

wrought have in China and caused a pandemic situation in the worldwide population, leading to disease outbreaks that have not been controlled to date, although extensive efforts are being put in place to counter this virus (25). This virus has been proposed to be designated/named severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) by the International Committee on Taxonomy of Viruses (ICTV), which determined the virus belongs to the Severe acute respiratory syndrome-related coronavirus category and found this virus is related to SARS-CoV (26). SARS-CoV-2 is a member of the order Nidovirales, family Coronaviridae, subfamily Orthocoronavirinae, which is subdivided into four genera, viz., Alphacoronavirus, Betacoronavirus, Gammacoronavirus, and Deltacoronavirus (3, 27). The genera Alphacoronavirus and Betacoronavirus originate from bats, while Gammacoronavirus and Deltacoronavirus have evolved from bird and swine gene pools (24, 28, 29, 275).

Coronaviruses possess an unsegmented, single-stranded, positive-sense RNA genome of around 30 kb, enclosed by a 5'-cap and 3'-poly(A) tail (30). The genome of SARS-CoV-2 is 29,891 bp long, with a G+C content of 38% (31). These viruses are enriched with an envelope containing viral