



May 26, 2020

Keio University  
Systems Biology Institute  
Okinawa Institute of Science and Technology Graduate University

## COVID-19 Disease Map

### - Building a computational repository of SARS-CoV-2 virus-host interaction mechanisms.

Researchers from Japan and around the world, including Assoc. Prof. Akira Funahashi of the Keio University Faculty of Science and Technology; Prof. Hiroaki Kitano of the Systems Biology Institute, the Okinawa Institute of Science and Technology Graduate University, and Sony Computer Science Laboratories, Inc.; and Dr. Marek Ostaszewski, Prof. Rudi Balling, and Prof. Reinhard Schneider of the University of Luxembourg, are teaming up to reconstruct the molecular processes of virus-host interactions to combat the ongoing COVID-19 pandemic. Comprising 163 members from 81 organizations in 29 countries, the research group have published the COVID-19 Disease Map to form a comprehensive, standardized knowledge repository of the interaction mechanisms between the SARS-CoV-2 virus and the host.

SBML (Systems Biology Markup Language, <http://sbml.org>) and SBGN (Systems Biology Graphical Notation, <http://sbgn.org>) are standardization technologies that Assoc. Prof. Funahashi and Prof. Kitano have been working on since the early 2000s. These were adopted as the computational platform underlying the COVID-19 Disease Map. And CellDesigner (<http://celldesigner.org>), a software tool also developed by Assoc. Prof. Funahashi and Prof. Kitano, is being used to construct the COVID-19 Disease Map. The COVID-19 Disease Map will provide a graphical, interactive representation of the disease mechanisms and be a computational resource for analyses and disease modeling. It currently contains 13 models, including the viral replication cycle, transcription mechanisms, and signal transduction. All of these resources are available at <https://fairdomhub.org/projects/190#models>.

#### Future developments

Such an open collaboration between clinical researchers, life scientists, pathway curators, computational biologists, and data scientists makes it possible to build a trustworthy, reliable, and useful resource for all projects that are looking into COVID-19 disease mechanisms. The cumulative knowledge will improve our understanding of susceptibility features of the host such as gender and age, disease progression, defense mechanisms, and responses to treatment. It will be an invaluable resource that will facilitate the development of efficient diagnostics and treatment strategies for COVID-19.

### Details of Original Paper

Title: COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms

Authors: Marek Ostaszewski, Akira Funahashi, Hiroaki Kitano, Charles Auffray, Rudi Balling & Reinhard Schneider

Journal: Scientific Data (DOI: 10.1038/s41597-020-0477-8)

<https://www.nature.com/articles/s41597-020-0477-8>

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