

LISTADO DE SECUENCIA

<110> Merial, Inc.
 David, Frederic
 Hannas-Djebbara , Zahia
 Poulet, Herve
 Minke, Jules

<120> VACUNAS DE PARTÍCULAS TIPO VIRUS (VLP) CONTRA EL PARVOVIRUS CANINO (CPV) Y SUS USOS

<130> MER 14-252

<150> 62/234,196
 <151> 2015-09-29

<160> 12

<170> PatentIn versión 3.5

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Glu Thr Leu Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp
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Arg Tyr Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly

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Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu Ile Thr Ala Asn
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Asp Ala Asn Ala Trp Gly Val Trp Phe Asn Pro Gly Asp Trp Gln Leu
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Glu Thr Leu Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp
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 Thr Asp Pro Ile Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe
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 Asn Thr Tyr Gly Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr
 450 455 460
 Pro Asn Gly Gln Ile Trp Asp Lys Glu Phe Asp Thr Asp Leu Lys Pro
 465 470 475 480
 Arg Leu His Val Asn Ala Pro Phe Val Cys Gln Asn Asn Cys Pro Gly
 485 490 495
 Gln Leu Phe Val Lys Val Ala Pro Asn Leu Thr Asn Glu Tyr Asp Pro
 500 505 510
 Asp Ala Ser Ala Asn Met Ser Arg Ile Val Thr Tyr Ser Asp Phe Trp
 515 520 525
 Trp Lys Gly Lys Leu Val Phe Lys Ala Lys Leu Arg Ala Ser His Thr
 530 535 540
 Trp Asn Pro Ile Gln Gln Met Ser Ile Asn Val Asp Asn Gln Phe Asn

545						550													560
Tyr	Val	Pro	Ser	Asn 565	Ile	Gly	Gly	Met	Lys 570	Ile	Val	Tyr	Glu	Lys 575	Ser				
Gln	Leu	Ala	Pro	Arg 580	Lys	Leu	Tyr												
<210>	4																		
<211>	584																		
<212>	PRT																		
<213>	Secuencia artificial																		
<220>																			
<223>	VP2 del CPV no truncado en el pMEB072																		
<400>	4																		
Met 1	Ser	Asp	Gly	Ala 5	Val	Gln	Pro	Asp	Gly 10	Gly	Gln	Pro	Ala	Val 15	Arg				
Asn	Glu	Arg	Ala 20	Thr	Gly	Ser	Gly	Asn 25	Gly	Ser	Gly	Gly	Gly 30	Gly	Gly	Gly			
Gly	Gly	Ser 35	Gly	Gly	Val	Gly	Ile 40	Ser	Thr	Gly	Thr	Phe 45	Asn	Asn	Gln				
Thr 50	Glu	Phe	Lys	Phe	Leu	Glu 55	Asn	Gly	Trp	Val	Glu 60	Ile	Thr	Ala	Asn				
Ser 65	Ser	Arg	Leu	Val	His 70	Leu	Asn	Met	Pro	Glu 75	Ser	Glu	Asn	Tyr	Arg 80				
Arg	Val	Val	Val	Asn 85	Asn	Leu	Asp	Lys	Thr 90	Ala	Val	Asn	Gly	Asn 95	Met				
Ala	Leu	Asp	Asp 100	Thr	His	Ala	Gln	Ile 105	Val	Thr	Pro	Trp	Ser 110	Leu	Val				
Asp	Ala	Asn 115	Ala	Trp	Gly	Val	Trp 120	Phe	Asn	Pro	Gly	Asp 125	Trp	Gln	Leu				
Ile 130	Val	Asn	Thr	Met	Ser	Glu 135	Leu	His	Leu	Val	Ser 140	Phe	Glu	Gln	Glu				
Ile 145	Phe	Asn	Val	Val	Leu 150	Lys	Thr	Val	Ser	Glu 155	Ser	Ala	Thr	Gln	Pro 160				
Pro	Thr	Lys	Val 165	Tyr	Asn	Asn	Asp	Leu	Thr 170	Ala	Ser	Leu	Met	Val 175	Ala				
Leu	Asp	Ser 180	Asn	Asn	Thr	Met	Pro	Phe 185	Thr	Pro	Ala	Ala	Met 190	Arg	Ser				
Glu	Thr	Leu 195	Gly	Phe	Tyr	Pro	Trp 200	Lys	Pro	Thr	Ile 205	Pro	Thr	Pro	Trp				
Arg 210	Tyr	Tyr	Phe	Gln	Trp	Asp 215	Arg	Thr	Leu	Ile	Pro 220	Ser	His	Thr	Gly				
Thr 225	Ser	Gly	Thr	Pro	Thr 230	Asn	Ile	Tyr	His	Gly 235	Thr	Asp	Pro	Asp	Asp 240				
Val	Gln	Phe	Tyr	Thr	Ile	Glu	Asn	Ser	Val	Pro	Val	His	Leu	Leu	Arg				

