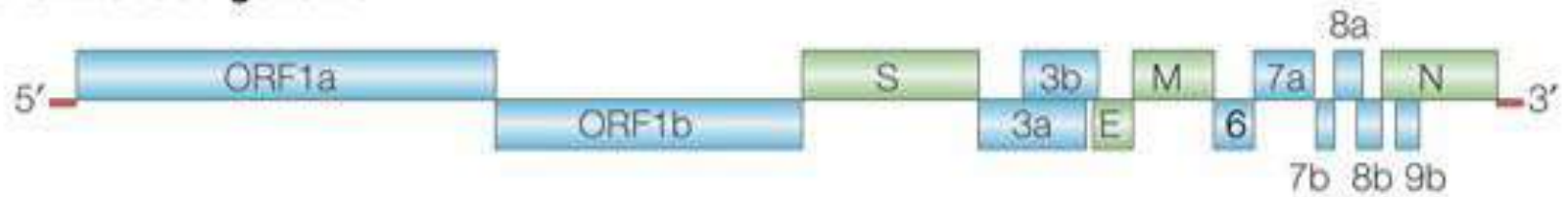
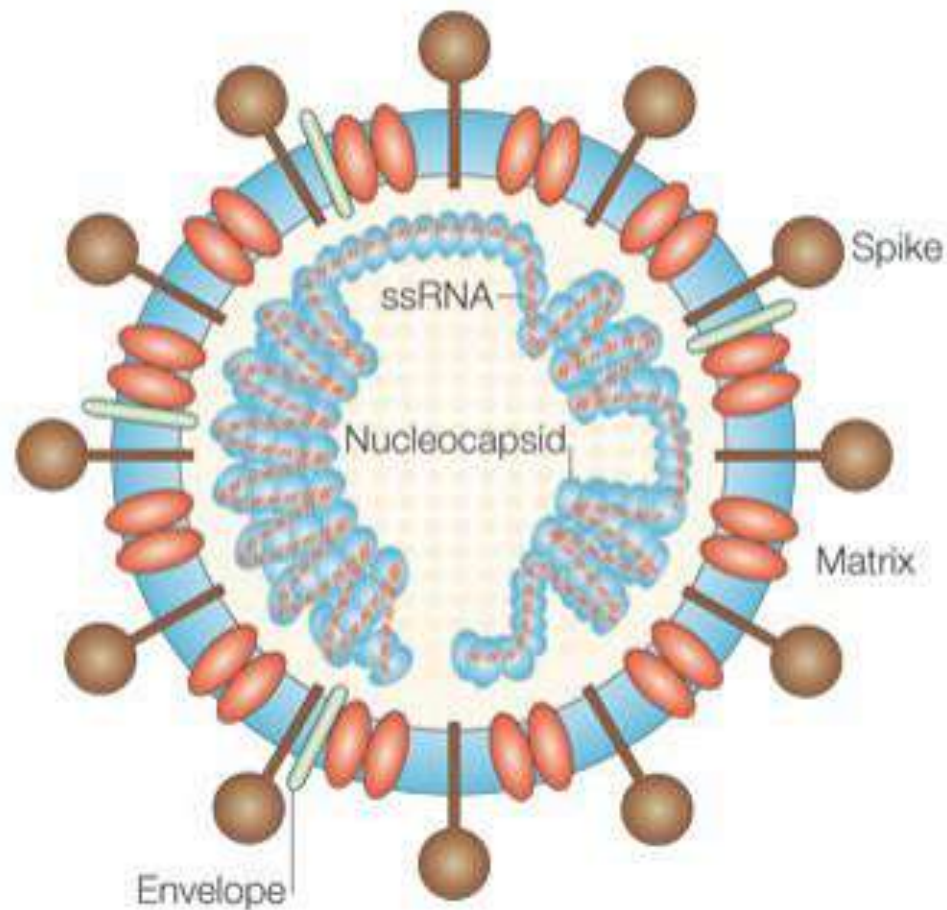
