

LISTADO DE SECUENCIAS

<110> KALIVIR IMMUNOTHERAPEUTICS, INC.

<120> VIRUS ONCOLÍTICOS PARA LA EXPRESIÓN MODIFICADA DEL MHC

<130> 199249-716601

<140>

<141>

<150> 63/182,243

<151> 2021-04-30

<160> 39

<170> PatentIn versión 3.5

<210> SEQ ID NO: 1

<211> 130

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 1

tcactaattc caaaccacc cgctttttat agtaagtttt tcaccataa ataataaata 60

caataattaa tttctcgtaa aagtagaaaa tatattctaa tttattgcac ggtaaggaag 120

tagatcataa 130

<210> SEQ ID NO: 2

<211> 210

<212> ADN

<213> Virus de la viruela vacuna

<400> 2

atgttcatca tgcgcgagag catttacgc gtgatgattg tcattttgta tttgagcttg 60

atttcttcgt ttttggttat ctgctctatg gagcacggct acttccagga gggcatcagc 120

cgcttcaaga tttgtcccta tcattggtat aaacaacaca tgagtttatt gtttcgctgt 180

tactatcaca agctggatag tatcatctag 210

<210> SEQ ID NO: 3

<211> 69

<212> PRT

<213> Virus de la viruela vacuna

<400> 3

Met Phe Ile Met Arg Glu Ser Ile Tyr Arg Val Met Ile Val Ile Leu
1 5 10 15

Tyr Leu Ser Leu Ile Ser Ser Phe Leu Val Ile Cys Ser Met Glu His
20 25 30

Gly Tyr Phe Gln Glu Gly Ile Ser Arg Phe Lys Ile Cys Pro Tyr His
35 40 45

Trp Tyr Lys Gln His Met Ser Leu Leu Phe Arg Arg Tyr Tyr His Lys
 50 55 60

Leu Asp Ser Ile Ile
 65

<210> SEQ ID NO: 4

<211> 645

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 4

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ggcaaaggag atcctaagaa gccgagaggc aaaatgtcat catatgcatt cttcgtgcaa      60
acttgctggg aggagcataa gaagaagcac ccagatgctg cagtcaactt cgctgagttt      120
gcaaagaagt gcgctgagag gtggaagacc atggcagcta aagagaaagg aaaatttgaa      180
gatatggcaa aagcggacaa ggcccgttat gaaagagaaa tgaaaaccta tatccctccc      240
aaaggggaga caaaaaagaa gttcaaggac cccaatgcac ccaagaggcc tccttcggcc      300
ttcttcctct tctgctctga gtatcgccca aaaatcaaag gagaacatcc tggcctgtcc      360
attggtgatg ttgcgaagaa actgggagag atgtggaata aactgctgc agatgacaag      420
cagccttatg aaaagaaggc tgcgaagctg aaggaaaaat atgaaaagga tattgctgca      480
tatcgagcta aaggaaagcc tgatgcagca aaaaaggagg ttgtcaaggc tgaaaaagcg      540
aagaaaaaga aggaagagga ggaagatgag gaagatgaag aggatgagga ggaggaggaa      600
gatgaagaag atgaagatga agaagaagat gatgatgatg aataa                      645
  
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<210> SEQ ID NO: 5

<211> 214

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido sintético

<400> 5

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Gly Lys Gly Asp Pro Lys Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala
1          5          10          15
Phe Phe Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His Pro Asp
          20          25          30
Ala Ala Val Asn Phe Ala Glu Phe Ala Lys Lys Cys Ala Glu Arg Trp
          35          40          45
Lys Thr Met Ala Ala Lys Glu Lys Gly Lys Phe Glu Asp Met Ala Lys
          50          55          60
Ala Asp Lys Ala Arg Tyr Glu Arg Glu Met Lys Thr Tyr Ile Pro Pro
65          70          75          80
Lys Gly Glu Thr Lys Lys Lys Phe Lys Asp Pro Asn Ala Pro Lys Arg
          85          90          95
  
```

Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu Tyr Arg Pro Lys Ile
100 105 110

Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys Lys Leu
115 120 125

Gly Glu Met Trp Asn Asn Thr Ala Ala Asp Asp Lys Gln Pro Tyr Glu
130 135 140

Lys Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile Ala Ala
145 150 155 160

Tyr Arg Ala Lys Gly Lys Pro Asp Ala Ala Lys Lys Gly Val Val Lys
165 170 175

Ala Glu Lys Ala Lys Lys Lys Lys Glu Glu Glu Glu Asp Glu Glu Asp
180 185 190

Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Asp Glu Asp Glu Glu
195 200 205

Glu Asp Asp Asp Asp Glu
210

<210> SEQ ID NO: 6

<211> 54

<212> ADN

<213> Desconocido

<220>

<223> Descripción de Desconocido: Secuencia señal derivada de IgE

<400> 6

atggactgga catggattct ctttctagtg gccgcagcca caaggggtcca ctcc

54

<210> SEQ ID NO: 7

<211> 18

<212> PRT

<213> Desconocido

<220>

<223> Descripción de Desconocido: Secuencia señal derivada de IgE

<400> 7

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser

<210> SEQ ID NO: 8

<211> 699

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 8

atggactgga catggattct ctttctagtg gccgcagcca caaggggtcca ctccggcaaa

60

ggagatccta agaagccgag aggcaaaatg tcatcatatg cattcttcgt gcaaacttgt

120

```

cgggaggagc ataagaagaa gcaccagat gctgcagtca acttcgctga gtttgcaaag      180
aagtgcgctg agaggtggaa gaccatggca gctaaagaga aaggaaaatt tgaagatatg      240
gcaaaagcgg acaaggcccg ttatgaaaga gaaatgaaaa cctatatccc tcccaaaggg      300
gagacaaaaa agaagttcaa ggacccaat gcaccaaga ggccctccttc ggcccttcttc      360
ctcttctgct ctgagtatcg cccaaaaatc aaaggagaac atcctggcct gtccattggt      420
gatgttgcca agaaactggg agagatgtgg aataacactg ctgcagatga caagcagcct      480
tatgaaaaga aggctgcgaa gctgaaggaa aaatatgaaa aggatattgc tgcatatcga      540
gctaaaggaa agcctgatgc agcaaaaaag ggagttgtca aggctgaaaa agcgaagaaa      600
aagaaggaag aggaggaaga tgaggaagat gaagaggatg aggaggagga ggaagatgaa      660
gaagatgaag atgaagaaga agatgatgat gatgaataa                             699

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<210> SEQ ID NO: 9

<211> 232

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido sintético

<400> 9

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Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1           5           10           15

```

```

His Ser Gly Lys Gly Asp Pro Lys Lys Pro Arg Gly Lys Met Ser Ser
          20           25           30

```

```

Tyr Ala Phe Phe Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His
      35           40           45

```

```

Pro Asp Ala Ala Val Asn Phe Ala Glu Phe Ala Lys Lys Cys Ala Glu
      50           55           60

```

```

Arg Trp Lys Thr Met Ala Ala Lys Glu Lys Gly Lys Phe Glu Asp Met
65           70           75           80

```

```

Ala Lys Ala Asp Lys Ala Arg Tyr Glu Arg Glu Met Lys Thr Tyr Ile
      85           90           95

```

```

Pro Pro Lys Gly Glu Thr Lys Lys Lys Phe Lys Asp Pro Asn Ala Pro
      100          105          110

```

```

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

```

```

Lys Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys
      130          135          140

```

```

Lys Leu Gly Glu Met Trp Asn Asn Thr Ala Ala Asp Asp Lys Gln Pro
      145          150          155          160

```

