Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: None
PI Accessory Mutations: None
PR Other Mutations: I13V 98% cov=37,617 • I15IV V: 68%, I: 30% cov=38,614 • R41K 99% cov=40,449 • L63P 90% cov=38,697 • I64V 91% cov=38,725 • V77I 90% cov=30,386

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: **S68N** 91% cov=13,473 • **L74I** 83% cov=11,731 • **M184I** 95% cov=25,614
NNRTI Mutations: **K101E** 91% cov=11,464 • **K103N** 98% cov=11,852 • **E138A** 95% cov=20,887 • **P225H** 95% cov=26,119
RT Other Mutations: V35T 98% cov=19,004 • V60I 98% cov=15,045 • V90I 91% cov=10,717 • D121H 94% cov=15,551 • K122E 98% cov=15,540 • T139S 94% cov=20,875 • I142V 95% cov=21,495 • I178L 95% cov=24,531 • T200A 98% cov=25,328 • Q207G 94% cov=21,790 • R211K 97% cov=25,557 • V245K 77% cov=24,571 • D250E 97% cov=24,881 • A272P 96% cov=24,353 • L282C 96% cov=24,322 • L283I 94% cov=24,389 • T286A 96% cov=26,139 • I293V 93% cov=27,200 • I329IV I: 57%, V: 36% cov=77 • P345PQ Q: 76%, P: 24% cov=50 • F346FY Y: 76%, F: 24% cov=50

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)	Intermediate Resistance
efavirenz (EFV)	High-Level Resistance
etravirine (ETR)	Low-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

- **K101E** is a non-polymorphic accessory mutation that confers intermediate resistance to NVP and RPV and low-level reductions in susceptibility to EFV, ETR, and DOR when it occurs with other NNRTI-resistance mutations.
- **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

- **V90I** is a polymorphic accessory mutation weakly selected by each of the NNRTIs. It is associated with minimal, if any, detectable reduction in NNRTI susceptibility.

Mutation scoring: RT

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Drug resistance mutation scores of NRTI: Download CSV

Rule	ABC	AZT	FTC	3TC	TDF
L74I	15	0	0	0	5
M184I	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
K101E	15	15	15	30	45
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
K101E + M184I	0	0	0	0	15
Total	45	120	25	135	75