

**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"> • T215A/C/D/E/G/H/I/L/N/S/V/Y/F [1, 2, 3, 4] • At least 3 mutations among: M41L, D67N, K70R, L210W, K219Q/E [1, 2, 3, 4] • Q151M • Insertion at codon 69 	
3TC/FTC	<ul style="list-style-type: none"> • K65R [8, 9, 11] • M184V/I • Insertion at codon 69 	<ul style="list-style-type: none"> • Q151M
ABC	<ul style="list-style-type: none"> • 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] • K65R [6, 8, 9, 24] • L74V/I [16, 17, 18, 19, 20, 24] • Y115F [24] • Q151M • Insertion at codon 69 	<ul style="list-style-type: none"> • 2 mutations among: M41L, D67N, L210W, T215A/C/D/E/G/H/I/L/N/S/V/Y/F [5, 20] • M184V/I [24]
TDF/TAF	<ul style="list-style-type: none"> • 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] • K65R/E/N [6, 7, 8, 9, 22, 23, 25, 26] • Insertion at codon 69 • K70E [13, 14, 15] 	<ul style="list-style-type: none"> • 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]

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 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"> • L100I • K101E • K103H/N/S/T [1] • V106M [2] • E138K [12, 13] • Y181C/I • Y188C/L • G190A/C/E/Q/S/T/V • P225H • M230L 	
NVP	<ul style="list-style-type: none"> • A98S (for HIV-1 subtype C only) [3] • L100I • K101E • K103H/N/S/T [1] • V106A/M [2] • Y181C/I • Y188C/H/L • G190A/C/E/Q/S/T/V • M230L 	<ul style="list-style-type: none"> • E138K [13]
ETR	<ul style="list-style-type: none"> • 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] • E138K [12, 13] • Y181C/I/V [5, 6] • H221Y [12,16] 	<ul style="list-style-type: none"> • 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] • E138A/G/Q/R/S [5, 6, 7, 8]
RPV	<ul style="list-style-type: none"> • K101E/P [9, 13] • E138A/G/K/Q/R/S [12, 13, 14] • V179L [9] • Y181C/I/V [13] • Y188L [9] • F227C [9] • H221Y [13] • M230I/L/V [9] • L100I + K103N/S [9, 15] • L100I + K103R + V179D [15] 	<ul style="list-style-type: none"> • V179D [9,15, 17]

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DOR	<ul style="list-style-type: none">• V106A/M [18, 19, 20, 21,22]• Y188L• G190S• M230L• L100I + K103N [18, 20]• K103N + Y181C• K103N + P225H• F227C [22]	
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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"> 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] I47A [8, 9] L76V [11, 12] 	<ul style="list-style-type: none"> 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]
ATV/RTV 300/100 mg QD	<ul style="list-style-type: none"> I50L [4] N88S [20,21,22] At least 3 mutations among: L10F/I/V, G16E, L33F/I/V, M46I/L, D60E, A71V/T, I84V, I85V, L90M [5, 7, 14, 23] 	<ul style="list-style-type: none"> 2 mutations among: L10F/I/V, G16E, L33F/I/V, M46I/L, D60E, A71V/T, I84V, I85V, L90M [5, 7, 14, 23]
TPV/RTV 500/200 mg BID	<ul style="list-style-type: none"> 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] 	<ul style="list-style-type: none"> A score of + 2*: M36I/L/V – F53L/W/Y + Q58E + H69I/K/N/Q/R/Y + L89I/M/R/T/V [6, 15]
DRV/RTV** 600/100 mg BID	<ul style="list-style-type: none"> At least 4 mutations among: V11I, V32I, L33F, I47V, I50V, I54L/M, T74P, L76V, I84V, L89V [10, 16, 17, 18, 19] 	<ul style="list-style-type: none"> 3 mutations among: V11I, V32I, L33F, I47V, I50V, I54L/M, T74P, L76V, I84V, L89V [10, 16, 17, 18, 19]
800/100 mg QD	<ul style="list-style-type: none"> 2 mutations among: V11I, V32I, L33F, I47V, I50V, I54L/M, T74P, L76V, I84V, L89V [10, 16, 17, 18, 19] 	

