Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: None
PI Accessory Mutations: None
PR Other Mutations: L19I 91% cov=40,020 • N37A 90% cov=46,334 • R41K 99% cov=49,700 • L63P 91% cov=37,424 • I64L 90% cov=37,443

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

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: **L74I** 95% cov=19,056 • **M184V** 97% cov=22,812
NNRTI Mutations: **K103N** 95% cov=20,188 • **P225H** 95% cov=24,372 • **F227C** 94% cov=24,293 • **M230L** 94% cov=24,745
RT Other Mutations: K32N 92% cov=19,750 • V35T 99% cov=18,994 • T39K 94% cov=19,229 • I47L 91% cov=18,807 • V60I 99% cov=19,659 • Q85R 94% cov=19,140 • K122E 100% cov=20,637 • D123S 95% cov=19,676 • S162C 95% cov=23,076 • K173L 94% cov=22,444 • Q174K 96% cov=22,449 • D177E 98% cov=21,821 • I178L 94% cov=21,824 • T200A 97% cov=22,115 • Q207E 95% cov=19,967 • R211K 95% cov=20,108 • V245K 95% cov=26,183 • A272P 97% cov=29,179 • K277R 95% cov=30,060 • L282C 96% cov=30,121 • L283I 95% cov=30,175 • T286V 94% cov=32,352 • I293V 98% cov=33,421 • I329IR I: 78%, R: 12% cov=59

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

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

RT comments

NRTI

- L74V causes intermediate ABC resistance. **L74I** causes low-level ABC resistance.
- **M184V/I** cause high-level in vitro resistance to 3TC and FTC and low/intermediate resistance to ABC (3-fold reduced susceptibility). **M184V/I** are not contraindications to continued treatment with 3TC or FTC because they increase susceptibility to AZT and TDF and are associated with clinically significant reductions in HIV-1 replication.

NNRTI

- **K103N** is a non-polymorphic mutation that confers high-level reductions in NVP and EFV susceptibility. It is the most commonly transmitted DRM.
- **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.
- **F227C** is a nonpolymorphic mutation selected in persons receiving DOR and rarely in persons receiving ETR and RPV. It usually occurs in combination with other DRMs and in this setting has consistently been associated with the highest possible levels of DOR resistance. It is also usually associated with intermediate or high-level reductions in susceptibility to NVP, EFV, ETR, and RPV.
- **M230L** is an uncommon non-polymorphic mutation selected in persons receiving EFV, NVP, and RPV. It causes intermediate to high-level resistance to each of the NNRTIs.

Mutation scoring: RT HIVDB 9.5.1 (2023-11-05)

Drug resistance mutation scores of NRTI: Download CSV

Rule	ABC	AZT	FTC	3TC	TDF
L74I	15	0	0	0	5
M184V	15	-10	60	60	-10
Total	30	-10	60	60	-5

Drug resistance mutation scores of NNRTI: Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
K103N + P225H	10	0	0	0	0
P225H	20	45	0	45	0
F227C	60	45	30	45	45
M230L	60	45	30	60	60
K103N	0	60	0	60	0
Total	150	195	60	210	105