Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: None
PI Accessory Mutations: L24I
PR Other Mutations: V11Q • T12C • I13T • K14V • I15R • G16* • G17K • Q18G • L19Q • K20* • E21K • A22K • D25R • T26S • L33* • M36X • N37K • P39T • R41K • R57K • L63Q • H69Q • L89M

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

PR comments

Accessory

- **L24I** is a non-polymorphic mutation selected by IDV and LPV. It contributes reduced susceptibility to ATV and LPV.

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
L24I	10	0	10	15	10	10	10	-5

Drug resistance interpretation: RT

HIVDB 9.5.1 (2023-11-05)

NRTI Mutations: K70E • M184V
NNRTI Mutations: L100I • K103N • H221Y • P236L
RT Other Mutations: K20R • V35M • T39A • K49R • I50V • L109I • K122E • D123S • I135T • I142V • S162C • K173S • Q174K • V179I • T200V • Q207A • R211K • F214S • P217S • K219X • E224D • F227Y • H235I • D237T • K238V • W239T • T240V • V241N • Q242L • P243* • I244T • V245A • L246R • P247K • K249S

Nucleoside Reverse Transcriptase Inhibitors	
abacavir (ABC)	Intermediate Resistance
zidovudine (AZT)	Susceptible
stavudine (D4T)	Low-Level Resistance
didanosine (DDI)	Low-Level Resistance
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

- **K70/E/Q/N/T/S/G** cause low-leve resistance to ABC and 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.

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.
- **H221Y** is a non-polymorphic accessory mutation selected primarily by NVP, RPV, and DOR. It frequently occurs in combination with Y181C.
- **P236L** is a rare mutation selected commonly by DLV, which appears to have little if any effect on current NNRTIs.

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.
- F227L is a non-polymorphic mutation that usually occurs in combination with V106A. It is selected in vivo and in vitro with both NVP and DOR. In this context it is associated with high-level reductions in NVP and DOR susceptibility and intermediate reductions in EFV susceptibility. F227I/V are extremely rare mutations that have been selected in vitro by DOR. 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. **F227Y** is a highly unusual mutation at this position.
- K238T/N are uncommon non-polymorphic mutations selected in persons receiving NVP and EFV usually in combination with K103N. Alone, K238T/N appear to have minimal effects on NNRTI susceptibility. **K238V** is a highly unusual mutation at this position.

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
K70E	15	0	15	15	10	10	15
M184V	15	-10	-10	10	60	60	-10
K70E + M184V	0	0	10	0	0	0	10
Total	30	-10	15	25	70	70	15

Drug resistance mutation scores of NNRTI: Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
L100I	15	60	30	60	60
L100I + K103N	15	0	0	0	0
H221Y	10	10	10	15	15
P236L	10	0	0	0	0
K103N	0	60	0	60	0
Total	50	130	40	135	75