Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: I54V • V82A
PI Accessory Mutations: L89V
PR Other Mutations: V11X • T12S • I13Q • K14* • I15* • G16S • G17L • Q18E • L19T • K20S • E21V • A22S • L23S • L24V • E35D • M36I • R41K • Y59C • Q61H • L63P • H69L • A71T • T91S

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

PR comments

Major

- **I54V** is a non-polymorphic PI-selected mutation that contributes reduced susceptibility to each of the PIs except DRV.
- **V82A** is a non-polymorphic mutation selected primarily by IDV and LPV. It is associated with reduced susceptibility to LPV and to a lesser extent ATV. It increases DRV susceptibility.

Accessory

- **L89V** is a nonpolymorphic accessory mutation weakly selected by each of the PIs. It appears to be minimally associated with reduced PI susceptibility. L89T is an uncommon non-polymorphic PI-selected mutation selected primarily by ATV.

Other

- L24I is a non-polymorphic mutation selected by IDV and LPV. It contributes reduced susceptibility to ATV and LPV. L24F/M are uncommon non-polymorphic PI-selected mutations. L24F has a susceptibility profile similar to L24I. **L24V** is a highly unusual mutation at this position.
- **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:

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Rule	ATV/r	DRV/r	FPV/r	IDV/r	LPV/r	NFV	SQV/r	TPV/r
I54V	15	0	10	15	15	20	15	20
I54V + V82A	10	0	10	10	10	10	10	0
V82A	15	0	15	30	30	30	15	0
L89V	0	5	10	5	0	10	0	0
Total	40	5	45	60	55	70	40	20

Drug resistance interpretation: RT

HIVDB 9.5.1 (2023-11-05)

NRTI Mutations: M41L • D67E • T69S_ST • V75M • L210W
NNRTI Mutations: Y181C • M230I • P236L
RT Other Mutations: V21I • V35T • K43Q • K49R • V60I • K64R • K122E • D177E • I178L • R199T • T200A • Q207E • R211N • T216P • D218E • K220* • K223X • L228R • W229G • D237I • K238Q • P247T • E248R • D250G • S251K • I257L

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

Non-nucleoside Reverse Transcriptase Inhibitors	
doravirine (DOR)	Intermediate Resistance
efavirenz (EFV)	Intermediate Resistance
etravirine (ETR)	Intermediate Resistance
nevirapine (NVP)	High-Level Resistance
rilpivirine (RPV)	High-Level Resistance

RT comments

NRTI

- **M41L** is a TAM that usually occurs with T215Y. In combination, **M41L** plus T215Y confer intermediate / high-level resistance to AZT and d4T and contribute to reduced ddI, ABC and TDF susceptibility.
- D67N is a non-polymorphic TAM associated with low-level resistance to AZT. **D67G/E/S/T/H** are non-polymorphic NRTI-selected mutations that generally occur in viruses with multiple TAMs.
- Amino acid insertions between codons 67 and 70 are by convention assigned to codon 69. Together with TAMs, they are associated with high-level resistance to AZT, ABC and TDF, and intermediate to 3TC and FTC.
- **V75T/M/A/S** are nonpolymorphic accessory NRTI-selected mutations. They appear to have minimal phenotypic effects on AZT, ABC, and TDF.
- **L210W** is a TAM that usually occurs in combination with M41L and T215Y. The combination of M41, **L210W** and T215Y causes high-level resistance to AZT and intermediate resistance to ABC and TDF.

NNRTI

- **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.
- **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.
- **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. **K238Q** 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
M41L	5	15	15	10	0	0	5
M41L + L210W	10	10	10	10	0	0	10
D67E	5	15	10	5	0	0	5
T69ins	60	60	60	60	30	30	60
L210W	5	15	15	10	0	0	5
V75M	0	10	30	15	0	0	0
Total	85	125	140	110	30	30	85

Drug resistance mutation scores of NNRTI: Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
Y181C	10	30	30	60	45
M230I	15	15	15	30	30
P236L	10	0	0	0	0
Total	35	45	45	90	75