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

PI Major Mutations: None

PI Accessory Mutations: None

PR Other Mutations: 115V \*\*\* • E35D \*\*\* • M36I \*\*\* • R41K \*\*\*

#### 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

No drug resistance mutations were found for PI.

# Drug resistance interpretation: RT

NRTI Mutations: None NNRTI Mutations: None

## Nucleoside Reverse Transcriptase Inhibitors

abacavir (ABC)

zidovudine (AZT)

stavudine (D4T)

didanosine (DDI)

emtricitabine (FTC)

lamivudine (3TC)

tenofovir (TDF)

Susceptible

Susceptible

Susceptible

Susceptible

Susceptible

## Non-nucleoside Reverse Transcriptase Inhibitors

doravirine (DOR)

efavirenz (EFV)

etravirine (ETR)

nevirapine (NVP)

rilpivirine (RPV)

Susceptible

Susceptible

Susceptible

No drug resistance mutations were found for NRTI.

No drug resistance mutations were found for NNRTI.

## Drug resistance interpretation: IN

Mutation scoring: RT

INSTI Major Mutations: None

INSTI Accessory Mutations: None

IN Other Mutations: \$17N = M50L = 172V = 172

## Integrase Strand Transfer Inhibitors

bictegravir (BIC) Susceptible
cabotegravir (CAB) Susceptible
dolutegravir (DTG) Susceptible
elvitegravir (EVG) Susceptible
raltegravir (RAL) Susceptible

#### IN comments

#### Other

• L741 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.

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

No drug resistance mutations were found for INSTI.

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