

P-2019-31598- Traducción secuencias notas.txt
LISTADO DE SECUENCIAS

<110> MODEARNTX, INC

<120> COMPOSICIONES TERAPÉUTICAS INMUNOMODULADORAS DE ARNm QUE CODIFICAN PÉPTIDOS DE ACTIVACIÓN DE MUTACIONES ONCOGÉNICAS

<130> MDN-015PC

<140> PCT/US2018/016510

<141> 2018-02-01

<150> US 62/453,465

<151> 2017-02-01

<150> US 62/467,063

<151> 2017-03-03

<150> US 62/490,523

<151> 2017-04-26

<150> US 62/541,571

<151> 2017-08-04

<160> 232

<170> PatentIn versión 3.5

<210> 1

<211> 379

<212> PRT

<213> Secuencia artificial

<220>

<223> Sintético: huSTING(V155M); sin etiqueta de epítipo

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Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
1 5 10 15

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
20 25 30

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
35 40 45

Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
50 55 60

Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65 70 75 80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
85 90 95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
100 105 110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
115 120 125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
130 135 140

Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu Ala
145 150 155 160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
165 170 175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
180 185 190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
195 200 205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
210 215 220

Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
225 230 235 240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
245 250 255

Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser

260

265

270

Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
 275 280 285

Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
 290 295 300

Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
 305 310 315 320

Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
 325 330 335

Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
 340 345 350

Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
 355 360 365

Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
 370 375

<210> 2
 <211> 379
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: Hu STING(R284T); sin etiqueta de epítipo

<400> 2

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 1 5 10 15

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
 20 25 30

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
 35 40 45

Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
 50 55 60

Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
 65 70 75 80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
 85 90 95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
 100 105 110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
 115 120 125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
 130 135 140

Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala
 145 150 155 160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
 165 170 175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
 180 185 190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
 195 200 205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
 210 215 220

Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
 225 230 235 240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
 245 250 255

Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
260 265 270

Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Thr Leu Glu Gln Ala
275 280 285

Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
290 295 300

Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305 310 315 320

Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
325 330 335

Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
340 345 350

Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
355 360 365

Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
370 375

<210> 3
<211> 379
<212> PRT
<213> Secuencia artificial

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<223> Sintético: hu STING (R284M); sin etiqueta de epítipo

<400> 3

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
1 5 10 15

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
20 25 30

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
35 40 45

Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
50 55 60

Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65 70 75 80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
85 90 95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
100 105 110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
115 120 125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
130 135 140

Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala
145 150 155 160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
165 170 175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
180 185 190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
195 200 205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
210 215 220

Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
225 230 235 240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
 245 250 255
 Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
 260 265 270
 Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Met Leu Glu Gln Ala
 275 280 285
 Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
 290 295 300
 Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
 305 310 315 320
 Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
 325 330 335
 Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
 340 345 350
 Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
 355 360 365
 Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
 370 375
 <210> 4
 <211> 379
 <212> PRT
 <213> Secuencia artificial
 <220>
 <223> Sintético: Hu STING (R284K); sin etiqueta de epítipo
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 Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 1 5 10 15
 Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
 20 25 30
 Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
 35 40 45
 Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
 50 55 60
 Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
 65 70 75 80
 Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
 85 90 95
 Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
 100 105 110
 Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
 115 120 125
 Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
 130 135 140
 Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala
 145 150 155 160
 Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
 165 170 175
 Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
 180 185 190
 Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
 195 200 205
 Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
 210 215 220

Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
 225 230 235 240
 Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
 245 250 255
 Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
 260 265 270
 Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Lys Leu Glu Gln Ala
 275 280 285
 Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
 290 295 300
 Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
 305 310 315 320
 Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
 325 330 335
 Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
 340 345 350
 Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
 355 360 365
 Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
 370 375

<210> 5
 <211> 379
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: Hu STING(N154S); sin etiqueta de epítipo
 <400> 5

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 1 5 10 15
 Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
 20 25 30
 Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
 35 40 45
 Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
 50 55 60
 Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
 65 70 75 80
 Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
 85 90 95
 Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
 100 105 110
 Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
 115 120 125
 Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
 130 135 140
 Ser Ala Val Cys Glu Lys Gly Asn Phe Ser Val Ala His Gly Leu Ala
 145 150 155 160
 Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
 165 170 175
 Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
 180 185 190
 Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
 195 200 205
 Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys

210 215 220

Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
225 230 235 240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
245 250 255

Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
260 265 270

Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
275 280 285

Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
290 295 300

Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305 310 315 320

Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
325 330 335

Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
340 345 350

Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
355 360 365

Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
370 375

<210> 6
<211> 379
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: Hu STING(V147L); sin etiqueta de epítipo

<400> 6

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
1 5 10 15

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
20 25 30

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
35 40 45

Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
50 55 60

Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65 70 75 80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
85 90 95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
100 105 110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
115 120 125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
130 135 140

Ser Ala Leu Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala
145 150 155 160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
165 170 175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
180 185 190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
195 200 205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
210 215 220

Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
225 230 235 240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
245 250 255

Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
260 265 270

Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
275 280 285

Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
290 295 300

Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305 310 315 320

Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
325 330 335

Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
340 345 350

Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
355 360 365

Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
370 375

<210> 7
<211> 379
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: Hu STING (E315Q); sin etiqueta de epítipo

<400> 7

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
1 5 10 15

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
20 25 30

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
35 40 45

Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
50 55 60

Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65 70 75 80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
85 90 95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
100 105 110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
115 120 125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
130 135 140

Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala
145 150 155 160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
165 170 175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
180 185 190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
 195 200 205
 Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
 210 215 220
 Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
 225 230 235 240
 Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
 245 250 255
 Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
 260 265 270
 Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
 275 280 285
 Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
 290 295 300
 Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Gln Pro Ala Asp Asp
 305 310 315 320
 Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
 325 330 335
 Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
 340 345 350
 Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
 355 360 365
 Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
 370 375
 <210> 8
 <211> 379
 <212> PRT
 <213> Secuencia artificial
 <220>
 <223> Sintético: Hu STING (R375A); sin etiqueta de epítipo
 <400> 8
 Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 1 5 10 15
 Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
 20 25 30
 Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
 35 40 45
 Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
 50 55 60
 Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
 65 70 75 80
 Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
 85 90 95
 Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
 100 105 110
 Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
 115 120 125
 Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
 130 135 140
 Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala
 145 150 155 160
 Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
 165 170 175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
180 185 190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
195 200 205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
210 215 220

Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
225 230 235 240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
245 250 255

Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
260 265 270

Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
275 280 285

Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
290 295 300

Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305 310 315 320

Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
325 330 335

Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
340 345 350

Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
355 360 365

Glu Lys Pro Leu Pro Leu Ala Thr Asp Phe Ser
370 375

<210> 9
<211> 379
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: Hu STING(V147L/N154S/V155M); sin etiqueta de epítipo

<400> 9

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
1 5 10 15

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
20 25 30

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
35 40 45

Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
50 55 60

Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65 70 75 80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
85 90 95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
100 105 110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
115 120 125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
130 135 140

Ser Ala Leu Cys Glu Lys Gly Asn Phe Ser Met Ala His Gly Leu Ala
145 150 155 160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln

165

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
180 185 190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
195 200 205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
210 215 220

Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
225 230 235 240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
245 250 255

Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
260 265 270

Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
275 280 285

Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
290 295 300

Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305 310 315 320

Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
325 330 335

Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
340 345 350

Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
355 360 365

Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
370 375

<210> 10

<211> 379

<212> PRT

<213> Secuencia artificial

<220>

<223> Sintético: Hu STING(R284M/V147L/N154S/V155M); sin etiqueta de epítipo

<400> 10

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
1 5 10 15

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
20 25 30

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
35 40 45

Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
50 55 60

Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65 70 75 80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
85 90 95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
100 105 110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
115 120 125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
130 135 140

Ser Ala Leu Cys Glu Lys Gly Asn Phe Ser Met Ala His Gly Leu Ala
145 150 155 160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
165 170 175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
180 185 190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
195 200 205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
210 215 220

Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
225 230 235 240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
245 250 255

Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
260 265 270

Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Met Leu Glu Gln Ala
275 280 285

Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
290 295 300

Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305 310 315 320

Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
325 330 335

Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
340 345 350

Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
355 360 365

Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
370 375

<210> 11
<211> 419
<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(419)
<223> superratón IRF3 S396D; sin etiqueta de epítipo
<400> 11

Met Glu Thr Pro Lys Pro Arg Ile Leu Pro Trp Leu Val Ser Gln Leu
1 5 10 15

Asp Leu Gly Gln Leu Glu Gly Val Ala Trp Leu Asp Glu Ser Arg Thr
20 25 30

Arg Phe Arg Ile Pro Trp Lys His Gly Leu Arg Gln Asp Ala Gln Met
35 40 45

Ala Asp Phe Gly Ile Phe Gln Ala Trp Ala Glu Ala Ser Gly Ala Tyr
50 55 60

Thr Pro Gly Lys Asp Lys Pro Asp Val Ser Thr Trp Lys Arg Asn Phe
65 70 75 80

Arg Ser Ala Leu Asn Arg Lys Glu Val Leu Arg Leu Ala Ala Asp Asn
85 90 95

Ser Lys Asp Pro Tyr Asp Pro His Lys Val Tyr Glu Phe Val Thr Pro
100 105 110

Gly Ala Arg Asp Phe Val His Leu Gly Ala Ser Pro Asp Thr Asn Gly
115 120 125

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

Gly Asn Ile

<210> 12
 <211> 427
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(427)
 <223> superhumano IRF3 S396D; sin etiqueta de epítipo

<400> 12

Met Gly Thr Pro Lys Pro Arg Ile Leu Pro Trp Leu Val Ser Gln Leu
 1 5 10 15
 Asp Leu Gly Gln Leu Glu Gly Val Ala Trp Val Asn Lys Ser Arg Thr
 20 25 30
 Arg Phe Arg Ile Pro Trp Lys His Gly Leu Arg Gln Asp Ala Gln Gln
 35 40 45
 Glu Asp Phe Gly Ile Phe Gln Ala Trp Ala Glu Ala Thr Gly Ala Tyr
 50 55 60

Val Pro Gly Arg Asp Lys Pro Asp Leu Pro Thr Trp Lys Arg Asn Phe
 65 70 75 80
 Arg Ser Ala Leu Asn Arg Lys Glu Gly Leu Arg Leu Ala Glu Asp Arg
 85 90 95
 Ser Lys Asp Pro His Asp Pro His Lys Ile Tyr Glu Phe Val Asn Ser
 100 105 110
 Gly Val Gly Asp Phe Ser Gln Pro Asp Thr Ser Pro Asp Thr Asn Gly
 115 120 125
 Gly Gly Ser Thr Ser Asp Thr Gln Glu Asp Ile Leu Asp Glu Leu Leu
 130 135 140
 Gly Asn Met Val Leu Ala Pro Leu Pro Asp Pro Gly Pro Pro Ser Leu
 145 150 155 160
 Ala Val Ala Pro Glu Pro Cys Pro Gln Pro Leu Arg Ser Pro Ser Leu
 165 170 175
 Asp Asn Pro Thr Pro Phe Pro Asn Leu Gly Pro Ser Glu Asn Pro Leu
 180 185 190
 Lys Arg Leu Leu Val Pro Gly Glu Glu Trp Glu Phe Glu Val Thr Ala
 195 200 205
 Phe Tyr Arg Gly Arg Gln Val Phe Gln Gln Thr Ile Ser Cys Pro Glu
 210 215 220
 Gly Leu Arg Leu Val Gly Ser Glu Val Gly Asp Arg Thr Leu Pro Gly
 225 230 235 240
 Trp Pro Val Thr Leu Pro Asp Pro Gly Met Ser Leu Thr Asp Arg Gly
 245 250 255
 Val Met Ser Tyr Val Arg His Val Leu Ser Cys Leu Gly Gly Gly Leu
 260 265 270
 Ala Leu Trp Arg Ala Gly Gln Trp Leu Trp Ala Gln Arg Leu Gly His
 275 280 285
 Cys His Thr Tyr Trp Ala Val Ser Glu Glu Leu Leu Pro Asn Ser Gly
 290 295 300
 His Gly Pro Asp Gly Glu Val Pro Lys Asp Lys Glu Gly Gly Val Phe
 305 310 315 320
 Asp Leu Gly Pro Phe Ile Val Asp Leu Ile Thr Phe Thr Glu Gly Ser
 325 330 335
 Gly Arg Ser Pro Arg Tyr Ala Leu Trp Phe Cys Val Gly Glu Ser Trp
 340 345 350
 Pro Gln Asp Gln Pro Trp Thr Lys Arg Leu Val Met Val Lys Val Val
 355 360 365
 Pro Thr Cys Leu Arg Ala Leu Val Glu Met Ala Arg Val Gly Gly Ala
 370 375 380
 Ser Ser Leu Glu Asn Thr Val Asp Leu His Ile Asp Asn Ser His Pro
 385 390 395 400
 Leu Ser Leu Thr Ser Asp Gln Tyr Lys Ala Tyr Leu Gln Asp Leu Val
 405 410 415
 Glu Gly Met Asp Phe Gln Gly Pro Gly Glu Thr
 420 425

<210> 13

<211> 503

<212> PRT

<213> Secuencia artificial

<220>

<223> Sintético: Wild-type Hu IRF7 isoform A; P037 sin etiqueta de epítipo

<400> 13

Met Ala Leu Ala Pro Glu Arg Ala Ala Pro Arg Val Leu Phe Gly Glu
 1 5 10 15
 Trp Leu Leu Gly Glu Ile Ser Ser Gly Cys Tyr Glu Gly Leu Gln Trp
 20 25 30
 Leu Asp Glu Ala Arg Thr Cys Phe Arg Val Pro Trp Lys His Phe Ala
 35 40 45
 Arg Lys Asp Leu Ser Glu Ala Asp Ala Arg Ile Phe Lys Ala Trp Ala
 50 55 60
 Val Ala Arg Gly Arg Trp Pro Pro Ser Ser Arg Gly Gly Gly Pro Pro
 65 70 75 80
 Pro Glu Ala Glu Thr Ala Glu Arg Ala Gly Trp Lys Thr Asn Phe Arg
 85 90 95
 Cys Ala Leu Arg Ser Thr Arg Arg Phe Val Met Leu Arg Asp Asn Ser
 100 105 110
 Gly Asp Pro Ala Asp Pro His Lys Val Tyr Ala Leu Ser Arg Glu Leu
 115 120 125
 Cys Trp Arg Glu Gly Pro Gly Thr Asp Gln Thr Glu Ala Glu Ala Pro
 130 135 140
 Ala Ala Val Pro Pro Pro Gln Gly Gly Pro Pro Gly Pro Phe Leu Ala
 145 150 155 160
 His Thr His Ala Gly Leu Gln Ala Pro Gly Pro Leu Pro Ala Pro Ala
 165 170 175
 Gly Asp Lys Gly Asp Leu Leu Leu Gln Ala Val Gln Gln Ser Cys Leu
 180 185 190
 Ala Asp His Leu Leu Thr Ala Ser Trp Gly Ala Asp Pro Val Pro Thr
 195 200 205
 Lys Ala Pro Gly Glu Gly Gln Glu Gly Leu Pro Leu Thr Gly Ala Cys
 210 215 220
 Ala Gly Gly Pro Gly Leu Pro Ala Gly Glu Leu Tyr Gly Trp Ala Val
 225 230 235 240
 Glu Thr Thr Pro Ser Pro Gly Pro Gln Pro Ala Ala Leu Thr Thr Gly
 245 250 255
 Glu Ala Ala Ala Pro Glu Ser Pro His Gln Ala Glu Pro Tyr Leu Ser
 260 265 270
 Pro Ser Pro Ser Ala Cys Thr Ala Val Gln Glu Pro Ser Pro Gly Ala
 275 280 285
 Leu Asp Val Thr Ile Met Tyr Lys Gly Arg Thr Val Leu Gln Lys Val
 290 295 300
 Val Gly His Pro Ser Cys Thr Phe Leu Tyr Gly Pro Pro Asp Pro Ala
 305 310 315 320
 Val Arg Ala Thr Asp Pro Gln Gln Val Ala Phe Pro Ser Pro Ala Glu
 325 330 335
 Leu Pro Asp Gln Lys Gln Leu Arg Tyr Thr Glu Glu Leu Leu Arg His
 340 345 350
 Val Ala Pro Gly Leu His Leu Glu Leu Arg Gly Pro Gln Leu Trp Ala
 355 360 365
 Arg Arg Met Gly Lys Cys Lys Val Tyr Trp Glu Val Gly Gly Pro Pro
 370 375 380
 Gly Ser Ala Ser Pro Ser Thr Pro Ala Cys Leu Leu Pro Arg Asn Cys
 385 390 395 400
 Asp Thr Pro Ile Phe Asp Phe Arg Val Phe Phe Gln Glu Leu Val Glu
 405 410 415

Phe Arg Ala Arg Gln Arg Arg Gly Ser Pro Arg Tyr Thr Ile Tyr Leu
420 425 430

Gly Phe Gly Gln Asp Leu Ser Ala Gly Arg Pro Lys Glu Lys Ser Leu
435 440 445

Val Leu Val Lys Leu Glu Pro Trp Leu Cys Arg Val His Leu Glu Gly
450 455 460

Thr Gln Arg Glu Gly Val Ser Ser Leu Asp Ser Ser Ser Leu Ser Leu
465 470 475 480

Cys Leu Ser Ser Ala Asn Ser Leu Tyr Asp Asp Ile Glu Cys Phe Leu
485 490 495

Met Glu Leu Glu Gln Pro Ala
500

<210> 14
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: Hu IRF7 constitutivamente activo S477D/S479D; P033 sin etiqueta de epítipo

<400> 14

Met Ala Leu Ala Pro Glu Arg Ala Ala Pro Arg Val Leu Phe Gly Glu
1 5 10 15

Trp Leu Leu Gly Glu Ile Ser Ser Gly Cys Tyr Glu Gly Leu Gln Trp
20 25 30

Leu Asp Glu Ala Arg Thr Cys Phe Arg Val Pro Trp Lys His Phe Ala
35 40 45

Arg Lys Asp Leu Ser Glu Ala Asp Ala Arg Ile Phe Lys Ala Trp Ala
50 55 60

Val Ala Arg Gly Arg Trp Pro Pro Ser Ser Arg Gly Gly Gly Pro Pro
65 70 75 80

Pro Glu Ala Glu Thr Ala Glu Arg Ala Gly Trp Lys Thr Asn Phe Arg
85 90 95

Cys Ala Leu Arg Ser Thr Arg Arg Phe Val Met Leu Arg Asp Asn Ser
100 105 110

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

Cys Trp Arg Glu Gly Pro Gly Thr Asp Gln Thr Glu Ala Glu Ala Pro
130 135 140

Ala Ala Val Pro Pro Pro Gln Gly Gly Pro Pro Gly Pro Phe Leu Ala
145 150 155 160

His Thr His Ala Gly Leu Gln Ala Pro Gly Pro Leu Pro Ala Pro Ala
165 170 175

Gly Asp Lys Gly Asp Leu Leu Leu Gln Ala Val Gln Gln Ser Cys Leu
180 185 190

Ala Asp His Leu Leu Thr Ala Ser Trp Gly Ala Asp Pro Val Pro Thr
195 200 205

Lys Ala Pro Gly Glu Gly Gln Glu Gly Leu Pro Leu Thr Gly Ala Cys
210 215 220

Ala Gly Gly Pro Gly Leu Pro Ala Gly Glu Leu Tyr Gly Trp Ala Val
225 230 235 240

Glu Thr Thr Pro Ser Pro Gly Pro Gln Pro Ala Ala Leu Thr Thr Gly
245 250 255

Glu Ala Ala Ala Pro Glu Ser Pro His Gln Ala Glu Pro Tyr Leu Ser
260 265 270

Pro Ser Pro Ser Ala Cys Thr Ala Val Gln Glu Pro Ser Pro Gly Ala
275 280 285

Leu Asp Val Thr Ile Met Tyr Lys Gly Arg Thr Val Leu Gln Lys Val
290 295 300

Val Gly His Pro Ser Cys Thr Phe Leu Tyr Gly Pro Pro Asp Pro Ala
305 310 315 320

Val Arg Ala Thr Asp Pro Gln Gln Val Ala Phe Pro Ser Pro Ala Glu
325 330 335

Leu Pro Asp Gln Lys Gln Leu Arg Tyr Thr Glu Glu Leu Leu Arg His
340 345 350

Val Ala Pro Gly Leu His Leu Glu Leu Arg Gly Pro Gln Leu Trp Ala
355 360 365

Arg Arg Met Gly Lys Cys Lys Val Tyr Trp Glu Val Gly Gly Pro Pro
370 375 380

Gly Ser Ala Ser Pro Ser Thr Pro Ala Cys Leu Leu Pro Arg Asn Cys
385 390 395 400

Asp Thr Pro Ile Phe Asp Phe Arg Val Phe Phe Gln Glu Leu Val Glu
405 410 415

Phe Arg Ala Arg Gln Arg Arg Gly Ser Pro Arg Tyr Thr Ile Tyr Leu
420 425 430

Gly Phe Gly Gln Asp Leu Ser Ala Gly Arg Pro Lys Glu Lys Ser Leu
435 440 445

Val Leu Val Lys Leu Glu Pro Trp Leu Cys Arg Val His Leu Glu Gly
450 455 460

Thr Gln Arg Glu Gly Val Ser Ser Leu Asp Ser Ser Asp Leu Asp Leu
465 470 475 480

Cys Leu Ser Ser Ala Asn Ser Leu Tyr Asp Asp Ile Glu Cys Phe Leu
485 490 495

Met Glu Leu Glu Gln Pro Ala
500

<210> 15
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: Hu IRF7 constitutivamente activo S475D/S477D/L480D; P034 sin etiqueta de epítipo
<400> 15

Met Ala Leu Ala Pro Glu Arg Ala Ala Pro Arg Val Leu Phe Gly Glu
1 5 10 15

Trp Leu Leu Gly Glu Ile Ser Ser Gly Cys Tyr Glu Gly Leu Gln Trp
20 25 30

Leu Asp Glu Ala Arg Thr Cys Phe Arg Val Pro Trp Lys His Phe Ala
35 40 45

Arg Lys Asp Leu Ser Glu Ala Asp Ala Arg Ile Phe Lys Ala Trp Ala
50 55 60

Val Ala Arg Gly Arg Trp Pro Pro Ser Ser Arg Gly Gly Gly Pro Pro
65 70 75 80

Pro Glu Ala Glu Thr Ala Glu Arg Ala Gly Trp Lys Thr Asn Phe Arg
85 90 95

Cys Ala Leu Arg Ser Thr Arg Arg Phe Val Met Leu Arg Asp Asn Ser
100 105 110

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

Cys Trp Arg Glu Gly Pro Gly Thr Asp Gln Thr Glu Ala Glu Ala Pro
 130 135 140
 Ala Ala Val Pro Pro Pro Gln Gly Gly Pro Pro Gly Pro Phe Leu Ala
 145 150 155 160
 His Thr His Ala Gly Leu Gln Ala Pro Gly Pro Leu Pro Ala Pro Ala
 165 170 175
 Gly Asp Lys Gly Asp Leu Leu Leu Gln Ala Val Gln Gln Ser Cys Leu
 180 185 190
 Ala Asp His Leu Leu Thr Ala Ser Trp Gly Ala Asp Pro Val Pro Thr
 195 200 205
 Lys Ala Pro Gly Glu Gly Gln Glu Gly Leu Pro Leu Thr Gly Ala Cys
 210 215 220
 Ala Gly Gly Pro Gly Leu Pro Ala Gly Glu Leu Tyr Gly Trp Ala Val
 225 230 235 240
 Glu Thr Thr Pro Ser Pro Gly Pro Gln Pro Ala Ala Leu Thr Thr Gly
 245 250 255
 Glu Ala Ala Ala Pro Glu Ser Pro His Gln Ala Glu Pro Tyr Leu Ser
 260 265 270
 Pro Ser Pro Ser Ala Cys Thr Ala Val Gln Glu Pro Ser Pro Gly Ala
 275 280 285
 Leu Asp Val Thr Ile Met Tyr Lys Gly Arg Thr Val Leu Gln Lys Val
 290 295 300
 Val Gly His Pro Ser Cys Thr Phe Leu Tyr Gly Pro Pro Asp Pro Ala
 305 310 315 320
 Val Arg Ala Thr Asp Pro Gln Gln Val Ala Phe Pro Ser Pro Ala Glu
 325 330 335
 Leu Pro Asp Gln Lys Gln Leu Arg Tyr Thr Glu Glu Leu Leu Arg His
 340 345 350
 Val Ala Pro Gly Leu His Leu Glu Leu Arg Gly Pro Gln Leu Trp Ala
 355 360 365
 Arg Arg Met Gly Lys Cys Lys Val Tyr Trp Glu Val Gly Gly Pro Pro
 370 375 380
 Gly Ser Ala Ser Pro Ser Thr Pro Ala Cys Leu Leu Pro Arg Asn Cys
 385 390 395 400
 Asp Thr Pro Ile Phe Asp Phe Arg Val Phe Phe Gln Glu Leu Val Glu
 405 410 415
 Phe Arg Ala Arg Gln Arg Arg Gly Ser Pro Arg Tyr Thr Ile Tyr Leu
 420 425 430
 Gly Phe Gly Gln Asp Leu Ser Ala Gly Arg Pro Lys Glu Lys Ser Leu
 435 440 445
 Val Leu Val Lys Leu Glu Pro Trp Leu Cys Arg Val His Leu Glu Gly
 450 455 460
 Thr Gln Arg Glu Gly Val Ser Ser Leu Asp Asp Ser Asp Leu Ser Asp
 465 470 475 480
 Cys Leu Ser Ser Ala Asn Ser Leu Tyr Asp Asp Ile Glu Cys Phe Leu
 485 490 495
 Met Glu Leu Glu Gln Pro Ala
 500

<210> 16
 <211> 503
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: Hu IRF7 constitutivamente activo S475D/S476D/S477D/S479D/S483D/S487D; P035 sin etiqueta de epítipo

<400> 16

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Met Ala Leu Ala Pro Glu Arg Ala Ala Pro Arg Val Leu Phe Gly Glu
1      5      10      15

Trp Leu Leu Gly Glu Ile Ser Ser Gly Cys Tyr Glu Gly Leu Gln Trp
20      25      30

Leu Asp Glu Ala Arg Thr Cys Phe Arg Val Pro Trp Lys His Phe Ala
35      40      45

Arg Lys Asp Leu Ser Glu Ala Asp Ala Arg Ile Phe Lys Ala Trp Ala
50      55      60

Val Ala Arg Gly Arg Trp Pro Pro Ser Ser Arg Gly Gly Gly Pro Pro
65      70      75      80

Pro Glu Ala Glu Thr Ala Glu Arg Ala Gly Trp Lys Thr Asn Phe Arg
85      90      95

Cys Ala Leu Arg Ser Thr Arg Arg Phe Val Met Leu Arg Asp Asn Ser
100     105     110

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

Cys Trp Arg Glu Gly Pro Gly Thr Asp Gln Thr Glu Ala Glu Ala Pro
130     135     140

Ala Ala Val Pro Pro Pro Gln Gly Gly Pro Pro Gly Pro Phe Leu Ala
145     150     155     160

His Thr His Ala Gly Leu Gln Ala Pro Gly Pro Leu Pro Ala Pro Ala
165     170     175

Gly Asp Lys Gly Asp Leu Leu Leu Gln Ala Val Gln Gln Ser Cys Leu
180     185     190

Ala Asp His Leu Leu Thr Ala Ser Trp Gly Ala Asp Pro Val Pro Thr
195     200     205

Lys Ala Pro Gly Glu Gly Gln Glu Gly Leu Pro Leu Thr Gly Ala Cys
210     215     220

Ala Gly Gly Pro Gly Leu Pro Ala Gly Glu Leu Tyr Gly Trp Ala Val
225     230     235     240

Glu Thr Thr Pro Ser Pro Gly Pro Gln Pro Ala Ala Leu Thr Thr Gly
245     250     255

Glu Ala Ala Ala Pro Glu Ser Pro His Gln Ala Glu Pro Tyr Leu Ser
260     265     270

Pro Ser Pro Ser Ala Cys Thr Ala Val Gln Glu Pro Ser Pro Gly Ala
275     280     285

Leu Asp Val Thr Ile Met Tyr Lys Gly Arg Thr Val Leu Gln Lys Val
290     295     300

Val Gly His Pro Ser Cys Thr Phe Leu Tyr Gly Pro Pro Asp Pro Ala
305     310     315     320

Val Arg Ala Thr Asp Pro Gln Gln Val Ala Phe Pro Ser Pro Ala Glu
325     330     335

Leu Pro Asp Gln Lys Gln Leu Arg Tyr Thr Glu Glu Leu Leu Arg His
340     345     350

Val Ala Pro Gly Leu His Leu Glu Leu Arg Gly Pro Gln Leu Trp Ala
355     360     365

Arg Arg Met Gly Lys Cys Lys Val Tyr Trp Glu Val Gly Gly Pro Pro
370     375     380

Gly Ser Ala Ser Pro Ser Thr Pro Ala Cys Leu Leu Pro Arg Asn Cys
385     390     395     400

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Asp Thr Pro Ile Phe Asp Phe Arg Val Phe Phe Gln Glu Leu Val Glu
405 410 415

Phe Arg Ala Arg Gln Arg Arg Gly Ser Pro Arg Tyr Thr Ile Tyr Leu
420 425 430

Gly Phe Gly Gln Asp Leu Ser Ala Gly Arg Pro Lys Glu Lys Ser Leu
435 440 445

Val Leu Val Lys Leu Glu Pro Trp Leu Cys Arg Val His Leu Glu Gly
450 455 460

Thr Gln Arg Glu Gly Val Ser Ser Leu Asp Asp Asp Asp Leu Asp Leu
465 470 475 480

Cys Leu Asp Ser Ala Asn Asp Leu Tyr Asp Asp Ile Glu Cys Phe Leu
485 490 495

Met Glu Leu Glu Gln Pro Ala
500

<210> 17
<211> 282
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: Hu IRF7 truncado constitutivamente activo 1-246 +
468-503; P032 sin etiqueta de epítipo

<400> 17

Met Ala Leu Ala Pro Glu Arg Ala Ala Pro Arg Val Leu Phe Gly Glu
1 5 10 15

Trp Leu Leu Gly Glu Ile Ser Ser Gly Cys Tyr Glu Gly Leu Gln Trp
20 25 30

Leu Asp Glu Ala Arg Thr Cys Phe Arg Val Pro Trp Lys His Phe Ala
35 40 45

Arg Lys Asp Leu Ser Glu Ala Asp Ala Arg Ile Phe Lys Ala Trp Ala
50 55 60

Val Ala Arg Gly Arg Trp Pro Pro Ser Ser Arg Gly Gly Gly Pro Pro
65 70 75 80

Pro Glu Ala Glu Thr Ala Glu Arg Ala Gly Trp Lys Thr Asn Phe Arg
85 90 95

Cys Ala Leu Arg Ser Thr Arg Arg Phe Val Met Leu Arg Asp Asn Ser
100 105 110

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

Cys Trp Arg Glu Gly Pro Gly Thr Asp Gln Thr Glu Ala Glu Ala Pro
130 135 140

Ala Ala Val Pro Pro Pro Gln Gly Gly Pro Pro Gly Pro Phe Leu Ala
145 150 155 160

His Thr His Ala Gly Leu Gln Ala Pro Gly Pro Leu Pro Ala Pro Ala
165 170 175

Gly Asp Lys Gly Asp Leu Leu Leu Gln Ala Val Gln Gln Ser Cys Leu
180 185 190

Ala Asp His Leu Leu Thr Ala Ser Trp Gly Ala Asp Pro Val Pro Thr
195 200 205

Lys Ala Pro Gly Glu Gly Gln Glu Gly Leu Pro Leu Thr Gly Ala Cys
210 215 220

Ala Gly Gly Pro Gly Leu Pro Ala Gly Glu Leu Tyr Gly Trp Ala Val
225 230 235 240

Glu Thr Thr Pro Ser Pro Glu Gly Val Ser Ser Leu Asp Ser Ser Ser
245 250 255

Leu Ser Leu Cys Leu Ser Ser Ala Asn Ser Leu Tyr Asp Asp Ile Glu
260 265 270

Cys Phe Leu Met Glu Leu Glu Gln Pro Ala
275 280

<210> 18
<211> 282
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: Hu IRF7 truncado constitutivamente activo 1-246 +
468-503 más S475D/S476D/S477D/S479D/S483D/S487D; P036 sin etiqueta de epítipo

<400> 18

Met Ala Leu Ala Pro Glu Arg Ala Ala Pro Arg Val Leu Phe Gly Glu
1 5 10 15

Trp Leu Leu Gly Glu Ile Ser Ser Gly Cys Tyr Glu Gly Leu Gln Trp
20 25 30

Leu Asp Glu Ala Arg Thr Cys Phe Arg Val Pro Trp Lys His Phe Ala
35 40 45

Arg Lys Asp Leu Ser Glu Ala Asp Ala Arg Ile Phe Lys Ala Trp Ala
50 55 60

Val Ala Arg Gly Arg Trp Pro Pro Ser Ser Arg Gly Gly Gly Pro Pro
65 70 75 80

Pro Glu Ala Glu Thr Ala Glu Arg Ala Gly Trp Lys Thr Asn Phe Arg
85 90 95

Cys Ala Leu Arg Ser Thr Arg Arg Phe Val Met Leu Arg Asp Asn Ser
100 105 110

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

Cys Trp Arg Glu Gly Pro Gly Thr Asp Gln Thr Glu Ala Glu Ala Pro
130 135 140

Ala Ala Val Pro Pro Pro Gln Gly Gly Pro Pro Gly Pro Phe Leu Ala
145 150 155 160

His Thr His Ala Gly Leu Gln Ala Pro Gly Pro Leu Pro Ala Pro Ala
165 170 175

Gly Asp Lys Gly Asp Leu Leu Leu Gln Ala Val Gln Gln Ser Cys Leu
180 185 190

Ala Asp His Leu Leu Thr Ala Ser Trp Gly Ala Asp Pro Val Pro Thr
195 200 205

Lys Ala Pro Gly Glu Gly Gln Glu Gly Leu Pro Leu Thr Gly Ala Cys
210 215 220

Ala Gly Gly Pro Gly Leu Pro Ala Gly Glu Leu Tyr Gly Trp Ala Val
225 230 235 240

Glu Thr Thr Pro Ser Pro Glu Gly Val Ser Ser Leu Asp Asp Asp Asp
245 250 255

Leu Asp Leu Cys Leu Asp Ser Ala Asn Asp Leu Tyr Asp Asp Ile Glu
260 265 270

Cys Phe Leu Met Glu Leu Glu Gln Pro Ala
275 280

<210> 19
<211> 408
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: Hu IRF7 truncado 1-151 + 247-503; P038 sin etiqueta de epítipo; mutación nula

