Patient ID: CAS0109

UNIVERSITY OF KWAZULU NATAL

DEPARTMENT OF HIV MEDICINE

Hasso Plattner Research Laboratory

# HIV-1 Drug Resistance Genotyping Report

**Participant Study Number:** **CAS0109**

**Processed by:** Hasso Plattner Research Laboratory

**HPRL Lab No.:** CAS0109

**Date Sample Received:** 18 November 2011

**Methodology:** In-House HIV-1 Resistance Genotyping Assay

**Interpretation Algorithm Used:** Stanford HIV-1 Drug Resistance Database (Version 6.0.5 last updated 10/16/09)

**Performed by:** _____ **Date:** 25 November 2011
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DISCLAIMER: **This document is only valid if signed by two of the three signatories.**
**Time lapse from last drug dose may influence the result. Results may not represent the full resistance profile. Results should be interpreted in conjunction with the patient's clinical history.**

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STANFORD UNIVERSITY
**HIV DRUG RESISTANCE DATABASE**
*A curated public database designed to represent, store, and analyze the divergent forms of data underlying HIV drug resistance.*



# HIVdb: Genotypic Resistance Interpretation Algorithm

Date: 25-Nov-2011 00:37:07 PST

**Seq ID: CAS0109**

**Summary Data**

Sequence includes PR: codons: 1 - 99

Sequence includes RT: codons: 1 - 432

RT AA Deletion: codon 69

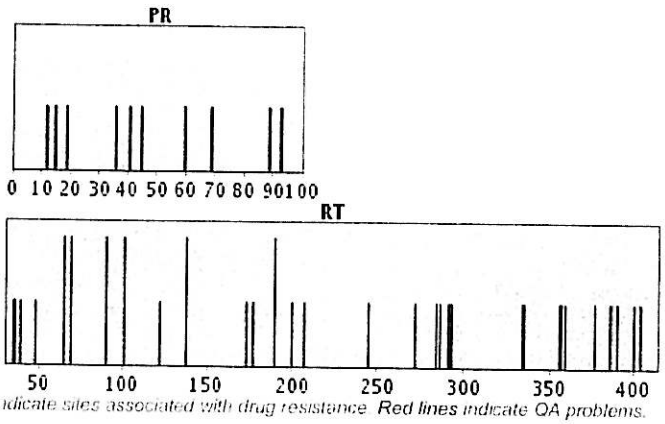
*Subtype and % similarity to closest reference isolate:*

1. *PR: C (94.3%)*
2. *RT: C (93.3%)*

**Sequence Quality Assessment**

| Gene | QA Problem | Codons |
|---|---|---|
| PR | Stop Codons, Frame Shifts: | *None* |
| PR | Ambiguous Positions: | *None* |
| PR | Unusual Residues: | *None* |

| Gene | QA Problem | Codons |
|---|---|---|
| RT | Stop Codons, Frame Shifts: | *None* |
| RT | Ambiguous Positions: | *None* |
| RT | Unusual Residues: | *None* |




***Blue lines** indicate differences from consensus B; **tall blue lines** indicate sites associated with drug resistance. **Red lines** indicate QA problems.*

**Drug Resistance Interpretation: PR**

| | |
|---|---|
| PI Major Resistance Mutations: | None |
| PI Minor Resistance Mutations: | None |
| Other Mutations: | T12S, I15V, L19V, M36I, R41K, K45R, D60E, H69K, L89M, I93L |

| Protease Inhibitors | |
|---|---|
| atazanavir/r (ATV/r) | Susceptible |
| darunavir/r (DRV/r) | Susceptible |
| fosamprenavir/r (FPV/r) | Susceptible |
| indinavir/r (IDV/r) | Susceptible |
| lopinavir/r (LPV/r) | Susceptible |
| nelfinavir (NFV) | Susceptible |
| saquinavir/r (SQV/r) | Susceptible |

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tipranavir/r (TPV/r) Susceptible

PR Comments

Other

M36I is weakly associated with PI resistance in subtype B viruses when present with other mutations. However, M36I is the consensus amino acid in most non-B subtypes.

