

Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations:None

PI Accessory Mutations:None

PR Other Mutations:L10LV100%
n=12,389 • G16GE100%
n=2,591 • E35D100%
n=3,523 • M36I100%
n=3,523 • R41K100%
n=3,575 • R57K100%
n=1,202 • H69K100%
n=1,862 • L89M100%
n=1,887

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

- L10I/V are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other 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:M184MV100%
n=3,523

NNRTI Mutations:K103N100%
n=12,385 • V108VI100%
n=3,309

RT Other Mutations:I5V100%
n=12,145 • K20R100%
n=12,207 • V35T100%
n=12,202 • I50V100%
n=12,378 • V60I100%
n=1,319 • W88C100%
n=1,342 • D121H100%
n=1,358 • K122E100%
n=1,358 • K173A100%
n=12,352 • Q174K100%
n=12,352 • D177E100%
n=12,362 • V179S100%
n=12,324 • V189VI100%
n=1,381 • T200TA100%
n=12,352 • I202V100%
n=12,375 • Q207A100%
n=12,372 • V245Q100%
n=12,362 • D250DE100%
n=12,228

Nucleoside Reverse Transcriptase Inhibitors

| | |
|---------------------|--------------------------------|
| abacavir (ABC) | Low-Level Resistance |
| zidovudine (AZT) | Susceptible |
| stavudine (D4T) | Susceptible |
| didanosine (DDI) | Potential Low-Level Resistance |
| emtricitabine (FTC) | High-Level Resistance |
| lamivudine (3TC) | High-Level Resistance |
| tenofovir (TDF) | Susceptible |

Non-nucleoside Reverse Transcriptase Inhibitors

| | |
|-------------------|--------------------------------|
| doravirine (DOR) | Potential Low-Level Resistance |
| efavirenz (EFV) | High-Level Resistance |
| etravirine (ETR) | Susceptible |
| nevirapine (NVP) | High-Level Resistance |
| rilpivirine (RPV) | Susceptible |

RT comments

NRTI

- 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.

NNRTI

- K103N is a non-polymorphic mutation that confers high-level reductions in NVP and EFV susceptibility. It is the most commonly transmitted DRM.
- V108I is a relatively non-polymorphic accessory mutation selected in vitro and/or in vivo with each of the NNRTIs. It appears to contribute to reduced susceptibility to most NNRTIs only in combination with other NNRTI-resistance mutations.

Other

- 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. V179F is a non-polymorphic mutation selected in combination with Y181C in persons receiving ETR. Alone it has little effect on NNRTI susceptibility, however in combination with Y181C it is associated with high-level reductions in ETR and RPV susceptibility. V179T is a rare non-polymorphic mutation occasionally selected in persons receiving NNRTIs. It is associated with minimal, if any, reduction in ETR and RPV susceptibility. V179L is a rare non-polymorphic mutation listed as a RPV-associated resistance mutation by the FDA package insert. Its effects on NNRTI susceptibility have not been well studied. V179S is an unusual mutation at this position.

Mutation scoring: RT

HIVDB 9.5.1 (2023-11-05)

Drug resistance mutation scores of NRTI:

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| Rule | ABC | AZT | D4T | DDI | FTC | 3TC | TDF |
|--------|-----|-----|-----|-----|-----|-----|-----|
| M184MV | 15 | -10 | -10 | 10 | 60 | 60 | -10 |

Drug resistance mutation scores of NNRTI:

