

Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	V11H • T12V • I13V • K14R • G16E • L19* • K20R • E21R • A22S • T26P • D29X • T31P • V32S • L33* • E34D • E35L • M36I • N37A • R41K • R57K • L63T • H69Q • L89M

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

PR comments

Other

- K20R is a highly polymorphic PI-selected accessory mutation that increases replication fitness in viruses with PI-resistance mutations.
- V32I is a non-polymorphic mutation selected by LPV, ATV, and DRV which is associated with reduced susceptibility to each of these PIs. V32S is a highly unusual mutation at this position.

Mutation scoring: PR	HIVDB 9.5.1 (2023-11-05)
No drug resistance mutations were found for PI.	

Drug resistance interpretation: RT

NRTI Mutations:

NNRTI Mutations:

RT Other Mutations:

L74V • M184V

L100I • K103N • L234I

E6D • V35T • V60I • K102R • K122E • D123N • I135T • I142V • K173S • Q174K • D177E • I178L • V179I • E204X • Q207A • R211S • F214L • P217S • K220S • Q222S • K223E • W229D • M230G • G231Y • Y232E • E233L • H235* • P236Q • D237* • K238Q • W239S • V241I • Δ242-245 • L246X • P247L • E248L • K249D • D250K • S251K • W252A • T253D • V254C • N255H

Nucleoside Reverse Transcriptase Inhibitors

abacavir (ABC)

zidovudine (AZT)

stavudine (D4T)

didanosine (DDI)

emtricitabine (FTC)

lamivudine (3TC)

tenofovir (TDF)

High-Level Resistance

Susceptible

Susceptible

High-Level Resistance

High-Level Resistance

High-Level Resistance

Susceptible

Non-nucleoside Reverse Transcriptase Inhibitors

doravirine (DOR)

efavirenz (EFV)

etravirine (ETR)

nevirapine (NVP)

rilpivirine (RPV)

High-Level Resistance

High-Level Resistance

Intermediate Resistance

High-Level Resistance

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

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.

L234I is a nonpolymorphic mutation selected in persons receiving NVP and EFV. It is also selected in vitro by ETR and DOR. In combination with V106A, it is associated with high-level DOR resistance. Its effect on susceptibility when it occurs alone has not been well characterized.

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.

M230L is an uncommon non-polymorphic mutation selected in persons receiving EFV, NVP, and RPV. It causes intermediate to high-level resistance to each of the NNRTIs. M230I is a rare mutation selected by RPV. Its effects on NNRTI susceptibility have not been well studied. It also often occurs as a result of APOBEC-mediated G-to-A hypermutation resulting in viruses that are likely to be noninfectious. M230G is a highly unusual mutation at this position.

P236L is a rare mutation selected commonly by DLV, which appears to have little if any effect on current NNRTIs. P236Q 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. K238Q is a highly unusual mutation at this position.

Mutation scoring: RT	HIVDB 9.5.1 (2023-11-05)
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Drug resistance mutation scores of NRTI:

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Rule	ABC	AZT	D4T	DDI	FTC	3TC	TDF
<u>L74V</u>	30	0	0	60	0	0	0
<u>L74V + M184V</u>	15	0	0	0	0	0	0
<u>M184V</u>	15	-10	-10	10	60	60	-10
Total	60	-10	-10	70	60	60	-10

Drug resistance mutation scores of NNRTI:

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Rule	DOR	EFV	ETR	NVP	RPV
<u>L100I</u>	15	60	30	60	60
<u>L100I + K103N</u>	15	0	0	0	0
<u>L234I</u>	45	0	0	0	0
<u>K103N</u>	0	60	0	60	0
Total	75	120	30	120	60