<400> 19

Met Ala Leu Ala Pro Glu Arg Ala Ala Pro Arg Val Leu Phe Gly Glu
1 5 10 15

Trp Leu Leu Gly Glu Ile Ser Ser Gly Cys Tyr Glu Gly Leu Gln Trp
 20 25 30
 Leu Asp Glu Ala Arg Thr Cys Phe Arg Val Pro Trp Lys His Phe Ala
 35 40 45
 Arg Lys Asp Leu Ser Glu Ala Asp Ala Arg Ile Phe Lys Ala Trp Ala
 50 55 60
 Val Ala Arg Gly Arg Trp Pro Pro Ser Ser Arg Gly Gly Gly Pro Pro
 65 70 75 80
 Pro Glu Ala Glu Thr Ala Glu Arg Ala Gly Trp Lys Thr Asn Phe Arg
 85 90 95
 Cys Ala Leu Arg Ser Thr Arg Arg Phe Val Met Leu Arg Asp Asn Ser
 100 105 110
 Gly Asp Pro Ala Asp Pro His Lys Val Tyr Ala Leu Ser Arg Glu Leu
 115 120 125
 Cys Trp Arg Glu Gly Pro Gly Thr Asp Gln Thr Glu Ala Glu Ala Pro
 130 135 140
 Ala Ala Val Pro Pro Pro Gln Gly Pro Gln Pro Ala Ala Leu Thr Thr
 145 150 155 160
 Gly Glu Ala Ala Ala Pro Glu Ser Pro His Gln Ala Glu Pro Tyr Leu
 165 170 175
 Ser Pro Ser Pro Ser Ala Cys Thr Ala Val Gln Glu Pro Ser Pro Gly
 180 185 190
 Ala Leu Asp Val Thr Ile Met Tyr Lys Gly Arg Thr Val Leu Gln Lys
 195 200 205
 Val Val Gly His Pro Ser Cys Thr Phe Leu Tyr Gly Pro Pro Asp Pro
 210 215 220
 Ala Val Arg Ala Thr Asp Pro Gln Gln Val Ala Phe Pro Ser Pro Ala
 225 230 235 240
 Glu Leu Pro Asp Gln Lys Gln Leu Arg Tyr Thr Glu Glu Leu Leu Arg
 245 250 255
 His Val Ala Pro Gly Leu His Leu Glu Leu Arg Gly Pro Gln Leu Trp
 260 265 270
 Ala Arg Arg Met Gly Lys Cys Lys Val Tyr Trp Glu Val Gly Gly Pro
 275 280 285
 Pro Gly Ser Ala Ser Pro Ser Thr Pro Ala Cys Leu Leu Pro Arg Asn
 290 295 300
 Cys Asp Thr Pro Ile Phe Asp Phe Arg Val Phe Phe Gln Glu Leu Val
 305 310 315 320
 Glu Phe Arg Ala Arg Gln Arg Arg Gly Ser Pro Arg Tyr Thr Ile Tyr
 325 330 335
 Leu Gly Phe Gly Gln Asp Leu Ser Ala Gly Arg Pro Lys Glu Lys Ser
 340 345 350
 Leu Val Leu Val Lys Leu Glu Pro Trp Leu Cys Arg Val His Leu Glu
 355 360 365
 Gly Thr Gln Arg Glu Gly Val Ser Ser Leu Asp Ser Ser Ser Leu Ser
 370 375 380
 Leu Cys Leu Ser Ser Ala Asn Ser Leu Tyr Asp Asp Ile Glu Cys Phe
 385 390 395 400
 Leu Met Glu Leu Glu Gln Pro Ala
 405

<211> 353
 <212> PRT
 <213> Secuencia artificial
 <220>
 <223> Sintético: Hu IRF7 truncado 152-503; P039 sin etiqueta de epítipo; mutación nula
 <400> 20

Met Gly Gly Pro Pro Gly Pro Phe Leu Ala His Thr His Ala Gly Leu
 1 5 10 15

Gln Ala Pro Gly Pro Leu Pro Ala Pro Ala Gly Asp Lys Gly Asp Leu
 20 25 30

Leu Leu Gln Ala Val Gln Gln Ser Cys Leu Ala Asp His Leu Leu Thr
 35 40 45

Ala Ser Trp Gly Ala Asp Pro Val Pro Thr Lys Ala Pro Gly Glu Gly
 50 55 60

Gln Glu Gly Leu Pro Leu Thr Gly Ala Cys Ala Gly Gly Pro Gly Leu
 65 70 75 80

Pro Ala Gly Glu Leu Tyr Gly Trp Ala Val Glu Thr Thr Pro Ser Pro
 85 90 95

Gly Pro Gln Pro Ala Ala Leu Thr Thr Gly Glu Ala Ala Ala Pro Glu
 100 105 110

Ser Pro His Gln Ala Glu Pro Tyr Leu Ser Pro Ser Pro Ser Ala Cys
 115 120 125

Thr Ala Val Gln Glu Pro Ser Pro Gly Ala Leu Asp Val Thr Ile Met
 130 135 140

Tyr Lys Gly Arg Thr Val Leu Gln Lys Val Val Gly His Pro Ser Cys
 145 150 155 160

Thr Phe Leu Tyr Gly Pro Pro Asp Pro Ala Val Arg Ala Thr Asp Pro
 165 170 175

Gln Gln Val Ala Phe Pro Ser Pro Ala Glu Leu Pro Asp Gln Lys Gln
 180 185 190

Leu Arg Tyr Thr Glu Glu Leu Leu Arg His Val Ala Pro Gly Leu His
 195 200 205

Leu Glu Leu Arg Gly Pro Gln Leu Trp Ala Arg Arg Met Gly Lys Cys
 210 215 220

Lys Val Tyr Trp Glu Val Gly Gly Pro Pro Gly Ser Ala Ser Pro Ser
 225 230 235 240

Thr Pro Ala Cys Leu Leu Pro Arg Asn Cys Asp Thr Pro Ile Phe Asp
 245 250 255

Phe Arg Val Phe Phe Gln Glu Leu Val Glu Phe Arg Ala Arg Gln Arg
 260 265 270

Arg Gly Ser Pro Arg Tyr Thr Ile Tyr Leu Gly Phe Gly Gln Asp Leu
 275 280 285

Ser Ala Gly Arg Pro Lys Glu Lys Ser Leu Val Leu Val Lys Leu Glu
 290 295 300

Pro Trp Leu Cys Arg Val His Leu Glu Gly Thr Gln Arg Glu Gly Val
 305 310 315 320

Ser Ser Leu Asp Ser Ser Ser Leu Ser Leu Cys Leu Ser Ser Ala Asn
 325 330 335

Ser Leu Tyr Asp Asp Ile Glu Cys Phe Leu Met Glu Leu Glu Gln Pro
 340 345 350

Ala

<210> 21
 <211> 92

<212> ADN
 <213> Secuencia artificial
 <220>
 <223> Sintético: 5 UTR
 <400> 21
 tcaagctttt ggaccctcgt acagaagcta atacgactca ctatagggaa ataagagaga 60
 aaagaagagt aagaagaaat ataagagcca cc 92
 <210> 22
 <211> 119
 <212> ADN
 <213> Secuencia artificial
 <220>
 <223> Sintético: 3 UTR
 <400> 22
 tgataatagg ctggagcctc ggtggccatg cttcttgccc cttgggcctc cccccagccc 60
 ctctctcccct tctgcaccc gtacccccgt ggtctttgaa taaagtctga gtgggcggc 119
 <210> 23
 <211> 164
 <212> ADN
 <213> Secuencia artificial
 <220>
 <223> Sintético: 3 UTR con sitios mi-122 y mi-142.3p
 <400> 23
 tgataatagg ctggagcctc ggtggccatg cttcttgccc cttgggcca aacaccattg 60
 tcacactcca tccccccagc ccctcctccc cttcctccat aaagtaggaa acactacatg 120
 caccgtacc cccgtggtct ttgaataaag tctgagtggg cggc 164
 <210> 24
 <211> 22
 <212> PRT
 <213> Secuencia artificial
 <220>
 <223> Sintético: secuencia de aminoácidos péptido 2A
 <400> 24
 Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
 1 5 10 15
 Glu Glu Asn Pro Gly Pro
 20
 <210> 25
 <211> 66
 <212> ADN
 <213> Secuencia artificial
 <220>
 <223> Sintético: secuencia de nucleótidos que codifica el péptido 2A
 <400> 25
 ggaagcggag ctactaactt cagcctgctg aagcaggctg gagacgtgga ggagaaccct 60
 ggacct 66
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 <211> 108
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 <223> Sintético: secuencia de nucleótidos que codifica el péptido 2A
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 tccggactca gatccgggga tctcaaaatt gtcgctcctg tcaaacaac tcttaacttt 60
 gatttactca aactggctgg ggatgtagaa agcaatccag gtccactc 108
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 <223> Sintético: miR-142
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 uccuacuuua uggaugagug uacugug 87
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 <223> Sintético: miR-142-3p
 <400> 28
 uguaguguuu ccuacuuuau gga 23

<210> 29
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 <223> Sintético: sitio de unión a miR-142-3p
 <400> 29
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<210> 30
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 <223> Sintético: miR-142-5p
 <400> 30
 cauaaaaguag aaagcacuac u 21

<210> 31
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 <223> Sintético: sitio de unión a miR-142-5p
 <400> 31
 aguagugcuu ucuacuuuau g 21

<210> 32
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 <223> Sintético: miR-122-3p
 <400> 32
 aacgccauua ucacacuaaa ua 22

<210> 33
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 <223> Sintético: miR-122-5p
 <400> 33
 uggaguguga caaugguguu ug 22

<210> 34
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 <223> Sintético: miR-21-5p
 <400> 34
 uagcuuauca gacugauguu ga 22

<210> 35
 <211> 21
 <212> ARN
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 <223> Sintético: miR-21-3p
 <400> 35
 caacaccagu cgaugggcug u 21

<210> 36
 <211> 16
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 <213> Secuencia artificial
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 <223> Sintético: KRAS(G12D)15mer

<400> 36

Met Lys Leu Val Val Val Gly Ala Asp Gly Val Gly Lys Ser Ala Leu
1 5 10 15

<210> 37

<211> 16

<212> PRT

<213> Secuencia artificial

<220>

<223> Sintético: KRAS(G12V)15mer

<400> 37

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

<210> 38

<211> 16

<212> PRT

<213> Secuencia artificial

<220>

<223> Sintético: KRAS(G13D)15mer

<400> 38

Met Leu Val Val Val Gly Ala Gly Asp Val Gly Lys Ser Ala Leu Thr
1 5 10 15

<210> 39

<211> 25

<212> PRT

<213> Secuencia artificial

<220>

<223> Sintético: KRAS(G12D)25mer

<400> 39

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Asp Gly Val Gly Lys
1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln
20 25

<210> 40

<211> 25

<212> PRT

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<220>

<223> Sintético: KRAS(G12V)25mer

<400> 40

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

Ser Ala Leu Thr Ile Gln Leu Ile Gln
20 25

<210> 41

<211> 25

<212> PRT

<213> Secuencia artificial

<220>

<223> Sintético: KRAS(G13D)25mer

<400> 41

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Asp Val Gly Lys
1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln
20 25

<210> 42

<211> 46

<212> PRT

<213> Secuencia artificial

<220>

<223> Sintético: KRAS(G12D)15mer^3

<400> 42

Met Lys Leu Val Val Val Gly Ala Asp Gly Val Gly Lys Ser Ala Leu
1 5 10 15

Lys Leu Val Val Val Gly Ala Asp Gly Val Gly Lys Ser Ala Leu Lys
Página 25

20

25

30

Leu Val Val Val Gly Ala Asp Gly Val Gly Lys Ser Ala Leu
 35 40 45

<210> 43
 <211> 46
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: KRAS(G12V)15mer^3

<400> 43

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

Lys Leu Val Val Val Gly Ala Val Gly Val Gly Lys Ser Ala Leu Lys
 20 25 30

Leu Val Val Val Gly Ala Val Gly Val Gly Lys Ser Ala Leu
 35 40 45

<210> 44
 <211> 46
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: KRAS(G13D)15mer^3

<400> 44

Met Leu Val Val Val Gly Ala Gly Asp Val Gly Lys Ser Ala Leu Thr
 1 5 10 15

Leu Val Val Val Gly Ala Gly Asp Val Gly Lys Ser Ala Leu Thr Leu
 20 25 30

Val Val Val Gly Ala Gly Asp Val Gly Lys Ser Ala Leu Thr
 35 40 45

<210> 45
 <211> 75
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 <213> Secuencia artificial

<220>
 <223> Sintético: KRAS(G12D)25mer^3

<400> 45

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Asp Gly Val Gly Lys
 1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Met Thr Glu Tyr Lys Leu Val
 20 25 30

Val Val Gly Ala Asp Gly Val Gly Lys Ser Ala Leu Thr Ile Gln Leu
 35 40 45

Ile Gln Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Asp Gly Val
 50 55 60

Gly Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln
 65 70 75

<210> 46
 <211> 75
 <212> PRT
 <213> Secuencia artificial

<220>
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<400> 46

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

Ser Ala Leu Thr Ile Gln Leu Ile Gln Met Thr Glu Tyr Lys Leu Val
 20 25 30

Val Val Gly Ala Val Gly Val Gly Lys Ser Ala Leu Thr Ile Gln Leu
 35 40 45

Ile Gln Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Val Gly Val
 50 55 60

Gly Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln
 65 70 75

<210> 47
 <211> 75
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: KRAS(G13D)25mer^3

<400> 47

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Asp Val Gly Lys
 1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Met Thr Glu Tyr Lys Leu Val
 20 25 30

Val Val Gly Ala Gly Asp Val Gly Lys Ser Ala Leu Thr Ile Gln Leu
 35 40 45

Ile Gln Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Asp Val
 50 55 60

Gly Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln
 65 70 75

<210> 48
 <211> 414
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: KRAS(G12D)15mer_nt.STING(V155M)

<400> 48

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 1 5 10 15

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
 20 25 30

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
 35 40 45

Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
 50 55 60

Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
 65 70 75 80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
 85 90 95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
 100 105 110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
 115 120 125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
 130 135 140

Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu Ala
 145 150 155 160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
 165 170 175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
 180 185 190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
 195 200 205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
 210 215 220

Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
 225 230 235 240
 Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
 245 250 255
 Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
 260 265 270
 Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
 275 280 285
 Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
 290 295 300
 Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
 305 310 315 320
 Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
 325 330 335
 Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
 340 345 350
 Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
 355 360 365
 Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser Ala Thr Asn Phe Ser
 370 375 380
 Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Lys
 385 390 395 400
 Leu Val Val Val Gly Ala Asp Gly Val Gly Lys Ser Ala Leu
 405 410
 <210> 49
 <211> 414
 <212> PRT
 <213> Secuencia artificial
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 <400> 49
 Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 1 5 10 15
 Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
 20 25 30
 Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
 35 40 45
 Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
 50 55 60
 Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
 65 70 75 80
 Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
 85 90 95
 Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
 100 105 110
 Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
 115 120 125
 Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
 130 135 140
 Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu Ala
 145 150 155 160
 Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
 165 170 175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
180 185 190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
195 200 205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
210 215 220

Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
225 230 235 240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
245 250 255

Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
260 265 270

Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
275 280 285

Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
290 295 300

Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305 310 315 320

Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
325 330 335

Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
340 345 350

Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
355 360 365

Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser Ala Thr Asn Phe Ser
370 375 380

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Lys
385 390 395 400

Leu Val Val Val Gly Ala Val Gly Val Gly Lys Ser Ala Leu
405 410

<210> 50
<211> 414
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: KRAS(G13D)15mer_nt.STING(V155M

<400> 50

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
1 5 10 15

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
20 25 30

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
35 40 45

Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
50 55 60

Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65 70 75 80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
85 90 95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
100 105 110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
115 120 125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile

130 135 140

Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu Ala
145 150 155 160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
165 170 175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
180 185 190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
195 200 205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
210 215 220

Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
225 230 235 240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
245 250 255

Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
260 265 270

Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
275 280 285

Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
290 295 300

Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305 310 315 320

Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
325 330 335

Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
340 345 350

Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
355 360 365

Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser Ala Thr Asn Phe Ser
370 375 380

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Leu
385 390 395 400

Val Val Val Gly Ala Gly Asp Val Gly Lys Ser Ala Leu Thr
405 410

<210> 51
<211> 423
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: KRAS(G12D)25mer_nt.STING(V155M)

<400> 51

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
1 5 10 15

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
20 25 30

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
35 40 45

Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
50 55 60

Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65 70 75 80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
85 90 95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
100 105 110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
115 120 125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
130 135 140

Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu Ala
145 150 155 160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
165 170 175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
180 185 190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
195 200 205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
210 215 220

Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
225 230 235 240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
245 250 255

Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
260 265 270

Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
275 280 285

Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
290 295 300

Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305 310 315 320

Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
325 330 335

Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
340 345 350

Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
355 360 365

Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser Ala Thr Asn Phe Ser
370 375 380

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Thr
385 390 395 400

Glu Tyr Lys Leu Val Val Val Gly Ala Asp Gly Val Gly Lys Ser Ala
405 410 415

Leu Thr Ile Gln Leu Ile Gln
420

<210> 52
<211> 423
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: KRAS(G12V)25mer_nt.STING(V155M)

<400> 52

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
1 5 10 15

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
20 25 30

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
 35 40 45
 Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
 50 55 60
 Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
 65 70 75 80
 Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
 85 90 95
 Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
 100 105 110
 Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
 115 120 125
 Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
 130 135 140
 Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu Ala
 145 150 155 160
 Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
 165 170 175
 Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
 180 185 190
 Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
 195 200 205
 Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
 210 215 220
 Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
 225 230 235 240
 Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
 245 250 255
 Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
 260 265 270
 Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
 275 280 285
 Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
 290 295 300
 Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
 305 310 315 320
 Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
 325 330 335
 Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
 340 345 350
 Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
 355 360 365
 Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser Ala Thr Asn Phe Ser
 370 375 380
 Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Thr
 385 390 395 400
 Glu Tyr Lys Leu Val Val Val Gly Ala Val Gly Val Gly Lys Ser Ala
 405 410 415
 Leu Thr Ile Gln Leu Ile Gln
 420

<210> 53
 <211> 423

<212> PRT

<213> Secuencia artificial

<220>

<223> Sintético: KRAS(G13D)25mer_nt.STING(V155M)

<400> 53

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
1 5 10 15

Gly Ala Gln Lys Ala Ala Leu Val Leu Ser Ala Cys Leu Val Thr
20 25 30

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
35 40 45

Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
50 55 60

Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65 70 75 80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
85 90 95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
100 105 110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
115 120 125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
130 135 140

Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu Ala
145 150 155 160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
165 170 175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
180 185 190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
195 200 205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
210 215 220

Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
225 230 235 240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
245 250 255

Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
260 265 270

Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
275 280 285

Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
290 295 300

Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305 310 315 320

Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
325 330 335

Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
340 345 350

Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
355 360 365

Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser Ala Thr Asn Phe Ser
370 375 380

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Thr
 385 390 395 400

 Glu Tyr Lys Leu Val Val Val Gly Ala Gly Asp Val Gly Lys Ser Ala
 405 410 415

 Leu Thr Ile Gln Leu Ile Gln
 420

 <210> 54
 <211> 444
 <212> PRT
 <213> Secuencia artificial

 <220>
 <223> Sintético: KRAS(G12D)15mer^3_nt.STING(V155M)

 <400> 54

 Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 1 5 10 15

 Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
 20 25 30

 Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
 35 40 45

 Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
 50 55 60

 Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
 65 70 75 80

 Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
 85 90 95

 Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
 100 105 110

 Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
 115 120 125

 Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
 130 135 140

 Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu Ala
 145 150 155 160

 Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
 165 170 175

 Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
 180 185 190

 Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
 195 200 205

 Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
 210 215 220

 Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
 225 230 235 240

 Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
 245 250 255

 Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
 260 265 270

 Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
 275 280 285

 Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
 290 295 300

 Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
 305 310 315 320

Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
325 330 335

Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
340 345 350

Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
355 360 365

Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser Ala Thr Asn Phe Ser
370 375 380

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Lys
385 390 395 400

Leu Val Val Val Gly Ala Asp Gly Val Gly Lys Ser Ala Leu Lys Leu
405 410 415

Val Val Val Gly Ala Asp Gly Val Gly Lys Ser Ala Leu Lys Leu Val
420 425 430

Val Val Gly Ala Asp Gly Val Gly Lys Ser Ala Leu
435 440

<210> 55
<211> 444
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: KRAS(G12V)15mer^3_nt.STING(V155M)

<400> 55

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
1 5 10 15

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
20 25 30

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
35 40 45

Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
50 55 60

Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65 70 75 80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
85 90 95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
100 105 110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
115 120 125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
130 135 140

Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu Ala
145 150 155 160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
165 170 175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
180 185 190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
195 200 205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
210 215 220

Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
225 230 235 240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr

245

250

255

Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
260 265 270

Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
275 280 285

Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
290 295 300

Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305 310 315 320

Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
325 330 335

Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
340 345 350

Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
355 360 365

Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser Ala Thr Asn Phe Ser
370 375 380

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Lys
385 390 395 400

Leu Val Val Val Gly Ala Val Gly Val Gly Lys Ser Ala Leu Lys Leu
405 410 415

Val Val Val Gly Ala Val Gly Val Gly Lys Ser Ala Leu Lys Leu Val
420 425 430

Val Val Gly Ala Val Gly Val Gly Lys Ser Ala Leu
435 440

<210> 56
<211> 444
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: KRAS(G13D)15mer^3_nt.STING(V155M

<400> 56

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
1 5 10 15

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
20 25 30

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
35 40 45

Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
50 55 60

Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65 70 75 80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
85 90 95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
100 105 110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
115 120 125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
130 135 140

Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu Ala
145 150 155 160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
165 170 175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
180 185 190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
195 200 205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
210 215 220

Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
225 230 235 240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
245 250 255

Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
260 265 270

Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
275 280 285

Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
290 295 300

Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305 310 315 320

Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
325 330 335

Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
340 345 350

Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
355 360 365

Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser Ala Thr Asn Phe Ser
370 375 380

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Leu
385 390 395 400

Val Val Val Gly Ala Gly Asp Val Gly Lys Ser Ala Leu Thr Leu Val
405 410 415

Val Val Gly Ala Gly Asp Val Gly Lys Ser Ala Leu Thr Leu Val Val
420 425 430

Val Gly Ala Gly Asp Val Gly Lys Ser Ala Leu Thr
435 440

<210> 57
<211> 473
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: KRAS(G12D)25mer^3_nt.STING(V155M)

<400> 57

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
1 5 10 15

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
20 25 30

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
35 40 45

Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
50 55 60

Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65 70 75 80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
85 90 95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
100 105 110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
115 120 125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
130 135 140

Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu Ala
145 150 155 160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
165 170 175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
180 185 190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
195 200 205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
210 215 220

Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
225 230 235 240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
245 250 255

Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
260 265 270

Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
275 280 285

Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
290 295 300

Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305 310 315 320

Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
325 330 335

Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
340 345 350

Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
355 360 365

Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser Ala Thr Asn Phe Ser
370 375 380

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Thr
385 390 395 400

Glu Tyr Lys Leu Val Val Val Gly Ala Asp Gly Val Gly Lys Ser Ala
405 410 415

Leu Thr Ile Gln Leu Ile Gln Met Thr Glu Tyr Lys Leu Val Val Val
420 425 430

Gly Ala Asp Gly Val Gly Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln
435 440 445

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

Ser Ala Leu Thr Ile Gln Leu Ile Gln
465 470

<210> 58

<211> 473

<212> PRT

<213> Secuencia artificial

<220>

<223> Sintético: KRAS(G12V)25mer^3_nt.STING(V155M

<400> 58

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
1 5 10 15

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
20 25 30

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
35 40 45

Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
50 55 60

Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65 70 75 80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
85 90 95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
100 105 110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
115 120 125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
130 135 140

Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu Ala
145 150 155 160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
165 170 175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
180 185 190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
195 200 205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
210 215 220

Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
225 230 235 240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
245 250 255

Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
260 265 270

Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
275 280 285

Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
290 295 300

Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305 310 315 320

Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
325 330 335

Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
340 345 350

Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
355 360 365

Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser Ala Thr Asn Phe Ser
370 375 380

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Thr
385 390 395 400

Glu Tyr Lys Leu Val Val Val Gly Ala Val Gly Val Gly Lys Ser Ala
 405 410 415
 Leu Thr Ile Gln Leu Ile Gln Met Thr Glu Tyr Lys Leu Val Val Val
 420 425 430
 Gly Ala Val Gly Val Gly Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln
 435 440 445
 Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Val Gly Val Gly Lys
 450 455 460
 Ser Ala Leu Thr Ile Gln Leu Ile Gln
 465 470
 <210> 59
 <211> 473
 <212> PRT
 <213> Secuencia artificial
 <220>
 <223> Sintético: KRAS(G13D)25mer^3_nt.STING(V155M
 <400> 59
 Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 1 5 10 15
 Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
 20 25 30
 Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
 35 40 45
 Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
 50 55 60
 Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
 65 70 75 80
 Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
 85 90 95
 Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
 100 105 110
 Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
 115 120 125
 Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
 130 135 140
 Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu Ala
 145 150 155 160
 Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
 165 170 175
 Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
 180 185 190
 Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
 195 200 205
 Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
 210 215 220
 Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
 225 230 235 240
 Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
 245 250 255
 Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
 260 265 270
 Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
 275 280 285

Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
 290 295 300
 Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
 305 310 315 320
 Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
 325 330 335
 Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
 340 345 350
 Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
 355 360 365
 Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser Ala Thr Asn Phe Ser
 370 375 380
 Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Thr
 385 390 395 400
 Glu Tyr Lys Leu Val Val Val Gly Ala Gly Asp Val Gly Lys Ser Ala
 405 410 415
 Leu Thr Ile Gln Leu Ile Gln Met Thr Glu Tyr Lys Leu Val Val Val
 420 425 430
 Gly Ala Gly Asp Val Gly Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln
 435 440 445
 Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Asp Val Gly Lys
 450 455 460
 Ser Ala Leu Thr Ile Gln Leu Ile Gln
 465 470

<210> 60
 <211> 414
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: KRAS(G12D)15mer_ct.STING(V155M)

<400> 60

Met Lys Leu Val Val Val Gly Ala Asp Gly Val Gly Lys Ser Ala Leu
 1 5 10 15
 Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
 20 25 30
 Pro Gly Pro Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro
 35 40 45
 Arg Gly His Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys
 50 55 60
 Leu Val Thr Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg
 65 70 75 80
 Tyr Leu Val Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn
 85 90 95
 Gly Val Cys Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr
 100 105 110
 Arg Gly Ser Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu
 115 120 125
 Arg Arg Gly Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu
 130 135 140
 Pro Asn Ala Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly
 145 150 155 160
 Leu Ser Gln Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro
 165 170 175
 Ala Glu Ile Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Met Ala His

180

185

190

Gly Leu Ala Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro
 195 200 205

Glu Leu Gln Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu
 210 215 220

Leu Arg Gly Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp
 225 230 235 240

Cys Gly Val Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe
 245 250 255

Leu Asp Lys Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp
 260 265 270

Arg Val Tyr Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg
 275 280 285

Ala Gly Thr Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe
 290 295 300

Ala Met Ser Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu
 305 310 315 320

Glu Gln Ala Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp
 325 330 335

Ala Pro Glu Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro
 340 345 350

Ala Asp Asp Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu
 355 360 365

Arg Gln Glu Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser
 370 375 380

Ala Val Pro Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile
 385 390 395 400

Ser Gly Met Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
 405 410

<210> 61
 <211> 414
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: KRAS(G12V)15mer_ct.STING(V155M

<400> 61

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

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

Pro Gly Pro Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro
 35 40 45

Arg Gly His Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys
 50 55 60

Leu Val Thr Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg
 65 70 75 80

Tyr Leu Val Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn
 85 90 95

Gly Val Cys Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr
 100 105 110

Arg Gly Ser Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu
 115 120 125

Arg Arg Gly Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu
 130 135 140

Pro Asn Ala Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly
145 150 155 160

Leu Ser Gln Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro
165 170 175

Ala Glu Ile Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Met Ala His
180 185 190

Gly Leu Ala Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro
195 200 205

Glu Leu Gln Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu
210 215 220

Leu Arg Gly Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp
225 230 235 240

Cys Gly Val Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe
245 250 255

Leu Asp Lys Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp
260 265 270

Arg Val Tyr Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg
275 280 285

Ala Gly Thr Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe
290 295 300

Ala Met Ser Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu
305 310 315 320

Glu Gln Ala Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp
325 330 335

Ala Pro Glu Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro
340 345 350

Ala Asp Asp Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu
355 360 365

Arg Gln Glu Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser
370 375 380

Ala Val Pro Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile
385 390 395 400

Ser Gly Met Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
405 410

<210> 62
<211> 414
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: KRAS(G13D)15mer_ct.STING(V155M)

<400> 62

Met Leu Val Val Val Gly Ala Gly Asp Val Gly Lys Ser Ala Leu Thr
1 5 10 15

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

Pro Gly Pro Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro
35 40 45

Arg Gly His Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys
50 55 60

Leu Val Thr Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg
65 70 75 80

Tyr Leu Val Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn
85 90 95

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

<210> 63
 <211> 423
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: KRAS(G12D)25mer_ct.STING(V155M)

<400> 63

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Asp Gly Val Gly Lys
 1 5 10 15
 Ser Ala Leu Thr Ile Gln Leu Ile Gln Ala Thr Asn Phe Ser Leu Leu
 20 25 30
 Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Pro His Ser
 35 40 45

Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His Gly Ala Gln Lys
 50 55 60
 Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr Leu Trp Gly Leu
 65 70 75 80
 Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val Leu His Leu Ala
 85 90 95
 Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys Ser Leu Ala Glu
 100 105 110
 Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser Tyr Trp Arg Thr
 115 120 125
 Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly Ala Leu Leu Leu
 130 135 140
 Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala Val Gly Pro Pro
 145 150 155 160
 Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln Ala Leu Asn Ile
 165 170 175
 Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala Val Cys
 180 185 190
 Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu Ala Trp Ser Tyr Tyr
 195 200 205
 Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln Ala Arg Ile Arg
 210 215 220
 Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly Ala Val Ser Gln
 225 230 235 240
 Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val Pro Asp Asn Leu
 245 250 255
 Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys Leu Pro Gln Gln
 260 265 270
 Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr Ser Asn Ser Ile
 275 280 285
 Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr Cys Val Leu Glu
 290 295 300
 Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser Gln Tyr Ser Gln
 305 310 315 320
 Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala Lys Leu Phe Cys
 325 330 335
 Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu Ser Gln Asn Asn
 340 345 350
 Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp Ser Ser Phe Ser
 355 360 365
 Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu Glu Lys Glu Glu
 370 375 380
 Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro Ser Thr Ser Thr
 385 390 395 400
 Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met Glu Lys Pro Leu
 405 410 415
 Pro Leu Arg Thr Asp Phe Ser
 420

<210> 64
 <211> 423
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: KRAS(G12V)25mer_ct.STING(V155M)

<400> 64

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

Ser Ala Leu Thr Ile Gln Leu Ile Gln Ala Thr Asn Phe Ser Leu Leu
20 25 30

Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Pro His Ser
35 40 45

Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His Gly Ala Gln Lys
50 55 60

Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr Leu Trp Gly Leu
65 70 75 80

Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val Leu His Leu Ala
85 90 95

Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys Ser Leu Ala Glu
100 105 110

Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser Tyr Trp Arg Thr
115 120 125

Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly Ala Leu Leu Leu
130 135 140

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

Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln Ala Leu Asn Ile
165 170 175

Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala Val Cys
180 185 190

Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu Ala Trp Ser Tyr Tyr
195 200 205

Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln Ala Arg Ile Arg
210 215 220

Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly Ala Val Ser Gln
225 230 235 240

Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val Pro Asp Asn Leu
245 250 255

Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys Leu Pro Gln Gln
260 265 270

Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr Ser Asn Ser Ile
275 280 285

Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr Cys Val Leu Glu
290 295 300

Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser Gln Tyr Ser Gln
305 310 315 320

Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala Lys Leu Phe Cys
325 330 335

Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu Ser Gln Asn Asn
340 345 350

Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp Ser Ser Phe Ser
355 360 365

Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu Glu Lys Glu Glu
370 375 380

Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro Ser Thr Ser Thr
385 390 395 400

Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met Glu Lys Pro Leu
 405 410 415

Pro Leu Arg Thr Asp Phe Ser
 420

<210> 65
 <211> 423
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: KRAS(G13D)25mer_ct.STING(V155M)

<400> 65

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Asp Val Gly Lys
 1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Ala Thr Asn Phe Ser Leu Leu
 20 25 30

Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Pro His Ser
 35 40 45

Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His Gly Ala Gln Lys
 50 55 60

Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr Leu Trp Gly Leu
 65 70 75 80

Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val Leu His Leu Ala
 85 90 95

Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys Ser Leu Ala Glu
 100 105 110

Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser Tyr Trp Arg Thr
 115 120 125

Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly Ala Leu Leu Leu
 130 135 140

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

Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln Ala Leu Asn Ile
 165 170 175

Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala Val Cys
 180 185 190

Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu Ala Trp Ser Tyr Tyr
 195 200 205

Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln Ala Arg Ile Arg
 210 215 220

Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly Ala Val Ser Gln
 225 230 235 240

Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val Pro Asp Asn Leu
 245 250 255

Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys Leu Pro Gln Gln
 260 265 270

Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr Ser Asn Ser Ile
 275 280 285

Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr Cys Val Leu Glu
 290 295 300

Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser Gln Tyr Ser Gln
 305 310 315 320

Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala Lys Leu Phe Cys
 325 330 335

Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu Ser Gln Asn Asn
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340

