



Genomic Variation and Epidemiology of SARS-CoV-2

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Deadline for manuscript
submissions:

closed (20 March 2023)

Message from the Guest Editors

The COVID-19 global pandemic caused by SARS-CoV-2 is currently ongoing. Genome-wide analyses of SARS-CoV-2 variants and epidemiological studies are critically important in order to identify changes in virus transmissibility and COVID-19 disease severity, the ability of the virus to avoid immunity induced by vaccination or postinfection, and how these features may impact pandemic progress. The most important mutations are those at the level of the spike protein of SARS-CoV-2, because this region is important for cellular receptor binding and endocellular penetration of the virus, and because vaccination-induced antibodies are directed against it.

This Special Issue of the International Journal of Molecular Sciences focuses on the research field of Genomic Variation and Epidemiology of SARS-CoV-2, and welcomes both original research articles and review articles with the aim of providing useful evidence for the global scientific community during the COVID-19 pandemic.





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Message from the Editor-in-Chief

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