```

Tyr Glu Lys Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile
      165          170          175

```

Ala Ala Tyr Arg Ala Lys Gly Lys Pro Asp Ala Ala Lys Lys Gly Val
180 185 190

Val Lys Ala Glu Lys Ala Lys Lys Lys Glu Glu Glu Glu Asp Glu
195 200 205

Glu Asp Glu Glu Asp Glu Glu Glu Glu Asp Glu Glu Asp Glu Asp
210 215 220

Glu Glu Glu Asp Asp Asp Asp Glu
225 230

<210> SEQ ID NO: 10

<211> 162

<212> PRT

<213> *Homo sapiens*

<400> 10

Met Arg Ile Ser Lys Pro His Leu Arg Ser Ile Ser Ile Gln Cys Tyr
1 5 10 15

Leu Cys Leu Leu Leu Asn Ser His Phe Leu Thr Glu Ala Gly Ile His
20 25 30

Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala
35 40 45

Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
50 55 60

Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
65 70 75 80

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
85 90 95

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
100 105 110

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
115 120 125

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
130 135 140

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
145 150 155 160

Thr Ser

<210> SEQ ID NO: 11

<211> 465

<212> ADN

<213> *Mus sp.*

<400> 11

atgttccatg tttcttttag atatatcttt ggaattcctc cactgatcct tgttctgctg 60

cctgtcacat catctgagtg ccacattaaa gacaaagaag gtaaagcata tgagagtgta 120

ctgatgatca gcatcgatga attggacaaa atgacaggaa ctgatagtaa ttgcccgaat 180

aatgaaccaa acttttttag aaaacatgta tgtgatgata caaaggaagc tgcttttcta 240
aatcgtgctg ctcgcaagtt gaagcaatth cttaaaatga atatcagtga agaattcaat 300
gtccacttac taacagtatc acaaggcaca caaacactgg tgaactgcac aagtaaggaa 360
gaaaaaaacg taaaggaaca gaaaaagaat gatgcatggt tcctaaagag actactgaga 420
gaaataaaaa cttgttggaa taaaattttg aagggcagta tataa 465

<210> SEQ ID NO: 12

<211> 534

<212> ADN

<213> *Homo sapiens*

<400> 12

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ccagtagcat catctgattg tgatattgaa ggtaaagatg gcaaacaata tgagagtgtt 120
ctaattggtc gcatcgatca attattggac agcatgaaag aaattggttag caattgcctg 180
aataatgaat ttaacttttt taaaagacat atctgtgatg ctaataagga aggtatgttt 240
ttattccgtg ctgctcgcaa gttgaggcaa tttcttaaaa tgaatagcac tgggtgatttt 300
gatctccact tattaaaagt ttcagaaggc acaacaatac tgttgaactg cactggccag 360
gttaaaggaa gaaaaccagc tgccctgggt gaagcccaac caacaaagag tttggaagaa 420
aataaatctt taaaggaaca gaaaaaactg aatgacttgt gtttcctaaa gagactatta 480
caagagataa aaacttggtg gaataaaatt ttgatgggca ctaaagaaca ctga 534

<210> SEQ ID NO: 13

<211> 154

<212> PRT

<213> *Mus sp.*

<400> 13

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
1 5 10 15
Leu Val Leu Leu Pro Val Thr Ser Ser Glu Cys His Ile Lys Asp Lys
20 25 30
Glu Gly Lys Ala Tyr Glu Ser Val Leu Met Ile Ser Ile Asp Glu Leu
35 40 45
Asp Lys Met Thr Gly Thr Asp Ser Asn Cys Pro Asn Asn Glu Pro Asn
50 55 60
Phe Phe Arg Lys His Val Cys Asp Asp Thr Lys Glu Ala Ala Phe Leu
65 70 75 80
Asn Arg Ala Ala Arg Lys Leu Lys Gln Phe Leu Lys Met Asn Ile Ser
85 90 95
Glu Glu Phe Asn Val His Leu Leu Thr Val Ser Gln Gly Thr Gln Thr
100 105 110
Leu Val Asn Cys Thr Ser Lys Glu Glu Lys Asn Val Lys Glu Gln Lys
115 120 125

Lys Asn Asp Ala Cys Phe Leu Lys Arg Leu Leu Arg Glu Ile Lys Thr
 130 135 140

Cys Trp Asn Lys Ile Leu Lys Gly Ser Ile
 145 150

<210> SEQ ID NO: 14

<211> 177

<212> PRT

<213> *Homo sapiens*

<400> 14

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Leu Pro Pro Leu Ile
 1 5 10 15

Leu Val Leu Leu Pro Val Ala Ser Ser Asp Cys Asp Ile Glu Gly Lys
 20 25 30

Asp Gly Lys Gln Tyr Glu Ser Val Leu Met Val Ser Ile Asp Gln Leu
 35 40 45

Leu Asp Ser Met Lys Glu Ile Gly Ser Asn Cys Leu Asn Asn Glu Phe
 50 55 60

Asn Phe Phe Lys Arg His Ile Cys Asp Ala Asn Lys Glu Gly Met Phe
 65 70 75 80

Leu Phe Arg Ala Ala Arg Lys Leu Arg Gln Phe Leu Lys Met Asn Ser
 85 90 95

Thr Gly Asp Phe Asp Leu His Leu Leu Lys Val Ser Glu Gly Thr Thr
 100 105 110

Ile Leu Leu Asn Cys Thr Gly Gln Val Lys Gly Arg Lys Pro Ala Ala
 115 120 125

Leu Gly Glu Ala Gln Pro Thr Lys Ser Leu Glu Glu Asn Lys Ser Leu
 130 135 140

Lys Glu Gln Lys Lys Leu Asn Asp Leu Cys Phe Leu Lys Arg Leu Leu
 145 150 155 160

Gln Glu Ile Lys Thr Cys Trp Asn Lys Ile Leu Met Gly Thr Lys Glu
 165 170 175

His

<210> SEQ ID NO: 15

<211> 1059

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 15

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tatgactcca tgaaggaacc ctgtttccgt gaagaaaatg ctaatttcaa taaaatcttc 120

ctgcccacca tctactccat catcttctta actggcattg tgggcaatgg attggtcac 180

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ctggtcatgg gttaccagaa gaaactgaga agcatgacgg acaagtacag gctgcacctg      240
tcagtggccg acctcctctt tgtcatcacg cttcccttct gggcagttga tgccgtggca      300
aactggtact ttgggaactt cctatgcaag gcagtccatg tcatctacac agtcaacctc      360
tacagcagtg tcctcatcct ggcccttcac agtctggacc gctacctggc catcgtccac      420
gccaccaaca gtcagaggcc aaggaagctg ttggctgaaa aggtggtcgc tgttggcgtc      480
tggatccctg ccctcctgct gactattccc gacttcatct ttgccaacgt cagtgaggca      540
gatgacagat atatctgtga ccgcttctac cccaatgact tgtgggtggg tgtgttccag      600
tttcagcaca tcatggttgg ccttctcctg cctgggtattg tcatcctgtc ctgctattgc      660
attatcatct ccaagctgtc aactccaag ggccaccaga agcgcaaggc cctcaagacc      720
acagtcatcc tcatcctggc tttcttcgcc tgttggctgc cttactacat tgggatcagc      780
atcgactcct tcatcctcct ggaaatcatc aagcaagggt gtgagtttga gaacactgtg      840
cacaagtgga tttccatcac cgaggcccta gctttcttcc actgttgtct gaaccccatc      900
ctctatgctt tccttggagc caaatTTaaa acctctgcc agcacgcact cacctctgtg      960
agcagagggt ccagcctcaa gatcctctcc aaaggaaagc gaggtggaca ttcactctgtt    1020
tccactgagt ctgagtcttc aagttttcac tccagctaa                                1059

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<210> SEQ ID NO: 16

<211> 1080

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 16

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ggagactatg actccaacaa ggaaccctgc ttccgggatg aaaacgtcca tttcaatagg      120
atcttcctgc ccaccatcta cttcatcatc ttcttgactg gcatagtcgg caatggattg      180
gtgatcctgg tcatgggtta ccagaagaag ctaaggagca tgacggacaa gtaccggctg      240
cacctgtcag tggctgacct cctctttgtc atcacactcc ccttctgggc agttgatgcc      300
atggctgact ggtacttttg gaaatTTTTg tgtaaggctg tccatatcat ctacactgtc      360
aacctctaca gcagcgttct catcctggcc ttcacagcc tggaccgata cctcgctatt      420
gtccacgcca ccaacagtca gaggccaagg aaactgctgg ctgaaaaggc agtcgctgtg      480
ggcgtctgga tcccagccct cctcctgact atacctgact tcatctttgc cgacgtcagc      540
cagggggaca tcagtcaggg ggatgacagg tacatctgtg accgccttta ccccgatagc      600
ctgtggatgg tgggttttca attccagcat ataatgggtg gtctcgtcct gcccggcac      660
gtcatcctct cctgttactg catcatcatc tctaagctgt cacactccaa gggccaccag      720

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```

aagcgcaagg ccctcaagac gacagtcac ctcacccatg cttctcttgc ctgctggctg      780
ccatattatg tggggatcag catcgactcc ttcatccttt tgggggtcat caagcaagga      840
tgtgacttcg agagcatcgt gcacaagtgg atctccatca cagaggccct cgccttcttc      900
cactgttgcc tgaaccccat cctctatgcc ttctctgggg ccaagttcaa aagctctgcc      960
cagcatgcac tcaactccat gagcagaggc tccagcctca agatcctttc caaaggaaag     1020
cggggtggac actcttccgt ctccacggag tcagaatcct ccagttttca ctccagctaa     1080

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<210> SEQ ID NO: 17

<211> 1059

<212> ADN

<213> *Homo sapiens*

<400> 17

