

NEWS | FEBRUARY 02 2024

# Navigating the free energy landscapes of COVID variants FREE

Chris Patrick



Scilight 2024, 051107 (2024)

<https://doi.org/10.1063/10.0024758>

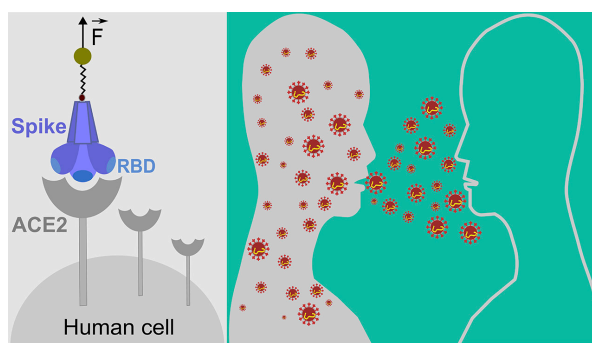


2 February 2024

## Navigating the free energy landscapes of COVID variants

Chris Patrick

Values that characterize the binding between virus and host may be able to predict transmission rates and inform the treatment of SARS-CoV-2 variants.



As the COVID-19 pandemic continues, variants of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) emerge, including Omicron and its subvariants. To better treat these variants, researchers must understand the interaction between the virus and human cells on the molecular level.

During the first step of infection, the receptor binding domain (RBD) of the virus's spike protein binds to the host cell's angiotensin-converting enzyme 2 (ACE2) receptor. Lan et al. used simulations to obtain the RBD-ACE2 complex's free energy landscape, which describes their binding affinity.

They found that Omicron has a higher unbinding free energy barrier and binds to ACE2 more strongly than the wild type, SARS-CoV-2, which may explain why Omicron infects faster.

The authors also used the free energy landscape to extract the distance between the transition state and the bound state,  $x_u$ . This value was the same for the wild type and the Omicron subvariants they studied. However, the researchers expect  $x_u$  to differ for other variants.

"One would expect that the larger the  $x_u$ , the lower the transmission rate," said author Mai Suan Li. "Therefore, given different free energy landscape parameters, such as  $x_u$  and the unbinding barrier, one should be able to estimate the virus infection rate."

The authors plan to construct free energy landscapes for many other variants to test their hypothesis.

"Once we have a large database, machine learning can be used to predict free energy landscape parameters instead of time-consuming molecular simulations," Li said.

**Source:** "Deciphering the free energy landscapes of SARS-CoV-2 wild type and omicron variant interacting with human ACE2," by Pham Dang Lan, Daniel A. Nissley, Edward P. O'Brien, Toan T. Nguyen, and Mai Suan Li, *Journal of Chemical Physics* (2024). The article can be accessed at <https://doi.org/10.1063/5.0188053>.

Published by AIP Publishing (<https://publishing.aip.org/authors/rights-and-permissions>).