

Página 1
LISTADO DE SECUENCIAS

<110> Consejo Superior de Investigaciones Científicas (CSIC)
 <120> Retrotranscriptasa del VIH-1 de grupo O modificada
 <130> ES.1641.330
 <160> 17
 <170> PatentIn version 3.5
 <210> 1
 <211> 560
 <212> PRT
 <213> Virus de la Inmunodeficiencia Humana Tipo 1 (VIH-1) de Grupo O
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Pro Ile Ser Pro Ile Ala Pro Val Pro Val Lys Leu Lys Pro Gly Met
 1 5 10 15

Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Ser Lys Glu Lys Ile Glu
 20 25 30

Ala Leu Thr Ala Ile Cys Gln Glu Met Glu Gln Glu Gly Lys Ile Ser
 35 40 45

Arg Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe Ala Ile Lys
 50 55 60

Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu
 65 70 75 80

Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His
 85 90 95

Pro Gly Gly Leu Lys Gln Lys Arg Ser Val Thr Val Leu Asp Val Gly
 100 105 110

Asp Ala Tyr Phe Ser Cys Pro Leu Asp Pro Asp Phe Arg Lys Tyr Thr
 115 120 125

Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly Ile Arg Tyr
 130 135 140

Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe
 145 150 155 160

Gln Ser Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys Asp Asn Pro
 165 170 175

Glu Leu Glu Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp
 180 185 190

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Leu Pro Leu Ala Glu His Arg Lys Arg Val Glu Leu Leu Arg Glu His
 195 200 205
 Leu Tyr Gln Trp Gly Phe Thr Thr Pro Asp Lys Lys His Gln Lys Glu
 210 215 220
 Pro Pro Phe Met Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr
 225 230 235 240
 Val Gln Pro Ile Lys Leu Pro Asn Lys Asp Val Trp Thr Val Asn Asp
 245 250 255
 Ile Gln Lys Leu Ile Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Gln
 260 265 270
 Gly Ile Arg Val Arg Glu Leu Cys Lys Leu Ile Arg Gly Thr Lys Ser
 275 280 285
 Leu Thr Glu Val Val Pro Leu Ser Lys Glu Ala Glu Met Glu Leu Glu
 290 295 300
 Glu Asn Arg Glu Lys Leu Lys Glu Pro Met His Gly Val Tyr Tyr Gln
 305 310 315 320
 Pro Asp Lys Asp Leu Trp Val Asn Ile Gln Lys Gln Gly Glu Gly Gln
 325 330 335
 Trp Thr Tyr Gln Ile Tyr Gln Asp Glu His Lys Asn Leu Lys Thr Gly
 340 345 350
 Lys Tyr Thr Arg Gln Lys Ala Ser His Thr Asn Asp Ile Arg Gln Leu
 355 360 365
 Ala Glu Val Ile Gln Lys Val Ser Gln Glu Ser Ile Val Ile Trp Gly
 370 375 380
 Lys Leu Pro Lys Phe Lys Leu Pro Val Thr Arg Glu Thr Trp Glu Thr
 385 390 395 400
 Trp Trp Ala Asp Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Asp Tyr
 405 410 415
 Val Ser Thr Pro Pro Leu Ile Lys Leu Trp Tyr Arg Leu Glu Ser Glu
 420 425 430
 Pro Ile Arg Gly Ala Glu Thr Tyr Tyr Val Asp Gly Ala Ala Asn Arg
 435 440 445
 Asp Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Glu Gln Gly Lys Gln

450

455

460

Lys Ile Ile Lys Leu Asp Glu Thr Thr Asn Gln Lys Ala Glu Leu Met
465 470 475 480

Ala Val Leu Leu Ala Leu Gln Asp Ser Lys Glu Lys Val Asn Ile Val
485 490 495

Thr Asp Ser Gln Tyr Val Leu Gly Ile Ile Ser Ser Gln Pro Thr Gln
500 505 510

Ser Glu Ser Pro Ile Val Gln Gln Ile Ile Glu Glu Leu Thr Lys Lys
515 520 525

Glu Gln Val Tyr Leu Thr Trp Val Pro Ala His Lys Gly Ile Gly Gly
530 535 540

Asn Glu Lys Ile Asp Lys Leu Val Ser Lys Asp Ile Arg Arg Val Leu
545 550 555 560

<210> 2
<211> 560
<212> PRT
<213> Artificial Sequence

<220>
<223> Secuencia de aminoácidos de la subunidad p66 de la RT del VIH-1 de grupo O modificada con la mutación V75I

