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Age / Gender	: 27 Years / Female	Registered on	: 18-Sep-2022 / 15:15 PM
Ref.By	: P.NO: R0642809	Collected on	: 18-Sep-2022 / 15:16 PM
Req.No		Reported on	: 18-Sep-2022 / 21:15 PM
	BIL1833279	TEST REPORT	

DEPARTMENT OF MOLECULAR PATHOLOGY
SARS-CoV-2, Targeted S-Gene Detection

Investigation	Result
Specimen Type	Nasopharyngeal/Oropharyngeal swab
N gene	Not Detected
ORF1ab	Not Detected
S gene	Not Detected
SARS-CoV-2 - RNA DETECTION	POSITIVE

Method: Real Time PCR

GenePath Dx CoViDelta - Targeted S - Gene Kit

Interpretation:

SARS-CoV-2 is a single stranded RNA virus, causing the disease COVID-19. Clinical presentation ranges from asymptomatic cases to mild, moderate and severe illness. Risk factors for severe COVID-19 infection may include advanced age, Immunocompromised state, Diabetes, Cardiovascular disease, Hypertension, Chronic pulmonary disease, Liver disease, Malignancy, Severe obesity.

This test is a real-time RT-PCR test intended for the qualitative detection of SARS-CoV-2 Nucleic Acid from respiratory samples of individuals suspected of COVID-19. SARS-CoV-2 RNA is generally detectable in respiratory specimens during the acute phase of infection. This is a multiplex assay that contains three primers/probes - N gene, ORF1ab gene, S gene- that are specific and confirmatory for SARS-CoV-2.

NOTE :

1. ICMR Regd No. For COVID-19 Testing : TDAUC001
2. All results relate only to the specimen tested and should be correlated with other clinical and radiographical findings.
3. A negative result, particularly from an upper respiratory sample does not rule out the possibility of COVID-19 infection as presence of inhibitors, mutations and insufficient RNA and other factors can influence the results. Repeat sampling and testing of lower respiratory specimen is strongly recommended in severe or progressive disease.
4. CT Values > 30 is suggestive of Borderline Positive and should be correlated clinically. Advised repeat test if clinically indicated.
5. Due to relatively fast molecular evolution of RNA viruses, there is an inherent risk that accumulation of mutations over time may lead to false negative results. Positive results do not rule out bacterial infection or co-infection with other viruses.
6. SARS-CoV-2 variants identification can only be done by genomic sequencing.

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