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atggagggga tcagtatata cacttcagat aactacaccg aggaaatggg ctgaggggac      60
tatgactcca tgaaggaacc ctgtttccgt gaagaaaatg ctaatttcaa taaaatcttc     120
ctgcccacca tctactccat catctttctta actggcattg tgggcaatgg attggtcatc     180
ctggtcatgg gttaccagaa gaaactgaga agcatgacgg acaagtacag gctgcacctg     240
tcagtggccg acctcctctt tgtcatcacg cttcccttct gggcagttga tgccgtggca     300
aactggtact ttgggaactt cctatgcaag gcagtcocatg tcactctacac agtcaacctc     360
tacagcagtg tctcctcctt ggcccttcac agtctggacc gctacctggc catcgccac     420
gccaccaaca gtcagaggcc aaggaagctg ttggctgaaa aggtggtcta tgttggcgctc     480
tggatccctg cctcctgct gactattccc gacttcatct ttgccaacgt cagtgaggca     540
gatgacagat atatctgtga ccgcttctac cccaatgact tgtgggtggg tgtgttccag     600
tttcagcaca tcatggttgg ccttatcctg cctgggtattg tcacccctgtc ctgctattgc     660
attatcatct ccaagctgtc aactccaag ggccaccaga agcgcaaggc cctcaagacc     720
acagtcatcc tcacccctggc tttcttctgc tgttggctgc cttactacat tgggatcagc     780
atcgactcct tcacccctcct ggaaatcac aagcaagggt gtgagtttga gaacactgtg     840
cacaagtgga tttccatcac cgaggcccta gctttcttcc actgttgtct gaaccccatc     900
ctctatgctt tccttggagc caaattttaa acctctgccc agcacgcact cacctctgtg     960
agcagagggt ccagcctcaa gatcctctcc aaaggaaagc gaggtggaca ttcacctgtt    1020
tccactgagt ctgagtcttc aagttttcac tccagctaa                               1059

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<210> SEQ ID NO: 18

<211> 352

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido sintético

<400> 18

Met	Glu	Gly	Ile	Ser	Ile	Tyr	Thr	Ser	Asp	Asn	Tyr	Thr	Glu	Glu	Met	1	5	10	15
Gly	Ser	Gly	Asp	Tyr	Asp	Ser	Met	Lys	Glu	Pro	Cys	Phe	Arg	Glu	Glu	20	25	30	
Asn	Ala	Asn	Phe	Asn	Lys	Ile	Phe	Leu	Pro	Thr	Ile	Tyr	Ser	Ile	Ile	35	40	45	
Phe	Leu	Thr	Gly	Ile	Val	Gly	Asn	Gly	Leu	Val	Ile	Leu	Val	Met	Gly	50	55	60	
Tyr	Gln	Lys	Lys	Leu	Arg	Ser	Met	Thr	Asp	Lys	Tyr	Arg	Leu	His	Leu	65	70	75	80
Ser	Val	Ala	Asp	Leu	Leu	Phe	Val	Ile	Thr	Leu	Pro	Phe	Trp	Ala	Val	85	90	95	
Asp	Ala	Val	Ala	Asn	Trp	Tyr	Phe	Gly	Asn	Phe	Leu	Cys	Lys	Ala	Val	100	105	110	
His	Val	Ile	Tyr	Thr	Val	Asn	Leu	Tyr	Ser	Ser	Val	Leu	Ile	Leu	Ala	115	120	125	
Phe	Ile	Ser	Leu	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Ala	Thr	Asn	Ser	130	135	140	
Gln	Arg	Pro	Arg	Lys	Leu	Leu	Ala	Glu	Lys	Val	Val	Ala	Val	Gly	Val	145	150	155	160
Trp	Ile	Pro	Ala	Leu	Leu	Leu	Thr	Ile	Pro	Asp	Phe	Ile	Phe	Ala	Asn	165	170	175	
Val	Ser	Glu	Ala	Asp	Asp	Arg	Tyr	Ile	Cys	Asp	Arg	Phe	Tyr	Pro	Asn	180	185	190	
Asp	Leu	Trp	Val	Val	Val	Phe	Gln	Phe	Gln	His	Ile	Met	Val	Gly	Leu	195	200	205	
Ile	Leu	Pro	Gly	Ile	Val	Ile	Leu	Ser	Cys	Tyr	Cys	Ile	Ile	Ile	Ser	210	215	220	
Lys	Leu	Ser	His	Ser	Lys	Gly	His	Gln	Lys	Arg	Lys	Ala	Leu	Lys	Thr	225	230	235	240
Thr	Val	Ile	Leu	Ile	Leu	Ala	Phe	Phe	Ala	Cys	Trp	Leu	Pro	Tyr	Tyr	245	250	255	
Ile	Gly	Ile	Ser	Ile	Asp	Ser	Phe	Ile	Leu	Leu	Glu	Ile	Ile	Lys	Gln	260	265	270	
Gly	Cys	Glu	Phe	Glu	Asn	Thr	Val	His	Lys	Trp	Ile	Ser	Ile	Thr	Glu	275	280	285	
Ala	Leu	Ala	Phe	Phe	His	Cys	Cys	Leu	Asn	Pro	Ile	Leu	Tyr	Ala	Phe	290	295	300	
Leu	Gly	Ala	Lys	Phe	Lys	Thr	Ser	Ala	Gln	His	Ala	Leu	Thr	Ser	Val	305	310	315	320
Ser	Arg	Gly	Ser	Ser	Leu	Lys	Ile	Leu	Ser	Lys	Gly	Lys	Arg	Gly	Gly	325	330	335	

His Ser Ser Val Ser Thr Glu Ser Glu Ser Ser Ser Phe His Ser Ser
 340 345 350

<210> SEQ ID NO: 19

<211> 359

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido sintético

<400> 19

Met Glu Pro Ile Ser Val Ser Ile Tyr Thr Ser Asp Asn Tyr Ser Glu
 1 5 10 15

Glu Val Gly Ser Gly Asp Tyr Asp Ser Asn Lys Glu Pro Cys Phe Arg
 20 25 30

Asp Glu Asn Val His Phe Asn Arg Ile Phe Leu Pro Thr Ile Tyr Phe
 35 40 45

Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val
 50 55 60

Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu
 65 70 75 80

His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp
 85 90 95

Ala Val Asp Ala Met Ala Asp Trp Tyr Phe Gly Lys Phe Leu Cys Lys
 100 105 110

Ala Val His Ile Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile
 115 120 125

Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr
 130 135 140

Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Ala Val Ala Val
 145 150 155 160

Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe
 165 170 175

Ala Asp Val Ser Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr Ile
 180 185 190

Cys Asp Arg Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln Phe
 195 200 205

Gln His Ile Met Val Gly Leu Val Leu Pro Gly Ile Val Ile Leu Ser
 210 215 220

Cys Tyr Cys Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly His Gln
 225 230 235 240

Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe Phe
 245 250 255

Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser Phe Ile
 260 265 270

Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser Ile Val His
275 280 285

Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys Leu
290 295 300

Asn Pro Ile Leu Tyr Ala Phe Leu Gly Ala Lys Phe Lys Ser Ser Ala
305 310 315 320

Gln His Ala Leu Asn Ser Met Ser Arg Gly Ser Ser Leu Lys Ile Leu
325 330 335

Ser Lys Gly Lys Arg Gly Gly His Ser Ser Val Ser Thr Glu Ser Glu
340 345 350

Ser Ser Ser Phe His Ser Ser
355

<210> SEQ ID NO: 20

<211> 352

<212> PRT

<213> *Homo sapiens*

<400> 20

Met Glu Gly Ile Ser Ile Tyr Thr Ser Asp Asn Tyr Thr Glu Glu Met
1 5 10 15

Gly Ser Gly Asp Tyr Asp Ser Met Lys Glu Pro Cys Phe Arg Glu Glu
20 25 30

Asn Ala Asn Phe Asn Lys Ile Phe Leu Pro Thr Ile Tyr Ser Ile Ile
35 40 45

Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val Met Gly
50 55 60

Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu His Leu
65 70 75 80

Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp Ala Val
85 90 95

Asp Ala Val Ala Asn Trp Tyr Phe Gly Asn Phe Leu Cys Lys Ala Val
100 105 110

His Val Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile Leu Ala
115 120 125

Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser
130 135 140

Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Val Val Tyr Val Gly Val
145 150 155 160

Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asn
165 170 175

Val Ser Glu Ala Asp Asp Arg Tyr Ile Cys Asp Arg Phe Tyr Pro Asn
180 185 190

Asp Leu Trp Val Val Val Phe Gln Phe Gln His Ile Met Val Gly Leu
195 200 205

Ile Leu Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys Ile Ile Ile Ser
 210 215 220
 Lys Leu Ser His Ser Lys Gly His Gln Lys Arg Lys Ala Leu Lys Thr
 225 230 235 240
 Thr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr Tyr
 245 250 255
 Ile Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Glu Ile Ile Lys Gln
 260 265 270
 Gly Cys Glu Phe Glu Asn Thr Val His Lys Trp Ile Ser Ile Thr Glu
 275 280 285
 Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile Leu Tyr Ala Phe
 290 295 300
 Leu Gly Ala Lys Phe Lys Thr Ser Ala Gln His Ala Leu Thr Ser Val
 305 310 315 320
 Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser Lys Gly Lys Arg Gly Gly
 325 330 335
 His Ser Ser Val Ser Thr Glu Ser Glu Ser Ser Ser Phe His Ser Ser
 340 345 350

<210> SEQ ID NO: 21

<211> 1125

<212> ADN

<213> *Homo sapiens*

<400> 21

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ggggcccaac tcctgcctcc gctctactcg ctgggtgttca tctttgggtt tgtgggcaac	180
atgctgggtcg tcctcatctt aataaactgc aaaaagctga agtgcttgac tgacatttac	240
ctgctcaacc tggccatctc tgatctgctt tttcttatta ctctccatt gtgggctcac	300
tctgctgcaa atgagtgggt ctttgggaat gcaatgtgca aattattcac agggctgtat	360