<400> 2

Pro Ile Ser Pro Ile Ala Pro Val Pro Val Lys Leu Lys Pro Gly Met
1 5 10 15

Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Ser Lys Glu Lys Ile Glu
20 25 30

Ala Leu Thr Ala Ile Cys Gln Glu Met Glu Gln Glu Gly Lys Ile Ser
35 40 45

Arg Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe Ala Ile Lys
50 55 60

Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Ile Asp Phe Arg Glu Leu
65 70 75 80

Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His
85 90 95

Pro Gly Gly Leu Lys Gln Lys Arg Ser Val Thr Val Leu Asp Val Gly
100 105 110

Asp Ala Tyr Phe Ser Cys Pro Leu Asp Pro Asp Phe Arg Lys Tyr Thr
 115 120 125
 Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly Ile Arg Tyr
 130 135 140
 Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe
 145 150 155 160
 Gln Ser Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys Asp Asn Pro
 165 170 175
 Glu Leu Glu Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp
 180 185 190
 Leu Pro Leu Ala Glu His Arg Lys Arg Val Glu Leu Leu Arg Glu His
 195 200 205
 Leu Tyr Gln Trp Gly Phe Thr Thr Pro Asp Lys Lys His Gln Lys Glu
 210 215 220
 Pro Pro Phe Met Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr
 225 230 235 240
 Val Gln Pro Ile Lys Leu Pro Asn Lys Asp Val Trp Thr Val Asn Asp
 245 250 255
 Ile Gln Lys Leu Ile Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Gln
 260 265 270
 Gly Ile Arg Val Arg Glu Leu Cys Lys Leu Ile Arg Gly Thr Lys Ser
 275 280 285
 Leu Thr Glu Val Val Pro Leu Ser Lys Glu Ala Glu Met Glu Leu Glu
 290 295 300
 Glu Asn Arg Glu Lys Leu Lys Glu Pro Met His Gly Val Tyr Tyr Gln
 305 310 315 320
 Pro Asp Lys Asp Leu Trp Val Asn Ile Gln Lys Gln Gly Glu Gly Gln
 325 330 335
 Trp Thr Tyr Gln Ile Tyr Gln Asp Glu His Lys Asn Leu Lys Thr Gly
 340 345 350
 Lys Tyr Thr Arg Gln Lys Ala Ser His Thr Asn Asp Ile Arg Gln Leu
 355 360 365
 Ala Glu Val Ile Gln Lys Val Ser Gln Glu Ser Ile Val Ile Trp Gly
 370 375 380

Lys Leu Pro Lys Phe Lys Leu Pro Val Thr Arg Glu Thr Trp Glu Thr
385 390 395 400

Trp Trp Ala Asp Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Asp Tyr
405 410 415

Val Ser Thr Pro Pro Leu Ile Lys Leu Trp Tyr Arg Leu Glu Ser Glu
420 425 430

Pro Ile Arg Gly Ala Glu Thr Tyr Tyr Val Asp Gly Ala Ala Asn Arg
435 440 445

Asp Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Glu Gln Gly Lys Gln
450 455 460

Lys Ile Ile Lys Leu Asp Glu Thr Thr Asn Gln Lys Ala Glu Leu Met
465 470 475 480

Ala Val Leu Leu Ala Leu Gln Asp Ser Lys Glu Lys Val Asn Ile Val
485 490 495

Thr Asp Ser Gln Tyr Val Leu Gly Ile Ile Ser Ser Gln Pro Thr Gln
500 505 510

Ser Glu Ser Pro Ile Val Gln Gln Ile Ile Glu Glu Leu Thr Lys Lys
515 520 525

Glu Gln Val Tyr Leu Thr Trp Val Pro Ala His Lys Gly Ile Gly Gly
530 535 540

Asn Glu Lys Ile Asp Lys Leu Val Ser Lys Asp Ile Arg Arg Val Leu
545 550 555 560

<210> 3
<211> 560
<212> PRT
<213> Artificial Sequence

<220>
<223> Secuencia de aminoácidos de la subunidad p66 de la RTdel VIH-1 de grupo O modificada con las mutaciones V75I y E478Q

<400> 3

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1 5 10 15

Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Ser Lys Glu Lys Ile Glu
20 25 30

