

**ANRS - AC 43: RESISTANCE GROUP  
GENOTYPE INTERPRETATION: NUCLEOSIDE AND NUCLEOTIDE REVERSE TRANSCRIPTASE INHIBITORS**

	Mutations associated with resistance	Mutations associated with « possible resistance »
ZDV	<ul style="list-style-type: none"> <li>• T215A/C/D/E/G/H/I/L/N/S/V/Y/F [1, 2, 3, 4]</li> <li>• At least 3 mutations among: M41L, D67N, K70R, L210W, K219Q/E [1, 2, 3, 4]</li> <li>• Q151M</li> <li>• Insertion at codon 69</li> </ul>	
3TC/FTC	<ul style="list-style-type: none"> <li>• K65R [8, 9, 11]</li> <li>• M184V/I</li> <li>• Insertion at codon 69</li> </ul>	<ul style="list-style-type: none"> <li>• Q151M</li> </ul>
ABC	<ul style="list-style-type: none"> <li>• At least 3 mutations among: M41L, D67N, M184V/I, L210W, T215A/C/D/E/G/H/I/L/N/S/V/Y/F [5, 20]</li> <li>• K65R [6, 8, 9, 24]</li> <li>• L74V/I [16, 17, 18, 19, 20, 24]</li> <li>• Y115F [24]</li> <li>• Q151M</li> <li>• Insertion at codon 69</li> </ul>	<ul style="list-style-type: none"> <li>• 2 mutations among: M41L, D67N, L210W, T215A/C/D/E/G/H/I/L/N/S/V/Y/F [5, 20]</li> <li>• M184V/I [24]</li> </ul>
TDF/TAF	<ul style="list-style-type: none"> <li>• At least 4 mutations among: M41L, E44D, D67N, T69D/N/S, L74V/I, L210W, T215A/C/D/E/G/H/I/L/N/S/V/Y/F [10, 12, 21, 25, 26]</li> <li>• K65R/E/N [6, 7, 8, 9, 22, 23, 25, 26]</li> <li>• Insertion at codon 69</li> <li>• K70E [13, 14, 15]</li> </ul>	<ul style="list-style-type: none"> <li>• 3 mutations among: M41L, E44D, D67N, T69D/N/S, L74V/I, L210W, T215A/C/D/E/G/H/I/L/N/S/V/Y/F [10, 21, 25, 26]</li> </ul>
ISL	<ul style="list-style-type: none"> <li>• M184V/I [27, 28, 29]</li> </ul>	<ul style="list-style-type: none"> <li>• A114S [29]</li> </ul>

ZDV: zidovudine, 3TC: lamivudine, FTC: emtricitabine, ABC: abacavir, TDF: tenofovir disoproxil fumarate, TAF: tenofovir alafenamide, ISL: islatravir

For didanosine and stavudine refer to previous rules (See Archives, September 2017, version 27)

For DNA provirus, Impact of stop codons and G to A mutations on ARV resistance is unknown

