but RNAs are somehow acting in accordance to the chaos theory in maths

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

Public health promotion. Why COVID getting out of control is because many doesn't care about health protocok

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

How to use quantum mechanics to predict the behavior of viruses, especially the RNA ones

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

Enjoy your self, have fun, and watch good movies :)