245	250	255
Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys Lys Pro 260 265 270		
Cys Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu Gly Leu Pro 275 280 285		
Pro Phe Leu Asn Ser Leu Pro Gln Ala Glu Gly Gly Thr Asn Phe Gly 290 295 300		
Tyr Ile Gly Val Gln Gln Asp Lys Arg Arg Gly Val Thr Gln Met Gly 305 310 315 320		
Asn Thr Asn Tyr Ile Thr Glu Ala Thr Ile Met Arg Pro Ala Glu Val 325 330 335		
Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe Glu Ala Ser Thr Gln Gly Pro 340 345 350		
Phe Lys Thr Pro Ile Ala Ala Gly Arg Gly Gly Ala Gln Thr Asp Glu 355 360 365		
Asn Gln Ala Ala Asp Gly Asp Pro Arg Tyr Ala Phe Gly Arg Gln His 370 375 380		
Gly Gln Lys Thr Thr Thr Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr 385 390 395 400		
Ile Ala His Gln Asp Thr Gly Arg Tyr Pro Glu Gly Asp Trp Ile Gln 405 410 415		
Asn Ile Asn Phe Asn Leu Pro Val Thr Glu Asp Asn Val Leu Leu Pro 420 425 430		
Thr Asp Pro Ile Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe 435 440 445		
Asn Thr Tyr Gly Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr 450 455 460		
Pro Asn Gly Gln Ile Trp Asp Lys Glu Phe Asp Thr Asp Leu Lys Pro 465 470 475 480		
Arg Leu His Val Asn Ala Pro Phe Val Cys Gln Asn Asn Cys Pro Gly 485 490 495		
Gln Leu Phe Val Lys Val Ala Pro Asn Leu Thr Asn Glu Tyr Asp Pro 500 505 510		
Asp Ala Ser Ala Asn Met Ser Arg Ile Val Thr Tyr Ser Asp Phe Trp 515 520 525		
Trp Lys Gly Lys Leu Val Phe Lys Ala Lys Leu Arg Ala Ser His Thr 530 535 540		
Trp Asn Pro Ile Gln Gln Met Ser Ile Asn Val Asp Asn Gln Phe Asn 545 550 555 560		
Tyr Val Pro Ser Asn Ile Gly Gly Met Lys Ile Val Tyr Glu Lys Ser 565 570 575		

Gln Leu Ala Pro Arg Lys Leu Tyr
580

<210> 5
<211> 1752
<212> ADN
<213> Secuencia artificial

<220>

<223> Ácidos nucleicos de codones optimizados del pMEB072 que codifica la VP2 del CPV (SEQ ID N°: 4)