cacatcggtt attttggcgg aatcttcttc atcatcctcc tgacaatcga tagataacctg	420
gctattgtcc atgctgtgtt tgctttaaaa gccaggacgg tcacctttgg ggtggtgaca	480
agtgtgatca cctgggttggg ggctgtgttt gcttctgtcc caggaatcat ctttactaaa	540
tgccagaaag aagattctgt ttatgtctgt ggcccttatt ttccacgagg atggaataat	600
ttccacacaa taatgaggaa catthtgggg ctgggtcctgc cgctgctcat catgggtcatc	660
tgctactcgg gaatcctgaa aaccctgctt cgggtgtcgaa acgagaagaa gaggcataagg	720
gcagtgagag tcattctcac catcatgatt gtttactttc tcttctggac tccctataat	780
attgtcattc tcctgaacac cttccaggaa ttcttcggcc tgagtaactg tgaaagcacc	840
agtcaactgg accaagccac gcagggtgaca gagactcttg ggatgactca ctgctgcac	900

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aatcccatca tctatgcctt cgttggggag aagttcagaa gcctttttca catagctctt      960
ggctgtagga ttgccccact ccaaaaacca gtgtgtggag gtccaggagt gagaccagga      1020
aagaatgtga aagtgactac acaaggactc ctcgatggtc gtggaaaagg aaagtcaatt      1080
ggcagagccc ctgaagccag tcttcaggac aaagaaggag cctag                        1125

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<210> SEQ ID NO: 22

<211> 1122

<212> ADN

<213> *Mus sp.*

<400> 22

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ctattttacac gaagtatcca agagcttgat gaagggggcca ccacaccgta tgactacgat      120
gatgggtgagc cttgtcataa aaccagtgtg aagcaaattg gagcttggat cctgcctcca      180
ctctactccc tgggtattcat ctttggtttt gtgggcaaca tgttgggtcat tataattctg      240
ataggctgta aaaagctgaa gagcatgact gatatctatc tgctcaactt ggccatctct      300
gacctgctct tctgtctcac attaccattc tgggctcact atgctgcaaa tgagtgggtc      360
tttggaata taatgtgtaa agtattcaca gggctctatc acattgggtta ttttgggtgga      420
atctttttca ttatcctcct gacaattgat aggtacttgg ctattgttca tgctgtgttt      480
gctttaaaaag ccaggacagt tacctttggg gtgataacaa gtgtagtcac ttgggtgggtg      540
gctgtgtttg cctctctacc aggaatcata ttactaaat ccaaacaaga tgatcaccat      600
tacacctgtg gcccttattt tacacaacta tggaagaatt tccaaacaat aatgagaaat      660
atcttgagcc tgatcctgcc tctacttgtc atgggtcatct gctactcagg aattctccac      720
accctgtttc gctgtaggaa tgagaagaag aggcacaggg ctgtgaggct catctttgcc      780
atcatgattg tctactttct cttctggact ccatacaata ttgttctctt cttgaccacc      840
ttccaggaat ccttggaat gagtaactgt gtgattgaca agcacttaga ccaggccatg      900
caggtgacag agactcttgg aatgacacac tgctgcatta atcctgtcat ttatgccttt      960
gttgagagaga agttccgaag gtatctctcc atatttttca gaaagcacat tgctaaacgt      1020
ctctgcaaac agtcccagc tttctatagg gagacagcag atcgagtaag ctctacattc      1080
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<210> SEQ ID NO: 23

<211> 374

<212> PRT

<213> *Homo sapiens*

<400> 23

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Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser
1           5           10          15
Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys
20          25          30

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His	Lys	Phe 35	Asp	Val	Lys	Gln	Ile 40	Gly	Ala	Gln	Leu	Leu 45	Pro	Pro	Leu
Tyr	Ser 50	Leu	Val	Phe	Ile	Phe 55	Gly	Phe	Val	Gly	Asn 60	Met	Leu	Val	Val
Leu 65	Ile	Leu	Ile	Asn	Cys 70	Lys	Lys	Leu	Lys	Cys 75	Leu	Thr	Asp	Ile	Tyr 80
Leu	Leu	Asn	Leu	Ala 85	Ile	Ser	Asp	Leu	Leu 90	Phe	Leu	Ile	Thr	Leu 95	Pro
Leu	Trp	Ala	His 100	Ser	Ala	Ala	Asn	Glu 105	Trp	Val	Phe	Gly	Asn 110	Ala	Met
Cys	Lys	Leu 115	Phe	Thr	Gly	Leu	Tyr 120	His	Ile	Gly	Tyr	Phe 125	Gly	Gly	Ile
Phe	Phe 130	Ile	Ile	Leu	Leu	Thr 135	Ile	Asp	Arg	Tyr	Leu 140	Ala	Ile	Val	His
Ala 145	Val	Phe	Ala	Leu	Lys 150	Ala	Arg	Thr	Val	Thr 155	Phe	Gly	Val	Val	Thr 160
Ser	Val	Ile	Thr	Trp 165	Leu	Val	Ala	Val	Phe 170	Ala	Ser	Val	Pro	Gly 175	Ile
Ile	Phe	Thr	Lys 180	Cys	Gln	Lys	Glu	Asp 185	Ser	Val	Tyr	Val	Cys 190	Gly	Pro
Tyr	Phe 195	Pro	Arg	Gly	Trp	Asn	Asn 200	Phe	His	Thr	Ile	Met 205	Arg	Asn	Ile
Leu	Gly 210	Leu	Val	Leu	Pro	Leu 215	Leu	Ile	Met	Val	Ile 220	Cys	Tyr	Ser	Gly
Ile 225	Leu	Lys	Thr	Leu	Leu 230	Arg	Cys	Arg	Asn	Glu 235	Lys	Lys	Arg	His	Arg 240
Ala	Val	Arg	Val	Ile 245	Phe	Thr	Ile	Met	Ile 250	Val	Tyr	Phe	Leu	Phe 255	Trp
Thr	Pro	Tyr	Asn 260	Ile	Val	Ile	Leu	Leu 265	Asn	Thr	Phe	Gln	Glu 270	Phe	Phe
Gly	Leu	Ser 275	Asn	Cys	Glu	Ser	Thr 280	Ser	Gln	Leu	Asp	Gln 285	Ala	Thr	Gln
Val	Thr 290	Glu	Thr	Leu	Gly	Met 295	Thr	His	Cys	Cys	Ile 300	Asn	Pro	Ile	Ile
Tyr 305	Ala	Phe	Val	Gly	Glu 310	Lys	Phe	Arg	Ser	Leu 315	Phe	His	Ile	Ala	Leu 320
Gly	Cys	Arg	Ile	Ala 325	Pro	Leu	Gln	Lys	Pro 330	Val	Cys	Gly	Gly	Pro 335	Gly
Val	Arg	Pro	Gly 340	Lys	Asn	Val	Lys	Val 345	Thr	Thr	Gln	Gly	Leu 350	Leu	Asp
Gly	Arg	Gly 355	Lys	Gly	Lys	Ser	Ile 360	Gly	Arg	Ala	Pro	Glu 365	Ala	Ser	Leu

Gln Asp Lys Glu Gly Ala
370

<210> SEQ ID NO: 24

<211> 373

<212> PRT

<213> *Mus sp.*

<400> 24

Met Glu Asp Asn Asn Met Leu Pro Gln Phe Ile His Gly Ile Leu Ser
1 5 10 15

Thr Ser His Ser Leu Phe Thr Arg Ser Ile Gln Glu Leu Asp Glu Gly
20 25 30

Ala Thr Thr Pro Tyr Asp Tyr Asp Asp Gly Glu Pro Cys His Lys Thr
35 40 45

Ser Val Lys Gln Ile Gly Ala Trp Ile Leu Pro Pro Leu Tyr Ser Leu
50 55 60

Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Ile Ile Ile Leu
65 70 75 80

Ile Gly Cys Lys Lys Leu Lys Ser Met Thr Asp Ile Tyr Leu Leu Asn
85 90 95

Leu Ala Ile Ser Asp Leu Leu Phe Leu Leu Thr Leu Pro Phe Trp Ala
100 105 110

His Tyr Ala Ala Asn Glu Trp Val Phe Gly Asn Ile Met Cys Lys Val
115 120 125

Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile Phe Phe Ile
130 135 140

Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
145 150 155 160

Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Ile Thr Ser Val Val
165 170 175

Thr Trp Val Val Ala Val Phe Ala Ser Leu Pro Gly Ile Ile Phe Thr
180 185 190

Lys Ser Lys Gln Asp Asp His His Tyr Thr Cys Gly Pro Tyr Phe Thr
195 200 205

Gln Leu Trp Lys Asn Phe Gln Thr Ile Met Arg Asn Ile Leu Ser Leu
210 215 220

Ile Leu Pro Leu Leu Val Met Val Ile Cys Tyr Ser Gly Ile Leu His
225 230 235 240

Thr Leu Phe Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg
245 250 255

Leu Ile Phe Ala Ile Met Ile Val Tyr Phe Leu Phe Trp Thr Pro Tyr
260 265 270

Asn Ile Val Leu Phe Leu Thr Thr Phe Gln Glu Ser Leu Gly Met Ser
275 280 285

Asn Cys Val Ile Asp Lys His Leu Asp Gln Ala Met Gln Val Thr Glu
 290 295 300
 Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Val Ile Tyr Ala Phe
 305 310 315 320
 Val Gly Glu Lys Phe Arg Arg Tyr Leu Ser Ile Phe Phe Arg Lys His
 325 330 335
 Ile Ala Lys Arg Leu Cys Lys Gln Cys Pro Val Phe Tyr Arg Glu Thr
 340 345 350
 Ala Asp Arg Val Ser Ser Thr Phe Thr Pro Ser Thr Gly Glu Gln Glu
 355 360 365
 Val Ser Val Gly Leu
 370

<210> SEQ ID NO: 25

<211> 1530

<212> ADN

<213> *Homo sapiens*

<400> 25

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cctcctgtta	ttccaaatgt	gcctttcctc	tgggcctgga	atgccccaa	tgaattttgt	180
cttgaaaaat	ttgatgagcc	actagatatg	agcctcttct	ctttcatagg	aagccccga	240
ataaacgcca	ccgggcaagg	tgttacaata	ttttatgttg	atagacttgg	ctactatcct	300
tacatagatt	caatcacagg	agtaactgtg	aatggaggaa	tccccagaa	gatttcctta	360
caagaccatc	tggacaaagc	taagaaagac	attacatctt	atatgccagt	agacaatttg	420
ggaatggctg	ttattgactg	ggaagaatgg	agaccactt	gggcaagaaa	ctggaaacct	480
aaagatgttt	acaagaatag	gtctattgaa	ttggttcagc	aacaaaatgt	acaacttagt	540
ctcacagagg	ccactgagaa	agcaaaacaa	gaatttgaaa	aggcagggaa	ggatttcctg	600
gtagagacta	taaaattggg	aaaattactt	cggccaaatc	acttgtgggg	ttattatctt	660
tttccggatt	gttacaacca	tcactataag	aaaccgggtt	acaatggaag	ttgcttcaat	720
gtagaaataa	aaagaaatga	tgatctcagc	tgggtgtgga	atgaaagcac	tgctctttac	780
