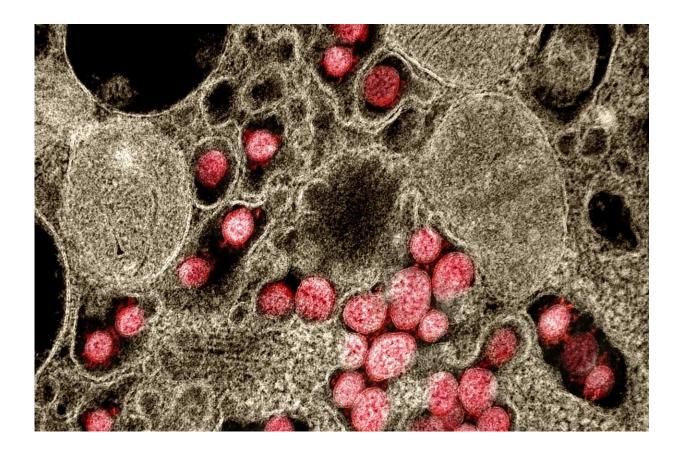


Computer simulation identifies SARS-CoV-2 viral membrane protein as potential vaccine target

April 16 2021



Transmission electron micrograph of SARS-CoV-2 virus particles isolated from a patient. Credit: NIAID

A new computational study suggests that a protein present in SARS-



CoV-2, the virus that causes COVID-19, could be a target for future vaccines. The study is published ahead of print in the *American Journal of Physiology—Lung Cellular and Molecular Physiology*.

Increased inflammation that leads to a "cytokine storm"—in which the body attacks its own tissues—is a serious complication affecting many people with COVID-19. SARS-CoV, the virus that caused a global outbreak of severe acute respiratory syndrome in Asia in 2003, encodes three viral membrane proteins—called viroporins—that play a role in activating inflammatory responses of the immune system. Previous studies have shown that the Viroporin E of SARS-CoV-2 has 94.7% similarity with the Viroporin E of SARS-CoV, which increases the probability that the two proteins have similar functions. Additionally, it was found that mutations in one region of the SARS-CoV-2 E protein could provide the basis for live, weakened and inactivated vaccines.

The researchers of a new study used the Universal Protein Resource database to obtain the Viroporin E sequence of SARS-CoV-2 for in silico (computer-based) analysis. Computer modeling has "changed the field of vaccinology, providing a time- and cost-effective strategy that aims at very focused, evidence-directed experimental investigation," the researchers of the new study wrote.

The Viroporin E of SARS-CoV-2 was identified as a "probable antigen"—a substance that is likely to trigger an immune response in the body. The predicted <u>vaccine</u> epitope candidates—the part of the antigen recognized by the immune system—were also found to fulfill prerequisites for vaccine safety. These findings "indicate that the SARS-CoV-2 viroporin E could serve as a promising vaccine target for this devastating disease," the researchers wrote. However, "<u>experimental data</u> are required to validate the in silico estimates."

"In silico investigation of the Viroporin E as a vaccine target against



SARS-CoV-2" ispublished ahead of print in the American Journal of Physiology-Lung Cellular and Molecular Physiology.

More information: Erasmia Rouka et al. In Silico investigation of the viroporin E as a vaccine target against SARS-CoV-2, *American Journal of Physiology—Lung Cellular and Molecular Physiology* (2021). DOI: 10.1152/ajplung.00443.2020

Provided by American Physiological Society

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