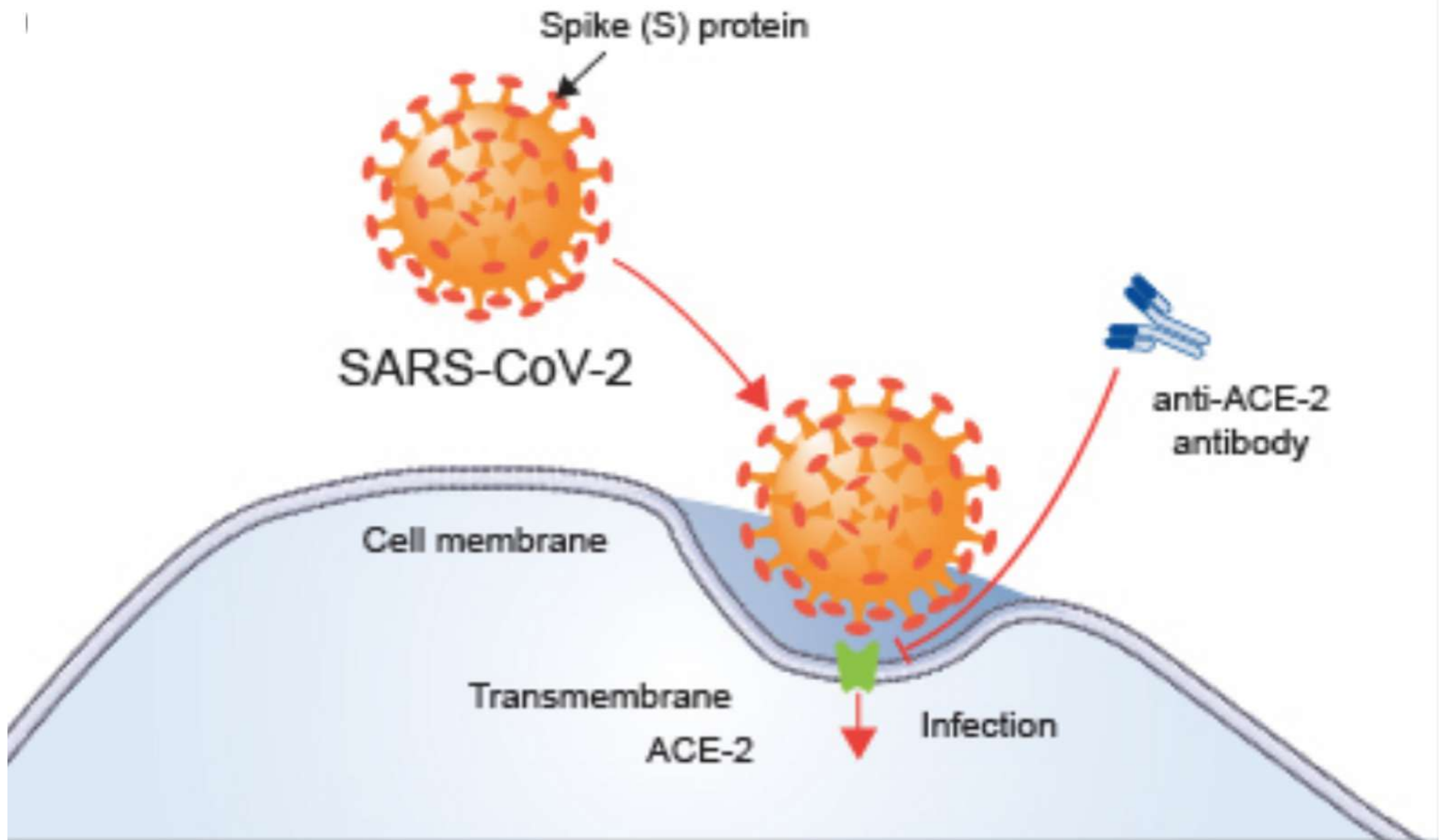


