

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

Physician: Doctor, Example

## **Patient: Patient, Example**

DOB	2/2/2025
Gender:	Unknown
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
<b>Collection Date:</b>	00/00/0000 00:00

## Cytomegalovirus Drug Resistance by Next Generation Sequencing, Ganciclovir, Foscarnet, Cidofovir, Maribavir, and Letermovir

ARUP test code 3004615

CMV Drug Resistance by NGS, 5 Drugs	Indeterminate Cytomegalovirus Drug Resistance by Next Generation Sequencing is Indeterminate.	
	In most cases, samples below the lower limit of detection of the assay cannot be sequenced. In addition to low viral load, other conditions such as inhibitors and viral genetic variation may cause sequencing failure and an indeterminate result.	
	CMVResistanceCaller software version: 2.2.1.1	
	CMV_resistance_mutations_20231228.db	

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 Jonathan R. Genzen, MD, PhD, Laboratory Director



INTERPRETIVE INFORMATION: CMV Drug Resistance by NGS, 5 Drugs

This assay assesses resistance to ganciclovir, foscarnet, This assay assesses resistance to ganciciovir, foscarnet, cidofovir, maribavir, and letermovir. Resistance-associated mutations in the UL97, UL54, UL27, and UL56 genes are sequenced using next generation sequencing. Drug resistance is assigned using an ARUP-developed database of published resistance mutations. For a list of resistance mutations refer to https://ltd.aruplab.com/Tests/Pub/3004615. This test detects populations down to 10% of the total This test detects populations down to 10% of the total population which may account for resistance interpretation differences between methods. Some insertions or deletions may be difficult to detect using this software. Drug Resistance Interpretations are defined as follows: -Not determined indicates incomplete sequence coverage across a given gape or gaped. Not determined indicates incomplete sequence coverage across a given gene or genes.
-Likely sensitive indicates that a single drug resistance mutation position did not have adequate coverage. However, the missing mutation is rarely observed.
-Sensitive indicates no drug resistance mutations were detected.
-Possible resistance indicates mutations were detected with berdenline-lovel drug resistance or conflicting resistance borderline-level drug resistance or conflicting resistance status reported in the literature. -Resistant indicates that mutations associated with drug resistance were detected. -Inadequate sequence coverage indicates a low number of sequence reads at a given drug resistance site. Mutations are classified as follows: -Drug Resistance Mutations reduce susceptibility of specific drug classes whether found in isolation or in combination with other drugs. -Additional mutations have not been associated with drug resistance. -Uncalled mutation sites are known locations of drug resistance mutations that have an inadequate number of sequencing reads to accurately determine if mutations are present. Drugs associated with each gene are as follows: UL97: ganciclovir, maribavir UL54: ganciclovir, foscarnet, cidofovir UL27: maribavir UL56: letermovir

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.

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VERIFIED/REPORTED DATES				
Procedure	Accession	Collected	Received	Verified/Reported
CMV Drug Resistance by NGS, 5 Drugs	24-357-108353	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00

## END OF CHART

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

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