Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: None
PI Accessory Mutations: None
PR Other Mutations: L19V • M36I • R41K • Q58QR • D60E • I62V • I64V • 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

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: D67ΔE • T69G • K70R • M184V • T215F • K219E
NNRTI Mutations: A98G • K101E • G190A • Y318F
RT Other Mutations: L26LW • V35T • T39TA • V60I • K66KR • V111I • D121H • K122E • D123E • I135K • I142V • S162SD • K173S • Q174K • D177E • T200A • E203K • Q207E • R211K • E224EK • V245K • D250E • A272Q • K281KR • L282C • T286A • I293V • A327AV • S515SL • E516A • S519N • K530R • A534S • A554N

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

Non-nucleoside Reverse Transcriptase Inhibitors	
doravirine (DOR)	High-Level Resistance
efavirenz (EFV)	High-Level Resistance
etravirine (ETR)	Intermediate Resistance
nevirapine (NVP)	High-Level Resistance
rilpivirine (RPV)	High-Level Resistance

RT comments

NRTI

- Amino acid deletions between codons 67 and 70 are rare and usually occur in combination with multiple TAMs, K65R, or the Q151M mutation complex. Deletions at position 67 are more often associated with multiple TAMs. Deletions at positions 69 and 70 are more often associated with K65R or the Q151M mutation complex. Deletions at codon 68 are extremely rare and less well characterized.
- D67N is a non-polymorphic TAM associated with low-level resistance to AZT. **D67G/E/S/T/H** are non-polymorphic NRTI-selected mutations that generally occur in viruses with multiple TAMs.
- **T69G** is a rare non-polymorphic mutation that usually occurs in viruses with a deletion at codon 67 and multiple other NRTI-resistance mutations.
- **K70R** is a TAM that confers intermediate resistance to AZT and contributes to reduced ABC and TDF susceptibility in combination with other TAMs.
- **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.
- **K219E/Q/N/R** are accessory TAMS that usually occur in combination with multiple other TAMs.

NNRTI

- **A98G** is a non-polymorphic accessory mutation associated with low-level reduced susceptibility to each of the NNRTIs.
- **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.
- **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.
- **Y318F** is a nonpolymorphic mutation that occurred in 2 of 10 persons with VF and HIVDR while receiving DOR. It confers about 11-fold reduced susceptibility to DOR but otherwise has minimal if any effect on NVP, EFV, and ETR.

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
D67-E	30	30	30	30	15	15	30
D67-E + K70R + M184V + K219E	10	0	0	0	0	0	0
D67-E + K70R + K219E	10	15	10	10	10	10	10
D67-E + T215F + K219E	5	5	5	5	0	0	5
T69G	10	5	10	10	0	0	5
K70R	5	30	15	10	0	0	5
M184V	15	-10	-10	10	60	60	-10
T215F	10	60	40	15	0	0	10
K219E	5	10	10	5	0	0	5
K70R + T215F	0	0	5	5	0	0	0
Total	100	145	115	100	85	85	60

Drug resistance mutation scores of NNRTI: Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
A98G	15	15	10	30	15
K101E	15	15	15	30	45
K101E + G190A	5	0	5	0	0
Y318F	60	10	0	30	0
G190A	0	45	10	60	15
Total	95	85	40	150	75

Drug resistance interpretation: IN

HIVDB 9.5.1 (2023-11-05)

INSTI Major Mutations: T66I • G118R • E138K

INSTI Accessory Mutations: E157Q

IN Other Mutations: S17N • R20K • M50L • L63V • I72V • L74I • G94A • T112TAV • I113V • T124S • T125A • V151VI • K160I • V165I • L172LJ • I200L • V201I • I204L • K211KR • T218I • L234I • C280CR • S283G

Integrase Strand Transfer Inhibitors

bictegravir (BIC)	High-Level Resistance
cabotegravir (CAB)	High-Level Resistance
dolutegravir (DTG)	High-Level Resistance
elvitegravir (EVG)	High-Level Resistance
raltegravir (RAL)	High-Level Resistance

IN comments

Major

- **T66A/I** are non-polymorphic mutations selected in persons receiving EVG, RAL, and DTG usually in combination with other INSTI-resistance mutations. They cause moderate reductions in EVG susceptibility but do not appear to reduce susceptibility to other INSTIs.
- **G118R** is a nonpolymorphic mutation reported in a significant proportion of persons with VF and emergent HIVDR in persons receiving a DTG-containing regimen. It has occasionally been reported in persons receiving other INSTIs. It is associated with 5-10-fold reduced susceptibility to RAL, EVG, DTG and CAB, and 2-3 fold reduced susceptibility to BIC.
- **E138K/A/T** are common nonpolymorphic accessory resistance mutations selected in patients receiving RAL, EVG, CAB, and DTG. Alone they do not reduce INSTI susceptibility. However, they contribute to reduced susceptibility in combination with other mutations particularly those at position 148.

Accessory

- **E157Q** is a polymorphic mutation selected in persons receiving RAL and EVG. It appears to have little effect on INSTI susceptibility.

Other

- **L74I** is a highly polymorphic mutation with a prevalence of 3% to 30% depending on subtype. It is the consensus amino acid in subtype A viruses belonging to the A6 clade. It does not appear to be selected by any of the INSTIs or to reduce their susceptibility.
- **V151I** is an accessory INSTI selected mutation that occurs in 1% to 3% of viruses from ART-naive persons depending on subtype. Alone, it appears to have little or no effect on INSTI susceptibility.
- There is evidence for high-level **DTG** resistance. If **DTG** is used, it should be administered twice daily.

Mutation scoring: IN

HIVDB 9.5.1 (2023-11-05)

Drug resistance mutation scores of INSTI: Download CSV

Rule	BIC	CAB	DTG	EVG	RAL
T66I	5	10	5	60	15
L74I + G118R	10	10	10	10	10
G118R	30	60	50	60	60
G118R + E138K	10	10	10	10	10
E138K	10	10	10	15	15
E157Q	0	0	0	10	10
Total	65	100	85	165	120