

**ANRS - AC 11: 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>

ZDV: zidovudine, 3TC: lamivudine, FTC: emtricitabine, ABC: abacavir, TDF: tenofovir, TAF: tenofovir alafenamide

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 11: 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>• V179D [9,15, 17]</li> </ul>

DOR	<ul style="list-style-type: none"><li>• V106A [18, 19, 20, 21]</li><li>• Y188L</li><li>• G190S</li><li>• M230L</li><li>• K103N + Y181C</li><li>• K103N + P225H</li></ul>	<ul style="list-style-type: none"><li>• L100I + K103N [18, 20]</li><li>• Y181C + G190A</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 11: 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, 13]</li> <li>I47A [8, 9]</li> <li>L76V [11, 12]</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, 13]</li> </ul>
ATV/RTV 300/100 mg QD	<ul style="list-style-type: none"> <li>I50L [4]</li> <li>N88S [20,21,22]</li> <li>At least 3 mutations among: L10F/I/V, G16E, L33F/I/V, M46I/L, D60E, A71V/T, I84V, I85V, L90M [5, 7, 14, 23]</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, 7, 14, 23]</li> </ul>
TPV/RTV 500/200 mg BID	<ul style="list-style-type: none"> <li>At least a score of + 3*: M36I/L/V – F53L/W/Y + Q58E + H69I/K/N/Q/R/Y + L89I/M/R/T/V [6, 15]</li> </ul>	<ul style="list-style-type: none"> <li>A score of + 2*: M36I/L/V – F53L/W/Y + Q58E + H69I/K/N/Q/R/Y + L89I/M/R/T/V [6, 15]</li> </ul>
DRV/RTV** 600/100 mg BID	<ul style="list-style-type: none"> <li>At least 4 mutations among: V11I, V32I, L33F, I47V, I50V, I54L/M, T74P, L76V, I84V, L89V [10, 16, 17, 18, 19]</li> </ul>	<ul style="list-style-type: none"> <li>3 mutations among: V11I, V32I, L33F, I47V, I50V, I54L/M, T74P, L76V, I84V, L89V [10, 16, 17, 18, 19]</li> </ul>
800/100 mg QD	<ul style="list-style-type: none"> <li>2 mutations among: V11I, V32I, L33F, I47V, I50V, I54L/M, T74P, L76V, I84V, L89V [10, 16, 17, 18, 19]</li> </ul>	

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

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

\* Insufficient data for HIV-1 subtype non-B

\*\* 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 11: 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**

ANRS - AC 11: 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>• T66K [10]</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>• 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, 33, 34, 35]</li> <li>• R263K [16, 18]</li> <li>• L74F + V75I [38]</li> </ul>	
EVG	<ul style="list-style-type: none"> <li>• T66I/A/K [6]</li> <li>• E92Q [6]</li> <li>• T97A [21,22]</li> <li>• G118R [17]</li> <li>• F121Y [9,17]</li> <li>• E138K</li> <li>• G140C/S</li> <li>• Y143A/C/G/H/R/S [14]</li> <li>• P145S [9]</li> <li>• S147G [21]</li> <li>• Q148H/R/K [6]</li> <li>• V151L [9]</li> <li>• N155H/S/T [6,9]</li> <li>• E157Q [11,37]</li> <li>• S230R [18, 33, 34, 35]</li> <li>• R263K [18]</li> <li>• L74F + V75I [38]</li> </ul>	

<p><b>DTG*</b> 50 mg BID</p>	<ul style="list-style-type: none"> <li>• G118R [12,13]</li> <li>• F121Y [17]</li> <li>• V151L [9,25]</li> <li>• S153F/Y [9, 25,28, 36]</li> <li>• R263K [16]</li> <li>• T66K + L74M [9]</li> <li>• E92Q + N155H [9, 23, 24]</li> <li>• Q148H/K/R + at least 2 mutations among: L74I or E138A/K/T or G140A/C/S [15]</li> <li>• Q148H/K/R + N155H [9, 29,30]</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>50 mg 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>• Q148H/K/R</li> <li>• V151L [9,25]</li> <li>• S153F/Y [9,25,28, 36]</li> <li>• N155H [18]</li> <li>• S230R [31]</li> <li>• R263K [16]</li> <li>• T66K + L74M [9]</li> <li>• L74I + E92Q [32]</li> </ul>	<ul style="list-style-type: none"> <li>• T66K [9]</li> <li>• E157Q [19, 20, 37]</li> </ul>
<p><b>CAB**</b></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>• Q148H/K/R</li> <li>• V151L [9,25]</li> <li>• S153F/Y [9,25,28, 36]</li> <li>• N155H [18]</li> <li>• S230R [31]</li> <li>• R263K [16]</li> <li>• T66K + L74M [9]</li> <li>• L74I + E92Q [32]</li> </ul>	<ul style="list-style-type: none"> <li>• T66K [9]</li> <li>• E157Q [19, 20, 37]</li> </ul>

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**RAL: raltegravir, EVG: elvitegravir, DTG: dolutegravir, CAB: cabotegravir**

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

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

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



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