Drug resistance interpretation: PR HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: M46I 93% - I54V 93% - L76V 93% - V82A 94% 009-38,177 009-38,707

PI Accessory Mutations: L33F 20%

Protease Inhibitors

 atazanavir/r (ATV/r)
 High-Level Resistance

 darunavir/r (DRV/r)
 Low-Level Resistance

 lopinavir/r (LPV/r)
 High-Level Resistance

PR comments

Major

- . 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.
- 154V is a non-polymorphic PI-selected mutation that contributes reduced susceptibility to each of the PIs except DRV.
- . L76V is a non-polymorphic mutation selected by IDV, LPV and DRV and reduces susceptibility to LPV and 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

L33F is a relatively non-polymorphic accessory mutation selected by each of the Pls. In combination with other Pl-resistance mutations, it is associated with reduced susceptibility to LPV, ATV, and DRV.

Other

- L10I/V are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.
- There is evidence for low-level DRV resistance. If DRV is administered it should be used twice daily.

Mutation scoring: PR HIVDB 9.5.1 (2023-11-05)

Drug resistance mutation scores of PI:

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ATV/r =	DRV/r =	LPV/r ≑
5	5	5
10	0	10
10	0	10
15	0	15
10	0	10
15	0	30
0	20	30
0	0	10
65	25	120
	5 10 10 15 10 15 0	5 5 10 0 10 0 15 0 10 0 15 0 0 0 0 0 0

Drug resistance interpretation: RT HIVDB 9.5.1 (2023-11-05)

NRTI Mutations: M41L 05% - D67N 05% - K70R 05% - V75M 05% - M184V 07% - L210W 05% - T215Y 05% - K219E 05% 05% 23,401

NNRTI Mutations: V108VI = 67%, V= 37% • Y188L 05% cpr-24.036

V276T 50% - K277KR x: 56%, R: 35% - K281R 85% - L282C 57% - L283I 56% - T286A 57% - J293V 56% 50% 53,675

Nucleoside Reverse Transcriptase Inhibitors

Non-nucleoside Reverse Transcriptase Inhibitors

abacavir (ABC)	High-Level Resistance	doravirine (DOR)	High-Level Resistance
zidovudine (AZT)	High-Level Resistance	efavirenz (EFV)	High-Level Resistance
emtricitabine (FTC)	High-Level Resistance	etravirine (ETR)	Potential Low-Level Resistance
lamivudine (3TC)	High-Level Resistance	nevirapine (NVP)	High-Level Resistance
tenofovir (TDF)	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 ddl, ABC and TDF susceptibility.
- D67N is a non-polymorphic TAM associated with low-level resistance to AZT.
- K70R is a TAM that confers intermediate resistance to AZT and contributes to reduced ABC and TDF susceptibility in combination with other TAMs.
- V75T/M/A/S are nonpolymorphic accessory NRTI-selected mutations. They appear to have minimal phenotypic effects on AZT, 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.
- 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.
- T215Y/F are TAMs that causes intermediate/high-level resistance to AZT and potentially low-level resistance to ABC and TDF.
- K219E/Q/N/R are accessory TAMS that usually occur in combination with multiple other TAMs.

NNRTI

- 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.
- Y188L is a non-polymorphic mutation that confers high-level resistance to NVP, EFV, RPV, and DOR, and potentially low-level resistance to ETR.

Mutation scoring: RT HIVDB 9.5.1 (2023-11-05)

HIVDB 9.5.1 (2023-11-05) Mutation scoring: RT

Drug resistance mutation scores of NRTI:

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Rule	ABC \$	AZT \$	FTC \$	зтс ≑	TDF \$
M41L	5	15	0	0	5
M41L + D67N + T215Y	5	5	0	0	5
M41L + M184V + T215Y	10	0	0	0	0
M41L + L210W	10	10	0	0	10
M41L + L210W + T215Y	10	0	15	15	10
M41L + T215Y	10	10	5	5	10
<u>D67N</u>	5	15	0	0	5
D67N + K70R + M184V + K219E	10	0	0	0	0
D67N + K70R + K219E	10	15	10	10	10
D67N + T215Y + K219E	5	5	0	0	5
<u>K70R</u>	5	30	0	0	5
M184V	15	-10	60	60	-10
<u>L210W</u>	5	15	0	0	5
L210W + T215Y	10	10	0	0	10
<u>T215Y</u>	10	60	0	0	10
<u>K219E</u>	5	10	0	0	5
<u>V75M</u>	0	10	0	0	0
K70R + T215Y	0	0	0	0	0
Total	130	200	90	90	85

Drug resistano	e mutation	scores o	f NNRTI
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Rule	DOR ÷	EFV \$	ETR \$	NVP ≑	RPV \$
V108VI	10	10	0	15	0
Y188L	60	60	10	60	60
Total	70	70	10	75	60