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Selected Publications on SARS-CoV-2 by EVBC Members

Science, not speculation, is essential to determine how SARS-CoV-2 reached humans. *Lancet*

[10.1016/S0140-6736\(21\)01419-7](https://doi.org/10.1016/S0140-6736(21)01419-7)

Untangling introductions and persistence in COVID-19 resurgence in Europe. *Nature* [10.1038/s41586-021-03754-2](https://doi.org/10.1038/s41586-021-03754-2)

Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. *Science* [10.1126/science.abj0113](https://doi.org/10.1126/science.abj0113)

SARS-CoV-2 rapid diagnostic tests for emerging variants. *Lancet Microbe* [10.1016/S2666-5247\(21\)00147-6](https://doi.org/10.1016/S2666-5247(21)00147-6)

Identification of SARS-CoV-2-induced pathways reveals drug repurposing strategies. *Sci Adv* [10.1126/sciadv.abh3032](https://doi.org/10.1126/sciadv.abh3032)

CVnCoV and CV2CoV protect human ACE2 transgenic mice from ancestral B BavPat1 and emerging B.1.351 SARS-CoV-2. Now published in *Nat Commun* [10.1038/s41467-021-24339-7](https://doi.org/10.1038/s41467-021-24339-7)

Lineage-specific protection and immune imprinting shape the age distributions of influenza B cases. *Nat Commun*

[10.1038/s41467-021-24566-y](https://doi.org/10.1038/s41467-021-24566-y)

Rapid feedback on hospital onset SARS-CoV-2 infections combining epidemiological and sequencing data. *eLife* [10.7554/eLife.65828](https://doi.org/10.7554/eLife.65828)

AmpliCoV: Rapid Whole-Genome Sequencing Using Multiplex PCR Amplification and Real-Time Oxford Nanopore MinION Sequencing Enables Rapid Variant Identification of SARS-CoV-2. *Front Microbiol* [10.3389/fmicb.2021.651151](https://doi.org/10.3389/fmicb.2021.651151)

Preprints

Reduced neutralisation of the Delta (B.1.617.2) SARS-CoV-2 variant of concern following vaccination. *medRxiv* [10.1101/2021.06.23.21259327](https://doi.org/10.1101/2021.06.23.21259327)

Heterologous immunisation with vector vaccine as prime followed by mRNA vaccine as boost leads to humoral immune response against SARS-CoV-2, which is comparable to that according to a homologous mRNA vaccination scheme. *medRxiv* [10.1101/2021.07.09.21260251](https://doi.org/10.1101/2021.07.09.21260251)

Leveraging of SARS-CoV-2 PCR cycle thresholds values (Ct) to forecast COVID-19 trends. *medRxiv* [10.1101/2021.07.17.21260679](https://doi.org/10.1101/2021.07.17.21260679)

Comparative analysis of ChAdOx1 nCoV-19 and Ad26.COV2.S SARS-CoV-2 vector vaccines. *Research Square* [10.21203/rs.3.rs-736157/v1](https://doi.org/10.21203/rs.3.rs-736157/v1)

 [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.

- [SpikePro](#) predicts the fitness of a SARS-CoV-2 strain from the sequence of its spike protein.
- [CoVigator](#): NGS variant calling on SARS-CoV-2

 [Coronavirus tools website](#)