

PI Major Mutations:None

PI Accessory Mutations:[G73GS](#)(G:K76, N:176)
score:5,832

PR Other Mutations:[I13V](#)100%
score:4,202 • [E35D](#)99%
score:5,790 • [M36I](#)100%
score:5,790 • [G40GE](#)(G:K76, N:176)
score:5,890 • [R41K](#)99%
score:5,890 • [W42W](#)(W:K76, N:176)
score:5,982 • [R57K](#)99%
score:5,875 • [H69K](#)99%
score:5,264 • [G78GR](#)(G:K76, N:176)
score:6,635 • [L89M](#)100%
score:6,645

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

PR comments

Accessory

- G73S/T/C/A are common non-polymorphic accessory mutations selected primarily by most PIs. They are associated with minimally reduced susceptibility to each of the PIs.

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
G73GS	10	0	10	15	5	15	15	0

NRTI Mutations:None

NNRTI Mutations:[K103N](#)100%
score:1,600

RT Other Mutations:[K11T](#)100%
score:6,284 • [K20KR](#)N:79%
score:5,122 • [V21I](#)99%
score:5,121 • [V35T](#)99%
score:5,200 • [T39R](#)99%
score:5,177 • [K43E](#)100%
score:5,029 • [V60I](#)100%
score:2,562 • [W88C](#)96%
score:1,046 • [K122E](#)99%
score:5,762 • [D123N](#)99%
score:1,762 • [K173S](#)99%
score:5,890 • [D177E](#)99%
score:5,509 • [V179I](#)100%
score:3,588 • [T200TA](#)N:40%
score:2,687 • [I202V](#)100%
score:12,852 • [Q207A](#)99%
score:12,138 • [R211K](#)99%
score:2,523 • [V245Q](#)100%
score:2,882 • [E248DN](#)(I:K76, N:201)
score:2,885 • [T286A](#)100%
score:1,130 • [E291D](#)99%
score:1,058 • [I293V](#)100%
score:927 • [P294T](#)99%
score:916 • [E312D](#)99%
score:269 • [V317E](#)99%
score:392 • [L517I](#)100%
score:5,863 • [Q520S](#)100%
score:6,725 • [Q524K](#)94%
score:7,679 • [K527E](#)99%
score:8,028 • [E529D](#)100%
score:8,328 •

Nucleoside Reverse Transcriptase Inhibitors		Non-nucleoside Reverse Transcriptase Inhibitors	
abacavir (ABC)	Susceptible	doravirine (DOR)	Susceptible
zidovudine (AZT)	Susceptible	efavirenz (EFV)	High-Level Resistance
stavudine (D4T)	Susceptible	etravirine (ETR)	Susceptible
didanosine (DDI)	Susceptible	nevirapine (NVP)	High-Level Resistance
emtricitabine (FTC)	Susceptible	rilpivirine (RPV)	Susceptible
lamivudine (3TC)	Susceptible		
tenofovir (TDF)	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.

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

INSTI Major Mutations:None

INSTI Accessory Mutations:None

IN Other Mutations:[S17N](#)100%
score:11,500 • [V31I](#)100%
score:12,058 • [I60M](#)100%
score:9,008 • [I72V](#)97%
score:1,533 • [T112V](#)100%
score:947 • [I113V](#)100%
score:947 • [T124A](#)100%
score:929 • [T125A](#)100%
score:929 • [V126F](#)100%
score:929 • [I135V](#)99%
score:927 • [K136Q](#)100%
score:919 • [F139Y](#)100%
score:963 • [D167E](#)100%
score:980 • [H171Q](#)100%
score:1,044 • [V201I](#)99%
score:1,068 • [S283G](#)100%
score:1,500

Integrase Strand Transfer Inhibitors	
bictegravir (BIC)	Susceptible
cabotegravir (CAB)	Susceptible
dolutegravir (DTG)	Susceptible
elvitegravir (EVG)	Susceptible
raltegravir (RAL)	Susceptible

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

No drug resistance mutations were found for INSTI.