Download CSV

| Rule | DOR | EFV | ETR | NVP | RPV |
|--------|-----|-----|-----|-----|-----|
| V108VI | 10 | 10 | 0 | 15 | 0 |
| K103N | 0 | 60 | 0 | 60 | 0 |
| Total | 10 | 70 | 0 | 75 | 0 |

| | | |
|--|--|--------------------------|
| Drug resistance interpretation: IN | | HIVDB 9.5.1 (2023-11-05) |
| INSTI Major Mutations: | None | |
| INSTI Accessory Mutations: | None | |
| IN Other Mutations: | D3DE <small>(D: 70%, N: 30%)</small> • K14R <small>(K: 100%, N: 0%)</small> • A21T <small>(A: 100%, N: 0%)</small> • V32V <small>(V: 100%, N: 0%)</small> • I72V <small>(I: 100%, N: 0%)</small> • E92EA <small>(E: 100%, N: 0%)</small> • L101I <small>(L: 100%, N: 0%)</small> • T112V <small>(T: 100%, N: 0%)</small> • I113V <small>(I: 100%, N: 0%)</small> • T124A <small>(T: 100%, N: 0%)</small> • T125A <small>(T: 100%, N: 0%)</small> • G134N <small>(G: 100%, N: 0%)</small> • K136Q <small>(K: 100%, N: 0%)</small> • M154M <small>(M: 100%, N: 0%)</small> • D167E <small>(D: 100%, N: 0%)</small> • V201I <small>(V: 100%, N: 0%)</small> • T218I <small>(T: 100%, N: 0%)</small> • Q221QKR <small>(Q: 100%, N: 0%)</small> • L234I <small>(L: 100%, N: 0%)</small> • R269RK <small>(R: 100%, N: 0%)</small> • C280C* <small>(C: 100%, N: 0%)</small> • S283G <small>(S: 100%, N: 0%)</small> • D288DG <small>(D: 100%, N: 0%)</small> | |
| Integrase Strand Transfer Inhibitors | | |
| bictegravir (BIC) | Susceptible | |
| cabotegravir (CAB) | Susceptible | |
| dolutegravir (DTG) | Susceptible | |
| elvitegravir (EVG) | Susceptible | |
| raltegravir (RAL) | Susceptible | |
| IN comments | | |
| Other | | |
| <ul style="list-style-type: none">E92Q is a common non-polymorphic mutation selected in persons receiving RAL and EVG. It reduces RAL susceptibility 5 to 10-fold and EVG susceptibility ~30-fold. It does not reduce susceptibility to BIC, CAB, and DTG. E92G/V are rare nonpolymorphic mutations that reduce EVG susceptibility >=10-fold but do not appear to reduce susceptibility to other INSTIs. E92A is an unusual mutation at this position. | | |
| Mutation scoring: IN | | HIVDB 9.5.1 (2023-11-05) |

No drug resistance mutations were found for INSTI.

Drug resistance interpretation: PRHIVDB 9.5.1 (2023-11-05)

PI Major Mutations:
PI Accessory Mutations:
PR Other Mutations:

None
None
I13V 100%
mut:1,301 • M36I 100%
mut:3,377 • R41K 99%
mut:4,432 • L63P 100%
mut:5,848 • H69K 99%
mut:5,791 • V82I 99%
mut:5,802 • L89I 100%
mut:5,749

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

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

Mutation scoring: PRHIVDB 9.5.1 (2023-11-05)

No drug resistance mutations were found for PI.

Drug resistance interpretation: RTHIVDB 9.5.1 (2023-11-05)

NRTI Mutations:
NNRTI Mutations:
RT Other Mutations:

