

Researchers studying proteomics to identify potential drugs for battling SARS-CoV-2

March 30 2020, by Bob Yirka



This scanning electron microscope image shows SARS-CoV-2 (yellow)—also known as 2019-nCoV, the virus that causes COVID-19—isolated from a patient, emerging from the surface of cells (blue/pink) cultured in the lab. Credit: NIAID-RML

A team of researchers at the University of California has been studying

proteins that the SARS-CoV-2 virus uses to bind to proteins in the lungs, and has identified multiple drug candidates that might be useful to treat patients with COVID-19. The team notes that many of them have already been approved for use by the FDA in treating other diseases. They have posted their paper on the BioRxiv preprint server as they await publication in an unspecified journal.

Not long after the SARS-CoV-2 virus was found to be infecting people, scientists sequenced its genome. The work in this new effort involved analyzing the sequenced data, from which the researchers identified 29 genes in the virus that were responsible for producing proteins involved in interacting with human proteins. Next, the team invited a group of chemists into their effort to help them find [small molecules](#) that could be used to target the host proteins they had found. That led to a list of drugs that might be useful in treating patients with COVID-19. The team is now currently testing the drugs on their list with infected cells to find those that are able to prevent the virus proteins from interacting with the human proteins. They note that they accomplished work in just a matter of weeks that would normally take months. They proceeded more rapidly by collaborating with hundreds of other scientists working in 21 laboratories around the world.

The team at UC was not the only one studying proteomics as a way to identify drugs that might help with COVID-19. A combined team from University Hospital Frankfurt and Goethe University used an isobaric labeling-based technique to study changes in [protein](#) translation and amounts following infection, which they believe could guide the search for therapies. And another team at IsoPlexis has been collaborating with researchers at the Institute for Systems Biology to study [immune response](#) in people who have recovered from COVID-19 infections, particularly the way proteins are prevented from interacting. Also, a combined team from the Virginia School of Medicine and Hood College has been looking into the possibility of using proteins as a way to

develop a test for the [virus](#).

More information: David E. Gordon et al. A SARS-CoV-2-Human Protein-Protein Interaction Map Reveals Drug Targets and Potential Drug-Repurposing, *BioRxiv* (2020). [DOI: 10.1101/2020.03.22.002386](https://doi.org/10.1101/2020.03.22.002386)

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