345

350

Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp Ser Ser Phe Ser
355 360 365

Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu Glu Lys Glu Glu
370 375 380

Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro Ser Thr Ser Thr
385 390 395 400

Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met Glu Lys Pro Leu
405 410 415

Pro Leu Arg Thr Asp Phe Ser
420

<210> 66
<211> 444
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: KRAS(G12D)15mer^3_ct.STING(V155M)

<400> 66

Met Lys Leu Val Val Val Gly Ala Asp Gly Val Gly Lys Ser Ala Leu
1 5 10 15

Lys Leu Val Val Val Gly Ala Asp Gly Val Gly Lys Ser Ala Leu Lys
20 25 30

Leu Val Val Val Gly Ala Asp Gly Val Gly Lys Ser Ala Leu Ala Thr
35 40 45

Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly
50 55 60

Pro Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly
65 70 75 80

His Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val
85 90 95

Thr Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu
100 105 110

Val Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val
115 120 125

Cys Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly
130 135 140

Ser Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg
145 150 155 160

Gly Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn
165 170 175

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

Gln Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu
195 200 205

Ile Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu
210 215 220

Ala Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu
225 230 235 240

Gln Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg
245 250 255

Gly Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly
260 265 270

Val Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp
275 280 285

Lys Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val
290 295 300

Tyr Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly
305 310 315 320

Thr Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met
325 330 335

Ser Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln
340 345 350

Ala Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro
355 360 365

Glu Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp
370 375 380

Asp Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln
385 390 395 400

Glu Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val
405 410 415

Pro Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly
420 425 430

Met Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
435 440

<210> 67
<211> 444
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: KRAS(G12V)15mer^3_ct.STING(V155M)

<400> 67

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

Lys Leu Val Val Val Gly Ala Val Gly Val Gly Lys Ser Ala Leu Lys
20 25 30

Leu Val Val Val Gly Ala Val Gly Val Gly Lys Ser Ala Leu Ala Thr
35 40 45

Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly
50 55 60

Pro Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly
65 70 75 80

His Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val
85 90 95

Thr Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu
100 105 110

Val Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val
115 120 125

Cys Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly
130 135 140

Ser Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg
145 150 155 160

Gly Ala Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn
165 170 175

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

Gln Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu
195 200 205

Ile Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu
 210 215 220
 Ala Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu
 225 230 235 240
 Gln Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg
 245 250 255
 Gly Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly
 260 265 270
 Val Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp
 275 280 285
 Lys Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val
 290 295 300
 Tyr Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly
 305 310 315 320
 Thr Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met
 325 330 335
 Ser Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln
 340 345 350
 Ala Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro
 355 360 365
 Glu Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp
 370 375 380
 Asp Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln
 385 390 395 400
 Glu Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val
 405 410 415
 Pro Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly
 420 425 430
 Met Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
 435 440
 <210> 68
 <211> 444
 <212> PRT
 <213> Secuencia artificial
 <220>
 <223> Sintético: KRAS(G13D)15mer^3_ct.STING(V155M
 <400> 68
 Met Leu Val Val Val Gly Ala Gly Asp Val Gly Lys Ser Ala Leu Thr
 1 5 10 15
 Leu Val Val Val Gly Ala Gly Asp Val Gly Lys Ser Ala Leu Thr Leu
 20 25 30
 Val Val Val Gly Ala Gly Asp Val Gly Lys Ser Ala Leu Thr Ala Thr
 35 40 45
 Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly
 50 55 60
 Pro Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly
 65 70 75 80
 His Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val
 85 90 95
 Thr Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu
 100 105 110
 Val Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val
 115 120 125

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

<210> 69
 <211> 473
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: KRAS(G12D)25mer^3_ct.STING(V155M)

<400> 69

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Asp Gly Val Gly Lys
 1 5 10 15
 Ser Ala Leu Thr Ile Gln Leu Ile Gln Met Thr Glu Tyr Lys Leu Val
 20 25 30
 Val Val Gly Ala Asp Gly Val Gly Lys Ser Ala Leu Thr Ile Gln Leu
 35 40 45
 Ile Gln Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Asp Gly Val

50 55 60

Gly Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Ala Thr Asn Phe Ser
65 70 75 80

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Pro
85 90 95

His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His Gly Ala
100 105 110

Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr Leu Trp
115 120 125

Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val Leu His
130 135 140

Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys Ser Leu
145 150 155 160

Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser Tyr Trp
165 170 175

Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly Ala Leu
180 185 190

Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala Val Gly
195 200 205

Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln Ala Leu
210 215 220

Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala
225 230 235 240

Val Cys Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu Ala Trp Ser
245 250 255

Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln Ala Arg
260 265 270

Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly Ala Val
275 280 285

Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val Pro Asp
290 295 300

Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys Leu Pro
305 310 315 320

Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr Ser Asn
325 330 335

Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr Cys Val
340 345 350

Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser Gln Tyr
355 360 365

Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala Lys Leu
370 375 380

Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu Ser Gln
385 390 395 400

Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp Ser Ser
405 410 415

Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu Glu Lys
420 425 430

Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro Ser Thr
435 440 445

Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met Glu Lys
450 455 460

Pro Leu Pro Leu Arg Thr Asp Phe Ser
465 470

<210> 70
<211> 473
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: KRAS(G12V)25mer^3_ct.STING(V155M

<400> 70

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

Ser Ala Leu Thr Ile Gln Leu Ile Gln Met Thr Glu Tyr Lys Leu Val
20 25 30

Val Val Gly Ala Val Gly Val Gly Lys Ser Ala Leu Thr Ile Gln Leu
35 40 45

Ile Gln Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Val Gly Val
50 55 60

Gly Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Ala Thr Asn Phe Ser
65 70 75 80

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Pro
85 90 95

His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His Gly Ala
100 105 110

Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr Leu Trp
115 120 125

Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val Leu His
130 135 140

Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys Ser Leu
145 150 155 160

Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser Tyr Trp
165 170 175

Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly Ala Leu
180 185 190

Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala Val Gly
195 200 205

Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln Ala Leu
210 215 220

Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala
225 230 235 240

Val Cys Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu Ala Trp Ser
245 250 255

Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln Ala Arg
260 265 270

Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly Ala Val
275 280 285

Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val Pro Asp
290 295 300

Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys Leu Pro
305 310 315 320

Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr Ser Asn
325 330 335

Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr Cys Val
340 345 350

Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser Gln Tyr

355

360

365

Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala Lys Leu
370 375 380

Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu Ser Gln
385 390 395 400

Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp Ser Ser
405 410 415

Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu Glu Lys
420 425 430

Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro Ser Thr
435 440 445

Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met Glu Lys
450 455 460

Pro Leu Pro Leu Arg Thr Asp Phe Ser
465 470

<210> 71
<211> 473
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: KRAS(G13D)25mer^3_ct.STING(V155M

<400> 71

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Asp Val Gly Lys
1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Met Thr Glu Tyr Lys Leu Val
20 25 30

Val Val Gly Ala Gly Asp Val Gly Lys Ser Ala Leu Thr Ile Gln Leu
35 40 45

Ile Gln Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Asp Val
50 55 60

Gly Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Ala Thr Asn Phe Ser
65 70 75 80

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Pro
85 90 95

His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His Gly Ala
100 105 110

Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr Leu Trp
115 120 125

Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val Leu His
130 135 140

Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys Ser Leu
145 150 155 160

Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser Tyr Trp
165 170 175

Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly Ala Leu
180 185 190

Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala Val Gly
195 200 205

Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln Ala Leu
210 215 220

Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala
225 230 235 240

Val Cys Glu Lys Gly Asn Phe Asn Met Ala His Gly Leu Ala Trp Ser
245 250 255

Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln Ala Arg
260 265 270

Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly Ala Val
275 280 285

Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val Pro Asp
290 295 300

Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys Leu Pro
305 310 315 320

Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr Ser Asn
325 330 335

Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr Cys Val
340 345 350

Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser Gln Tyr
355 360 365

Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala Lys Leu
370 375 380

Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu Ser Gln
385 390 395 400

Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp Ser Ser
405 410 415

Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu Glu Lys
420 425 430

Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro Ser Thr
435 440 445

Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met Glu Lys
450 455 460

Pro Leu Pro Leu Arg Thr Asp Phe Ser
465 470

<210> 72
<211> 25
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: KRAS(G12C)25mer

<400> 72

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Cys Gly Val Gly Lys
1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln
20 25

<210> 73
<211> 75
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: KRAS(G12C)25mer^3

<400> 73

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Cys Gly Val Gly Lys
1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Met Thr Glu Tyr Lys Leu Val
20 25 30

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

Ile Gln Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Cys Gly Val
50 55 60

Gly Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln

65

70

<210> 74
<211> 25
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: KRAS(WT)25mer

<400> 74

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

Ser Ala Leu Thr Ile Gln Leu Ile Gln
20 25

<210> 75
<211> 296
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(296)
<223> myd88(L265P) humano; P4027 sin etiqueta de epítipo

<400> 75

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

Met Phe Ser Ile Pro Leu Val Ala Leu Asn Val Gly Val Arg Arg Arg
20 25 30

Leu Ser Leu Phe Leu Asn Pro Arg Thr Pro Val Ala Ala Asp Trp Thr
35 40 45

Leu Leu Ala Glu Glu Met Gly Phe Glu Tyr Leu Glu Ile Arg Glu Leu
50 55 60

Glu Thr Arg Pro Asp Pro Thr Arg Ser Leu Leu Asp Ala Trp Gln Gly
65 70 75 80

Arg Ser Gly Ala Ser Val Gly Arg Leu Leu Glu Leu Leu Ala Leu Leu
85 90 95

Asp Arg Glu Asp Ile Leu Lys Glu Leu Lys Ser Arg Ile Glu Glu Asp
100 105 110

Cys Gln Lys Tyr Leu Gly Lys Gln Gln Asn Gln Glu Ser Glu Lys Pro
115 120 125

Leu Gln Val Ala Arg Val Glu Ser Ser Val Pro Gln Thr Lys Glu Leu
130 135 140

Gly Gly Ile Thr Thr Leu Asp Asp Pro Leu Gly Gln Thr Pro Glu Leu
145 150 155 160

Phe Asp Ala Phe Ile Cys Tyr Cys Pro Asn Asp Ile Glu Phe Val Gln
165 170 175

Glu Met Ile Arg Gln Leu Glu Gln Thr Asp Tyr Arg Leu Lys Leu Cys
180 185 190

Val Ser Asp Arg Asp Val Leu Pro Gly Thr Cys Val Trp Ser Ile Ala
195 200 205

Ser Glu Leu Ile Glu Lys Arg Cys Arg Arg Met Val Val Val Val Ser
210 215 220

Asp Asp Tyr Leu Gln Ser Lys Glu Cys Asp Phe Gln Thr Lys Phe Ala
225 230 235 240

Leu Ser Leu Ser Pro Gly Val Gln Gln Lys Arg Pro Ile Pro Ile Lys
245 250 255

Tyr Lys Ala Met Lys Lys Asp Phe Pro Ser Ile Leu Arg Phe Ile Thr
260 265 270

Ile Cys Asp Tyr Thr Asn Pro Cys Thr Lys Ser Trp Phe Trp Thr Arg

275

280

Leu Ala Lys Ala Leu Ser Leu Pro
290 295

<210> 76
<211> 296
<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(296)
<223> myd88(L265P) de ratón; P4028 sin etiqueta de epítopo
<400> 76

Met Ala Ala Gly Gly Pro Gly Ala Gly Ser Ala Ala Pro Val Ser Ser
1 5 10 15

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

Leu Ser Leu Phe Leu Asn Val Arg Thr Gln Val Ala Ala Asp Trp Thr
35 40 45

Ala Leu Ala Glu Glu Met Asp Phe Glu Tyr Leu Glu Ile Arg Gln Leu
50 55 60

Glu Thr Gln Ala Asp Pro Thr Gly Arg Leu Leu Asp Ala Trp Gln Gly
65 70 75 80

Arg Pro Gly Ala Ser Val Gly Arg Leu Leu Glu Leu Leu Thr Lys Leu
85 90 95

Gly Arg Asp Asp Val Leu Leu Glu Leu Gly Pro Ser Ile Glu Glu Asp
100 105 110

Cys Gln Lys Tyr Ile Leu Lys Gln Gln Gln Glu Glu Ala Glu Lys Pro
115 120 125

Leu Gln Val Ala Ala Val Asp Ser Ser Val Pro Arg Thr Ala Glu Leu
130 135 140

Ala Gly Ile Thr Thr Leu Asp Asp Pro Leu Gly His Met Pro Glu Arg
145 150 155 160

Phe Asp Ala Phe Ile Cys Tyr Cys Pro Ser Asp Ile Gln Phe Val Gln
165 170 175

Glu Met Ile Arg Gln Leu Glu Gln Thr Asn Tyr Arg Leu Lys Leu Cys
180 185 190

Val Ser Asp Arg Asp Val Leu Pro Gly Thr Cys Val Trp Ser Ile Ala
195 200 205

Ser Glu Leu Ile Glu Lys Arg Cys Arg Arg Met Val Val Val Val Ser
210 215 220

Asp Asp Tyr Leu Gln Ser Lys Glu Cys Asp Phe Gln Thr Lys Phe Ala
225 230 235 240

Leu Ser Leu Ser Pro Gly Ala His Gln Lys Arg Pro Ile Pro Ile Lys
245 250 255

Tyr Lys Ala Met Lys Lys Glu Phe Pro Ser Ile Leu Arg Phe Ile Thr
260 265 270

Val Cys Asp Tyr Thr Asn Pro Cys Thr Lys Ser Trp Phe Trp Thr Arg
275 280 285

Leu Ala Lys Ala Leu Ser Leu Pro
290 295

<210> 77
<211> 232
<212> PRT
<213> Mus musculus

<220>

<221> misc_feature

<222> (1)..(232)

<223> TRAM (TICAM2) de ratón; P4033 sin etiqueta de epítopo

<400> 77

Met Gly Val Gly Lys Ser Lys Leu Asp Lys Cys Pro Leu Ser Trp His
1 5 10 15Lys Lys Asp Ser Val Asp Ala Asp Gln Asp Gly His Glu Ser Asp Ser
20 25 30Lys Asn Ser Glu Glu Ala Cys Leu Arg Gly Phe Val Glu Gln Ser Ser
35 40 45Gly Ser Glu Pro Pro Thr Gly Glu Gln Asp Gln Pro Glu Ala Lys Gly
50 55 60Ala Gly Pro Glu Glu Gln Asp Glu Glu Glu Phe Leu Lys Phe Val Ile
65 70 75 80Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val Gln Asp Leu
85 90 95Leu Gln Asn Asp Phe Gly Ile Arg Pro Gly Ile Val Phe Ala Glu Met
100 105 110Pro Cys Gly Arg Leu His Leu Gln Asn Leu Asp Asp Ala Val Asn Gly
115 120 125Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu Arg Asp Thr
130 135 140Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser Val Ser Arg
145 150 155 160Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu Asn Ser Pro
165 170 175Leu Pro Arg Glu Arg Thr Pro Leu Ala Leu Gln Thr Ile Asn Ala Leu
180 185 190Glu Glu Glu Ser Gln Gly Phe Ser Thr Gln Val Glu Arg Ile Phe Arg
195 200 205Glu Ser Val Phe Glu Arg Gln Gln Ser Ile Trp Lys Glu Thr Arg Ser
210 215 220Val Ser Gln Lys Gln Phe Ile Ala
225 230

<210> 78

<211> 847

<212> PRT

<213> Secuencia artificial

<220>

<223> Sintético: STAT6 V547A/T548A); P008 sin etiqueta de epítopo

<400> 78

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

Gln Phe Arg His Leu Pro Met Pro Phe His Trp Lys Gln Glu Glu Leu
 115 120 125
 Lys Phe Lys Thr Gly Leu Arg Arg Leu Gln His Arg Val Gly Glu Ile
 130 135 140
 His Leu Leu Arg Glu Ala Leu Gln Lys Gly Ala Glu Ala Gly Gln Val
 145 150 155 160
 Ser Leu His Ser Leu Ile Glu Thr Pro Ala Asn Gly Thr Gly Pro Ser
 165 170 175
 Glu Ala Leu Ala Met Leu Leu Gln Glu Thr Thr Gly Glu Leu Glu Ala
 180 185 190
 Ala Lys Ala Leu Val Leu Lys Arg Ile Gln Ile Trp Lys Arg Gln Gln
 195 200 205
 Gln Leu Ala Gly Asn Gly Ala Pro Phe Glu Glu Ser Leu Ala Pro Leu
 210 215 220
 Gln Glu Arg Cys Glu Ser Leu Val Asp Ile Tyr Ser Gln Leu Gln Gln
 225 230 235 240
 Glu Val Gly Ala Ala Gly Gly Glu Leu Glu Pro Lys Thr Arg Ala Ser
 245 250 255
 Leu Thr Gly Arg Leu Asp Glu Val Leu Arg Thr Leu Val Thr Ser Cys
 260 265 270
 Phe Leu Val Glu Lys Gln Pro Pro Gln Val Leu Lys Thr Gln Thr Lys
 275 280 285
 Phe Gln Ala Gly Val Arg Phe Leu Leu Gly Leu Arg Phe Leu Gly Ala
 290 295 300
 Pro Ala Lys Pro Pro Leu Val Arg Ala Asp Met Val Thr Glu Lys Gln
 305 310 315 320
 Ala Arg Glu Leu Ser Val Pro Gln Gly Pro Gly Ala Gly Ala Glu Ser
 325 330 335
 Thr Gly Glu Ile Ile Asn Asn Thr Val Pro Leu Glu Asn Ser Ile Pro
 340 345 350
 Gly Asn Cys Cys Ser Ala Leu Phe Lys Asn Leu Leu Leu Lys Lys Ile
 355 360 365
 Lys Arg Cys Glu Arg Lys Gly Thr Glu Ser Val Thr Glu Glu Lys Cys
 370 375 380
 Ala Val Leu Phe Ser Ala Ser Phe Thr Leu Gly Pro Gly Lys Leu Pro
 385 390 395 400
 Ile Gln Leu Gln Ala Leu Ser Leu Pro Leu Val Val Ile Val His Gly
 405 410 415
 Asn Gln Asp Asn Asn Ala Lys Ala Thr Ile Leu Trp Asp Asn Ala Phe
 420 425 430
 Ser Glu Met Asp Arg Val Pro Phe Val Val Ala Glu Arg Val Pro Trp
 435 440 445
 Glu Lys Met Cys Glu Thr Leu Asn Leu Lys Phe Met Ala Glu Val Gly
 450 455 460
 Thr Asn Arg Gly Leu Leu Pro Glu His Phe Leu Phe Leu Ala Gln Lys
 465 470 475 480
 Ile Phe Asn Asp Asn Ser Leu Ser Met Glu Ala Phe Gln His Arg Ser
 485 490 495
 Val Ser Trp Ser Gln Phe Asn Lys Glu Ile Leu Leu Gly Arg Gly Phe
 500 505 510
 Thr Phe Trp Gln Trp Phe Asp Gly Val Leu Asp Leu Thr Lys Arg Cys
 515 520 525

Leu Arg Ser Tyr Trp Ser Asp Arg Leu Ile Ile Gly Phe Ile Ser Lys
530 535 540

Gln Tyr Ala Ala Ser Leu Leu Leu Asn Glu Pro Asp Gly Thr Phe Leu
545 550 555 560

Leu Arg Phe Ser Asp Ser Glu Ile Gly Gly Ile Thr Ile Ala His Val
565 570 575

Ile Arg Gly Gln Asp Gly Ser Pro Gln Ile Glu Asn Ile Gln Pro Phe
580 585 590

Ser Ala Lys Asp Leu Ser Ile Arg Ser Leu Gly Asp Arg Ile Arg Asp
595 600 605

Leu Ala Gln Leu Lys Asn Leu Tyr Pro Lys Lys Pro Lys Asp Glu Ala
610 615 620

Phe Arg Ser His Tyr Lys Pro Glu Gln Met Gly Lys Asp Gly Arg Gly
625 630 635 640

Tyr Val Pro Ala Thr Ile Lys Met Thr Val Glu Arg Asp Gln Pro Leu
645 650 655

Pro Thr Pro Glu Leu Gln Met Pro Thr Met Val Pro Ser Tyr Asp Leu
660 665 670

Gly Met Ala Pro Asp Ser Ser Met Ser Met Gln Leu Gly Pro Asp Met
675 680 685

Val Pro Gln Val Tyr Pro Pro His Ser His Ser Ile Pro Pro Tyr Gln
690 695 700

Gly Leu Ser Pro Glu Glu Ser Val Asn Val Leu Ser Ala Phe Gln Glu
705 710 715 720

Pro His Leu Gln Met Pro Pro Ser Leu Gly Gln Met Ser Leu Pro Phe
725 730 735

Asp Gln Pro His Pro Gln Gly Leu Leu Pro Cys Gln Pro Gln Glu His
740 745 750

Ala Val Ser Ser Pro Asp Pro Leu Leu Cys Ser Asp Val Thr Met Val
755 760 765

Glu Asp Ser Cys Leu Ser Gln Pro Val Thr Ala Phe Pro Gln Gly Thr
770 775 780

Trp Ile Gly Glu Asp Ile Phe Pro Pro Leu Leu Pro Pro Thr Glu Gln
785 790 795 800

Asp Leu Thr Lys Leu Leu Leu Glu Gly Gln Gly Glu Ser Gly Gly Gly
805 810 815

Ser Leu Gly Ala Gln Pro Leu Leu Gln Pro Ser His Tyr Gly Gln Ser
820 825 830

Gly Ile Ser Met Ser His Met Asp Leu Arg Ala Asn Pro Ser Trp
835 840 845

<210> 79
<211> 847
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: STAT6 (S407D); P009 sin etiqueta de epítipo

<400> 79

Met Ser Leu Trp Gly Leu Val Ser Lys Met Pro Pro Glu Lys Val Gln
1 5 10 15

Arg Leu Tyr Val Asp Phe Pro Gln His Leu Arg His Leu Leu Gly Asp
20 25 30

Trp Leu Glu Ser Gln Pro Trp Glu Phe Leu Val Gly Ser Asp Ala Phe
35 40 45

Cys Cys Asn Leu Ala Ser Ala Leu Leu Ser Asp Thr Val Gln His Leu
 50 55 60
 Gln Ala Ser Val Gly Glu Gln Gly Glu Gly Ser Thr Ile Leu Gln His
 65 70 75 80
 Ile Ser Thr Leu Glu Ser Ile Tyr Gln Arg Asp Pro Leu Lys Leu Val
 85 90 95
 Ala Thr Phe Arg Gln Ile Leu Gln Gly Glu Lys Lys Ala Val Met Glu
 100 105 110
 Gln Phe Arg His Leu Pro Met Pro Phe His Trp Lys Gln Glu Glu Leu
 115 120 125
 Lys Phe Lys Thr Gly Leu Arg Arg Leu Gln His Arg Val Gly Glu Ile
 130 135 140
 His Leu Leu Arg Glu Ala Leu Gln Lys Gly Ala Glu Ala Gly Gln Val
 145 150 155 160
 Ser Leu His Ser Leu Ile Glu Thr Pro Ala Asn Gly Thr Gly Pro Ser
 165 170 175
 Glu Ala Leu Ala Met Leu Leu Gln Glu Thr Thr Gly Glu Leu Glu Ala
 180 185 190
 Ala Lys Ala Leu Val Leu Lys Arg Ile Gln Ile Trp Lys Arg Gln Gln
 195 200 205
 Gln Leu Ala Gly Asn Gly Ala Pro Phe Glu Glu Ser Leu Ala Pro Leu
 210 215 220
 Gln Glu Arg Cys Glu Ser Leu Val Asp Ile Tyr Ser Gln Leu Gln Gln
 225 230 235 240
 Glu Val Gly Ala Ala Gly Gly Glu Leu Glu Pro Lys Thr Arg Ala Ser
 245 250 255
 Leu Thr Gly Arg Leu Asp Glu Val Leu Arg Thr Leu Val Thr Ser Cys
 260 265 270
 Phe Leu Val Glu Lys Gln Pro Pro Gln Val Leu Lys Thr Gln Thr Lys
 275 280 285
 Phe Gln Ala Gly Val Arg Phe Leu Leu Gly Leu Arg Phe Leu Gly Ala
 290 295 300
 Pro Ala Lys Pro Pro Leu Val Arg Ala Asp Met Val Thr Glu Lys Gln
 305 310 315 320
 Ala Arg Glu Leu Ser Val Pro Gln Gly Pro Gly Ala Gly Ala Glu Ser
 325 330 335
 Thr Gly Glu Ile Ile Asn Asn Thr Val Pro Leu Glu Asn Ser Ile Pro
 340 345 350
 Gly Asn Cys Cys Ser Ala Leu Phe Lys Asn Leu Leu Leu Lys Lys Ile
 355 360 365
 Lys Arg Cys Glu Arg Lys Gly Thr Glu Ser Val Thr Glu Glu Lys Cys
 370 375 380
 Ala Val Leu Phe Ser Ala Ser Phe Thr Leu Gly Pro Gly Lys Leu Pro
 385 390 395 400
 Ile Gln Leu Gln Ala Leu Asp Leu Pro Leu Val Val Ile Val His Gly
 405 410 415
 Asn Gln Asp Asn Asn Ala Lys Ala Thr Ile Leu Trp Asp Asn Ala Phe
 420 425 430
 Ser Glu Met Asp Arg Val Pro Phe Val Val Ala Glu Arg Val Pro Trp
 435 440 445
 Glu Lys Met Cys Glu Thr Leu Asn Leu Lys Phe Met Ala Glu Val Gly
 450 455 460

Thr Asn Arg Gly Leu Leu Pro Glu His Phe Leu Phe Leu Ala Gln Lys
465 470 475 480

Ile Phe Asn Asp Asn Ser Leu Ser Met Glu Ala Phe Gln His Arg Ser
485 490 495

Val Ser Trp Ser Gln Phe Asn Lys Glu Ile Leu Leu Gly Arg Gly Phe
500 505 510

Thr Phe Trp Gln Trp Phe Asp Gly Val Leu Asp Leu Thr Lys Arg Cys
515 520 525

Leu Arg Ser Tyr Trp Ser Asp Arg Leu Ile Ile Gly Phe Ile Ser Lys
530 535 540

Gln Tyr Val Thr Ser Leu Leu Leu Asn Glu Pro Asp Gly Thr Phe Leu
545 550 555 560

Leu Arg Phe Ser Asp Ser Glu Ile Gly Gly Ile Thr Ile Ala His Val
565 570 575

Ile Arg Gly Gln Asp Gly Ser Pro Gln Ile Glu Asn Ile Gln Pro Phe
580 585 590

Ser Ala Lys Asp Leu Ser Ile Arg Ser Leu Gly Asp Arg Ile Arg Asp
595 600 605

Leu Ala Gln Leu Lys Asn Leu Tyr Pro Lys Lys Pro Lys Asp Glu Ala
610 615 620

Phe Arg Ser His Tyr Lys Pro Glu Gln Met Gly Lys Asp Gly Arg Gly
625 630 635 640

Tyr Val Pro Ala Thr Ile Lys Met Thr Val Glu Arg Asp Gln Pro Leu
645 650 655

Pro Thr Pro Glu Leu Gln Met Pro Thr Met Val Pro Ser Tyr Asp Leu
660 665 670

Gly Met Ala Pro Asp Ser Ser Met Ser Met Gln Leu Gly Pro Asp Met
675 680 685

Val Pro Gln Val Tyr Pro Pro His Ser His Ser Ile Pro Pro Tyr Gln
690 695 700

Gly Leu Ser Pro Glu Glu Ser Val Asn Val Leu Ser Ala Phe Gln Glu
705 710 715 720

Pro His Leu Gln Met Pro Pro Ser Leu Gly Gln Met Ser Leu Pro Phe
725 730 735

Asp Gln Pro His Pro Gln Gly Leu Leu Pro Cys Gln Pro Gln Glu His
740 745 750

Ala Val Ser Ser Pro Asp Pro Leu Leu Cys Ser Asp Val Thr Met Val
755 760 765

Glu Asp Ser Cys Leu Ser Gln Pro Val Thr Ala Phe Pro Gln Gly Thr
770 775 780

Trp Ile Gly Glu Asp Ile Phe Pro Pro Leu Leu Pro Pro Thr Glu Gln
785 790 795 800

Asp Leu Thr Lys Leu Leu Leu Glu Gly Gln Gly Glu Ser Gly Gly Gly
805 810 815

Ser Leu Gly Ala Gln Pro Leu Leu Gln Pro Ser His Tyr Gly Gln Ser
820 825 830

Gly Ile Ser Met Ser His Met Asp Leu Arg Ala Asn Pro Ser Trp
835 840 845

<210> 80
<211> 847
<212> PRT
<213> Secuencia artificial

<220>

<223> Sintético: STAT6 (S407D/V547A/T548A); P010 sin etiqueta de epítipo

<400> 80

Met Ser Leu Trp Gly Leu Val Ser Lys Met Pro Pro Glu Lys Val Gln
 1 5 10 15

Arg Leu Tyr Val Asp Phe Pro Gln His Leu Arg His Leu Leu Gly Asp
 20 25 30

Trp Leu Glu Ser Gln Pro Trp Glu Phe Leu Val Gly Ser Asp Ala Phe
 35 40 45

Cys Cys Asn Leu Ala Ser Ala Leu Leu Ser Asp Thr Val Gln His Leu
 50 55 60

Gln Ala Ser Val Gly Glu Gln Gly Glu Gly Ser Thr Ile Leu Gln His
 65 70 75 80

Ile Ser Thr Leu Glu Ser Ile Tyr Gln Arg Asp Pro Leu Lys Leu Val
 85 90 95

Ala Thr Phe Arg Gln Ile Leu Gln Gly Glu Lys Lys Ala Val Met Glu
 100 105 110

Gln Phe Arg His Leu Pro Met Pro Phe His Trp Lys Gln Glu Glu Leu
 115 120 125

Lys Phe Lys Thr Gly Leu Arg Arg Leu Gln His Arg Val Gly Glu Ile
 130 135 140

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

Ser Leu His Ser Leu Ile Glu Thr Pro Ala Asn Gly Thr Gly Pro Ser
 165 170 175

Glu Ala Leu Ala Met Leu Leu Gln Glu Thr Thr Gly Glu Leu Glu Ala
 180 185 190

Ala Lys Ala Leu Val Leu Lys Arg Ile Gln Ile Trp Lys Arg Gln Gln
 195 200 205

Gln Leu Ala Gly Asn Gly Ala Pro Phe Glu Glu Ser Leu Ala Pro Leu
 210 215 220

Gln Glu Arg Cys Glu Ser Leu Val Asp Ile Tyr Ser Gln Leu Gln Gln
 225 230 235 240

Glu Val Gly Ala Ala Gly Gly Glu Leu Glu Pro Lys Thr Arg Ala Ser
 245 250 255

Leu Thr Gly Arg Leu Asp Glu Val Leu Arg Thr Leu Val Thr Ser Cys
 260 265 270

Phe Leu Val Glu Lys Gln Pro Pro Gln Val Leu Lys Thr Gln Thr Lys
 275 280 285

Phe Gln Ala Gly Val Arg Phe Leu Leu Gly Leu Arg Phe Leu Gly Ala
 290 295 300

Pro Ala Lys Pro Pro Leu Val Arg Ala Asp Met Val Thr Glu Lys Gln
 305 310 315 320

Ala Arg Glu Leu Ser Val Pro Gln Gly Pro Gly Ala Gly Ala Glu Ser
 325 330 335

Thr Gly Glu Ile Ile Asn Asn Thr Val Pro Leu Glu Asn Ser Ile Pro
 340 345 350

Gly Asn Cys Cys Ser Ala Leu Phe Lys Asn Leu Leu Leu Lys Lys Ile
 355 360 365

Lys Arg Cys Glu Arg Lys Gly Thr Glu Ser Val Thr Glu Glu Lys Cys
 370 375 380

Ala Val Leu Phe Ser Ala Ser Phe Thr Leu Gly Pro Gly Lys Leu Pro
 385 390 395 400

Ile Gln Leu Gln Ala Leu Asp Leu Pro Leu Val Val Ile Val His Gly
 405 410 415
 Asn Gln Asp Asn Asn Ala Lys Ala Thr Ile Leu Trp Asp Asn Ala Phe
 420 425 430
 Ser Glu Met Asp Arg Val Pro Phe Val Val Ala Glu Arg Val Pro Trp
 435 440 445
 Glu Lys Met Cys Glu Thr Leu Asn Leu Lys Phe Met Ala Glu Val Gly
 450 455 460
 Thr Asn Arg Gly Leu Leu Pro Glu His Phe Leu Phe Leu Ala Gln Lys
 465 470 475 480
 Ile Phe Asn Asp Asn Ser Leu Ser Met Glu Ala Phe Gln His Arg Ser
 485 490 495
 Val Ser Trp Ser Gln Phe Asn Lys Glu Ile Leu Leu Gly Arg Gly Phe
 500 505 510
 Thr Phe Trp Gln Trp Phe Asp Gly Val Leu Asp Leu Thr Lys Arg Cys
 515 520 525
 Leu Arg Ser Tyr Trp Ser Asp Arg Leu Ile Ile Gly Phe Ile Ser Lys
 530 535 540
 Gln Tyr Ala Ala Ser Leu Leu Leu Asn Glu Pro Asp Gly Thr Phe Leu
 545 550 555 560
 Leu Arg Phe Ser Asp Ser Glu Ile Gly Gly Ile Thr Ile Ala His Val
 565 570 575
 Ile Arg Gly Gln Asp Gly Ser Pro Gln Ile Glu Asn Ile Gln Pro Phe
 580 585 590
 Ser Ala Lys Asp Leu Ser Ile Arg Ser Leu Gly Asp Arg Ile Arg Asp
 595 600 605
 Leu Ala Gln Leu Lys Asn Leu Tyr Pro Lys Lys Pro Lys Asp Glu Ala
 610 615 620
 Phe Arg Ser His Tyr Lys Pro Glu Gln Met Gly Lys Asp Gly Arg Gly
 625 630 635 640
 Tyr Val Pro Ala Thr Ile Lys Met Thr Val Glu Arg Asp Gln Pro Leu
 645 650 655
 Pro Thr Pro Glu Leu Gln Met Pro Thr Met Val Pro Ser Tyr Asp Leu
 660 665 670
 Gly Met Ala Pro Asp Ser Ser Met Ser Met Gln Leu Gly Pro Asp Met
 675 680 685
 Val Pro Gln Val Tyr Pro Pro His Ser His Ser Ile Pro Pro Tyr Gln
 690 695 700
 Gly Leu Ser Pro Glu Glu Ser Val Asn Val Leu Ser Ala Phe Gln Glu
 705 710 715 720
 Pro His Leu Gln Met Pro Pro Ser Leu Gly Gln Met Ser Leu Pro Phe
 725 730 735
 Asp Gln Pro His Pro Gln Gly Leu Leu Pro Cys Gln Pro Gln Glu His
 740 745 750
 Ala Val Ser Ser Pro Asp Pro Leu Leu Cys Ser Asp Val Thr Met Val
 755 760 765
 Glu Asp Ser Cys Leu Ser Gln Pro Val Thr Ala Phe Pro Gln Gly Thr
 770 775 780
 Trp Ile Gly Glu Asp Ile Phe Pro Pro Leu Leu Pro Pro Thr Glu Gln
 785 790 795 800
 Asp Leu Thr Lys Leu Leu Leu Glu Gly Gln Gly Glu Ser Gly Gly Gly