M41L 100%
mut:1,481 • V75M 100%
mut:98 • F77L 100%
mut:72 • M184V 99%
mut:132
A98G 100%
mut:54 • K103N 100%
mut:52
V21I 10%
mut:1,611 • V35ΔT 100%
mut:1,481 • E36EΔ 100%
mut:1,481 • E37Δ 100%
mut:1,481 • C38CΔ 100%
mut:1,481 • T39TΔ 100%
mut:1,481 • E40EΔ 100%
mut:1,481 • E42EΔ 100%
mut:1,481 • K43KΔ 100%
mut:1,481 • Δ44 100%
mut:1,481 • G45GΔ 100%
mut:1,481 • Δ46 100%
mut:1,481 • H47Δ 100%
mut:1,481 • S48SΔ 100%
mut:1,481 • K49KΔ 100%
mut:1,481 • I50Δ 100%
mut:1,481 • G51GΔ 100%
mut:1,481 • Δ52-55 100%
mut:1,481 • V60I 99%
mut:1,481 • K122E 100%
mut:1,481 • I135T 100%
mut:1,481 • T165I 100%
mut:1,481 • K173A 100%
mut:1,481 • Q174K 100%
mut:1,481 • D177E 100%
mut:1,481 • T200A 99%
mut:1,481 • K512R 100%
mut:1,481 • S519N 100%
mut:1,481
Q524K 99%
mut:1,481 • K527E 100%
mut:1,481 • E529N 99%
mut:1,481 • A534S 100%
mut:1,481 • A554S 100%
mut:1,481 • I556V 100%
mut:1,481

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

RT comments

NRTI

- M41L is a TAM that usually occurs with T215Y. In combination, **M41L** plus T215Y confer intermediate / high-level resistance to AZT and d4T and contribute to reduced ddi, ABC and TDF susceptibility.
- V75T)M)A)S are nonpolymorphic accessory NRTI-selected mutations. They appear to have minimal phenotypic effects on AZT, ABC, and TDF.
- F77L usually occurs in combination with the multi-NRTI resistance mutation Q151M. When it occurs alone, its clinical significance is uncertain.
- 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.

NNRTI

- A98G is a non-polymorphic accessory mutation associated with low-level reduced susceptibility to each of the NNRTIs.
- K103N is a non-polymorphic mutation that confers high-level reductions in NVP and EPV susceptibility. It is the most commonly transmitted DRM.

- This virus is predicted to have low-level reduced susceptibility to **RPV**. The use of the combination of CAB/**RPV** should be considered to be relatively contraindicated.

Mutation scoring: RTHIVDB 9.5.1 (2023-11-05)

Drug resistance mutation scores of NRTI:

Download CSV

| Rule | ABC | AZT | D4T | DDI | FTC | 3TC | TDF |
|-------|-----|-----|-----|-----|-----|-----|-----|
| M41-L | 5 | 15 | 15 | 10 | 0 | 0 | 5 |
| F77L | 5 | 10 | 10 | 10 | 5 | 5 | 5 |
| M184V | 15 | -10 | -10 | 10 | 60 | 60 | -10 |
| V75M | 0 | 10 | 30 | 15 | 0 | 0 | 0 |
| Total | 25 | 25 | 45 | 45 | 65 | 65 | 0 |

| Rule | DOR ↕ | EFV ↕ | ETR ↕ | NVP ↕ | RPV ↕ |
|--------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| <u>A98G</u> | 15 | 15 | 10 | 30 | 15 |
| <u>K103N</u> | 0 | 60 | 0 | 60 | 0 |
| Total | 15 | 75 | 10 | 90 | 15 |

Drug resistance interpretation: IN

HIVDB 9.5.1 (2023-11-05)

INSTI Major Mutations:

None

INSTI Accessory Mutations:

None

IN Other Mutations:

K14R ^{10%}_{score:827} • S24A ^{100%}_{score:822} • V31I ^{10%}_{score:886} • I60V ^{100%}_{score:880} • I72V ^{100%}_{score:882} • Q95A ^{10%}_{score:852} • E96D ^{10%}_{score:883} • T112V ^{100%}_{score:897} • I113V ^{10%}_{score:897} • T124A ^{100%}_{score:884} • T125A ^{10%}_{score:884} • K136Q ^{10%}_{score:878} • D167E ^{10%}_{score:878} • V201I ^{10%}_{score:882} • I203M ^{10%}_{score:888} • K219N ^{100%}_{score:887} • N222K ^{10%}_{score:881} • L234V ^{100%}_{score:887} • M275V ^{100%}_{score:1,000}

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

Mutation scoring: IN

HIVDB 9.5.1 (2023-11-05)

No drug resistance mutations were found for INSTI.