Patient ID: CAS0107

HIV-1 Drug Resistance Genotyping Report

Participant Study Number: CAS0107

Processed by: Hasso Plattner Research Laboratory
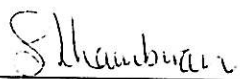
HPRL Lab No.:   CAS0107

Date Sample Received: 11 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)
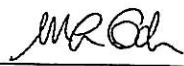
Performed by: _____   **Date:** 25 November 2011
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DISCLAIMER: This document is only valid if signed by two of the three signatories.
Time lapse from last drug dose may influence the result. Results may not represent the full resistance profile. Results should be interpreted in conjunction with the patient's clinical history.

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.

HOME GENOTYPE-RX GENOTYPE-PHENO GENOTYPE-CLINICAL HIVDB PROGRAM

HIVdb: Genotypic Resistance Interpretation Algorithm

Date: 25-Nov-2011 00:28:42 PST

Seq ID: CAS0107

Summary Data

Sequence includes PR: codons: 1 - 99

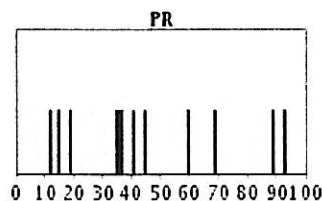Sequence includes RT: codons: 1 - 429

There are no insertions or deletions

Subtype and % similarity to closest reference isolate:
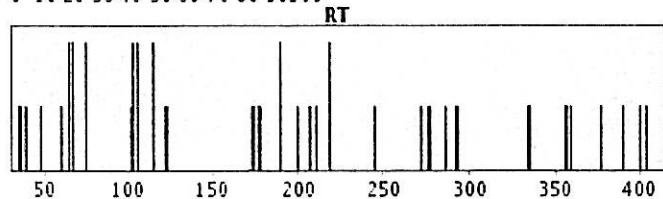
1. *PR: C (93.9%)*

2. *RT: C (92.1%)*

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, L19I, E35D, M36I, N37E, 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

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saquinavir/r (SQV/r)   Susceptible
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, D67N, V75I, Y115F, K219E
NNRTI Resistance Mutations: K103R, V106A, G190E
Other Mutations: V35T, E36A, T39E, S48T, V60I, K102R, K122E, D123S, K173A, Q174K, D177E, I178M, T200A, Q207A, R211K, V245K, A272P, V276T, K277R, T286V, V292I, I293V, Q334D, G335D, R356K, M357R, G359A, T377V, K390R, A400T, E404D

Nucleoside RTI		Non-Nucleoside RTI	
lamivudine (3TC)	Intermediate resistance	efavirenz (EFV)	High-level resistance
abacavir (ABC)	High-level resistance	etravirine (ETR)	Potential low-level resistance
zidovudine (AZT)	Intermediate resistance	nevirapine (NVP)	High-level resistance
stavudine (D4T)	Intermediate resistance	rilpivirine (RPV)	Potential low-level resistance
didanosine (DDI)	Intermediate 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.

D67N contributes some degree of resistance to each of the NRTIs except 3TC and FTC. It usually occurs with mutations at positions 70 or 215.

V75I increases multinucleoside resistance caused by Q151M when present with F77L and F116Y; its effect in the absence of Q151M is not known.

Y115F causes intermediate resistance to ABC and low-level resistance to TDF.

K219Q/E decrease AZT and probably d4T susceptibility when present with K70R or T215Y/F but have

little if any effect on the remaining NRTIs.

NNRTI

K103R occurs in about 1%-2% of untreated persons and by itself has no effect on NNRTI susceptibility. However, K103R + V179D reduces NVP and EFV susceptibility >10-fold and decreases ETR susceptibility by a lesser amount.

V106A causes high-level resistance to NVP and low/intermediate resistance to EFV.

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	-	-	-	-
D67N	0	8	15	12	8	0	5	-	-	-	-
V75I	5	5	5	10	10	5	5	-	-	-	-
Y115F	0	30	0	0	0	0	15	-	-	-	-
K219E	0	0	15	10	0	0	0	-	-	-	-
K103R	-	-	-	-	-	-	-	0	0	0	0
V106A	-	-	-	-	-	-	-	30	0	60	0
G190E	-	-	-	-	-	-	-	60	10	60	10
K65R+Y115F	-	-	-	-	-	-	15	-	-	-	-
Total:	35	83	30	47	58	35	85	90	10	120	10