D60E is a polymorphic mutation that is slightly more common in viruses from PI-treated compared with untreated persons.

L89M is a common polymorphism that is not associated with decreased PI susceptibility.

I93L is a common polymorphism. It is the consensus residue in most subtypes. In subtype B, it is weakly associated with PI treatment.

**Drug Resistance Interpretation: RT**

| | |
|---|---|
| **NRTI Resistance Mutations:** | **K65R, T69d** |
| **NNRTI Resistance Mutations:** | **V90I, K101E, E138K, G190E** |
| **Other Mutations:** | V35T, E36A, T39E, S48T, K122E, K173T, D177E, T200A, Q207E, V245K, A272P, R284K, T286A, E291D, V292I, I293V, Q334H, G335D, R356K, M357R, G359T, T377R, T386I, K390R, A400I, E404D |

| Nucleoside RTI | | Non-Nucleoside RTI | |
|---|---|---|---|
| **lamivudine (3TC)** | Intermediate resistance | **efavirenz (EFV)** | High-level resistance |
| **abacavir (ABC)** | High-level resistance | **etravirine (ETR)** | Intermediate resistance |
| **zidovudine (AZT)** | Low-level resistance | **nevirapine (NVP)** | High-level resistance |
| **stavudine (D4T)** | Intermediate resistance | **rilpivirine (RPV)** | Intermediate resistance |
| **didanosine (DDI)** | High-level resistance | | |
| **emtricitabine (FTC)** | Intermediate resistance | | |
| **tenofovir (TDF)** | High-level resistance | | |

RT Comments

NRTI

K65R causes intermediate resistance to ddI, ABC, 3TC, FTC, and TDF, and low-level resistance to d4T. K65R causes AZT hypersusceptibility.

Deletions at codon 69 occur at a frequency of about 0.1%. Their phenotypic and clinical significance is not known.

T69D/N/S/G/A/I are NRTI-selected mutations. T69d is a highly unusual mutation at this position.

NNRTI

V90I is a common polymorphism that is associated with decreased ETR susceptibility in combination with other ETR-resistance mutations.

K101E causes intermediate resistance to NVP and low-level resistance to EFV, ETR, and probably RPV.

E138K is the most common RPV-selected mutation. In this setting it usually occurs with M184I (rather than M184V) and reduces RPV susceptibility >5-fold. E138K is selected less frequently by ETR and reduces its susceptibility by ~5-fold. E138K reduces NVP and EFV ~2 to 5-fold.

G190E/Q cause high-level resistance to NVP and EFV and are synergistic with Y181C at reducing ETR susceptibility.

**Mutation Scoring**

| PR | ATV/r | DRV/r | FPV/r | IDV/r | LPV/r | NFV | SQV/r | TPV/r |
|---|---|---|---|---|---|---|---|---|
| Total: | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

| RT | 3TC | ABC | AZT | D4T | DDI | FTC | TDF | EFV | ETR | NVP | RPV |
|---|---|---|---|---|---|---|---|---|---|---|---|
| K65R | 30 | 40 | -5 | 15 | 40 | 30 | 45 | - | - | - | - |
| T69d | 15 | 25 | 30 | 30 | 25 | 15 | 15 | - | - | - | - |
| V90I | - | - | - | - | - | - | - | 0 | 0 | 0 | 0 |
| K101E | - | - | - | - | - | - | - | 15 | 10 | 30 | 10 |
| E138K | - | - | - | - | - | - | - | 15 | 15 | 15 | 30 |
| G190E | - | - | - | - | - | - | - | 60 | 10 | 60 | 10 |
| Total: | 45 | 65 | 25 | 45 | 65 | 45 | 60 | 90 | 35 | 105 | 50 |