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Eurofins unveils NGS service to identify viral mutations

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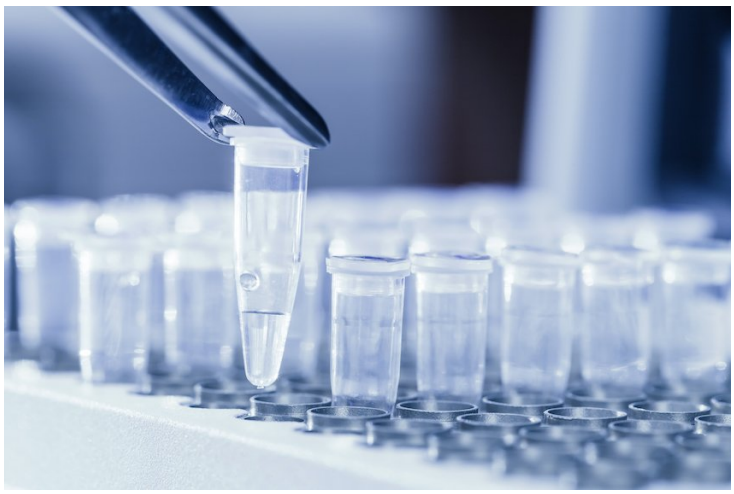

Eurofins Genomics has launched an optimised, cost-effective, SARS-CoV-2, next-generation sequencing service providing full length viral genome sequences. The best-in-class ARTIC NGS Oligo mix synthesised by Eurofins Genomics' Synthesis branch will be commercially available shortly.

The new NGS service and ARTIC NGS oligo kit are Eurofins' latest additions to a comprehensive product portfolio to support researchers globally in the development of vaccines and in their fight against the COVID-19 pandemic.

The increasing diversity of SARS-CoV-2 variants and the potential threat of increased virulence, higher infectivity and altered epitopes of these newly evolving viral strains, underline the need to identify, trace and track mutations over the complete viral genome. Whole genome SARS-CoV-2 sequencing identify mutant strains and spot emerging risks, including potentially immune and vaccine evasive variants, at an early stage.

The service and oligo mix are based on a protocol by the ARTIC consortium, which is used for SARS-CoV-2 sequencing worldwide. The ARTIC approach utilises an oligo pool for multiplexed PCR amplification of the complete viral genome.

Eurofins Genomics' sophisticated bioinformatic pipeline assembles and compares the resulting contiguous full-length SARS-CoV-2 isolate sequences and delivers a report for conclusive interpretation. The new service exploits Eurofins Genomics scalable, automated, standardised laboratory information management system (LIMS) controlled high throughput next generation sequencing facility.

As announced on December 23, 2020, Eurofins is offering part of its sequencing capacity for free to public healthcare authorities who do not have emergency budgets available to detect the VUI2020-12/01 strain reported to be currently fast-spreading in the UK.