ccatccatct	atttgaacac	tcagcagtct	cctgtagctg	ctacactcta	tgtgcgcaat	840
cgagttcggg	aagccatcag	agtttccaaa	atacctgatg	caaaaagtcc	acttccgggt	900
tttgcatata	cccgcatagt	ttttactgat	caagttttga	aattcctttc	tcaagatgaa	960
cttgtgtata	catttggcga	aactgttgct	ctgggtgctt	ctggaattgt	aatatgggga	1020
accctcagta	taatgcgaag	tatgaaatct	tgcttgctcc	tagacaatta	catggagact	1080
atactgaatc	cttacataat	caacgtcaca	ctagcagcca	aatgtgtag	ccaagtgtct	1140

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tgccaggagc aaggagtgtg tataaggaaa aactggaatt caagtgacta tcttcacctc      1200
aaccagata attttgctat tcaacttgag aaaggtggaa agttcacagt acgtggaaaa      1260
ccgacacttg aagacctgga gcaatcttct gaaaaatttt attgcagctg ttatagcacc      1320
ttgagttgta aggagaaagc tgatgtaaaa gacactgatg ctgttgatgt gtgtattgct      1380
gatggtgtct gtatagatgc ttttctaaaa cctcccatgg agacagaaga acctcaaatt      1440
ttctacaatg cttcaccctc cacactatct gccacaatgt tcattgttag tattttgttt      1500
cttatcattt cttctgtagc gagtttgtaa                                     1530

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<210> SEQ ID NO: 26

<211> 509

<212> PRT

<213> *Homo sapiens*

<400> 26

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Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
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Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
          20           25           30

Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
          35           40           45

Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
          50           55           60

Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
65           70           75           80

Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
          85           90           95

Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
          100          105          110

Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
          115          120          125

Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
130          135          140

Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
145          150          155          160

Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
          165          170          175

Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
          180          185          190

Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
          195          200          205

Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
210          215          220

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Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
 465 470 475 480
 Phe Tyr Asn Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val
 485 490 495
 Ser Ile Leu Phe Leu Ile Ile Ser Ser Val Ala Ser Leu
 500 505

<210> SEQ ID NO: 27

<211> 2398

<212> ADN

<213> Desconocido

<220>

<223> Descripción de Desconocido: Secuencia de la hialuronidasa

<400> 27

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taactacggt tatgatcagt atgatgagaa gaatgacgca atgaagaaga agtttgatgc	120
tacggagaaa gaggcagaga aattactcag tagcatgaaa actgaaagtg gaaggactta	180
cttgtgggat agtgcaaaag atttagataa caagtctgcg gatatgactc gtacctatcg	240
taatattgag aaaatcgag aagcgatgaa gcataaagat actaagttaa atactccgga	300
taataaaaaac aaagttaaag atgcccttga gtggctgcat aaaaatgcct atggaaaaga	360
accggtgaaa aaacttgaag aactaaaaac aaatttctca aaatcagcac ctcaaaagaa	420
tacaaactta aattggtggg attatgaaat tggaacacct agagcactaa caaatacctt	480
tatactctta aaagaagatt ttactgatga agaaaagaaa aaatacactg cccctattaa	540
aactttcgcc caaaaagtg atgaaatatt atcttctgta ggaaaagctg aacctgctaa	600
aggcggaat ttagtagaca tttctaaagt aaaactttta gaaagtatta tcgaagaaga	660
tgcaactatg atgaaagaat caatagaggc atttaataaa gtcttcactt acgttcaaag	720
taatgcaact ggtaaagaac gtaatggatt ctataaagac ggctcttata ttgatcatca	780
agacgtcca tacactggtg cttatggcgt tgtactctta gaggggattt ctcaaagat	840
gccgatgata aaagaaacac cttttaaaga tagtaatcaa aatgatacaa cattaaagtc	900
gtggattgat gaaggattta tgccactcat ttataaagggt gaaatgatgg atttatcacg	960
tggtagagcc attagccgtg aaaatgaaac gagtcactca acatctgcaa ctgtaatgaa	1020
atcattgttg agattaagtg atgccatgga tgagtcaaca aaagctaaat ataagcaaat	1080
cgttaaaact tctgttaaat ctgattcaag ttataaacia aacgattatt taagctctta	1140
ttcagatata agcaaatga agtctttaat tgaagacagc actatttcta ctaacggttt	1200
aacacaacia cttaaaatat ataatgacat gaatcgtgtc acctatcata acaaagactt	1260
agactttgca tttggcttaa gtatgacgtc gaaaaacgtc gcacattacg aaagtatcaa	1320
cggagagaac ttaaaagggt ggacactgg tgctggaatg tcttatttat acaatagcga	1380
tgtgaaacac taccgtgata acttctgggc gacagctgat atgaaacgtt tagcaggtac	1440
tacaacttta gataatgaag aacctaaaga aaataagaac tccgataaaa cttttgtagg	1500
cggaacaaaa ttcgatgacc aacatgctag tatcggaatg gattttgaaa atcaggacaa	1560
aactttaact gccaaaaaat catatttcat attaaacgat aaaattgtct tcttaggaac	1620
tggcattaaa agtactgatt catcaaagaa tccagtgaca acgattgaaa atcgcaaadc	1680
gaatgggtat acgttattta cagacgataa acaacaacc gttcaaata ttaatgatca	1740
ggaaaccaat tcagtctttt tagagtccac agatacaaaa aagaacatcg gttatcattt	1800
tttaaacgaa tcgaaaataa ctgtaaaaaa agaaagtcac actggtaagt ggagtgatat	1860

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aaataaaagt caaaagtcag atgacaaaac tgatgagtat tatgaagtaa ctcaaaagca      1920
ttctaataca gatgataaat atgcatatgt cttgtatcca ggcttatcta aagataatTTT      1980
taaataccaaa gcaagccaag taactatcgt taaacaagat gatgacttcc acattgtgaa      2040
agataatgaa tcggtttggg ctggtgtcaa ttatagtaat agcactcaaa cttttgacat      2100
taacaacacc aagggttgagg ttaaagcgaa agggatgttc attttgaaaa acaaggacga      2160
taatacgtac gaatgctcat tctataatcc tgagtctacg aatacggctt cagacataga      2220
aagtaagatc agtatgacgg gatactcaat cacgaataaa aacacaagta cgtccaacga      2280
aagtgggtgtg catttcgagt tgactaaata tgctgccgcg atgtctggag cagggtccgtg      2340
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<210> SEQ ID NO: 28

<211> 799

<212> PRT

<213> Desconocido

<220>

<223> Descripción de Desconocido: Secuencia de la hialuronidasa

<400> 28

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Gly Arg Asp Thr Asn Val Gln Thr Pro Asp Tyr Glu Lys Leu Arg Asn
1              5              10              15

Thr Trp Leu Asn Val Asn Tyr Gly Tyr Asp Gln Tyr Asp Glu Lys Asn
                20              25              30

Asp Ala Met Lys Lys Lys Phe Asp Ala Thr Glu Lys Glu Ala Glu Lys
          35              40              45

Leu Leu Ser Ser Met Lys Thr Glu Ser Gly Arg Thr Tyr Leu Trp Asp
          50              55              60

Ser Ala Lys Asp Leu Asp Asn Lys Ser Ala Asp Met Thr Arg Thr Tyr
65              70              75              80

Arg Asn Ile Glu Lys Ile Ala Glu Ala Met Lys His Lys Asp Thr Lys
          85              90              95

Leu Asn Thr Pro Asp Asn Lys Asn Lys Val Lys Asp Ala Leu Glu Trp
          100             105             110

Leu His Lys Asn Ala Tyr Gly Lys Glu Pro Val Lys Lys Leu Glu Glu
          115             120             125

Leu Lys Thr Asn Phe Ser Lys Ser Ala Pro Gln Lys Asn Thr Asn Leu
          130             135             140

Asn Trp Trp Asp Tyr Glu Ile Gly Thr Pro Arg Ala Leu Thr Asn Thr
145             150             155             160

Leu Ile Leu Leu Lys Glu Asp Phe Thr Asp Glu Glu Lys Lys Lys Tyr
          165             170             175

Thr Ala Pro Ile Lys Thr Phe Ala Pro Lys Ser Asp Glu Ile Leu Ser
          180             185             190