Ala Leu Thr Ala Ile Cys Gln Glu Met Glu Gln Glu Gly Lys Ile Ser

35	40	45
Arg Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe Ala Ile Lys		
50	55	60
Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Ile Asp Phe Arg Glu Leu		
65	70	75
Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His		
85	90	95
Pro Gly Gly Leu Lys Gln Lys Arg Ser Val Thr Val Leu Asp Val Gly		
100	105	110
Asp Ala Tyr Phe Ser Cys Pro Leu Asp Pro Asp Phe Arg Lys Tyr Thr		
115	120	125
Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly Ile Arg Tyr		
130	135	140
Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe		
145	150	155
Gln Ser Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys Asp Asn Pro		
165	170	175
Glu Leu Glu Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp		
180	185	190
Leu Pro Leu Ala Glu His Arg Lys Arg Val Glu Leu Leu Arg Glu His		
195	200	205
Leu Tyr Gln Trp Gly Phe Thr Thr Pro Asp Lys Lys His Gln Lys Glu		
210	215	220
Pro Pro Phe Met Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr		
225	230	235
Val Gln Pro Ile Lys Leu Pro Asn Lys Asp Val Trp Thr Val Asn Asp		
245	250	255
Ile Gln Lys Leu Ile Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Gln		
260	265	270
Gly Ile Arg Val Arg Glu Leu Cys Lys Leu Ile Arg Gly Thr Lys Ser		
275	280	285
Leu Thr Glu Val Val Pro Leu Ser Lys Glu Ala Glu Met Glu Leu Glu		
290	295	300

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Glu Asn Arg Glu Lys Leu Lys Glu Pro Met His Gly Val Tyr Tyr Gln
 305 310 315 320
 Pro Asp Lys Asp Leu Trp Val Asn Ile Gln Lys Gln Gly Glu Gly Gln
 325 330 335
 Trp Thr Tyr Gln Ile Tyr Gln Asp Glu His Lys Asn Leu Lys Thr Gly
 340 345 350
 Lys Tyr Thr Arg Gln Lys Ala Ser His Thr Asn Asp Ile Arg Gln Leu
 355 360 365
 Ala Glu Val Ile Gln Lys Val Ser Gln Glu Ser Ile Val Ile Trp Gly
 370 375 380
 Lys Leu Pro Lys Phe Lys Leu Pro Val Thr Arg Glu Thr Trp Glu Thr
 385 390 395 400
 Trp Trp Ala Asp Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Asp Tyr
 405 410 415
 Val Ser Thr Pro Pro Leu Ile Lys Leu Trp Tyr Arg Leu Glu Ser Glu
 420 425 430
 Pro Ile Arg Gly Ala Glu Thr Tyr Tyr Val Asp Gly Ala Ala Asn Arg
 435 440 445
 Asp Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Glu Gln Gly Lys Gln
 450 455 460
 Lys Ile Ile Lys Leu Asp Glu Thr Thr Asn Gln Lys Ala Gln Leu Met
 465 470 475 480
 Ala Val Leu Leu Ala Leu Gln Asp Ser Lys Glu Lys Val Asn Ile Val
 485 490 495
 Thr Asp Ser Gln Tyr Val Leu Gly Ile Ile Ser Ser Gln Pro Thr Gln
 500 505 510
 Ser Glu Ser Pro Ile Val Gln Gln Ile Ile Glu Glu Leu Thr Lys Lys
 515 520 525
 Glu Gln Val Tyr Leu Thr Trp Val Pro Ala His Lys Gly Ile Gly Gly
 530 535 540
 Asn Glu Lys Ile Asp Lys Leu Val Ser Lys Asp Ile Arg Arg Val Leu
 545 550 555 560

<211> 99
 <212> PRT
 <213> Virus de la Inmunodeficiencia Humana Tipo 1 (VIH-1) de Grupo B Suptipo M

<400> 4

Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
 1 5 10 15

Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45

Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile
 50 55 60

Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95

Leu Asn Phe

<210> 5
 <211> 1720
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Secuencia del inserto portador de la región codificante para la subunidad p66 de la RT del VIH-1 de Grupo O con una cola de seis residuos de histidina, flanqueada por un sitio de restricción EcoRI en el extremo 5' y codones de terminación en el extremo 3'

<400> 5
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 accaaaagta aaacaatggc ccctatctaa agaaaaaata gaagccttaa cagcaatatg 120
 ccaggaaatg gaacaagaag gaaaaatttc aagaatagga cctgaaaatc cttataatac 180
 acctatcttt gctataaaaa agaaagatag tactaagtgg agaaagctgg tagactttag 240
 ggaattaaac aagagaacac aagatTTTTT ggaggtacag ttaggtatcc cacatccggg 300
 gggTTTTaaag caaaagcgat ctgttacagt cttagatgta ggagatgcct atttctcatg 360
 ccccttagac ccagatttta gaaaatatac tgctttcact attcctagtg taaacaatga 420
 gaccccagga ataagatacc agtacaatgt cctcccgcaa ggatggaaag gtTCGCCagc 480
 catattccaa agttcaatga caaaaatttt agatccattt aggaaagaca acccagaatt 540
 agaaatttgt cagtacatgg atgacctata tgtaggatca gatttaccCC tggcagaaca 600


