

Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations:

PI Accessory Mutations:

PR Other Mutations:

None

None

I15V ^{91%}_{cons:190} • L19V ^{100%}_{cons:483} • M36I ^{100%}_{cons:2,378} • N37K ^{100%}_{cons:2,378} • R41N ^{99%}_{cons:2,392} • H69K ^{100%}_{cons:2,335} • V82I ^{100%}_{cons:603} • L89M ^{100%}_{cons:526} • I93L ^{99%}_{cons:853}

Protease Inhibitors

atazanavir/r (ATV/r)

darunavir/r (DRV/r)

fosamprenavir/r (FPV/r)

indinavir/r (IDV/r)

lopinavir/r (LPV/r)

nelfinavir (NFV)

saquinavir/r (SQV/r)

tipranavir/r (TPV/r)

Susceptible

Susceptible

Susceptible

Susceptible

Susceptible

Susceptible

Susceptible

Susceptible

PR comments

Other

V82I is a highly polymorphic mutation that is not selected by PIs. It is the consensus amino acid in subtype G viruses.

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| Mutation scoring: PR | HIVDB 9.5.1 (2023-11-05) |
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No drug resistance mutations were found for PI.

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| Drug resistance interpretation: RT | HIVDB 9.5.1 (2023-11-05) |
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| NRTI Mutations: | None | |
| NNRTI Mutations: | None | |
| RT Other Mutations: | V35T ^{100%} _{cons:73} • E36A ^{100%} _{cons:73} • T39E ^{100%} _{cons:73} • S48T ^{100%} _{cons:63} • K122E ^{100%} _{cons:1,214} • D123S ^{100%} _{cons:1,344} • A158S ^{99%} _{cons:1,860} • K173A ^{100%} _{cons:1,983} • D177EG ^{9-10%, G: 42%} _{cons:2,344} • T200A ^{100%} _{cons:1,304} • E204Q ^{99%} _{cons:1,375} • Q207E ^{99%} _{cons:1,890} • V245K ^{100%} _{cons:735} • S519N ^{99%} _{cons:72} • Q524E ^{100%} _{cons:19} • K530R ^{100%} _{cons:42} • A534S ^{99%} _{cons:96} • A554N ^{100%} _{cons:126} | |

| Nucleoside Reverse Transcriptase Inhibitors | | Non-nucleoside Reverse Transcriptase Inhibitors | |
|---|-------------|---|-------------|
| abacavir (ABC) | Susceptible | doravirine (DOR) | Susceptible |
| zidovudine (AZT) | Susceptible | efavirenz (EFV) | Susceptible |
| stavudine (D4T) | Susceptible | etravirine (ETR) | Susceptible |
| didanosine (DDI) | Susceptible | nevirapine (NVP) | Susceptible |
| emtricitabine (FTC) | Susceptible | rilpivirine (RPV) | Susceptible |
| lamivudine (3TC) | Susceptible | | |
| tenofovir (TDF) | Susceptible | | |

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| Mutation scoring: RT | HIVDB 9.5.1 (2023-11-05) |
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No drug resistance mutations were found for NRTI.

No drug resistance mutations were found for NNRTI.

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| Drug resistance interpretation: IN | HIVDB 9.5.1 (2023-11-05) |
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| INSTI Major Mutations: | None | |
| INSTI Accessory Mutations: | A128T ^{9-41%, N: 10%} _{cons:242} | |
| IN Other Mutations: | D6E ^{100%} _{cons:752} • E13D ^{100%} _{cons:1,437} • S17N ^{100%} _{cons:1,505} • V31I ^{100%} _{cons:1,797} • S39N ^{100%} _{cons:1,898} • E96D ^{100%} _{cons:219} • L101I ^{100%} _{cons:137} • T112IV ^{9-100%, L: 43%} _{cons:138} • T124NQ ^{10-72%, N: 20%} _{cons:132} • T125A ^{99%} _{cons:132} • K127KR ^{9-43%, R: 42%} _{cons:243} • K136Q ^{100%} _{cons:459} • D167E ^{100%} _{cons:1,076} • K173KR ^{9-46%, R: 13%} _{cons:1,434} • F181FL ^{9-100%, L: 43%} _{cons:1,732} • V201I ^{100%} _{cons:1,762} • K211R ^{100%} _{cons:1,076} • T218I ^{100%} _{cons:1,484} • L234I ^{100%} _{cons:1,244} • D270E ^{100%} _{cons:591} • D278A ^{100%} _{cons:312} • S283SG ^{10-42%, S: 98%} _{cons:293} | |

| Integrase Strand Transfer Inhibitors | |
|--------------------------------------|-------------|
| bictegravir (BIC) | Susceptible |
| cabotegravir (CAB) | Susceptible |
| dolutegravir (DTG) | Susceptible |
| elvitegravir (EVG) | Susceptible |
| raltegravir (RAL) | Susceptible |

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| IN comments | |
| Accessory | |
| • A128T is a relatively nonpolymorphic possible INSTI-selected mutation, which does not appear to reduce INSTI susceptibility. | |

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| Mutation scoring: IN | HIVDB 9.5.1 (2023-11-05) |
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No drug resistance mutations were found for INSTI.