a SARS-CoV genome



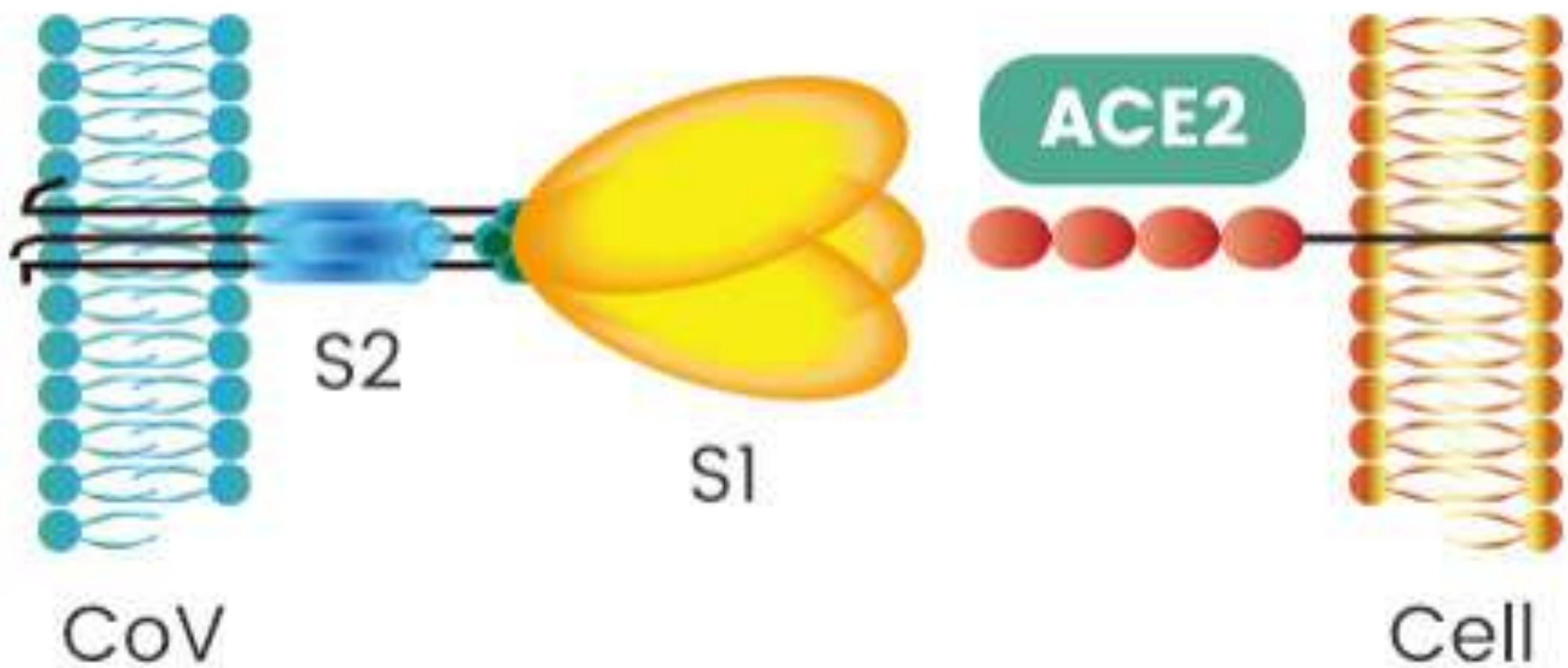
b SARS-CoV virion

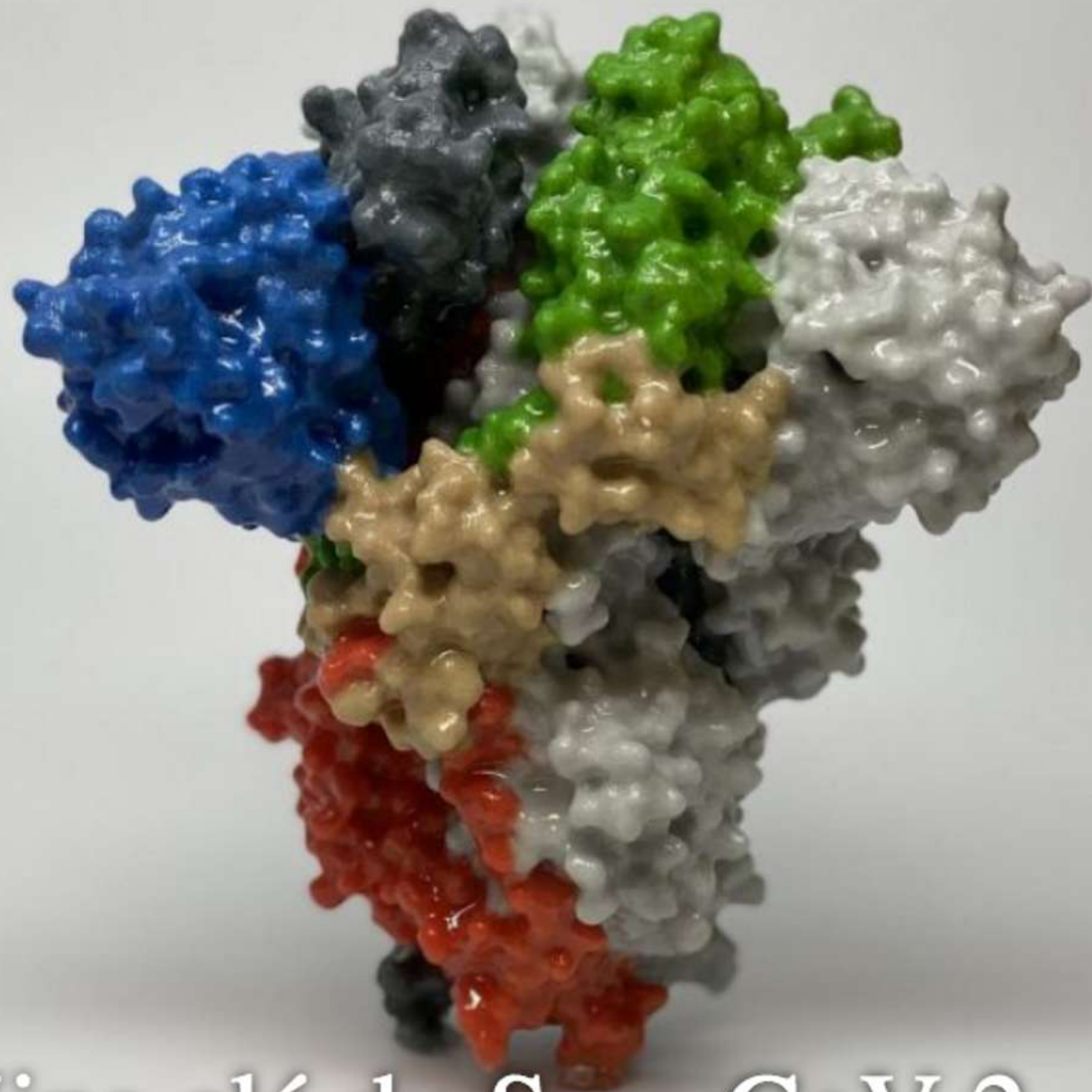




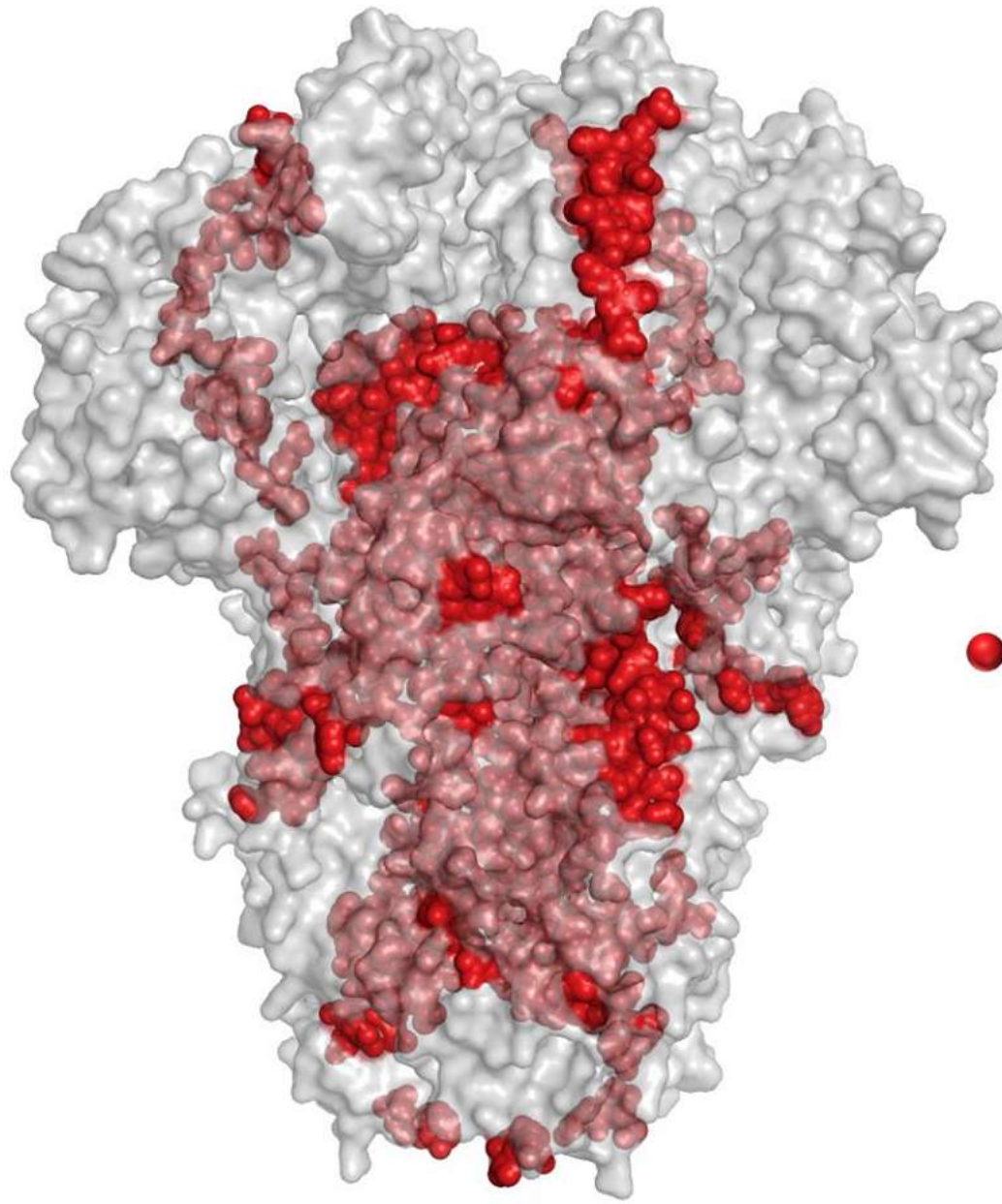
R&D Systems

ACE-2 is shown to be the entry receptor for SARS-CoV-2