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tagaaaaagg gttgaattgc ttagagaaca cttatatcag tggggattca ctaccctga      660
taaaaagcat caaaaggaac ctccctttat gtggatgggg tatgagctcc atccagataa      720
atggacagta cagcccatca aattgcctaa caaagatgtg tggacagtaa atgatataca      780
aaaactaata ggaaagttaa attgggcaag tcaaatctat caaggaatta gagtaagaga      840
atttgttaag ttaattagag gcaccaagtc attaacagaa gtagtaccat taagcaaaga      900
ggcagagatg gaattagagg agaacagaga gaaattaaaa gaaccaatgc atggtgtata      960
ctatcaacct gataaagact tatgggttaa tattcagaag caaggagaag ggcaatggac     1020
ttaccagata tatcaggatg aacataagaa cctcaaaaca gggaaatata ctaggcaaaa     1080
ggcctccac acaaatgaca taagacaatt agcagaagta atccagaagg tgtctcaaga     1140
atctatagtt atctggggaa aattgcctaa atttaagctg ccagtcacta gagaaacttg     1200
ggaaacatgg tgggcagatt attggcaagc cacctggatc ccagaatggg attatgtcag     1260
cacaccccca ttgatcaaat tatggtaccg gttagaaagt gaacctatta ggggggcaga     1320
aacctattat gtagatggag cagctaatag agatacaaaa ttaggaaaag caggatatgt     1380
tacagaacaa gggaaacaga aaataataaa attagatgag accaccaatc aaaaggctga     1440
attaatggca gtattattag ccttacagga ttccaaagaa aaagtaaata tagtaacaga     1500
ctcacaatat gtattgggca ttatctcttc ccagcctaca cagagtgaat cccctatagt     1560
tcagcagata atagaggaac taacaaaaaa ggaacaggtg tatcttacat gggttcctgc     1620
tcataaaggc ataggaggaa atgaaaaaat agataaatta gtaagcaagg atattagaag     1680
agtcctcgag tcgactcacc accaccacca cactgataa      1720

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<210> 6

<211> 572

<212> PRT

<213> Artificial sequence

<220>

<223> subunidad p66 de la RT del VIH-1 de Grupo O con modificaciones en los extremos N- y C-terminales que incluyen una cola de seis residuos de histidina

<400> 6

Met Asn Ser Pro Ile Ser Pro Ile Ala Pro Val Pro Val Lys Leu Lys
1 5 10 15

Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Ser Lys Glu
20 25 30

Lys Ile Glu Ala Leu Thr Ala Ile Cys Gln Glu Met Glu Gln Glu Gly
35 40 45

Lys Ile Ser Arg Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
50 55 60

Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
65 70 75 80

Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
85 90 95

Ile Pro His Pro Gly Gly Leu Lys Gln Lys Arg Ser Val Thr Val Leu
100 105 110

Asp Val Gly Asp Ala Tyr Phe Ser Cys Pro Leu Asp Pro Asp Phe Arg
115 120 125

Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly
130 135 140

Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
145 150 155 160

Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys
165 170 175

Asp Asn Pro Glu Leu Glu Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val
180 185 190

Gly Ser Asp Leu Pro Leu Ala Glu His Arg Lys Arg Val Glu Leu Leu
195 200 205

Arg Glu His Leu Tyr Gln Trp Gly Phe Thr Thr Pro Asp Lys Lys His
210 215 220

Gln Lys Glu Pro Pro Phe Met Trp Met Gly Tyr Glu Leu His Pro Asp
225 230 235 240

Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Asn Lys Asp Val Trp Thr
245 250 255

Val Asn Asp Ile Gln Lys Leu Ile Gly Lys Leu Asn Trp Ala Ser Gln
260 265 270

Ile Tyr Gln Gly Ile Arg Val Arg Glu Leu Cys Lys Leu Ile Arg Gly
275 280 285

Thr Lys Ser Leu Thr Glu Val Val Pro Leu Ser Lys Glu Ala Glu Met
290 295 300

Glu Leu Glu Glu Asn Arg Glu Lys Leu Lys Glu Pro Met His Gly Val
305 310 315 320

Tyr Tyr Gln Pro Asp Lys Asp Leu Trp Val Asn Ile Gln Lys Gln Gly
325 330 335

Glu Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Asp Glu His Lys Asn Leu
340 345 350

