# HIV1 Genotype and Integrase Inhibitor Resistance by Sequencing

ARUP LABORATORIES

**Patient:** [redacted]
DOB: [redacted] Age: [redacted] Gender: [redacted]
**Patient Identifiers:** [redacted]
**Visit Number (FIN):** [redacted]

Client: [redacted]
Physician: [redacted]

ARUP Test Code: 2009256

Collection Date: 01/09/2020
Received in lab: 01/16/2020
Completion Date: 01/19/2020

## Human Immunodeficiency Virus 1, Genotype by Sequencing

| Drug Class | Drug | | Evidence of Resistance |
|---|---|---|---|
| NRTI | 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 |
| NNRTI | SUSTIVA | (efavirenz, EFV) | Possible Resistance |
| | VIRAMUNE | (nevirapine, NVP) | Resistance |
| | INTELENCE | (etravirine, ETR) | Possible Resistance |
| | EDURANT | (rilpivirine, RVP) | Possible Resistance |
| PI + | 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 |

| Drug Class | Drug Resistance Mutations Identified |
|---|---|
| NRTI | None |
| NNRTI | Y181C |
| PI | A71T |

**Notes on Evidence of Resistance:**

| | |
|---|---|
| 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. |

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 non-boosted PIs. (ref. 2,3)



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| | |
|---|---|
| + | Evidence of Resistance for Protease Inhibitors estimates response to ritonavir boosted regimens. Refer to titled "Notes on Evidence of Resistance". |
| * | At least one mutation used to determine Evidence of Resistance for this drug has not been fully validated. |
| ** | At least one mutation used to determine Evidence of Resistance for this drug has not been clinically verified. |
| *** | For at least one mutation used to evaluate Evidence of Resistance for this drug, both notes above apply. |

**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

**Reverse Transcriptase:**

V35T, T39L, E122K, D123E, I135T, T200A, Q207E, L228H, P272A, T286A, P294T, T296S, E297K, R307K

Software Version: ViroSeq HIV-1 System v2.0; ViroSeq Software v3.0
Profile Version: hiv3.4-xml1.1

**Additional Information**

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

**Full report for HIV1 Genotype and Integrase Inhibitor Resistance by Sequencing continues on next page.**



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**Patient:** [redacted] | **Date of Birth:** [redacted] | **Gender:** [redacted] | **Physician:** [redacted]
**Patient Identifiers:** [redacted] | **Visit Number (FIN):** [redacted]

## HIV-1 Integrase Inhibitors Resistance by Sequencing

**HIV INT Result:**

**SEE NOTE**

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**HIV INT Result Comment:**

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

## Additional Information

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