

Drug resistance interpretation: PR

PI Major Mutations:

None

PI Accessory Mutations:

None

PR Other Mutations:

L10V<sup>92%</sup>  
cons=28,207 • I13V<sup>98%</sup>  
cons=27,203 • I15V<sup>92%</sup>  
cons=27,205 • G16E<sup>76%</sup>  
cons=27,211 • K20R<sup>92%</sup>  
cons=25,795 • E35D<sup>93%</sup>  
cons=23,939 • M36I<sup>98%</sup>  
cons=23,932 • R41K<sup>99%</sup>  
cons=24,344 • R57K<sup>98%</sup>  
cons=21,989 • L63V<sup>100%</sup>  
cons=28,000 • H69K<sup>93%</sup>  
cons=25,389 • I72V<sup>79%</sup>  
cons=20,240 • L89M<sup>97%</sup>  
cons=28,000

Protease Inhibitors

atazanavir/r (ATV/r)

Susceptible

darunavir/r (DRV/r)

Susceptible

lopinavir/r (LPV/r)

Susceptible

PR comments

Other

- L10I/V are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.
- K20R is a highly polymorphic PI-selected accessory mutation that increases replication fitness in viruses with PI-resistance mutations.

Mutation scoring: PR

No drug resistance mutations were found for PI.

Drug resistance interpretation: RT

NRTI Mutations:

L74V<sup>96%</sup>  
cons=9,225 • Y115F<sup>96%</sup>  
cons=6,112 • M184V<sup>96%</sup>  
cons=24,528 • K219N<sup>96%</sup>  
cons=25,262

NNRTI Mutations:

L100I<sup>96%</sup>  
cons=6,789 • K103N<sup>96%</sup>  
cons=6,828

RT Other Mutations:

K11T<sup>92%</sup>  
cons=25,000 • K20R<sup>92%</sup>  
cons=25,719 • V35T<sup>98%</sup>  
cons=20,086 • T39R<sup>96%</sup>  
cons=25,705 • K49R<sup>92%</sup>  
cons=23,704 • V60I<sup>96%</sup>  
cons=11,342 • R63RK<sup>91, 75%</sup>  
cons=40,219 • K122E<sup>96%</sup>  
cons=6,204 • D123N<sup>96%</sup>  
cons=6,284 • E169A<sup>96%</sup>  
cons=12,703 • K173S<sup>96%</sup>  
cons=22,000 • Q174K<sup>96%</sup>  
cons=22,900 • D177E<sup>96%</sup>  
cons=11,072 • V179I<sup>96%</sup>  
cons=11,011 • T200E<sup>96%</sup>  
cons=10,040 • I202V<sup>96%</sup>  
cons=20,907 • Q207A<sup>96%</sup>  
cons=19,400 • R211K<sup>96%</sup>  
cons=22,770 • V245Q<sup>96%</sup>  
cons=24,000 • E248D<sup>96%</sup>  
cons=18,111 • T286TA<sup>91, 76%</sup>  
cons=24,528 T-127% • I293V<sup>96%</sup>  
cons=10,002 • P294A<sup>96%</sup>  
cons=10,000

Nucleoside Reverse Transcriptase Inhibitors

abacavir (ABC)

High-Level Resistance

zidovudine (AZT)

Susceptible

emtricitabine (FTC)

High-Level Resistance

lamivudine (3TC)

High-Level Resistance

tenofovir (TDF)

Low-Level Resistance

Non-nucleoside Reverse Transcriptase Inhibitors

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

- L74V causes intermediate ABC resistance. L74I causes low-level ABC resistance.
- Y115F causes intermediate resistance to ABC and low-level resistance to TDF.
- 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.
- K219E/Q/N/R are accessory TAMs that usually occur in combination with multiple other TAMs.

NNRTI

- L100I is a non-polymorphic mutation that usually occurs in combination with K103N. In this setting it confers high-level resistance to NVP, EFV, and RPV and intermediate resistance to ETR and DOR.
- 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: RT

Drug resistance mutation scores of NRTI: 

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Rule	ABC ⇅	AZT ⇅	FTC ⇅	3TC ⇅	TDF ⇅
<u>L74V</u>	30	0	0	0	0
<u>L74V + M184V</u>	15	0	0	0	0
<u>Y115F</u>	30	0	0	0	15
<u>Y115F + M184V</u>	15	0	0	0	5
<u>M184V</u>	15	-10	60	60	-10
<u>K219N</u>	5	10	0	0	5
Total	110	0	60	60	15

Drug resistance mutation scores of NNRTI: 

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Rule	DOR ⇅	EFV ⇅	ETR ⇅	NVP ⇅	RPV ⇅
<u>L100I</u>	15	60	30	60	60
<u>L100I + K103N</u>	15	0	0	0	0
<u>K103N</u>	0	60	0	60	0
Total	30	120	30	120	60