

Drug resistance interpretation: PR		HIVDB 9.5.1 (2023-11-05)
PI Major Mutations:	None	
PI Accessory Mutations:	None	
PR Other Mutations:	I13V ^{100%} _{cons=2,084} • K14R ^{94%} _{cons=2,083} • G16E ^{99%} _{cons=2,070} • K20I ^{99%} _{cons=2,113} • E35N ^{99%} _{cons=2,817} • M36I ^{100%} _{cons=2,816} • R41K ^{99%} _{cons=2,813} • I62V ^{99%} _{cons=2,801} • L63S ^{100%} _{cons=2,801} • I64L ^{100%} _{cons=2,801} • H69K ^{99%} _{cons=2,811} • K70KR ^{91.75%} _{cons=2,811} R 221K • T74S ^{99%} _{cons=2,891} • L89M ^{100%} _{cons=3,140}	
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		
<ul style="list-style-type: none">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.T74S is a PI-selected accessory mutation that is polymorphic in most non-B subtypes.		

Mutation scoring: PR	HIVDB 9.5.1 (2023-11-05)
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No drug resistance mutations were found for PI.

Drug resistance interpretation: RT	HIVDB 9.5.1 (2023-11-05)
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NRTI Mutations:	K65R 100% cons=3,540 • S685G 91.54% cons=3,203 • M184V 99% cons=3,243		
NNRTI Mutations:	K103S 94% cons=4,018 • V106VI 91.80% cons=3,119 • V179T 99% cons=3,512 • Y181YC 91.93% cons=3,541 • G190A 99% cons=370		
RT Other Mutations:	I50V 91.93% cons=2,291 • K11Q 100% cons=2,312 • K20KR 91.93% cons=2,313 • E28A 100% cons=2,314 • V35T 100% cons=2,309 • T39D 94% cons=1,900 • A98AS 91.75% cons=510 • K122E 99% cons=526 • D123N 99% cons=525 • I135T 100% cons=1,042 • I142V 99% cons=1,110 • K173ST 91.51% cons=1,428 • Q174K 99% cons=1,428 • D177E 100% cons=1,611 • V189VI 91.93% cons=1,092 • T200A 100% cons=1,511 • I202V 100% cons=1,841 • Q207A 94% cons=1,820 • P243T 100% cons=240 • V243Q 99% cons=230 • A554S 100% cons=39 • I556V 97% cons=210 • K558KR 91.93% cons=214		
Nucleoside Reverse Transcriptase Inhibitors		Non-nucleoside Reverse Transcriptase Inhibitors	
abacavir (ABC)	High-Level Resistance	doravirine (DOR)	Intermediate Resistance
zidovudine (AZT)	Susceptible	efavirenz (EFV)	High-Level Resistance
stavudine (D4T)	Intermediate Resistance	etravirine (ETR)	High-Level Resistance
didanosine (DDI)	High-Level Resistance	nevirapine (NVP)	High-Level Resistance
emtricitabine (FTC)	High-Level Resistance	rilpivirine (RPV)	High-Level Resistance
lamivudine (3TC)	High-Level Resistance		
tenofovir (TDF)	Intermediate Resistance		

RT comments	
NRTI	
<ul style="list-style-type: none">K65R confers intermediate reductions in susceptibility to TDF, ABC, and 3TC/FTC. It increases AZT susceptibility. In NRTI-experienced, INSTI-naïve patients with K65R, TDF+3TC+DTG is usually highly effective and more effective than AZT/3TC/DTG. However, in patients receiving TDF+3TC+DTG, there is a risk of emergent DTG resistance that does not arise in NRTI-naïve patients receiving TDF+3TC+DTG.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.	
NNRTI	
<ul style="list-style-type: none">K103S is a non-polymorphic mutation that causes high-level reductions in NVP susceptibility but intermediate reductions in EFV susceptibility. Because K103S is a 2-bp change from the wildtype K and a 1-bp change from K103N, persons with K103S may be likely to have once had K103N.V106I occurs in 1% to 2% of viruses from untreated persons. It contributes to reduced NNRTI susceptibility only in combination with other NNRTI-resistance mutations. It is commonly selected in persons receiving DOR in combination with mutations at position 227.V179T is a rare non-polymorphic mutation occasionally selected in persons receiving NNRTIs. It is associated with minimal, if any, reduction in ETR and RPV susceptibility.Y181C is a non-polymorphic mutation selected in persons receiving NVP, ETR and RPV. It confers high-level resistance to NVP, intermediate resistance to ETR and RPV, and low-level resistance to EFV. It does not significantly reduce DOR susceptibility.G190A is a non-polymorphic mutation that causes high-level resistance to NVP and intermediate resistance to EFV. It does not significantly reduce susceptibility to RPV, ETR, or DOR.	