Lys Thr Gly Lys Tyr Thr Arg Gln Lys Ala Ser His Thr Asn Asp Ile
355 360 365

Arg Gln Leu Ala Glu Val Ile Gln Lys Val Ser Gln Glu Ser Ile Val
370 375 380

Ile Trp Gly Lys Leu Pro Lys Phe Lys Leu Pro Val Thr Arg Glu Thr
385 390 395 400

Trp Glu Thr Trp Trp Ala Asp Tyr Trp Gln Ala Thr Trp Ile Pro Glu
405 410 415

Trp Asp Tyr Val Ser Thr Pro Pro Leu Ile Lys Leu Trp Tyr Arg Leu
420 425 430

Glu Ser Glu Pro Ile Arg Gly Ala Glu Thr Tyr Tyr Val Asp Gly Ala
435 440 445

Ala Asn Arg Asp Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Glu Gln
450 455 460

Gly Lys Gln Lys Ile Ile Lys Leu Asp Glu Thr Thr Asn Gln Lys Ala
465 470 475 480

Glu Leu Met Ala Val Leu Leu Ala Leu Gln Asp Ser Lys Glu Lys Val
485 490 495

Asn Ile Val Thr Asp Ser Gln Tyr Val Leu Gly Ile Ile Ser Ser Gln
500 505 510

Pro Thr Gln Ser Glu Ser Pro Ile Val Gln Gln Ile Ile Glu Glu Leu
515 520 525

Thr Lys Lys Glu Gln Val Tyr Leu Thr Trp Val Pro Ala His Lys Gly
530 535 540

Ile Gly Gly Asn Glu Lys Ile Asp Lys Leu Val Ser Lys Asp Ile Arg
545 550 555 560

Arg Val Leu Glu Ser Thr His His His His His His
565 570

<210> 7
<211> 36

<212> DNA
 <213> Artificial Sequence

<220>
 <223> cebador "sentido" empleado para introducir la mutación V75I en la subunidad p66 de la RT del VIH-1 de Grupo O

<400> 7
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<210> 8
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> cebador "antisentido" empleado para introducir la mutación V75I en la subunidad p66 de la RT del VIH-1 de Grupo O

<400> 8
 gtttaattcc ctaaagtcta tcagctttct ccactt 36

<210> 9
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> cebador "sentido" empleado para introducir la mutación E478Q en la subunidad p66 de la RT del VIH-1 de Grupo O

<400> 9
 ccaatcaaaa ggctcaatta atggcag 27

<210> 10
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> cebador "antisentido" empleado para introducir la mutación E478Q en la subunidad p66 de la RT del VIH-1 de Grupo O

<400> 10
 ctgccattaa ttgagccttt tgattgg 27

<210> 11
 <211> 1720
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Secuencia del inserto portador de la región codificante para la subunidad p66 de la RT del VIH-1 de Grupo O modificada mediante la mutación V75I, con modificaciones en los extremos N- y C-terminales que incluyen una cola de 6 residuos de histidina

<400> 11
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 accaaaagta aaacaatggc ccctatctaa agaaaaaata gaagccttaa cagcaatatg 120

