

Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations:

PI Accessory Mutations:

PR Other Mutations:

None

None

L10LV 1-10%, 0-40% • K20KR 4-50%, 0-30% • M36I 100% cons=0.110 • R41K 90% cons=0.141 • L63C 100% cons=0.190 • I64V 90% cons=0.190 • I72V 100% cons=0.640

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

- L10I/V are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.
- K20R is a highly polymorphic PI-selected accessory mutation that increases replication fitness in viruses with PI-resistance mutations.

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:	S68G <small>100% cons=0.860</small> • K70KT <small>0-10%, 0-20%</small> • T215F <small>90% cons=1.100</small>
NNRTI Mutations:	K103N <small>90% cons=0.300</small>
RT Other Mutations:	V35T <small>90% cons=0.111</small> • K49KR <small>0-40%, 0-10%</small> • V60I <small>100% cons=0.100</small> • A98S <small>90% cons=0.101</small> • K101R <small>90% cons=0.160</small> • K122E <small>90% cons=0.160</small> • I135IT <small>0-10%, 0-10%</small> • D177G <small>100% cons=0.100</small> • T200K <small>10% cons=0.100</small> • Q207E <small>90% cons=0.100</small> • R211K <small>100% cons=0.100</small> • P243PAS <small>0-10%, 0-10%, 0-10%</small> • V245K <small>100% cons=0.100</small> • E248ED <small>0-10%, 0-10%</small> • D250E <small>90% cons=0.100</small> • A554N <small>100% cons=0.100</small>

Nucleoside Reverse Transcriptase Inhibitors		Non-nucleoside Reverse Transcriptase Inhibitors	
abacavir (ABC)	Low-Level Resistance	doravirine (DOR)	Susceptible
zidovudine (AZT)	High-Level Resistance	efavirenz (EFV)	High-Level Resistance
stavudine (D4T)	Intermediate Resistance	etravirine (ETR)	Susceptible
didanosine (DDI)	Intermediate Resistance	nevirapine (NVP)	High-Level Resistance
emtricitabine (FTC)	Potential Low-Level Resistance	rilpivirine (RPV)	Susceptible
lamivudine (3TC)	Potential Low-Level Resistance		
tenofovir (TDF)	Low-Level Resistance		

RT comments	
NRTI	
<ul style="list-style-type: none">S68G is a polymorphic mutation that is often selected in combination with K65R. It partially restores the replication defect associated with K65R.K70/E/Q/N/T/S/G cause low-level resistance to ABC and TDF.T215V/F are TAMs that causes intermediate/high-level resistance to AZT and potentially low-level resistance to ABC and TDF.	
NNRTI	
<ul style="list-style-type: none">K103N is a non-polymorphic mutation that confers high-level reductions in NVP and EFV susceptibility. It is the most commonly transmitted DRM.	

Mutation scoring: RT	HIVDB 9.5.1 (2023-11-05)
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Drug resistance mutation scores of NRTI:								Download CSV	▼
Rule	ABC	AZT	D4T	DDI	FTC	3TC	TDF		
K70KT	15	0	15	15	10	10	15		
T215F	10	60	40	15	0	0	10		
Total	25	60	55	30	10	10	25		

Drug resistance mutation scores of NNRTI:						Download CSV	▼
Rule	DOR	EFV	ETR	NVP	RPV		
K103N	0	60	0	60	0		

INSTI Major Mutations:None

INSTI Accessory Mutations:None

IN Other Mutations:

K77Q

8, 12%, 0, 38%

cons:262

•S17N

100%

cons:252

•M50L

100%

cons:240

•L101I

100%

cons:211

•T112M

17%

cons:212

•T124A

100%

cons:252

•T125A

94%

cons:252

•D167DE

0, 10%, 0, 30%

cons:252

•V201I

100%

cons:212

•T206TS

1, 47%, 0, 13%

cons:225

•T218I

100%

cons:252

•K219Q

100%

cons:252

•L234I

100%

cons:252

•D256E

100%

cons:242

•D286N

100%

cons:252

Integrase Strand Transfer Inhibitors

bictegravir (BIC)Susceptible

cabotegravir (CAB)Susceptible

dolutegravir (DTG)Susceptible

elvitegravir (EVG)Susceptible

raltegravir (RAL)Susceptible

No drug resistance mutations were found for INSTI.

Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations:

M46I100%
from 13,217 • V82A100%
from 7,667

PI Accessory Mutations:

None

PR Other Mutations:

L10I100%
from 4,702 • I13V100%
from 1,411 • E35D100%
from 11,118 • M36I100%
from 11,118 • R41K99%
from 11,205 • I62N100%
from 10,424 • L63P100%
from 9,892 • C67Y100%
from 9,892 • H69K99%
from 9,822 • L89I100%
from 7,387

Protease Inhibitors

atazanavir/r (ATV/r)	Intermediate Resistance
darunavir/r (DRV/r)	Susceptible
fosamprenavir/r (FPV/r)	Intermediate Resistance
indinavir/r (IDV/r)	Intermediate Resistance
lopinavir/r (LPV/r)	Intermediate Resistance
nelfinavir (NFV)	High-Level Resistance
saquinavir/r (SQV/r)	Intermediate Resistance
tipranavir/r (TPV/r)	Susceptible

PR comments

Major

- M46I/L are relatively non-polymorphic PI-selected mutations. In combination with other PI-resistance mutations, they are associated with reduced susceptibility to each of the PIs except DRV.
- V82A is a non-polymorphic mutation selected primarily by IDV and LPV. It is associated with reduced susceptibility to LPV and to a lesser extent ATV. It increases DRV susceptibility.

Other

- L10I/V are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.

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

[Download CSV](#)

Rule	ATV/r	DRV/r	FPV/r	IDV/r	LPV/r	NFV	SQV/r	TPV/r
M46I	10	0	10	10	10	30	10	5
M46I + V82A	10	0	10	10	10	10	10	0
V82A	15	0	15	30	30	30	15	0
Total	35	0	35	50	50	70	35	5

Drug resistance interpretation: RT	HIVDB 9.5.1 (2023-11-05)
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NRTI Mutations:	M41L <small>100% from 10,000</small> • M184V <small>100% from 104</small> • T215Y <small>100% from 104</small>
NNRTI Mutations:	K103N <small>97% from 181</small>
RT Other Mutations:	ISV <small>100% from 9,400</small> • V35T <small>100% from 10,276</small> • T39A <small>100% from 10,368</small> • V50I <small>100% from 6,002</small> • D121Y <small>100% from 216</small> • K122E <small>99% from 236</small> • S162C <small>99% from 126</small> • K173A <small>100% from 105</small> • Q174K <small>100% from 105</small> • T200A <small>100% from 104</small> • Q207A <small>100% from 104</small> • R211K <small>100% from 104</small>

Nucleoside Reverse Transcriptase Inhibitors		Non-nucleoside Reverse Transcriptase Inhibitors	
abacavir (ABC)	Intermediate Resistance	doravirine (DOR)	Susceptible
zidovudine (AZT)	High-Level Resistance	efavirenz (EFV)	High-Level Resistance
stavudine (D4T)	Intermediate Resistance	etravirine (ETR)	Susceptible
didanosine (DDI)	Intermediate Resistance	nevirapine (NVP)	High-Level Resistance
emtricitabine (FTC)	High-Level Resistance	rilpivirine (RPV)	Susceptible
lamivudine (3TC)	High-Level Resistance		
tenofovir (TDF)	Low-Level Resistance		

RT comments
NRTI
<ul style="list-style-type: none">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.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.T215Y/F are TAMs that causes intermediate/high-level resistance to AZT and potentially low-level resistance to ABC and TDF.
NNRTI
<ul style="list-style-type: none">K103N is a non-polymorphic mutation that confers high-level reductions in NVP and EFV susceptibility. It is the most commonly transmitted DRM.

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Drug resistance mutation scores of NRTI:

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Rule	ABC	AZT	D4T	DDI	FTC	3TC	TDF
M41L	5	15	15	10	0	0	5
M41L + M184V + T215Y	10	0	0	0	0	0	0
M41L + T215Y	10	10	10	10	5	5	10
M184V	15	-10	-10	10	60	60	-10
T215Y	10	60	40	15	0	0	10
Total	50	75	55	45	65	65	15

Drug resistance mutation scores of NNRTI:

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Rule	DOR	EFV	ETR	NVP	RPV
K103N	0	60	0	60	0