Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: None

PI Accessory Mutations: None

PR Other Mutations: I13V (97%, n=1,135) • E35D (97%, n=1,011) • M36I (97%, n=1,011) • N37D (100%, n=1,011) • R41K (99%, n=1,024) • L63T (100%, n=1,036) • H69K (91%, n=1,024) • K70R (92%, n=1,024) • I72T (83%, n=1,011) • L89M (97%, n=1,014)

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

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: M184V (100%, n=218)

NNRTI Mutations: K103N (92%, n=160) • E138A (100%, n=171) • P225H (98%, n=161)

RT Other Mutations: K20R (98%, n=1,175) • V35T (100%, n=1,178) • T39KR (L: 52%, R: 45%, n=1,253) • K43E (93%, n=1,088) • K102HQ (H: 73%, Q: 26%, n=1,180) • D123E (99%, n=113) • I135L (100%, n=119) • K173S (93%, n=141) • V179I (97%, n=117) • T200EK (E: 86%, K: 13%, n=279) • I202V (98%, n=240) • Q207A (100%, n=104) • R211K (100%, n=113) • V245Q (100%, n=121) • E248D (100%, n=121)

Nucleoside Reverse Transcriptase Inhibitors	
abacavir (ABC)	Low-Level Resistance
zidovudine (AZT)	Susceptible
stavudine (D4T)	Susceptible
didanosine (DDI)	Potential Low-Level Resistance
emtricitabine (FTC)	High-Level Resistance
lamivudine (3TC)	High-Level Resistance
tenofovir (TDF)	Susceptible

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

RT comments

NRTI

- **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.
- **E138A** is a common polymorphic accessory mutation weakly selected in persons receiving ETR and RPV. It reduces ETR and RPV susceptibility ~2-fold. Its effect on ETR- and RPV-containing regimens is likely to be minimal.
- **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.

Other

- **V179I** is a polymorphic mutation that is frequently selected in persons receiving ETR and RPV. However, it has little, if any, direct effect on NNRTI susceptibility.
- This virus is predicted to have low-level reduced susceptibility to **RPV**. The use of the combination of CAB/**RPV** should be considered to be relatively contraindicated.

Mutation scoring: RT

HIVDB 9.5.1 (2023-11-05)

Drug resistance mutation scores of NRTI: Download CSV

Rule	ABC	AZT	D4T	DDI	FTC	3TC	TDF
M184V	15	-10	-10	10	60	60	-10

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
K103N	0	60	0	60	0
E138A	0	0	10	0	15
Total	30	105	10	105	15