Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: I84IV

PI Accessory Mutations: L10LF • K20T • L89T

PR Other Mutations: I13IV • K14R • G17D • E35D • M36I • R41K • K45R • R57K • L63P • H69K • A71GI • I72IV

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

PR comments

Major

- **I84V** is a nonpolymorphic substrate-cleft mutation selected by each of the PIs. **I84V** reduces susceptibility to LPV, ATV, and DRV.

Accessory

- **L10F** is a common non-polymorphic, PI-selected accessory mutation associated with reduced in vitro susceptibility to LPV and DRV.
- **K20T** is a non-polymorphic accessory PI-selected mutation associated with reduced susceptibility to ATV and LPV.
- *L89V* is a nonpolymorphic accessory mutation weakly selected by each of the PIs. It appears to be minimally associated with reduced PI susceptibility. **L89T** is an uncommon non-polymorphic PI-selected mutation selected primarily by ATV.

Other

- **A71I/L** are non-polymorphic, PI-selected accessory mutations that appear to increase the replication of viruses with other PI-resistance mutations.
- There is evidence for low-level **DRV** resistance. If **DRV** is administered it should be used twice daily.

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
K20T	5	0	5	5	0	15	5	0
I84IV	60	15	60	60	30	60	60	30
L10LF	0	5	15	10	5	15	0	0
Total	65	20	80	75	35	90	65	30

Drug resistance interpretation: RT

HIVDB 9.5.1 (2023-11-05)

NRTI Mutations: None

NNRTI Mutations: None

RT Other Mutations: V35T • T39A • A554S

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

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.

Drug resistance interpretation: IN

HIVDB 9.5.1 (2023-11-05)

INSTI Major Mutations: G140S • Q148H

INSTI Accessory Mutations: T97A

IN Other Mutations: K14R • P30PS • V31I • Q55N • I60V • L63I • L74I • L101I • T112L • T124A • T125A • K136Q • K160R • D167E • V201I • L234I • 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

- **G140S/A/C** are non-polymorphic mutations that usually occur with Q148 mutations. Alone, they have minimal effects on INSTI susceptibility. However, in combination with Q148 mutations they are associated with high-level resistance to RAL and EVG and intermediate reductions in DTG and BIC susceptibility.
- **Q148H/K/R** are nonpolymorphic mutations reported in persons receiving RAL, EVG, CAB, and DTG. They nearly always occur in combination with G140A/S or E138K. In this setting they are associated with near complete resistance to RAL and EVG, high-levels of reduction in CAB susceptibility, and low-to-intermediate reductions in DTG and BIC susceptibility.

Accessory

- **T97A** is a polymorphic INSTI-selected mutation that, depending on subtype, occurs in 1% to 5% of viruses from untreated persons. Alone, it has minimal effects on INSTI susceptibility but in combination with other major resistance mutations, it synergistically reduces susceptibility to each of the INSTIs.

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.
- 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
L74I + Q148H	15	15	15	15	15
T97A + Q148H	15	20	15	0	0
G140S	10	10	10	30	30
G140S + Q148H	10	20	10	0	0
Q148H	25	30	25	60	60
T97A	0	0	0	10	10
Total	75	95	75	115	115