Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	P9X • L10C • V11Y • T12G • I13P • K14E • I15E • G16K • L19P • E35D • M36I • N37K • R41K • M46R • R57K • L63T • H69K • 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

- L10F is a common non-polymorphic, PI-selected accessory mutation associated with reduced in vitro susceptibility to LPV and DRV. L10I/V are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations. L10R/Y are rare, non-polymorphic PI-selected mutations. Their effects on PI susceptibility have not been well studied. **L10C** is a highly unusual mutation at this position.
- 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. **M46R** 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

HIVDB 9.5.1 (2023-11-05)

NRTI Mutations:	M184V • T215F
NNRTI Mutations:	A98G • V108I • Y188H • G190A
RT Other Mutations:	K11T • K20R • V21I • V35T • T39N • K43R • P52L • V60I • W88C • K101Q • K122E • D123N • I135T • K166* • K173A • D177E • V179I • Q182X • V189I • T200A • I202* • E203R • Q207A • R211S • K220N • Δ221 • Q222I • K223R • E224R • H235I • P236* • D237Q • K238M • W239T • T240Y • V241S • Q242Y

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

RT comments

NRTI

- **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.

NNRTI

- **A98G** is a non-polymorphic accessory mutation associated with low-level reduced susceptibility to each of the NNRTIs.
- **V108I** is a relatively non-polymorphic accessory mutation selected in vitro and/or in vivo with each of the NNRTIs. It appears to contribute to reduced susceptibility to most NNRTIs only in combination with other NNRTI-resistance mutations.
- **Y188H** is a non-polymorphic mutation selected in persons receiving NVP and EFV. It causes about 5 to 10-fold reduced susceptibility to NVP and EFV. It appears to cause little if any reduction in susceptibility to RPV, ETR, or DOR.
- **G190A** is a non-polymorphic mutation that causes high-level resistance to NVP and intermediate resistance to EFV. It does not significantly reduce susceptibility to RPV, ETR, or DOR.

Other

- **K101Q** is a relatively non-polymorphic mutation that is weakly selected in persons receiving NVP and EFV. It is of uncertain phenotypic and clinical significance.
- **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.
- 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. **K238M** is a highly unusual mutation at this position.

- This virus is predicted to have intermediate-level reduced susceptibility to **RPV**. The use of the combination of CAB/**RPV** should be considered to be contraindicated.

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
M184V	15	-10	-10	10	60	60	-10
T215F	10	60	40	15	0	0	10
Total	25	50	30	25	60	60	0

Drug resistance mutation scores of NNRTI: Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
A98G	15	15	10	30	15
V108I	10	10	0	15	0
Y188H	5	30	0	60	0
G190A	0	45	10	60	15
Total	30	100	20	165	30