**ANRS - AC 43: RESISTANCE GROUP  
GENOTYPE INTERPRETATION: NON-NUCLEOSIDE REVERSE TRANSCRIPTASE INHIBITORS**

	Mutations associated with resistance	Mutations associated with « possible resistance »
EFV	<ul style="list-style-type: none"> <li>• L100I</li> <li>• K101E</li> <li>• K103H/N/S/T [1]</li> <li>• V106M [2]</li> <li>• E138K [12, 13]</li> <li>• Y181C/I</li> <li>• Y188C/L</li> <li>• G190A/C/E/Q/S/T/V</li> <li>• P225H</li> <li>• M230L</li> </ul>	
NVP	<ul style="list-style-type: none"> <li>• A98S (for HIV-1 subtype C only) [3]</li> <li>• L100I</li> <li>• K101E</li> <li>• K103H/N/S/T [1]</li> <li>• V106A/M [2]</li> <li>• Y181C/I</li> <li>• Y188C/H/L</li> <li>• G190A/C/E/Q/S/T/V</li> <li>• M230L</li> </ul>	<ul style="list-style-type: none"> <li>• E138K [13]</li> </ul>
ETR	<ul style="list-style-type: none"> <li>• At least 3 among: V90I, A98G, L100I, K101E/H/I/P/R, V106I, V179D/F/I/L/M/T, G190A/S, M230L [4, 7, 8, 9, 10, 11]</li> <li>• E138K [12, 13]</li> <li>• Y181C/I/V [5, 6]</li> <li>• H221Y [12,16]</li> </ul>	<ul style="list-style-type: none"> <li>• 2 mutations among: V90I, A98G, L100I, K101E/H/I/P/R, V106I, V179D/F/I/L/M/T, G190A/S, M230L [4, 7, 8, 9, 10, 11]</li> <li>• E138A/G/Q/R/S [5, 6, 7, 8]</li> </ul>
RPV	<ul style="list-style-type: none"> <li>• K101E/P [9, 13]</li> <li>• E138A/G/K/Q/R/S [12, 13, 14]</li> <li>• V179L [9]</li> <li>• Y181C/I/V [13]</li> <li>• Y188L [9]</li> <li>• F227C [9]</li> <li>• H221Y [13]</li> <li>• M230I/L/V [9]</li> <li>• L100I + K103N/S [9, 15]</li> <li>• L100I + K103R + V179D [15]</li> </ul>	<ul style="list-style-type: none"> <li>• A98G [22]</li> </ul>

DOR	<ul style="list-style-type: none"><li>• V106A/M [17, 18, 19, 20 ,21]</li><li>• Y188L</li><li>• G190E/S [21]</li><li>• M230L</li><li>• L100I + K103N [17, 19]</li><li>• K103N + Y181C</li><li>• K103N + P225H</li><li>• F227C [21]</li><li>• At least 4 among: A98G, L100I, K101E, V106I, E138K, , Y181C/V, G190A or H221Y [23]</li></ul>	<ul style="list-style-type: none"><li>• At least 2 among: A98G, L100I, K101E, V106I, E138K, Y181C/V, G190A or H221Y [23]</li></ul>
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EFV: efavirenz, NVP: nevirapine, ETR: etravirine, RPV : rilpivirine, DOR : doravirine.

For DNA provirus, Impact of stop codons and G to A mutations on ARV resistance is unknown

**ANRS - AC 43: RESISTANCE GROUP  
GENOTYPE INTERPRETATION: PROTEASE INHIBITORS**

	Mutations associated with resistance	Mutations associated with « possible resistance »
LPV/r	<ul style="list-style-type: none"> <li>At least 4 mutations among: L10F/I/R/V, K20M/R, L24I, L33F, M46I/L, I50V, F53L, I54M/L/T/V, L63P, A71I/L/V/T, V82A/F/S/T, I84V, L90M [1, 2, 3, 12]</li> <li>I47A [7, 8]</li> <li>L76V [10, 11]</li> </ul>	<ul style="list-style-type: none"> <li>3 mutations among: L10F/I/R/V, K20M/R, L24I, L33F, M46I/L, I50V, F53L, I54M/L/T/V, L63P, A71I/L/V/T, V82A/F/S/T, I84V, L90M [1, 2, 3, 12]</li> </ul>
ATV/RTV 300/100 mg QD	<ul style="list-style-type: none"> <li>I50L [4]</li> <li>N88S [18,19,20]</li> <li>At least 3 mutations among: L10F/I/V, G16E, L33F/I/V, M46I/L, D60E, A71V/T, I84V, I85V, L90M [5, 6, 13, 21]</li> </ul>	<ul style="list-style-type: none"> <li>2 mutations among: L10F/I/V, G16E, L33F/I/V, M46I/L, D60E, A71V/T, I84V, I85V, L90M [5, 6, 13, 21]</li> </ul>
DRV/RTV* 600/100 mg BID  800/100 mg QD	<ul style="list-style-type: none"> <li>At least 4 mutations among: V11I, V32I, L33F, I47V, I50V, I54L/M, T74P, L76V, I84V, L89V [9, 14, 15, 16, 17]</li> <li>At least 2 mutations among: V11I, V32I, L33F, I47V, I50V, I54L/M, T74P, L76V, I84V, L89V [9, 14, 15, 16, 17]</li> </ul>	<ul style="list-style-type: none"> <li>3 mutations among: V11I, V32I, L33F, I47V, I50V, I54L/M, T74P, L76V, I84V, L89V [9, 14, 15, 16, 17]</li> </ul>

