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

Virological Assessment of Hospitalized Patients With COVID-19. 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
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

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
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
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

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.
- CoV-GLUE for data analysis that integrates virus-human interactions for SARS-CoV-2 and SARS-CoV-1.
- 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.
- PoSelIDon 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 Coronavirus / 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.