Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: None
PI Accessory Mutations: None
PR Other Mutations: L10LV (I: 67%, L: 32%) • K14KR (K: 71%, R: 29%) • L19I (40%, n=1,285) • L33LV (L: 75%, V: 24%) • M36MI (I: 77%, M: 22%) • R41K (99%, n=6,180) • I72IV (I: 62%, V: 38%, n=1,991)

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
tipranavir/r (TPV/r)	Susceptible

PR comments

Other

- **L10I/V** are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.
- **L33I/V** are minimally polymorphic mutations that do not appear to be selected by PIs or to reduce their susceptibility.

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: None
NNRTI Mutations: K103N (98%, n=1,403)
RT Other Mutations: V10A (100%, n=2,586) • K11KT (I: 82%, K: 14%, n=2,762) • V35T (100%, n=2,584) • T39A (99%, n=2,327) • E40D (100%, n=2,308) • K49R (100%, n=2,342) • V60I (100%, n=2,307) • K102Q (100%, n=1,754) • D121Y (99%, n=1,992) • K122E (100%, n=1,992) • T165I (100%, n=2,568) • D177E (100%, n=2,531) • I178IM (I: 77%, M: 22%, n=2,570) • T200A (100%, n=2,924) • Q207E (100%, n=2,790) • V245N (100%, n=733) • E248D (100%, n=729) • D250E (100%, n=686) • A554N (99%, n=46) • V559I (100%, n=135)

Nucleoside Reverse Transcriptase Inhibitors	
abacavir (ABC)	Susceptible
zidovudine (AZT)	Susceptible
stavudine (D4T)	Susceptible
didanosine (DDI)	Susceptible
emtricitabine (FTC)	Susceptible
lamivudine (3TC)	Susceptible
tenofovir (TDF)	Susceptible

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

RT comments

NNRTI

- **K103N** is a non-polymorphic mutation that confers high-level reductions in NVP and EFV susceptibility. It is the most commonly transmitted DRM.

Mutation scoring: RT

HIVDB 9.5.1 (2023-11-05)

No drug resistance mutations were found for NRTI.

Drug resistance mutation scores of NNRTI: Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
K103N	0	60	0	60	0

Drug resistance interpretation: IN

HIVDB 9.5.1 (2023-11-05)

INSTI Major Mutations: None
INSTI Accessory Mutations: None
IN Other Mutations: K14R (100%, n=297) • L45V (100%, n=529) • I72V (100%, n=509) • T112V (100%, n=187) • I113V (100%, n=187) • S119T (100%, n=240) • H171Q (100%, n=275) • V201I (100%, n=182) • L234I (100%, n=154) • A265V (97%, n=471) • S283G (100%, n=83)

Integrase Strand Transfer Inhibitors	
bictegravir (BIC)	Susceptible
cabotegravir (CAB)	Susceptible
dolutegravir (DTG)	Susceptible
elvitegravir (EVG)	Susceptible
raltegravir (RAL)	Susceptible

Mutation scoring: IN

HIVDB 9.5.1 (2023-11-05)

No drug resistance mutations were found for INSTI.