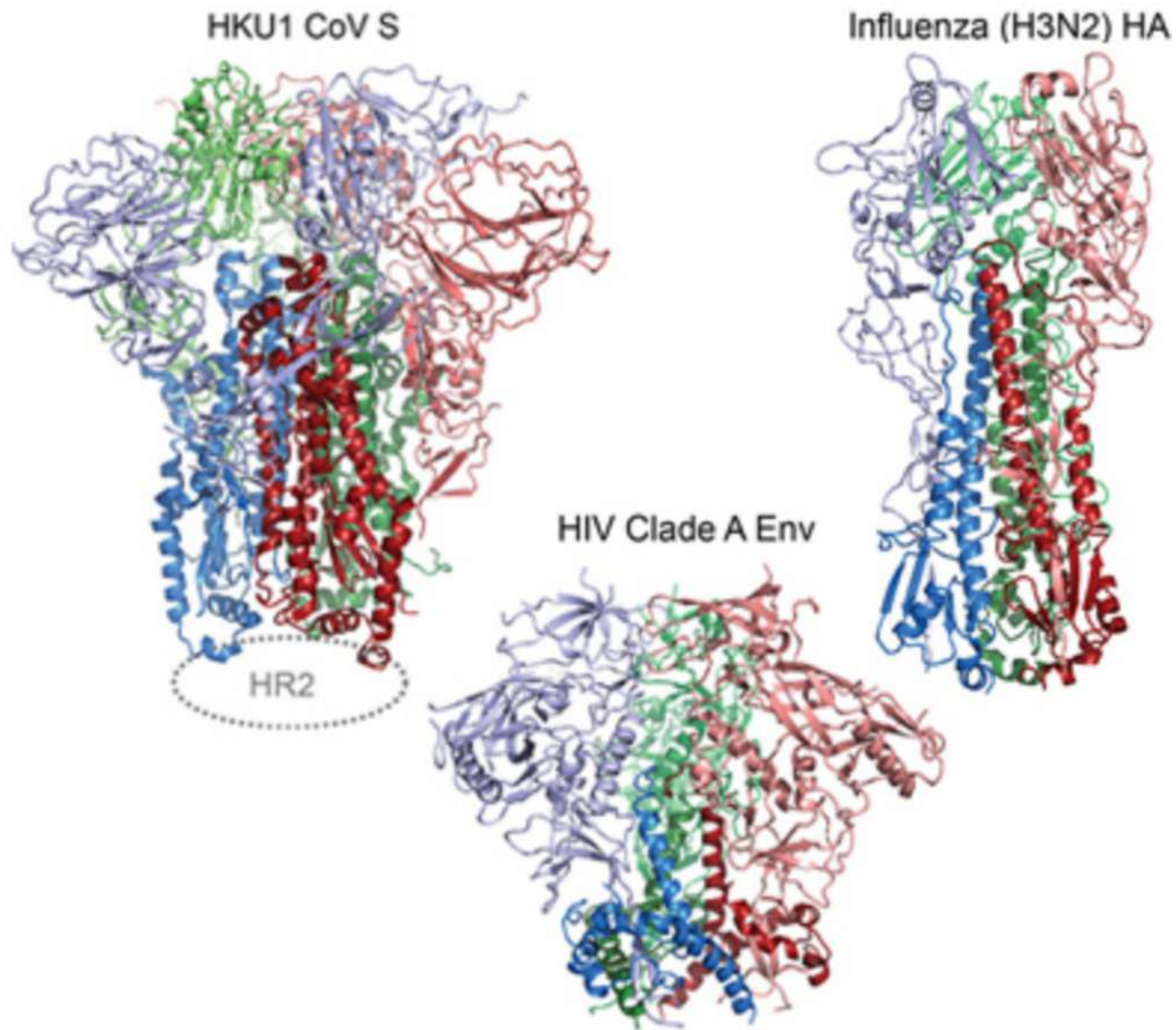
protéine clé du Sras-CoV-2



● B cell epitopes that map identically to SARS-CoV-2

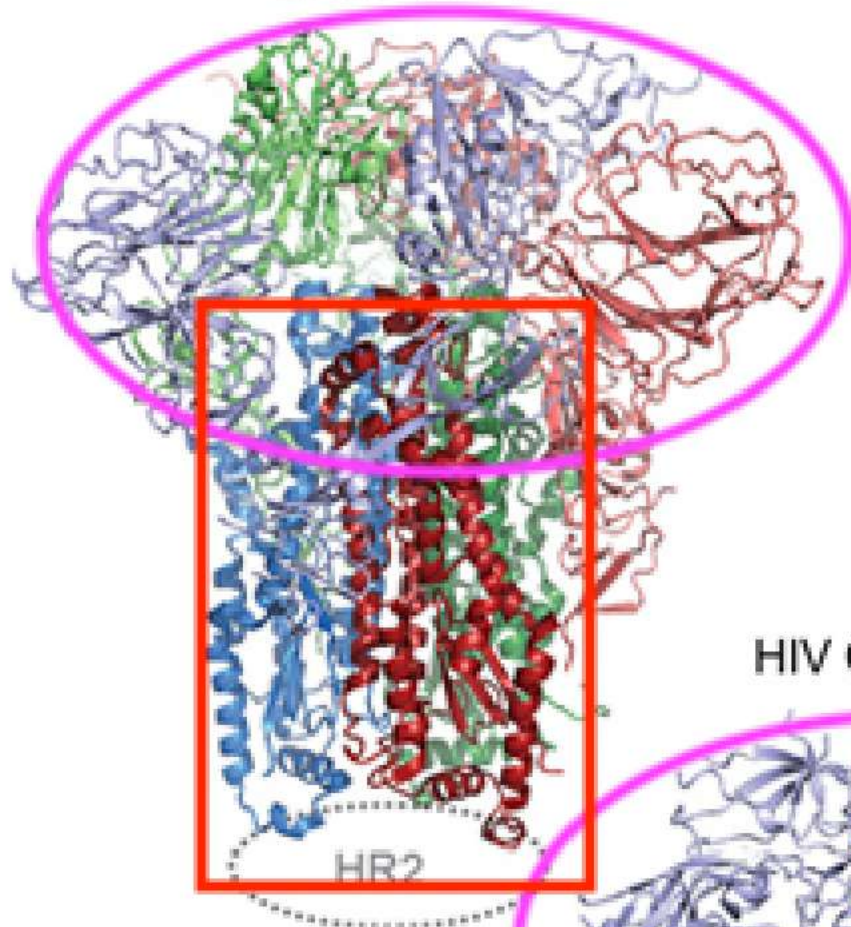
SARS-CoV spike protein

B cell epitopes that map identically to SARS-CoV-2. Credit: HKUST

