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Selected Publications by EVBC Members

 [All publications on Pubmed](#)

Introducing the Bacterial and Viral Bioinformatics Resource Center (BV-BRC): a resource combining PATRIC, IRD and ViPR. (Nucleic Acids Res: [10.1093/nar/gkac1003](#))

IMG/VR provides access to the largest collection of viral sequences obtained from (meta)genomes, along with functional annotation and rich metadata. (Nucleic Acids Res: [10.1093/nar/gkac1037](#))

Leveraging the epitope information available in the Immune Epitope Database on vaccinia-based vaccines to predict potential mpox virus targets recognized by CD4+ and CD8+ T cell responses. (Cell Host Microbe: [10.1016/j.chom.2022.11.003](#))

Generation of an Attenuated Chimeric Bat Influenza A Virus Live-Vaccine Prototype. (Microbiol Spectr: [10.1128/spectrum.01424-22](#))

What the Phage: an easy-to-use and parallel multitool approach for phage prediction combined with an annotation and classification downstream strategy. (GigaScience: [10.1093/gigascience/giac110](#))

Defining the characteristics of interferon-alpha-stimulated human genes: insight from expression data and machine learning. (GigaScience: [10.1093/gigascience/giac103](#))

Utility of viral metagenomics in exploring the archaeal virome and new insights into the diversity, distribution and evolution of marine archaeal viruses. (Environ Microbiol: [10.1111/1462-2920.16287](#))

Assessing the dynamics and impact of a host antiviral defense mechanism: cytidine deaminase activity leading to C to U editing in anelloviruses-on the stability of the anellome. (mSphere: [10.1128/msphere.00506-22](#))

Two murine cytomegalovirus microRNAs target the major viral immediate early 3 gene. (J Gen Virol: [10.1099/jgv.0.001804](#))

Early Genomic Surveillance and Phylogeographic Analysis of Getah Virus, a Reemerging Arbovirus, in Livestock in China. (J Virol: [10.1128/jvi.01091-22](#))

A viral metagenomic protocol for nanopore sequencing of group A rotavirus that

generates both high quality and accurate RVA WGS extracted from faecal samples. (J Virol Methods: [10.1016/j.jviromet.2022.114664](#))

Reviews / Commentaries / Editorials

Changes in the gut virome through life, health, and disease, as well as interactions between the virome, the microbiome, and the human host and their contribution to gut disease and disease of distant organs. (FEMS Microbiol Rev: [10.1093/femsre/fuac027](#))

Recent advances in 'soil viromics', that is, virus-focused metagenome and meta-transcriptome analyses that offer unprecedented windows into the soil virosphere. (Trends Microbiol: [10.1016/j.tim.2022.05.003](#))

Ecological and functional roles of bacteriophages in contrasting environments: marine, terrestrial and human gut. (Curr Opin Microbiol: [10.1016/j.mib.2022.102229](#))

Recent findings about signals able to trigger prophage induction in the gut. (Mol Microbiol: [10.1111/mmi.14983](#))

Preprints

Recombination-aware phylogenetic analysis sheds light on the evolutionary origin of SARS-CoV-2. (Research Square: [10.21203/rs.3.rs-2189993/v1](#))

Convergent evolution of the SARS-CoV-2 Omicron subvariants leading to the emergence of BQ.1.1 variant. (bioRxiv: [10.1101/2022.12.05.519085](#))

The mutation process of SARS-CoV-2 is itself a dynamic variable during SARS-CoV-2 evolution, and suggests that human SARS-CoV-2 may be trending towards a mutation spectrum more similar to that of other animal sarbecoviruses. (bioRxiv: [10.1101/2022.11.19.517207](#))

Highly diverse and unknown viruses may enhance Antarctic endoliths' adaptability. (bioRxiv: [10.1101/2022.12.02.518905](#))

Unraveling the viral dark matter of the rumen microbiome with a new global virome database. (bioRxiv: [10.1101/2022.11.30.518432](#))

Spatial scale influences taxon conservation in the eukaryotic virome of a mosquito. (bioRxiv: [10.1101/2022.11.23.517782](#))

Publication shortcuts: If you would like us to add a shortcut to a specific virus (family) or topic, drop us an [email](#).

SARS-CoV-2


influenza






HIV

monkeypox

Tools and Resources

 [Virus tools website](#)

Tools that have been added to our [collection](#) this month, or have now been published in a journal. Tools developed by EVBC members are marked .

-  **BV-BRC:** Bacterial and Viral Bioinformatics Resource Center
-  **Gsub:** easy annotation and submission of virus contigs.
-  **IMG/VR:** largest collection of viral sequences obtained from (meta)genomes.
-  **ISGPRES:** Tools for predicting interferon stimulated human genes.
-  **What the Phage:** a scalable workflow for the identification and analysis of phage sequences.

ViBioM 2023

 [Save the date](#)

We are happy to announce the RdRp Summit on the 22–23 May 2023 as a satellite meeting of ViBioM 2023.

The RdRp Summit is the first international, discussion-centric conference dedicated to improving interoperability in the fields of RNA virus discovery and characterization.

The RdRp Summit will take place in Valencia in the days leading to ViBioM 2023 at the same venue. It will also include an online video format to accommodate active participation from remote attendees.

If you have any questions, ideas or just want to get in touch, feel free to contact the [organizers](#).