<400> 5
atgtccgacg gtgctgtgca gcccagcggg gccagcccg ctgtgcgtaa cgagcgtgct 60
accggttccg gtaacggttc aggcggaggt ggaggtggtg gttccggcgg tgtgggcatc 120
tccaccggca ccttcaacaa ccagaccgag ttcaagttcc tcgagaacgg ttgggtggag 180
atcacgcgta actcctcccg tctggtgcac ctgaacatgc ccgagtcga gaactaccgt 240
cgtgtggtgg tgaacaacct ggacaagacc gctgtgaacg gtaacatggc tctggacgac 300
acccacgctc agatcgtgac cccctggtcc ctggtggacg ctaacgcttg gggcgtgtgg 360
ttcaaccccg gtgactggca gctgatcgtg aacacatgt ccgagctgca cctggtgtcc 420
ttcgagcaag agatcttcaa cgtcgtcctc aagaccgtgt ccgagtcgc taccagccc 480
cccaccaagg tgtacaacaa cgactgacc gcttccctga tggctcgtct ggactccaac 540
aacacatgc ccttcaaccc cgtgctatg cgttccgaga ccctgggctt ctaccctgg 600
aagcccacca tccccacccc ctggcggttac tacttccagt gggaccgtac cctgatcccc 660
tcccacaccg gtacttccg cacccccacc aacatctacc acggcaccga ccccgacgac 720
gtgcagttct acaccatcga gaactccgtg cccgtgcacc tgctgcgtac cggtgacgag 780
ttcgctaccg gaaccttctt cttcgactgc aagccctgcc gtctgacca cacctggcag 840
accaaccgtg ctctgggtct gcctccctc ctgaactccc tgcccaggc tgaggggtggc 900
accaacttcg gttacatcgg tgtgcagcag gacaagcgtc gtggtgtgac ccagatgggt 960
aacaccaact acatcacga ggctaccatc atgcgtcccg ctgaggtcgg ctactccgt 1020
ccctactact ccttcgaggc ttccaccag gccccttca agaccccat cgtgctggt 1080
cgtggtggtg ctcagaccga cgagaaccag gctgctgacg gtgaccccg ttacgctttc 1140
ggtcgtcagc acggcaaaa gaccaccacc accggcgaga ccccgagcg ttccacctac 1200
atcgctcacc aggacaccg tcgttaccac gagggcgact ggattcagaa catcaacttc 1260
aacctgccc tgaccgagga caacgtgctg ctgcccaccg acccatcgg tggaagacc 1320
ggtatcaact aactaacat cttcaacacc tacggctctc tgaccgtct gaacaacgtg 1380
cccccggtg acccaacgg ccagatctgg gacaaggagt tcgacaccga cctgaagccc 1440
cgtctgcacg tgaacgctcc cttcgtgtgc cagaacaact gccctggcca gctgttcgtc 1500
aaggtggccc ccaacctgac caacgagtac gaccctgacg cttccgctaa catgtcccgt 1560
atcgtgacct actccgactt ctggtggaag ggcaagctgg tgttcaaggc caagctgcgt 1620
gtttctcaca cctggaaccc catccagcag atgtccatca acgtggacaa ccagttcaac 1680
tacgtgccct ccaacatcgg tggaatgaag atcgtgtacg agaagtccca gctggctccc 1740
cgtaagctgt ac 1752

<210> 6
<211> 578
<212> PRT
<213> Secuencia artificial

<220>

<223> VP2 del CPV truncada en el pMEB073

<400> 6

Met Leu Lys Gly Gly Gln Pro Ala Val Arg Asn Glu Arg Ala Thr Gly
1 5 10 15

Ser Gly Asn Gly Ser Gly Gly Gly Gly Gly Gly Ser Gly Gly Val
20 25 30

Gly Ile Ser Thr Gly Thr Phe Asn Asn Gln Thr Glu Phe Lys Phe Leu
35 40 45

Glu Asn Gly Trp Val Glu Ile Thr Ala Asn Ser Ser Arg Leu Val His
50 55 60

Leu Asn Met Pro Glu Ser Glu Asn Tyr Arg Arg Val Val Val Asn Asn
65 70 75 80

Leu Asp Lys Thr Ala Val Asn Gly Asn Met Ala Leu Asp Asp Thr His
85 90 95

Ala Gln Ile Val Thr Pro Trp Ser Leu Val Asp Ala Asn Ala Trp Gly
100 105 110

Val Trp Phe Asn Pro Gly Asp Trp Gln Leu Ile Val Asn Thr Met Ser
115 120 125

Glu Leu His Leu Val Ser Phe Glu Gln Glu Ile Phe Asn Val Val Leu
130 135 140

Lys Thr Val Ser Glu Ser Ala Thr Gln Pro Pro Thr Lys Val Tyr Asn
145 150 155 160

Asn Asp Leu Thr Ala Ser Leu Met Val Ala Leu Asp Ser Asn Asn Thr
165 170 175

Met Pro Phe Thr Pro Ala Ala Met Arg Ser Glu Thr Leu Gly Phe Tyr
180 185 190

Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp Arg Tyr Tyr Phe Gln Trp
195 200 205

