## Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: None
PI Accessory Mutations: None
PR Other Mutations: T12P 96% (n=3,111) • I13V 99% (n=3,213) • K14R 99% (n=3,213) • E35D 96% (n=3,077) • M36I 99% (n=3,077) • R41K 94% (n=3,124) • K45R 96% (n=3,139) • R57K 97% (n=3,025) • L63P 96% (n=3,171) • C67Y 95% (n=2,966) • H69K 95% (n=2,965) • V82I 95% (n=2,969) • L89M 99% (n=2,109)

| Protease Inhibitors | |
|---|---|
| **atazanavir/r (ATV/r)** | Susceptible |
| **darunavir/r (DRV/r)** | Susceptible |
| **lopinavir/r (LPV/r)** | Susceptible |

**PR comments**

**Other**

- **V82I** is a highly polymorphic mutation that is not selected by PIs. It is the consensus amino acid in subtype G viruses.

## Mutation scoring: PR

HIVDB 9.5.1 (2023-11-05)

*No drug resistance mutations were found for PI.*

## Drug resistance interpretation: RT

HIVDB 9.5.1 (2023-11-05)

NRTI Mutations: K65R 95% (n=3,153) • Y115F 95% (n=796)
NNRTI Mutations: K103N 96% (n=1,009) • Y181C 98% (n=817) • P225H 95% (n=1,131)
RT Other Mutations: K11T 97% (n=2,054) • K20R 97% (n=1,962) • V35T 99% (n=2,154) • T39A 97% (n=2,148) • K46Q 96% (n=2,073) • K122E 100% (n=726) • D123S 96% (n=830) • K173S 96% (n=829) • D177E 99% (n=829) • Q197K 94% (n=720) • T200E 93% (n=710) • E203D 95% (n=724) • Q207A 96% (n=828) • V245Q 97% (n=1,419) • E248D 97% (n=1,449) • A272P 94% (n=1,190) • T286A 97% (n=966) • E291D 96% (n=810) • V292I 95% (n=809) • P294T 96% (n=850) • E312N 89% (n=710)

| Nucleoside Reverse Transcriptase Inhibitors | |
|---|---|
| **abacavir (ABC)** | High-Level Resistance |
| **zidovudine (AZT)** | Susceptible |
| **emtricitabine (FTC)** | Intermediate Resistance |
| **lamivudine (3TC)** | Intermediate Resistance |
| **tenofovir (TDF)** | High-Level Resistance |

| Non-nucleoside Reverse Transcriptase Inhibitors | |
|---|---|
| **doravirine (DOR)** | Intermediate Resistance |
| **efavirenz (EFV)** | High-Level Resistance |
| **etravirine (ETR)** | Intermediate Resistance |
| **nevirapine (NVP)** | High-Level Resistance |
| **rilpivirine (RPV)** | Intermediate Resistance |

**RT comments**

**NRTI**

- **K65R** confers intermediate reductions in susceptibility to TDF, ABC, and 3TC/FTC. It increases AZT susceptibility. In NRTI-experienced, INSTI-naive patients with **K65R**, TDF+3TC+DTG is usually highly effective and more effective than AZT/3TC/DTG. However, in patients receiving TDF+3TC+DTG, there is a risk of emergent DTG resistance that does not arise in NRTI-naive patients receiving TDF+3TC+DTG.
- **Y115F** causes intermediate resistance to ABC and low-level resistance to TDF.

**NNRTI**

- **K103N** is a non-polymorphic mutation that confers high-level reductions in NVP and EFV susceptibility. It is the most commonly transmitted DRM.
- **Y181C** is a non-polymorphic mutation selected in persons receiving NVP, ETR and RPV. It confers high-level resistance to NVP, intermediate resistance to ETR and RPV, and low-level resistance to EFV. It does not significantly reduce DOR susceptibility.
- **P225H** is a non-polymorphic EFV-selected mutation that usually occurs in combination with K103N. The combination of **P225H** and K103N synergistically reduces NVP, EFV and DOR susceptibility.

- This virus is predicted to have intermediate-level reduced susceptibility to **RPV**. The use of the combination of CAB/**RPV** should be considered to be contraindicated.

## Mutation scoring: RT

HIVDB 9.5.1 (2023-11-05)

*Drug resistance mutation scores of NRTI:* Download CSV

| Rule | ABC | AZT | FTC | 3TC | TDF |
|---|---|---|---|---|---|
| K65R | 45 | -10 | 30 | 30 | 50 |
| Y115F | 30 | 0 | 0 | 0 | 15 |
| Total | 75 | -10 | 30 | 30 | 65 |

*Drug resistance mutation scores of NNRTI:* Download CSV

| Rule | DOR | EFV | ETR | NVP | RPV |
|---|---|---|---|---|---|
| K103N + Y181C | 5 | 0 | 0 | 0 | 0 |
| K103N + P225H | 10 | 0 | 0 | 0 | 0 |
| Y181C | 10 | 30 | 30 | 60 | 45 |
| P225H | 20 | 45 | 0 | 45 | 0 |
| K103N | 0 | 60 | 0 | 60 | 0 |
| Total | 45 | 135 | 30 | 165 | 45 |