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Selected Publications on SARS-CoV-2 by EVBC Members

Spatial and temporal fluctuations in COVID-19 fatality rates in Brazilian hospitals: approximately half of the COVID-19 deaths in hospitals in the 14 cities could have been avoided without pre-pandemic geographic inequities and without pandemic healthcare pressure. (Nat Med: [10.1038/s41591-022-01807-1](https://doi.org/10.1038/s41591-022-01807-1))

SARS-CoV-2-specific T-cell epitope repertoire in convalescent and mRNA-vaccinated individuals. (Nat Microbiol: [10.1038/s41564-022-01106-y](https://doi.org/10.1038/s41564-022-01106-y))

Antibodies from convalescent plasma promote SARS-CoV-2 clearance in individuals with and without endogenous antibody response. (J Clin Invest: [10.1172/JCI158190](https://doi.org/10.1172/JCI158190))

Genome-wide CRISPR screens: GATA6 may represent a target for the development of anti-SARS-CoV-2 therapeutic strategies. (Nat Commun: [10.1038/s41467-022-29896-z](https://doi.org/10.1038/s41467-022-29896-z))

Minimal adaptation was required for onward transmission in mink and deer following human-to-animal spillover, highlighting the 'generalist' nature of SARS-CoV-2 as a mammalian pathogen. (Nat Commun: [10.1038/s41467-022-30698-6](https://doi.org/10.1038/s41467-022-30698-6))

Routine screening of hospitalized COVID-19 patients for rapid identification of patients with IFN-AABs (early biomarker for the development of severe COVID-19) who most likely benefit from specific therapies. (J Clin Immunol: [10.1007/s10875-022-01252-2](https://doi.org/10.1007/s10875-022-01252-2))

Tracking SARS-CoV-2 mutations and variants through the COG-UK-Mutation Explorer. (Viurs Evol: [10.1093/ve/veac023](https://doi.org/10.1093/ve/veac023))

A naturally occurring mutation can liberate SARS-CoV-2 from ACE2-dependence. The ACE2-independent entry may protect the virus from neutralization by an antibody used for COVID-19 therapy. (mBio: [10.1128/mbio.00364-22](https://doi.org/10.1128/mbio.00364-22))

Wastewater surveillance for monitoring SARS-CoV-2 infections and its effectiveness in identifying circulating variants which may prove useful when sequencing capacity is limited. (Sci Total Environ: [10.1016/j.scitotenv.2022.155828](https://doi.org/10.1016/j.scitotenv.2022.155828))

Reduced interferon-antagonizing activity explains at least in part why Omicron variant infections are inherently less severe than infections with other SARS-CoV-2 variants. (Cell Discov: [10.1038/s41421-022-00408-z](https://doi.org/10.1038/s41421-022-00408-z))

SARS-CoV-2-specific T cell responses are preserved in SARS-CoV-2-vaccinated or -infected anti-CD20-treated multiple sclerosis. (Mult Scler: [10.1177/13524585221094478](https://doi.org/10.1177/13524585221094478))

Transmission of infectious SARS-CoV-2 via fomites is possible upon extensive moistening, but unlikely to occur in real-life scenarios and from droplet-contaminated fomites. (J Infect Dis: [10.1093/infdis/jiac170](https://doi.org/10.1093/infdis/jiac170))

Duplex one-step RT-qPCR assays that concurrently detect genomic and subgenomic SARS-CoV-2 targets. (Viruses: [10.3390/v14051066](https://doi.org/10.3390/v14051066))

For a single person, the risk of contracting COVID-19 via person-to-person cash transactions is very low. (Risk Anal: [10.1111/risa.13935](https://doi.org/10.1111/risa.13935))

Vaccination of previously infected convalescent plasma donors induced high levels of broadly neutralising antibodies against circulating antigenic variants of SARS-CoV-2. (Transfusion: [10.1111/trf.16934](https://doi.org/10.1111/trf.16934))

Advancing genomic epidemiology by addressing the bioinformatics bottleneck: Challenges, design principles, and a Swiss example. (Epidemics: [10.1016/j.epidem.2022.100576](https://doi.org/10.1016/j.epidem.2022.100576))

Reviews / Commentaries

Dysregulated Immune Responses in SARS-CoV-2-Infected Patients: A Comprehensive Overview. (Viruses: [10.3390/v14051082](https://doi.org/10.3390/v14051082))

Preprints

Predictive power of computational heuristics for SARS-CoV-2 host prediction based on variation in the ACE2 receptor derives from strong correlations with host phylogeny rather than processes which can be mechanistically linked to infection biology. (bioRxiv: [10.1101/2022.05.16.492068](https://doi.org/10.1101/2022.05.16.492068))

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

Tools and Resources

[COG-UK-Mutation Explorer](#): Tracking SARS-CoV-2 mutations and variants

 [Coronavirus tools website](#)