Ser Leu Gly Ala Gln Pro Leu Leu Gln Pro Ser His Tyr Gly Gln Ser
820 825 830

Gly Ile Ser Met Ser His Met Asp Leu Arg Ala Asn Pro Ser Trp
835 840 845

<210> 81
<211> 847
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: STAT6 (V547A/T548A/Y641F); P011 sin etiqueta de epítipo
<400> 81

Met Ser Leu Trp Gly Leu Val Ser Lys Met Pro Pro Glu Lys Val Gln
1 5 10 15

Arg Leu Tyr Val Asp Phe Pro Gln His Leu Arg His Leu Leu Gly Asp
20 25 30

Trp Leu Glu Ser Gln Pro Trp Glu Phe Leu Val Gly Ser Asp Ala Phe
35 40 45

Cys Cys Asn Leu Ala Ser Ala Leu Leu Ser Asp Thr Val Gln His Leu
50 55 60

Gln Ala Ser Val Gly Glu Gln Gly Glu Gly Ser Thr Ile Leu Gln His
65 70 75 80

Ile Ser Thr Leu Glu Ser Ile Tyr Gln Arg Asp Pro Leu Lys Leu Val
85 90 95

Ala Thr Phe Arg Gln Ile Leu Gln Gly Glu Lys Lys Ala Val Met Glu
100 105 110

Gln Phe Arg His Leu Pro Met Pro Phe His Trp Lys Gln Glu Glu Leu
115 120 125

Lys Phe Lys Thr Gly Leu Arg Arg Leu Gln His Arg Val Gly Glu Ile
130 135 140

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

Ser Leu His Ser Leu Ile Glu Thr Pro Ala Asn Gly Thr Gly Pro Ser
165 170 175

Glu Ala Leu Ala Met Leu Leu Gln Glu Thr Thr Gly Glu Leu Glu Ala
180 185 190

Ala Lys Ala Leu Val Leu Lys Arg Ile Gln Ile Trp Lys Arg Gln Gln
195 200 205

Gln Leu Ala Gly Asn Gly Ala Pro Phe Glu Glu Ser Leu Ala Pro Leu
210 215 220

Gln Glu Arg Cys Glu Ser Leu Val Asp Ile Tyr Ser Gln Leu Gln Gln
225 230 235 240

Glu Val Gly Ala Ala Gly Gly Glu Leu Glu Pro Lys Thr Arg Ala Ser
245 250 255

Leu Thr Gly Arg Leu Asp Glu Val Leu Arg Thr Leu Val Thr Ser Cys
260 265 270

Phe Leu Val Glu Lys Gln Pro Pro Gln Val Leu Lys Thr Gln Thr Lys
275 280 285

Phe Gln Ala Gly Val Arg Phe Leu Leu Gly Leu Arg Phe Leu Gly Ala
290 295 300

Pro Ala Lys Pro Pro Leu Val Arg Ala Asp Met Val Thr Glu Lys Gln
305 310 315 320

Ala Arg Glu Leu Ser Val Pro Gln Gly Pro Gly Ala Gly Ala Glu Ser
325 330 335

Thr Gly Glu Ile Ile Asn Asn Thr Val Pro Leu Glu Asn Ser Ile Pro
 340 345 350
 Gly Asn Cys Cys Ser Ala Leu Phe Lys Asn Leu Leu Leu Lys Lys Ile
 355 360 365
 Lys Arg Cys Glu Arg Lys Gly Thr Glu Ser Val Thr Glu Glu Lys Cys
 370 375 380
 Ala Val Leu Phe Ser Ala Ser Phe Thr Leu Gly Pro Gly Lys Leu Pro
 385 390 395 400
 Ile Gln Leu Gln Ala Leu Ser Leu Pro Leu Val Val Ile Val His Gly
 405 410 415
 Asn Gln Asp Asn Asn Ala Lys Ala Thr Ile Leu Trp Asp Asn Ala Phe
 420 425 430
 Ser Glu Met Asp Arg Val Pro Phe Val Val Ala Glu Arg Val Pro Trp
 435 440 445
 Glu Lys Met Cys Glu Thr Leu Asn Leu Lys Phe Met Ala Glu Val Gly
 450 455 460
 Thr Asn Arg Gly Leu Leu Pro Glu His Phe Leu Phe Leu Ala Gln Lys
 465 470 475 480
 Ile Phe Asn Asp Asn Ser Leu Ser Met Glu Ala Phe Gln His Arg Ser
 485 490 495
 Val Ser Trp Ser Gln Phe Asn Lys Glu Ile Leu Leu Gly Arg Gly Phe
 500 505 510
 Thr Phe Trp Gln Trp Phe Asp Gly Val Leu Asp Leu Thr Lys Arg Cys
 515 520 525
 Leu Arg Ser Tyr Trp Ser Asp Arg Leu Ile Ile Gly Phe Ile Ser Lys
 530 535 540
 Gln Tyr Ala Ala Ser Leu Leu Leu Asn Glu Pro Asp Gly Thr Phe Leu
 545 550 555 560
 Leu Arg Phe Ser Asp Ser Glu Ile Gly Gly Ile Thr Ile Ala His Val
 565 570 575
 Ile Arg Gly Gln Asp Gly Ser Pro Gln Ile Glu Asn Ile Gln Pro Phe
 580 585 590
 Ser Ala Lys Asp Leu Ser Ile Arg Ser Leu Gly Asp Arg Ile Arg Asp
 595 600 605
 Leu Ala Gln Leu Lys Asn Leu Tyr Pro Lys Lys Pro Lys Asp Glu Ala
 610 615 620
 Phe Arg Ser His Tyr Lys Pro Glu Gln Met Gly Lys Asp Gly Arg Gly
 625 630 635 640
 Phe Val Pro Ala Thr Ile Lys Met Thr Val Glu Arg Asp Gln Pro Leu
 645 650 655
 Pro Thr Pro Glu Leu Gln Met Pro Thr Met Val Pro Ser Tyr Asp Leu
 660 665 670
 Gly Met Ala Pro Asp Ser Ser Met Ser Met Gln Leu Gly Pro Asp Met
 675 680 685
 Val Pro Gln Val Tyr Pro Pro His Ser His Ser Ile Pro Pro Tyr Gln
 690 695 700
 Gly Leu Ser Pro Glu Glu Ser Val Asn Val Leu Ser Ala Phe Gln Glu
 705 710 715 720
 Pro His Leu Gln Met Pro Pro Ser Leu Gly Gln Met Ser Leu Pro Phe
 725 730 735
 Asp Gln Pro His Pro Gln Gly Leu Leu Pro Cys Gln Pro Gln Glu His

740

745

750

Ala Val Ser Ser Pro Asp Pro Leu Leu Cys Ser Asp Val Thr Met Val
755 760 765

Glu Asp Ser Cys Leu Ser Gln Pro Val Thr Ala Phe Pro Gln Gly Thr
770 775 780

Trp Ile Gly Glu Asp Ile Phe Pro Pro Leu Leu Pro Pro Thr Glu Gln
785 790 795 800

Asp Leu Thr Lys Leu Leu Leu Glu Gly Gln Gly Glu Ser Gly Gly Gly
805 810 815

Ser Leu Gly Ala Gln Pro Leu Leu Gln Pro Ser His Tyr Gly Gln Ser
820 825 830

Gly Ile Ser Met Ser His Met Asp Leu Arg Ala Asn Pro Ser Trp
835 840 845

<210> 82

<211> 479

<212> PRT

<213> Secuencia artificial

<220>

<223> Sintético: hu-cFLIP-L; P1006 sin etiqueta de epítipo

<400> 82

Ser Ala Glu Val Ile His Gln Val Glu Glu Ala Leu Asp Thr Asp Glu
1 5 10 15

Lys Glu Met Leu Leu Phe Leu Cys Arg Asp Val Ala Ile Asp Val Val
20 25 30

Pro Pro Asn Val Arg Asp Leu Leu Asp Ile Leu Arg Glu Arg Gly Lys
35 40 45

Leu Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg Phe
50 55 60

Asp Leu Leu Lys Arg Ile Leu Lys Met Asp Arg Lys Ala Val Glu Thr
65 70 75 80

His Leu Leu Arg Asn Pro His Leu Val Ser Asp Tyr Arg Val Leu Met
85 90 95

Ala Glu Ile Gly Glu Asp Leu Asp Lys Ser Asp Val Ser Ser Leu Ile
100 105 110

Phe Leu Met Lys Asp Tyr Met Gly Arg Gly Lys Ile Ser Lys Glu Lys
115 120 125

Ser Phe Leu Asp Leu Val Val Glu Leu Glu Lys Leu Asn Leu Val Ala
130 135 140

Pro Asp Gln Leu Asp Leu Leu Glu Lys Cys Leu Lys Asn Ile His Arg
145 150 155 160

Ile Asp Leu Lys Thr Lys Ile Gln Lys Tyr Lys Gln Ser Val Gln Gly
165 170 175

Ala Gly Thr Ser Tyr Arg Asn Val Leu Gln Ala Ala Ile Gln Lys Ser
180 185 190

Leu Lys Asp Pro Ser Asn Asn Phe Arg Leu His Asn Gly Arg Ser Lys
195 200 205

Glu Gln Arg Leu Lys Glu Gln Leu Gly Ala Gln Gln Glu Pro Val Lys
210 215 220

Lys Ser Ile Gln Glu Ser Glu Ala Phe Leu Pro Gln Ser Ile Pro Glu
225 230 235 240

Glu Arg Tyr Lys Met Lys Ser Lys Pro Leu Gly Ile Cys Leu Ile Ile
245 250 255

Asp Cys Ile Gly Asn Glu Thr Glu Leu Leu Arg Asp Thr Phe Thr Ser
260 265 270

Leu Gly Tyr Glu Val Gln Lys Phe Leu His Leu Ser Met His Gly Ile
275 280 285

Ser Gln Ile Leu Gly Gln Phe Ala Cys Met Pro Glu His Arg Asp Tyr
290 295 300

Asp Ser Phe Val Cys Val Leu Val Ser Arg Gly Gly Ser Gln Ser Val
305 310 315 320

Tyr Gly Val Asp Gln Thr His Ser Gly Leu Pro Leu His His Ile Arg
325 330 335

Arg Met Phe Met Gly Asp Ser Cys Pro Tyr Leu Ala Gly Lys Pro Lys
340 345 350

Met Phe Phe Ile Gln Asn Tyr Val Val Ser Glu Gly Gln Leu Glu Asp
355 360 365

Ser Ser Leu Leu Glu Val Asp Gly Pro Ala Met Lys Asn Val Glu Phe
370 375 380

Lys Ala Gln Lys Arg Gly Leu Cys Thr Val His Arg Glu Ala Asp Phe
385 390 395 400

Phe Trp Ser Leu Cys Thr Ala Asp Met Ser Leu Leu Glu Gln Ser His
405 410 415

Ser Ser Pro Ser Leu Tyr Leu Gln Cys Leu Ser Gln Lys Leu Arg Gln
420 425 430

Glu Arg Lys Arg Pro Leu Leu Asp Leu His Ile Glu Leu Asn Gly Tyr
435 440 445

Met Tyr Asp Trp Asn Ser Arg Val Ser Ala Lys Glu Lys Tyr Tyr Val
450 455 460

Trp Leu Gln His Thr Leu Arg Lys Lys Leu Ile Leu Ser Tyr Thr
465 470 475

<210> 83
<211> 226
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: hu-cFLIP-S(1-227); P1007 sin etiqueta de epítopo

<400> 83

Ser Ala Glu Val Ile His Gln Val Glu Glu Ala Leu Asp Thr Asp Glu
1 5 10 15

Lys Glu Met Leu Leu Phe Leu Cys Arg Asp Val Ala Ile Asp Val Val
20 25 30

Pro Pro Asn Val Arg Asp Leu Leu Asp Ile Leu Arg Glu Arg Gly Lys
35 40 45

Leu Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg Phe
50 55 60

Asp Leu Leu Lys Arg Ile Leu Lys Met Asp Arg Lys Ala Val Glu Thr
65 70 75 80

His Leu Leu Arg Asn Pro His Leu Val Ser Asp Tyr Arg Val Leu Met
85 90 95

Ala Glu Ile Gly Glu Asp Leu Asp Lys Ser Asp Val Ser Ser Leu Ile
100 105 110

Phe Leu Met Lys Asp Tyr Met Gly Arg Gly Lys Ile Ser Lys Glu Lys
115 120 125

Ser Phe Leu Asp Leu Val Val Glu Leu Glu Lys Leu Asn Leu Val Ala
130 135 140

Pro Asp Gln Leu Asp Leu Leu Glu Lys Cys Leu Lys Asn Ile His Arg
145 150 155 160

Ile Asp Leu Lys Thr Lys Ile Gln Lys Tyr Lys Gln Ser Val Gln Gly
165 170 175

Ala Gly Thr Ser Tyr Arg Asn Val Leu Gln Ala Ala Ile Gln Lys Ser
180 185 190

Leu Lys Asp Pro Ser Asn Asn Phe Arg Leu His Asn Gly Arg Ser Lys
195 200 205

Glu Gln Arg Leu Lys Glu Gln Leu Gly Ala Gln Gln Glu Pro Val Lys
210 215 220

Lys Ser
225

<210> 84
<211> 195
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: hu-cFLIP-p22(1-198); P1008 sin etiqueta de epítipo

<400> 84

Ser Ala Glu Val Ile His Gln Val Glu Glu Ala Leu Asp Thr Asp Glu
1 5 10 15

Lys Glu Met Leu Leu Phe Leu Cys Arg Asp Val Ala Ile Asp Val Val
20 25 30

Pro Pro Asn Val Arg Asp Leu Leu Asp Ile Leu Arg Glu Arg Gly Lys
35 40 45

Leu Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg Phe
50 55 60

Asp Leu Leu Lys Arg Ile Leu Lys Met Asp Arg Lys Ala Val Glu Thr
65 70 75 80

His Leu Leu Arg Asn Pro His Leu Val Ser Asp Tyr Arg Val Leu Met
85 90 95

Ala Glu Ile Gly Glu Asp Leu Asp Lys Ser Asp Val Ser Ser Leu Ile
100 105 110

Phe Leu Met Lys Asp Tyr Met Gly Arg Gly Lys Ile Ser Lys Glu Lys
115 120 125

Ser Phe Leu Asp Leu Val Val Glu Leu Glu Lys Leu Asn Leu Val Ala
130 135 140

Pro Asp Gln Leu Asp Leu Leu Glu Lys Cys Leu Lys Asn Ile His Arg
145 150 155 160

Ile Asp Leu Lys Thr Lys Ile Gln Lys Tyr Lys Gln Ser Val Gln Gly
165 170 175

Ala Gly Thr Ser Tyr Arg Asn Val Leu Gln Ala Ala Ile Gln Lys Ser
180 185 190

Leu Lys Asp
195

<210> 85
<211> 375
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: hu-cFLIP-p43(1-376); P1009 sin etiqueta de epítipo

<400> 85

Ser Ala Glu Val Ile His Gln Val Glu Glu Ala Leu Asp Thr Asp Glu
1 5 10 15

Lys Glu Met Leu Leu Phe Leu Cys Arg Asp Val Ala Ile Asp Val Val
20 25 30

Pro Pro Asn Val Arg Asp Leu Leu Asp Ile Leu Arg Glu Arg Gly Lys
35 40 45

Leu Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg Phe
50 55 60

Asp Leu Leu Lys Arg Ile Leu Lys Met Asp Arg Lys Ala Val Glu Thr
65 70 75 80

His Leu Leu Arg Asn Pro His Leu Val Ser Asp Tyr Arg Val Leu Met
85 90 95

Ala Glu Ile Gly Glu Asp Leu Asp Lys Ser Asp Val Ser Ser Leu Ile
100 105 110

Phe Leu Met Lys Asp Tyr Met Gly Arg Gly Lys Ile Ser Lys Glu Lys
115 120 125

Ser Phe Leu Asp Leu Val Val Glu Leu Glu Lys Leu Asn Leu Val Ala
130 135 140

Pro Asp Gln Leu Asp Leu Leu Glu Lys Cys Leu Lys Asn Ile His Arg
145 150 155 160

Ile Asp Leu Lys Thr Lys Ile Gln Lys Tyr Lys Gln Ser Val Gln Gly
165 170 175

Ala Gly Thr Ser Tyr Arg Asn Val Leu Gln Ala Ala Ile Gln Lys Ser
180 185 190

Leu Lys Asp Pro Ser Asn Asn Phe Arg Leu His Asn Gly Arg Ser Lys
195 200 205

Glu Gln Arg Leu Lys Glu Gln Leu Gly Ala Gln Gln Glu Pro Val Lys
210 215 220

Lys Ser Ile Gln Glu Ser Glu Ala Phe Leu Pro Gln Ser Ile Pro Glu
225 230 235 240

Glu Arg Tyr Lys Met Lys Ser Lys Pro Leu Gly Ile Cys Leu Ile Ile
245 250 255

Asp Cys Ile Gly Asn Glu Thr Glu Leu Leu Arg Asp Thr Phe Thr Ser
260 265 270

Leu Gly Tyr Glu Val Gln Lys Phe Leu His Leu Ser Met His Gly Ile
275 280 285

Ser Gln Ile Leu Gly Gln Phe Ala Cys Met Pro Glu His Arg Asp Tyr
290 295 300

Asp Ser Phe Val Cys Val Leu Val Ser Arg Gly Gly Ser Gln Ser Val
305 310 315 320

Tyr Gly Val Asp Gln Thr His Ser Gly Leu Pro Leu His His Ile Arg
325 330 335

Arg Met Phe Met Gly Asp Ser Cys Pro Tyr Leu Ala Gly Lys Pro Lys
340 345 350

Met Phe Phe Ile Gln Asn Tyr Val Val Ser Glu Gly Gln Leu Glu Asp
355 360 365

Ser Ser Leu Leu Glu Val Asp
370 375

<210> 86
<211> 104
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: hu-cFLIP-p12(377-480); P1010 sin etiqueta de epítipo

<400> 86

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

Cys Thr Val His Arg Glu Ala Asp Phe Phe Trp Ser Leu Cys Thr Ala
20 25 30

Asp Met Ser Leu Leu Glu Gln Ser His Ser Ser Pro Ser Leu Tyr Leu
 35 40 45
 Gln Cys Leu Ser Gln Lys Leu Arg Gln Glu Arg Lys Arg Pro Leu Leu
 50 55 60
 Asp Leu His Ile Glu Leu Asn Gly Tyr Met Tyr Asp Trp Asn Ser Arg
 65 70 75 80
 Val Ser Ala Lys Glu Lys Tyr Tyr Val Trp Leu Gln His Thr Leu Arg
 85 90 95
 Lys Lys Leu Ile Leu Ser Tyr Thr
 100
 <210> 87
 <211> 756
 <212> PRT
 <213> Secuencia artificial
 <220>
 <223> Sintético: huIKK2ca(S177E/S181E); P4005 sin etiqueta de epítipo
 <400> 87
 Met Ser Trp Ser Pro Ser Leu Thr Thr Gln Thr Cys Gly Ala Trp Glu
 1 5 10 15
 Met Lys Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Ile Arg Trp
 20 25 30
 His Asn Gln Glu Thr Gly Glu Gln Ile Ala Ile Lys Gln Cys Arg Gln
 35 40 45
 Glu Leu Ser Pro Arg Asn Arg Glu Arg Trp Cys Leu Glu Ile Gln Ile
 50 55 60
 Met Arg Arg Leu Thr His Pro Asn Val Val Ala Ala Arg Asp Val Pro
 65 70 75 80
 Glu Gly Met Gln Asn Leu Ala Pro Asn Asp Leu Pro Leu Leu Ala Met
 85 90 95
 Glu Tyr Cys Gln Gly Gly Asp Leu Arg Lys Tyr Leu Asn Gln Phe Glu
 100 105 110
 Asn Cys Cys Gly Leu Arg Glu Gly Ala Ile Leu Thr Leu Leu Ser Asp
 115 120 125
 Ile Ala Ser Ala Leu Arg Tyr Leu His Glu Asn Arg Ile Ile His Arg
 130 135 140
 Asp Leu Lys Pro Glu Asn Ile Val Leu Gln Gln Gly Glu Gln Arg Leu
 145 150 155 160
 Ile His Lys Ile Ile Asp Leu Gly Tyr Ala Lys Glu Leu Asp Gln Gly
 165 170 175
 Glu Leu Cys Thr Glu Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu
 180 185 190
 Leu Leu Glu Gln Gln Lys Tyr Thr Val Thr Val Asp Tyr Trp Ser Phe
 195 200 205
 Gly Thr Leu Ala Phe Glu Cys Ile Thr Gly Phe Arg Pro Phe Leu Pro
 210 215 220
 Asn Trp Gln Pro Val Gln Trp His Ser Lys Val Arg Gln Lys Ser Glu
 225 230 235 240
 Val Asp Ile Val Val Ser Glu Asp Leu Asn Gly Thr Val Lys Phe Ser
 245 250 255
 Ser Ser Leu Pro Tyr Pro Asn Asn Leu Asn Ser Val Leu Ala Glu Arg
 260 265 270
 Leu Glu Lys Trp Leu Gln Leu Met Leu Met Trp His Pro Arg Gln Arg
 275 280 285

Gly Thr Asp Pro Thr Tyr Gly Pro Asn Gly Cys Phe Lys Ala Leu Asp
 290 295 300

Asp Ile Leu Asn Leu Lys Leu Val His Ile Leu Asn Met Val Thr Gly
 305 310 315 320

Thr Ile His Thr Tyr Pro Val Thr Glu Asp Glu Ser Leu Gln Ser Leu
 325 330 335

Lys Ala Arg Ile Gln Gln Asp Thr Gly Ile Pro Glu Glu Asp Gln Glu
 340 345 350

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

Gln Cys Ile Ser Asp Gly Lys Leu Asn Glu Gly His Thr Leu Asp Met
 370 375 380

Asp Leu Val Phe Leu Phe Asp Asn Ser Lys Ile Thr Tyr Glu Thr Gln
 385 390 395 400

Ile Ser Pro Arg Pro Gln Pro Glu Ser Val Ser Cys Ile Leu Gln Glu
 405 410 415

Pro Lys Arg Asn Leu Ala Phe Phe Gln Leu Arg Lys Val Trp Gly Gln
 420 425 430

Val Trp His Ser Ile Gln Thr Leu Lys Glu Asp Cys Asn Arg Leu Gln
 435 440 445

Gln Gly Gln Arg Ala Ala Met Met Asn Leu Leu Arg Asn Asn Ser Cys
 450 455 460

Leu Ser Lys Met Lys Asn Ser Met Ala Ser Met Ser Gln Gln Leu Lys
 465 470 475 480

Ala Lys Leu Asp Phe Phe Lys Thr Ser Ile Gln Ile Asp Leu Glu Lys
 485 490 495

Tyr Ser Glu Gln Thr Glu Phe Gly Ile Thr Ser Asp Lys Leu Leu Leu
 500 505 510

Ala Trp Arg Glu Met Glu Gln Ala Val Glu Leu Cys Gly Arg Glu Asn
 515 520 525

Glu Val Lys Leu Leu Val Glu Arg Met Met Ala Leu Gln Thr Asp Ile
 530 535 540

Val Asp Leu Gln Arg Ser Pro Met Gly Arg Lys Gln Gly Gly Thr Leu
 545 550 555 560

Asp Asp Leu Glu Glu Gln Ala Arg Glu Leu Tyr Arg Arg Leu Arg Glu
 565 570 575

Lys Pro Arg Asp Gln Arg Thr Glu Gly Asp Ser Gln Glu Met Val Arg
 580 585 590

Leu Leu Leu Gln Ala Ile Gln Ser Phe Glu Lys Lys Val Arg Val Ile
 595 600 605

Tyr Thr Gln Leu Ser Lys Thr Val Val Cys Lys Gln Lys Ala Leu Glu
 610 615 620

Leu Leu Pro Lys Val Glu Glu Val Val Ser Leu Met Asn Glu Asp Glu
 625 630 635 640

Lys Thr Val Val Arg Leu Gln Glu Lys Arg Gln Lys Glu Leu Trp Asn
 645 650 655

Leu Leu Lys Ile Ala Cys Ser Lys Val Arg Gly Pro Val Ser Gly Ser
 660 665 670

Pro Asp Ser Met Asn Ala Ser Arg Leu Ser Gln Pro Gly Gln Leu Met
 675 680 685

Ser Gln Pro Ser Thr Ala Ser Asn Ser Leu Pro Glu Pro Ala Lys Lys
 690 695 700

Ser Glu Glu Leu Val Ala Glu Ala His Asn Leu Cys Thr Leu Leu Glu
 705 710 715 720

 Asn Ala Ile Gln Asp Thr Val Arg Glu Gln Asp Gln Ser Phe Thr Ala
 725 730 735

 Leu Asp Trp Ser Trp Leu Gln Thr Glu Glu Glu Glu His Ser Cys Leu
 740 745 750

 Glu Gln Ala Ser
 755

 <210> 88
 <211> 756
 <212> PRT
 <213> Secuencia artificial

 <220>
 <223> Sintético: huIKK2null(S177A/S181A); P4006 sin etiqueta de epítipo

 <400> 88

 Met Ser Trp Ser Pro Ser Leu Thr Thr Gln Thr Cys Gly Ala Trp Glu
 1 5 10 15

 Met Lys Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Ile Arg Trp
 20 25 30

 His Asn Gln Glu Thr Gly Glu Gln Ile Ala Ile Lys Gln Cys Arg Gln
 35 40 45

 Glu Leu Ser Pro Arg Asn Arg Glu Arg Trp Cys Leu Glu Ile Gln Ile
 50 55 60

 Met Arg Arg Leu Thr His Pro Asn Val Val Ala Ala Arg Asp Val Pro
 65 70 75 80

 Glu Gly Met Gln Asn Leu Ala Pro Asn Asp Leu Pro Leu Leu Ala Met
 85 90 95

 Glu Tyr Cys Gln Gly Gly Asp Leu Arg Lys Tyr Leu Asn Gln Phe Glu
 100 105 110

 Asn Cys Cys Gly Leu Arg Glu Gly Ala Ile Leu Thr Leu Leu Ser Asp
 115 120 125

 Ile Ala Ser Ala Leu Arg Tyr Leu His Glu Asn Arg Ile Ile His Arg
 130 135 140

 Asp Leu Lys Pro Glu Asn Ile Val Leu Gln Gln Gly Glu Gln Arg Leu
 145 150 155 160

 Ile His Lys Ile Ile Asp Leu Gly Tyr Ala Lys Glu Leu Asp Gln Gly
 165 170 175

 Ala Leu Cys Thr Ala Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu
 180 185 190

 Leu Leu Glu Gln Gln Lys Tyr Thr Val Thr Val Asp Tyr Trp Ser Phe
 195 200 205

 Gly Thr Leu Ala Phe Glu Cys Ile Thr Gly Phe Arg Pro Phe Leu Pro
 210 215 220

 Asn Trp Gln Pro Val Gln Trp His Ser Lys Val Arg Gln Lys Ser Glu
 225 230 235 240

 Val Asp Ile Val Val Ser Glu Asp Leu Asn Gly Thr Val Lys Phe Ser
 245 250 255

 Ser Ser Leu Pro Tyr Pro Asn Asn Leu Asn Ser Val Leu Ala Glu Arg
 260 265 270

 Leu Glu Lys Trp Leu Gln Leu Met Leu Met Trp His Pro Arg Gln Arg
 275 280 285

 Gly Thr Asp Pro Thr Tyr Gly Pro Asn Gly Cys Phe Lys Ala Leu Asp
 290 295 300

Asp Ile Leu Asn Leu Lys Leu Val His Ile Leu Asn Met Val Thr Gly
 305 310 315 320
 Thr Ile His Thr Tyr Pro Val Thr Glu Asp Glu Ser Leu Gln Ser Leu
 325 330 335
 Lys Ala Arg Ile Gln Gln Asp Thr Gly Ile Pro Glu Glu Asp Gln Glu
 340 345 350
 Leu Leu Gln Glu Ala Gly Leu Ala Leu Ile Pro Asp Lys Pro Ala Thr
 355 360 365
 Gln Cys Ile Ser Asp Gly Lys Leu Asn Glu Gly His Thr Leu Asp Met
 370 375 380
 Asp Leu Val Phe Leu Phe Asp Asn Ser Lys Ile Thr Tyr Glu Thr Gln
 385 390 395 400
 Ile Ser Pro Arg Pro Gln Pro Glu Ser Val Ser Cys Ile Leu Gln Glu
 405 410 415
 Pro Lys Arg Asn Leu Ala Phe Phe Gln Leu Arg Lys Val Trp Gly Gln
 420 425 430
 Val Trp His Ser Ile Gln Thr Leu Lys Glu Asp Cys Asn Arg Leu Gln
 435 440 445
 Gln Gly Gln Arg Ala Ala Met Met Asn Leu Leu Arg Asn Asn Ser Cys
 450 455 460
 Leu Ser Lys Met Lys Asn Ser Met Ala Ser Met Ser Gln Gln Leu Lys
 465 470 475 480
 Ala Lys Leu Asp Phe Phe Lys Thr Ser Ile Gln Ile Asp Leu Glu Lys
 485 490 495
 Tyr Ser Glu Gln Thr Glu Phe Gly Ile Thr Ser Asp Lys Leu Leu Leu
 500 505 510
 Ala Trp Arg Glu Met Glu Gln Ala Val Glu Leu Cys Gly Arg Glu Asn
 515 520 525
 Glu Val Lys Leu Leu Val Glu Arg Met Met Ala Leu Gln Thr Asp Ile
 530 535 540
 Val Asp Leu Gln Arg Ser Pro Met Gly Arg Lys Gln Gly Gly Thr Leu
 545 550 555 560
 Asp Asp Leu Glu Glu Gln Ala Arg Glu Leu Tyr Arg Arg Leu Arg Glu
 565 570 575
 Lys Pro Arg Asp Gln Arg Thr Glu Gly Asp Ser Gln Glu Met Val Arg
 580 585 590
 Leu Leu Leu Gln Ala Ile Gln Ser Phe Glu Lys Lys Val Arg Val Ile
 595 600 605
 Tyr Thr Gln Leu Ser Lys Thr Val Val Cys Lys Gln Lys Ala Leu Glu
 610 615 620
 Leu Leu Pro Lys Val Glu Glu Val Val Ser Leu Met Asn Glu Asp Glu
 625 630 635 640
 Lys Thr Val Val Arg Leu Gln Glu Lys Arg Gln Lys Glu Leu Trp Asn
 645 650 655
 Leu Leu Lys Ile Ala Cys Ser Lys Val Arg Gly Pro Val Ser Gly Ser
 660 665 670
 Pro Asp Ser Met Asn Ala Ser Arg Leu Ser Gln Pro Gly Gln Leu Met
 675 680 685
 Ser Gln Pro Ser Thr Ala Ser Asn Ser Leu Pro Glu Pro Ala Lys Lys
 690 695 700
 Ser Glu Glu Leu Val Ala Glu Ala His Asn Leu Cys Thr Leu Leu Glu
 705 710 715 720

Asn Ala Ile Gln Asp Thr Val Arg Glu Gln Asp Gln Ser Phe Thr Ala
725 730 735

Leu Asp Trp Ser Trp Leu Gln Thr Glu Glu Glu Glu His Ser Cys Leu
740 745 750

Glu Gln Ala Ser
755

<210> 89
<211> 757
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: muIKK2ca(S177E/S181E); P4002 sin etiqueta de epítipo

<400> 89

Met Ser Trp Ser Pro Ser Leu Pro Thr Gln Thr Cys Gly Ala Trp Glu
1 5 10 15

Met Lys Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Ile Arg Trp
20 25 30

His Asn Gln Ala Thr Gly Glu Gln Ile Ala Ile Lys Gln Cys Arg Gln
35 40 45

Glu Leu Ser Pro Lys Asn Arg Asn Arg Trp Cys Leu Glu Ile Gln Ile
50 55 60

Met Arg Arg Leu Asn His Pro Asn Val Val Ala Ala Arg Asp Val Pro
65 70 75 80

Glu Gly Met Gln Asn Leu Ala Pro Asn Asp Leu Pro Leu Leu Ala Met
85 90 95

Glu Tyr Cys Gln Gly Gly Asp Leu Arg Arg Tyr Leu Asn Gln Phe Glu
100 105 110

Asn Cys Cys Gly Leu Arg Glu Gly Ala Val Leu Thr Leu Leu Ser Asp
115 120 125

Ile Ala Ser Ala Leu Arg Tyr Leu His Glu Asn Arg Ile Ile His Arg
130 135 140

Asp Leu Lys Pro Glu Asn Ile Val Leu Gln Gln Gly Glu Lys Arg Leu
145 150 155 160

Ile His Lys Ile Ile Asp Leu Gly Tyr Ala Lys Glu Leu Asp Gln Gly
165 170 175

Glu Leu Cys Thr Glu Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu
180 185 190