ccaggaaatg gaacaagaag gaaaaatttc aagaatagga cctgaaaatc cttataatac	180
acctatcttt gctataaaaa agaaagatag tactaagtgg agaaagctga tagacttttag	240
ggaattaaac aagagaacac aagatTTTTT ggaggtacag ttaggtatcc cacatccggg	300
gggttttaaag caaaagcgat ctgttacagt cttagatgta ggagatgcct atttctcatg	360
ccccttagac ccagatttta gaaaatatac tgctttcact attcctagtg taaacaatga	420
gaccccagga ataagatacc agtacaatgt cctcccgcaa ggatggaaag gttcgccagc	480
catattccaa agttcaatga caaaaatttt agatccattt aggaaagaca acccagaatt	540
agaaatttgt cagtacatgg atgacctata tgtaggatca gatttaccctc tggcagaaca	600
tagaaaaagg gttgaattgc ttagagaaca cttatatcag tggggattca ctacccctga	660
taaaaagcat caaaaggaac ctccctttat gtggatgggg tatgagctcc atccagataa	720
atggacagta cagcccatca aattgcctaa caaagatgtg tggacagtaa atgatataca	780
aaaactaata ggaaagttaa attgggcaag tcaaatctat caaggaatta gagtaagaga	840
attgtgtaag ttaattagag gcaccaagtc attaacagaa gtagtaccat taagcaaaga	900
ggcagagatg gaattagagg agaacagaga gaaattaaaa gaaccaatgc atggtgtata	960
ctatcaacct gataaagact tatgggttaa tattcagaag caaggagaag ggcaatggac	1020
ttaccagata tatcaggatg aacataagaa cctcaaaaca gggaaatata ctaggcaaaa	1080
ggcctccac acaaatgaca taagacaatt agcagaagta atccagaagg tgtctcaaga	1140
atctatagtt atctggggaa aattgcctaa atttaagctg ccagtcacta gagaaacttg	1200
ggaaacatgg tgggcagatt attggcaagc cacctggatc ccagaatggg attatgtcag	1260
cacaccccca ttgatcaaat tatggtaccg gttagaaagt gaacctatta ggggggcaga	1320
aacctattat gtagatggag cagctaatag agatacaaaa ttaggaaaag caggatatgt	1380
tacagaacaa gggaaacaga aaataataaa attagatgag accaccaatc aaaaggctga	1440
attaatggca gtattattag ccttacagga ttccaaagaa aaagtaaata tagtaacaga	1500
ctcacaatat gtattgggca ttatctcttc ccagcctaca cagagtgaat cccctatagt	1560
tcagcagata atagaggaac taacaaaaaa ggaacaggtg tatcttacat gggttcctgc	1620
tcataaaggc ataggaggaa atgaaaaaat agataaatta gtaagcaagg atattagaag	1680
agtcctcgag tcgactcacc accaccacca ccaactgataa	1720

<210> 12

<211> 1720

<212> DNA

<213> Artificial Sequence

<220>

<223> Secuencia del inserto portador de la región codificante para la subunidad p66 de la RT del VIH-1 de Grupo O modificada mediante las mutaciones V75I y E478Q, con modificaciones en los extremos N- y C-terminales que incluyen una cola de 6 residuos de

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<400> 12
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ccaggaaatg gaacaagaag gaaaaatttc aagaatagga cctgaaaatc cttataatac      180
acctatcttt gctataaaaa agaaagatag tactaagtgg agaaagctga tagactttag      240
ggaattaaac aagagaacac aagatTTTTT ggagggtacag ttaggtatcc cacatccggg      300
gggttttaaag caaaagcgat ctgttacagt cttagatgta ggagatgcct atttctcatg      360
ccccttagac ccagatttta gaaaatatac tgctttcact attcctagtg taaacaatga      420
gacccagga ataagatacc agtacaatgt cctcccgcaa ggatggaaag gttcgccagc      480
catattccaa agttcaatga caaaaatttt agatccattt aggaaagaca acccagaatt      540
agaaatttgt cagtacatgg atgacctata tgtaggatca gatttacccc tggcagaaca      600
tagaaaaagg gttgaattgc ttagagaaca cttatatcag tggggattca ctacccctga      660
taaaaagcat caaaaggaac ctccctttat gtggatgggg tatgagctcc atccagataa      720
atggacagta cagcccatca aattgcctaa caaagatgtg tggacagtaa atgatataca      780
aaaactaata ggaaagttaa attgggcaag tcaaatctat caaggaatta gagtaagaga      840
attgtgtaag ttaattagag gcaccaagtc attaacagaa gtagtaccat taagcaaaga      900
ggcagagatg gaattagagg agaacagaga gaaattaaaa gaaccaatgc atggtgtata      960
ctatcaacct gataaagact tatgggttaa tattcagaag caaggagaag ggcaatggac     1020
ttaccagata tatcaggatg aacataagaa cctcaaaaca gggaaatata ctaggcaaaa     1080
ggcctccac acaaatgaca taagacaatt agcagaagta atccagaagg tgtctcaaga     1140
atctatagtt atctggggaa aattgcctaa atttaagctg ccagtcacta gagaaaacttg     1200
ggaaacatgg tgggcagatt attggcaagc cacctggatc ccagaatggg attatgtcag     1260
cacaccccca ttgatcaaat tatggtaccg gttagaaagt gaacctatta ggggggcaga     1320
aacctattat gtagatggag cagctaatag agatacaaaa ttaggaaaag caggatatgt     1380
tacagaacaa gggaaacaga aaataataaa attagatgag accaccaatc aaaaggctca     1440
attaatggca gtattattag ccttacagga ttccaaagaa aaagtaaata tagtaacaga     1500
ctcacaatat gtattgggca ttatctcttc ccagcctaca cagagtgaat cccctatagt     1560
tcagcagata atagaggaac taacaaaaaa ggaacagggtg tatcttacat ggggttcctgc     1620
tcataaaggc ataggaggaa atgaaaaaat agataaatta gtaagcaagg atattagaag     1680
agtcctcgag tcgactcacc accaccacca ccaactgataa                        1720

