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

PI Major Mutations: PI Accessory Mutations: None

PR Other Mutations: V11L - T12G - 113R - K14D - 115G - G16A - Q18A - L19A - E21T - A22M - L23H - D25R - T26" - T31P - E35D - M36I - N37D - R41K - 154F - R57Q - 1799" - D60E - H69K - K70R - A71V - L89M

Protease Inhibitors

atazanavir/r (ATV/r) Potential Low-Level Resistance Susceptible darunavir/r (DRV/r) Potential Low-Level Resistance fosamprenavir/r (FPV/r) indinavir/r (IDV/r) Low-Level Resistance lopinavir/r (LPV/r) Potential Low-Level Resistance nelfinavir (NFV) Potential Low-Level Resistance saguinavir/r (SQV/r) Potential Low-Level Resistance

tipranavir/r (TPV/r) Susceptible

PR comments

Accessory

L24I is a non-polymorphic mutation selected by IDV and LPV. It contributes reduced susceptibility to ATV and LPV.

Other

- V111/L are relatively non-polymorphic accessory mutation selected in persons receiving DRV. V11L is a nonpolymorphic PI-selected mutation associated with reduced in vitro DRV susceptibility when it occurs in combination with other PI-resistance mutations.
- 154V is a non-polymorphic PI-selected mutation that contributes reduced susceptibility to each of the PIs except DRV. 154M/L are non-polymorphic mutations that occur almost exclusively in viruses with multiple PI-resistance mutations that occur almost exclusively in viruses with multiple PI-resistance mutations that occur almost exclusively in viruses with multiple PI-resistance mutations. 154M/T/S are non-polymorphic PI-selected mutations that occur almost exclusively in viruses with multiple PI-resistance mutations. 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: Download CSV Rule ATV/r
DRV/r FPV/r ≑ IDV/r

LPV/r NFV

SQV/r

TPV/r L24I 10 0 10 15 10 10 10 -5

Drug resistance interpretation: RT

HIVDB 9.5.1 (2023-11-05)

NRTI Mutations: None

K103N • P225H • P236L • K238T NNRTI Mutations:

E6D - K20R - V351 - V601 - K122E - 1142V - K173L - Q174K - D177E - V1791 - T200A - Q207A - R2115 - F214L - K229F - K223F - K22 RT Other Mutations:

Nucleoside Reverse Transcriptase Inhibitors

abacavir (ABC) Susceptible zidovudine (AZT) Susceptible stavudine (D4T) Susceptible didanosine (DDI) Susceptible emtricitabine (FTC) Susceptible lamivudine (3TC) Susceptible tenofovir (TDF) Susceptible

Non-nucleoside Reverse Transcriptase Inhibitors

doravirine (DOR) Intermediate Resistance efavirenz (EFV) High-Level Resistance etravirine (ETR) Susceptible nevirapine (NVP) High-Level Resistance rilpivirine (RPV) Susceptible

RT comments

NNRTI

- K103N is a non-polymorphic mutation that confers high-level reductions in NVP and EFV susceptibility. It is the most commonly transmitted DRM.
- P225H is a non-polymorphic EFV-selected mutation that usually occurs in combination with K103N. The combination of P225H and K103N synergistically reduces NVP, EFV and DOR susceptibility.
- P236L is a rare mutation selected commonly by DLV, which appears to have little if any effect on current NNRTIs.
- 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.

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.

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

NORTI:		Download CSV	
FV ÷	ETR ÷	NVP ≑	RPV ÷
0	0	0	0
45	0	45	0
0	0	0	0

135 0

135 0

Rule DOR ≑

20

10

K103N + P225H 10

P225H P236L

K103N K238T Total