Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: None
PI Accessory Mutations: None
PR Other Mutations: L10X • V11I • T12A • I13D • K14T • G16E • Q18T • L19A • E35D • M36I • R41K • R57K • L63C • 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

- **V11I/L** are relatively non-polymorphic accessory mutation selected in persons receiving DRV. V11L is a nonpolymorphic PI-selected mutation associated with reduced in vitro DRV susceptibility when it occurs in combination with other 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: K219E
NNRTI Mutations: E138A
RT Other Mutations: E6K • V35T • S48T • V60I • K103I • K122E • D123E • I135T • K166T • K173S • Q174K • N175H • D177E • V179I • T200A • I202V • Q207E • F214L • P217S • E224D • P225X • P226H • H235M • Δ236 • K238* • W239Q • T240* • V241Q • Q242S • P243T • L246* • P247L • S251C • N255M • D256N • Q257T • Q258E • K259L • L260V • V261G • G262N • K263* • L264M • N265G • W266S

Nucleoside Reverse Transcriptase Inhibitors	
abacavir (ABC)	Susceptible
zidovudine (AZT)	Potential Low-Level Resistance
stavudine (D4T)	Potential Low-Level Resistance
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)	Potential Low-Level Resistance
nevirapine (NVP)	Susceptible
rilpivirine (RPV)	Low-Level Resistance

RT comments

NRTI

- **K219E/Q/N/R** are accessory TAMS that usually occur in combination with multiple other TAMs.

NNRTI

- **E138A** is a common polymorphic accessory mutation weakly selected in persons receiving ETR and RPV. It reduces ETR and RPV susceptibility ~2-fold. Its effect on ETR- and RPV-containing regimens is likely to be minimal.

Other

- K103N is a non-polymorphic mutation that confers high-level reductions in NVP and EFV susceptibility. K103S is a non-polymorphic mutation that causes high-level reductions in NVP susceptibility but intermediate reductions in EFV susceptibility. Because K103S is a 2-bp change from the wildtype K and a 1-bp change from K103N, persons with K103S may be likely to have once had K103N. It is the most commonly transmitted DRM. K103T is an extremely rare non-polymorphic mutation that appears to confer intermediate/high-level resistance to NVP but it has little if any effect on EFV susceptibility. K103H is a rare non-polymorphic mutation that confers high-level resistance to NVP and EFV. K103E/Q are rare mutations that have not been associated with reduced NNRTI susceptibility. **K103I** is a highly unusual mutation at this position.
- **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.
- P236L is a rare mutation selected commonly by DLV, which appears to have little if any effect on current NNRTIs. **P236del** is a highly unusual mutation at this position.
- This virus is predicted to have low-level reduced susceptibility to **RPV**. The use of the combination of CAB/**RPV** should be considered to be relatively contraindicated.

Mutation scoring: RT

HIVDB 9.5.1 (2023-11-05)

Drug resistance mutation scores of NRTI: Download CSV

Rule	ABC	AZT	D4T	DDI	FTC	3TC	TDF
K219E	5	10	10	5	0	0	5

Drug resistance mutation scores of NNRTI: Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
E138A	0	0	10	0	15