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

Physician: Doctor, Example

Patient: Patient, Example

DOB	3/16/1999
Gender:	Male
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
Collection Date:	01/01/2017 12:34

HIV1 Genotype and Integrase Inhibitor Resistance by Sequencing

ARUP test code 2009256

HIV-1 Genotype by Sequencing	See Note

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

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
EPIVIR, (lamivudine, 3TC)	None

NRTI drug resistance mutations identified: None

NNRTI Drug Class

SUSTIVA, (efavirenz, EFV)	Possible Resistance
VIRAMUNE, (nevirapine, NVP)	Resistance
INTELENCE, (etravirine, ETR)	Possible Resistance
EDURANT, (rilpivirine, RPV)	Possible Resistance

NNRTI drug resistance mutations identified: Y181C

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: A71T

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, S37D, K45R, R57K, D60E, Q61E, I62V, L63P, I64L
RT: V35T, T39L, E122K, D123E, I135T, T200A, Q207E, L228H, P272A, T286A, P294T, T296S, E297K, R307K

+ 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 Pls(ref. 2,3)

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 v3.0

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

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

HIV-1 Integrase Inhib. Resistance, Seq	See Note

Drug Resistance Interpretation: IN

IN Major Resistance Mutations: None
IN Accessory Resistance Mutations: None

Other Mutations: K7R, E11D, A38N, S39C, L45Q, I72V, L101I, T124A, T125A, I182V, V201I, D207N, K211T

Integrase Strand Transfer Inhibitors

bictegravir (BIC): Susceptible
dolutegravir (DTG): Susceptible
elvitegravir (EVG): Susceptible
raltegravir (RAL): Susceptible

INTERPRETIVE INFORMATION: HIV-1 Integrase Inhibitor Resistance

The entire integrase-encoding region is sequenced. Mutations associated with resistance to integrase inhibitors are reported. Mutations in viral sub-populations below 20% of total may not be detected.

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

EER HIV-1 Genotype by Seq for Panel	See Note

Access ARUP Enhanced Report using the link below:

-Direct access:

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

VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
HIV-1 Genotype by Sequencing	20-015-400637	1/9/2020 10:10:00 AM	1/16/2020 7:04:41 AM	1/18/2020 7:09:00 PM
HIV-1 Integrase Inhib. Resistance, Seq	20-015-400637	1/9/2020 10:10:00 AM	1/16/2020 7:04:41 AM	1/18/2020 7:49:00 AM
EER HIV-1 Genotype by Seq for Panel	20-015-400637	1/9/2020 10:10:00 AM	1/16/2020 7:04:41 AM	1/19/2020 4:54:00 PM

END OF CHART