

Current altona Diagnostics SARS-CoV-2 test kits reactivity analysis (Sep 10, 2023)

Section 1 does focus specifically on the S gene mutations as these are of the highest public concern. Not only due to the possible implications for molecular diagnostic assays but even more so due to potential devastating effects on vaccine efficiency and possible immune evasion of these variants.

Section 2 shows the summarized results from our latest bioinformatical analysis including all newly retrieved sequences collected from different online sources between Aug 14, 2023 to Sep 10, 2023.

Section 1: Variants of concern and other spike mutations

The Omicron viruses account for over 98% of the publicly available sequences since February 2022 and constitute the genetic background from which new SARS-CoV-2 variants will likely emerge, although the emergence of variants derived from previously circulating VOCs or of completely new variants remains possible. Therefore, the Omicron sublineages are independently classified as variants of different public importance. Among those are the variants listed in Table 1:

Table 1: SARS-CoV-2 variants

	WHO Label	PANGOLIN Lineage	Nextstrain clade	Earliest documented samples
Variants of interest (VOIs)	Omicron	XBB.1.5	23A	21-10-2022
	Omicron	XBB.1.16	23B	09-01-2023
	Omicron	EG.5	Not assigned	17-02-2023
Variants under monitoring (VUMs)	Omicron	BA.2.75	22D	31-12-2021
	Omicron	CH.1.1	22D	27-07-2022
	Omicron	XBB	22F	19-08-2022
	Omicron	XBB.1.9.1	23D	05-12-2022
	Omicron	XBB.1.9.2	23D	05-12-2022
	Omicron	XBB.2.3	23E	09-12-2022
	Omicron	BA.2.86	Not assigned	24-07-2023

None of the mutations contained in the above-mentioned variants does impact the performance of the S gene detection system included in the RealStar®, FlexStar® and AltoStar® kits for detection of SARS-CoV-2.

Section 2: *In silico* reactivity analysis

Inclusivity data were collected from 14.08.2023 to 10.09.2023 and *in silico* analysis was performed using the newly published sequences and data from the indicated time period (see Table 2).

Table 2: Inclusivity (*In silico* analysis for **82,810** whole genome sequences of SARS-CoV-2 published via GISAID e.V. (www.gisaid.org) and via National Center for biotechnology Information (www.ncbi.nlm.nih.gov) as of Aug 14, 2023 to Sep 10, 2023 for the E gene and the S gene target included in the RealStar®, FlexStar® and AltoStar® kits for detection of SARS-CoV-2.

82810 whole genome sequences (14.08.-10.09.)		Percentage of sequences showing mismatches
E gene	Forward Primer	92.81
	Reverse Primer	0.11
	Probe	0.21
S gene	Forward Primer	2.63
	Reverse Primer	0.33
	Probe	0.48

Depending on the mutation frequency and position wet lab experiments in the cause of the post market surveillance activities for the RealStar®, FlexStar® and AltoStar® kits for detection of SARS-CoV-2 were done and so far confirmed that the performance was not affected by such mutations.

Including all previous and this latest data analysis, we have not yet found sequences in the database rendering the respective products for SARS-CoV-2 detection useless or severely diminishing their performance.