




Stanford University  
**HIV DRUG RESISTANCE DATABASE**

*A curated public database to represent, store and analyze HIV drug resistance data.*

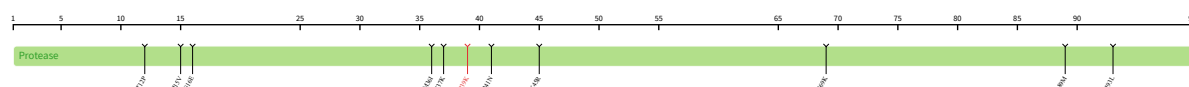
## 1. userInput

## Sequence summary

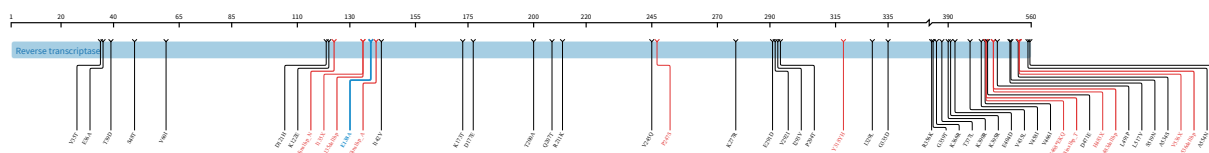
Sequence includes PR: codons 1 - 99  
Sequence includes RT: codons 1 - 560  
Sequence includes IN: codons 1 - 288 (missing: 206-237)  
Subtype:  C (4.79%)

## Sequence quality assessment

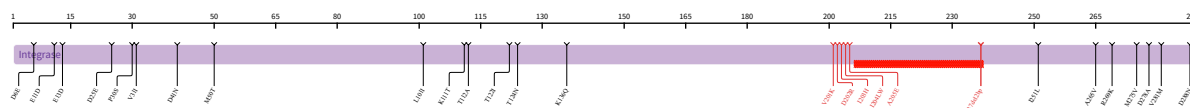
### Protease (PR)



### Reverse transcriptase (RT)



### Integrase (IN)



- **Severe warning:** The RT gene has 6 frameshifts: 124ins1bp\_N, 135del1bp, 140ins1bp\_A, 468ins1bp\_T, 483del1bp, 536del1bp.
- **Warning:** The IN gene has a frameshift: 237del2bp.
- **Warning:** There are 6 unusual mutations in RT: I135X, P247S, Y318H, S468\*EK, H483X, V536X.
- **Warning:** There are 5 unusual mutations in IN: V201K, D202R, I203H, I204W, A205E.
- **Note:** 32 positions were not sequenced or aligned: IN 206-237. Of them, 2 are at drug-resistance positions: IN 230, 232.
- **Note:** There is one stop codon in RT: RT:S468\*.
- **Note:** There is one unusual mutation at a drug-resistance position in RT: Y318H.

Drug resistance interpretation: PR

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PI Major Mutations: None

PI Accessory Mutations:None

PR Other Mutations:T12P • I15V • G16E • M36I • N37K • P39K • R41N • K45R • H69K • L89M • I93L

Protease Inhibitors	
atazanavir/r (ATV/r)	Susceptible
darunavir/r (DRV/r)	Susceptible
lopinavir/r (LPV/r)	Susceptible

Mutation scoring: PR

HIVDB 9.8 (2025-01-05)

No drug resistance mutations were found for PI.

Drug resistance interpretation: RT

HIVDB 9.8 (2025-01-05)

NRTI Mutations:None

NNRTI Mutations:E138A

RT Other Mutations:V35T • E36A • T39D • S48T • V60I • D121H • K122E • I135X • I142V • K173T • D177E • T200A • Q207T • R211K • V245Q • P247S • K277R • E291D • V292I • I293V • P294T • Y318YH • I329L • G335D • R356K • G359T • K366R • T377L • K390R • K395R • E404D • V435L • V458I • V466I • S468\*EKQ • D471E • H483X • L491P • L517V • S519N • A534S • V536X • A554N • K558R

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

RT comments

NNRTI

- E138A is a common polymorphic accessory mutation weakly selected in persons receiving ETR and RPV. It reduces ETR and RPV susceptibility ~2-fold. Its effect on ETR- and RPV-containing regimens is likely to be minimal.

Other

- Y318F is a nonpolymorphic mutation that occurred in 2 of 10 persons with VF and HIVDR while receiving DOR. It confers about 11-fold reduced susceptibility to DOR but otherwise has minimal if any effect on NVP, EFV, and ETR. Y318H is a highly unusual mutation at this position.

Dosage

- 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 9.8 (2025-01-05)

No drug resistance mutations were found for NRTI.

Drug resistance mutation scores of NNRTI:

Rule	DOR	EFV	ETR	NVP	RPV
E138A	0	0	10	0	15

Drug resistance interpretation: IN

HIVDB 9.8 (2025-01-05)

INSTI Major Mutations:None

INSTI Accessory Mutations:None

IN Other Mutations:D6E • E11D • E13D • D25E • P30S • V31I • D41N • M50T • L101I • K111T • T112A • T122I • T124N • K136Q • V201K • D202R • I203H • I204LW • A205E • I251L • A265V • R269K • M275V • D278A • V281M • D288N

Integrase Strand Transfer Inhibitors	
bictegravir (BIC)	Susceptible
cabotegravir (CAB)	Susceptible
dolutegravir (DTG)	Susceptible

elvitegravir (EVG)

Susceptible

raltegravir (RAL)

Susceptible

Mutation scoring: IN

HIVDB 9.8 (2025-01-05)

No drug resistance mutations were found for INSTI.