Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: None

PI Accessory Mutations: L33F 93% cov=37,290

PR Other Mutations: I13V 99% cov=29,322 • K14R 94% cov=29,347 • G16E 95% cov=30,660 • M36I 99% cov=37,811 • N37ND N: 73%, D: 26% cov=37,939 • P39S 93% cov=37,850 • R57K 96% cov=35,557 • D60E 93% cov=32,658 • E65D 88% cov=28,610 • H69K 96% cov=28,512 • L89M 98% cov=38,476

Protease Inhibitors	
atazanavir/r (ATV/r)	Susceptible
darunavir/r (DRV/r)	Susceptible
fosamprenavir/r (FPV/r)	Potential Low-Level Resistance
indinavir/r (IDV/r)	Susceptible
lopinavir/r (LPV/r)	Susceptible
nelfinavir (NFV)	Potential Low-Level Resistance
saquinavir/r (SQV/r)	Susceptible
tipranavir/r (TPV/r)	Potential Low-Level Resistance

PR comments

Accessory

- **L33F** is a relatively non-polymorphic accessory mutation selected by each of the PIs. In combination with other PI-resistance mutations, it is associated with reduced susceptibility to LPV, ATV, and DRV.

Mutation scoring: PR

HIVDB 9.5.1 (2023-11-05)

Drug resistance mutation scores of PI: Download CSV

Rule	ATV/r	DRV/r	FPV/r	IDV/r	LPV/r	NFV	SQV/r	TPV/r
L33F	5	5	10	5	5	10	5	10

Drug resistance interpretation: RT

HIVDB 9.5.1 (2023-11-05)

NRTI Mutations: D67N 92% cov=12,556 • K70R 95% cov=12,905 • M184V 89% cov=6,417 • T215FI I: 63%, F: 27% cov=8,149 • K219E 92% cov=8,493

NNRTI Mutations: L100LI I: 81%, L: 17% cov=13,089 • K103N 98% cov=13,042

RT Other Mutations: E6N 91% cov=16,039 • V35T 94% cov=15,051 • T39TL T: 52%, L: 39% cov=14,050 • E40ED D: 53%, E: 44% cov=14,055 • K49R 93% cov=13,864 • V60I 99% cov=13,708 • K102KR K: 63%, R: 36% cov=13,172 • K122E 98% cov=10,444 • D123N 91% cov=10,434 • I135T 95% cov=8,681 • K166T 88% cov=6,690 • K173S 86% cov=6,215 • Q174K 79% cov=6,217 • D177E 92% cov=6,380 • V179I 77% cov=6,343 • T200A 96% cov=7,319 • I202V 92% cov=7,441 • E203EK E: 76%, K: 18% cov=7,452 • Q207D 85% cov=7,505 • L210F 85% cov=7,440 • R211K 92% cov=7,457 • D218E 91% cov=8,497 • L228R 88% cov=9,068 • V245E 95% cov=15,713 • E248D 95% cov=16,036 • K249KR K: 51%, R: 45% cov=16,037 • D250E 98% cov=16,040 • L283I 96% cov=25,387 • I293V 99% cov=28,766 • P294T 92% cov=28,780 • L295M 91% cov=28,777 • V314VA V: 75%, A: 23% cov=29,002 • G335D 97% cov=257 • R356K 89% cov=227 • M357K 94% cov=227 • G359S 94% cov=215 • K366R 92% cov=181 • T369A 83% cov=179 • E370A 92% cov=176 • A371V 93% cov=176 • I375IV V: 86%, I: 12% cov=168 • A376V 93% cov=165 • T377M 84% cov=165

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

RT comments

NRTI

- **D67N** is a non-polymorphic TAM associated with low-level resistance to AZT.
- **K70R** is a TAM that confers intermediate resistance to AZT and contributes to reduced ABC and TDF susceptibility in combination with other TAMs.
- **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.
- **T215Y/F** are TAMs that causes intermediate/high-level resistance to AZT and potentially low-level resistance to ABC and TDF.
- T215Y/F are TAMs that causes intermediate/high-level resistance to AZT and potentially low-level resistance to ABC and TDF. **T215S/C/D/E/I/V/N/A/L** do not reduce NRTI susceptibility but arise from viruses that once contained T215Y/F. The presence of one of these revertant mutations suggests that the patient may have once been infected with a virus containing T215Y/F.
- **K219E/Q/N/R** are accessory TAMS that usually occur in combination with multiple other TAMs.

NNRTI

- **L100I** is a non-polymorphic mutation that usually occurs in combination with K103N. In this setting it confers high-level resistance to NVP, EFV, and RPV and intermediate resistance to ETR and DOR.
- **K103N** is a non-polymorphic mutation that confers high-level reductions in NVP and EFV susceptibility. It is the most commonly transmitted DRM.

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.

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
D67N	5	15	15	5	0	0	5
D67N + K70R + M184V + K219E	10	0	0	0	0	0	0
D67N + K70R + K219E	10	15	10	10	10	10	10
D67N + T215FI + K219E	5	5	5	5	0	0	5
K70R	5	30	15	10	0	0	5
M184V	15	-10	-10	10	60	60	-10
T215FI	10	60	40	15	0	0	10
K219E	5	10	10	5	0	0	5
K70R + T215FI	0	0	5	5	0	0	0
Total	65	125	90	65	70	70	30

Drug resistance mutation scores of NNRTI: Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
L100LI	15	60	30	60	60
L100LI + K103N	15	0	0	0	0
K103N	0	60	0	60	0
Total	30	120	30	120	60