Asp Arg Thr Leu Ile Pro Ser His Thr Gly Thr Ser Gly Thr Pro Thr
210 215 220

Asn Ile Tyr His Gly Thr Asp Pro Asp Asp Val Gln Phe Tyr Thr Ile
225 230 235 240

Glu Asn Ser Val Pro Val His Leu Leu Arg Thr Gly Asp Glu Phe Ala
245 250 255

Thr Gly Thr Phe Phe Phe Asp Cys Lys Pro Cys Arg Leu Thr His Thr
260 265 270

Trp Gln Thr Asn Arg Ala Leu Gly Leu Pro Pro Phe Leu Asn Ser Leu
275 280 285

Pro Gln Ala Glu Gly Gly Thr Asn Phe Gly Tyr Ile Gly Val Gln Gln
290 295 300

Asp Lys Arg Arg Gly Val Thr Gln Met Gly Asn Thr Asn Tyr Ile Thr
305 310 315 320

Glu Ala Thr Ile Met Arg Pro Ala Glu Val Gly Tyr Ser Ala Pro Tyr
 325 330 335
 Tyr Ser Phe Glu Ala Ser Thr Gln Gly Pro Phe Lys Thr Pro Ile Ala
 340 345 350
 Ala Gly Arg Gly Gly Ala Gln Thr Asp Glu Asn Gln Ala Ala Asp Gly
 355 360 365
 Asp Pro Arg Tyr Ala Phe Gly Arg Gln His Gly Gln Lys Thr Thr Thr
 370 375 380
 Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr Ile Ala His Gln Asp Thr
 385 390 395 400
 Gly Arg Tyr Pro Glu Gly Asp Trp Ile Gln Asn Ile Asn Phe Asn Leu
 405 410 415
 Pro Val Thr Glu Asp Asn Val Leu Leu Pro Thr Asp Pro Ile Gly Gly
 420 425 430
 Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe Asn Thr Tyr Gly Pro Leu
 435 440 445
 Thr Ala Leu Asn Asn Val Pro Pro Val Tyr Pro Asn Gly Gln Ile Trp
 450 455 460
 Asp Lys Glu Phe Asp Thr Asp Leu Lys Pro Arg Leu His Val Asn Ala
 465 470 475 480
 Pro Phe Val Cys Gln Asn Asn Cys Pro Gly Gln Leu Phe Val Lys Val
 485 490 495
 Ala Pro Asn Leu Thr Asn Glu Tyr Asp Pro Asp Ala Ser Ala Asn Met
 500 505 510
 Ser Arg Ile Val Thr Tyr Ser Asp Phe Trp Trp Lys Gly Lys Leu Val
 515 520 525
 Phe Lys Ala Lys Leu Arg Ala Ser His Thr Trp Asn Pro Ile Gln Gln
 530 535 540
 Met Ser Ile Asn Val Asp Asn Gln Phe Asn Tyr Val Pro Ser Asn Ile
 545 550 555 560
 Gly Gly Met Lys Ile Val Tyr Glu Lys Ser Gln Leu Ala Pro Arg Lys
 565 570 575

Leu Tyr

<210> 7

<211> 1536

<212> ADN

<213> Secuencia artificial

<220>

<223> Secuencia de ácidos nucleicos de codones optimizados del pMEB073 que codifica la VP2 del CPV (SEQ ID N°: 6)

