## ANRS - AC 11: RESISTANCE GROUP

### GENOTYPE INTERPRETATION: NUCLEOSIDE AND NUCLEOTIDE REVERSE TRANSCRIPTASE INHIBITORS

<table>
<thead>
<tr>
<th>Drug</th>
<th>Mutations associated with resistance</th>
<th>Mutations associated with “possible resistance”</th>
</tr>
</thead>
</table>
| ZDV     | 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 | K65R [8, 9, 11]  
M184V/I  
Insertion at codon 69 | Q151M                                           |
| ABC     | 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 | 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 | 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] | 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 11: RESISTANCE GROUP

**GENOTYPE INTERPRETATION: NON-NUCLEOSIDE REVERSE TRANSCRIPTASE INHIBITORS**

<table>
<thead>
<tr>
<th>Mutations associated with resistance</th>
<th>Mutations associated with « possible resistance »</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>EFV</strong></td>
<td></td>
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<tr>
<td>L100I</td>
<td></td>
</tr>
<tr>
<td>K101E</td>
<td></td>
</tr>
<tr>
<td>K103H/N/S/T [1]</td>
<td></td>
</tr>
<tr>
<td>V106M [2]</td>
<td></td>
</tr>
<tr>
<td>E138K [12, 13]</td>
<td></td>
</tr>
<tr>
<td>Y181C/I</td>
<td></td>
</tr>
<tr>
<td>Y188C/L</td>
<td></td>
</tr>
<tr>
<td>G190A/C/E/Q/S/T/V</td>
<td></td>
</tr>
<tr>
<td>P225H</td>
<td></td>
</tr>
<tr>
<td>M230L</td>
<td></td>
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<tr>
<td><strong>NVP</strong></td>
<td></td>
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<tr>
<td>L100I</td>
<td></td>
</tr>
<tr>
<td>K101E</td>
<td></td>
</tr>
<tr>
<td>K103H/N/S/T [1]</td>
<td></td>
</tr>
<tr>
<td>V106A/M [2]</td>
<td></td>
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<tr>
<td>Y181C/I</td>
<td></td>
</tr>
<tr>
<td>Y188C/H/L</td>
<td></td>
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<tr>
<td>G190A/C/E/Q/S/T/V</td>
<td></td>
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<tr>
<td>M230L</td>
<td></td>
</tr>
<tr>
<td><strong>ETR</strong></td>
<td></td>
</tr>
<tr>
<td>E138K [12, 13]</td>
<td>E138A/G/Q/R/S [5, 6, 7, 8]</td>
</tr>
<tr>
<td>Y181C/I/V</td>
<td></td>
</tr>
<tr>
<td>H221Y [12,16]</td>
<td></td>
</tr>
<tr>
<td><strong>RPV</strong></td>
<td></td>
</tr>
<tr>
<td>K101E/P [9, 13]</td>
<td>V179D [9,15, 17]</td>
</tr>
<tr>
<td>E138A/G/K/Q/R/S [12, 13, 14]</td>
<td></td>
</tr>
<tr>
<td>V179L [9]</td>
<td></td>
</tr>
<tr>
<td>Y181C/I/V [13]</td>
<td></td>
</tr>
<tr>
<td>Y188L [9]</td>
<td></td>
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<tr>
<td>F227C [9]</td>
<td></td>
</tr>
<tr>
<td>H221Y [13]</td>
<td></td>
</tr>
<tr>
<td>M230I/L/V [9]</td>
<td></td>
</tr>
<tr>
<td>L100I + K103N/S [9, 15]</td>
<td></td>
</tr>
<tr>
<td>L100I + K103R + V179D [15]</td>
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</tbody>
</table>
**DOR**

- V106A [18, 19, 20, 21]
- Y188L
- G190S
- M230L
- K103N + Y181C
- K103N + P225H

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<table>
<thead>
<tr>
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<tbody>
<tr>
<td></td>
<td>L100I + K103N [18, 20]</td>
</tr>
<tr>
<td></td>
<td>Y181C + G190A</td>
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</tbody>
</table>


