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PATIENT REPORT

Patient Age/Sex: 24 years Male

Specimen Collected: 17-Jun-24 14:26

HCV Quant with Reflex to HCV Genotype | **Received: 17-Jun-24 14:33** **Report/Verified: 17-Jun-24 14:40**

Procedure	Result	Units	Reference Interval
HCV Qnt by NAAT (IU/mL)	124,000	IU/mL	
HCV Qnt by NAAT (log IU/mL)	5.09 [f1]	log IU/mL	
HCV Qnt by NAAT Interp	**Detected** * [i1]		[Not Detected]

HCV Genotype by PCR and Sequencing | **Received: 17-Jun-24 14:33** **Report/Verified: 18-Jun-24 10:07**

Procedure	Result	Units	Reference Interval
HCV Genotype by Sequencing	1a or 1b [i2]		

Result Footnote

f1: HCV Qnt by NAAT (log IU/mL)

Hepatitis C Virus Genotype by Sequencing added.

Test Information

i1: HCV Qnt by NAAT Interp

INTERPRETIVE INFORMATION: HCV by Quantitative NAAT

The quantitative range of this test is 15-100,000,000 IU/mL (1.18-8.0 log IU/mL).

A result of "Not Detected" does not rule out the presence of inhibitors in the patient specimen or hepatitis C virus RNA concentrations below the level of detection of the test. Care should be taken when interpreting any single viral load determination.

This test is intended for use as an aid in the diagnosis of HCV infection in the following populations: individuals with antibody evidence of HCV with evidence of liver disease, individuals suspected to be actively infected with HCV antibody evidence, and individuals at risk for HCV infection with antibodies to HCV. Detection of HCV RNA indicates that the virus is replicating and therefore is evidence of active infection.

This test is also intended for use as an aid in the management of patients with an HCV infection undergoing antiviral therapy. The assay can be used to measure HCV RNA levels at baseline, during treatment, at the end of treatment, and at the end of follow-up of treatment to determine sustained or nonsustained viral response. The results must be interpreted within the context of all relevant clinical and laboratory findings.

This test should not be used for blood donor screening, associated reentry protocols, or for screening human cells, tissues, and cellular tissue-based products (HCT/P).

i2: HCV Genotype by Sequencing

INTERPRETIVE INFORMATION: Hepatitis C Genotyping

*=Abnormal, #=Corrected, C=Critical, f=Result Footnote, H-High, i-Test Information, L-Low, t-Interpretive Text, @=Performing lab

Test Information

i2: HCV Genotype by Sequencing

Hepatitis C viral RNA is tested using reverse transcription polymerase chain reaction (RT-PCR) to amplify a specific portion of the 5' untranslated region (5' UTR) of the viral genome. The amplified nucleic acid is sequenced bidirectionally using dye-terminator chemistry (ABI). Sequencing data is compared to a database of characterized sequences.

Isolates of hepatitis C virus are grouped into six major genotypes (1-6). These genotypes are subtyped according to sequence characteristics. Due to high conservation of the 5' untranslated region of the HCV genome, this test has limitations in differentiating subtype 1a from 1b. Therefore, these subtypes will be reported as "1a or 1b." In rare instances, type 6 virus may be misclassified as type 1.

This test was developed and its performance characteristics determined by ARUP Laboratories. It has not been cleared or approved by the U.S. Food and Drug Administration. This test was performed in a CLIA-certified laboratory and is intended for clinical purposes.