

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

Virological Assessment of Hospitalized Patients With COVID-2019. *Nature* [10.1038/s41586-020-2196-x](#)

Molecular characterization of SARS-CoV-2 from the first case of COVID-19 in Italy. *Clin Microbiol Infect* [10.1016/j.cmi.2020.03.025](#)

Will COVID-19 Become the Next Neglected Tropical Disease? *PLoS Negl Trop Dis* [10.1371/journal.pntd.0008271](#)

Severe Acute Respiratory Syndrome Coronavirus 2-Specific Antibody Responses in Coronavirus Disease 2019 Patients. *Emerg Infect Dis* [10.3201/eid2607.200841](#)

Comparative Pathogenesis of COVID-19, MERS, and SARS in a Nonhuman Primate Model. Now published in *Science* [10.1126/science.abb7314](#)

Inactivation of Severe Acute Respiratory Syndrome Coronavirus 2 by WHO-Recommended Hand Rub Formulations and Alcohols. Now published in *Emerg Infect Dis* [10.3201/eid2607.200915](#)

Remdesivir and SARS-CoV-2: Structural Requirements at Both nsp12 RdRp and nsp14 Exonuclease Active-Sites. *Antiviral Res* [10.1016/j.antiviral.2020.104793](#)

Nafamostat mesylate blocks activation of SARS-CoV-2: New treatment option for COVID-19. *Antimicrob Agents Chemother* [10.1128/AAC.00754-20](#)

Preprints

Combined prophylactic and therapeutic use maximizes hydroxychloroquine anti-SARS-CoV-2 effects *in vitro*. *bioRxiv* [10.1101/2020.03.29.014407](#)

Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic. *bioRxiv* [10.1101/2020.03.30.015008](#)

SARS-CoV-2 and SARS-CoV differ in their cell tropism and drug sensitivity profiles. *bioRxiv* [10.1101/2020.04.03.024257](#)

Analysis of SARS-CoV-2-controlled autophagy reveals spermidine, MK-2206, and niclosamide as putative antiviral therapeutics. *bioRxiv* [10.1101/2020.04.15.997254](#)

TMPRSS2 and furin are both essential for proteolytic activation and spread of SARS-CoV-2 in human airway epithelial cells and provide promising drug targets. *bioRxiv* [10.1101/2020.04.15.042085](#)

The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) envelope (E) protein harbors a conserved BH3-like sequence. *bioRxiv* [10.1101/2020.04.09.033522](#)

Presence of SARS-CoV-2 reactive T cells in COVID-19 patients and healthy donors. *medRxiv* [10.1101/2020.04.17.20061440](#)

Disparate temperature-dependent virus - host dynamics for SARS-CoV-2 and SARS-CoV in the human respiratory epithelium. *bioRxiv* [10.1101/2020.04.27.062315](#)

STAT2 signaling as double-edged sword restricting viral dissemination but driving severe pneumonia in SARS-CoV-2 infected hamsters. *bioRxiv* [10.1101/2020.04.23.056838](#)

SARS-CoV-2 RNA titers in wastewater anticipated COVID-19 occurrence in a low prevalence area. *medRxiv* [10.1101/2020.04.22.20075200](#)

Rapid SARS-CoV-2 whole genome sequencing for informed public health decision making in the Netherlands. *bioRxiv* [10.1101/2020.04.21.050633](#)

For more frequent updates on SARS-CoV-2 publications, please follow us on Twitter [@EVirusBioinfC](#) or check our [publications website](#).

Virus Bioinformatics Tools and Resources

We are curating a list of [bioinformatics tools specifically for coronaviruses](#). Please let us know about the tools you have developed to advance the field.

- [ARTIC Workflow for nCoV](#) for working with nanopore sequencing data.
- [COPASI](#) for simulation and analysis of biochemical networks and their dynamics.
- [CORDITE](#) collects drug interactions that could be used to treat COVID.
- [CoVex](#) for data analysis that integrates virus-human interactions for SARS-CoV-2 and SARS-CoV-1.
- [CoV-GLUE](#) will help to track nucleotide changes in the SARSCoV2 genomes.
- [Covidex](#) is an alignment-free machine learning subtyping tool for viral species.
- [Covid-19 Simulator](#) is a daily updated epidemiological model that includes projections of hospital resources needed in the next weeks as well as effects of contact reduction measures.
- The [Covid-19 Data Portal](#) developed and hosted by EMBL-EBI brings together relevant datasets and includes some tools as well.
- [NFDI4Microbiota](#) and EVBC is offering sequencing and assembly of SARS-CoV-2 genomes at net costs, as well as the immediate storage of the resulting sequences in public repositories.
- [Pangolin](#) will assign your query SARS-CoV-2 genomes a lineage based on the global lineages.
- [P-HIPSTER](#) contains predicted viral-host PPIs for 15 human-infecting coronaviruses.
- [PoSeiDon](#) detects significantly positively selected sites and possible recombination events in an alignment of multiple coding sequences.
- [Rfam](#) release that includes new and updated Coronavirus families.
- [VBRC](#) tools have been adapted for coronaviruses.
- [VIGOR4](#) to predict protein sequences encoded in SARS-CoV-2.
- [VIPR](#) has a dedicated page with several bioinformatics tools for SARS-CoV-2 analysis.
- The latest [VirHostNet](#) 2.0 release contains manual biocuration of experimentally validated physical Coronaviridae / host protein-protein interactions.
- [VIRULIGN](#) for fast codon-correct alignments of large datasets has been adapted to SARS-CoV-2.
- [V-Pipe](#) allows for the detection of within-host genetic variation of SARS-CoV-2 from viral NGS data.

