Stanford University
HIV DRUG RESISTANCE DATABASE
A curated public database to represent, store and analyze HIV drug resistance data.

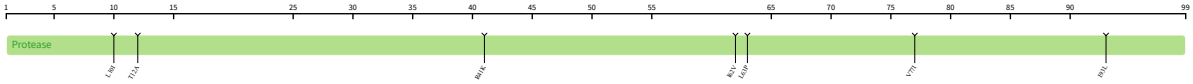
1. userinput unamed sample: 1

Sequence summary

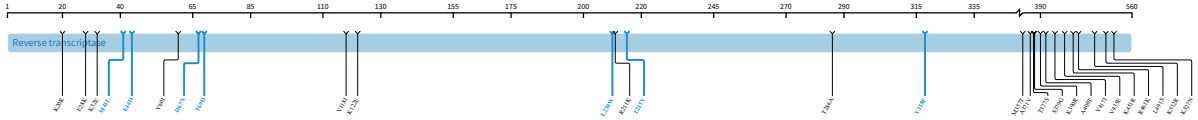
Sequence includes PR:	codons 1 - 99
Sequence includes RT:	codons 1 - 560
Sequence includes IN:	codons 1 - 288
Subtype:	⊞ B (2.99%)

Sequence quality assessment

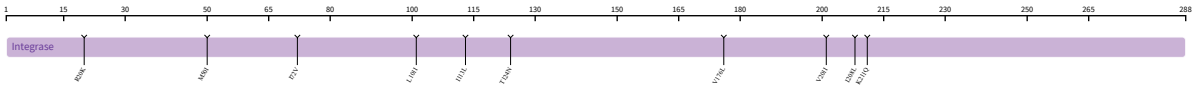
Protease (PR)



Reverse transcriptase (RT)



Integrase (IN)



There are no known sequence quality issues.

Drug resistance interpretation: PR

HIVDB 9.8 (2025-01-05)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	L10I • T12A • R41K • I62V • L63P • V77I • I93L

Protease Inhibitors	
atazanavir/r (ATV/r)	Susceptible
darunavir/r (DRV/r)	Susceptible
lopinavir/r (LPV/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 9.8 (2025-01-05)

No drug resistance mutations were found for PI.

Drug resistance interpretation: RT

HIVDB 9.8 (2025-01-05)

NRTI Mutations: **M41L** • **E44D** • **D67N** • **T69D** • **L210W** • **T215Y**
NNRTI Mutations: **Y318F**
RT Other Mutations: K20R • E28K • K32E • V60I • V118I • K122E • R211K • T286A • M357T • A371V • T377S • S379G • K390R • A400T • V417I • V435E • K451R • R461K • L491S • K512R • K527N

Nucleoside Reverse Transcriptase Inhibitors		Non-nucleoside Reverse Transcriptase Inhibitors	
abacavir (ABC)	High-Level Resistance	**doravirine (DOR)**	High-Level Resistance
zidovudine (AZT)	High-Level Resistance	**efavirenz (EFV)**	Potential Low-Level Resistance
emtricitabine (FTC)	Low-Level Resistance	**etravirine (ETR)**	Susceptible
lamivudine (3TC)	Low-Level Resistance	**nevirapine (NVP)**	Intermediate Resistance
tenofovir (TDF)	High-Level Resistance	**rilpivirine (RPV)**	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.
- **E44D** is a relatively non-polymorphic accessory mutation; E44A is a nonpolymorphic accessory mutation. Each usually occurs with multiple TAMs.
- **D67N** is a non-polymorphic TAM associated with low-level resistance to AZT.
- **T69D** is a nonpolymorphic mutation selected by early NRTIs that does not appear to reduce AZT, ABC, or TDF susceptibility.
- **L210W** is a TAM that usually occurs in combination with M41L and T215Y. The combination of M41, **L210W** and T215Y causes high-level resistance to AZT and intermediate resistance to ABC and TDF.
- **T215Y/F** are TAMs that causes intermediate/high-level resistance to AZT and potentially low-level resistance to ABC and TDF.

NNRTI

- **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.

Other

- **V118I** is a polymorphic accessory NRTI-resistance mutation that often occurs in combination with multiple TAMs.

Mutation scoring: RT

HIVDB 9.8 (2025-01-05)

Drug resistance mutation scores of NRTI:

Rule	ABC	AZT	FTC	3TC	TDF
M41L	5	15	0	0	5
M41L + E44D + L210W + T215Y	5	5	0	0	5
M41L + D67N + T215Y	5	5	0	0	5
M41L + L210W	10	10	0	0	10
M41L + L210W + T215Y	10	0	15	15	10
M41L + T215Y	10	10	0	0	10
D67N	5	15	0	0	5
L210W	5	15	0	0	5
L210W + T215Y	10	10	0	0	10
T215Y	10	60	0	0	10
T69D	0	0	0	0	0
Total	75	145	15	15	75

Drug resistance mutation scores of NNRTI:

Rule	DOR	EFV	ETR	NVP	RPV
Y318F	60	10	0	30	0

Drug resistance interpretation: IN

HIVDB 9.8 (2025-01-05)

INSTI Major Mutations: None
INSTI Accessory Mutations: None
IN Other Mutations: R20K • M50I • I72V • L101I • I113L • T124N • V176L • V201I • I208L • K211Q

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

IN comments

Other

- **M50I** is a highly polymorphic mutation, which has a prevalence of 3% to 34% in INSTI-naïve persons depending on subtype. It has been selected in vitro by DTG and BIC in combination with R263K. It also appears to frequently occur in combination with R263K in patients receiving DTG and BIC. It is uncertain whether it contributes to reduced DTG and CAB susceptibility in combination with R263K.

Mutation scoring: IN

HIVDB 9.8 (2025-01-05)

No drug resistance mutations were found for INSTI.