

Drug resistance interpretation: PR		HIVDB 9.5.1 (2023-11-05)
PI Major Mutations:	None	
PI Accessory Mutations:	None	
PR Other Mutations:	V11H • T12L • I13V • K14R • I15V • K20I • E35D • M36I • N37D • R41K • I64M • H69K • L89M	
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		
<ul style="list-style-type: none">K20I is the consensus amino acid in subtype G and CRF02_AG. In subtypes B and C, K20I is a PI-selected mutation of uncertain effects on currently used PIs.		

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:	M184I • T215L • K219E		
NNRTI Mutations:	K101E • Y181C • G190A • H221Y		
RT Other Mutations:	P4T • I5V • V35T • T39N • V60I • V90I • K103R • K122E • D123S • I142V • P176S • D177E • I178L • E204K • Q207E • R211K • E224T • P225S • P226X • L234X • P236S • P243L • V245Q • P247Q • E248K • K249R • D250S • S251W • W252T • T253V • V254M • N255T • D256Y		
Nucleoside Reverse Transcriptase Inhibitors		Non-nucleoside Reverse Transcriptase Inhibitors	
abacavir (ABC)	Low-Level Resistance	doravirine (DOR)	High-Level Resistance
zidovudine (AZT)	Potential Low-Level Resistance	efavirenz (EFV)	High-Level Resistance
stavudine (D4T)	Low-Level Resistance	etravirine (ETR)	High-Level Resistance
didanosine (DDI)	Low-Level Resistance	nevirapine (NVP)	High-Level Resistance
emtricitabine (FTC)	High-Level Resistance	rilpivirine (RPV)	High-Level Resistance
lamivudine (3TC)	High-Level Resistance		
tenofovir (TDF)	Susceptible		

RT comments

NRTI

- **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. **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

- **K101E** is a non-polymorphic accessory mutation that confers intermediate resistance to NVP and RPV and low-level reductions in susceptibility to EFV, ETR, and DOR when it occurs with other NNRTI-resistance mutations.
- **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.
- **G190A** is a non-polymorphic mutation that causes high-level resistance to NVP and intermediate resistance to EFV. It does not significantly reduce susceptibility to RPV, ETR, or DOR.
- **H221Y** is a non-polymorphic accessory mutation selected primarily by NVP, RPV, and DOR. It frequently occurs in combination with Y181C.

Other

- **V90I** is a polymorphic accessory mutation weakly selected by each of the NNRTIs. It is associated with minimal, if any, detectable reduction in NNRTI susceptibility.
- **K103R** is a polymorphic mutation that alone has no effect on NNRTI susceptibility. However, in combination with V179D, it reduces NVP and EFV susceptibility about 15-fold.
- 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. **P225S** is a highly unusual mutation at this position.
- P236L is a rare mutation selected commonly by DLV, which appears to have little if any effect on current NNRTIs. **P236S** is a highly unusual mutation at this position.

Mutation scoring: RT

HIVDB 9.5.1 (2023-11-05)

Drug resistance mutation scores of NRTI:

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Rule	ABC ⇅	AZT ⇅	D4T ⇅	DDI ⇅	FTC ⇅	3TC ⇅	TDF ⇅
M184I	15	-10	-10	10	60	60	-10
K219E	5	10	10	5	0	0	5
T215L	0	10	20	10	0	0	0
Total	20	10	20	25	60	60	-5

Drug resistance mutation scores of NNRTI:

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Rule	DOR ⇅	EFV ⇅	ETR ⇅	NVP ⇅	RPV ⇅
K101E	15	15	15	30	45
K101E + G190A	5	0	5	0	0
Y181C	10	30	30	60	45
Y181C + G190A	10	0	10	0	10
Y181C + H221Y	10	0	0	0	10
H221Y	10	10	10	15	15
K101E + Y181C	0	5	5	5	0
G190A	0	45	10	60	15
K101E + M184I	0	0	0	0	15
Total	60	105	85	170	155