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

HIVDB 9.5.1 (2023-11-05)

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: None PI Accessory Mutations: K20T

PR Other Mutations: V11Q - T12G - 113\* - K14P - 115D - G16R - Q18N - E35D - M36I - R41K - R57K - H69K - K70R - 185V - L89M

### Protease Inhibitors

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

saquinavir/r (SQV/r) Susceptible Susceptible tipranavir/r (TPV/r)

#### PR comments

#### Accessory

K20T is a non-polymorphic accessory PI-selected mutation associated with reduced susceptibility to ATV and LPV.

### Other

185V is a non-polymorphic PI-selected mutation. It has minimal, if any, effects on PI susceptibility.

Mutation scoring: PR

L	Drug re	sistance m		Download CSV					
	Rule	ATV/r ≎	DRV/r ‡	FPV/r ‡	IDV/r ≎	LPV/r ‡	NFV 🗢	sqv/r 🗢	TPV/r 🕏
	K20T	5	0	5	5	0	15	5	0

# Drug resistance interpretation: RT

NRTI Mutations: L74I - M184V

NNRTI Mutations: A98G - K103N - P225H

E6K - K11Q - V35T - V60I - L100\* - V111I - K122E - D123S - I135T - I142V - K173S - Q174K - D177E - T200X - Q207A - K220S - Q222S - K223E - H235I - D237T - K238S - W239D - T240S - V245T - L246A - P247A - D250E - D256\* - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - I257Y - Q258T - K259E - L260I - S268V - Q269K - Q26 RT Other Mutations:

V276L - K281N - L282S - R284S - G285A - T286A - K287\*

# **Nucleoside Reverse Transcriptase Inhibitors**

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

# Non-nucleoside Reverse Transcriptase Inhibitors

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

#### RT comments

#### NRTI

- L74V causes intermediate ABC resistance. L74I causes low-level ABC resistance.
- 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

- . A986 is a non-polymorphic accessory mutation associated with low-level reduced susceptibility to each of the NNRTIs.
- . 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.

### 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. K238S is a highly unusual mutation at this position.
- . This virus is predicted to have low-level reduced susceptibility to RPV. The use of the combination of CAB/RPV should be considered to be relatively contraindicated.

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

Drug resistance mutation scores of NRTI:

Download CSV

Rule	ABC \$	AZT \$	D4T \$	DDI \$	FTC \$	3ТС ≑	TDF \$	
<u>L741</u>	15	0	0	60	0	0	5	
M184V	15	-10	-10	10	60	60	-10	
Total	30	-10	-10	70	60	60	-5	

Drug resistance mutation scores of NNRTI:

Download CSV

Rule	DOR \$	EFV ≑	ETR ‡	NVP \$	RPV \$
<u>A98G</u>	15	15	10	30	15
K103N + P225H	10	0	0	0	0
P225H	20	45	0	45	0
K103N	0	60	0	60	0
Total	45	120	10	135	15