

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

Physician: Doctor, Example

Patient: Patient, Example

DOB: 11/10/1974
Gender: Male
Patient Identifiers: 01234567890ABCD, 012345
Visit Number (FIN): 01234567890ABCD
Collection Date: 00/00/0000 00:00

Human Immunodeficiency Virus 1 (HIV-1) by Quantitative NAAT with Reflex to HIV-1 Genotype by Sequencing

ARUP test code 3000870

HIV-1 Qnt by NAAT (copies/mL) 1,803,796

HIV-1 Qnt by NAAT (log copies/mL) 6.26 log cpy/mL

HIV-1 Genotype by Sequencing will be added.

HIV-1 Qnt by NAAT Interp

Detected * (Ref Interval: Not Detected)

INTERPRETIVE INFORMATION: HIV-1 by Quantitative NAAT, Plasma

Normal range for this assay is "Not Detected".
 The quantitative range of this assay is 1.47-7.00 log copies/mL (30-10,000,000 copies/mL).

An interpretation of "Not Detected" does not rule out the presence of inhibitors or HIV-1 RNA concentration below the level of detection of the assay. Care should be taken in the interpretation of any single viral load determination. The clinical significance of changes in HIV-1 RNA concentration has not been fully established; however, a change of 0.5 log copies/mL may be significant.

This assay 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).

Human Immunodeficiency Virus 1, Genotype by Sequencing

ARUP test code 0055670

HIV-1 Genotype by Sequencing

See Note

Drug Resistance:
 NRTI Drug Class

VIDEX, (didanosine, ddI)	None
VIREAD, (tenofovir, TDF)	None
ZERIT, (stavudine, d4T)	None
ZIAGEN, (abacavir, ABC)	None
EMTRIVA, (emtricitabine, FTC)	None
RETROVIR, (zidovudine, ZDV)	None

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

EPIVIR, (lamivudine, 3TC) None

NRTI drug resistance mutations identified: None

NNRTI Drug Class

SUSTIVA, (efavirenz, EFV)	Resistance***
VIRAMUNE, (nevirapine, NVP)	Resistance***
INTELENCE, (etravirine, ETR)	None
EDURANT, (rilpivirine, RPV)	None

NNRTI drug resistance mutations identified: K101Q, K103N

PI+ Drug Class

VIRACEPT, (nelfinavir, NFV)	None
APTIVUS, (tipranavir, TPV)	None
CRIXIVAN, (indinavir, IDV)	None
KALETRA, (lopinavir + ritonavir, LPV)	None
REYATAZ, (atazanavir, ATV)	None
PREZISTA, (darunavir, DRV)	None
LEXIVA, (fosamprenavir, FPV)	None
FORTOVASE / INVIRASE, (saquinavir, SQV)	None

PI+ drug resistance mutations identified: None

Additional Mutations: The following amino acids differing from the reference sequence (HXB-2, accession number K03455) at the indicated codon positions were identified and may be useful as a baseline determination of virus genotype.

Protease: V3I, I13V, K14R, K20I, M36I, S37D, R41K, H69K, L89M

RT: K20R, V35T, E36A, V60I, E122K, D123E, I135V, S162A, K173T, Q174K, D177E, T200A, Q207E, R211K, L214F, V245Q, E248D, P272A, R277K, K281R, T286A, E291D, V292I, I293V, S322A, G335D

+ Evidence of Resistance for Protease Inhibitors estimates response to ritonavir boosted regimens. Refer to "Evidence of Resistance Legend." The protease inhibitor (PI) evidence of resistance interpretations were developed to estimate the expected virological response to standard doses of protease inhibitors with pharmacokinetic boosting by ritonavir. This has become the most common method of administering each of the protease inhibitors, except nelfinavir (ref. 1), to ensure adequate drug levels in all patients. Boosted PIs are more active in the presence of resistance than nonboosted PIs(ref. 2,3)

* NOTE: At least one mutation used to determine Evidence of Resistance for this drug has not been fully validated.

** NOTE: At least one mutation used to determine Evidence of Resistance for this drug has not been clinically verified.

*** NOTE: For at least one mutation used to evaluate Evidence of Resistance for this drug, both notes above apply.

Evidence of Resistance Legend:

Resistance: Mutations present constitute a high level of genetic evidence for viral resistance.

Possible Resistance: Mutations present suggest the possibility of viral resistance.

None: There is insufficient evidence for viral resistance.

Software Version: ViroSeq HIV-1 System v2.0; ViroSeq Software

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

v3.0

INTERPRETIVE INFORMATION: HIV-1 Genotyping

This assay predicts HIV-1 resistance to protease and reverse transcriptase inhibitor anti-retroviral drugs. The protease gene and codons 1-335 of the reverse transcriptase gene of the viral genome are sequenced using the Viroseq HIV-1 Genotyping System kit. Drug resistance is assigned using ViroSeq software. The most current resistance algorithm and drug list is available by selecting the Drug Resistance Report found in the test directory.

This test should be used in conjunction with clinical presentation and other laboratory markers. A patient's response to therapy depends on multiple factors, including patient compliance, percentage of resistant virus population, dosing, and drug pharmacology issues. Resistance interpretations may vary with methodology.

Some insertions or deletions may be difficult to detect using this software. This test may not detect minor HIV-1 populations less than 20 percent of the total population.

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

EER HIV-1 Genotype by Sequencing

See Note

Access ARUP Enhanced Report using either link below:

-Direct access:

-Enter Username, Password:

Username:
 Password:

VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
HIV-1 Qnt by NAAT (copies/mL)	19-197-108798	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
HIV-1 Qnt by NAAT (log copies/mL)	19-197-108798	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
HIV-1 Qnt by NAAT Interp	19-197-108798	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
HIV-1 Genotype by Sequencing	19-197-108798	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
EER HIV-1 Genotype by Sequencing	19-197-108798	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