

1. userinput

unnamed sample: 1

Sequence summary

Sequence includes PR:codons 1 - 99

Sequence includes RT:codons 1 - 560

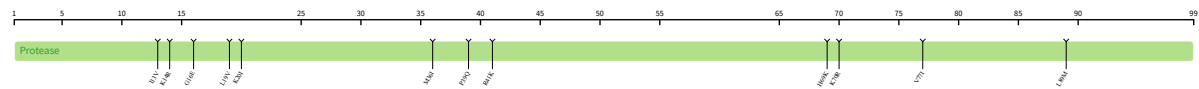
Sequence includes IN:codons 1 - 288

Subtype:

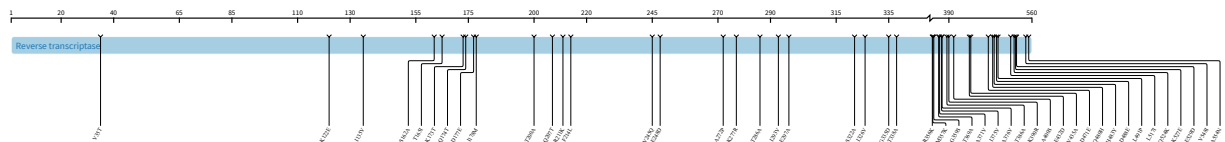
CRF02_AG (5.32%)

Sequence quality assessment

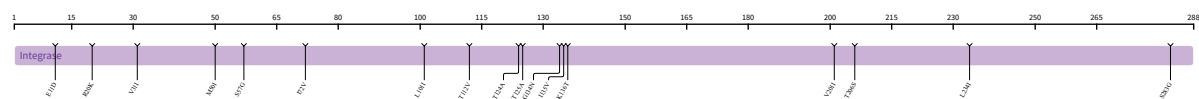
Protease (PR)



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:I13V • K14R • G16E • L19V • K20I • M36I • P39Q • R41K • H69K • K70R • V77I • L89M

Protease Inhibitors

atazanavir/r (ATV/r)Susceptible

darunavir/r (DRV/r)Susceptible

lopinavir/r (LPV/r)Susceptible

PR comments

Other

- K20I** is the consensus amino acid in subtype G and CRF02_AG. In subtypes B and C, **K20I** is a PI-selected mutation of uncertain effects on currently used PIs.

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:None

RT Other Mutations:V35T • K122E • I135V • S162A • T165I • K173T • Q174T • D177E • I178M • T200A • Q207T • R211K • F214L • V245Q • E248D • A272P • K277R • T286A • I293V • E297A • S322A • I326V • G335D • T338A • R356K • M357K • G359S • T369A • A371V • I375V • A376V • T386A • K390R • A400S • E432D • V435A • D471E • Q480H • H483Y • D488E • L491P • L517I • Q524K • K527E • E529D • V548I • A554N

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)	Susceptible
lamivudine (3TC)	Susceptible	nevirapine (NVP)	Susceptible
tenofovir (TDF)	Susceptible	rilpivirine (RPV)	Susceptible

Mutation scoring: RT

HIVDB 9.8 (2025-01-05)

No drug resistance mutations were found for NRTI.

No drug resistance mutations were found for NNRTI.

Drug resistance interpretation: IN

HIVDB 9.8 (2025-01-05)

INSTI Major Mutations:None

INSTI Accessory Mutations:None

IN Other Mutations:E11D • R20K • V31I • M50I • S57G • I72V • L101I • T112V • T124A • T125A • G134N • I135V • K136T • V201I • T206S • L234I • S283G

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.