Leu Leu Glu Gln Gln Lys Tyr Thr Val Thr Val Asp Tyr Trp Ser Phe
195 200 205

Gly Thr Leu Ala Phe Glu Cys Ile Thr Gly Phe Arg Pro Phe Leu Pro
210 215 220

Asn Trp Gln Pro Val Gln Trp His Ser Lys Val Arg Gln Lys Ser Glu
225 230 235 240

Val Asp Ile Val Val Ser Glu Asp Leu Asn Gly Ala Val Lys Phe Ser
245 250 255

Ser Ser Leu Pro Phe Pro Asn Asn Leu Asn Ser Val Leu Ala Glu Arg
260 265 270

Leu Glu Lys Trp Leu Gln Leu Met Leu Met Trp His Pro Arg Gln Arg
275 280 285

Gly Thr Asp Pro Gln Tyr Gly Pro Asn Gly Cys Phe Arg Ala Leu Asp
290 295 300

Asp Ile Leu Asn Leu Lys Leu Val His Val Leu Asn Met Val Thr Gly
305 310 315 320

Thr Val His Thr Tyr Pro Val Thr Glu Asp Glu Ser Leu Gln Ser Leu
 325 330 335
 Lys Thr Arg Ile Gln Glu Asn Thr Gly Ile Leu Glu Thr Asp Gln Glu
 340 345 350
 Leu Leu Gln Lys Ala Gly Leu Val Leu Leu Pro Asp Lys Pro Ala Thr
 355 360 365
 Gln Cys Ile Ser Asp Ser Lys Thr Asn Glu Gly Leu Thr Leu Asp Met
 370 375 380
 Asp Leu Val Phe Leu Leu Asp Asn Ser Lys Ile Asn Tyr Glu Thr Gln
 385 390 395 400
 Ile Thr Pro Arg Pro Pro Pro Glu Ser Val Ser Cys Ile Leu Gln Glu
 405 410 415
 Pro Lys Arg Asn Leu Ser Phe Phe Gln Leu Arg Lys Val Trp Gly Gln
 420 425 430
 Val Trp His Ser Ile Gln Thr Leu Lys Glu Asp Cys Asn Arg Leu Gln
 435 440 445
 Gln Gly Gln Arg Ala Ala Met Met Ser Leu Leu Arg Asn Asn Ser Cys
 450 455 460
 Leu Ser Lys Met Lys Asn Ala Met Ala Ser Thr Ala Gln Gln Leu Lys
 465 470 475 480
 Ala Lys Leu Asp Phe Phe Lys Thr Ser Ile Gln Ile Asp Leu Glu Lys
 485 490 495
 Tyr Lys Glu Gln Thr Glu Phe Gly Ile Thr Ser Asp Lys Leu Leu Leu
 500 505 510
 Ala Trp Arg Glu Met Glu Gln Ala Val Glu Gln Cys Gly Arg Glu Asn
 515 520 525
 Asp Val Lys His Leu Val Glu Arg Met Met Ala Leu Gln Thr Asp Ile
 530 535 540
 Val Asp Leu Gln Arg Ser Pro Met Gly Arg Lys Gln Gly Gly Thr Leu
 545 550 555 560
 Asp Asp Leu Glu Glu Gln Ala Arg Glu Leu Tyr Arg Lys Leu Arg Glu
 565 570 575
 Lys Pro Arg Asp Gln Arg Thr Glu Gly Asp Ser Gln Glu Met Val Arg
 580 585 590
 Leu Leu Leu Gln Ala Ile Gln Ser Phe Glu Lys Lys Val Arg Val Ile
 595 600 605
 Tyr Thr Gln Leu Ser Lys Thr Val Val Cys Lys Gln Lys Ala Leu Glu
 610 615 620
 Leu Leu Pro Lys Val Glu Glu Val Val Ser Leu Met Asn Glu Asp Glu
 625 630 635 640
 Arg Thr Val Val Arg Leu Gln Glu Lys Arg Gln Lys Glu Leu Trp Asn
 645 650 655
 Leu Leu Lys Ile Ala Cys Ser Lys Val Arg Gly Pro Val Ser Gly Ser
 660 665 670
 Pro Asp Ser Met Asn Val Ser Arg Leu Ser His Pro Gly Gln Leu Met
 675 680 685
 Ser Gln Pro Ser Ser Ala Cys Asp Ser Leu Pro Glu Ser Asp Lys Lys
 690 695 700
 Ser Glu Glu Leu Val Ala Glu Ala His Ala Leu Cys Ser Arg Leu Glu
 705 710 715 720
 Ser Ala Leu Gln Asp Thr Val Lys Glu Gln Asp Arg Ser Phe Thr Thr
 725 730 735

Leu Asp Trp Ser Trp Leu Gln Met Glu Asp Glu Glu Arg Cys Ser Leu
740 745 750

Glu Gln Ala Cys Asp
755

<210> 90
<211> 757
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: muIKK2null(S177A/S181A); P4003 sin etiqueta de epítipo
<400> 90

Met Ser Trp Ser Pro Ser Leu Pro Thr Gln Thr Cys Gly Ala Trp Glu
1 5 10 15

Met Lys Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Ile Arg Trp
20 25 30

His Asn Gln Ala Thr Gly Glu Gln Ile Ala Ile Lys Gln Cys Arg Gln
35 40 45

Glu Leu Ser Pro Lys Asn Arg Asn Arg Trp Cys Leu Glu Ile Gln Ile
50 55 60

Met Arg Arg Leu Asn His Pro Asn Val Val Ala Ala Arg Asp Val Pro
65 70 75 80

Glu Gly Met Gln Asn Leu Ala Pro Asn Asp Leu Pro Leu Leu Ala Met
85 90 95

Glu Tyr Cys Gln Gly Gly Asp Leu Arg Arg Tyr Leu Asn Gln Phe Glu
100 105 110

Asn Cys Cys Gly Leu Arg Glu Gly Ala Val Leu Thr Leu Leu Ser Asp
115 120 125

Ile Ala Ser Ala Leu Arg Tyr Leu His Glu Asn Arg Ile Ile His Arg
130 135 140

Asp Leu Lys Pro Glu Asn Ile Val Leu Gln Gln Gly Glu Lys Arg Leu
145 150 155 160

Ile His Lys Ile Ile Asp Leu Gly Tyr Ala Lys Glu Leu Asp Gln Gly
165 170 175

Ala Leu Cys Thr Ala Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu
180 185 190

Leu Leu Glu Gln Gln Lys Tyr Thr Val Thr Val Asp Tyr Trp Ser Phe
195 200 205

Gly Thr Leu Ala Phe Glu Cys Ile Thr Gly Phe Arg Pro Phe Leu Pro
210 215 220

Asn Trp Gln Pro Val Gln Trp His Ser Lys Val Arg Gln Lys Ser Glu
225 230 235 240

Val Asp Ile Val Val Ser Glu Asp Leu Asn Gly Ala Val Lys Phe Ser
245 250 255

Ser Ser Leu Pro Phe Pro Asn Asn Leu Asn Ser Val Leu Ala Glu Arg
260 265 270

Leu Glu Lys Trp Leu Gln Leu Met Leu Met Trp His Pro Arg Gln Arg
275 280 285

Gly Thr Asp Pro Gln Tyr Gly Pro Asn Gly Cys Phe Arg Ala Leu Asp
290 295 300

Asp Ile Leu Asn Leu Lys Leu Val His Val Leu Asn Met Val Thr Gly
305 310 315 320

Thr Val His Thr Tyr Pro Val Thr Glu Asp Glu Ser Leu Gln Ser Leu
325 330 335

Lys Thr Arg Ile Gln Glu Asn Thr Gly Ile Leu Glu Thr Asp Gln Glu
 340 345 350
 Leu Leu Gln Lys Ala Gly Leu Val Leu Leu Pro Asp Lys Pro Ala Thr
 355 360 365
 Gln Cys Ile Ser Asp Ser Lys Thr Asn Glu Gly Leu Thr Leu Asp Met
 370 375 380
 Asp Leu Val Phe Leu Leu Asp Asn Ser Lys Ile Asn Tyr Glu Thr Gln
 385 390 395 400
 Ile Thr Pro Arg Pro Pro Glu Ser Val Ser Cys Ile Leu Gln Glu
 405 410 415
 Pro Lys Arg Asn Leu Ser Phe Phe Gln Leu Arg Lys Val Trp Gly Gln
 420 425 430
 Val Trp His Ser Ile Gln Thr Leu Lys Glu Asp Cys Asn Arg Leu Gln
 435 440 445
 Gln Gly Gln Arg Ala Ala Met Met Ser Leu Leu Arg Asn Asn Ser Cys
 450 455 460
 Leu Ser Lys Met Lys Asn Ala Met Ala Ser Thr Ala Gln Gln Leu Lys
 465 470 475 480
 Ala Lys Leu Asp Phe Phe Lys Thr Ser Ile Gln Ile Asp Leu Glu Lys
 485 490 495
 Tyr Lys Glu Gln Thr Glu Phe Gly Ile Thr Ser Asp Lys Leu Leu Leu
 500 505 510
 Ala Trp Arg Glu Met Glu Gln Ala Val Glu Gln Cys Gly Arg Glu Asn
 515 520 525
 Asp Val Lys His Leu Val Glu Arg Met Met Ala Leu Gln Thr Asp Ile
 530 535 540
 Val Asp Leu Gln Arg Ser Pro Met Gly Arg Lys Gln Gly Gly Thr Leu
 545 550 555 560
 Asp Asp Leu Glu Glu Gln Ala Arg Glu Leu Tyr Arg Lys Leu Arg Glu
 565 570 575
 Lys Pro Arg Asp Gln Arg Thr Glu Gly Asp Ser Gln Glu Met Val Arg
 580 585 590
 Leu Leu Leu Gln Ala Ile Gln Ser Phe Glu Lys Lys Val Arg Val Ile
 595 600 605
 Tyr Thr Gln Leu Ser Lys Thr Val Val Cys Lys Gln Lys Ala Leu Glu
 610 615 620
 Leu Leu Pro Lys Val Glu Glu Val Val Ser Leu Met Asn Glu Asp Glu
 625 630 635 640
 Arg Thr Val Val Arg Leu Gln Glu Lys Arg Gln Lys Glu Leu Trp Asn
 645 650 655
 Leu Leu Lys Ile Ala Cys Ser Lys Val Arg Gly Pro Val Ser Gly Ser
 660 665 670
 Pro Asp Ser Met Asn Val Ser Arg Leu Ser His Pro Gly Gln Leu Met
 675 680 685
 Ser Gln Pro Ser Ser Ala Cys Asp Ser Leu Pro Glu Ser Asp Lys Lys
 690 695 700
 Ser Glu Glu Leu Val Ala Glu Ala His Ala Leu Cys Ser Arg Leu Glu
 705 710 715 720
 Ser Ala Leu Gln Asp Thr Val Lys Glu Gln Asp Arg Ser Phe Thr Thr
 725 730 735
 Leu Asp Trp Ser Trp Leu Gln Met Glu Asp Glu Glu Arg Cys Ser Leu
 740 745 750

Glu Gln Ala Cys Asp
755

<210> 91
<211> 744
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(744)
<223> IKK alfa constitutivamente activo humano (mutación PEST) P.4013 sin etiqueta de epítipo

<400> 91

Met Glu Arg Pro Pro Gly Leu Arg Pro Gly Ala Gly Gly Pro Trp Glu
1 5 10 15

Met Arg Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Cys Leu Tyr
20 25 30

Gln His Arg Glu Leu Asp Leu Lys Ile Ala Ile Lys Ser Cys Arg Leu
35 40 45

Glu Leu Ser Thr Lys Asn Arg Glu Arg Trp Cys His Glu Ile Gln Ile
50 55 60

Met Lys Lys Leu Asn His Ala Asn Val Val Lys Ala Cys Asp Val Pro
65 70 75 80

Glu Glu Leu Asn Ile Leu Ile His Asp Val Pro Leu Leu Ala Met Glu
85 90 95

Tyr Cys Ser Gly Gly Asp Leu Arg Lys Leu Leu Asn Lys Pro Glu Asn
100 105 110

Cys Cys Gly Leu Lys Glu Ser Gln Ile Leu Ser Leu Leu Ser Asp Ile
115 120 125

Gly Ser Gly Ile Arg Tyr Leu His Glu Asn Lys Ile Ile His Arg Asp
130 135 140

Leu Lys Pro Glu Asn Ile Val Leu Gln Asp Val Gly Gly Lys Ile Ile
145 150 155 160

His Lys Ile Ile Asp Leu Gly Tyr Ala Lys Asp Val Asp Gln Gly Glu
165 170 175

Leu Cys Thr Glu Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu Leu
180 185 190

Phe Glu Asn Lys Pro Tyr Thr Ala Thr Val Asp Tyr Trp Ser Phe Gly
195 200 205

Thr Met Val Phe Glu Cys Ile Ala Gly Tyr Arg Pro Phe Leu His His
210 215 220

Leu Gln Pro Phe Thr Trp His Glu Lys Ile Lys Lys Lys Asp Pro Lys
225 230 235 240

Cys Ile Phe Ala Cys Glu Glu Met Ser Gly Glu Val Arg Phe Ser Ser
245 250 255

His Leu Pro Gln Pro Asn Ser Leu Cys Ser Leu Val Val Glu Pro Met
260 265 270

Glu Asn Trp Leu Gln Leu Met Leu Asn Trp Asp Pro Gln Gln Arg Gly
275 280 285

Gly Pro Val Asp Leu Thr Leu Lys Gln Pro Arg Cys Phe Val Leu Met
290 295 300

Asp His Ile Leu Asn Leu Lys Ile Val His Ile Leu Asn Met Thr Ser
305 310 315 320

Ala Lys Ile Ile Ser Phe Leu Leu Pro Pro Asp Glu Ser Leu His Ser
325 330 335

Leu Gln Ser Arg Ile Glu Arg Glu Thr Gly Ile Asn Thr Gly Ser Gln
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340

345

350

Glu Leu Leu Ser Glu Thr Gly Ile Ser Leu Asp Pro Arg Lys Pro Ala
 355 360 365

Ser Gln Cys Val Leu Asp Gly Val Arg Gly Cys Asp Ser Tyr Met Val
 370 375 380

Tyr Leu Phe Asp Lys Ser Lys Thr Val Tyr Glu Gly Pro Phe Ala Ser
 385 390 395 400

Arg Ser Leu Ser Asp Cys Val Asn Tyr Ile Val Gln Asp Ser Lys Ile
 405 410 415

Gln Leu Pro Ile Ile Gln Leu Arg Lys Val Trp Ala Glu Ala Val His
 420 425 430

Tyr Val Ser Gly Leu Lys Glu Asp Tyr Ser Arg Leu Phe Gln Gly Gln
 435 440 445

Arg Ala Ala Met Leu Ser Leu Leu Arg Tyr Asn Ala Asn Leu Thr Lys
 450 455 460

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

Glu Phe Phe His Lys Ser Ile Gln Leu Asp Leu Glu Arg Tyr Ser Glu
 485 490 495

Gln Met Thr Tyr Gly Ile Ser Ser Glu Lys Met Leu Lys Ala Trp Lys
 500 505 510

Glu Met Glu Glu Lys Ala Ile His Tyr Ala Glu Val Gly Val Ile Gly
 515 520 525

Tyr Leu Glu Asp Gln Ile Met Ser Leu His Ala Glu Ile Met Glu Leu
 530 535 540

Gln Lys Ser Pro Tyr Arg Arg Gln Gly Asp Leu Met Glu Ser Leu Glu
 545 550 555 560

Gln Arg Ala Ile Asp Leu Tyr Lys Gln Leu Lys His Arg Pro Ser Asp
 565 570 575

His Ser Tyr Ser Asp Ser Thr Glu Met Val Lys Ile Ile Val His Thr
 580 585 590

Val Gln Ser Gln Asp Arg Val Leu Lys Glu Leu Phe Gly His Leu Ser
 595 600 605

Lys Leu Leu Gly Cys Lys Gln Lys Ile Ile Asp Leu Leu Pro Lys Val
 610 615 620

Glu Val Ala Leu Ser Asn Ile Lys Glu Ala Asp Asn Thr Val Met Phe
 625 630 635 640

Met Gln Gly Lys Arg Gln Lys Glu Ile Trp His Leu Leu Lys Ile Ala
 645 650 655

Cys Thr Gln Ala Ala Arg Ala Leu Val Gly Ala Ala Leu Glu Gly
 660 665 670

Ala Val Ala Pro Gln Ala Ala Ala Trp Leu Pro Pro Ala Ala Ala Glu
 675 680 685

His Asp His Ala Leu Ala Cys Val Val Ala Pro Gln Asp Gly Glu Ala
 690 695 700

Ala Ala Gln Met Ile Glu Glu Asn Leu Asn Cys Leu Gly His Leu Ala
 705 710 715 720

Ala Ile Ile His Glu Ala Asn Glu Glu Gln Gly Asn Ser Met Met Asn
 725 730 735

Leu Asp Trp Ser Trp Leu Thr Glu
 740

<210> 92
 <211> 744
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(744)
 <223> IKK alfa constitutivamente activo humano (mutación PEST) P.4014 sin etiqueta de epítipo

<400> 92

Met Glu Arg Pro Pro Gly Leu Arg Pro Gly Ala Gly Gly Pro Trp Glu
 1 5 10 15

Met Arg Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Cys Leu Tyr
 20 25 30

Gln His Arg Glu Leu Asp Leu Lys Ile Ala Ile Lys Ser Cys Arg Leu
 35 40 45

Glu Leu Ser Thr Lys Asn Arg Glu Arg Trp Cys His Glu Ile Gln Ile
 50 55 60

Met Lys Lys Leu Asn His Ala Asn Val Val Lys Ala Cys Asp Val Pro
 65 70 75 80

Glu Glu Leu Asn Ile Leu Ile His Asp Val Pro Leu Leu Ala Met Glu
 85 90 95

Tyr Cys Ser Gly Gly Asp Leu Arg Lys Leu Leu Asn Lys Pro Glu Asn
 100 105 110

Cys Cys Gly Leu Lys Glu Ser Gln Ile Leu Ser Leu Leu Ser Asp Ile
 115 120 125

Gly Ser Gly Ile Arg Tyr Leu His Glu Asn Lys Ile Ile His Arg Asp
 130 135 140

Leu Lys Pro Glu Asn Ile Val Leu Gln Asp Val Gly Gly Lys Ile Ile
 145 150 155 160

His Lys Ile Ile Asp Leu Gly Tyr Ala Lys Asp Val Asp Gln Gly Glu
 165 170 175

Leu Cys Thr Glu Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu Leu
 180 185 190

Phe Glu Asn Lys Pro Tyr Thr Ala Thr Val Asp Tyr Trp Ser Phe Gly
 195 200 205

Thr Met Val Phe Glu Cys Ile Ala Gly Tyr Arg Pro Phe Leu His His
 210 215 220

Leu Gln Pro Phe Thr Trp His Glu Lys Ile Lys Lys Lys Asp Pro Lys
 225 230 235 240

Cys Ile Phe Ala Cys Glu Glu Met Ser Gly Glu Val Arg Phe Ser Ser
 245 250 255

His Leu Pro Gln Pro Asn Ser Leu Cys Ser Leu Val Val Glu Pro Met
 260 265 270

Glu Asn Trp Leu Gln Leu Met Leu Asn Trp Asp Pro Gln Gln Arg Gly
 275 280 285

Gly Pro Val Asp Leu Thr Leu Lys Gln Pro Arg Cys Phe Val Leu Met
 290 295 300

Asp His Ile Leu Asn Leu Lys Ile Val His Ile Leu Asn Met Thr Ser
 305 310 315 320

Ala Lys Ile Ile Ser Phe Leu Leu Pro Pro Asp Glu Ser Leu His Ser
 325 330 335

Leu Gln Ser Arg Ile Glu Arg Glu Thr Gly Ile Asn Thr Gly Ser Gln
 340 345 350

Glu Leu Leu Ser Glu Thr Gly Ile Ser Leu Asp Pro Arg Lys Pro Ala
 355 360 365

Ser Gln Cys Val Leu Asp Gly Val Arg Gly Cys Asp Ser Tyr Met Val
 370 375 380
 Tyr Leu Phe Asp Lys Ser Lys Thr Val Tyr Glu Gly Pro Phe Ala Ser
 385 390 395 400
 Arg Ser Leu Ser Asp Cys Val Asn Tyr Ile Val Gln Asp Ser Lys Ile
 405 410 415
 Gln Leu Pro Ile Ile Gln Leu Arg Lys Val Trp Ala Glu Ala Val His
 420 425 430
 Tyr Val Ser Gly Leu Lys Glu Asp Tyr Ser Arg Leu Phe Gln Gly Gln
 435 440 445
 Arg Ala Ala Met Leu Ser Leu Leu Arg Tyr Asn Ala Asn Leu Thr Lys
 450 455 460
 Met Lys Asn Thr Leu Ile Ser Ala Ser Gln Gln Leu Lys Ala Lys Leu
 465 470 475 480
 Glu Phe Phe His Lys Ser Ile Gln Leu Asp Leu Glu Arg Tyr Ser Glu
 485 490 495
 Gln Met Thr Tyr Gly Ile Ser Ser Glu Lys Met Leu Lys Ala Trp Lys
 500 505 510
 Glu Met Glu Glu Lys Ala Ile His Tyr Ala Glu Val Gly Val Ile Gly
 515 520 525
 Tyr Leu Glu Asp Gln Ile Met Ser Leu His Ala Glu Ile Met Glu Leu
 530 535 540
 Gln Lys Ser Pro Tyr Arg Arg Gln Gly Asp Leu Met Glu Ser Leu Glu
 545 550 555 560
 Gln Arg Ala Ile Asp Leu Tyr Lys Gln Leu Lys His Arg Pro Ser Asp
 565 570 575
 His Ser Tyr Ser Asp Ser Thr Glu Met Val Lys Ile Ile Val His Thr
 580 585 590
 Val Gln Ser Gln Asp Arg Val Leu Lys Glu Leu Phe Gly His Leu Ser
 595 600 605
 Lys Leu Leu Gly Cys Lys Gln Lys Ile Ile Asp Leu Leu Pro Lys Val
 610 615 620
 Glu Val Ala Leu Ser Asn Ile Lys Glu Ala Asp Asn Thr Val Met Phe
 625 630 635 640
 Met Gln Gly Lys Arg Gln Lys Glu Ile Trp His Leu Leu Lys Ile Ala
 645 650 655
 Cys Thr Gln Ala Ala Ala Arg Ala Leu Val Gly Ala Ala Leu Glu Gly
 660 665 670
 Ala Val Ala Pro Gln Ala Ala Ala Trp Leu Pro Pro Ala Ala Ala Glu
 675 680 685
 His Asp His Ala Leu Ala Cys Val Val Ala Pro Gln Asp Gly Glu Ala
 690 695 700
 Ala Ala Gln Met Ile Glu Glu Asn Leu Asn Cys Leu Gly His Leu Ala
 705 710 715 720
 Ala Ile Ile His Glu Ala Asn Glu Glu Gln Gly Asn Ser Met Met Asn
 725 730 735
 Leu Asp Trp Ser Trp Leu Thr Glu
 740

<210> 93
 <211> 756
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(756)
 <223> IKK beta constitutivamente activo humano (mutación PEST) P.4015 sin etiqueta de epítipo

<400> 93

Met Ser Trp Ser Pro Ser Leu Thr Thr Gln Thr Cys Gly Ala Trp Glu
 1 5 10 15

Met Lys Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Ile Arg Trp
 20 25 30

His Asn Gln Glu Thr Gly Glu Gln Ile Ala Ile Lys Gln Cys Arg Gln
 35 40 45

Glu Leu Ser Pro Arg Asn Arg Glu Arg Trp Cys Leu Glu Ile Gln Ile
 50 55 60

Met Arg Arg Leu Thr His Pro Asn Val Val Ala Ala Arg Asp Val Pro
 65 70 75 80

Glu Gly Met Gln Asn Leu Ala Pro Asn Asp Leu Pro Leu Leu Ala Met
 85 90 95

Glu Tyr Cys Gln Gly Gly Asp Leu Arg Lys Tyr Leu Asn Gln Phe Glu
 100 105 110

Asn Cys Cys Gly Leu Arg Glu Gly Ala Ile Leu Thr Leu Leu Ser Asp
 115 120 125

Ile Ala Ser Ala Leu Arg Tyr Leu His Glu Asn Arg Ile Ile His Arg
 130 135 140

Asp Leu Lys Pro Glu Asn Ile Val Leu Gln Gln Gly Glu Gln Arg Leu
 145 150 155 160

Ile His Lys Ile Ile Asp Leu Gly Tyr Ala Lys Glu Leu Asp Gln Gly
 165 170 175

Glu Leu Cys Thr Glu Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu
 180 185 190

Leu Leu Glu Gln Gln Lys Tyr Thr Val Thr Val Asp Tyr Trp Ser Phe
 195 200 205

Gly Thr Leu Ala Phe Glu Cys Ile Thr Gly Phe Arg Pro Phe Leu Pro
 210 215 220

Asn Trp Gln Pro Val Gln Trp His Ser Lys Val Arg Gln Lys Ser Glu
 225 230 235 240

Val Asp Ile Val Val Ser Glu Asp Leu Asn Gly Thr Val Lys Phe Ser
 245 250 255

Ser Ser Leu Pro Tyr Pro Asn Asn Leu Asn Ser Val Leu Ala Glu Arg
 260 265 270

Leu Glu Lys Trp Leu Gln Leu Met Leu Met Trp His Pro Arg Gln Arg
 275 280 285

Gly Thr Asp Pro Thr Tyr Gly Pro Asn Gly Cys Phe Lys Ala Leu Asp
 290 295 300

Asp Ile Leu Asn Leu Lys Leu Val His Ile Leu Asn Met Val Thr Gly
 305 310 315 320

Thr Ile His Thr Tyr Pro Val Thr Glu Asp Glu Ser Leu Gln Ser Leu
 325 330 335

Lys Ala Arg Ile Gln Gln Asp Thr Gly Ile Pro Glu Glu Asp Gln Glu
 340 345 350

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

Gln Cys Ile Ser Asp Gly Lys Leu Asn Glu Gly His Thr Leu Asp Met
 370 375 380

Asp Leu Val Phe Leu Phe Asp Asn Ser Lys Ile Thr Tyr Glu Thr Gln
 385 390 395 400
 Ile Ser Pro Arg Pro Gln Pro Glu Ser Val Ser Cys Ile Leu Gln Glu
 405 410 415
 Pro Lys Arg Asn Leu Ala Phe Phe Gln Leu Arg Lys Val Trp Gly Gln
 420 425 430
 Val Trp His Ser Ile Gln Thr Leu Lys Glu Asp Cys Asn Arg Leu Gln
 435 440 445
 Gln Gly Gln Arg Ala Ala Met Met Asn Leu Leu Arg Asn Asn Ser Cys
 450 455 460
 Leu Ser Lys Met Lys Asn Ser Met Ala Ser Met Ser Gln Gln Leu Lys
 465 470 475 480
 Ala Lys Leu Asp Phe Phe Lys Thr Ser Ile Gln Ile Asp Leu Glu Lys
 485 490 495
 Tyr Ser Glu Gln Thr Glu Phe Gly Ile Thr Ser Asp Lys Leu Leu Leu
 500 505 510
 Ala Trp Arg Glu Met Glu Gln Ala Val Glu Leu Cys Gly Arg Glu Asn
 515 520 525
 Glu Val Lys Leu Leu Val Glu Arg Met Met Ala Leu Gln Thr Asp Ile
 530 535 540
 Val Asp Leu Gln Arg Ser Pro Met Gly Arg Lys Gln Gly Gly Thr Leu
 545 550 555 560
 Asp Asp Leu Glu Glu Gln Ala Arg Glu Leu Tyr Arg Arg Leu Arg Glu
 565 570 575
 Lys Pro Arg Asp Gln Arg Thr Glu Gly Asp Ser Gln Glu Met Val Arg
 580 585 590
 Leu Leu Leu Gln Ala Ile Gln Ser Phe Glu Lys Lys Val Arg Val Ile
 595 600 605
 Tyr Thr Gln Leu Ser Lys Thr Val Val Cys Lys Gln Lys Ala Leu Glu
 610 615 620
 Leu Leu Pro Lys Val Glu Glu Val Val Ser Leu Met Asn Glu Asp Glu
 625 630 635 640
 Lys Thr Val Val Arg Leu Gln Glu Lys Arg Gln Lys Glu Leu Trp Asn
 645 650 655
 Leu Leu Lys Ile Ala Cys Ser Lys Val Arg Gly Pro Val Ala Gly Ala
 660 665 670
 Pro Asp Ala Met Asn Ala Ala Arg Leu Ala Gln Pro Gly Gln Leu Met
 675 680 685
 Ala Gln Pro Ala Thr Ala Ala Asn Ala Leu Pro Glu Pro Ala Lys Lys
 690 695 700
 Ala Glu Glu Leu Val Ala Glu Ala His Asn Leu Cys Thr Leu Leu Glu
 705 710 715 720
 Asn Ala Ile Gln Asp Thr Val Arg Glu Gln Asp Gln Ser Phe Thr Ala
 725 730 735
 Leu Asp Trp Ser Trp Leu Gln Thr Glu Glu Glu Glu His Ser Cys Leu
 740 745 750
 Glu Gln Ala Ser
 755

<210> 94
 <211> 756
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(756)
 <223> IKK beta constitutivamente activo humano (Mutación PEST) P.4016 sin etiqueta de epítipo

<400> 94

Met Ser Trp Ser Pro Ser Leu Thr Thr Gln Thr Cys Gly Ala Trp Glu
 1 5 10 15

Met Lys Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Ile Arg Trp
 20 25 30

His Asn Gln Glu Thr Gly Glu Gln Ile Ala Ile Lys Gln Cys Arg Gln
 35 40 45

Glu Leu Ser Pro Arg Asn Arg Glu Arg Trp Cys Leu Glu Ile Gln Ile
 50 55 60

Met Arg Arg Leu Thr His Pro Asn Val Val Ala Ala Arg Asp Val Pro
 65 70 75 80

Glu Gly Met Gln Asn Leu Ala Pro Asn Asp Leu Pro Leu Leu Ala Met
 85 90 95

Glu Tyr Cys Gln Gly Gly Asp Leu Arg Lys Tyr Leu Asn Gln Phe Glu
 100 105 110

Asn Cys Cys Gly Leu Arg Glu Gly Ala Ile Leu Thr Leu Leu Ser Asp
 115 120 125

Ile Ala Ser Ala Leu Arg Tyr Leu His Glu Asn Arg Ile Ile His Arg
 130 135 140

Asp Leu Lys Pro Glu Asn Ile Val Leu Gln Gln Gly Glu Gln Arg Leu
 145 150 155 160

Ile His Lys Ile Ile Asp Leu Gly Tyr Ala Lys Glu Leu Asp Gln Gly
 165 170 175

Glu Leu Cys Thr Glu Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu
 180 185 190

Leu Leu Glu Gln Gln Lys Tyr Thr Val Thr Val Asp Tyr Trp Ser Phe
 195 200 205

Gly Thr Leu Ala Phe Glu Cys Ile Thr Gly Phe Arg Pro Phe Leu Pro
 210 215 220

Asn Trp Gln Pro Val Gln Trp His Ser Lys Val Arg Gln Lys Ser Glu
 225 230 235 240

Val Asp Ile Val Val Ser Glu Asp Leu Asn Gly Thr Val Lys Phe Ser
 245 250 255

Ser Ser Leu Pro Tyr Pro Asn Asn Leu Asn Ser Val Leu Ala Glu Arg
 260 265 270

Leu Glu Lys Trp Leu Gln Leu Met Leu Met Trp His Pro Arg Gln Arg
 275 280 285

Gly Thr Asp Pro Thr Tyr Gly Pro Asn Gly Cys Phe Lys Ala Leu Asp
 290 295 300

Asp Ile Leu Asn Leu Lys Leu Val His Ile Leu Asn Met Val Thr Gly
 305 310 315 320

Thr Ile His Thr Tyr Pro Val Thr Glu Asp Glu Ser Leu Gln Ser Leu
 325 330 335

Lys Ala Arg Ile Gln Gln Asp Thr Gly Ile Pro Glu Glu Asp Gln Glu
 340 345 350

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

Gln Cys Ile Ser Asp Gly Lys Leu Asn Glu Gly His Thr Leu Asp Met
 370 375 380

Asp Leu Val Phe Leu Phe Asp Asn Ser Lys Ile Thr Tyr Glu Thr Gln
 385 390 395 400
 Ile Ser Pro Arg Pro Gln Pro Glu Ser Val Ser Cys Ile Leu Gln Glu
 405 410 415
 Pro Lys Arg Asn Leu Ala Phe Phe Gln Leu Arg Lys Val Trp Gly Gln
 420 425 430
 Val Trp His Ser Ile Gln Thr Leu Lys Glu Asp Cys Asn Arg Leu Gln
 435 440 445
 Gln Gly Gln Arg Ala Ala Met Met Asn Leu Leu Arg Asn Asn Ser Cys
 450 455 460
 Leu Ser Lys Met Lys Asn Ser Met Ala Ser Met Ser Gln Gln Leu Lys
 465 470 475 480
 Ala Lys Leu Asp Phe Phe Lys Thr Ser Ile Gln Ile Asp Leu Glu Lys
 485 490 495
 Tyr Ser Glu Gln Thr Glu Phe Gly Ile Thr Ser Asp Lys Leu Leu Leu
 500 505 510
 Ala Trp Arg Glu Met Glu Gln Ala Val Glu Leu Cys Gly Arg Glu Asn
 515 520 525
 Glu Val Lys Leu Leu Val Glu Arg Met Met Ala Leu Gln Thr Asp Ile
 530 535 540
 Val Asp Leu Gln Arg Ser Pro Met Gly Arg Lys Gln Gly Gly Thr Leu
 545 550 555 560
 Asp Asp Leu Glu Glu Gln Ala Arg Glu Leu Tyr Arg Arg Leu Arg Glu
 565 570 575
 Lys Pro Arg Asp Gln Arg Thr Glu Gly Asp Ser Gln Glu Met Val Arg
 580 585 590
 Leu Leu Leu Gln Ala Ile Gln Ser Phe Glu Lys Lys Val Arg Val Ile
 595 600 605
 Tyr Thr Gln Leu Ser Lys Thr Val Val Cys Lys Gln Lys Ala Leu Glu
 610 615 620
 Leu Leu Pro Lys Val Glu Glu Val Val Ser Leu Met Asn Glu Asp Glu
 625 630 635 640
 Lys Thr Val Val Arg Leu Gln Glu Lys Arg Gln Lys Glu Leu Trp Asn
 645 650 655
 Leu Leu Lys Ile Ala Cys Ser Lys Val Arg Gly Pro Val Ala Gly Ala
 660 665 670
 Pro Asp Ala Met Asn Ala Ala Arg Leu Ala Gln Pro Gly Gln Leu Met
 675 680 685
 Ala Gln Pro Ala Thr Ala Ala Asn Ala Leu Pro Glu Pro Ala Lys Lys
 690 695 700
 Ala Glu Glu Leu Val Ala Glu Ala His Asn Leu Cys Thr Leu Leu Glu
 705 710 715 720
 Asn Ala Ile Gln Asp Thr Val Arg Glu Gln Asp Gln Ser Phe Thr Ala
 725 730 735
 Leu Asp Trp Ser Trp Leu Gln Thr Glu Glu Glu Glu His Ser Cys Leu
 740 745 750