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<210> 13
<211> 572
<212> PRT
<213> Artificial Sequence

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<220>

<223> Subunidad p66 de la RT del VIH-1 de Grupo O modificada mediante la mutación V75I con modificaciones en los extremos N- y C-terminales que incluyen una cola de 6 residuos de histidina

<400> 13

Met Asn Ser Pro Ile Ser Pro Ile Ala Pro Val Pro Val Lys Leu Lys
1 5 10 15

Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Ser Lys Glu
20 25 30

Lys Ile Glu Ala Leu Thr Ala Ile Cys Gln Glu Met Glu Gln Glu Gly
35 40 45

Lys Ile Ser Arg Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
50 55 60

Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Ile Asp Phe
65 70 75 80

Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
85 90 95

Ile Pro His Pro Gly Gly Leu Lys Gln Lys Arg Ser Val Thr Val Leu
100 105 110

Asp Val Gly Asp Ala Tyr Phe Ser Cys Pro Leu Asp Pro Asp Phe Arg
115 120 125

Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly
130 135 140

Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
145 150 155 160

Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys
165 170 175

Asp Asn Pro Glu Leu Glu Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val
180 185 190

Gly Ser Asp Leu Pro Leu Ala Glu His Arg Lys Arg Val Glu Leu Leu
195 200 205

Arg Glu His Leu Tyr Gln Trp Gly Phe Thr Thr Pro Asp Lys Lys His
210 215 220

Gln Lys Glu Pro Pro Phe Met Trp Met Gly Tyr Glu Leu His Pro Asp
225 230 235 240

Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Asn Lys Asp Val Trp Thr
 245 250 255
 Val Asn Asp Ile Gln Lys Leu Ile Gly Lys Leu Asn Trp Ala Ser Gln
 260 265 270
 Ile Tyr Gln Gly Ile Arg Val Arg Glu Leu Cys Lys Leu Ile Arg Gly
 275 280 285
 Thr Lys Ser Leu Thr Glu Val Val Pro Leu Ser Lys Glu Ala Glu Met
 290 295 300
 Glu Leu Glu Glu Asn Arg Glu Lys Leu Lys Glu Pro Met His Gly Val
 305 310 315 320
 Tyr Tyr Gln Pro Asp Lys Asp Leu Trp Val Asn Ile Gln Lys Gln Gly
 325 330 335
 Glu Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Asp Glu His Lys Asn Leu
 340 345 350
 Lys Thr Gly Lys Tyr Thr Arg Gln Lys Ala Ser His Thr Asn Asp Ile
 355 360 365
 Arg Gln Leu Ala Glu Val Ile Gln Lys Val Ser Gln Glu Ser Ile Val
 370 375 380
 Ile Trp Gly Lys Leu Pro Lys Phe Lys Leu Pro Val Thr Arg Glu Thr
 385 390 395 400
 Trp Glu Thr Trp Trp Ala Asp Tyr Trp Gln Ala Thr Trp Ile Pro Glu
 405 410 415
 Trp Asp Tyr Val Ser Thr Pro Pro Leu Ile Lys Leu Trp Tyr Arg Leu
 420 425 430
 Glu Ser Glu Pro Ile Arg Gly Ala Glu Thr Tyr Tyr Val Asp Gly Ala
 435 440 445
 Ala Asn Arg Asp Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Glu Gln
 450 455 460
 Gly Lys Gln Lys Ile Ile Lys Leu Asp Glu Thr Thr Asn Gln Lys Ala
 465 470 475 480
 Glu Leu Met Ala Val Leu Leu Ala Leu Gln Asp Ser Lys Glu Lys Val
 485 490 495
 Asn Ile Val Thr Asp Ser Gln Tyr Val Leu Gly Ile Ile Ser Ser Gln

500

505

510

Pro Thr Gln Ser Glu Ser Pro Ile Val Gln Gln Ile Ile Glu Glu Leu
515 520 525

Thr Lys Lys Glu Gln Val Tyr Leu Thr Trp Val Pro Ala His Lys Gly
530 535 540

Ile Gly Gly Asn Glu Lys Ile Asp Lys Leu Val Ser Lys Asp Ile Arg
545 550 555 560

Arg Val Leu Glu Ser Thr His His His His His His
565 570

<210> 14

<211> 572

<212> PRT

<213> Artificial Sequence

<220>

<223> Subunidad p66 de la RT del VIH-1 de Grupo O modificada mediante las mutaciones V75I y E478Q con modificaciones en los extremos N- y C-terminales que incluyen una cola de 6 residuos de histidina