```

Ser	Val	Gly	Lys	Ala	Glu	Pro	Ala	Lys	Gly	Gly	Asn	Leu	Val	Asp	Ile	195	200	205
Ser	Lys	Val	Lys	Leu	Leu	Glu	Ser	Ile	Ile	Glu	Glu	Asp	Ala	Thr	Met	210	215	220
Met	Lys	Glu	Ser	Ile	Glu	Ala	Phe	Asn	Lys	Val	Phe	Thr	Tyr	Val	Gln	225	230	235
Ser	Asn	Ala	Thr	Gly	Lys	Glu	Arg	Asn	Gly	Phe	Tyr	Lys	Asp	Gly	Ser	245	250	255
Tyr	Ile	Asp	His	Gln	Asp	Val	Pro	Tyr	Thr	Gly	Ala	Tyr	Gly	Val	Val	260	265	270
Leu	Leu	Glu	Gly	Ile	Ser	Gln	Met	Met	Pro	Met	Ile	Lys	Glu	Thr	Pro	275	280	285
Phe	Lys	Asp	Ser	Asn	Gln	Asn	Asp	Thr	Thr	Leu	Lys	Ser	Trp	Ile	Asp	290	295	300
Glu	Gly	Phe	Met	Pro	Leu	Ile	Tyr	Lys	Gly	Glu	Met	Met	Asp	Leu	Ser	305	310	315
Arg	Gly	Arg	Ala	Ile	Ser	Arg	Glu	Asn	Glu	Thr	Ser	His	Ser	Thr	Ser	325	330	335
Ala	Thr	Val	Met	Lys	Ser	Leu	Leu	Arg	Leu	Ser	Asp	Ala	Met	Asp	Glu	340	345	350
Ser	Thr	Lys	Ala	Lys	Tyr	Lys	Gln	Ile	Val	Lys	Thr	Ser	Val	Lys	Ser	355	360	365
Asp	Ser	Ser	Tyr	Lys	Gln	Asn	Asp	Tyr	Leu	Ser	Ser	Tyr	Ser	Asp	Ile	370	375	380
Ser	Lys	Met	Lys	Ser	Leu	Ile	Glu	Asp	Ser	Thr	Ile	Ser	Thr	Asn	Gly	385	390	395
Leu	Thr	Gln	Gln	Leu	Lys	Ile	Tyr	Asn	Asp	Met	Asn	Arg	Val	Thr	Tyr	405	410	415
His	Asn	Lys	Asp	Leu	Asp	Phe	Ala	Phe	Gly	Leu	Ser	Met	Thr	Ser	Lys	420	425	430
Asn	Val	Ala	His	Tyr	Glu	Ser	Ile	Asn	Gly	Glu	Asn	Leu	Lys	Gly	Trp	435	440	445
His	Thr	Gly	Ala	Gly	Met	Ser	Tyr	Leu	Tyr	Asn	Ser	Asp	Val	Lys	His	450	455	460
Tyr	Arg	Asp	Asn	Phe	Trp	Ala	Thr	Ala	Asp	Met	Lys	Arg	Leu	Ala	Gly	465	470	475
Thr	Thr	Thr	Leu	Asp	Asn	Glu	Glu	Pro	Lys	Glu	Asn	Lys	Asn	Ser	Asp	485	490	495
Lys	Thr	Phe	Val	Gly	Gly	Thr	Lys	Phe	Asp	Asp	Gln	His	Ala	Ser	Ile	500	505	510
Gly	Met	Asp	Phe	Glu	Asn	Gln	Asp	Lys	Thr	Leu	Thr	Ala	Lys	Lys	Ser	515	520	525

Tyr Phe Ile Leu Asn Asp Lys Ile Val Phe Leu Gly Thr Gly Ile Lys
530 535 540

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

Ser Asn Gly Tyr Thr Leu Phe Thr Asp Asp Lys Gln Thr Thr Ala Ser
565 570 575

Asn Ile Asn Asp Gln Glu Thr Asn Ser Val Phe Leu Glu Ser Thr Asp
580 585 590

Thr Lys Lys Asn Ile Gly Tyr His Phe Leu Asn Glu Ser Lys Ile Thr
595 600 605

Val Lys Lys Glu Ser His Thr Gly Lys Trp Ser Asp Ile Asn Lys Ser
610 615 620

Gln Lys Ser Asp Asp Lys Thr Asp Glu Tyr Tyr Glu Val Thr Gln Lys
625 630 635 640

His Ser Asn Thr Asp Asp Lys Tyr Ala Tyr Val Leu Tyr Pro Gly Leu
645 650 655

Ser Lys Asp Asn Phe Lys Ser Lys Ala Ser Gln Val Thr Ile Val Lys
660 665 670

Gln Asp Asp Asp Phe His Ile Val Lys Asp Asn Glu Ser Val Trp Ala
675 680 685

Gly Val Asn Tyr Ser Asn Ser Thr Gln Thr Phe Asp Ile Asn Asn Thr
690 695 700

Lys Val Glu Val Lys Ala Lys Gly Met Phe Ile Leu Lys Asn Lys Asp
705 710 715 720

Asp Asn Thr Tyr Glu Cys Ser Phe Tyr Asn Pro Glu Ser Thr Asn Thr
725 730 735

Ala Ser Asp Ile Glu Ser Lys Ile Ser Met Thr Gly Tyr Ser Ile Thr
740 745 750

Asn Lys Asn Thr Ser Thr Ser Asn Glu Ser Gly Val His Phe Glu Leu
755 760 765

Thr Lys Tyr Ala Ala Ala Met Ser Gly Ala Gly Pro Trp Ala Ala Trp
770 775 780

Pro Phe Leu Leu Ser Leu Ala Leu Met Leu Leu Trp Leu Leu Ser
785 790 795

<210> SEQ ID NO: 29

<211> 2454

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 29

atggactgga catggattct ctttctagtg gccgcagcca caaggggtcca cagcggccgc

gatacgaatg ttcaaacgcc agattatgaa aagttgagga acacatggct gaacgttaac	120
tacggttatg atcagtatga tgagaagaat gacgcaatga agaagaagtt tgatgctacg	180
gagaaagagg cagagaaatt actcagtagc atgaaaactg aaagtggaag gacttacttg	240
tgggatagtg caaaagattht agataacaag tctgctggata tgactcgtac ctatcgtaat	300
attgagaaaa tcgcagaagc gatgaagcat aaagatacta agttaaatac tccggataat	360
aaaaacaaag ttaaagatgc ccttgagtgg ctgcataaaa atgcctatgg aaaagaaccg	420
gtgaaaaaac ttgaagaact aaaaacaaat ttctcaaaat cagcacctca aaagaatata	480
aacttaaat ggtgggatta tgaaattgga acacctagag cactaacaaa tacccttata	540
ctcttaaaag aagatthtac tgatgaagaa aagaaaaaat acactgcccc tattaaaact	600
ttcgcccaa aaagtgatga aatattatct tctgtaggaa aagctgaacc tgctaaaggc	660
ggaaatthtag tagacatthc taaagtaaaa cththtagaaa gtattatcga agaagatgca	720
actatgatga aagaatcaat agaggcattht aataaagtct tcacttacgt tcaaagtaat	780
gcaactggta aagaacgtaa tggattctat aaagacggct cttatattga tcatcaagac	840
gtcccatata ctgggtgctta tggcgttgta ctcttagagg ggattthctca aatgatgccg	900
atgataaaaag aaacaccttht taaagatagt aatcaaaatg atacaacatt aaagtcgtgg	960
attgatgaag gatthtatgcc actcattht aaaggtgaaa tgatggattht atcacgtgg	1020
agagccatta gccgtgaaaa tgaaacgagt cactcaacat ctgcaactgt aatgaaatca	1080
ttgttgagat taagtgatgc catggatgag tcaacaaaag ctaaataataa gcaaatcgtht	1140
aaaactthctg ttaaactctga ttcaagtht aaacaaaacg attatthtaag ctcttattca	1200
gatataagca aaatgaagtc thtaattgaa gacagcacta thtctactaa cggthtaaca	1260
caacaactta aaatatataa tgacatgaat cgtgtcacct atcataacaa agacttagac	1320
thtgcattht gcttaagtat gacgtcgaaa aacgtcgac attacgaaag tatcaacgga	1380
gagaacttaa aaggttgga cactggtgct ggaatgtctt atthatacaa tagcgatgtg	1440
aaacactacc gtgataactt ctgggcgaca gctgatatga aacgtthtagc aggtactaca	1500
actthtagata atgaagaacc taaagaaaat aagaactccg ataaaacttht tgtaggcgga	1560
acaaaatthc atgaccaaca tgctagtatc ggaatggatt ttgaaaatca ggacaaaact	1620
thtaactgcca aaaaatcata thtcatatta aacgataaaa thgtctthctt aggaactggc	1680
atthaaagta ctgattcatc aaagaatcca gtgacaacga ttgaaaatcg caaatcgat	1740
gggtatacgt taththacaga cgataaacaa acaaccgctt caaatatthaa tgatcaggaa	1800
accaatthcag ththththtaga gtccacagat acaaaaaaga acatcggtta ththththta	1860
aacgaatcga aaataactgt aaaaaaagaa agtcatactg gtaagtggag tgatataaat	1920

```

aaaagtcaaa agtcagatga caaaactgat gagtattatg aagtaactca aaagcattct      1980
aatacagatg ataaatatgc atatgtcttg tatccaggct tatctaaaga taatttttaa      2040
tccaaagcaa gccaaagtaac tatcggttaa caagatgatg acttccacat tgtgaaagat      2100
aatgaatcgg tttgggctgg tgtcaattat agtaatagca ctcaaacttt tgacattaac      2160
aacaccaagg ttgagggttaa agcgaaaggg atgttcattt tgaaaaacaa ggacgataat      2220
acgtacgaat gctcattcta taatcctgag tctacgaata cggcttcaga catagaaagt      2280
aagatcagta tgacgggata ctcaatcacg aataaaaaca caagtacgtc caacgaaagt      2340
gggtgtgcatt tcgagttgac taaatatgct gccgcgatgt ctggagcagg tccgtgggca      2400
gcctggccat tctactctc actggcgctc atgctactat ggctgctctc atga          2454

```

<210> SEQ ID NO: 30

<211> 817

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido sintético

<400> 30

```

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1              5              10              15

```

```

His Ser Gly Arg Asp Thr Asn Val Gln Thr Pro Asp Tyr Glu Lys Leu
              20              25              30

```

```

Arg Asn Thr Trp Leu Asn Val Asn Tyr Gly Tyr Asp Gln Tyr Asp Glu
              35              40              45

```

```

Lys Asn Asp Ala Met Lys Lys Lys Phe Asp Ala Thr Glu Lys Glu Ala
50              55              60

```

```

Glu Lys Leu Leu Ser Ser Met Lys Thr Glu Ser Gly Arg Thr Tyr Leu
65              70              75              80

```

```

Trp Asp Ser Ala Lys Asp Leu Asp Asn Lys Ser Ala Asp Met Thr Arg
              85              90              95

```

```

Thr Tyr Arg Asn Ile Glu Lys Ile Ala Glu Ala Met Lys His Lys Asp
100              105              110

