Drug resistance interpretation: PR — HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: **M46MI** L: 83%, M: 16% cov=35,025 • **I47A** 87% cov=35,724

PI Accessory Mutations: **F53L** 84% cov=35,062

PR Other Mutations: L10I 91% cov=34,549 • K20R 90% cov=35,431 • E35D 95% cov=37,963 • M36I 98% cov=37,952 • R41K 99% cov=37,645 • K45R 90% cov=37,090 • R57K 93% cov=34,113 • L63P 90% cov=32,825 • I64IL L: 55%, I: 42% cov=33,127 • A71V 89% cov=31,915 • I72V 90% cov=31,929

Protease Inhibitors	
atazanavir/r (ATV/r)	Low-Level Resistance
darunavir/r (DRV/r)	Potential Low-Level Resistance
lopinavir/r (LPV/r)	High-Level Resistance

PR comments

Major

- **M46I/L** are relatively non-polymorphic PI-selected mutations. In combination with other PI-resistance mutations, they are associated with reduced susceptibility to each of the PIs except DRV.
- **I47A** is a non-polymorphic mutation selected by LPV. It usually occurs in combination with V32I and in this context it confers high-level resistance to LPV and low-level resistance to DRV.

Accessory

- **F53L** is a nonpolymorphic accessory mutation selected primarily by SQV, IDV, ATV and LPV. In combination with other mutations, It is associated with reduced susceptibility to ATV and possibly LPV. F53Y is an uncommon nonpolymorphic accessory PI-selected mutation that has not been well studied.

Other

- **L10I/V** are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.
- **K20R** is a highly polymorphic PI-selected accessory mutation that increases replication fitness in viruses with PI-resistance mutations.
- **A71V/T** are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.

Mutation scoring: PR — HIVDB 9.5.1 (2023-11-05)

Drug resistance mutation scores of PI: Download CSV

Rule	ATV/r	DRV/r	LPV/r
M46MI	10	0	10
F53L	10	0	0
I47A	0	10	60
Total	20	10	70

Drug resistance interpretation: RT — HIVDB 9.5.1 (2023-11-05)

NRTI Mutations: **L74V** 90% cov=10,866 • **Y115F** 92% cov=11,187 • **M184V** 96% cov=18,426 • **K219E** 88% cov=15,234

NNRTI Mutations: **L100I** 90% cov=9,500 • **K103NS** N: 68%, S: 26% cov=9,968

RT Other Mutations: E6K 92% cov=29,498 • V21VI I: 52%, V: 45% cov=29,250 • K32R 86% cov=26,069 • V35T 99% cov=25,111 • T39R 79% cov=15,692 • E40EK K: 63%, E: 29% cov=15,643 • K43E 90% cov=15,462 • V60I 98% cov=13,260 • K122E 100% cov=12,156 • D123S 89% cov=12,108 • T139A 92% cov=15,025 • K173S 95% cov=18,946 • Q174K 86% cov=18,955 • T200A 95% cov=15,698 • Q207A 83% cov=13,731 • R211S 93% cov=15,378 • L228Q 91% cov=16,010 • V245Q 97% cov=16,879 • D250E 95% cov=17,767 • A272Q 92% cov=19,632 • T286A 94% cov=17,974 • V292VI I: 71%, V: 29% cov=18,170 • I293V 98% cov=18,113 • Q334N 92% cov=7,467 • G335GD D: 84%, G: 14% cov=7,491 • R356K 93% cov=6,615 • G359T 100% cov=5,782 • T377Q 98% cov=4,696 • S379C 94% cov=4,695

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

- **L74V** causes intermediate ABC resistance. L74I causes low-level ABC resistance.
- **Y115F** causes intermediate resistance to ABC and low-level resistance to TDF.
- **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.
- **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.
- **K103S** is a non-polymorphic mutation that causes high-level reductions in NVP susceptibility but intermediate reductions in EFV susceptibility. Because **K103S** is a 2-bp change from the wildtype K and a 1-bp change from K103N, persons with **K103S** may be likely to have once had K103N.

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

Drug resistance mutation scores of NRTI: Download CSV

Rule	ABC	AZT	FTC	3TC	TDF
L74V	30	0	0	0	0
L74V + M184V	15	0	0	0	0
Y115F	30	0	0	0	15
Y115F + M184V	15	0	0	0	5
M184V	15	-10	60	60	-10
K219E	5	10	0	0	5
Total	110	0	60	60	15

Drug resistance mutation scores of NNRTI: Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
L100I	15	60	30	60	60
L100I + K103NS	15	0	0	0	0
K103NS	0	60	0	60	0
Total	30	120	30	120	60