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Detection and Assessment of SARS-CoV-2 Variants

Guest Editor:

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Deadline for manuscript submissions:
closed (31 August 2023)

Message from the Guest Editor

Dear Colleagues,

Since the first severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variant Alpha was identified in England in late November 2021, mutations in the viral genome can increase transmissibility, facilitate escape from the human immune system, and/or alter biologically important phenotypes. The SARS-CoV-2 variants are classified as variants being monitored (VBMs), variants of interest (VOIs), variants of concern (VOCs), and variants of high consequence (VOHCs). There are two currently circulating SARS-CoV-2 VOCs (Delta and Omicron), and three previously circulating VOCs (Alpha, Beta, and Gamma) in a way that confers a fitness advantage to the virus.

Previous studies have pointed out that viral genomic mutations leading to new variants of SARS-CoV-2 are a real challenge in tackling the global coronavirus disease (COVID-19). Understanding SARS-CoV-2 variants remains an issue of concern for all local government authorities and are critical for establishing and implementing effective public health measures.

This Special Issue will cover all related areas, such as diagnostic applications, VOC pathogen detection, biomarker monitoring, and others of concern.

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Message from the Editor-in-Chief

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