

Drug resistance interpretation: PR		HVDB 9.5.1 (2023-11-05)
PI Major Mutations:	None	
PI Accessory Mutations:	None	
PR Other Mutations:	I13V ^{100%} _{cons=3,171} • K20KR ^{N: 42%, R: 57%} _{cons=3,112} • E35D ^{100%} _{cons=4,404} • M36I ^{100%} _{cons=4,404} • R41K ^{99%} _{cons=4,410} • R57K ^{100%} _{cons=4,398} • H69K ^{99%} _{cons=3,984} • L89M ^{100%} _{cons=2,713}	
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		
• K20R is a highly polymorphic PI-selected accessory mutation that increases replication fitness in viruses with PI-resistance mutations.		

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

Drug resistance interpretation: RT		HVDB 9.5.1 (2023-11-05)	
NRTI Mutations:	None		
NNRTI Mutations:	None		
RT Other Mutations:	P95P ^{N: 90%, S: 10%} _{cons=3,135} • K11T ^{99%} _{cons=2,360} • V21I ^{100%} _{cons=3,139} • V35T ^{100%} _{cons=3,326} • T39KR ^{N: 90%, R: 10%} _{cons=2,362} • V60I ^{100%} _{cons=2,264} • K122E ^{99%} _{cons=2,317} • D123N ^{100%} _{cons=2,327} • K173S ^{99%} _{cons=3,225} • D177E ^{100%} _{cons=3,175} • V179I ^{99%} _{cons=3,163} • T200E ^{99%} _{cons=2,097} • I202V ^{100%} _{cons=2,117} • Q207AK ^{N: 67%, R: 33%} _{cons=3,332} • R211K ^{99%} _{cons=3,330} • D218DG ^{N: 97%, G: 3%} _{cons=3,320} • V245Q ^{100%} _{cons=496} • E248DN ^{N: 10%, G: 20%} _{cons=676} • K281R ^{99%} _{cons=313} • T286A ^{100%} _{cons=529} • E291D ^{100%} _{cons=139} • I293V ^{100%} _{cons=120} • P294T ^{100%} _{cons=120} • K512S ^{99%} _{cons=2,466} • S519N ^{99%} _{cons=3,309} • Q520L ^{100%} _{cons=3,309} • Q524K ^{99%} _{cons=3,320} • I526IV ^{N: 70%, G: 20%} _{cons=4,355} • K527G ^{100%} _{cons=4,355} • E529D ^{99%} _{cons=3,214} • V531V ^{N: 71%, S: 29%} _{cons=3,329} • A534S ^{99%} _{cons=3,320} • A554N ^{99%} _{cons=7,311} • V559I ^{100%} _{cons=7,363}		
Nucleoside Reverse Transcriptase Inhibitors		Non-nucleoside Reverse Transcriptase Inhibitors	
abacavir (ABC)	Susceptible	doravirine (DOR)	Susceptible
zidovudine (AZT)	Susceptible	efavirenz (EFV)	Susceptible
stavudine (D4T)	Susceptible	etravirine (ETR)	Susceptible
didanosine (DDI)	Susceptible	nevirapine (NVP)	Susceptible
emtricitabine (FTC)	Susceptible	rilpivirine (RPV)	Susceptible
lamivudine (3TC)	Susceptible		
tenofovir (TDF)	Susceptible		
RT comments			
Other			
<ul style="list-style-type: none">V179I is a polymorphic mutation that is frequently selected in persons receiving ETR and RPV. However, it has little, if any, direct effect on NNRTI susceptibility.			

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

Drug resistance interpretation: IN		HVDB 9.5.1 (2023-11-05)
INSTI Major Mutations:	None	
INSTI Accessory Mutations:	None	
IN Other Mutations:	E10A ^{100%} _{cons=7,372} • E11D ^{100%} _{cons=6,340} • S17N ^{99%} _{cons=6,404} • D25E ^{100%} _{cons=6,402} • V31V ^{N: 79%, S: 21%} _{cons=7,104} • I60M ^{100%} _{cons=4,396} • I72V ^{100%} _{cons=3,961} • K111KR ^{N: 77%, R: 23%} _{cons=2,410} • T112V ^{99%} _{cons=3,395} • I113V ^{99%} _{cons=3,395} • T124A ^{100%} _{cons=2,394} • T125A ^{100%} _{cons=2,394} • G134D ^{99%} _{cons=3,403} • K136Q ^{99%} _{cons=3,361} • V165I ^{100%} _{cons=4,326} • D167E ^{99%} _{cons=3,310} • V201I ^{99%} _{cons=10,114} • S255SGN ^{N: 90%, G: 90%, S: 20%} _{cons=11,362} • S283G ^{99%} _{cons=3,967}	
Integrase Strand Transfer Inhibitors		
bictegravir (BIC)	Susceptible	
cabotegravir (CAB)	Susceptible	
dolutegravir (DTG)	Susceptible	
elvitegravir (EVG)	Susceptible	
raltegravir (RAL)	Susceptible	
Mutation scoring: IN		HVDB 9.5.1 (2023-11-05)
No drug resistance mutations were found for INSTI.		