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

<table>
<thead>
<tr>
<th>Drug Combination</th>
<th>Mutations associated with resistance</th>
<th>Mutations associated with « possible resistance »</th>
</tr>
</thead>
</table>
• I47A [8, 9]  
| **ATV/RTV 300/100 mg QD** | • 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] | • 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** | • 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] | • 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  
800/100 mg QD | • At least 4 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
ANRS - AC 11: RESISTANCE GROUP
GENOTYPE INTERPRETATION: FUSION INHIBITOR

<table>
<thead>
<tr>
<th>ENF T20</th>
<th>Mutations associated with resistance</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>• G36A/D/E/S/V [1, 2, 3, 4, 5, 6, 7]</td>
</tr>
<tr>
<td></td>
<td>• V38A/E/K/M</td>
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<tr>
<td></td>
<td>• Q40H/K/P/T</td>
</tr>
<tr>
<td></td>
<td>• N42D/T</td>
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<tr>
<td></td>
<td>• N43D/H/K/S</td>
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<tr>
<td></td>
<td>• L44M</td>
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<tr>
<td></td>
<td>• L45Q/M</td>
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</tbody>
</table>

ENF (T20): enfuvirtide
### ANRS - AC 11: RESISTANCE GROUP

**GENOTYPE INTERPRETATION: INTEGRASE STRAND TRANSFER INHIBITORS**

<table>
<thead>
<tr>
<th>Mutations associated with resistance</th>
<th>Mutations associated with « possible resistance »</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>RAL</strong></td>
<td></td>
</tr>
<tr>
<td>T66K [10]</td>
<td></td>
</tr>
<tr>
<td>E92Q [1, 2]</td>
<td></td>
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<tr>
<td>G118R [10, 17]</td>
<td></td>
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<tr>
<td>F121Y [10,17]</td>
<td></td>
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<tr>
<td>G140A/S [7]</td>
<td></td>
</tr>
<tr>
<td>Y143A/C/G/H/R/S [1, 3, 4, 5, 8, 14]</td>
<td></td>
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<tr>
<td>Q148E/G/H/K/R [1, 2]</td>
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<tr>
<td>V151L [9]</td>
<td></td>
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<tr>
<td>N155H/S/T [1, 2, 9]</td>
<td></td>
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<tr>
<td>E157Q [2]</td>
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<tr>
<td>S230R [18, 33, 34, 35]</td>
<td></td>
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<tr>
<td>R263K [16, 18]</td>
<td></td>
</tr>
<tr>
<td>L74F + V75I [38]</td>
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<tr>
<td><strong>EVG</strong></td>
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<tr>
<td>T66I/A/K [6]</td>
<td></td>
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<tr>
<td>E92Q [6]</td>
<td></td>
</tr>
<tr>
<td>T97A [21,22]</td>
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<tr>
<td>G118R [17]</td>
<td></td>
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<tr>
<td>F121Y [9,17]</td>
<td></td>
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<tr>
<td>E138K</td>
<td></td>
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<tr>
<td>G140C/S</td>
<td></td>
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<tr>
<td>Y143A/C/G/H/R/S [14]</td>
<td></td>
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<tr>
<td>P145S [9]</td>
<td></td>
</tr>
<tr>
<td>S147G [21]</td>
<td></td>
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<tr>
<td>Q148H/R/K [6]</td>
<td></td>
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<tr>
<td>V151L [9]</td>
<td></td>
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<tr>
<td>N155H/S/T [6,9]</td>
<td></td>
</tr>
<tr>
<td>E157Q [11,37]</td>
<td></td>
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<tr>
<td>S230R [18, 33, 34, 35]</td>
<td></td>
</tr>
<tr>
<td>R263K [18]</td>
<td></td>
</tr>
<tr>
<td>L74F + V75I [38]</td>
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</tbody>
</table>
| DTG* 50 mg BID | 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]  
| 50 mg QD | 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]  
| CAB** | 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]  
|                | T66K [9]  
|                | Q148H/K/R + 1 mutation among: L74I or E138A/K/T or G140A/C/S [15]  
|                | T66K [9]  
|                | E157Q [19, 20, 37]  
|                | T66K [9]  
|                | E157Q [19, 20, 37]  
|                | T66K [9]  
|                | E157Q [19, 20, 37]  
|
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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Avril 2018 - Version n°28


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