

Biophysicists' continued outstanding response to COVID-19

As we head into a promising summer in some parts of the world after an unprecedented pandemic year, it is astounding to recall the rapid progress of science from the time we first heard about a mysterious respiratory illness with an alarming infection and death rate in China's Hubei Province at the end of 2019. Already, we are witnessing massive vaccination campaigns against this deadly COVID-19 disease, and many of us are returning to our workplaces and in-person activities, spiriting a more hopeful view into the future.

Scientists across numerous disciplines have shifted research gears to aid in understanding the spread of the infection, determining optimal protocols to protect ourselves with cloth coverings and physical distancing, developing rapid and inexpensive tests for COVID-19, repurposing known drugs to combat the disease, inventing new drugs, and unraveling the complex and multifarious biophysical aspects of the virus life cycle and infection trajectory. This amassed knowledge along with related prior research on RNAs, proteins, and other biomolecules has been instrumental to the success of the current vaccines. It is likely that this remarkable momentum of research will continue and will be invaluable for better handling of future epidemics that inevitably will arise. Much work remains to be done to manage COVID-19 around the globe, but the scientific progress to date provides cause for optimism.

Biophysicists' response to our two special issues of COVID-19-related studies, of which this is the second, has been overwhelming. Many Biophysical Society members sent us their premier work and helped us review the other articles with the rigor and speed that we strive for in *Biophysical Journal*.

In coordination with the special Biophysical Society Symposium on COVID-19, held in October 2020, we invited original article contributions from scientists working to advance our understanding of all aspects of the COVID-19 disease and the SARS-Cov-2 virus on multiple scales, levels, and points of view by using novel experimental, mathematical, statistical, and computational approaches.

In this issue, you will read these excellent works that were submitted by early 2021. The many techniques include

molecular dynamics simulations, coarse-grained elastic network modeling, Markov state models, computational protein design, molecular docking, cryo electron microscopy, NMR spectroscopy, circular dichroism spectroscopy, cross-linking strategies, multi-angle light scattering, analytical ultracentrifugation, and mass spectrometry. The problems addressed range from tracing the stages of the epidemic from growth to decay, decontamination of N95 masks, COVID-19 infection impact on blood cells, dynamic fluctuations and transitions of viral proteins (spike and Nsp16), features of key interfaces or interactions (ACE2 with receptor-binding domains, fusion peptide to human membranes, viral proteins, and ion channels), and the RNA interactions and packaging with nucleocapsid proteins. Not surprisingly, these investigations suggest new practical tools to follow pandemic stages and symptoms, as well as strategies and compounds for antiviral therapy of many disease targets.

These continued efforts, collaborations, and related clinical experiments will help us better address future threats. Although the virus may continue to confound us with more variants, relatives, and strange symptoms, the continued innovation of our community provides a reassuring certainty. We look forward to discussing with you these scientific developments and others in person at the upcoming Biophysical Society meeting.

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