Drug resistance interpretation: PR — HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: None
PI Accessory Mutations: L24F • L33F
PR Other Mutations: L10E • V11Y • T12R • I13R • K14E • I15R • G16K • G17V • Q18N • L19Q • E21R • A22L • L23P • P39A • R41K • R57K • L63P • I64L • H69L • L89M

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

PR comments

Accessory

- L24I is a non-polymorphic mutation selected by IDV and LPV. It contributes reduced susceptibility to ATV and LPV. **L24F/M** are uncommon non-polymorphic PI-selected mutations. **L24F** has a susceptibility profile similar to L24I.
- **L33F** is a relatively non-polymorphic accessory mutation selected by each of the PIs. In combination with other PI-resistance mutations, it is associated with reduced susceptibility to LPV, ATV, and DRV.

Other

- L10F is a common non-polymorphic, PI-selected accessory mutation associated with reduced in vitro susceptibility to LPV and DRV. L10I/V are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations. L10R/Y are rare, non-polymorphic PI-selected mutations. Their effects on PI susceptibility have not been well studied. **L10E** is a highly unusual mutation at this position.

Mutation scoring: PR — HIVDB 9.5.1 (2023-11-05)

Drug resistance mutation scores of PI: Download CSV

Rule	ATV/r	DRV/r	FPV/r	IDV/r	LPV/r	NFV	SQV/r	TPV/r
L24F	5	0	5	5	5	10	5	0
L33F	5	5	10	5	5	10	5	10
Total	10	5	15	10	10	20	10	10

Drug resistance interpretation: RT — HIVDB 9.5.1 (2023-11-05)

NRTI Mutations: None
NNRTI Mutations: None
RT Other Mutations: K11T • K20R • V35I • K49R • V60I • D121H • K122E • D177E • I178M • Y181L • Q182S • T200L • I202* • E203R • Q207E • R211K • P217Q • D218T • K220A • Δ221-222 • K223S • P225E • F227H • L228F • W229L • M230D • K238X • P243S • Δ245 • L246X • P247L • E248Q • D250E • N255X • K263I • L264N • N265G • W266Q • S268D • Q269Y • I270Q • Y271M • A272Q • G273* • I274D • K275N • V276M • K277Q • Q278C • L279I • C280G • K281S

Nucleoside Reverse Transcriptase Inhibitors	
abacavir (ABC)	Susceptible
zidovudine (AZT)	Susceptible
stavudine (D4T)	Susceptible
didanosine (DDI)	Susceptible
emtricitabine (FTC)	Susceptible
lamivudine (3TC)	Susceptible
tenofovir (TDF)	Susceptible

Non-nucleoside Reverse Transcriptase Inhibitors	
doravirine (DOR)	Susceptible
efavirenz (EFV)	Susceptible
etravirine (ETR)	Susceptible
nevirapine (NVP)	Susceptible
rilpivirine (RPV)	Susceptible

RT comments

Other

- 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. 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. **Y181L** is a highly unusual mutation at this position.
- 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. **P225E** is a highly unusual mutation at this position.
- F227L is a non-polymorphic mutation that usually occurs in combination with V106A. It is selected in vivo and in vitro with both NVP and DOR. In this context it is associated with high-level reductions in NVP and DOR susceptibility and intermediate reductions in EFV susceptibility. F227I/V are extremely rare mutations that have been selected in vitro by DOR. F227C is a nonpolymorphic mutation selected in persons receiving DOR and rarely in persons receiving ETR and RPV. It usually occurs in combination with other DRMs and in this setting has consistently been associated with the highest possible levels of DOR resistance. It is also usually associated with intermediate or high-level reductions in susceptibility to NVP, EFV, ETR, and RPV. **F227H** is a highly unusual mutation at this position.
- M230L is an uncommon non-polymorphic mutation selected in persons receiving EFV, NVP, and RPV. It causes intermediate to high-level resistance to each of the NNRTIs. M230I is a rare mutation selected by RPV. Its effects on NNRTI susceptibility have not been well studied. It also often occurs as a result of APOBEC-mediated G-to-A hypermutation resulting in viruses that are likely to be noninfectious. **M230D** is a highly unusual mutation at this position.

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

No drug resistance mutations were found for NRTI.

No drug resistance mutations were found for NNRTI.