

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

Genetic Diversity and Ecology of Coronaviruses Hosted by Cave-Dwelling Bats in Gabon. *Sci Rep* [10.1038/s41598-020-64159-1](https://doi.org/10.1038/s41598-020-64159-1)

Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-CoV-2 infections unreliable. *Proc Natl Acad Sci USA* [10.1073/pnas.2007295117](https://doi.org/10.1073/pnas.2007295117)

Rapid Reconstruction of SARS-CoV-2 Using a Synthetic Genomics Platform. Now published in *Nature* [10.1038/s41586-020-2294-9](https://doi.org/10.1038/s41586-020-2294-9)

Imbalanced Host Response to SARS-CoV-2 Drives Development of COVID-19. *Cell* [10.1016/j.cell.2020.04.026](https://doi.org/10.1016/j.cell.2020.04.026)

Understanding evolution of SARS-CoV-2: a perspective from analysis of genetic diversity of RdRp gene. *J Med Virol* [10.1002/jmv.25909](https://doi.org/10.1002/jmv.25909) Nursing Homes and the Elderly Regarding the COVID-19 Pandemic: Situation Report From Hungary. *Geroscience* [10.1007/s11357-020-00195-z](https://doi.org/10.1007/s11357-020-00195-z)

SARS-CoV-2 RNA in Wastewater Anticipated COVID-19 Occurrence in a Low Prevalence Area. Now published in *Water Res* [10.1016/j.watres.2020.115942](https://doi.org/10.1016/j.watres.2020.115942)

Investigation of a COVID-19 Outbreak in Germany Resulting From a Single Travel-Associated Primary Case: A Case Series. *Lancet Infect Dis* [10.1016/S1473-3099\(20\)30314-5](https://doi.org/10.1016/S1473-3099(20)30314-5)

Preprints

Clinical classifiers of COVID-19 infection from novel ultra-high-throughput proteomics. *medRxiv* [10.1101/2020.04.27.20081810](https://doi.org/10.1101/2020.04.27.20081810)

Cross-talk between the airway epithelium and activated immune cells defines severity in COVID-19. *medRxiv* [10.1101/2020.04.29.20084327](https://doi.org/10.1101/2020.04.29.20084327)

Temporal signal and the phylodynamic threshold of SARS-CoV-2. *bioRxiv* [10.1101/2020.05.04.077735](https://doi.org/10.1101/2020.05.04.077735)

COVID-19 in healthcare workers in three hospitals in the South of the Netherlands, March 2020. *medRxiv* [10.1101/2020.04.26.20079418](https://doi.org/10.1101/2020.04.26.20079418)

Computational Strategies to Combat COVID-19: Useful Tools to Accelerate SARS-CoV-2 and Coronavirus Research. *Preprints* [10.20944/preprints202005.0376.v1](https://doi.org/10.20944/preprints202005.0376.v1)

Risk of Human-to-Wildlife Transmission of SARS-CoV-2. *Preprints* [10.20944/preprints202005.0141.v1](https://doi.org/10.20944/preprints202005.0141.v1)

A putative new SARS-CoV protein, 3a*, encoded in an ORF overlapping ORF3a. *bioRxiv* [10.1101/2020.05.12.088088](https://doi.org/10.1101/2020.05.12.088088)

Upregulation of Human Endogenous Retroviruses in Bronchoalveolar Lavage Fluid of COVID-19 Patients. *medRxiv* [10.1101/2020.05.10.20096958](https://doi.org/10.1101/2020.05.10.20096958)

Identification of five antiviral compounds from the Pandemic Response Box targeting SARS-CoV-2. *bioRxiv* [10.1101/2020.05.17.100404](https://doi.org/10.1101/2020.05.17.100404)

Modelling the SARS-CoV-2 first epidemic wave in Greece: social contact patterns for impact assessment and an exit strategy from social distancing measures. *medRxiv* [10.1101/2020.05.27.20114017](https://doi.org/10.1101/2020.05.27.20114017)

Multiple SARS-CoV-2 introductions shaped the early outbreak in Central Eastern Europe: comparing Hungarian data to a worldwide sequence data-matrix. *bioRxiv* [10.1101/2020.05.06.080119](https://doi.org/10.1101/2020.05.06.080119)

ACE2-Variants Indicate Potential SARS-CoV-2-Susceptibility in Animals: An Extensive Molecular Dynamics Study. *bioRxiv* [10.1101/2020.05.14.092767](https://doi.org/10.1101/2020.05.14.092767)

The emergence of SARS-CoV-2 in Europe and the US. *bioRxiv* [10.1101/2020.05.21.109322](https://doi.org/10.1101/2020.05.21.109322)

Human coronavirus reinfection dynamics: lessons for SARS-CoV-2. *bioRxiv* [10.1101/2020.05.11.20086439](https://doi.org/10.1101/2020.05.11.20086439)

Evidence of significant natural selection in the evolution of SARS-CoV-2 in bats, not humans. *bioRxiv* [10.1101/2020.05.28.122366](https://doi.org/10.1101/2020.05.28.122366)

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

SARS-CoV-2 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.

- **Ensembl COVID-19 resource**: SARS-CoV-2 genome browser and related resources, including gene annotation, information on gene functions, ...
- **COVID19 tissue simulator** simulates replication dynamics of SARS-CoV-2 in a layer of epithelium. It is being rapidly prototyped and refined with community support.
- **CoVPipe**: fully automated workflow for reference-based reconstruction of SARS-CoV-2 genomes.
- **Coronavirus typing tool** is designed to use Blast and phylogenetic methods in order to identify the Coronavirus types and genotypes of a nucleotide sequence.
- **Haploflow** for detection and full-length reconstruction of SARS-CoV-2 multi-strain infections.
- **Nextstrain** is incorporating SARS-CoV-2 genomes as soon as they are shared and providing analyses and situation reports.
- **Pfam** protein families database for large-scale functional annotation of proteins contains an updated set of models that comprehensively cover the proteins encoded by SARS-CoV-2.
- **Uniprot**: latest knowledge on proteins relevant to COVID-19 for both the virus and human host.