Glu Gln Ala Ser
 755

<210> 95
 <211> 745
 <212> PRT
 <213> Mus musculus

<220>

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<221> misc_feature
<222> (1)..(745)
<223> IKK alfa constitutivamente activo de ratón (mutación PEST) P.4017 sin etiqueta de epítopo

<400> 95
Met Glu Arg Pro Pro Gly Leu Arg Pro Gly Ala Gly Gly Pro Trp Glu
1      5      10
Met Arg Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Ser Leu Tyr
20     25
Gln His Arg Glu Leu Asp Leu Lys Ile Ala Ile Lys Ser Cys Arg Leu
35     40     45
Glu Leu Ser Ser Lys Asn Arg Glu Arg Trp Cys His Glu Ile Gln Ile
50     55     60
Met Lys Lys Leu Asp His Ala Asn Val Val Lys Ala Cys Asp Val Pro
65     70     75     80
Glu Glu Leu Asn Phe Leu Ile Asn Asp Val Pro Leu Leu Ala Met Glu
85     90     95
Tyr Cys Ser Gly Gly Asp Leu Arg Lys Leu Leu Asn Lys Pro Glu Asn
100    105    110
Cys Cys Gly Leu Lys Glu Ser Gln Ile Leu Ser Leu Leu Ser Asp Ile
115    120    125
Gly Ser Gly Ile Arg Tyr Leu His Glu Asn Lys Ile Ile His Arg Asp
130    135    140
Leu Lys Pro Glu Asn Ile Val Leu Gln Asp Val Gly Gly Lys Thr Ile
145    150    155    160
His Lys Ile Ile Asp Leu Gly Tyr Ala Lys Asp Val Asp Gln Gly Glu
165    170    175
Leu Cys Thr Glu Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu Leu
180    185    190
Phe Glu Asn Lys Pro Tyr Thr Ala Thr Val Asp Tyr Trp Ser Phe Gly
195    200    205
Thr Met Val Phe Glu Cys Ile Ala Gly Tyr Arg Pro Phe Leu His His
210    215    220
Leu Gln Pro Phe Thr Trp His Glu Lys Ile Lys Lys Lys Asp Pro Lys
225    230    235    240
Cys Ile Phe Ala Cys Glu Glu Met Thr Gly Glu Val Arg Phe Ser Ser
245    250    255
His Leu Pro Gln Pro Asn Ser Leu Cys Ser Leu Ile Val Glu Pro Met
260    265    270
Glu Ser Trp Leu Gln Leu Met Leu Asn Trp Asp Pro Gln Gln Arg Gly
275    280    285
Gly Pro Ile Asp Leu Thr Leu Lys Gln Pro Arg Cys Phe Ala Leu Met
290    295    300
Asp His Ile Leu Asn Leu Lys Ile Val His Ile Leu Asn Met Thr Ser
305    310    315    320
Ala Lys Ile Ile Ser Phe Leu Leu Pro Cys Asp Glu Ser Leu His Ser
325    330    335
Leu Gln Ser Arg Ile Glu Arg Glu Thr Gly Ile Asn Thr Gly Ser Gln
340    345    350
Glu Leu Leu Ser Glu Thr Gly Ile Ser Leu Asp Pro Arg Lys Pro Ala
355    360    365
Ser Gln Cys Val Leu Asp Gly Val Arg Gly Cys Asp Ser Tyr Met Val
370    375    380
Tyr Leu Phe Asp Lys Ser Lys Thr Val Tyr Glu Gly Pro Phe Ala Ser

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385          390          395          400
Arg Ser Leu Ser Asp Cys Val Asn Tyr Ile Val Gln Asp Ser Lys Ile
      405      410      415
Gln Leu Pro Ile Ile Gln Leu Arg Lys Val Trp Ala Glu Ala Val His
      420      425      430
Tyr Val Ser Gly Leu Lys Glu Asp Tyr Ser Arg Leu Phe Gln Gly Gln
      435      440      445
Arg Ala Ala Met Leu Ser Leu Leu Arg Tyr Asn Ala Asn Leu Thr Lys
      450      455      460
Met Lys Asn Thr Leu Ile Ser Ala Ser Gln Gln Leu Lys Ala Lys Leu
      465      470      475
Glu Phe Phe Arg Lys Ser Ile Gln Leu Asp Leu Glu Arg Tyr Ser Glu
      485      490      495
Gln Met Thr Tyr Gly Ile Ser Ser Glu Lys Met Leu Lys Ala Trp Lys
      500      505      510
Glu Met Glu Glu Lys Ala Ile His Tyr Ser Glu Val Gly Val Ile Gly
      515      520      525
Tyr Leu Glu Asp Gln Ile Met Ser Leu His Thr Glu Ile Met Glu Leu
      530      535      540
Gln Lys Ser Pro Tyr Gly Arg Arg Gln Gly Asp Leu Met Glu Ser Leu
      545      550      555      560
Glu Gln Arg Ala Ile Asp Leu Tyr Lys Gln Leu Lys His Arg Pro Pro
      565      570      575
Asp His Leu Tyr Ser Asp Ser Thr Glu Met Val Lys Ile Ile Val His
      580      585      590
Thr Val Gln Ser Gln Asp Arg Val Leu Lys Glu Leu Phe Gly His Leu
      595      600      605
Ser Lys Leu Leu Gly Cys Lys Gln Lys Ile Ile Asp Leu Leu Pro Lys
      610      615      620
Val Glu Val Ala Leu Ser Asn Ile Lys Glu Ala Asp Asn Thr Val Met
      625      630      635      640
Phe Met Gln Gly Lys Arg Gln Lys Glu Ile Trp His Leu Leu Lys Ile
      645      650      655
Ala Cys Thr Gln Ala Ala Ala Arg Ala Leu Val Gly Ala Ala Leu Glu
      660      665      670
Gly Ala Val Ala Pro Pro Val Ala Ala Trp Leu Pro Pro Ala Leu Ala
      675      680      685
Asp Arg Glu His Pro Leu Thr Cys Val Val Ala Pro Gln Asp Gly Glu
      690      695      700
Ala Leu Ala Gln Met Ile Glu Glu Asn Leu Asn Cys Leu Gly His Leu
      705      710      715      720
Ala Ala Ile Ile Arg Glu Ala Asn Glu Asp Gln Ser Ser Ser Leu Met
      725      730      735
Ser Leu Asp Trp Ser Trp Leu Ala Glu
      740      745

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<210> 96
 <211> 745
 <212> PRT
 <213> Mus musculus

<220>
 <221> misc_feature
 <222> (1)..(745)
 <223> IKK alfa constitutivamente activo de ratón (mutación PEST) P.4018 sin etiqueta de epítopo

<400> 96

Met Glu Arg Pro Pro Gly Leu Arg Pro Gly Ala Gly Gly Pro Trp Glu
 1 5 10 15
 Met Arg Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Ser Leu Tyr
 20 25 30
 Gln His Arg Glu Leu Asp Leu Lys Ile Ala Ile Lys Ser Cys Arg Leu
 35 40 45
 Glu Leu Ser Ser Lys Asn Arg Glu Arg Trp Cys His Glu Ile Gln Ile
 50 55 60
 Met Lys Lys Leu Asp His Ala Asn Val Val Lys Ala Cys Asp Val Pro
 65 70 75 80
 Glu Glu Leu Asn Phe Leu Ile Asn Asp Val Pro Leu Leu Ala Met Glu
 85 90 95
 Tyr Cys Ser Gly Gly Asp Leu Arg Lys Leu Leu Asn Lys Pro Glu Asn
 100 105 110
 Cys Cys Gly Leu Lys Glu Ser Gln Ile Leu Ser Leu Leu Ser Asp Ile
 115 120 125
 Gly Ser Gly Ile Arg Tyr Leu His Glu Asn Lys Ile Ile His Arg Asp
 130 135 140
 Leu Lys Pro Glu Asn Ile Val Leu Gln Asp Val Gly Gly Lys Thr Ile
 145 150 155 160
 His Lys Ile Ile Asp Leu Gly Tyr Ala Lys Asp Val Asp Gln Gly Glu
 165 170 175
 Leu Cys Thr Glu Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu Leu
 180 185 190
 Phe Glu Asn Lys Pro Tyr Thr Ala Thr Val Asp Tyr Trp Ser Phe Gly
 195 200 205
 Thr Met Val Phe Glu Cys Ile Ala Gly Tyr Arg Pro Phe Leu His His
 210 215 220
 Leu Gln Pro Phe Thr Trp His Glu Lys Ile Lys Lys Lys Asp Pro Lys
 225 230 235 240
 Cys Ile Phe Ala Cys Glu Glu Met Thr Gly Glu Val Arg Phe Ser Ser
 245 250 255
 His Leu Pro Gln Pro Asn Ser Leu Cys Ser Leu Ile Val Glu Pro Met
 260 265 270
 Glu Ser Trp Leu Gln Leu Met Leu Asn Trp Asp Pro Gln Gln Arg Gly
 275 280 285
 Gly Pro Ile Asp Leu Thr Leu Lys Gln Pro Arg Cys Phe Ala Leu Met
 290 295 300
 Asp His Ile Leu Asn Leu Lys Ile Val His Ile Leu Asn Met Thr Ser
 305 310 315 320
 Ala Lys Ile Ile Ser Phe Leu Leu Pro Cys Asp Glu Ser Leu His Ser
 325 330 335
 Leu Gln Ser Arg Ile Glu Arg Glu Thr Gly Ile Asn Thr Gly Ser Gln
 340 345 350
 Glu Leu Leu Ser Glu Thr Gly Ile Ser Leu Asp Pro Arg Lys Pro Ala
 355 360 365
 Ser Gln Cys Val Leu Asp Gly Val Arg Gly Cys Asp Ser Tyr Met Val
 370 375 380
 Tyr Leu Phe Asp Lys Ser Lys Thr Val Tyr Glu Gly Pro Phe Ala Ser
 385 390 395 400
 Arg Ser Leu Ser Asp Cys Val Asn Tyr Ile Val Gln Asp Ser Lys Ile
 405 410 415

Gln Leu Pro Ile Ile Gln Leu Arg Lys Val Trp Ala Glu Ala Val His
420 425 430

Tyr Val Ser Gly Leu Lys Glu Asp Tyr Ser Arg Leu Phe Gln Gly Gln
435 440 445

Arg Ala Ala Met Leu Ser Leu Leu Arg Tyr Asn Ala Asn Leu Thr Lys
450 455 460

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

Glu Phe Phe Arg Lys Ser Ile Gln Leu Asp Leu Glu Arg Tyr Ser Glu
485 490 495

Gln Met Thr Tyr Gly Ile Ser Ser Glu Lys Met Leu Lys Ala Trp Lys
500 505 510

Glu Met Glu Glu Lys Ala Ile His Tyr Ser Glu Val Gly Val Ile Gly
515 520 525

Tyr Leu Glu Asp Gln Ile Met Ser Leu His Thr Glu Ile Met Glu Leu
530 535 540

Gln Lys Ser Pro Tyr Gly Arg Arg Gln Gly Asp Leu Met Glu Ser Leu
545 550 555 560

Glu Gln Arg Ala Ile Asp Leu Tyr Lys Gln Leu Lys His Arg Pro Pro
565 570 575

Asp His Leu Tyr Ser Asp Ser Thr Glu Met Val Lys Ile Ile Val His
580 585 590

Thr Val Gln Ser Gln Asp Arg Val Leu Lys Glu Leu Phe Gly His Leu
595 600 605

Ser Lys Leu Leu Gly Cys Lys Gln Lys Ile Ile Asp Leu Leu Pro Lys
610 615 620

Val Glu Val Ala Leu Ser Asn Ile Lys Glu Ala Asp Asn Thr Val Met
625 630 635 640

Phe Met Gln Gly Lys Arg Gln Lys Glu Ile Trp His Leu Leu Lys Ile
645 650 655

Ala Cys Thr Gln Ala Ala Ala Arg Ala Leu Val Gly Ala Ala Leu Glu
660 665 670

Gly Ala Val Ala Pro Pro Val Ala Ala Trp Leu Pro Pro Ala Leu Ala
675 680 685

Asp Arg Glu His Pro Leu Thr Cys Val Val Ala Pro Gln Asp Gly Glu
690 695 700

Ala Leu Ala Gln Met Ile Glu Glu Asn Leu Asn Cys Leu Gly His Leu
705 710 715 720

Ala Ala Ile Ile Arg Glu Ala Asn Glu Asp Gln Ser Ser Ser Leu Met
725 730 735

Ser Leu Asp Trp Ser Trp Leu Ala Glu
740 745

<210> 97
<211> 757
<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(757)
<223> IKK beta constitutivamente activo de ratón (mutación PEST) P.4019 sin etiqueta de epítipo

<400> 97

Met Ser Trp Ser Pro Ser Leu Pro Thr Gln Thr Cys Gly Ala Trp Glu
1 5 10 15

Met Lys Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Ile Arg Trp
 20 25 30
 His Asn Gln Ala Thr Gly Glu Gln Ile Ala Ile Lys Gln Cys Arg Gln
 35 40 45
 Glu Leu Ser Pro Lys Asn Arg Asn Arg Trp Cys Leu Glu Ile Gln Ile
 50 55 60
 Met Arg Arg Leu Asn His Pro Asn Val Val Ala Ala Arg Asp Val Pro
 65 70 75 80
 Glu Gly Met Gln Asn Leu Ala Pro Asn Asp Leu Pro Leu Leu Ala Met
 85 90 95
 Glu Tyr Cys Gln Gly Gly Asp Leu Arg Arg Tyr Leu Asn Gln Phe Glu
 100 105 110
 Asn Cys Cys Gly Leu Arg Glu Gly Ala Val Leu Thr Leu Leu Ser Asp
 115 120 125
 Ile Ala Ser Ala Leu Arg Tyr Leu His Glu Asn Arg Ile Ile His Arg
 130 135 140
 Asp Leu Lys Pro Glu Asn Ile Val Leu Gln Gln Gly Glu Lys Arg Leu
 145 150 155 160
 Ile His Lys Ile Ile Asp Leu Gly Tyr Ala Lys Glu Leu Asp Gln Gly
 165 170 175
 Glu Leu Cys Thr Glu Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu
 180 185 190
 Leu Leu Glu Gln Gln Lys Tyr Thr Val Thr Val Asp Tyr Trp Ser Phe
 195 200 205
 Gly Thr Leu Ala Phe Glu Cys Ile Thr Gly Phe Arg Pro Phe Leu Pro
 210 215 220
 Asn Trp Gln Pro Val Gln Trp His Ser Lys Val Arg Gln Lys Ser Glu
 225 230 235 240
 Val Asp Ile Val Val Ser Glu Asp Leu Asn Gly Ala Val Lys Phe Ser
 245 250 255
 Ser Ser Leu Pro Phe Pro Asn Asn Leu Asn Ser Val Leu Ala Glu Arg
 260 265 270
 Leu Glu Lys Trp Leu Gln Leu Met Leu Met Trp His Pro Arg Gln Arg
 275 280 285
 Gly Thr Asp Pro Gln Tyr Gly Pro Asn Gly Cys Phe Arg Ala Leu Asp
 290 295 300
 Asp Ile Leu Asn Leu Lys Leu Val His Val Leu Asn Met Val Thr Gly
 305 310 315 320
 Thr Val His Thr Tyr Pro Val Thr Glu Asp Glu Ser Leu Gln Ser Leu
 325 330 335
 Lys Thr Arg Ile Gln Glu Asn Thr Gly Ile Leu Glu Thr Asp Gln Glu
 340 345 350
 Leu Leu Gln Lys Ala Gly Leu Val Leu Leu Pro Asp Lys Pro Ala Thr
 355 360 365
 Gln Cys Ile Ser Asp Ser Lys Thr Asn Glu Gly Leu Thr Leu Asp Met
 370 375 380
 Asp Leu Val Phe Leu Leu Asp Asn Ser Lys Ile Asn Tyr Glu Thr Gln
 385 390 395 400
 Ile Thr Pro Arg Pro Pro Pro Glu Ser Val Ser Cys Ile Leu Gln Glu
 405 410 415
 Pro Lys Arg Asn Leu Ser Phe Phe Gln Leu Arg Lys Val Trp Gly Gln
 420 425 430

Val Trp His Ser Ile Gln Thr Leu Lys Glu Asp Cys Asn Arg Leu Gln
435 440 445

Gln Gly Gln Arg Ala Ala Met Met Ser Leu Leu Arg Asn Asn Ser Cys
450 455 460

Leu Ser Lys Met Lys Asn Ala Met Ala Ser Thr Ala Gln Gln Leu Lys
465 470 475 480

Ala Lys Leu Asp Phe Phe Lys Thr Ser Ile Gln Ile Asp Leu Glu Lys
485 490 495

Tyr Lys Glu Gln Thr Glu Phe Gly Ile Thr Ser Asp Lys Leu Leu Leu
500 505 510

Ala Trp Arg Glu Met Glu Gln Ala Val Glu Gln Cys Gly Arg Glu Asn
515 520 525

Asp Val Lys His Leu Val Glu Arg Met Met Ala Leu Gln Thr Asp Ile
530 535 540

Val Asp Leu Gln Arg Ser Pro Met Gly Arg Lys Gln Gly Gly Thr Leu
545 550 555 560

Asp Asp Leu Glu Glu Gln Ala Arg Glu Leu Tyr Arg Lys Leu Arg Glu
565 570 575

Lys Pro Arg Asp Gln Arg Thr Glu Gly Asp Ser Gln Glu Met Val Arg
580 585 590

Leu Leu Leu Gln Ala Ile Gln Ser Phe Glu Lys Lys Val Arg Val Ile
595 600 605

Tyr Thr Gln Leu Ser Lys Thr Val Val Cys Lys Gln Lys Ala Leu Glu
610 615 620

Leu Leu Pro Lys Val Glu Glu Val Val Ser Leu Met Asn Glu Asp Glu
625 630 635 640

Arg Thr Val Val Arg Leu Gln Glu Lys Arg Gln Lys Glu Leu Trp Asn
645 650 655

Leu Leu Lys Ile Ala Cys Ser Lys Val Arg Gly Pro Val Ala Gly Ala
660 665 670

Pro Asp Ala Met Asn Val Ala Arg Leu Ala His Pro Gly Gln Leu Met
675 680 685

Ala Gln Pro Ala Ser Ala Cys Asp Ala Leu Pro Glu Ser Asp Lys Lys
690 695 700

Ala Glu Glu Leu Val Ala Glu Ala His Ala Leu Cys Ser Arg Leu Glu
705 710 715 720

Ser Ala Leu Gln Asp Thr Val Lys Glu Gln Asp Arg Ser Phe Thr Thr
725 730 735

Leu Asp Trp Ser Trp Leu Gln Met Glu Asp Glu Glu Arg Cys Ser Leu
740 745 750

Glu Gln Ala Cys Asp
755

<210> 98
<211> 757
<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(757)
<223> IKK beta constitutivamente activo de ratón (mutación PEST) P.4020 sin etiqueta de epítopo
<400> 98

Met Ser Trp Ser Pro Ser Leu Pro Thr Gln Thr Cys Gly Ala Trp Glu
1 5 10 15

Met Lys Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Ile Arg Trp
Página 92

20	25	30																	
His	Asn	Gln	Ala	Thr	Gly	Glu	Gln	Ile	Ala	Ile	Lys	Gln	Cys	Arg	Gln				
	35					40					45								
Glu	Leu	Ser	Pro	Lys	Asn	Arg	Asn	Arg	Trp	Cys	Leu	Glu	Ile	Gln	Ile				
	50				55					60									
Met	Arg	Arg	Leu	Asn	His	Pro	Asn	Val	Val	Ala	Ala	Arg	Asp	Val	Pro				
65				70						75				80					
Glu	Gly	Met	Gln	Asn	Leu	Ala	Pro	Asn	Asp	Leu	Pro	Leu	Leu	Ala	Met				
			85					90						95					
Glu	Tyr	Cys	Gln	Gly	Gly	Asp	Leu	Arg	Arg	Tyr	Leu	Asn	Gln	Phe	Glu				
			100					105					110						
Asn	Cys	Cys	Gly	Leu	Arg	Glu	Gly	Ala	Val	Leu	Thr	Leu	Leu	Ser	Asp				
		115					120					125							
Ile	Ala	Ser	Ala	Leu	Arg	Tyr	Leu	His	Glu	Asn	Arg	Ile	Ile	His	Arg				
	130					135					140								
Asp	Leu	Lys	Pro	Glu	Asn	Ile	Val	Leu	Gln	Gln	Gly	Glu	Lys	Arg	Leu				
145					150				155						160				
Ile	His	Lys	Ile	Ile	Asp	Leu	Gly	Tyr	Ala	Lys	Glu	Leu	Asp	Gln	Gly				
			165						170					175					
Glu	Leu	Cys	Thr	Glu	Phe	Val	Gly	Thr	Leu	Gln	Tyr	Leu	Ala	Pro	Glu				
			180					185					190						
Leu	Leu	Glu	Gln	Gln	Lys	Tyr	Thr	Val	Thr	Val	Asp	Tyr	Trp	Ser	Phe				
		195					200					205							
Gly	Thr	Leu	Ala	Phe	Glu	Cys	Ile	Thr	Gly	Phe	Arg	Pro	Phe	Leu	Pro				
	210					215					220								
Asn	Trp	Gln	Pro	Val	Gln	Trp	His	Ser	Lys	Val	Arg	Gln	Lys	Ser	Glu				
225					230					235					240				
Val	Asp	Ile	Val	Val	Ser	Glu	Asp	Leu	Asn	Gly	Ala	Val	Lys	Phe	Ser				
			245						250					255					
Ser	Ser	Leu	Pro	Phe	Pro	Asn	Asn	Leu	Asn	Ser	Val	Leu	Ala	Glu	Arg				
			260					265					270						
Leu	Glu	Lys	Trp	Leu	Gln	Leu	Met	Leu	Met	Trp	His	Pro	Arg	Gln	Arg				
		275					280					285							
Gly	Thr	Asp	Pro	Gln	Tyr	Gly	Pro	Asn	Gly	Cys	Phe	Arg	Ala	Leu	Asp				
	290					295					300								
Asp	Ile	Leu	Asn	Leu	Lys	Leu	Val	His	Val	Leu	Asn	Met	Val	Thr	Gly				
305					310					315					320				
Thr	Val	His	Thr	Tyr	Pro	Val	Thr	Glu	Asp	Glu	Ser	Leu	Gln	Ser	Leu				
				325					330					335					
Lys	Thr	Arg	Ile	Gln	Glu	Asn	Thr	Gly	Ile	Leu	Glu	Thr	Asp	Gln	Glu				
			340					345					350						
Leu	Leu	Gln	Lys	Ala	Gly	Leu	Val	Leu	Leu	Pro	Asp	Lys	Pro	Ala	Thr				
		355					360					365							
Gln	Cys	Ile	Ser	Asp	Ser	Lys	Thr	Asn	Glu	Gly	Leu	Thr	Leu	Asp	Met				
	370					375					380								
Asp	Leu	Val	Phe	Leu	Leu	Asp	Asn	Ser	Lys	Ile	Asn	Tyr	Glu	Thr	Gln				
385					390					395					400				
Ile	Thr	Pro	Arg	Pro	Pro	Pro	Glu	Ser	Val	Ser	Cys	Ile	Leu	Gln	Glu				
				405					410					415					
Pro	Lys	Arg	Asn	Leu	Ser	Phe	Phe	Gln	Leu	Arg	Lys	Val	Trp	Gly	Gln				
			420					425					430						

Val Trp His Ser Ile Gln Thr Leu Lys Glu Asp Cys Asn Arg Leu Gln
435 440 445

Gln Gly Gln Arg Ala Ala Met Met Ser Leu Leu Arg Asn Asn Ser Cys
450 455 460

Leu Ser Lys Met Lys Asn Ala Met Ala Ser Thr Ala Gln Gln Leu Lys
465 470 475 480

Ala Lys Leu Asp Phe Phe Lys Thr Ser Ile Gln Ile Asp Leu Glu Lys
485 490 495

Tyr Lys Glu Gln Thr Glu Phe Gly Ile Thr Ser Asp Lys Leu Leu Leu
500 505 510

Ala Trp Arg Glu Met Glu Gln Ala Val Glu Gln Cys Gly Arg Glu Asn
515 520 525

Asp Val Lys His Leu Val Glu Arg Met Met Ala Leu Gln Thr Asp Ile
530 535 540

Val Asp Leu Gln Arg Ser Pro Met Gly Arg Lys Gln Gly Gly Thr Leu
545 550 555 560

Asp Asp Leu Glu Glu Gln Ala Arg Glu Leu Tyr Arg Lys Leu Arg Glu
565 570 575

Lys Pro Arg Asp Gln Arg Thr Glu Gly Asp Ser Gln Glu Met Val Arg
580 585 590

Leu Leu Leu Gln Ala Ile Gln Ser Phe Glu Lys Lys Val Arg Val Ile
595 600 605

Tyr Thr Gln Leu Ser Lys Thr Val Val Cys Lys Gln Lys Ala Leu Glu
610 615 620

Leu Leu Pro Lys Val Glu Glu Val Val Ser Leu Met Asn Glu Asp Glu
625 630 635 640

Arg Thr Val Val Arg Leu Gln Glu Lys Arg Gln Lys Glu Leu Trp Asn
645 650 655

Leu Leu Lys Ile Ala Cys Ser Lys Val Arg Gly Pro Val Ala Gly Ala
660 665 670

Pro Asp Ala Met Asn Val Ala Arg Leu Ala His Pro Gly Gln Leu Met
675 680 685

Ala Gln Pro Ala Ser Ala Cys Asp Ala Leu Pro Glu Ser Asp Lys Lys
690 695 700

Ala Glu Glu Leu Val Ala Glu Ala His Ala Leu Cys Ser Arg Leu Glu
705 710 715 720

Ser Ala Leu Gln Asp Thr Val Lys Glu Gln Asp Arg Ser Phe Thr Thr
725 730 735

Leu Asp Trp Ser Trp Leu Gln Met Glu Asp Glu Glu Arg Cys Ser Leu
740 745 750

Glu Gln Ala Cys Asp
755

<210> 99
<211> 585
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: huRIPK1(1-555).IZ.TM; TH1021 sin etiqueta de epítipo

<400> 99

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

Phe Leu Glu Ser Ala Glu Leu Asp Ser Gly Gly Phe Gly Lys Val Ser
20 25 30

Leu Cys Phe His Arg Thr Gln Gly Leu Met Ile Met Lys Thr Val Tyr

35

40

45

Lys Gly Pro Asn Cys Ile Glu His Asn Glu Ala Leu Leu Glu Glu Ala
50 55 60

Lys Met Met Asn Arg Leu Arg His Ser Arg Val Val Lys Leu Leu Gly
65 70 75 80

Val Ile Ile Glu Glu Gly Lys Tyr Ser Leu Val Met Glu Tyr Met Glu
85 90 95

Lys Gly Asn Leu Met His Val Leu Lys Ala Glu Met Ser Thr Pro Leu
100 105 110

Ser Val Lys Gly Arg Ile Ile Leu Glu Ile Ile Glu Gly Met Cys Tyr
115 120 125

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

Leu Val Asp Asn Asp Phe His Ile Lys Ile Ala Asp Leu Gly Leu Ala
145 150 155 160

Ser Phe Lys Met Trp Ser Lys Leu Asn Asn Glu Glu His Asn Glu Leu
165 170 175

Arg Glu Val Asp Gly Thr Ala Lys Lys Asn Gly Gly Thr Leu Tyr Tyr
180 185 190

Met Ala Pro Glu His Leu Asn Asp Val Asn Ala Lys Pro Thr Glu Lys
195 200 205

Ser Asp Val Tyr Ser Phe Ala Val Val Leu Trp Ala Ile Phe Ala Asn
210 215 220

Lys Glu Pro Tyr Glu Asn Ala Ile Cys Glu Gln Gln Leu Ile Met Cys
225 230 235 240

Ile Lys Ser Gly Asn Arg Pro Asp Val Asp Asp Ile Thr Glu Tyr Cys
245 250 255

Pro Arg Glu Ile Ile Ser Leu Met Lys Leu Cys Trp Glu Ala Asn Pro
260 265 270

Glu Ala Arg Pro Thr Phe Pro Gly Ile Glu Glu Lys Phe Arg Pro Phe
275 280 285

Tyr Leu Ser Gln Leu Glu Glu Ser Val Glu Glu Asp Val Lys Ser Leu
290 295 300

Lys Lys Glu Tyr Ser Asn Glu Asn Ala Val Val Lys Arg Met Gln Ser
305 310 315 320

Leu Gln Leu Asp Cys Val Ala Val Pro Ser Ser Arg Ser Asn Ser Ala
325 330 335

Thr Glu Gln Pro Gly Ser Leu His Ser Ser Gln Gly Leu Gly Met Gly
340 345 350

Pro Val Glu Glu Ser Trp Phe Ala Pro Ser Leu Glu His Pro Gln Glu
355 360 365

Glu Asn Glu Pro Ser Leu Gln Ser Lys Leu Gln Asp Glu Ala Asn Tyr
370 375 380

His Leu Tyr Gly Ser Arg Met Asp Arg Gln Thr Lys Gln Gln Pro Arg
385 390 395 400

Gln Asn Val Ala Tyr Asn Arg Glu Glu Glu Arg Arg Arg Arg Val Ser
405 410 415

His Asp Pro Phe Ala Gln Gln Arg Pro Tyr Glu Asn Phe Gln Asn Thr
420 425 430

Glu Gly Lys Gly Thr Ala Tyr Ser Ser Ala Ala Ser His Gly Asn Ala
435 440 445

Val His Gln Pro Ser Gly Leu Thr Ser Gln Pro Gln Val Leu Tyr Gln
 450 455 460

Asn Asn Gly Leu Tyr Ser Ser His Gly Phe Gly Thr Arg Pro Leu Asp
 465 470 475 480

Pro Gly Thr Ala Gly Pro Arg Val Trp Tyr Arg Pro Ile Pro Ser His
 485 490 495

Met Pro Ser Leu His Asn Ile Pro Val Pro Glu Thr Asn Tyr Leu Gly
 500 505 510

Asn Thr Pro Thr Met Pro Phe Ser Ser Leu Pro Pro Thr Asp Glu Ser
 515 520 525

Ile Lys Tyr Thr Ile Tyr Asn Ser Thr Gly Ile Gln Ile Gly Ala Tyr
 530 535 540

Asn Tyr Met Glu Ile Gly Gly Thr Ser Ser Ser Gly Gly Ile Lys Lys
 545 550 555 560

Glu Ile Glu Ala Ile Lys Lys Glu Gln Glu Ala Ile Lys Lys Lys Ile
 565 570 575

Glu Ala Ile Glu Lys Glu Ile Glu Ala
 580 585

<210> 100
 <211> 609
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: huRIPK1(1-555).EE.DM; TH1022 sin etiqueta de epítipo