LPV: lopinavir, ATV: atazanavir, DRV: darunavir, RTV: ritonavir

For indinavir, saquinavir, nelfinavir and fosamprenavir refer to previous rules (See Archives, September 2017, version 27)

\* Please note that rules are different for DRV/RTV 600/100 mg BID and 800/100 mg QD  
For DNA provirus, Impact of stop codons and G to A mutations on ARV resistance is unknown

**ANRS - AC 43: RESISTANCE GROUP  
GENOTYPE INTERPRETATION: FUSION INHIBITOR**

<b>Mutations associated with resistance</b>	
<b>ENF T20</b>	<ul style="list-style-type: none"> <li>• G36A/D/E/S/V [1, 2, 3, 4, 5, 6, 7]</li> <li>• V38A/E/K/M</li> <li>• Q40H/K/P/T</li> <li>• N42D/T</li> <li>• N43D/H/K/S</li> <li>• L44M</li> <li>• L45Q/M</li> </ul>

ENF (T20): enfuvirtide

**GENOTYPE INTERPRETATION: ATTACHMENT INHIBITOR**

<b>Mutations associated with “possible resistance” (gp120)</b>	
<b>FTR*</b>	<ul style="list-style-type: none"> <li>• At least one mutation among: S375H/I/M/N/T, M426L/P, M434I/K, M475I [5]</li> </ul>

FTR: fostemsavir

\*HIV-1 CRF01\_AE and HIV-1 group non-M strains are naturally resistant to Fostemsavir [1, 2, 3, 4]

ANRS - AC 43: RESISTANCE GROUP

GENOTYPE INTERPRETATION: INTEGRASE STRAND TRANSFER INHIBITORS

	Mutations associated with resistance	Mutations associated with « possible resistance »
RAL	<ul style="list-style-type: none"> <li>• T66A/K [10, 40]</li> <li>• E92Q [1, 2]</li> <li>• G118R [10, 17]</li> <li>• F121Y [10,17]</li> <li>• G140A/S [7]</li> <li>• Y143A/C/G/H/R/S [1, 3, 4, 5, 8, 14]</li> <li>• N144D [42]</li> <li>• Q148E/G/H/K/R [1, 2]</li> <li>• V151L [9]</li> <li>• N155H/S/T [1, 2, 9]</li> <li>• E157Q [2]</li> <li>• S230R [18, 31, 32, 33]</li> <li>• R263K [16, 18]</li> <li>• L74 F/I + V75I [36]</li> </ul>	
EVG	<ul style="list-style-type: none"> <li>• T66A/I/K [6]</li> <li>• E92Q [6]</li> <li>• T97A [19,20]</li> <li>• G118R [17]</li> <li>• F121Y [9,17]</li> <li>• E138K</li> <li>• G140A/C/S [34, 41]</li> <li>• Y143A/C/G/H/R/S [14]</li> <li>• N144D [42]</li> <li>• P145S [9]</li> <li>• S147G [19]</li> <li>• Q148E/G/H/K/R [6]</li> <li>• V151L [9]</li> <li>• N155H/S/T [6, 9]</li> <li>• E157Q [11, 35]</li> <li>• S230R [18, 31, 32, 33]</li> <li>• R263K [18]</li> <li>• L74F/I + V75I [36]</li> </ul>	

