Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	V11R • T12D • I13S • K14T • I15G • K20S • L23Y • L24* • D25I • T26R • G27S • A28D • D30H • T31Q • V32R • Δ34 • E35X • M36S • N37P • L38M • R41K • R57K • I62V • L63V • E65D • H69K • T74S • 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

- D30N is a non-polymorphic mutation NFV-selected mutation that causes high-level resistance to NFV but not to other PIs. **D30H** is a highly unusual mutation at this position.
- V32I is a non-polymorphic mutation selected by LPV, ATV, and DRV which is associated with reduced susceptibility to each of these PIs. **V32R** is a highly unusual mutation at this position.
- **T74S** is a PI-selected accessory mutation that is polymorphic in most non-B subtypes.

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:	L74V • Y115F • M184V
NNRTI Mutations:	K103N • V108I • Y181C • H221Y • F227L • P236L
RT Other Mutations:	E6D • V35T • T39A • V60I • K101R • D123E • I135T • I142V • T165L • K173A • Q174K • D177E • I178M • E194D • T200A • Q207A • R211S • F214S • P217S • K219X • P225X • P226S • H235I • D237T • K238V • W239D • T240S • V241Q • Q242L • P243L • I244Q • V245L • Δ247 • D250E • Δ255 • I257* • Q258Y • K259T • L260E • V261I • G262V • K263R • L264N • N265L • W266T • A267G • I274T • K275E • K277N • K281Q

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

Non-nucleoside Reverse Transcriptase Inhibitors	
doravirine (DOR)	High-Level 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.

NNRTI

- **K103N** is a non-polymorphic mutation that confers high-level reductions in NVP and EFV susceptibility. It is the most commonly transmitted DRM.
- **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.
- **Y181C** is a non-polymorphic mutation selected in persons receiving NVP, ETR and RPV. It confers high-level resistance to NVP, intermediate resistance to ETR and RPV, and low-level resistance to EFV. It does not significantly reduce DOR susceptibility.
- **H221Y** is a non-polymorphic accessory mutation selected primarily by NVP, RPV, and DOR. It frequently occurs in combination with Y181C.
- **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.
- **P236L** is a rare mutation selected commonly by DLV, which appears to have little if any effect on current NNRTIs.

Other

- 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
L74V	30	0	0	60	0	0	0
L74V + M184V	15	0	0	0	0	0	0
Y115F	30	0	0	0	0	0	15
Y115F + M184V	15	0	0	0	0	0	5
M184V	15	-10	-10	10	60	60	-10
Total	105	-10	-10	70	60	60	10

Drug resistance mutation scores of NNRTI: Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
K103N + Y181C	5	0	0	0	0
V108I	10	10	0	15	0
V108I + Y181C	5	0	0	0	0
Y181C	10	30	30	60	45
Y181C + H221Y	10	0	0	0	10
H221Y	10	10	10	15	15
F227L	60	15	0	30	0
P236L	10	0	0	0	0
K103N	0	60	0	60	0
Total	120	125	40	180	70