

Drug resistance interpretation: PR

PI Major Mutations:

PI Accessory Mutations:

PR Other Mutations:

None

None

L10I

100%

score=2,283

•

T12V

100%

score=2,283

•

I13V

100%

score=2,283

•

E35D

100%

score=3,281

•

M36I

100%

score=3,281

•

R41K

99%

score=3,281

•

K45R

100%

score=2,384

•

R57K

99%

score=2,317

•

L63V

100%

score=2,338

•

H69K

99%

score=2,287

•

V77I

100%

score=2,352

•

L89I

100%

score=2,296

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:

NNRTI Mutations:

RT Other Mutations:

M41L

100%

score=2,096

•

S68G

99%

score=3,627

•

M184V

99%

score=3,282

•

T215F

99%

score=1,625

A98G

99%

score=2,252

•

K103N

97%

score=1,376

•

V108I

99%

score=1,212

E6A

100%

score=2,357

•

E28A

100%

score=2,290

•

V35T

100%

score=2,235

•

V60I

100%

score=1,879

•

K122E

100%

score=2,091

•

D123S

99%

score=387

•

R125RG

9.94%

score=1,270

•

I135T

100%

score=2,224

•

K173M

100%

score=3,314

•

Q174K

100%

score=3,332

•

D177E

100%

score=3,589

•

I202V

100%

score=2,404

•

Q207D

99%

score=1,372

•

R211S

100%

score=2,375

•

L228H

100%

score=1,354

•

V245E

99%

score=820

•

D250E

98%

score=290

Nucleoside Reverse Transcriptase Inhibitors

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

Non-nucleoside Reverse Transcriptase Inhibitors

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

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.
- S68G is a polymorphic mutation that is often selected in combination with K65R. It partially restores the replication defect associated with K65R.
- 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.

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 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.

- 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: 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
M41L	5	15	15	10	0	0	5
M41L + M184V + T215F	10	0	0	0	0	0	0
M41L + T215F	10	10	10	10	5	5	10
M184V	15	-10	-10	10	60	60	-10
T215F	10	60	40	15	0	0	10
Total	50	75	55	45	65	65	15

Rule	DOR ⚡	EFV ⚡	ETR ⚡	NVP ⚡	RPV ⚡
<u>A98G</u>	15	15	10	30	15
<u>V108I</u>	10	10	0	15	0
<u>K103N</u>	0	60	0	60	0
Total	25	85	10	105	15

Drug resistance interpretation: IN

HIVDB 9.5.1 (2023-11-05)

INSTI Major Mutations:

N155H 100%
seen 14

INSTI Accessory Mutations:

None

IN Other Mutations:

K14R 100%
seen 231 • A21T 99%
seen 139 • L28I 100%
seen 255 • V31I 99%
seen 242 • I60M 99%
seen 148 • I72V 11.72%
seen 42 • K156N 100%
seen 75 • D167E 100%
seen 98 • V201I 100%
seen 111 • K211R 100%
seen 117 • L234I 100%
seen 111 • I268L 99%
seen 87 • S283G 100%
seen 159

Integrase Strand Transfer Inhibitors	
bictegravir (BIC)	Potential Low-Level Resistance
cabotegravir (CAB)	Low-Level Resistance
dolutegravir (DTG)	Potential Low-Level Resistance
elvitegravir (EVG)	High-Level Resistance
raltegravir (RAL)	High-Level Resistance

IN comments

Major

- N155H** is a common nonpolymorphic INSTI-resistance mutations. It has been reported in a high proportion of persons developing VF and HIVDR while receiving RAL, EVG, DTG, and CAB. Alone, it reduces RAL and EVG susceptibility about 10 and 30-fold, respectively. It has minimal effect on susceptibility to DTG, BIC, and CAB.
- This virus is predicted to have low-level reduced susceptibility to **CAB**. The use of the combination of **CAB**/RPV should be considered to be relatively contraindicated.

Mutation scoring: IN

HIVDB 9.5.1 (2023-11-05)

Rule	BIC ⚡	CAB ⚡	DTG ⚡	EVG ⚡	RAL ⚡
<u>N155H</u>	10	25	10	60	60