

Send us your news to [evbc@uni-jena.de](mailto:evbc@uni-jena.de).

For more frequent updates, please follow us on Twitter [EVirusBioinfC](https://twitter.com/EVirusBioinfC).

## Selected Publications by EVBC Members

[All publications on Pubmed](#)

Highly virulent variant of subtype-B HIV-1 in the Netherlands arose in the 1990s from de novo mutation, not recombination, with increased transmissibility and an unfamiliar molecular mechanism of virulence. (Science: [10.1126/science.abk1688](https://doi.org/10.1126/science.abk1688))

Computational approach to predict the capsid architecture (T-number) of tailed phages using the sequence of a single gene: the major capsid protein. (Comput Struct Biotechnol J: [10.1016/j.csbj.2021.12.032](https://doi.org/10.1016/j.csbj.2021.12.032))

Recent and ongoing efforts to create the necessary taxonomic framework to accommodate the expected flood of novel viruses belonging to the order *Jingchuvirales*. (Appl Environ Microbiol: [10.1128/AEM.01954-21](https://doi.org/10.1128/AEM.01954-21))

New statistical test to detect selection in the HIV-1 genome during transmission based on comparing the transmitter and recipient virus population and accounting for the transmission bottleneck. (Viruses: [10.3390/v14020406](https://doi.org/10.3390/v14020406))

Comparative genomics approaches to explore the genetic diversity of the Acinetobacter phages propose the creation of five new subfami-

lies and suggest a reorganisation of the genus Obolenskvirus. (Viruses: [10.3390/v14020181](https://doi.org/10.3390/v14020181))

Numerical approaches for the rapid analysis of prophylactic efficacy against HIV with arbitrary drug-dosing schemes. (PLoS Comput Biol: [10.1371/journal.pcbi.1009295](https://doi.org/10.1371/journal.pcbi.1009295))

Data-driven approach for the analysis and prediction of the HIV-1 interacting proteins (VIPs) with a focus on the directionality of the interaction: host-dependency versus antiviral factors. (PLoS Comput Biol: [10.1371/journal.pcbi.1009720](https://doi.org/10.1371/journal.pcbi.1009720))

### Preprints

A five-fold expansion of the global RNA virome reveals multiple new clades of RNA bacteriophages. (bioRxiv: [10.1101/2022.02.15.480533](https://doi.org/10.1101/2022.02.15.480533))

Tendency to rapidly revert to a consensus-like state can explain much of the time dependence of evolutionary rate estimates in HIV-1. (bioRxiv: [10.1101/2022.02.13.480259](https://doi.org/10.1101/2022.02.13.480259))

## Tools and Resources

[Virus tools website](#)

**HIVPRE:** analysis and prediction of the HIV-1 interacting proteins.

**PrEP estimator:** compute the prophylactic efficacy of DTG using different methods.

**Dark matter:** Virus discovery: A collection of Python tools for filtering and visualizing Next Generation Sequencing reads.

## EVBC Special Issues

[Special issue list](#)

We remind you to submit to our Special Issue [Virus Bioinformatics 2022](#) which will present articles covering computational approaches in virology, and we welcome any contribution within this cross-disciplinary field.

Deadline for manuscript submissions: **30 April 2022**

## New Members

[EVBC members website](#)

We are happy to welcome our new members:

**Francois Balloux**, University College London, UK | **Georgii Bazykin**, Skolkovo Institute of Science and Technology, RU | **Roman Biek**, University of Glasgow, UK | **Noriko Cassman**, Friedrich Schiller University Jena, DE | **Volker Deckert**, Friedrich Schiller University Jena, DE | **Emma Hodcroft**, University of Bern, CH | **Mart Krupovic**, Institut Pasteur, FR | **Jens H. Kuhn**, Tunnell Government Services, US | **Elliot J. Lefkowitz**, University of Alabama at Birmingham, US | **Aine Niamh O'Toole**, University of Edinburgh, UK | **Kai Papenfort**, Friedrich Schiller University Jena, DE | **Alejandro Reyes Muñoz**, Universidad de los Andes, CO | **Marc A. Suchard**, University of California, Los Angeles, US | **Emma Thomson**, University of Glasgow, UK

Please see the [back of the newsletter](#) to get to know our members!

## ViBioM 2022

[Register](#)

Check out the [programme schedule](#) for ViBioM 2022!

