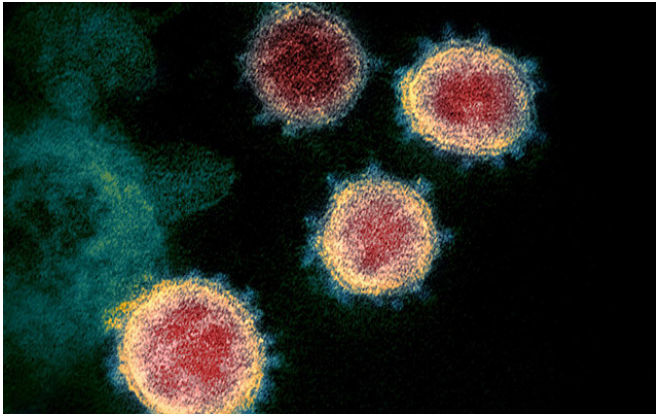


Immunodominant epitopes identified for designing peptide-based vaccine against SARS-CoV-2

10 June 2020



A colorized scanning electron micrograph of the SARS-CoV-2 virus. Credit: NIAID

There are currently no licensed vaccines available for COVID-19. While several antiviral drugs have been tested, none has proved to be completely effective against the disease. In a study just published in the journal MDPI *Vaccines*, researchers from Bar-Ilan University have identified a set of potential immunodominant epitopes from the SARS-CoV-2 proteome. These epitopes are capable of generating both antibody- and cell-mediated immune responses. The findings of this work may thus contribute to developing a peptide vaccine against SARS-CoV-2 infections which can stop the COVID-19 outbreak and future pandemics caused by coronaviruses.

Led by Dr. Milana Frenkel-Morgenstern, Head of the Cancer Genomics and BioComputing of Complex Diseases Lab at Bar-Ilan University's Azrieli Faculty of Medicine, the researchers took an immunoinformatics-based computational approach to mine the [protein](#) content of SARS-CoV-2 and subsequently identified immunodominant epitopes

of the virus. Immune responses that are based on specific immunodominant epitopes involve the generation of both antibody- and cell-mediated immunity against pathogens presenting such epitopes. Such immunity can facilitate fast and effective elimination of the pathogen.

The team of researchers that also includes Sumit Mukherjee, Dmitry Tworowski, Rajesh Detroja and Sunanda Biswas Mukherjee, identified 15 potential immunogenic regions from three proteins of SARS-CoV-2, and mapped 25 immunodominant epitopes on other SARS-CoV-2 proteins. To confirm that these epitopes could serve to provide immunity to a [global population](#), the percentage of individuals that express a major histocompatibility complex (MHC) capable of recognizing any of these epitopes was determined. Accordingly, seven epitopes were deemed to be present in more than 87% of the worldwide virus-affected population. Further structural molecular docking analyses estimated the binding interaction of these potential epitopes with human MHC. Complete lists of MHC proteins that recognize each epitope have been generated and are presented in both the submitted manuscript and a provisional US patent application (US 63/034.416).

The seven epitopes were tested using multiple tools to verify their non-allergenic and non-toxic natures, as well as to demonstrate that they carry a low risk of triggering any autoimmune responses. Together, such results indicate that these seven epitopes represent potentially effective [vaccine](#) candidates. Indeed, the development of vaccines using these immunodominant epitopes could activate both humoral and cellular immune responses in humans comprising a major fraction of the world's population.

More information: Sumit Mukherjee et al,

Immunoinformatics and Structural Analysis for Identification of Immunodominant Epitopes in SARS-CoV-2 as Potential Vaccine Targets, *Vaccines* (2020). DOI: [10.3390/vaccines8020290](https://doi.org/10.3390/vaccines8020290)

Provided by Bar-Ilan University

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