```

```

Thr Lys Leu Asn Thr Pro Asp Asn Lys Asn Lys Val Lys Asp Ala Leu
115              120              125

```

```

Glu Trp Leu His Lys Asn Ala Tyr Gly Lys Glu Pro Val Lys Lys Leu
130              135              140

```

```

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

```

```

Asn Leu Asn Trp Trp Asp Tyr Glu Ile Gly Thr Pro Arg Ala Leu Thr
165              170              175

```

```

Asn Thr Leu Ile Leu Leu Lys Glu Asp Phe Thr Asp Glu Glu Lys Lys
180              185              190

```

Lys	Tyr	Thr 195	Ala	Pro	Ile	Lys	Thr 200	Phe	Ala	Pro	Lys	Ser 205	Asp	Glu	Ile
Leu	Ser 210	Ser	Val	Gly	Lys	Ala 215	Glu	Pro	Ala	Lys	Gly 220	Gly	Asn	Leu	Val
Asp 225	Ile	Ser	Lys	Val	Lys 230	Leu	Leu	Glu	Ser	Ile 235	Ile	Glu	Glu	Asp	Ala 240
Thr	Met	Met	Lys	Glu 245	Ser	Ile	Glu	Ala	Phe 250	Asn	Lys	Val	Phe	Thr 255	Tyr
Val	Gln	Ser	Asn 260	Ala	Thr	Gly	Lys	Glu 265	Arg	Asn	Gly	Phe	Tyr 270	Lys	Asp
Gly	Ser	Tyr 275	Ile	Asp	His	Gln	Asp 280	Val	Pro	Tyr	Thr	Gly 285	Ala	Tyr	Gly
Val	Val 290	Leu	Leu	Glu	Gly	Ile 295	Ser	Gln	Met	Met	Pro 300	Met	Ile	Lys	Glu
Thr 305	Pro	Phe	Lys	Asp	Ser 310	Asn	Gln	Asn	Asp	Thr 315	Thr	Leu	Lys	Ser	Trp 320
Ile	Asp	Glu	Gly	Phe 325	Met	Pro	Leu	Ile	Tyr 330	Lys	Gly	Glu	Met	Met 335	Asp
Leu	Ser	Arg	Gly 340	Arg	Ala	Ile	Ser	Arg 345	Glu	Asn	Glu	Thr	Ser 350	His	Ser
Thr	Ser	Ala 355	Thr	Val	Met	Lys	Ser 360	Leu	Leu	Arg	Leu	Ser 365	Asp	Ala	Met
Asp 370	Glu	Ser	Thr	Lys	Ala	Lys 375	Tyr	Lys	Gln	Ile	Val 380	Lys	Thr	Ser	Val
Lys 385	Ser	Asp	Ser	Ser	Tyr 390	Lys	Gln	Asn	Asp	Tyr 395	Leu	Ser	Ser	Tyr	Ser 400
Asp	Ile	Ser	Lys	Met 405	Lys	Ser	Leu	Ile	Glu 410	Asp	Ser	Thr	Ile	Ser 415	Thr
Asn	Gly	Leu	Thr 420	Gln	Gln	Leu	Lys	Ile	Tyr 425	Asn	Asp	Met	Asn 430	Arg	Val
Thr	Tyr	His 435	Asn	Lys	Asp	Leu	Asp 440	Phe	Ala	Phe	Gly	Leu 445	Ser	Met	Thr
Ser	Lys 450	Asn	Val	Ala	His	Tyr 455	Glu	Ser	Ile	Asn	Gly 460	Glu	Asn	Leu	Lys
Gly 465	Trp	His	Thr	Gly	Ala 470	Gly	Met	Ser	Tyr	Leu 475	Tyr	Asn	Ser	Asp	Val 480
Lys	His	Tyr	Arg	Asp 485	Asn	Phe	Trp	Ala	Thr 490	Ala	Asp	Met	Lys	Arg 495	Leu
Ala	Gly	Thr	Thr 500	Thr	Leu	Asp	Asn	Glu 505	Glu	Pro	Lys	Glu	Asn 510	Lys	Asn
Ser	Asp	Lys 515	Thr	Phe	Val	Gly	Gly 520	Thr	Lys	Phe	Asp	Asp 525	Gln	His	Ala

Ser Ile Gly Met Asp Phe Glu Asn Gln Asp Lys Thr Leu Thr Ala Lys
 530 535 540
 Lys Ser Tyr Phe Ile Leu Asn Asp Lys Ile Val Phe Leu Gly Thr Gly
 545 550 555 560
 Ile Lys Ser Thr Asp Ser Ser Lys Asn Pro Val Thr Thr Ile Glu Asn
 565 570 575
 Arg Lys Ser Asn Gly Tyr Thr Leu Phe Thr Asp Asp Lys Gln Thr Thr
 580 585 590
 Ala Ser Asn Ile Asn Asp Gln Glu Thr Asn Ser Val Phe Leu Glu Ser
 595 600 605
 Thr Asp Thr Lys Lys Asn Ile Gly Tyr His Phe Leu Asn Glu Ser Lys
 610 615 620
 Ile Thr Val Lys Lys Glu Ser His Thr Gly Lys Trp Ser Asp Ile Asn
 625 630 635 640
 Lys Ser Gln Lys Ser Asp Asp Lys Thr Asp Glu Tyr Tyr Glu Val Thr
 645 650 655
 Gln Lys His Ser Asn Thr Asp Asp Lys Tyr Ala Tyr Val Leu Tyr Pro
 660 665 670
 Gly Leu Ser Lys Asp Asn Phe Lys Ser Lys Ala Ser Gln Val Thr Ile
 675 680 685
 Val Lys Gln Asp Asp Asp Phe His Ile Val Lys Asp Asn Glu Ser Val
 690 695 700
 Trp Ala Gly Val Asn Tyr Ser Asn Ser Thr Gln Thr Phe Asp Ile Asn
 705 710 715 720
 Asn Thr Lys Val Glu Val Lys Ala Lys Gly Met Phe Ile Leu Lys Asn
 725 730 735
 Lys Asp Asp Asn Thr Tyr Glu Cys Ser Phe Tyr Asn Pro Glu Ser Thr
 740 745 750
 Asn Thr Ala Ser Asp Ile Glu Ser Lys Ile Ser Met Thr Gly Tyr Ser
 755 760 765
 Ile Thr Asn Lys Asn Thr Ser Thr Ser Asn Glu Ser Gly Val His Phe
 770 775 780
 Glu Leu Thr Lys Tyr Ala Ala Ala Met Ser Gly Ala Gly Pro Trp Ala
 785 790 795 800
 Ala Trp Pro Phe Leu Leu Ser Leu Ala Leu Met Leu Leu Trp Leu Leu
 805 810 815

Ser

<210> SEQ ID NO: 31

<211> 418

<212> ADN

<213> *Mus sp.*

<400> 31

```

aattctatgg ctccgacttc aagttctacc aagaagaccc agcttcaatt agaacattta      60
cttctagatt tacaaatgat tctgaatggg atcaacaatt ataagaatcc aaagcttact      120
cgtatgttga cctttaaatt ctatatgcct aagaaggcta ctgaattaaa acacctgcag      180
tgtttagaag aagagctcaa accgttagaa gaagttctga atctggctca atctaaaaac      240
ttccatttac gtccacgaga tcttatctct aatattaacg taatcgtttt ggaacttaaa      300
ggatccgaaa ctaccttcac gtgtgaatat gctgacgaaa ccgctacgat cgtagaattt      360
cttaatcgat ggattacttt ctgtcaatct attatctcta ccttaacttg agtcgacg      418

```

<210> SEQ ID NO: 32

<211> 462

<212> ADN

<213> *Homo sapiens*

<400> 32

```

atgtacagga tgcaactcct gtcttgcatc gcactaagtc ttgcacttgt cacaaacagt      60
gcacctactt caagttctac aaagaaaaca cagctacaac tggagcattt actgctggat      120
ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc      180
acatttaagt ttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa      240
gaagaactca aacctctgga ggaagtgcct aatttagctc aaagcaaaaa ctttacttta      300
agaccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa      360
acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga      420
tggattacct tttgtcaaag catcatctca acactgactt ga                        462

```

<210> SEQ ID NO: 33

<211> 169

<212> PRT

<213> *Mus sp.*

<400> 33

```

Met Tyr Ser Met Gln Leu Ala Ser Cys Val Thr Leu Thr Leu Val Leu
1              5              10              15

Leu Val Asn Ser Ala Pro Thr Ser Ser Ser Thr Ser Ser Ser Thr Ala
                20              25              30

Glu Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His Leu
                35              40              45

Glu Gln Leu Leu Met Asp Leu Gln Glu Leu Leu Ser Arg Met Glu Asn
                50              55              60

Tyr Arg Asn Leu Lys Leu Pro Arg Met Leu Thr Phe Lys Phe Tyr Leu
65              70              75              80

Pro Lys Gln Ala Thr Glu Leu Lys Asp Leu Gln Cys Leu Glu Asp Glu
                85              90              95

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