<400> 14

Met Asn Ser Pro Ile Ser Pro Ile Ala Pro Val Pro Val Lys Leu Lys
1 5 10 15

Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Ser Lys Glu
20 25 30

Lys Ile Glu Ala Leu Thr Ala Ile Cys Gln Glu Met Glu Gln Glu Gly
35 40 45

Lys Ile Ser Arg Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
50 55 60

Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Ile Asp Phe
65 70 75 80

Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
85 90 95

Ile Pro His Pro Gly Gly Leu Lys Gln Lys Arg Ser Val Thr Val Leu
100 105 110

Asp Val Gly Asp Ala Tyr Phe Ser Cys Pro Leu Asp Pro Asp Phe Arg
115 120 125

Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly
130 135 140

Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
145 150 155 160

Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys
165 170 175

Asp Asn Pro Glu Leu Glu Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val
180 185 190

Gly Ser Asp Leu Pro Leu Ala Glu His Arg Lys Arg Val Glu Leu Leu
195 200 205

Arg Glu His Leu Tyr Gln Trp Gly Phe Thr Thr Pro Asp Lys Lys His
210 215 220

Gln Lys Glu Pro Pro Phe Met Trp Met Gly Tyr Glu Leu His Pro Asp
225 230 235 240

Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Asn Lys Asp Val Trp Thr
245 250 255

Val Asn Asp Ile Gln Lys Leu Ile Gly Lys Leu Asn Trp Ala Ser Gln
260 265 270

Ile Tyr Gln Gly Ile Arg Val Arg Glu Leu Cys Lys Leu Ile Arg Gly
275 280 285

Thr Lys Ser Leu Thr Glu Val Val Pro Leu Ser Lys Glu Ala Glu Met
290 295 300

Glu Leu Glu Glu Asn Arg Glu Lys Leu Lys Glu Pro Met His Gly Val
305 310 315 320

Tyr Tyr Gln Pro Asp Lys Asp Leu Trp Val Asn Ile Gln Lys Gln Gly
325 330 335

Glu Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Asp Glu His Lys Asn Leu
340 345 350

Lys Thr Gly Lys Tyr Thr Arg Gln Lys Ala Ser His Thr Asn Asp Ile
355 360 365

Arg Gln Leu Ala Glu Val Ile Gln Lys Val Ser Gln Glu Ser Ile Val
370 375 380

Ile Trp Gly Lys Leu Pro Lys Phe Lys Leu Pro Val Thr Arg Glu Thr
385 390 395 400

Trp Glu Thr Trp Trp Ala Asp Tyr Trp Gln Ala Thr Trp Ile Pro Glu

405

415

Trp Asp Tyr Val Ser Thr Pro Pro Leu Ile Lys Leu Trp Tyr Arg Leu
420 425 430

Glu Ser Glu Pro Ile Arg Gly Ala Glu Thr Tyr Tyr Val Asp Gly Ala
435 440 445

Ala Asn Arg Asp Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Glu Gln
450 455 460

Gly Lys Gln Lys Ile Ile Lys Leu Asp Glu Thr Thr Asn Gln Lys Ala
465 470 475 480

Gln Leu Met Ala Val Leu Leu Ala Leu Gln Asp Ser Lys Glu Lys Val
485 490 495

Asn Ile Val Thr Asp Ser Gln Tyr Val Leu Gly Ile Ile Ser Ser Gln
500 505 510

Pro Thr Gln Ser Glu Ser Pro Ile Val Gln Gln Ile Ile Glu Glu Leu
515 520 525

Thr Lys Lys Glu Gln Val Tyr Leu Thr Trp Val Pro Ala His Lys Gly
530 535 540

Ile Gly Gly Asn Glu Lys Ile Asp Lys Leu Val Ser Lys Asp Ile Arg
545 550 555 560

Arg Val Leu Glu Ser Thr His His His His His His
565 570

<210> 15
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> cebador "sentido" para amplificar el gen actina (ACT1)

<400> 15
cctaggcacc aggggtgtgat

20

<210> 16
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> cebador "antisentido" para amplificar el gen actina (ACT2)

<400> 16
cggtcaggat cttcatgagg

20

<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> cebador "antisentido" para amplificar el gen actina (ACT3)

<400> 17
cgtactcctg cttgctgac c