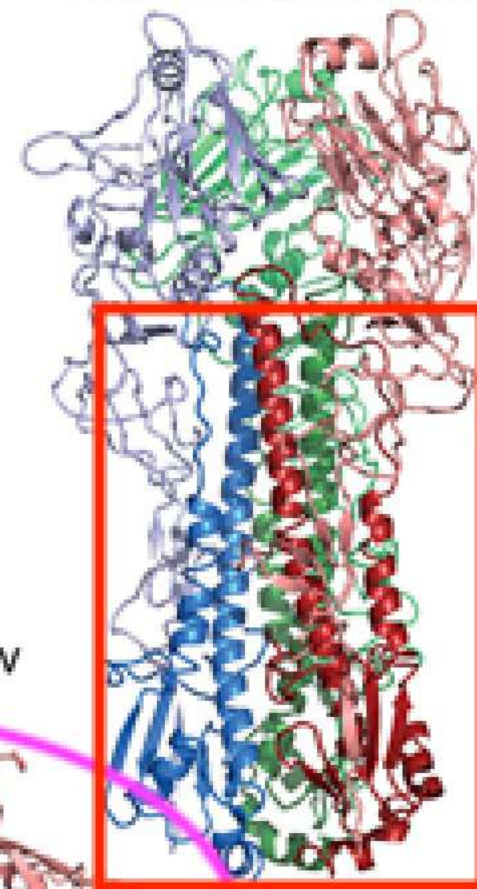


The coronavirus spike (CoV S) is the largest class I fusion protein known and displays structural similarities to the spike proteins of influenza virus and HIV. (Image courtesy of Robert Kirchdoerfer.)

