

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).

## Recent Selected Publications on SARS-CoV-2 by EVBC Members

SARS-CoV-2 uses a multipronged strategy to impede host protein synthesis. *Nature* [10.1038/s41586-021-03610-3](https://doi.org/10.1038/s41586-021-03610-3)

Investigate the origins of COVID-19. *Science* [10.1126/science.abj0016](https://doi.org/10.1126/science.abj0016)

Estimating infectiousness throughout SARS-CoV-2 infection course. *Science* [10.1126/science.abi5273](https://doi.org/10.1126/science.abi5273)

Structural basis of ribosomal frameshifting during translation of the SARS-CoV-2 RNA genome. Now published in *Science* [10.1126/science.abf3546](https://doi.org/10.1126/science.abf3546)

Clonal analysis of immunodominance and cross-reactivity of the CD4 T cell response to SARS-CoV-2. *Science* [10.1126/science.abg8985](https://doi.org/10.1126/science.abg8985)

Kinetics and correlates of the neutralizing antibody response to SARS-CoV-2 infection in humans. Now published in *Cell Host Microbe* [10.1016/j.chom.2021.04.015](https://doi.org/10.1016/j.chom.2021.04.015)

Genome-wide bioinformatic analyses predict key host and viral factors in SARS-CoV-2 pathogenesis. Now published in *Commun Biol* [10.1038/s42003-021-02095-0](https://doi.org/10.1038/s42003-021-02095-0)

SARS-CoV-2 variants of concern partially escape humoral but not T-cell responses in COVID-19 convalescent donors and vaccinees. *Sci Immunol* [10.1126/sciimmunol.abj1750](https://doi.org/10.1126/sciimmunol.abj1750)

Detection of SARS-CoV-2 RNA in bivalve mollusks and marine sediments. *Sci Total Environ* [10.1016/j.scitotenv.2021.147534](https://doi.org/10.1016/j.scitotenv.2021.147534)

Dispersal dynamics of SARS-CoV-2 lineages during the first epidemic wave in New York City. *PLoS Pathog* [10.1371/journal.ppat.1009571](https://doi.org/10.1371/journal.ppat.1009571)

Characterization of the SARS-CoV-2 Neutralization Potential of COVID-19-Convalescent Donors. *J Immunol* [10.4049/jimmunol.2100036](https://doi.org/10.4049/jimmunol.2100036)

Virological and serological characterization of critically ill patients with COVID-19 in the UK: Interactions of viral load, antibody status and B.1.1.7 variant infection. *J Infect Dis* [10.1093/infdis/jiab283](https://doi.org/10.1093/infdis/jiab283)

Sensitive immunodetection of SARS-CoV-2 variants-of-concern 501Y.V2 and 501Y.V1. *J Infect Dis* [10.1093/infdis/jiab278](https://doi.org/10.1093/infdis/jiab278)

The Significance of Phenotyping and Quantification of Plasma Extracellular Vesicles Levels Using High-Sensitivity Flow Cytometry during COVID-19 Treatment. *Viruses* [10.3390/v13050767](https://doi.org/10.3390/v13050767)

Glycyrrhizin Effectively Inhibits SARS-CoV-2 Replication by Inhibiting the Viral Main Protease. *Viruses* [10.3390/v13040609](https://doi.org/10.3390/v13040609)

Surveillance of SARS-CoV-2 in Frankfurt am Main from October to December 2020 Reveals High Viral Diversity Including Spike Mutation

N501Y in B.1.1.70 and B.1.1.7. *Microorganisms* [10.3390/microorganisms9040748](https://doi.org/10.3390/microorganisms9040748)

No Evidence for Human Monocyte-Derived Macrophage Infection and Antibody-Mediated Enhancement of SARS-CoV-2 Infection. *Front Cell Infect Microbiol* [10.3389/fcimb.2021.644574](https://doi.org/10.3389/fcimb.2021.644574)

Temporal Dominance of B.1.1.7 over B.1.354 SARS-CoV-2 Variant: A Hypothesis Based on Areas of Variant Co-Circulation. *Life* [10.3390/life11050375](https://doi.org/10.3390/life11050375)

### Reviews & Book Chapters

Novel SARS-CoV-2 variants: the pandemics within the pandemic. *Clin Microbiol Infect* [10.1016/j.cmi.2021.05.022](https://doi.org/10.1016/j.cmi.2021.05.022)

The Transmission of SARS-CoV-2 Infection on the Ocular Surface and Prevention Strategies. *Cells* [10.3390/cells10040796](https://doi.org/10.3390/cells10040796)

One year into the pandemic: Short-term evolution of SARS-CoV-2 and emergence of new lineages. *Infect Genet Evol* [10.1016/j.meegid.2021.104869](https://doi.org/10.1016/j.meegid.2021.104869)

### Preprints

The BNT162b2 mRNA vaccine against SARS-CoV-2 reprograms both adaptive and innate immune responses. *medRxiv* [10.1101/2021.05.03.21256520](https://doi.org/10.1101/2021.05.03.21256520)

Travel-driven emergence and spread of SARS-CoV-2 lineage B.1.620 with multiple VOC-like mutations and deletions in Europe. *medRxiv* [10.1101/2021.05.04.21256637](https://doi.org/10.1101/2021.05.04.21256637)

Fatal COVID-19 outcomes are associated with an antibody response targeting epitopes shared with endemic coronaviruses. *medRxiv* [10.1101/2021.05.04.21256571](https://doi.org/10.1101/2021.05.04.21256571)

A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. *medRxiv* [10.1101/2021.05.12.21257080](https://doi.org/10.1101/2021.05.12.21257080)

A Prenylated dsRNA Sensor Protects Against Severe COVID-19 and is Absent in Horseshoe Bats. *medRxiv* [10.1101/2021.05.05.21256681](https://doi.org/10.1101/2021.05.05.21256681)

poreCov - an easy to use, fast, and robust workflow for SARS-CoV-2 genome reconstruction via nanopore sequencing. *bioRxiv* [10.1101/2021.05.07.443089](https://doi.org/10.1101/2021.05.07.443089)

Rapid incidence estimation from SARS-CoV-2 genomes reveals decreased case detection in Europe during summer 2020. *medRxiv* [10.1101/2021.05.14.21257234](https://doi.org/10.1101/2021.05.14.21257234)

An appeal for an open scientific debate about the proximal origin of SARS-CoV-2. *arXiv* [10.13140/RG.2.2.15356.46727](https://doi.org/10.13140/RG.2.2.15356.46727)

 [EVBC publications on SARS-CoV-2](#)

## SARS-CoV-2 Bioinformatics Tools and Resources

We are very happy to announce our revised and redesigned [collection of virus bioinformatics tools](#). Don't hesitate to contact us if you want a tool to be added or require any further features for this collection. We strongly encourage you to leave comments and/or send us feedback on the tools.

- **GlnPipe**: reconstruct the SARS-CoV-2 incidence dynamics through time.
- **poreCov**: easy to use, highly parallel, and robust workflow written

in Nextflow for SARS-CoV-2 genome reconstruction via nanopore sequencing.

 [Coronavirus tools website](#)