Mutation scoring: RT	HIVDB 9.5.1 (2023-11-05)
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Drug resistance mutation scores of NRTI:

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Rule	ABC	AZT	D4T	DDI	FTC	3TC	TDF
K65R	45	-10	60	60	30	30	50
M184V	15	-10	-10	10	60	60	-10
K65R + S68SG	0	0	0	0	0	0	5
Total	60	-20	50	70	90	90	45

Drug resistance mutation scores of NNRTI:

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Rule	DOR ⚡	EFV ⚡	ETR ⚡	NVP ⚡	RPV ⚡
<u>V106M</u>	10	0	10	10	10
<u>V106M + Y181YC</u>	5	0	0	0	10
<u>Y181YC</u>	10	30	30	60	45
<u>Y181YC + G190A</u>	10	0	10	0	10
<u>K103S</u>	0	45	0	60	0
<u>G190A</u>	0	45	10	60	15
<u>V179T + Y181YC</u>	0	0	10	0	10
Total	35	120	70	190	100

Drug resistance interpretation: IN

HIVDB 9.5.1 (2023-11-05)

INSTI Major Mutations:

E138K

100%
seen=358

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G140A

100%
seen=352

•

Q148K

100%
seen=354

INSTI Accessory Mutations:

None

IN Other Mutations:

K14R
100%
seen=351

•

V31I

100%
seen=324

•

D41N

100%
seen=324

•

I60M

100%
seen=336

•

Q62QE

0: 40%
seen=372

Q: 60%
seen=372

•

I72V

100%
seen=384

•

V75W

1: 75%
seen=352

Q: 25%
seen=352

•

Q95HR

16: 75%
seen=329

R: 25%
seen=329

•

T112T1S

0: 60%
seen=329

T: 20%
seen=329

S: 20%
seen=329

•

I113V

100%
seen=329

•

T124A

100%
seen=327

•

T125A

100%
seen=321

•

V126F

100%
seen=321

•

G134D

100%
seen=355

•

K136Q

100%
seen=355

•

K156KN

6: 40%
seen=387

R: 10%
seen=387

•

D167E

100%
seen=384

•

K173R

100%
seen=329

•

V201I

100%
seen=341

•

Q221S

100%
seen=321

•

L234V

100%
seen=372

•

S283G

100%
seen=384

Integrase Strand Transfer Inhibitors

bictegravir (BIC)	High-Level Resistance
cabotegravir (CAB)	High-Level Resistance
dolutegravir (DTG)	High-Level Resistance
elvitegravir (EVG)	High-Level Resistance
raltegravir (RAL)	High-Level Resistance

IN comments

Major

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E138K/A/T are common nonpolymorphic accessory resistance mutations selected in patients receiving RAL, EVG, CAB, and DTG. Alone they do not reduce INSTI susceptibility. However, they contribute to reduced susceptibility in combination with other mutations particularly those at position 148.

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G140S/A/C are non-polymorphic mutations that usually occur with Q148 mutations. Alone, they have minimal effects on INSTI susceptibility. However, in combination with Q148 mutations they are associated with high-level resistance to RAL and EVG and intermediate reductions in DTG and BIC susceptibility.

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Q148H/K/R are nonpolymorphic mutations reported in persons receiving RAL, EVG, CAB, and DTG. They nearly always occur in combination with G140A/S or E138K. In this setting they are associated with near complete resistance to RAL and EVG, high-levels of reduction in CAB susceptibility, and low-to-intermediate reductions in DTG and BIC susceptibility.

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There is evidence for high-level DTG resistance. If DTG is used, it should be administered twice daily.

Mutation scoring: IN

HIVDB 9.5.1 (2023-11-05)

Drug resistance mutation scores of INSTI:

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Rule	BIC ⚡	CAB ⚡	DTG ⚡	EVG ⚡	RAL ⚡
<u>E138K</u>	10	10	10	15	15
<u>E138K + G140A</u>	10	15	10	15	15
<u>E138K + Q148K</u>	10	20	10	0	0
<u>G140A</u>	10	10	10	30	30
<u>G140A + Q148K</u>	10	20	10	0	0
<u>Q148K</u>	30	50	30	60	60
Total	80	125	80	120	120