<p>DTG* 50mg BID</p>	<ul style="list-style-type: none"> <li>• G118R [12,13]</li> <li>• F121Y [17]</li> <li>• N144D [42]</li> <li>• V151L [9,23]</li> <li>• S153F/Y [9, 23, 26, 34]</li> <li>• R263K [16]</li> <li>• T66K + L74M [9]</li> <li>• E92Q + N155H [9, 21, 22]</li> <li>• Q148H/K/R + at least 2 mutations among: L74I or T97A or E138A/K/T or G140A/C/S [15, 38, 39]</li> <li>• Q148H/K/R + N155H [9, 27, 28]</li> </ul>	<ul style="list-style-type: none"> <li>• T66K [9]</li> <li>• Q148H/K/R + 1 mutation among: L74I or E138A/K/T or G140A/C/S [15]</li> </ul>
<p><b>DTG*</b> 50mg QD</p>	<ul style="list-style-type: none"> <li>• G118R [12, 13]</li> <li>• F121Y [17]</li> <li>• E138A/K/T</li> <li>• G140A/C/S</li> <li>• N144D [42]</li> <li>• Q148H/K/R</li> <li>• V151L [9, 23]</li> <li>• S153F/Y [9, 23, 26, 34]</li> <li>• N155H [18]</li> <li>• S230R [29]</li> <li>• R263K [16]</li> <li>• T66K + L74M [9]</li> <li>• L74I + E92Q [30]</li> </ul>	<ul style="list-style-type: none"> <li>• T66K [9]</li> </ul>

<p>CAB**</p>	<ul style="list-style-type: none"> <li>• G118R [12, 13]</li> <li>• F121Y [17]</li> <li>• E138A/K/T</li> <li>• G140A/C/R/S [37]</li> <li>• N144D [42]</li> <li>• Q148H/K/R</li> <li>• V151L [9, 23]</li> <li>• S153F/Y [9, 23, 26, 34]</li> <li>• N155H [18]</li> <li>• S230R [29]</li> <li>• R263K [16]</li> <li>• T66K + L74M [9]</li> <li>• L74I + E92Q [30]</li> </ul>	<ul style="list-style-type: none"> <li>• T66K [9]</li> </ul>
<p>BIC**</p>	<ul style="list-style-type: none"> <li>• G118R [12, 13]</li> <li>• F121Y [17]</li> <li>• E138A/K/T</li> <li>• G140A/C/S</li> <li>• N144D [42]</li> <li>• Q148H/K/R</li> <li>• V151L [9, 23]</li> <li>• S153F/Y [9, 23, 26, 34]</li> <li>• N155H [18]</li> <li>• S230R [29]</li> <li>• R263K [16]</li> <li>• T66K + L74M [9]</li> <li>• L74I + E92Q [30]</li> </ul>	<ul style="list-style-type: none"> <li>• T66K [9]</li> </ul>

RAL: raltegravir, EVG: elvitegravir, DTG: dolutegravir, CAB: cabotegravir, BIC: bicitegravir

\* Please note that rules are different for DTG 50 mg BID and **DTG** 50 mg QD

\*\*Due to few data and to the very close structures of dolutegravir, cabotegravir and bicitegravir some rules for dolutegravir QD are transposed to cabotegravir and bicitegravir

For DNA provirus, Impact of stop codons and G to A mutations on ARV resistance is unknown



ANRS - AC 43: RESISTANCE GROUP  
GENOTYPE INTERPRETATION: CAPSID INHIBITORS

	Mutations associated with resistance	Mutations associated with « possible resistance »
LEN	<ul style="list-style-type: none"><li>• L56I [1]</li><li>• M66I [1]</li><li>• Q67H/K/N [1,3,4, 5]</li><li>• K70H/N/R/S [1,2,3,4,5]</li><li>• N74D/S [1]</li><li>• T107A/C/N [1,3, 4]</li></ul>	

LEN: lenacapavir

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