<400> 7

atgcccgaga gcgagaacta ccggagagtg gtggtgaaca acctggacaa gaccgccgtg 60

aacggcaata tggccctgga tgacaccac gccagatcg tgacccttg gagcctggtg 120

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gacgccaacg cctggggagt gtggttcaac cctggcgact ggcagctgat cgtgaacacc 180
atgagcgagc tgcacctggt gtccttcgag caggagattt tcaacgtggt gctgaaaacc 240
gtgtccgaga gcgccaccca gccccccacc aaagtgtaca acaacgacct gaccgcctcc 300
ctgatggtgg ccctggacag caacaacacc atgcccttca cccctgccgc catgagaagc 360
gagaccctgg gcttctaccc ttggaagccc accatcccca ccccttggcg gtactacttc 420
cagtgggaca ggacctgat ccccgccac accggcacca gcggcacccc taccaatatc 480
taccacggca ccgacctga tgactgagc ttctacacca tcgagaacag cgtgcctgtg 540
cacctgctga gaaccggcga cgagttcgcc accggcacat tcttcttcga ctgcaagccc 600
tgcagactga cccacacctg gcagaccaac agagccctgg gcctgcctcc tttcctgaac 660
agcctgcccc aggccgaggg cggcaccaac ttcggctaca tcggcggtga gcaggacaag 720
agaagaggcg tgacctgat gggcaacacc aactacatca ccgaggccac catcatgaga 780
cccgccgaag tgggctacag cgcctctac tacagcttcg aggccagcac ccagggcccc 840
ttcaagacct ccatcgccgc tggcagaggc ggagcccaga ccgacgagaa ccaggccgcc 900
gacggcgacc ccagatacgc cttcggcaga cagcacggcc agaaaaccac caccaccggc 960
gagacccccg agagattcac ctacatcgcc caccaggaca ccggcagata ccccgagggc 1020
gactggattc agaacatcaa cttcaacctg cccgtgaccg aggataatgt gctgctgccc 1080
accgacccca tcggcggcaa gaccggcadc aactacacca acatcttcaa cacctacggc 1140
cccctgaccg ccctgaataa cgtgcccccc gtgtacccca acggccagat ttgggacaag 1200
gagttcgaca ccgacctgaa gcctaggctg cacgtgaatg ccccttcgtg gtgtcagaac 1260
aactgcctg gccagctgtt tgtgaaagtg gcccacaacc tgaccaacga gtacgatcct 1320
gacgccagcg ccaacatgag ccgcatgctg acctacagcg acttctggtg gaagggcaag 1380
ctggtgttca aggccaagct gagagccagc cacacatgga accccatcca gcagatgagc 1440
atcaacgtgg acaaccagtt caactacgtg cccagcaata tcggcgggcat gaagatcgtg 1500
tacgagaaga gccagctggc ccccgagaaag ctgtac 1536

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<210> 8
<211> 584
<212> PRT
<213> Secuencia artificial

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<220>
<223> GenBank: AHW47988.1

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<400> 8

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Met Ser Asp Gly Ala Val Gln Pro Asp Gly Gly Gln Pro Ala Val Arg
1           5           10          15

```

```

Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly Gly Gly
20          25          30

```

```

Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe Asn Asn Gln
35          40          45

```

```

Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu Ile Thr Ala Asn
50          55          60

```

```

Ser Ser Arg Leu Val His Leu Asn Met Pro Glu Ser Glu Asn Tyr Lys
65          70          75          80

```