<400> 100

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

Phe Leu Glu Ser Ala Glu Leu Asp Ser Gly Gly Phe Gly Lys Val Ser
 20 25 30

Leu Cys Phe His Arg Thr Gln Gly Leu Met Ile Met Lys Thr Val Tyr
 35 40 45

Lys Gly Pro Asn Cys Ile Glu His Asn Glu Ala Leu Leu Glu Glu Ala
 50 55 60

Lys Met Met Asn Arg Leu Arg His Ser Arg Val Val Lys Leu Leu Gly
 65 70 75 80

Val Ile Ile Glu Glu Gly Lys Tyr Ser Leu Val Met Glu Tyr Met Glu
 85 90 95

Lys Gly Asn Leu Met His Val Leu Lys Ala Glu Met Ser Thr Pro Leu
 100 105 110

Ser Val Lys Gly Arg Ile Ile Leu Glu Ile Ile Glu Gly Met Cys Tyr
 115 120 125

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

Leu Val Asp Asn Asp Phe His Ile Lys Ile Ala Asp Leu Gly Leu Ala
 145 150 155 160

Ser Phe Lys Met Trp Ser Lys Leu Asn Asn Glu Glu His Asn Glu Leu
 165 170 175

Arg Glu Val Asp Gly Thr Ala Lys Lys Asn Gly Gly Thr Leu Tyr Tyr
 180 185 190

Met Ala Pro Glu His Leu Asn Asp Val Asn Ala Lys Pro Thr Glu Lys
 195 200 205

Ser Asp Val Tyr Ser Phe Ala Val Val Leu Trp Ala Ile Phe Ala Asn
 210 215 220

Lys Glu Pro Tyr Glu Asn Ala Ile Cys Glu Gln Gln Leu Ile Met Cys

225 230 235 240

Ile Lys Ser Gly Asn Arg Pro Asp Val Asp Asp Ile Thr Glu Tyr Cys
245 250 255

Pro Arg Glu Ile Ile Ser Leu Met Lys Leu Cys Trp Glu Ala Asn Pro
260 265 270

Glu Ala Arg Pro Thr Phe Pro Gly Ile Glu Glu Lys Phe Arg Pro Phe
275 280 285

Tyr Leu Ser Gln Leu Glu Glu Ser Val Glu Glu Asp Val Lys Ser Leu
290 295 300

Lys Lys Glu Tyr Ser Asn Glu Asn Ala Val Val Lys Arg Met Gln Ser
305 310 315 320

Leu Gln Leu Asp Cys Val Ala Val Pro Ser Ser Arg Ser Asn Ser Ala
325 330 335

Thr Glu Gln Pro Gly Ser Leu His Ser Ser Gln Gly Leu Gly Met Gly
340 345 350

Pro Val Glu Glu Ser Trp Phe Ala Pro Ser Leu Glu His Pro Gln Glu
355 360 365

Glu Asn Glu Pro Ser Leu Gln Ser Lys Leu Gln Asp Glu Ala Asn Tyr
370 375 380

His Leu Tyr Gly Ser Arg Met Asp Arg Gln Thr Lys Gln Gln Pro Arg
385 390 395 400

Gln Asn Val Ala Tyr Asn Arg Glu Glu Glu Arg Arg Arg Arg Val Ser
405 410 415

His Asp Pro Phe Ala Gln Gln Arg Pro Tyr Glu Asn Phe Gln Asn Thr
420 425 430

Glu Gly Lys Gly Thr Ala Tyr Ser Ser Ala Ala Ser His Gly Asn Ala
435 440 445

Val His Gln Pro Ser Gly Leu Thr Ser Gln Pro Gln Val Leu Tyr Gln
450 455 460

Asn Asn Gly Leu Tyr Ser Ser His Gly Phe Gly Thr Arg Pro Leu Asp
465 470 475 480

Pro Gly Thr Ala Gly Pro Arg Val Trp Tyr Arg Pro Ile Pro Ser His
485 490 495

Met Pro Ser Leu His Asn Ile Pro Val Pro Glu Thr Asn Tyr Leu Gly
500 505 510

Asn Thr Pro Thr Met Pro Phe Ser Ser Leu Pro Pro Thr Asp Glu Ser
515 520 525

Ile Lys Tyr Thr Ile Tyr Asn Ser Thr Gly Ile Gln Ile Gly Ala Tyr
530 535 540

Asn Tyr Met Glu Ile Gly Gly Thr Ser Ser Ser Gly Ser Asp Gly Ser
545 550 555 560

Gly Ser Gly Ser Gly Ser Ile Thr Ile Arg Ala Ala Phe Leu Glu Lys
565 570 575

Glu Asn Thr Ala Leu Arg Thr Glu Ile Ala Glu Leu Glu Lys Glu Val
580 585 590

Gly Arg Cys Glu Asn Ile Val Ser Lys Tyr Glu Thr Arg Tyr Gly Pro
595 600 605

Leu

<210> 101
<211> 609
<212> PRT
<213> Secuencia artificial

<220>

<223> Sintético: huRIPK1(1-555).RR.DM; TH1023 sin etiqueta de epítipo

<400> 101

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

Phe Leu Glu Ser Ala Glu Leu Asp Ser Gly Gly Phe Gly Lys Val Ser
 20 25 30

Leu Cys Phe His Arg Thr Gln Gly Leu Met Ile Met Lys Thr Val Tyr
 35 40 45

Lys Gly Pro Asn Cys Ile Glu His Asn Glu Ala Leu Leu Glu Glu Ala
 50 55 60

Lys Met Met Asn Arg Leu Arg His Ser Arg Val Val Lys Leu Leu Gly
 65 70 75 80

Val Ile Ile Glu Glu Gly Lys Tyr Ser Leu Val Met Glu Tyr Met Glu
 85 90 95

Lys Gly Asn Leu Met His Val Leu Lys Ala Glu Met Ser Thr Pro Leu
 100 105 110

Ser Val Lys Gly Arg Ile Ile Leu Glu Ile Ile Glu Gly Met Cys Tyr
 115 120 125

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

Leu Val Asp Asn Asp Phe His Ile Lys Ile Ala Asp Leu Gly Leu Ala
 145 150 155 160

Ser Phe Lys Met Trp Ser Lys Leu Asn Asn Glu Glu His Asn Glu Leu
 165 170 175

Arg Glu Val Asp Gly Thr Ala Lys Lys Asn Gly Gly Thr Leu Tyr Tyr
 180 185 190

Met Ala Pro Glu His Leu Asn Asp Val Asn Ala Lys Pro Thr Glu Lys
 195 200 205

Ser Asp Val Tyr Ser Phe Ala Val Val Leu Trp Ala Ile Phe Ala Asn
 210 215 220

Lys Glu Pro Tyr Glu Asn Ala Ile Cys Glu Gln Gln Leu Ile Met Cys
 225 230 235 240

Ile Lys Ser Gly Asn Arg Pro Asp Val Asp Asp Ile Thr Glu Tyr Cys
 245 250 255

Pro Arg Glu Ile Ile Ser Leu Met Lys Leu Cys Trp Glu Ala Asn Pro
 260 265 270

Glu Ala Arg Pro Thr Phe Pro Gly Ile Glu Glu Lys Phe Arg Pro Phe
 275 280 285

Tyr Leu Ser Gln Leu Glu Glu Ser Val Glu Glu Asp Val Lys Ser Leu
 290 295 300

Lys Lys Glu Tyr Ser Asn Glu Asn Ala Val Val Lys Arg Met Gln Ser
 305 310 315 320

Leu Gln Leu Asp Cys Val Ala Val Pro Ser Ser Arg Ser Asn Ser Ala
 325 330 335

Thr Glu Gln Pro Gly Ser Leu His Ser Ser Gln Gly Leu Gly Met Gly
 340 345 350

Pro Val Glu Glu Ser Trp Phe Ala Pro Ser Leu Glu His Pro Gln Glu
 355 360 365

Glu Asn Glu Pro Ser Leu Gln Ser Lys Leu Gln Asp Glu Ala Asn Tyr
 370 375 380

His Leu Tyr Gly Ser Arg Met Asp Arg Gln Thr Lys Gln Gln Pro Arg
 385 390 395 400

385 390 395 400
 Gln Asn Val Ala Tyr Asn Arg Glu Glu Glu Arg Arg Arg Arg Val Ser
 405 410 415
 His Asp Pro Phe Ala Gln Gln Arg Pro Tyr Glu Asn Phe Gln Asn Thr
 420 425 430
 Glu Gly Lys Gly Thr Ala Tyr Ser Ser Ala Ala Ser His Gly Asn Ala
 435 440 445
 Val His Gln Pro Ser Gly Leu Thr Ser Gln Pro Gln Val Leu Tyr Gln
 450 455 460
 Asn Asn Gly Leu Tyr Ser Ser His Gly Phe Gly Thr Arg Pro Leu Asp
 465 470 475 480
 Pro Gly Thr Ala Gly Pro Arg Val Trp Tyr Arg Pro Ile Pro Ser His
 485 490 495
 Met Pro Ser Leu His Asn Ile Pro Val Pro Glu Thr Asn Tyr Leu Gly
 500 505 510
 Asn Thr Pro Thr Met Pro Phe Ser Ser Leu Pro Pro Thr Asp Glu Ser
 515 520 525
 Ile Lys Tyr Thr Ile Tyr Asn Ser Thr Gly Ile Gln Ile Gly Ala Tyr
 530 535 540
 Asn Tyr Met Glu Ile Gly Gly Thr Ser Ser Ser Gly Ser Asp Gly Ser
 545 550 555 560
 Gly Ser Gly Ser Gly Ser Leu Glu Ile Arg Ala Ala Phe Leu Glu Lys
 565 570 575
 Glu Asn Thr Ala Leu Arg Thr Arg Ala Ala Glu Leu Arg Lys Arg Val
 580 585 590
 Gly Arg Cys Arg Asn Ile Val Ser Lys Tyr Glu Thr Arg Tyr Gly Pro
 595 600 605

Leu

<210> 102
 <211> 585
 <212> PRT
 <213> Secuencia artificial

 <220>
 <223> Sintético: msRIPK1(1-555).IZ.TM; TH1024 sin etiqueta de epítopo

 <400> 102

Met Gln Pro Asp Met Ser Leu Asp Asn Ile Lys Met Ala Ser Ser Asp
 1 5 10 15
 Leu Leu Glu Lys Thr Asp Leu Asp Ser Gly Gly Phe Gly Lys Val Ser
 20 25 30
 Leu Cys Tyr His Arg Ser His Gly Phe Val Ile Leu Lys Lys Val Tyr
 35 40 45
 Thr Gly Pro Asn Arg Ala Glu Tyr Asn Glu Val Leu Leu Glu Glu Gly
 50 55 60
 Lys Met Met His Arg Leu Arg His Ser Arg Val Val Lys Leu Leu Gly
 65 70 75 80
 Ile Ile Ile Glu Glu Gly Asn Tyr Ser Leu Val Met Glu Tyr Met Glu
 85 90 95
 Lys Gly Asn Leu Met His Val Leu Lys Thr Gln Ile Asp Val Pro Leu
 100 105 110
 Ser Leu Lys Gly Arg Ile Ile Val Glu Ala Ile Glu Gly Met Cys Tyr
 115 120 125
 Leu His Asp Lys Gly Val Ile His Lys Asp Leu Lys Pro Glu Asn Ile
 130 135 140

Leu Val Asp Arg Asp Phe His Ile Lys Ile Ala Asp Leu Gly Val Ala
 145 150 155 160
 Ser Phe Lys Thr Trp Ser Lys Leu Thr Lys Glu Lys Asp Asn Lys Gln
 165 170 175
 Lys Glu Val Ser Ser Thr Thr Lys Lys Asn Asn Gly Gly Thr Leu Tyr
 180 185 190
 Tyr Met Ala Pro Glu His Leu Asn Asp Ile Asn Ala Lys Pro Thr Glu
 195 200 205
 Lys Ser Asp Val Tyr Ser Phe Gly Ile Val Leu Trp Ala Ile Phe Ala
 210 215 220
 Lys Lys Glu Pro Tyr Glu Asn Val Ile Cys Thr Glu Gln Phe Val Ile
 225 230 235 240
 Cys Ile Lys Ser Gly Asn Arg Pro Asn Val Glu Glu Ile Leu Glu Tyr
 245 250 255
 Cys Pro Arg Glu Ile Ile Ser Leu Met Glu Arg Cys Trp Gln Ala Ile
 260 265 270
 Pro Glu Asp Arg Pro Thr Phe Leu Gly Ile Glu Glu Glu Phe Arg Pro
 275 280 285
 Phe Tyr Leu Ser His Phe Glu Glu Tyr Val Glu Glu Asp Val Ala Ser
 290 295 300
 Leu Lys Lys Glu Tyr Pro Asp Gln Ser Pro Val Leu Gln Arg Met Phe
 305 310 315 320
 Ser Leu Gln His Asp Cys Val Pro Leu Pro Pro Ser Arg Ser Asn Ser
 325 330 335
 Glu Gln Pro Gly Ser Leu His Ser Ser Gln Gly Leu Gln Met Gly Pro
 340 345 350
 Val Glu Glu Ser Trp Phe Ser Ser Ser Pro Glu Tyr Pro Gln Asp Glu
 355 360 365
 Asn Asp Arg Ser Val Gln Ala Lys Leu Gln Glu Glu Ala Ser Tyr His
 370 375 380
 Ala Phe Gly Ile Phe Ala Glu Lys Gln Thr Lys Pro Gln Pro Arg Gln
 385 390 395 400
 Asn Glu Ala Tyr Asn Arg Glu Glu Glu Arg Lys Arg Arg Val Ser His
 405 410 415
 Asp Pro Phe Ala Gln Gln Arg Ala Arg Glu Asn Ile Lys Ser Ala Gly
 420 425 430
 Ala Arg Gly His Ser Asp Pro Ser Thr Thr Ser Arg Gly Ile Ala Val
 435 440 445
 Gln Gln Leu Ser Trp Pro Ala Thr Gln Thr Val Trp Asn Asn Gly Leu
 450 455 460
 Tyr Asn Gln His Gly Phe Gly Thr Thr Gly Thr Gly Val Trp Tyr Pro
 465 470 475 480
 Pro Asn Leu Ser Gln Met Tyr Ser Thr Tyr Lys Thr Pro Val Pro Glu
 485 490 495
 Thr Asn Ile Pro Gly Ser Thr Pro Thr Met Pro Tyr Phe Ser Gly Pro
 500 505 510
 Val Ala Asp Asp Leu Ile Lys Tyr Thr Ile Phe Asn Ser Ser Gly Ile
 515 520 525
 Gln Ile Gly Asn His Asn Tyr Met Asp Val Gly Leu Asn Ser Gln Pro
 530 535 540
 Pro Asn Asn Thr Cys Lys Glu Glu Ser Thr Ser Gly Gly Ile Lys Lys

545 550 555 560
 Glu Ile Glu Ala Ile Lys Lys Glu Gln Glu Ala Ile Lys Lys Lys Ile
 565 570 575

 Glu Ala Ile Glu Lys Glu Ile Glu Ala
 580 585

 <210> 103
 <211> 609
 <212> PRT
 <213> Secuencia artificial

 <220>
 <223> Sintético: msRIPK1(1-555).EE.DM; TH1025 sin etiqueta de epítipo

 <400> 103

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

 Leu Leu Glu Lys Thr Asp Leu Asp Ser Gly Gly Phe Gly Lys Val Ser
 20 25 30

 Leu Cys Tyr His Arg Ser His Gly Phe Val Ile Leu Lys Lys Val Tyr
 35 40 45

 Thr Gly Pro Asn Arg Ala Glu Tyr Asn Glu Val Leu Leu Glu Glu Gly
 50 55 60

 Lys Met Met His Arg Leu Arg His Ser Arg Val Val Lys Leu Leu Gly
 65 70 75 80

 Ile Ile Ile Glu Glu Gly Asn Tyr Ser Leu Val Met Glu Tyr Met Glu
 85 90 95

 Lys Gly Asn Leu Met His Val Leu Lys Thr Gln Ile Asp Val Pro Leu
 100 105 110

 Ser Leu Lys Gly Arg Ile Ile Val Glu Ala Ile Glu Gly Met Cys Tyr
 115 120 125

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

 Leu Val Asp Arg Asp Phe His Ile Lys Ile Ala Asp Leu Gly Val Ala
 145 150 155 160

 Ser Phe Lys Thr Trp Ser Lys Leu Thr Lys Glu Lys Asp Asn Lys Gln
 165 170 175

 Lys Glu Val Ser Ser Thr Thr Lys Lys Asn Asn Gly Gly Thr Leu Tyr
 180 185 190

 Tyr Met Ala Pro Glu His Leu Asn Asp Ile Asn Ala Lys Pro Thr Glu
 195 200 205

 Lys Ser Asp Val Tyr Ser Phe Gly Ile Val Leu Trp Ala Ile Phe Ala
 210 215 220

 Lys Lys Glu Pro Tyr Glu Asn Val Ile Cys Thr Glu Gln Phe Val Ile
 225 230 235 240

 Cys Ile Lys Ser Gly Asn Arg Pro Asn Val Glu Glu Ile Leu Glu Tyr
 245 250 255

 Cys Pro Arg Glu Ile Ile Ser Leu Met Glu Arg Cys Trp Gln Ala Ile
 260 265 270

 Pro Glu Asp Arg Pro Thr Phe Leu Gly Ile Glu Glu Glu Phe Arg Pro
 275 280 285

 Phe Tyr Leu Ser His Phe Glu Glu Tyr Val Glu Glu Asp Val Ala Ser
 290 295 300

 Leu Lys Lys Glu Tyr Pro Asp Gln Ser Pro Val Leu Gln Arg Met Phe
 305 310 315 320

 Ser Leu Gln His Asp Cys Val Pro Leu Pro Pro Ser Arg Ser Asn Ser
 325 330 335

Glu Gln Pro Gly Ser Leu His Ser Ser Gln Gly Leu Gln Met Gly Pro
340 345 350

Val Glu Glu Ser Trp Phe Ser Ser Ser Pro Glu Tyr Pro Gln Asp Glu
355 360 365

Asn Asp Arg Ser Val Gln Ala Lys Leu Gln Glu Glu Ala Ser Tyr His
370 375 380

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

Asn Glu Ala Tyr Asn Arg Glu Glu Glu Arg Lys Arg Arg Val Ser His
405 410 415

Asp Pro Phe Ala Gln Gln Arg Ala Arg Glu Asn Ile Lys Ser Ala Gly
420 425 430

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

Gln Gln Leu Ser Trp Pro Ala Thr Gln Thr Val Trp Asn Asn Gly Leu
450 455 460

Tyr Asn Gln His Gly Phe Gly Thr Thr Gly Thr Gly Val Trp Tyr Pro
465 470 475 480

Pro Asn Leu Ser Gln Met Tyr Ser Thr Tyr Lys Thr Pro Val Pro Glu
485 490 495

Thr Asn Ile Pro Gly Ser Thr Pro Thr Met Pro Tyr Phe Ser Gly Pro
500 505 510

Val Ala Asp Asp Leu Ile Lys Tyr Thr Ile Phe Asn Ser Ser Gly Ile
515 520 525

Gln Ile Gly Asn His Asn Tyr Met Asp Val Gly Leu Asn Ser Gln Pro
530 535 540

Pro Asn Asn Thr Cys Lys Glu Glu Ser Thr Ser Gly Ser Asp Gly Ser
545 550 555 560

Gly Ser Gly Ser Gly Ser Ile Thr Ile Arg Ala Ala Phe Leu Glu Lys
565 570 575

Glu Asn Thr Ala Leu Arg Thr Glu Ile Ala Glu Leu Glu Lys Glu Val
580 585 590

Gly Arg Cys Glu Asn Ile Val Ser Lys Tyr Glu Thr Arg Tyr Gly Pro
595 600 605

Leu

<210> 104
<211> 609
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: msRIPK1(1-555).RR.DM; TH1026 sin etiqueta de epítipo

<400> 104

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

Leu Leu Glu Lys Thr Asp Leu Asp Ser Gly Gly Phe Gly Lys Val Ser
20 25 30

Leu Cys Tyr His Arg Ser His Gly Phe Val Ile Leu Lys Lys Val Tyr
35 40 45

Thr Gly Pro Asn Arg Ala Glu Tyr Asn Glu Val Leu Leu Glu Glu Gly
50 55 60

Lys Met Met His Arg Leu Arg His Ser Arg Val Val Lys Leu Leu Gly
65 70 75 80

Ile Ile Ile Glu Glu Gly Asn Tyr Ser Leu Val Met Glu Tyr Met Glu
 85 90 95
 Lys Gly Asn Leu Met His Val Leu Lys Thr Gln Ile Asp Val Pro Leu
 100 105 110
 Ser Leu Lys Gly Arg Ile Ile Val Glu Ala Ile Glu Gly Met Cys Tyr
 115 120 125
 Leu His Asp Lys Gly Val Ile His Lys Asp Leu Lys Pro Glu Asn Ile
 130 135 140
 Leu Val Asp Arg Asp Phe His Ile Lys Ile Ala Asp Leu Gly Val Ala
 145 150 155 160
 Ser Phe Lys Thr Trp Ser Lys Leu Thr Lys Glu Lys Asp Asn Lys Gln
 165 170 175
 Lys Glu Val Ser Ser Thr Thr Lys Lys Asn Asn Gly Gly Thr Leu Tyr
 180 185 190
 Tyr Met Ala Pro Glu His Leu Asn Asp Ile Asn Ala Lys Pro Thr Glu
 195 200 205
 Lys Ser Asp Val Tyr Ser Phe Gly Ile Val Leu Trp Ala Ile Phe Ala
 210 215 220
 Lys Lys Glu Pro Tyr Glu Asn Val Ile Cys Thr Glu Gln Phe Val Ile
 225 230 235 240
 Cys Ile Lys Ser Gly Asn Arg Pro Asn Val Glu Glu Ile Leu Glu Tyr
 245 250 255
 Cys Pro Arg Glu Ile Ile Ser Leu Met Glu Arg Cys Trp Gln Ala Ile
 260 265 270
 Pro Glu Asp Arg Pro Thr Phe Leu Gly Ile Glu Glu Glu Phe Arg Pro
 275 280 285
 Phe Tyr Leu Ser His Phe Glu Glu Tyr Val Glu Glu Asp Val Ala Ser
 290 295 300
 Leu Lys Lys Glu Tyr Pro Asp Gln Ser Pro Val Leu Gln Arg Met Phe
 305 310 315 320
 Ser Leu Gln His Asp Cys Val Pro Leu Pro Pro Ser Arg Ser Asn Ser
 325 330 335
 Glu Gln Pro Gly Ser Leu His Ser Ser Gln Gly Leu Gln Met Gly Pro
 340 345 350
 Val Glu Glu Ser Trp Phe Ser Ser Ser Pro Glu Tyr Pro Gln Asp Glu
 355 360 365
 Asn Asp Arg Ser Val Gln Ala Lys Leu Gln Glu Glu Ala Ser Tyr His
 370 375 380
 Ala Phe Gly Ile Phe Ala Glu Lys Gln Thr Lys Pro Gln Pro Arg Gln
 385 390 395 400
 Asn Glu Ala Tyr Asn Arg Glu Glu Glu Arg Lys Arg Arg Val Ser His
 405 410 415
 Asp Pro Phe Ala Gln Gln Arg Ala Arg Glu Asn Ile Lys Ser Ala Gly
 420 425 430
 Ala Arg Gly His Ser Asp Pro Ser Thr Thr Ser Arg Gly Ile Ala Val
 435 440 445
 Gln Gln Leu Ser Trp Pro Ala Thr Gln Thr Val Trp Asn Asn Gly Leu
 450 455 460
 Tyr Asn Gln His Gly Phe Gly Thr Thr Gly Thr Gly Val Trp Tyr Pro
 465 470 475 480
 Pro Asn Leu Ser Gln Met Tyr Ser Thr Tyr Lys Thr Pro Val Pro Glu
 485 490 495

Thr Asn Ile Pro Gly Ser Thr Pro Thr Met Pro Tyr Phe Ser Gly Pro
500 505 510

Val Ala Asp Asp Leu Ile Lys Tyr Thr Ile Phe Asn Ser Ser Gly Ile
515 520 525

Gln Ile Gly Asn His Asn Tyr Met Asp Val Gly Leu Asn Ser Gln Pro
530 535 540

Pro Asn Asn Thr Cys Lys Glu Glu Ser Thr Ser Gly Ser Asp Gly Ser
545 550 555 560

Gly Ser Gly Ser Gly Ser Leu Glu Ile Arg Ala Ala Phe Leu Glu Lys
565 570 575

Glu Asn Thr Ala Leu Arg Thr Arg Ala Ala Glu Leu Arg Lys Arg Val
580 585 590

Gly Arg Cys Arg Asn Ile Val Ser Lys Tyr Glu Thr Arg Tyr Gly Pro
595 600 605

Leu

<210> 105
<211> 378
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(378)
<223> TAK1-TAB1 humano; P4031 sin etiqueta de epítipo

<400> 105

Met Ser Thr Ala Ser Ala Ala Ser Ser Ser Ser Ser Ser Ala Gly
1 5 10 15

Glu Met Ile Glu Ala Pro Ser Gln Val Leu Asn Phe Glu Glu Ile Asp
20 25 30

Tyr Lys Glu Ile Glu Val Glu Glu Val Val Gly Arg Gly Ala Phe Gly
35 40 45

Val Val Cys Lys Ala Lys Trp Arg Ala Lys Asp Val Ala Ile Lys Gln
50 55 60

Ile Glu Ser Glu Ser Glu Arg Lys Ala Phe Ile Val Glu Leu Arg Gln
65 70 75 80

Leu Ser Arg Val Asn His Pro Asn Ile Val Lys Leu Tyr Gly Ala Cys
85 90 95

Leu Asn Pro Val Cys Leu Val Met Glu Tyr Ala Glu Gly Gly Ser Leu
100 105 110

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

His Ala Met Ser Trp Cys Leu Gln Cys Ser Gln Gly Val Ala Tyr Leu
130 135 140

His Ser Met Gln Pro Lys Ala Leu Ile His Arg Asp Leu Lys Pro Pro
145 150 155 160

Asn Leu Leu Leu Val Ala Gly Gly Thr Val Leu Lys Ile Cys Asp Phe
165 170 175

Gly Thr Ala Cys Asp Ile Gln Thr His Met Thr Asn Asn Lys Gly Ser
180 185 190

Ala Ala Trp Met Ala Pro Glu Val Phe Glu Gly Ser Asn Tyr Ser Glu
195 200 205

Lys Cys Asp Val Phe Ser Trp Gly Ile Ile Leu Trp Glu Val Ile Thr
210 215 220

Arg Arg Lys Pro Phe Asp Glu Ile Gly Gly Pro Ala Phe Arg Ile Met
 225 230 235 240
 Trp Ala Val His Asn Gly Thr Arg Pro Pro Leu Ile Lys Asn Leu Pro
 245 250 255
 Lys Pro Ile Glu Ser Leu Met Thr Arg Cys Trp Ser Lys Asp Pro Ser
 260 265 270
 Gln Arg Pro Ser Met Glu Glu Ile Val Lys Ile Met Thr His Leu Met
 275 280 285
 Arg Tyr Phe Pro Gly Ala Asp Glu Pro Leu Gln Tyr Pro Cys Gln Glu
 290 295 300
 Phe Gly Gly Gly Gly Gly Gly Gln Ser Pro Thr Leu Thr Leu Gln Ser Thr
 305 310 315 320
 Asn Thr His Thr Gln Ser Ser Ser Ser Ser Ser Asp Gly Gly Leu Phe
 325 330 335
 Arg Ser Arg Pro Ala His Ser Leu Pro Pro Gly Glu Asp Gly Arg Val
 340 345 350
 Glu Pro Tyr Val Asp Phe Ala Glu Phe Tyr Arg Leu Trp Ser Val Asp
 355 360 365
 His Gly Glu Gln Ser Val Val Thr Ala Pro
 370 375

<210> 106

<211> 239

<212> PRT

<213> Secuencia artificial

<220>

<223> Sintético: Diablo.1; sin etiqueta de epítipo

<400> 106

Met Ala Ala Leu Lys Ser Trp Leu Ser Arg Ser Val Thr Ser Phe Phe
 1 5 10 15
 Arg Tyr Arg Gln Cys Leu Cys Val Pro Val Val Ala Asn Phe Lys Lys
 20 25 30
 Arg Cys Phe Ser Glu Leu Ile Arg Pro Trp His Lys Thr Val Thr Ile
 35 40 45
 Gly Phe Gly Val Thr Leu Cys Ala Val Pro Ile Ala Gln Lys Ser Glu
 50 55 60
 Pro His Ser Leu Ser Ser Glu Ala Leu Met Arg Arg Ala Val Ser Leu
 65 70 75 80
 Val Thr Asp Ser Thr Ser Thr Phe Leu Ser Gln Thr Thr Tyr Ala Leu
 85 90 95
 Ile Glu Ala Ile Thr Glu Tyr Thr Lys Ala Val Tyr Thr Leu Thr Ser
 100 105 110
 Leu Tyr Arg Gln Tyr Thr Ser Leu Leu Gly Lys Met Asn Ser Glu Glu
 115 120 125
 Glu Asp Glu Val Trp Gln Val Ile Ile Gly Ala Arg Ala Glu Met Thr
 130 135 140
 Ser Lys His Gln Glu Tyr Leu Lys Leu Glu Thr Thr Trp Met Thr Ala
 145 150 155 160
 Val Gly Leu Ser Glu Met Ala Ala Glu Ala Ala Tyr Gln Thr Gly Ala
 165 170 175
 Asp Gln Ala Ser Ile Thr Ala Arg Asn His Ile Gln Leu Val Lys Leu
 180 185 190
 Gln Val Glu Glu Val His Gln Leu Ser Arg Lys Ala Glu Thr Lys Leu
 195 200 205
 Ala Glu Ala Gln Ile Glu Glu Leu Arg Gln Lys Thr Gln Glu Glu Gly

210 215
Glu Glu Arg Ala Glu Ser Glu Gln Glu Ala Tyr Leu Arg Glu Asp
225 230 235

<210> 107
<211> 239
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: Diablo.1(S126L); sin etiqueta de epítipo

<400> 107

Met Ala Ala Leu Lys Ser Trp Leu Ser Arg Ser Val Thr Ser Phe Phe
1 5 10 15

Arg Tyr Arg Gln Cys Leu Cys Val Pro Val Val Ala Asn Phe Lys Lys
20 25 30

Arg Cys Phe Ser Glu Leu Ile Arg Pro Trp His Lys Thr Val Thr Ile
35 40 45

Gly Phe Gly Val Thr Leu Cys Ala Val Pro Ile Ala Gln Lys Ser Glu
50 55 60

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

Val Thr Asp Ser Thr Ser Thr Phe Leu Ser Gln Thr Thr Tyr Ala Leu
85 90 95

Ile Glu Ala Ile Thr Glu Tyr Thr Lys Ala Val Tyr Thr Leu Thr Ser
100 105 110

Leu Tyr Arg Gln Tyr Thr Ser Leu Leu Gly Lys Met Asn Leu Glu Glu
115 120 125

Glu Asp Glu Val Trp Gln Val Ile Ile Gly Ala Arg Ala Glu Met Thr
130 135 140

Ser Lys His Gln Glu Tyr Leu Lys Leu Glu Thr Thr Trp Met Thr Ala
145 150 155 160

Val Gly Leu Ser Glu Met Ala Ala Glu Ala Ala Tyr Gln Thr Gly Ala
165 170 175

Asp Gln Ala Ser Ile Thr Ala Arg Asn His Ile Gln Leu Val Lys Leu
180 185 190

Gln Val Glu Glu Val His Gln Leu Ser Arg Lys Ala Glu Thr Lys Leu
195 200 205

Ala Glu Ala Gln Ile Glu Glu Leu Arg Gln Lys Thr Gln Glu Glu Gly
210 215 220

Glu Glu Arg Ala Glu Ser Glu Gln Glu Ala Tyr Leu Arg Glu Asp
225 230 235

<210> 108
<211> 185
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: Diablo.1(56-239); sin etiqueta de epítipo

<400> 108

Met Ala Val Pro Ile Ala Gln Lys Ser Glu Pro His Ser Leu Ser Ser
1 5 10 15

Glu Ala Leu Met Arg Arg Ala Val Ser Leu Val Thr Asp Ser Thr Ser
20 25 30

Thr Phe Leu Ser Gln Thr Thr Tyr Ala Leu Ile Glu Ala Ile Thr Glu
35 40 45

Tyr Thr Lys Ala Val Tyr Thr Leu Thr Ser Leu Tyr Arg Gln Tyr Thr
50 55 60

Ser Leu Leu Gly Lys Met Asn Ser Glu Glu Glu Asp Glu Val Trp Gln
65 70 75 80

Val Ile Ile Gly Ala Arg Ala Glu Met Thr Ser Lys His Gln Glu Tyr
85 90 95

Leu Lys Leu Glu Thr Thr Trp Met Thr Ala Val Gly Leu Ser Glu Met
100 105 110

Ala Ala Glu Ala Ala Tyr Gln Thr Gly Ala Asp Gln Ala Ser Ile Thr
115 120 125

Ala Arg Asn His Ile Gln Leu Val Lys Leu Gln Val Glu Glu Val His
130 135 140

Gln Leu Ser Arg Lys Ala Glu Thr Lys Leu Ala Glu Ala Gln Ile Glu
145 150 155 160

Glu Leu Arg Gln Lys Thr Gln Glu Glu Gly Glu Glu Arg Ala Glu Ser
165 170 175

Glu Gln Glu Ala Tyr Leu Arg Glu Asp
180 185

<210> 109
<211> 185
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: Diablo.1(56-239/S126L); sin etiqueta de epítipo

<400> 109

Met Ala Val Pro Ile Ala Gln Lys Ser Glu Pro His Ser Leu Ser Ser
1 5 10 15

Glu Ala Leu Met Arg Arg Ala Val Ser Leu Val Thr Asp Ser Thr Ser
20 25 30

Thr Phe Leu Ser Gln Thr Thr Tyr Ala Leu Ile Glu Ala Ile Thr Glu
35 40 45

Tyr Thr Lys Ala Val Tyr Thr Leu Thr Ser Leu Tyr Arg Gln Tyr Thr
50 55 60

Ser Leu Leu Gly Lys Met Asn Leu Glu Glu Glu Asp Glu Val Trp Gln
65 70 75 80

Val Ile Ile Gly Ala Arg Ala Glu Met Thr Ser Lys His Gln Glu Tyr
85 90 95

Leu Lys Leu Glu Thr Thr Trp Met Thr Ala Val Gly Leu Ser Glu Met
100 105 110

Ala Ala Glu Ala Ala Tyr Gln Thr Gly Ala Asp Gln Ala Ser Ile Thr
115 120 125

Ala Arg Asn His Ile Gln Leu Val Lys Leu Gln Val Glu Glu Val His
130 135 140

Gln Leu Ser Arg Lys Ala Glu Thr Lys Leu Ala Glu Ala Gln Ile Glu
145 150 155 160

Glu Leu Arg Gln Lys Thr Gln Glu Glu Gly Glu Glu Arg Ala Glu Ser
165 170 175

Glu Gln Glu Ala Tyr Leu Arg Glu Asp
180 185

<210> 110
<211> 195
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: Diablo.3; TH2003 sin etiqueta de epítipo