```

Gln Leu Glu Asp Ala Glu Asn Phe Ile Ser Asn Ile Arg Val Thr Val
115 120 125

Val Lys Leu Lys Gly Ser Asp Asn Thr Phe Glu Cys Gln Phe Asp Asp
130 135 140

Glu Ser Ala Thr Val Val Asp Phe Leu Arg Arg Trp Ile Ala Phe Cys
145 150 155 160

Gln Ser Ile Ile Ser Thr Ser Pro Gln
165

<210> SEQ ID NO: 34

<211> 153

<212> PRT

<213> *Homo sapiens*

<400> 34

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu
20 25 30

Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile
35 40 45

Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe
50 55 60

Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu
65 70 75 80

Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys
85 90 95

Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile
100 105 110

Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala
115 120 125

Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe
130 135 140

Cys Gln Ser Ile Ile Ser Thr Leu Thr
145 150

<210> SEQ ID NO: 35

<211> 34

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Oligonucleótido sintético

<400> 35

ataacttcgt atagcataca ttatacgaag ttat

34

<210> SEQ ID NO: 36

<211> 834

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 36

```

atgccagggc tccctgctgg ggagctgtac ggggtgggcag tagagacgac cccagcccc      60
gggccccagc ccgcggcact aacgacaggc gaggccgcgg cccagagtc cccgcaccag      120
gcagagccgt acctgtcacc ctccccaaagc gcctgcaccg cgggtgcaaga gccagcccc      180
ggggcgctgg acgtgaccat catgtacaag ggccgcacgg tgctgcagaa ggtggtggga      240
caccagagct gcacgttcct atacggcccc ccagaccag ctgtccgggc cacagacccc      300
cagcaggtag cattccccag ccttgccgag ctaccggacc agaagcagct gcgctacacg      360
gaggaactgc tgcggcacgt ggcccctggg ttgcacctgg agcttcgggg gccacagctg      420
tgggcccggc gcatgggcaa gtgcaagggtg tactgggagg tgggcggacc cccaggctcc      480
gccagcccct ccaccccagc ctgcctgctg cctcggaact gtgacacccc catcttcgac      540
ttcagagtct tcttccaaga gctggtggaa ttccgggcac ggcagcgccg tggtcccca      600
cgctatacca tctacctggg cttcgggcag gacctgtcag ctgggaggcc caaggagaag      660
agcctggtcc tggatgaagct ggaaccctgg ctgtgccgag tgcacctaga gggcacgcag      720
cgtgaggggtg tgtcttcctt ggatagcagc agcctcagcc tctgcctgtc cagcgccaac      780
agcctctatg acgacatcga gtgcttcctt atggagctgg agcagcccgc ctag          834

```

<210> SEQ ID NO: 37

<211> 277

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido sintético

<400> 37

```

Met Pro Gly Leu Pro Ala Gly Glu Leu Tyr Gly Trp Ala Val Glu Thr
1              5              10              15

Thr Pro Ser Pro Gly Pro Gln Pro Ala Ala Leu Thr Thr Gly Glu Ala
              20              25              30

Ala Ala Pro Glu Ser Pro His Gln Ala Glu Pro Tyr Leu Ser Pro Ser
              35              40              45

Pro Ser Ala Cys Thr Ala Val Gln Glu Pro Ser Pro Gly Ala Leu Asp
              50              55              60

Val Thr Ile Met Tyr Lys Gly Arg Thr Val Leu Gln Lys Val Val Gly
65              70              75              80

His Pro Ser Cys Thr Phe Leu Tyr Gly Pro Pro Asp Pro Ala Val Arg
              85              90              95

Ala Thr Asp Pro Gln Gln Val Ala Phe Pro Ser Pro Ala Glu Leu Pro
              100              105              110

```

Asp Gln Lys Gln Leu Arg Tyr Thr Glu Glu Leu Leu Arg His Val Ala
 115 120 125
 Pro Gly Leu His Leu Glu Leu Arg Gly Pro Gln Leu Trp Ala Arg Arg
 130 135 140
 Met Gly Lys Cys Lys Val Tyr Trp Glu Val Gly Gly Pro Pro Gly Ser
 145 150 155 160
 Ala Ser Pro Ser Thr Pro Ala Cys Leu Leu Pro Arg Asn Cys Asp Thr
 165 170 175
 Pro Ile Phe Asp Phe Arg Val Phe Phe Gln Glu Leu Val Glu Phe Arg
 180 185 190
 Ala Arg Gln Arg Arg Gly Ser Pro Arg Tyr Thr Ile Tyr Leu Gly Phe
 195 200 205
 Gly Gln Asp Leu Ser Ala Gly Arg Pro Lys Glu Lys Ser Leu Val Leu
 210 215 220
 Val Lys Leu Glu Pro Trp Leu Cys Arg Val His Leu Glu Gly Thr Gln
 225 230 235 240
 Arg Glu Gly Val Ser Ser Leu Asp Ser Ser Ser Leu Ser Leu Cys Leu
 245 250 255
 Ser Ser Ala Asn Ser Leu Tyr Asp Asp Ile Glu Cys Phe Leu Met Glu
 260 265 270
 Leu Glu Gln Pro Ala
 275

<210> SEQ ID NO: 38

<211> 1701

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 38

atggcaggca gacggcttac atggatcagc gagtttatcg taggtgccct ggactctgat	60
aagtaccct tggtaaaatg gcttgatcgg tcaacgggaa cttttctggc tcccgctgcg	120
agaaatgacg taataccact ggattccctg cagtttttca tagattttaa gagggagtgt	180
ttgtcaaagg ggctccacc cggagatctt ttgggtagtc caataactgc gttcggtaag	240
atttgataca ctagccgacg gctgagacga ttgcccggtg aagagtacga agttgtccaa	300
ggaatcaact gccggcggtg gcggcttctc tgcgccgaag tgaaagaatg ctggtggtgt	360
gtacacgcgc gaacacatct gactccgga agcagccttt gggaaattct ctaccagcat	420
tccgtaagac ttgaaaagca ccgacgaagg cccaggccct ttgtaggaga gaacagtgat	480
tcttctgagg aagaccacc tgctttctgc gatgtgcccg taacacaaac gggcgcgag	540
agcgaggaca gcggcgatga aggtccttcc accagacaca ggcctcagg tgtccaaccg	600
gtagacgatg ctaatgccga ctcccctggt tctggagacg aaggtcccag caccgcocat	660

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agcgacagtc aacctcctcc cgccgatgaa accactgtcc acacagacaa tgtagaggac      720
gatttgacac tccttgataa agagtccgcg tgcgcattga tgtatcacgt ggggcaggag      780
atggacatgc ttatgcgagc gatgtgcgat gaagacttgt ttgatttgct tgggatccct      840
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<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido sintético

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Leu Asp Ser Asp Lys Tyr Pro Leu Val Lys Trp Leu Asp Arg Ser Thr
          20           25           30

```

```

Gly Thr Phe Leu Ala Pro Ala Ala Arg Asn Asp Val Ile Pro Leu Asp
35           40           45

```

```

Ser Leu Gln Phe Phe Ile Asp Phe Lys Arg Glu Cys Leu Ser Lys Gly
50           55           60

```

```

Leu His Pro Arg Asp Leu Leu Gly Ser Pro Ile Thr Ala Phe Gly Lys
65           70           75           80

```

```

Ile Cys Thr Thr Ser Arg Arg Leu Arg Arg Leu Pro Gly Glu Glu Tyr
85           90           95

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Glu Val Val Gln Gly Ile Asn Cys Arg Arg Trp Arg Leu Leu Cys Ala
 100 105 110
 Glu Val Lys Glu Cys Trp Trp Cys Val His Ala Arg Thr His Leu His
 115 120 125
 Ser Gly Ser Ser Leu Trp Glu Ile Leu Tyr Gln His Ser Val Arg Leu
 130 135 140
 Glu Lys His Arg Arg Arg Pro Arg Pro Phe Val Gly Glu Asn Ser Asp
 145 150 155 160
 Ser Ser Glu Glu Asp His Pro Ala Phe Cys Asp Val Pro Val Thr Gln
 165 170 175
 Thr Gly Ala Glu Ser Glu Asp Ser Gly Asp Glu Gly Pro Ser Thr Arg
 180 185 190
 His Ser Ala Ser Gly Val Gln Pro Val Asp Asp Ala Asn Ala Asp Ser
 195 200 205
 Pro Gly Ser Gly Asp Glu Gly Pro Ser Thr Arg His Ser Asp Ser Gln
 210 215 220
 Pro Pro Pro Ala Asp Glu Thr Thr Val His Thr Asp Asn Val Glu Asp
 225 230 235 240
 Asp Leu Thr Leu Leu Asp Lys Glu Ser Ala Cys Ala Leu Met Tyr His
 245 250 255
 Val Gly Gln Glu Met Asp Met Leu Met Arg Ala Met Cys Asp Glu Asp
 260 265 270
 Leu Phe Asp Leu Leu Gly Ile Pro Glu Asp Val Ile Ala Thr Ser Gln
 275 280 285
 Pro Gly Gly Asp Thr Asp Ala Ser Gly Val Val Thr Glu Gly Ser Ile
 290 295 300
 Ala Ala Ser Ala Val Gly Ala Gly Val Glu Asp Val Tyr Leu Ala Gly
 305 310 315 320
 Ala Leu Glu Ala Gln Asn Val Ala Gly Glu Tyr Val Leu Glu Ile Ser
 325 330 335
 Asp Glu Glu Val Asp Asp Gly Ala Gly Leu Pro Pro Ala Ser Arg Arg
 340 345 350
 Arg Pro Val Val Gly Glu Phe Leu Trp Asp Asp Gly Pro Arg Arg His
 355 360 365
 Glu Arg Pro Thr Thr Arg Arg Ile Arg His Arg Lys Leu Arg Ser Ala
 370 375 380
 Tyr Tyr Arg Val Ala Arg Pro Pro Val Met Ile Thr Asp Arg Leu Gly
 385 390 395 400
 Val Glu Val Phe Tyr Phe Gly Arg Pro Ala Met Ser Leu Glu Val Glu
 405 410 415
 Arg Lys Val Phe Ile Leu Cys Ser Gln Asn Pro Leu Ala Asp Ile Ser
 420 425 430

