

Drug resistance interpretation: PRHIVDB 9.5.1 (2023-11-05)

PI Major Mutations:None

PI Accessory Mutations:None

PR Other Mutations:I13V 100%
HIV-2.138 • K20R 100%
HIV-2.289 • E35D 100%
HIV-1.216 • M36I 100%
HIV-3.275 • R41K 100%
HIV-5.229 • R57K 100%
HIV-2.711 • H69K 100%
HIV-2.351 • K70R 100%
HIV-2.391 • I72IV 1.107%
HIV-2.506¹ 0.107% • L89M 100%
HIV-2.520

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

- K20R is a highly polymorphic PI-selected accessory mutation that increases replication fitness in viruses with PI-resistance mutations.

Mutation scoring: PRHIVDB 9.5.1 (2023-11-05)

No drug resistance mutations were found for PI.

Drug resistance interpretation: RTHIVDB 9.5.1 (2023-11-05)

NRTI Mutations:None

NNRTI Mutations:[K103N](#) 100%
HIV-1.811

RT Other Mutations:K11T 100%
HIV-2.875 • V35T 100%
HIV-1.289 • S48T 100%
HIV-1.285 • V60I 100%
HIV-1.235 • K66KR 0.71%
HIV-1.228¹ 0.104% • K122E 100%
HIV-6.027 • D123N 100%
HIV-6.117 • I135T 100%
HIV-1.963 • I142N 1.147%
HIV-1.234¹ 0.104% • K173L 100%
HIV-1.367 • Q174K 100%
HIV-1.367 • D177E 100%
HIV-1.145 • I178V 100%
HIV-1.145 • V179I 100%
HIV-1.145 • T200A 100%
HIV-1.807 • Q207E 100%
HIV-6.114 • F214L 100%
HIV-1.331 • E514D 100%
HIV-1.225 • S519N 100%
HIV-1.147 • Q524R 100%
HIV-1.342 • K527G 100%
HIV-1.342 • E529D 100%
HIV-1.224 • A534S 100%
HIV-1.217 • A554S 100%
HIV-1.855

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)

Susceptible

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.

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.

Mutation scoring: RTHIVDB 9.5.1 (2023-11-05)

No drug resistance mutations were found for NRTI.

Drug resistance mutation scores of NNRTI:

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Rule	DOR	EFV	ETR	NVP	RPV
K103N	0	60	0	60	0

Drug resistance interpretation: INHIVDB 9.5.1 (2023-11-05)

INSTI Major Mutations:None

INSTI Accessory Mutations:[T97TA](#) 1.147%
HIV-1.258¹ 0.104%

IN Other Mutations:K14R 100%
HIV-1.671 • I60M 100%
HIV-1.221 • I72V 100%
HIV-1.302 • L101LIM 11.305%
HIV-1.272¹ 1.105% 1.105% • T112N 1.147%
HIV-1.258¹ 0.104% • I113V 100%
HIV-1.302 • T124A 100%
HIV-1.235 • T125A 100%
HIV-1.235 • V126F 100%
HIV-1.235 • G134N 100%
HIV-1.235 • I135V 100%
HIV-1.235 • D167E 100%
HIV-1.421 • V201I 100%
HIV-1.517 • T206S 100%
HIV-1.501 • I208IL 1.105%
HIV-1.404¹ 1.105% • K211KR 1.147%
HIV-1.302¹ 0.104% • Y227F 100%
HIV-1.412 • S255N 100%
HIV-1.511 • D256E 100%
HIV-1.501 • S283G 100%
HIV-1.727

Integrase Strand Transfer Inhibitors

bictegravir (BIC)

Susceptible

cabotegravir (CAB)

Susceptible

dolutegravir (DTG)

Susceptible

elvitegravir (EVG)

Potential Low-Level Resistance

raltegravir (RAL)

Potential Low-Level Resistance

IN comments

Accessory

- **T97A** is a polymorphic INSTI-selected mutation that, depending on subtype, occurs in 1% to 5% of viruses from untreated persons. Alone, it has minimal effects on INSTI susceptibility but in combination with other major resistance mutations, it synergistically reduces susceptibility to each of the INSTIs.

Mutation scoring: IN

HIVDB 9.5.1 (2023-11-05)

Drug resistance mutation scores of INSTI:

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Rule	BIC ⚡	CAB ⚡	DTG ⚡	EVG ⚡	RAL ⚡
<u>T97TA</u>	0	0	0	10	10