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Selected Publications on SARS-CoV-2 by EVBC Members

Selected humoral fluid-phase pattern recognition molecules can play an important role in resistance to, and pathogenesis of, COVID-19.

(Nat Immunol: [10.1038/s41590-021-01114-w](https://doi.org/10.1038/s41590-021-01114-w))

Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data and integration of new tools such as the Ensembl Variant Effect Predictor. (Nucleic Acids Res: [10.1093/nar/gkab889](https://doi.org/10.1093/nar/gkab889))

Mutations that adapt SARS-CoV-2 to mink or ferret do not increase fitness in the human airway. (Cell Rep: [10.1016/j.celrep.2022.110344](https://doi.org/10.1016/j.celrep.2022.110344))

Investigation of a Limited but Explosive COVID-19 Outbreak in a German Secondary School. (Viruses: [10.3390/v14010087](https://doi.org/10.3390/v14010087))

Non-covalent SARS-CoV-2 M pro inhibitors developed from in silico screen hits could form the basis for medicinal chemistry efforts that could lead to the development of clinically relevant inhibitors. (Sci Rep: [10.1038/s41598-022-06306-4](https://doi.org/10.1038/s41598-022-06306-4))

Need for dramatically more wildlife sampling to (i) pinpoint the exact origins of SARS-CoV-2's animal progenitor, (ii) the intermediate species that facilitated transmission from bats to humans (if there is one), and (iii) survey the extent of the diversity in the related sarbecoviruses' phylogeny that present high risk for future spillovers.

(Genome Biol Evol: [10.1093/gbe/evac018](https://doi.org/10.1093/gbe/evac018))

Reviews / Commentaries

SARS-CoV-2 variants preferentially emerge at intrinsically disordered protein sites helping immune evasion. (FEBS J: [10.1111/febs.16379](https://doi.org/10.1111/febs.16379))

Preprints

Detectable Omicron-neutralizing activity in elderly individuals was nearly absent after two vaccinations but elicited in 89% of individuals by the booster immunization. (medRxiv: [10.1101/2022.02.02.22270302](https://doi.org/10.1101/2022.02.02.22270302))

Omicron BA.1 and BA.2 have evolved as two distinct antigenic outliers and escape (vaccine-induced) antibody responses as a result of different antigenic characteristics. (bioRxiv: [10.1101/2022.02.23.481644](https://doi.org/10.1101/2022.02.23.481644))

An updated vaccine with more diverse epitopes capable of inducing neutralizing antibodies against VOCs would be a future direction for boosters. (medRxiv: [10.1101/2022.02.19.22271215](https://doi.org/10.1101/2022.02.19.22271215))

Easy-to-use SARS-CoV-2 genome assembler to facilitate the analysis of NGS sequencing data obtained from amplicon-based sequencing methods. (bioRxiv: [10.1101/2021.05.21.445156](https://doi.org/10.1101/2021.05.21.445156))

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

Tools and Resources

ESCA: Easy-to-use SARS-CoV-2 genome Assembler

sars2seq: summarize changes from a given reference sequence.


 [Coronavirus tools website](#)

Upcoming Events

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

**International Virus Bioinformatics Meeting 2022:
Satellite Meeting on SARS-CoV-2**

23 March 2022 | online

 Keynote Speakers: Francois Balloux, Philippe Lemey

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