Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: None
PI Accessory Mutations: None
PR Other Mutations: P9G • L10O • V11W • T12Q • I13Q • K14E • I15S • G17E • Q18A • L19S • K20R • E21R • A22L • M36I • R41K • L63P • H69K • L89M • I93L

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

- 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. **L10D** is a highly unusual mutation at this position.
- **K20R** is a highly polymorphic PI-selected accessory mutation that increases replication fitness in viruses with 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: K219R
NNRTI Mutations: V106M • V179D
RT Other Mutations: K20R • V35T • E36A • T39E • I50V • K122E • D123S • A158S • K173T • Q174K • D177E • T200X • Q207E • R211K • F214L • K220N • H221I • Q222R • K223R • E224P • L228F • W229G • G231E • L234H • P236X • Q242H • V245Q • E248D • V254G • N255D • D256* • I257Y • Q258N • K259R • L260S

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)	Intermediate Resistance
efavirenz (EFV)	High-Level Resistance
etravirine (ETR)	Potential Low-Level Resistance
nevirapine (NVP)	High-Level Resistance
rilpivirine (RPV)	Potential Low-Level Resistance

RT comments

NRTI

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

NNRTI

- **V106M** is a non-polymorphic mutation that confers high-level resistance to NVP and EFV. It is selected in vitro and in vivo by DOR and preliminary data suggests it reduces DOR susceptibility about 3-fold.
- **V179D/E** are somewhat polymorphic accessory NNRTI-selected mutation. In combination with other NNRTI DRMs, they appear to contribute low-levels of reduced susceptibility to each of the NNRTIs. In particular, the combinations of K103R/**V179D** and V106I/**V179D** act synergistically to reduce NVP and EFV susceptibility.

Other

- L234I is a nonpolymorphic mutation selected in persons receiving NVP and EFV. It is also selected in vitro by ETR and DOR. In combination with V106A, it is associated with high-level DOR resistance. Its effect on susceptibility when it occurs alone has not been well characterized. **L234H** is a highly unusual mutation at this position.

Mutation scoring: RT

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Drug resistance mutation scores of NRTI: Download CSV

Rule	ABC	AZT	D4T	DDI	FTC	3TC	TDF
K219R	5	10	10	5	0	0	5

Drug resistance mutation scores of NNRTI: Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
V106M	30	60	0	60	0
V179D	0	10	10	10	10
Total	30	70	10	70	10