

Drug resistance interpretation: PR		HIVDB 9.5.1 (2023-11-05)
PI Major Mutations:	None	
PI Accessory Mutations:	None	
PR Other Mutations:	L10LV <small>(1: 5.0%, 1: 4.0%) from 20,358</small> • E35D <small>100% from 11,054</small> • M36I <small>98% from 11,053</small> • N37D <small>98% from 11,355</small> • R41K <small>98% from 11,381</small> • R57RQ <small>(1: 6.0%, 1: 3.0%) from 22,476</small> • D60E <small>98% from 7,715</small> • I62V <small>100% from 7,735</small> • L63E <small>100% from 7,735</small> • I64V <small>100% from 7,735</small> • E65D <small>98% from 5,290</small> • C67CW <small>(1: 1.0%, 1: 2.0%) from 9,736</small>	
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.		

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

Drug resistance interpretation: RT	HNDB 9.5.1 (2023-11-05)
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NRTI Mutations:	None	
NNRTI Mutations:	None	
RT Other Mutations:	K20R <small>98% from 3,525</small> • V35T <small>100% from 3,514</small> • T39K <small>98% from 3,325</small> • K43KE <small>(1: 7.0%, 1: 2.0%) from 2,313</small> • K49R <small>98% from 2,321</small> • V60I <small>98% from 2,358</small> • K102KQ <small>(1: 7.0%, 1: 2.0%) from 2,333</small> • D121Y <small>98% from 1,336</small> • K122E <small>98% from 1,551</small> • E169ED <small>(1: 6.0%, 1: 3.0%) from 2,329</small> • Q174R <small>98% from 2,353</small> • D177E <small>98% from 2,352</small> • I178M <small>98% from 2,355</small> • T200A <small>98% from 1,381</small> • Q207E <small>98% from 1,902</small> • R211K <small>98% from 2,371</small> • V245Q <small>100% from 1,265</small> • D250E <small>98% from 1,261</small> • T286V <small>100% from 377</small> • I293V <small>100% from 1,352</small> • V531VI <small>(1: 5.0%, 1: 2.0%) from 2,867</small> • A554S <small>100% from 2,852</small> • K558R <small>98% from 2,853</small>	
Nucleoside Reverse Transcriptase Inhibitors		
abacavir (ABC)	Susceptible	
zidovudine (AZT)	Susceptible	
stavudine (D4T)	Susceptible	
didanosine (DDI)	Susceptible	
emtricitabine (FTC)	Susceptible	
lamivudine (3TC)	Susceptible	
tenofovir (TDF)	Susceptible	
Non-nucleoside Reverse Transcriptase Inhibitors		
doravirine (DOR)	Susceptible	
efavirenz (EFV)	Susceptible	
etravirine (ETR)	Susceptible	
nevirapine (NVP)	Susceptible	
rilpivirine (RPV)	Susceptible	

Mutation scoring: RT	HNDB 9.5.1 (2023-11-05)
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No drug resistance mutations were found for NRTI.

No drug resistance mutations were found for NNRTI.

Drug resistance interpretation: IN	HNDB 9.5.1 (2023-11-05)
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INSTI Major Mutations:	None
INSTI Accessory Mutations:	None
IN Other Mutations:	S17N <small>100% from 2,382</small> • I72IV <small>(1: 8.0%, 1: 3.0%) from 2,490</small> • L101L <small>(1: 7.0%, 1: 2.0%) from 2,223</small> • T112V <small>98% from 1,395</small> • I113V <small>100% from 1,395</small> • S119P <small>98% from 1,383</small> • T124A <small>98% from 1,857</small> • T125A <small>100% from 1,857</small> • K188KR <small>(1: 7.0%, 1: 2.0%) from 3,138</small> • V201I <small>98% from 2,914</small> • T206S <small>100% from 3,278</small> • D207E <small>100% from 3,435</small> • L234I <small>98% from 3,175</small> • N254H <small>100% from 3,258</small> • A265V <small>98% from 3,333</small> • R269RK <small>(1: 1.0%, 1: 3.0%) from 4,323</small>
Integrase Strand Transfer Inhibitors	
bictegravir (BIC)	Susceptible
cabotegravir (CAB)	Susceptible
dolutegravir (DTG)	Susceptible
elvitegravir (EVG)	Susceptible
raltegravir (RAL)	Susceptible

Mutation scoring: IN	HNDB 9.5.1 (2023-11-05)
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No drug resistance mutations were found for INSTI.