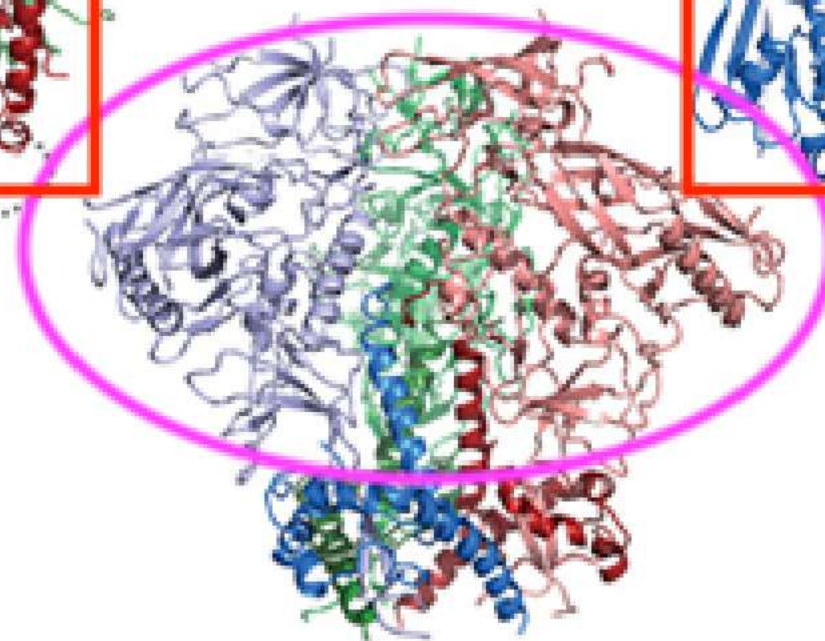
HKU1 CoV S



Influenza (H3N2) HA



HIV Clade A Env



S230, an antibody known to have neutralizing activity against the Severe Acute Respiratory Syndrome coronavirus, is predicted to interact with an initial model of a surface protein on the novel coronavirus. This computational estimate can quickly provide researchers with structural insights without waiting for time-consuming X-ray crystallography images of the actual protein.

