

Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	L10I <small>100% seen=2,300</small> • I13V <small>99% seen=2,714</small> • E35D <small>99% seen=3,100</small> • M36I <small>100% seen=3,100</small> • R41K <small>99% seen=3,107</small> • H69K <small>99% seen=2,944</small> • L89M <small>100% seen=3,101</small>

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

- L10I/V 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)
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No drug resistance mutations were found for PI.

Drug resistance interpretation: RT	HIVDB 9.5.1 (2023-11-05)
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NRTI Mutations:	D67ES <small>91.72% seen=1,149</small> • T215C <small>100% seen=354</small> • K219E <small>100% seen=200</small>
NNRTI Mutations:	K103N <small>90% seen=1,800</small> • V179T <small>100% seen=2,110</small> • Y181V <small>99% seen=2,114</small>
RT Other Mutations:	K11T <small>100% seen=2,994</small> • K20KR <small>91.40% seen=2,140</small> • V21I <small>100% seen=2,144</small> • V35T <small>100% seen=2,106</small> • T39N <small>99% seen=1,391</small> • V60I <small>100% seen=3,912</small> • T69N <small>99% seen=3,981</small> • D121H <small>99% seen=1,922</small> • K122E <small>100% seen=3,929</small> • D123S <small>97% seen=1,906</small> • I142V <small>99% seen=1,902</small> • K173S <small>99% seen=2,106</small> • Q174K <small>99% seen=2,106</small> • D177E <small>100% seen=2,114</small> • T200K <small>99% seen=2,100</small> • I202V <small>99% seen=2,100</small> • Q207A <small>99% seen=874</small> • R211S <small>100% seen=594</small> • Q524K <small>100% seen=206</small> • K527E <small>99% seen=212</small> • E529D <small>97% seen=226</small> • A534S <small>100% seen=217</small> • A554S <small>99% seen=4076</small>

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

RT comments	
NRTI	
• D67N is a non-polymorphic TAM associated with low-level resistance to AZT. D67G/E/S/T/H are non-polymorphic NRTI-selected mutations that generally occur in viruses with multiple TAMs.	
• T215Y/F are TAMs that causes intermediate/high-level resistance to AZT and potentially low-level resistance to ABC and TDF. T215S/C/D/E/I/V/N/A/L do not reduce NRTI susceptibility but arise from viruses that once contained T215Y/F. The presence of one of these revertant mutations suggests that the patient may have once been infected with a virus containing T215Y/F.	
• K219E/Q/N/R are accessory TAMs that usually occur in combination with multiple other TAMs.	
NNRTI	
• K103N is a non-polymorphic mutation that confers high-level reductions in NVP and EFV susceptibility. It is the most commonly transmitted DRM.	
• V179T is a rare non-polymorphic mutation occasionally selected in persons receiving NNRTIs. It is associated with minimal, if any, reduction in ETR and RPV susceptibility.	
• Y181I/V are 2-base pair non-polymorphic mutations selected by NVP and ETR. They cause high-level resistance to NVP, ETR, and RPV but not EFV. Their effects on DOR have not been well-characterized.	
Other	
• T69N/S/A/I/E are relatively non-polymorphic mutations weakly selected in persons receiving NRTIs. They may minimally contribute reduced AZT 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
D67ES	5	15	10	5	0	0	5
K219E	5	10	10	5	0	0	5
T215C	0	10	20	10	0	0	0
Total	10	35	40	20	0	0	10

Rule	DOR ⇅	EFV ⇅	ETR ⇅	NVP ⇅	RPV ⇅
<u>Y181V</u>	20	30	60	60	60
<u>K103N</u>	0	60	0	60	0
Total	20	90	60	120	60

Drug resistance interpretation: IN

HIVDB 9.5.1 (2023-11-05)

INSTI Major Mutations:None

INSTI Accessory Mutations:None

IN Other Mutations:

E11D94%
seen=823 • K14R111%
seen=873 • S17ST15.04%
seen=123 • V31I100%
seen=1,038 • M50I94%
seen=877 • I72V100%
seen=364 • G106A100%
seen=285 • S119P100%
seen=214 • T124A94%
seen=314 • T125A95%
seen=314 • K136Q100%
seen=347 • D167E100%
seen=835 • G193E100%
seen=1,032 • V201I100%
seen=876 • T218S94%
seen=753 • N222K94%
seen=1,030 • Y227F100%
seen=770 • N254K100%
seen=832 • S255G95%
seen=832 • S283G95%
seen=1,030

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.

Mutation scoring: IN

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No drug resistance mutations were found for INSTI.