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

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GENOTYPE INTERPRETATION: FUSION INHIBITOR**

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

ENF (T20): enfuvirtide

GENOTYPE INTERPRETATION: ATTACHMENT INHIBITOR

	Mutations associated with resistance (gp120)
FTR*	<ul style="list-style-type: none">• S375H/I/N [1, 2, 3]• M426L [1, 2, 3]

FTR: fostemsavir

*HIV-1 CRF01_AE and HIV-1 group non-M strains are naturally resistant to Fostemsavir [1, 2, 3, 4]

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GENOTYPE INTERPRETATION: INTEGRASE STRAND TRANSFER INHIBITORS

	Mutations associated with resistance	Mutations associated with « possible resistance »
RAL	<ul style="list-style-type: none"> • T66K [10] • E92Q [1, 2] • G118R [10, 17] • F121Y [10,17] • G140A/S [7] • Y143A/C/G/H/R/S [1, 3, 4, 5, 8, 14] • Q148E/G/H/K/R [1, 2] • V151L [9] • N155H/S/T [1, 2, 9] • E157Q [2] • S230R [18, 33, 34, 35] • R263K [16, 18] • L74F + V75I [38] 	
EVG	<ul style="list-style-type: none"> • T66I/A/K [6] • E92Q [6] • T97A [21,22] • G118R [17] • F121Y [9,17] • E138K • G140C/S • Y143A/C/G/H/R/S [14] • P145S [9] • S147G [21] • Q148H/R/K [6] • V151L [9] • N155H/S/T [6,9] • E157Q [11,37] • S230R [18, 33, 34, 35] • R263K [18] • L74F + V75I [38] 	

<p>DTG* 50 mg BID</p>	<ul style="list-style-type: none"> • G118R [12,13] • F121Y [17] • V151L [9,25] • S153F/Y [9, 25,28, 36] • R263K [16] • T66K + L74M [9] • E92Q + N155H [9, 23, 24] • Q148H/K/R + at least 2 mutations among: L74I or E138A/K/T or G140A/C/S [15] • Q148H/K/R + N155H [9, 29,30] 	<ul style="list-style-type: none"> • T66K [9] • Q148H/K/R + 1 mutation among: L74I or E138A/K/T or G140A/C/S [15]
<p>50 mg QD</p>	<ul style="list-style-type: none"> • G118R [12,13] • F121Y [17] • E138A/K/T • G140A/C/S • Q148H/K/R • V151L [9,25] • S153F/Y [9,25,28, 36] • N155H [18] • S230R [31] • R263K [16] • T66K + L74M [9] • L74I + E92Q [32] 	<ul style="list-style-type: none"> • T66K [9] • E157Q [19, 20, 37]
<p>CAB**</p>	<ul style="list-style-type: none"> • G118R [12,13] • F121Y [17] • E138A/K/T • G140A/C/S • Q148H/K/R • V151L [9,25] • S153F/Y [9,25,28, 36] • N155H [18] • S230R [31] • R263K [16] • T66K + L74M [9] • L74I + E92Q [32] 	<ul style="list-style-type: none"> • T66K [9] • E157Q [19, 20, 37]

BIC**	<ul style="list-style-type: none">• G118R [12,13]• F121Y [17]• E138A/K/T• G140A/C/S• Q148H/K/R• V151L [9,25]• S153F/Y [9,25,28, 36]• N155H [18]• S230R [31]• R263K [16]• T66K + L74M [9]• L74I + E92Q [32]	<ul style="list-style-type: none">• T66K [9]• E157Q [19, 20, 37]
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RAL: raltegravir, EVG: elvitegravir, DTG: dolutegravir, CAB: cabotegravir, BIC: bictegravir

* 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, cabotegravir and bictegravir rules for dolutegravir QD are transposed to cabotegravir and bictegravir

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

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