## ECR Viromics Webinar Series

[Register](#)

**Virus discovery now and then – from Koch's postulate to browsing viruses on the internet**

09 Mar 2022 | 04 pm CET


online

*Dr. Florian Pfaff, Friedrich-Loeffler-Institute, Germany*

**We would like to invite you to nominate speakers for the webinar series.**

## Upcoming Events

[Subscribe to Calendar](#)

EVBC does not endorse any of the listings. EVBC members are involved in events marked .

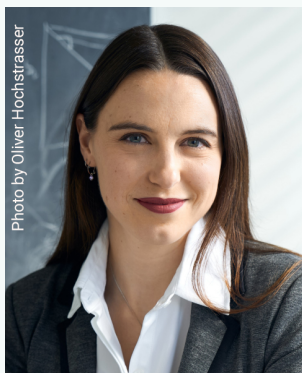
**Negative Strand RNA Virus (NSV2022) meeting**

12–17 June 2022 | Braga, Portugal

Registration/Abstract Deadline:

**11 April 2022**

## Member Profile: Emma Hodcroft



**Name:** Emma Hodcroft

**Position:** Senior Postdoctoral Researcher

**Research focus:** Phylogenetics and viral evolution



[Full interview online](#)

### What do you love about viruses?

The fact that you can open up their genomes in a alignment viewer! I worked on bacteria for a while and not being able to just open up alignments and check them out drove me crazy. But also - their fast evolutionary rate, which keeps things interesting and makes a lot of my work possible!

### Who is your favourite scientist and why?

Sir David Attenborough. He's done so much for awareness of our world, nature, and climate change - and all with a voice that immediately drains away your stress and transports you into the magical natural world. I would love to meet him.

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

A super-cheap, high-throughput, rugged sequencer with reagents that are also cheap and accessible. The fact that it's so difficult for so many countries around the world to get a sequencer or reagents, or get one with a warranty, or access servicing, or only at extortionate markups, really shocks me. Countries are really hindered in their ability to further their own research or understanding of the pathogens that matter to them without access to cheap and reliable sequencing. Plus, the rest of us are blind to what we might learn about these pathogens or a more complete understanding of the global distribution or circulation. It's in everyone's interest to work on creating more accessible and equitable sequencing and sequence sharing.

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

I think due to publicity during the pandemic, some people think I'm perhaps a bit big-headed - I'm really not! Being a precariously employed post-doc during the pandemic is a very effective anecdote to illusions of grandeur. If anything, I feel more pressure than ever to ensure my work is accurate, convey scientific communication clearly, and live up to expectations. I'm honoured both that I've been able to help during the pandemic, and that I've been able to provide good communication to so many people, but the responsibility that comes with this weighs really heavily, and I take it very seriously.

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

Virus evolution and phylogenetics - exactly what I do!

### Is there anything you would like to share with the EVBC members?

"All evolutionary biologists know that variation itself is nature's only irreducible essence. Variation is the hard reality, not a set of imperfect measures for a central tendency. Means and medians are the abstractions." - S J Gould

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## Member Profile: Diego Simón



**Name:** Diego Simón

**Position:** PhD student, Laboratory of Molecular Virology, Universidad de la República, Uruguay

**Research focus:** How viruses, in particular arboviruses, are affected by the compositional biases and immune systems of their hosts.



### What do you love about viruses?

Viruses are relatively simple yet full of emergent properties (many worrisome but all fascinating).

### Who is your favourite scientist and why?

Perhaps Alfred Sturtevant, and how he developed the first genetic-linkage map.

### What is your favourite way to spend a day off?

As a computational biologist, the amount of time I spend indoors and in front of a screen is excessive. So I try to spend most of my free time outdoors.

### What are you currently learning?

I am revisiting immunology.

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

Which came first: the virus or the cell?

### What is the coolest thing about your research?

As I am interested not only in viruses but also in their hosts, I have worked on all three domains of life (Archaea, Bacteria and Eukaryota) in addition to viruses.

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

I try to be transparent enough and not have to worry about that.

### What was your most surprising scientific finding?

I have found many cool things, but others have found it months, decades and even centuries earlier.

### What was your biggest achievement, & what your biggest failure?

I remain positive either way, so it is best to look ahead to the next challenge.

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

I think it is crucial to learn more about the diversity of viruses in less studied hosts and environments.

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

I might see myself leaning towards even more curiosity-driven research.

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

Be more focused from Monday to Friday, and switch off at weekends.

## Board of Directors

Martin Beer, Li Deng, Bas E. Dutilh, Philippe Le Mercier, Manja Marz, Volker Thiel