

Drug resistance interpretation: PR		HIVDB 9.5.1 (2023-11-05)
PI Major Mutations:	None	
PI Accessory Mutations:	None	
PR Other Mutations:	I13V ^{10%} _{cons=3,845} • K14R ^{10%} _{cons=1,838} • G17GE ^{G-13%, G-20%} _{cons=8,222} • L19LI ^{L-10%, L-20%} _{cons=8,283} • K20KR ^{R-13%, R-27%} _{cons=4,138} • E35D ^{10%} _{cons=6,122} • M36I ^{100%} _{cons=6,122} • R41K ^{10%} _{cons=6,128} • K43KR ^{R-107%, R-10%} _{cons=6,121} • R57K ^{10%} _{cons=6,286} • L63S ^{100%} _{cons=8,974} • I64IV ^{I-107%, V-20%} _{cons=1,064} • H69K ^{10%} _{cons=6,915} • L89M ^{10%} _{cons=1,136}	
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: PR	HIVDB 9.5.1 (2023-11-05)
No drug resistance mutations were found for PI.	

Drug resistance interpretation: RT

HIVDB 9.5.1 (2023-11-05)

NRTI Mutations:

NNRTI Mutations:

RT Other Mutations:

M184V10%cons=1,114

T215TF100%cons=262

A98AG100%cons=326

K103KN100%cons=267

Y181YC100%cons=362

K11T10%cons=2,317

K20R10%cons=1,478

V21I10%cons=1,479

V35T10%cons=362

T39K10%cons=362

K122E10%cons=1,681

D123S10%cons=1,681

T165L10%cons=161

K173S10%cons=1,681

D177E100%cons=1,138

T200TA100%cons=338

I202V100%cons=339

Q207A100%cons=339

R211RS100%cons=455

V245Q100%cons=1,587

E248D100%cons=1,536

V261VI100%cons=656

A272AP100%cons=384

T286A100%cons=386

E291D100%cons=1,281

V292I100%cons=1,281

I293V100%cons=1,281

P294T100%cons=1,281

E312D100%cons=1,271

E514D100%cons=1,106

S519SN100%cons=7,100

Q524K100%cons=8,967

K527E100%cons=9,286

E529D100%cons=11,081

A534S100%cons=11,111

Nucleoside Reverse Transcriptase Inhibitors

Non-nucleoside Reverse Transcriptase Inhibitors

abacavir (ABC)

Low-Level Resistance

zidovudine (AZT)

Intermediate Resistance

stavudine (D4T)

Intermediate Resistance

didanosine (DDI)

Low-Level Resistance

emtricitabine (FTC)

High-Level Resistance

lamivudine (3TC)

High-Level Resistance

tenofovir (TDF)

Susceptible

doravirine (DOR)

Intermediate Resistance

efavirenz (EFV)

High-Level Resistance

etravirine (ETR)

Intermediate Resistance

nevirapine (NVP)

High-Level Resistance

rilpivirine (RPV)

High-Level Resistance

RT comments

NRTI

NNRTI

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.

T215Y/F are TAMs that causes intermediate/high-level resistance to AZT and potentially low-level resistance to ABC and TDF.

A98G 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.

Y181C is a non-polymorphic mutation selected in persons receiving NVP, ETR and RPV. It confers high-level resistance to NVP, intermediate resistance to ETR and RPV, and low-level resistance to EFV. It does not significantly reduce DOR susceptibility.

Mutation scoring: RT	HIVDB 9.5.1 (2023-11-05)
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Drug resistance mutation scores of NRTI:

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Rule	ABC	AZT	D4T	DDI	FTC	3TC	TDF
M184V	15	-10	-10	10	60	60	-10
T215TF	10	60	40	15	0	0	10
Total	25	50	30	25	60	60	0

Drug resistance mutation scores of NNRTI:

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Rule	DOR	EFV	ETR	NVP	RPV
A98AG	15	15	10	30	15
A98AG + Y181YC	5	5	5	5	5
K103KN + Y181YC	5	0	0	0	0
Y181YC	10	30	30	60	45
K103KN	0	60	0	60	0
Total	35	110	45	155	65

INSTI Major Mutations:None

INSTI Accessory Mutations:None

IN Other Mutations:

V31I

100%

cons:26,333

 • M50I

94%

cons:11,334

 • I60M

100%

cons:9,300

82%

cons:3,546

99%

cons:3,229

100%

cons:3,229

100%

cons:5,378

94%

cons:5,660

100%

cons:5,629

99%

cons:1,5129

94%

cons:6,863

99%

cons:10,254

99%

cons:10,088

82%

cons:10,096

99%

cons:10,228

81%

cons:9,910

92%

cons:9,602

Integrase Strand Transfer Inhibitors

bictegravir (BIC)Susceptible

cabotegravir (CAB)Susceptible

dolutegravir (DTG)Susceptible

elvitegravir (EVG)Susceptible

raltegravir (RAL)Susceptible

IN comments

Other

- M50I is a highly polymorphic mutation, which has a prevalence of 3% to 34% in INSTI-naïve persons depending on subtype. It has been selected in vitro by DTG and BIC in combination with R263K. It may contribute to reduced DTG and CAB susceptibility in combination with R263K.

No drug resistance mutations were found for INSTI.