```

Arg Val Val Val Asn Asn Met Asp Lys Thr Ala Val Lys Gly Asn Met
85          90          95

```

Ala Leu Asp Asp Thr His Val Gln Ile Val Thr Pro Trp Ser Leu Val
100 105 110

Asp Ala Asn Ala Trp Gly Val Trp Phe Asn Pro Gly Asp Trp Gln Leu
115 120 125

Ile Val Asn Thr Met Ser Glu Leu His Leu Val Ser Phe Glu Arg Glu
130 135 140

Ile Phe Asn Val Val Leu Lys Thr Val Ser Glu Ser Ala Thr Gln Pro
145 150 155 160

Pro Thr Lys Val Tyr Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala
165 170 175

Leu Asp Ser Asn Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser
180 185 190

Glu Thr Leu Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp
195 200 205

Arg Tyr Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly
210 215 220

Thr Ser Gly Thr Pro Thr Asn Val Tyr His Gly Ser Asp Pro Asp Asp
225 230 235 240

Val Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu Arg
245 250 255

Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys Lys Pro
260 265 270

Cys Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu Gly Leu Pro
275 280 285

Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ile Thr Asn Phe Gly
290 295 300

Asp Ile Gly Val Gln Gln Asp Lys Arg Arg Gly Val Thr Gln Met Gly
305 310 315 320

Asn Thr Asp Tyr Ile Thr Glu Ala Thr Ile Met Arg Pro Ala Glu Val
325 330 335

Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe Glu Ala Ser Thr Gln Gly Pro
340 345 350

Phe Lys Thr Pro Ile Ala Ala Gly Arg Gly Gly Ala Gln Thr Asp Glu
355 360 365

Asn Gln Ala Ala Asp Gly Asp Pro Lys Tyr Ala Phe Gly Arg Gln His
370 375 380

Gly Gln Lys Thr Thr Thr Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr
385 390 395 400

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

Asn Ile Asn Phe Asn Leu Pro Val Thr Lys Asp Asn Val Leu Leu Pro

420 425 430
 Thr Asp Pro Ile Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe
 435 440 445
 Asn Thr Tyr Gly Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr
 450 455 460
 Pro Asn Gly Gln Ile Trp Asp Lys Glu Phe Asp Thr Asp Leu Lys Pro
 465 470 475 480
 Arg Leu His Val Asn Ala Pro Phe Val Cys Gln Asn Asn Cys Pro Gly
 485 490 495
 Gln Leu Phe Val Lys Val Ala Pro Asn Leu Thr Asn Glu Tyr Asp Pro
 500 505
 Asp Ala Ser Ala Asn Met Ser Arg Ile Val Thr Tyr Ser Asp Phe Trp
 515 520 525
 Trp Lys Gly Lys Leu Val Phe Lys Ala Lys Leu Arg Ala Ser His Thr
 530 535 540
 Trp Asn Pro Ile Gln Gln Met Ser Ile Asn Val Asp Asn Gln Phe Asn
 545 550 555 560
 Tyr Val Pro Asn Asn Ile Gly Ala Met Lys Ile Val Tyr Glu Lys Ser
 565 570 575
 Gln Leu Ala Pro Arg Lys Leu Tyr
 580
 <210> 9
 <211> 584
 <212> PRT
 <213> Secuencia artificial
 <220>
 <223> GenBank: AHW47989.1
 <400> 9
 Met Ser Asp Gly Ala Val Gln Pro Asp Gly Gly Gln Pro Ala Val Arg
 1 5 10 15
 Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly Gly Gly
 20 25 30
 Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe Asn Asn Gln
 35 40 45
 Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu Ile Thr Ala Asn
 50 55 60
 Ser Ser Arg Leu Val His Leu Asn Met Pro Glu Ser Glu Asn Tyr Lys
 65 70 75 80
 Arg Val Val Val Asn Asn Met Asp Lys Thr Ala Val Lys Gly Asn Met
 85 90 95
 Ala Leu Asp Asp Thr His Val Gln Ile Val Thr Pro Trp Ser Leu Val
 100 105 110
 Asp Ala Asn Ala Trp Gly Val Trp Phe Asn Pro Gly Asp Trp Gln Leu

115	120	125
Ile Val Asn Thr Met Ser Glu 130	Leu His Leu Val Ser Phe 135	Glu Gln Glu 140
Ile Phe Asn Val Val Leu Lys Thr Val Ser Glu Ser Ala Thr Gln Pro 145	150	155 160
Pro Thr Lys Val Tyr Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala 165	170	175
Leu Asp Ser Asn Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser 180	185	190
Glu Thr Leu Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp 195	200	205
Arg Tyr Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly 210	215	220
Thr Ser Gly Thr Pro Thr Asn Val Tyr His Gly Ser Asp Pro Asp Asp 225	230	235 240
Val Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu Arg 245	250	255
Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys Lys Pro 260	265	270
Cys Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu Gly Leu Pro 275	280	285
Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ile Thr Asn Phe Gly 290	295	300
Asp Ile Gly Val Gln Gln Asp Lys Arg Arg Gly Val Thr Gln Met Gly 305	310	315 320