Retrospective: Microbial Genomics workshop

The Microbial Genomics workshop was truly excellent, especially in the face of all the adversity created by the ongoing invasion by Russia. As one can imagine, it made things incredibly difficult for the organizers and for the participants. The workshop received a lot of interest from Ukrainian scientists, but also from other participants in Georgia, Poland, and Egypt - reaching 300 registered participants by the registration deadline - a clear success for a first edition. Because of the war, the organizers had early on decided to hold the workshop online via Zoom, this allowed them to invite international lecturers that would not have been able to travel to Ukraine, but especially allowed participants in Ukraine to participate remotely and avoid unnecessary and risky travels. Unfortunately, around the time of the workshop, Russia had started to systematically bomb the electrical infrastructure of the country, creating blackouts and preventing many participants to join online. The organizers anticipated this issue and asked all the lecturers a few days before the workshop if they could record the online lectures to make them made available later to those who could not join. In total, between 70 and 100 people were able to join live and interact with us during the lectures, while many more will now have access to the recorded material.

The content covered included all items from microbial genomics, from the sequencing technologies to comparative genomics. Myself, I covered the topics of post-sequencing data analysis and genome assembly, focusing on aspects of quality control of these steps. The theoretical sessions were followed by hands-on practical exercises from the BV-BRC (formerly known as PATRIC) coordinated by Rebecca Wattam.

All credits to the fantastic organizers of this workshop: Marichka Zlatohorska, Natalia Shenderovska, Nadiia Korotaieva, and Yuliia Faidiuk. They strove to provide an excellent scientific workshop and a break from all the darkness created by this ongoing tragedy. Together, they managed to deliver on their original objective, which was to provide a comprehensive introduction and practical training of microbial genomics to the scientists of Ukraine and beyond.

– by Cédric Lood –

Vacancies

 Find a job

Joint PostDoc position at FSU Jena, Germany, and EMBL/EBI, Hinxton, UK. This project is about virus alignments with secondary structures and covariance models for Rfam. The position will be 1 year in Jena and 2 years in Hinxton. If you are interested, you will have to apply for an EIPOD-LinC fellowship together with Manja Marz (FSU Jena) and Blake Sweeney (EMBL-EBI). Please contact [Manja](#) to learn how to proceed.

Call deadline:

18 January 2023

Professorship Virology at Medical University of Innsbruck, Austria. The Medical University of Innsbruck invites applications for the position of a University Professor of Virology.

Application deadline:

21 December 2022

Assistant Professor (tenure-track) in Viral Phylodynamics at University Stockholm, Sweden. within the SciLifeLab Fellows program, a career program aiming at strengthening Swedish research in Molecular Biosciences.

Application deadline:

28 December 2022

Postdoctoral computational biologist / bioinformatician at Hannover Medical School. To further expand the bioinformatics infrastructure available within the RESIST cluster, we are seeking to hire a postdoctoral computational biologist or bioinformatician who can provide informatics and data analysis support to ongoing projects that focus on understanding host-pathogen interactions in the context of infection susceptibility.

Application deadline:

ASAP

As the holiday season is upon us, we would like to thank all of you for your continued support and commitment to the EVBC and for advancing the field. The team at EVBC wishes you a peaceful and restful Christmas time. We look forward to new ideas, advanced bioinformatics tools to be applied in virology, and many fruitful scientific cooperations in the year to come.



Member Profile: Neta Zuckerman



Name: Neta Zuckerman

Position: Head of the Bioinformatics and Genomics National Center in Israel's Ministry of Health National Virology Laboratory

Research focus: Clinical and environmental surveillance of viruses within the interest of public health in Israel



What do you love about viruses?

It always fascinated me how a thing so small and invisible can cause so much trouble.

Who is your favourite scientist and why?

In the world of viruses it is Emma Hodcroft, who stepped up to the challenge in the very beginning of the COVID pandemic, and came up with coherent SARS-CoV-2 variant nomenclature and tools for the world to use.

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

SARS-CoV-2 variant surveillance in Israel from 2020 to today.

What is your favourite way to spend a day off?

At the beach

What are you currently learning?

Following one poliovirus outbreak and into the second, I'm currently learning the "insides" of poliovirus-related global regulations, mutation counting and molecular clocks.

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

Definitely teleportation!

What is the coolest thing about your research?

The coolest thing about my research is that it has an impact on public health in Israel.

For which project idea are you still looking for a cooperation partner?

I'm always looking for collaborations, any project that has to do with viruses of public health interest is great.

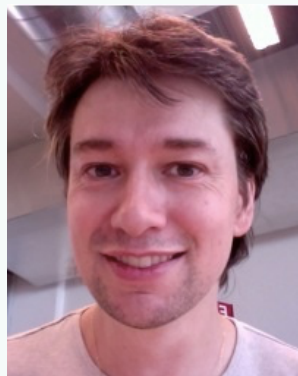
If you were completely free to choose a scientific topic to work on, which would it be?

exactly what I'm doing now :)

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

Do only what makes you excited when you wake up every morning.

Member Profile: Philippe Le Mercier



Name: Philippe Le Mercier

Position: SIB resource manager

Research focus: Virus genome and proteome annotation



What do you love about viruses?

They don't respect the rules

Who is your favourite scientist and why?

I got too many and can't choose one!

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

The taste of truth.

What is your favourite way to spend a day off?

painting

What are you currently learning?

The truth.

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

A microscope strong enough to see the color of viruses!

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

Unifying quantum mechanics with Einstein's general relativity

What is the coolest thing about your research?

Knowledge is always evolving, dogmas are shaken and new wonder continues to be discovered

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

quantum biochemistry

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

What's wrong with bats? They harbor too many viruses, it's unreasonable.