

Client: Example Client ABC123
123 Test Drive
Salt Lake City, UT 84108
UNITED STATES

Physician: Doctor, Example

Patient: Patient, Example

DOB: 6/10/1964
Gender: Male
Patient Identifiers: 01234567890ABCD, 012345
Visit Number (FIN): 01234567890ABCD
Collection Date: 01/01/2017 12:34

Hepatitis C Virus (HCV) by Quantitative NAAT with Reflex to HCV High-Resolution Genotype by Sequencing

ARUP test code 3000577

HCV Qnt by NAAT (IU/mL) 10,495,898 IU/mL

HCV Qnt by NAAT (log IU/mL) 7.02 log IU/mL

Hepatitis C Virus High-Resolution Genotype by Sequencing added.

HCV Qnt by NAAT Interp

Detected * (Ref Interval: Not Detected)

INTERPRETIVE INFORMATION: HCV by Quantitative NAAT

Normal range for this assay is "Not Detected".
The quantitative range of this assay is 10 - 100,000,000 IU/mL (1.0 - 8.0 log IU/mL).

Lower limit of quantitation (LLOQ):

10 IU/mL (1.0 log IU/mL)

LLOQ values do not apply to diluted specimens.

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 should not be used for blood donor screening, associated re-entry protocols, or for screening Human Cell, Tissues and Cellular Tissue-Based Products (HCT/P).

Hepatitis C Virus High-Resolution Genotype by Sequencing

ARUP test code 2006898

Hepatitis C High-Res Genotype by Seq 1a

H=High, L=Low, *=Abnormal, C=Critical

Unless otherwise indicated, testing performed at:

ARUP LABORATORIES | 800-522-2787 | aruplab.com
500 Chipeta Way, Salt Lake City, UT 84108-1221
Tracy I. George, MD, Laboratory Director

Patient: Patient, Example
ARUP Accession: 20-064-136534
Patient Identifiers: 01234567890ABCD, 012345
Visit Number (FIN): 01234567890ABCD
Page 1 of 2 | Printed: 1/7/2021 2:23:18 PM
4848

INTERPRETIVE INFORMATION: Hepatitis C High Resolution Genotype

Hepatitis C viral RNA is assayed using reverse transcription polymerase chain reaction (RT-PCR) to amplify specific portions of both the Core and NS5B regions of the viral genome. The amplified nucleic acid is sequenced bi-directionally 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. Sequencing both the Core and NS5B regions allows for subtyping of all confirmed and most provisional genotypes, including differentiation of 1a from 1b and typing of genotype 6.

Test developed and characteristics determined by ARUP Laboratories. See Compliance Statement B: aruplab.com/CS

VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
HCV Qnt by NAAT (IU/mL)	20-064-136534	3/4/2020 2:45:00 PM	3/6/2020 1:58:06 PM	3/7/2020 11:01:00 AM
HCV Qnt by NAAT (log IU/mL)	20-064-136534	3/4/2020 2:45:00 PM	3/6/2020 1:58:06 PM	3/7/2020 11:01:00 AM
HCV Qnt by NAAT Interp	20-064-136534	3/4/2020 2:45:00 PM	3/6/2020 1:58:06 PM	3/7/2020 11:01:00 AM
Hepatitis C High-Res Genotype by Seq	20-064-136534	3/4/2020 2:45:00 PM	3/7/2020 11:00:55 AM	3/10/2020 10:11:00 AM

END OF CHART

H=High, L=Low, *=Abnormal, C=Critical

Unless otherwise indicated, testing performed at:

ARUP LABORATORIES | 800-522-2787 | aruplab.com
500 Chipeta Way, Salt Lake City, UT 84108-1221
Tracy I. George, MD, Laboratory Director

Patient: Patient, Example
ARUP Accession: 20-064-136534
Patient Identifiers: 01234567890ABCD, 012345
Visit Number (FIN): 01234567890ABCD
Page 2 of 2 | Printed: 1/7/2021 2:23:18 PM
4848