Asn Thr Asp Tyr Ile Thr Glu Ala Thr Ile Met Arg Pro Ala Glu Val 325	330	335
Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe Glu Ala Ser Thr Gln Gly Pro 340	345	350
Phe Lys Thr Pro Ile Ala Ala Gly Arg Gly Gly Ala Gln Thr Asp Glu 355	360	365
Asn Gln Ala Ala Asp Gly Asp Pro Lys Tyr Ala Phe Gly Arg Gln His 370	375	380
Gly Gln Lys Thr Thr Thr Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr 385	390	395 400
Ile Ser His Gln Asp Thr Gly Arg Tyr Pro Glu Gly Asp Trp Ile Gln 405	410	415
Asn Ile Asn Phe Asn Leu Pro Val Thr Lys Asp Asn Val Leu Leu Pro 420	425	430
Thr Asp Pro Ile Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe 435	440	445

Asn Thr Tyr Gly Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr
 450 455 460

Pro Asn Gly Gln Ile Trp Asp Lys Glu Phe Asp Thr Asp Leu Lys Pro
 465 470 475 480

Arg Leu His Val Asn Ala Pro Phe Val Cys Gln Asn Asn Cys Pro Gly
 485 490 495

Gln Leu Phe Val Lys Val Ala Pro Asn Leu Thr Asn Glu Tyr Asp Pro
 500 505 510

Asp Ala Ser Ala Asn Met Ser Arg Ile Val Thr Tyr Ser Asp Phe Trp
 515 520 525

Trp Lys Gly Lys Leu Val Phe Lys Ala Lys Leu Arg Ala Ser His Thr
 530 535 540

Trp Asn Pro Ile Gln Gln Met Ser Ile Asn Val Asp Asn Gln Phe Asn
 545 550 555 560

Tyr Val Pro Asn Asn Ile Gly Ala Met Lys Ile Val Tyr Glu Lys Ser
 565 570 575

Gln Leu Ala Pro Arg Lys Leu Tyr
 580

<210> 10
 <211> 584
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> GenBank: ADA61118.1

<400> 10

Met Ser Asp Gly Ala Val Gln Pro Asp Gly Gly Gln Pro Ala Val Arg
 1 5 10 15

Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly Gly Gly
 20 25 30

Gly Gly Ser Gly Gly Gly Gly Ile Ser Thr Gly Ala Phe Asn Asn Gln
 35 40 45

Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu Ile Thr Ala Asn
 50 55 60

Ser Ser Arg Leu Val His Leu Asn Met Pro Glu Ser Glu Asn Tyr Arg
 65 70 75 80

Arg Val Val Val Asn Asn Met Asp Lys Thr Ala Val Asn Gly Asn Met
 85 90 95

Ala Leu Asp Asp Ile His Ala Gln Ile Val Thr Pro Trp Ser Leu Val
 100 105 110

Asp Ala Asn Ala Trp Gly Val Trp Phe Asn Pro Gly Asp Trp Gln Leu
 115 120 125

Ile Val Asn Thr Met Ser Glu Leu His Leu Val Ser Phe Glu Gln Glu
 130 135 140

Ile Phe Asn Val Val Leu Lys Thr Val Ser Glu Ser Ala Thr Gln Pro
 145 150 155 160

 Pro Thr Lys Val Tyr Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala
 165 170 175

 Leu Asp Ser Asn Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser
 180 185 190

 Glu Thr Leu Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp
 195 200 205

 Arg Tyr His Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly
 210 215 220

 Thr Ser Gly Thr Pro Thr Asn Ile Tyr His Gly Thr Asp Pro Asp Asp
 225 230 235 240

 Val Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu Arg
 245 250 255

 Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys Thr Pro
 260 265 270

 Cys Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu Gly Leu Pro
 275 280 285

 Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ala Thr Asn Phe Gly
 290 295 300

 Asp Ile Gly Val Gln Gln Asp Lys Arg Arg Gly Val Thr Gln Met Gly
 305 310 315 320

 Asn Thr Asn Tyr Ile Thr Glu Ala Thr Ile Met Arg Pro Ala Glu Val
 325 330 335

 Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe Glu Ala Ser Thr Gln Gly Pro
 340 345 350

 Phe Lys Thr Pro Ile Ala Ala Gly Arg Gly Gly Ala Gln Thr Asp Glu
 355 360 365

 Asn Gln Ala Ala Asp Gly Glu Pro Arg Tyr Ala Phe Gly Arg Gln His
 370 375 380

 Gly Gln Lys Thr Thr Thr Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr
 385 390 395 400

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

 Asn Ile Asn Phe Asn Leu Pro Val Thr Asn Asp Asn Val Leu Leu Pro
 420 425 430

 Thr Asp Pro Ile Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe
 435 440 445

 Asn Thr Tyr Gly Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr
 450 455 460

 Pro Asn Gly Gln Ile Trp Asp Lys Glu Phe Asp Thr Asp Leu Lys Pro

[illegible]

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<210> 11
<211> 11387
<212> ADN
<213> Secuencia artificial
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<220>
<223> pMEB072

<400>	11	
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gaaagcacgt	gtaaaatggt tcccgcgcgt tggcacaact atttacaatg cggccaagt	120
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