Given that the SARS-CoV-2 Omicron (B.1.1.529) variant was just recently discovered, only its sequence information is available. This variant poses multiple questions surrounding existing vaccine efficacy, potential for reinfection, transmissibility, and pathogenicity. The exact structure of the Omicron receptor binding domain (RBD) is not yet available, thus the questions pertaining to antibody interaction remain unanswered. In this work, we used machine learning-based predictive methods to create a predicted structure of the Omicron RBD and simulated the interaction with known neutralizing antibody structures. This helps us posit potential affects of the Omicron variant on vaccine efficacy.

While we expect these results to be overwritten by experimentally derived results in the coming months, in silico models like ours certainly provide a more rapid way to gain understanding in the ever-changing COVID-19 landscape. Thus, we feel this article will serve as a reference for future variant modeling and predictive analyses.

The preprint versions of this work have been read online over 800 times in the last week. This work was referenced by an article in The Economist and subsequently featured by LinkedIn News, garnering over five thousand additional views.