



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

Sequence summary

Sequence includes PR: codons 1 - 99
Sequence includes RT: codons 1 - 560
Sequence includes IN: codons 1 - 288
Subtype: **+** C (4.29%)

Sequence quality assessment

Linear map of the HIV-1 genome showing the location of the integrase gene and various proteins. The map is a horizontal bar with a scale from 15 to 265. The integrase gene is highlighted in purple. Proteins are indicated by vertical lines with labels: gag (15), pol (30), tat (45), rev (60), pro (75), gag (100), pol (115), tat (130), rev (145), gag (160), pol (175), tat (190), rev (205), gag (220), pol (235), tat (250), rev (265).

There are no known sequence quality issues.

HIVDB 9.8 (2025-01-05)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	T12S • I15V • L19I • M36I • N37K • R41N • L63T • I64V • H69K • V82I • I93L

Protease Inhibitors

atazanavir/r (ATV/r)	Susceptible
darunavir/r (DRV/r)	Susceptible
lopinavir/r (LPV/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: PR

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No drug resistance mutations were found for PI.

Drug resistance interpretation: RT

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NRTI Mutations:None

NNRTI Mutations:None

RT Other Mutations:V35T • E36A • T39E • K122E • D123S • A158S • K173A • Q174K • D177E • T200A • Q207E • V245Q • K277R • E291D • V292I • I293V • V317A • Q334H • G335D • R356K • G359T • T377L • K390R • E404D • V435A • A446S • L452M • S468P • D471E • H483Q • L491S • S519N • K530R • A534S • 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

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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:**E157Q**

IN Other Mutations:K14R • D25E • V31I • K34R • I72V • A98G • L101I • T112V • T124N • T125A • K136T • K160Q • D167E • K211R • L234I

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

IN comments

Accessory

- E157Q** is a polymorphic mutation selected in persons receiving RAL, EVG, and possibly the second generation INSTIs. Alone, it appears to have little effect on INSTI susceptibility. It is uncertain whether it contributes to reduced susceptibility in combination with R263K.

Mutation scoring: IN

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Drug resistance mutation scores of INSTI:

Rule	BIC	CAB	DTG	EVG	RAL
E157Q	0	0	0	10	10