<400> 110

Met Ala Ala Leu Lys Ser Trp Leu Ser Arg Ser Val Thr Ser Phe Phe
1 5 10 15

Arg Tyr Arg Gln Cys Leu Cys Val Pro Val Val Ala Asn Phe Lys Lys
 20 25 30
 Arg Cys Phe Ser Glu Leu Ile Arg Pro Trp His Lys Thr Val Thr Ile
 35 40 45
 Gly Phe Gly Val Thr Leu Cys Ala Val Pro Ile Ala Gln Ala Val Tyr
 50 55 60
 Thr Leu Thr Ser Leu Tyr Arg Gln Tyr Thr Ser Leu Leu Gly Lys Met
 65 70 75 80
 Asn Ser Glu Glu Glu Asp Glu Val Trp Gln Val Ile Ile Gly Ala Arg
 85 90 95
 Ala Glu Met Thr Ser Lys His Gln Glu Tyr Leu Lys Leu Glu Thr Thr
 100 105 110
 Trp Met Thr Ala Val Gly Leu Ser Glu Met Ala Ala Glu Ala Ala Tyr
 115 120 125
 Gln Thr Gly Ala Asp Gln Ala Ser Ile Thr Ala Arg Asn His Ile Gln
 130 135 140
 Leu Val Lys Leu Gln Val Glu Glu Val His Gln Leu Ser Arg Lys Ala
 145 150 155 160
 Glu Thr Lys Leu Ala Glu Ala Gln Ile Glu Glu Leu Arg Gln Lys Thr
 165 170 175
 Gln Glu Glu Gly Glu Glu Arg Ala Glu Ser Glu Gln Glu Ala Tyr Leu
 180 185 190
 Arg Glu Asp
 195
 <210> 111
 <211> 195
 <212> PRT
 <213> Secuencia artificial
 <220>
 <223> Sintético: Diablo.3(S82L); TH2001 sin etiqueta de epítipo
 <400> 111
 Met Ala Ala Leu Lys Ser Trp Leu Ser Arg Ser Val Thr Ser Phe Phe
 1 5 10 15
 Arg Tyr Arg Gln Cys Leu Cys Val Pro Val Val Ala Asn Phe Lys Lys
 20 25 30
 Arg Cys Phe Ser Glu Leu Ile Arg Pro Trp His Lys Thr Val Thr Ile
 35 40 45
 Gly Phe Gly Val Thr Leu Cys Ala Val Pro Ile Ala Gln Ala Val Tyr
 50 55 60
 Thr Leu Thr Ser Leu Tyr Arg Gln Tyr Thr Ser Leu Leu Gly Lys Met
 65 70 75 80
 Asn Leu Glu Glu Glu Asp Glu Val Trp Gln Val Ile Ile Gly Ala Arg
 85 90 95
 Ala Glu Met Thr Ser Lys His Gln Glu Tyr Leu Lys Leu Glu Thr Thr
 100 105 110
 Trp Met Thr Ala Val Gly Leu Ser Glu Met Ala Ala Glu Ala Ala Tyr
 115 120 125
 Gln Thr Gly Ala Asp Gln Ala Ser Ile Thr Ala Arg Asn His Ile Gln
 130 135 140
 Leu Val Lys Leu Gln Val Glu Glu Val His Gln Leu Ser Arg Lys Ala
 145 150 155 160
 Glu Thr Lys Leu Ala Glu Ala Gln Ile Glu Glu Leu Arg Gln Lys Thr
 165 170 175

Gln Glu Glu Gly Glu Glu Arg Ala Glu Ser Glu Gln Glu Ala Tyr Leu
 180 185 190

Arg Glu Asp
 195

<210> 112
 <211> 141
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: Diablo.3(56-195); TH2002 sin etiqueta de epítipo

<400> 112

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

Arg Gln Tyr Thr Ser Leu Leu Gly Lys Met Asn Ser Glu Glu Glu Asp
 20 25 30

Glu Val Trp Gln Val Ile Ile Gly Ala Arg Ala Glu Met Thr Ser Lys
 35 40 45

His Gln Glu Tyr Leu Lys Leu Glu Thr Thr Trp Met Thr Ala Val Gly
 50 55 60

Leu Ser Glu Met Ala Ala Glu Ala Ala Tyr Gln Thr Gly Ala Asp Gln
 65 70 75 80

Ala Ser Ile Thr Ala Arg Asn His Ile Gln Leu Val Lys Leu Gln Val
 85 90 95

Glu Glu Val His Gln Leu Ser Arg Lys Ala Glu Thr Lys Leu Ala Glu
 100 105 110

Ala Gln Ile Glu Glu Leu Arg Gln Lys Thr Gln Glu Glu Gly Glu Glu
 115 120 125

Arg Ala Glu Ser Glu Gln Glu Ala Tyr Leu Arg Glu Asp
 130 135 140

<210> 113
 <211> 141
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: Diablo.3(56-195/S82L); sin etiqueta de epítipo

<400> 113

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

Arg Gln Tyr Thr Ser Leu Leu Gly Lys Met Asn Leu Glu Glu Glu Asp
 20 25 30

Glu Val Trp Gln Val Ile Ile Gly Ala Arg Ala Glu Met Thr Ser Lys
 35 40 45

His Gln Glu Tyr Leu Lys Leu Glu Thr Thr Trp Met Thr Ala Val Gly
 50 55 60

Leu Ser Glu Met Ala Ala Glu Ala Ala Tyr Gln Thr Gly Ala Asp Gln
 65 70 75 80

Ala Ser Ile Thr Ala Arg Asn His Ile Gln Leu Val Lys Leu Gln Val
 85 90 95

Glu Glu Val His Gln Leu Ser Arg Lys Ala Glu Thr Lys Leu Ala Glu
 100 105 110

Ala Gln Ile Glu Glu Leu Arg Gln Lys Thr Gln Glu Glu Gly Glu Glu
 115 120 125

Arg Ala Glu Ser Glu Gln Glu Ala Tyr Leu Arg Glu Asp
 130 135 140

<210> 114
 <211> 659
 <212> PRT

<213> Secuencia artificial

<220>

<223> Sintético: Btk(E41K); P4029 sin etiqueta de epítipo

<400> 114

Met Ala Ala Val Ile Leu Glu Ser Ile Phe Leu Lys Arg Ser Gln Gln
1 5 10 15Lys Lys Lys Thr Ser Pro Leu Asn Phe Lys Lys Arg Leu Phe Leu Leu
20 25 30Thr Val His Lys Leu Ser Tyr Tyr Lys Tyr Asp Phe Glu Arg Gly Arg
35 40 45Arg Gly Ser Lys Lys Gly Ser Ile Asp Val Glu Lys Ile Thr Cys Val
50 55 60Glu Thr Val Val Pro Glu Lys Asn Pro Pro Pro Glu Arg Gln Ile Pro
65 70 75 80Arg Arg Gly Glu Glu Ser Ser Glu Met Glu Gln Ile Ser Ile Ile Glu
85 90 95Arg Phe Pro Tyr Pro Phe Gln Val Val Tyr Asp Glu Gly Pro Leu Tyr
100 105 110Val Phe Ser Pro Thr Glu Glu Leu Arg Lys Arg Trp Ile His Gln Leu
115 120 125Lys Asn Val Ile Arg Tyr Asn Ser Asp Leu Val Gln Lys Tyr His Pro
130 135 140Cys Phe Trp Ile Asp Gly Gln Tyr Leu Cys Cys Ser Gln Thr Ala Lys
145 150 155 160Asn Ala Met Gly Cys Gln Ile Leu Glu Asn Arg Asn Gly Ser Leu Lys
165 170 175Pro Gly Ser Ser His Arg Lys Thr Lys Lys Pro Leu Pro Pro Thr Pro
180 185 190Glu Glu Asp Gln Ile Leu Lys Lys Pro Leu Pro Pro Glu Pro Ala Ala
195 200 205Ala Pro Val Ser Thr Ser Glu Leu Lys Lys Val Val Ala Leu Tyr Asp
210 215 220Tyr Met Pro Met Asn Ala Asn Asp Leu Gln Leu Arg Lys Gly Asp Glu
225 230 235 240Tyr Phe Ile Leu Glu Glu Ser Asn Leu Pro Trp Trp Arg Ala Arg Asp
245 250 255Lys Asn Gly Gln Glu Gly Tyr Ile Pro Ser Asn Tyr Val Thr Glu Ala
260 265 270Glu Asp Ser Ile Glu Met Tyr Glu Trp Tyr Ser Lys His Met Thr Arg
275 280 285Ser Gln Ala Glu Gln Leu Leu Lys Gln Glu Gly Lys Glu Gly Gly Phe
290 295 300Ile Val Arg Asp Ser Ser Lys Ala Gly Lys Tyr Thr Val Ser Val Phe
305 310 315 320Ala Lys Ser Thr Gly Asp Pro Gln Gly Val Ile Arg His Tyr Val Val
325 330 335Cys Ser Thr Pro Gln Ser Gln Tyr Tyr Leu Ala Glu Lys His Leu Phe
340 345 350Ser Thr Ile Pro Glu Leu Ile Asn Tyr His Gln His Asn Ser Ala Gly
355 360 365Leu Ile Ser Arg Leu Lys Tyr Pro Val Ser Gln Gln Asn Lys Asn Ala
370 375 380

Pro Ser Thr Ala Gly Leu Gly Tyr Gly Ser Trp Glu Ile Asp Pro Lys
 385 390 395 400
 Asp Leu Thr Phe Leu Lys Glu Leu Gly Thr Gly Gln Phe Gly Val Val
 405 410 415
 Lys Tyr Gly Lys Trp Arg Gly Gln Tyr Asp Val Ala Ile Lys Met Ile
 420 425 430
 Lys Glu Gly Ser Met Ser Glu Asp Glu Phe Ile Glu Glu Ala Lys Val
 435 440 445
 Met Met Asn Leu Ser His Glu Lys Leu Val Gln Leu Tyr Gly Val Cys
 450 455 460
 Thr Lys Gln Arg Pro Ile Phe Ile Ile Thr Glu Tyr Met Ala Asn Gly
 465 470 475 480
 Cys Leu Leu Asn Tyr Leu Arg Glu Met Arg His Arg Phe Gln Thr Gln
 485 490 495
 Gln Leu Leu Glu Met Cys Lys Asp Val Cys Glu Ala Met Glu Tyr Leu
 500 505 510
 Glu Ser Lys Gln Phe Leu His Arg Asp Leu Ala Ala Arg Asn Cys Leu
 515 520 525
 Val Asn Asp Gln Gly Val Val Lys Val Ser Asp Phe Gly Leu Ser Arg
 530 535 540
 Tyr Val Leu Asp Asp Glu Tyr Thr Ser Ser Val Gly Ser Lys Phe Pro
 545 550 555 560
 Val Arg Trp Ser Pro Pro Glu Val Leu Met Tyr Ser Lys Phe Ser Ser
 565 570 575
 Lys Ser Asp Ile Trp Ala Phe Gly Val Leu Met Trp Glu Ile Tyr Ser
 580 585 590
 Leu Gly Lys Met Pro Tyr Glu Arg Phe Thr Asn Ser Glu Thr Ala Glu
 595 600 605
 His Ile Ala Gln Gly Leu Arg Leu Tyr Arg Pro His Leu Ala Ser Glu
 610 615 620
 Lys Val Tyr Thr Ile Met Tyr Ser Cys Trp His Glu Lys Ala Asp Glu
 625 630 635 640
 Arg Pro Thr Phe Lys Ile Leu Leu Ser Asn Ile Leu Asp Val Met Asp
 645 650 655
 Glu Glu Ser

<210> 115
 <211> 225
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: SOCS3; P4030 sin etiqueta de epítipo
 <400> 115

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

85

Cys Glu Gly Gly Ser Phe Ser Leu Gln Ser Asp Pro Arg Ser Thr Gln
100 105 110

Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu Val His His Tyr Met
115 120 125

Pro Pro Pro Gly Ala Pro Ser Phe Pro Ser Pro Pro Thr Glu Pro Ser
130 135 140

Ser Glu Val Pro Glu Gln Pro Ser Ala Gln Pro Leu Pro Gly Ser Pro
145 150 155 160

Pro Arg Arg Ala Tyr Tyr Ile Tyr Ser Gly Gly Glu Lys Ile Pro Leu
165 170 175

Val Leu Ser Arg Pro Leu Ser Ser Asn Val Ala Thr Leu Gln His Leu
180 185 190

Cys Arg Lys Thr Val Asn Gly His Leu Asp Ser Tyr Glu Lys Val Thr
195 200 205

Gln Leu Pro Gly Pro Ile Arg Glu Phe Leu Asp Gln Tyr Asp Ala Pro
210 215 220

Leu
225

<210> 116
<211> 347
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(347)
<223> IZ_hsCASP1 (Caspasa 1 humana autoactivante); P2024 sin etiqueta de epítipo
<400> 116

Met Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys
1 5 10 15

Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly
20 25 30

Glu Ala Asp Gln Thr Ser Gly Asn Tyr Leu Asn Met Gln Asp Ser Gln
35 40 45

Gly Val Leu Ser Ser Phe Pro Ala Pro Gln Ala Val Gln Asp Asn Pro
50 55 60

Ala Met Pro Thr Ser Ser Gly Ser Glu Gly Asn Val Lys Leu Cys Ser
65 70 75 80

Leu Glu Glu Ala Gln Arg Ile Trp Lys Gln Lys Ser Ala Glu Ile Tyr
85 90 95

Pro Ile Met Asp Lys Ser Ser Arg Thr Arg Leu Ala Leu Ile Ile Cys
100 105 110

Asn Glu Glu Phe Asp Ser Ile Pro Arg Arg Thr Gly Ala Glu Val Asp
115 120 125

Ile Thr Gly Met Thr Met Leu Leu Gln Asn Leu Gly Tyr Ser Val Asp
130 135 140

Val Lys Lys Asn Leu Thr Ala Ser Asp Met Thr Thr Glu Leu Glu Ala
145 150 155 160

Phe Ala His Arg Pro Glu His Lys Thr Ser Asp Ser Thr Phe Leu Val
165 170 175

Phe Met Ser His Gly Ile Arg Glu Gly Ile Cys Gly Lys Lys His Ser
180 185 190

Glu Gln Val Pro Asp Ile Leu Gln Leu Asn Ala Ile Phe Asn Met Leu
195 200 205

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Asn Thr Lys Asn Cys Pro Ser Leu Lys Asp Lys Pro Lys Val Ile Ile
 210          215          220

Ile Gln Ala Cys Arg Gly Asp Ser Pro Gly Val Val Trp Phe Lys Asp
 225          230          235          240

Ser Val Gly Val Ser Gly Asn Leu Ser Leu Pro Thr Thr Glu Glu Phe
          245          250          255

Glu Asp Asp Ala Ile Lys Lys Ala His Ile Glu Lys Asp Phe Ile Ala
          260          265          270

Phe Cys Ser Ser Thr Pro Asp Asn Val Ser Trp Arg His Pro Thr Met
          275          280          285

Gly Ser Val Phe Ile Gly Arg Leu Ile Glu His Met Gln Glu Tyr Ala
 290          295          300

Cys Ser Cys Asp Val Glu Glu Ile Phe Arg Lys Val Arg Phe Ser Phe
 305          310          315          320

Glu Gln Pro Asp Gly Arg Ala Gln Met Pro Thr Thr Glu Arg Val Thr
          325          330          335

Leu Thr Arg Cys Phe Tyr Leu Phe Pro Gly His
          340          345

<210> 117
<211> 347
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(347)
<223> DM_hscASP1 (Caspasa 1 humana autoactivante); P2025 sin etiqueta de epítipo

<400> 117

Met Arg Met Lys Gln Leu Glu Asp Lys Ile Glu Glu Leu Leu Ser Lys
 1          5          10          15

Ile Tyr His Leu Glu Asn Glu Ile Ala Arg Leu Lys Lys Leu Ile Gly
          20          25          30

Glu Ala Asp Gln Thr Ser Gly Asn Tyr Leu Asn Met Gln Asp Ser Gln
          35          40          45

Gly Val Leu Ser Ser Phe Pro Ala Pro Gln Ala Val Gln Asp Asn Pro
 50          55          60

Ala Met Pro Thr Ser Ser Gly Ser Glu Gly Asn Val Lys Leu Cys Ser
 65          70          75          80

Leu Glu Glu Ala Gln Arg Ile Trp Lys Gln Lys Ser Ala Glu Ile Tyr
          85          90          95

Pro Ile Met Asp Lys Ser Ser Arg Thr Arg Leu Ala Leu Ile Ile Cys
          100          105          110

Asn Glu Glu Phe Asp Ser Ile Pro Arg Arg Thr Gly Ala Glu Val Asp
          115          120          125

Ile Thr Gly Met Thr Met Leu Leu Gln Asn Leu Gly Tyr Ser Val Asp
          130          135          140

Val Lys Lys Asn Leu Thr Ala Ser Asp Met Thr Thr Glu Leu Glu Ala
          145          150          155          160

Phe Ala His Arg Pro Glu His Lys Thr Ser Asp Ser Thr Phe Leu Val
          165          170          175

Phe Met Ser His Gly Ile Arg Glu Gly Ile Cys Gly Lys Lys His Ser
          180          185          190

Glu Gln Val Pro Asp Ile Leu Gln Leu Asn Ala Ile Phe Asn Met Leu
          195          200          205

Asn Thr Lys Asn Cys Pro Ser Leu Lys Asp Lys Pro Lys Val Ile Ile

```

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

<210> 118
<211> 346
<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(346)
<223> IZ_mmCASP1 (Caspasa 1 de ratón autoactivante); P2026 sin etiqueta de epitopo

<400> 118

Met Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys
1 5 10 15
Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly
20 25 30
Glu Arg Ser Ala Pro Ser Ala Glu Thr Phe Val Ala Thr Glu Asp Ser
35 40 45
Lys Gly Gly His Pro Ser Ser Ser Glu Thr Lys Glu Glu Gln Asn Lys
50 55 60
Glu Asp Gly Thr Phe Pro Gly Leu Thr Gly Thr Leu Lys Phe Cys Pro
65 70 75 80
Leu Glu Lys Ala Gln Lys Leu Trp Lys Glu Asn Pro Ser Glu Ile Tyr
85 90 95
Pro Ile Met Asn Thr Thr Thr Arg Thr Arg Leu Ala Leu Ile Ile Cys
100 105 110
Asn Thr Glu Phe Gln His Leu Ser Pro Arg Val Gly Ala Gln Val Asp
115 120 125
Leu Arg Glu Met Lys Leu Leu Leu Glu Asp Leu Gly Tyr Thr Val Lys
130 135 140
Val Lys Glu Asn Leu Thr Ala Leu Glu Met Val Lys Glu Val Lys Glu
145 150 155 160
Phe Ala Ala Cys Pro Glu His Lys Thr Ser Asp Ser Thr Phe Leu Val
165 170 175
Phe Met Ser His Gly Ile Gln Glu Gly Ile Cys Gly Thr Thr Tyr Ser
180 185 190
Asn Glu Val Ser Asp Ile Leu Lys Val Asp Thr Ile Phe Gln Met Met
195 200 205
Asn Thr Leu Lys Cys Pro Ser Leu Lys Asp Lys Pro Lys Val Ile Ile
210 215 220

Ile Gln Ala Cys Arg Gly Glu Lys Gln Gly Val Val Leu Leu Lys Asp
225 230 235 240

Ser Val Arg Asp Ser Glu Glu Asp Phe Leu Thr Asp Ala Ile Phe Glu
245 250 255

Asp Asp Gly Ile Lys Lys Ala His Ile Glu Lys Asp Phe Ile Ala Phe
260 265 270

Cys Ser Ser Thr Pro Asp Asn Val Ser Trp Arg His Pro Val Arg Gly
275 280 285

Ser Leu Phe Ile Glu Ser Leu Ile Lys His Met Lys Glu Tyr Ala Trp
290 295 300

Ser Cys Asp Leu Glu Asp Ile Phe Arg Lys Val Arg Phe Ser Phe Glu
305 310 315 320

Gln Pro Glu Phe Arg Leu Gln Met Pro Thr Ala Asp Arg Val Thr Leu
325 330 335

Thr Lys Arg Phe Tyr Leu Phe Pro Gly His
340 345

<210> 119
<211> 346
<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(346)
<223> DM_mmCASP1 (Caspasa 1 de ratón autoactivante); P2027 sin etiqueta de epítipo
<400> 119

Met Arg Met Lys Gln Leu Glu Asp Lys Ile Glu Glu Leu Leu Ser Lys
1 5 10 15

Ile Tyr His Leu Glu Asn Glu Ile Ala Arg Leu Lys Lys Leu Ile Gly
20 25 30

Glu Arg Ser Ala Pro Ser Ala Glu Thr Phe Val Ala Thr Glu Asp Ser
35 40 45

Lys Gly Gly His Pro Ser Ser Ser Glu Thr Lys Glu Glu Gln Asn Lys
50 55 60

Glu Asp Gly Thr Phe Pro Gly Leu Thr Gly Thr Leu Lys Phe Cys Pro
65 70 75 80

Leu Glu Lys Ala Gln Lys Leu Trp Lys Glu Asn Pro Ser Glu Ile Tyr
85 90 95

Pro Ile Met Asn Thr Thr Thr Arg Thr Arg Leu Ala Leu Ile Ile Cys
100 105 110

Asn Thr Glu Phe Gln His Leu Ser Pro Arg Val Gly Ala Gln Val Asp
115 120 125

Leu Arg Glu Met Lys Leu Leu Leu Glu Asp Leu Gly Tyr Thr Val Lys
130 135 140

Val Lys Glu Asn Leu Thr Ala Leu Glu Met Val Lys Glu Val Lys Glu
145 150 155 160

Phe Ala Ala Cys Pro Glu His Lys Thr Ser Asp Ser Thr Phe Leu Val
165 170 175

Phe Met Ser His Gly Ile Gln Glu Gly Ile Cys Gly Thr Thr Tyr Ser
180 185 190

Asn Glu Val Ser Asp Ile Leu Lys Val Asp Thr Ile Phe Gln Met Met
195 200 205

Asn Thr Leu Lys Cys Pro Ser Leu Lys Asp Lys Pro Lys Val Ile Ile
210 215 220

Ile Gln Ala Cys Arg Gly Glu Lys Gln Gly Val Val Leu Leu Lys Asp

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<210> 120
<211> 106
<212> PRT
<213> Secuencia artificial
```

<220>
<223> Sintético: Concatémoro de ADR con etiqueta HIS

$\langle 400 \rangle$ 120

Met His His His His His His His His His His Gly Lys Pro Ile Pro
1 5 10 15

Asn Pro Leu Leu Gly Leu Asp Ser Thr Gly Ile Pro Val His Leu Glu
20 25 30

Leu Ala Ser Met Thr Asn Met Glu Leu Met Ser Ser Ile Val His Gln
35 40 45

Gln Val Phe Pro Thr Glu Ala Gly Gln Ser Leu Val Ile Ser Ala Ser
50 55 60

Ile Ile Val Phe Asn Leu Leu Glu Leu Glu Gly Asp Tyr Arg Gly Arg
65 70 75 80

Val Leu Glu Leu Phe Arg Ala Ala Gln Leu Ala Asn Asp Val Val Leu
85 90 95

Gln Ile Met Glu Leu Cys Gly Ala Thr Arg
100 105

```
<210> 121
<211> 9
<212> PRT
<213> Secuencia artificial
```

<220>
<223> Sintético: KRAS G12D 9mer

$\langle 400 \rangle$ 121

Val Val Gly Ala Asp Gly Val Gly Lys
1 5

```
<210> 122
<211> 9
<212> PRT
<213> Secuencia artificial
```

<220>
<223> Sintético: KRAS G12V 9mer

<400> 122

Val Val Gly Ala Val Gly Val Gly Lys
1 5

```
<210> 123
<211> 9
<212> PRT
<213> Secuencia artificial
```

$\langle 220 \rangle$

<223> Sintético: KRAS G13D 9mer

<400> 123

Val Gly Ala Gly Asp Val Gly Lys Ser
1 5

<210> 124

<211> 9

<212> PRT

<213> Secuencia artificial

<220>

<223> Sintético: KRAS G12C 9mer

<400> 124

Val Val Gly Ala Cys Gly Val Gly Lys
1 5

<210> 125

<211> 15

<212> PRT

<213> Secuencia artificial

<220>

<223> Sintético: KRAS G12C 15mer

<400> 125

Met Lys Leu Val Val Val Gly Ala Cys Gly Val Gly Lys Ser Ala
1 5 10 15

<210> 126

<211> 75

<212> ADN

<213> Secuencia artificial

<220>

<223> Sintético: Secuencia de nucleótidos de KRAS G12D 25mer

<400> 126

atgaccgagt acaagctggt ggtggtgggc gccgacggcg tgggcaagag cgccctgacc 60

atccagctga tccag 75

<210> 127

<211> 75

<212> ADN

<213> Secuencia artificial

<220>

<223> Sintético: Secuencia de nucleótidos de KRAS G12V 25mer

<400> 127

atgaccgagt acaagctggt ggtggtgggc gccgtgggcg tgggcaagag cgccctgacc 60

atccagctga tccag 75

<210> 128

<211> 75

<212> ADN

<213> Secuencia artificial

<220>

<223> Sintético: Secuencia de nucleótidos de KRAS G13D 25mer

<400> 128

atgaccgagt acaagctggt ggtggtgggc gccggcgacg tgggcaagag cgccctgacc 60

atccagctga tccag 75

<210> 129

<211> 225

<212> ADN

<213> Secuencia artificial

<220>

<223> Sintético: Secuencia de nucleótidos de KRAS G12D 25mer^3

<400> 129

atgaccgagt acaagttagt ggttgtgggc gccgacggcg tgggcaagag cgccctcacc 60

atccagctta tccagatgac ggaatataag ttagtagtag tgggagccga cggtgtcggc 120

aagtccgctt tgaccattca acttattcag atgacagagt ataagctggt cgttgtaggc 180

gcagacggcg ttggaaagtc ggcactgacg atccagttga tccag 225

<210> 130

<211> 225

<212> ADN

<213> Secuencia artificial

<220>

<223> Sintético: Secuencia de nucleótidos de KRAS G12V 25mer^3

<400> 130
 atgaccgagt acaagctcgt cgtggtgggc gccgtgggcg tgggcaagag cgccctaacc 60
 atccagtga tccagatgac cgaatataag ctcgtggttag tcggagcggg gggcgttggc 120
 aagtcagcgc taacaataca actaatccaa atgaccgaat acaagctagt ttagtcggg 180
 gccgtcggcg ttggaaagtc agcccttaca attcagctca ttcag 225

<210> 131
 <211> 225
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Sintético: Secuencia de nucleótidos de KRAS G13D 25mer^3

<400> 131
 atgaccgagt acaagctcgt agtgggtggc gccggcgacg tgggcaagag cgccctaacc 60
 atccagctca tccagatgac agaataaag cttgtggttg tgggagcagg agacgtggga 120
 aagagtgcgt tgacgattca actcatacag atgaccgaat acaagttggt ggtggtcggc 180
 gcaggtgacg ttggaagtc tgcactaact atacaactga tccag 225

<210> 132
 <211> 75
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Sintético: Secuencia de nucleótidos de KRAS G12C 25mer

<400> 132
 atgaccgagt acaagctggt ggtgggtgggc gcctgcggcg tgggcaagag cgccctgacc 60
 atccagctga tccag 75

<210> 133
 <211> 75
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Sintético: Secuencia de nucleótidos de KRAS WT 25mer

<400> 133
 atgaccgagt acaagctggt ggtgggtgggc gccggcgggcg tgggcaagag cgccctgacc 60
 atccagctga tccag 75

<210> 134
 <211> 47
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Sintético: Secuencia 5 UTR; sin promotor

<400> 134
 gggaaataag agagaaaaga agagtaagaa gaaatataag agccacc 47

<210> 135
 <211> 75
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: sec. aa. KRAS(G12D G12V G13D) 75mer 3MUT

<400> 135
 Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Asp Gly Val Gly Lys
 1 5 10 15
 Ser Ala Leu Thr Ile Gln Leu Ile Gln Met Thr Glu Tyr Lys Leu Val
 20 25 30
 Val Val Gly Ala Val Gly Val Gly Lys Ser Ala Leu Thr Ile Gln Leu
 35 40 45
 Ile Gln Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Asp Val
 50 55 60
 Gly Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln
 65 70 75

<210> 136
 <211> 225
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Sintético: sec. nt. KRAS(G12D G12V G13D) 75mer 3MUT
 <400> 136
 atgaccgagt acaagctcgt ttagtcggc gccgacggcg tgggcaagag cgccttgacc 60
 atccagttga tccagatgac cgaatataag ttggtggtgg taggcgcagt gggagttggc 120
 aagtcagcac tcacaattca gctcattcaa atgacagaat acaagttagt cgtttagga 180
 gcaggcgacg tcggcaagag tgccttaacc attcaactaa tccag 225

<210> 137
 <211> 100
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: sec. aa. KRAS(G12D G12V G13D G12C) 100mer 4MUT

<400> 137

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Asp Gly Val Gly Lys
 1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Met Thr Glu Tyr Lys Leu Val
 20 25 30

Val Val Gly Ala Val Gly Val Gly Lys Ser Ala Leu Thr Ile Gln Leu
 35 40 45

Ile Gln Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Asp Val
 50 55 60

Gly Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Met Thr Glu Tyr Lys
 65 70 75 80

Leu Val Val Val Gly Ala Cys Gly Val Gly Lys Ser Ala Leu Thr Ile
 85 90 95

Gln Leu Ile Gln
 100

<210> 138
 <211> 300
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Sintético: sec. nt. KRAS(G12D G12V G13D G12C) 100mer 4MUT

<400> 138
 atgaccgagt acaagctcgt ggtcgtcggc gccgacgggg taggcaagtc cgctctgacc 60
 attcagctca tccagatgac ggagtacaaa ctcgtggttag tgggagccgt ggggtgtggc 120
 aagagcgcgc tcacatcca actcatccaa atgaccgaat ataaactcgt cgtggtggga 180
 gccggcgacg tgggaaagag cgcccttacc atccagtaa tccagatgac agaatacaag 240
 ctggtggtgg tcggtgcctg cggcgtgggt aagtcgccc tgacaatcca gctgatccag 300

<210> 139
 <211> 1137
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Sintético: huSTING(V155M); sin etiqueta de epítipo; secuencia de nucleótidos

<400> 139
 atgccccaca gtagcctcca cccagcatc ccctgcccc gaggccacgg cgcacagaag 60
 gccgccctgg tgctgctgag cgctgtctg gtgacctgt ggggtctgg cgagcccccc 120
 gagcacacc tcggtacct cgtgctgcat ctggccagcc tgcagctgg cctgctgctg 180
 aacggcgtgt gcagcctggc cgaagagctg agacacatcc acagcagata cagaggctcc 240
 tactggagaa ccgtcagagc ctgcctcggc tgtcccctga gaagaggcgc cctgctgctc 300
 ctgagcatct acttctacta cagcctgccc aacgccgtgg gccccccctt cacctggatg 360
 ctggccctgc tgggcctgag ccaggccctg aacatcctgc tgggcctgaa gggcttgcc 420
 cccgccgaga tctccgccgt gtgcgagaag ggcaactca acatggcca tggccttgcc 480
 tggctctact acatcggcta cctgagactg atcctgccc agctgcaggc cagaatcaga 540
 acctacaacc agcactacaa caacctgctg agaggcgccg tgagccaaag actgtacatc 600
 ctgctgcccc tggactgcgg cgtgcccgc aaccttagca tggccgaccc caacatcaga 660

ttcctggaca	agctgcccc	gcagaccggc	gaccacgccg	gcatcaagga	cagagtgtac	720
agcaacagca	tctacgagct	gctggagaac	ggccagagag	ccggcacctg	ctgtctggag	780
tacgccaccc	ccctgcagac	cctgttcgcc	atgagccagt	acagccaggc	cggcttcagc	840
agagaggaca	gactggagca	agccaagctg	ttctgcagaa	ccctggagga	catcctggcg	900
gacgcccccg	agagccaaaa	caactgcaga	ctgatcgctt	accaggagcc	cgccgacgac	960
agcagcttca	gcctgagcca	ggaagtgtct	agacacctga	gacaggaaga	gaaggaggag	1020
gtgaccgtgg	gaagcctgaa	gaccagcgcc	gtgcccagca	ccagcaccat	gagccaggag	1080
cccagactgc	tgatcagcgg	catggagaag	cccctgcccc	tgagaaccga	cttcagc	1137

<210> 140
 <211> 1137
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Sintético: Hu STING(R284T); sin etiqueta de epítipo; secuencia de nucleótidos

<400> 140	atgcctcaca	gcagcctgca	ccctagcatc	ccttgcccta	gaggccacgg	cgcccagaag	60
	gccgccctgg	tgctgctgag	cgctgcctg	gtgacctgt	ggggcctggg	cgagcctcct	120
	gagcacaccc	tgagatacct	ggtgctgcac	ctggccagcc	tgagctggg	cctgctgctg	180
	aacggcgtgt	gcagcctggc	cgaggagctg	agacacatcc	acagcagata	cagaggcagc	240
	tactggagaa	ccgtgagagc	ctgcctgggc	tgccctctga	gaagaggcgc	cctgctgctg	300
	ctgagcatct	acttctacta	cagcctgcct	aacgccgtgg	gccctccttt	cacctggatg	360
	ctggccctgc	tgggcctgag	ccaggccctg	aacatcctgc	tgggcctgaa	gggcctggcc	420
	cctgccgaga	tcagcgccgt	gtgcgagaag	ggcaacttca	acgtggccca	cggcctggcc	480
	tggagctact	acatcggcta	cctgagactg	atcctgcctg	agctgcaggc	cagaatcaga	540
	acctacaacc	agcactacaa	caacctgctg	agaggcgccg	tgagccagag	actgtacatc	600
	ctgctgcctc	tggactgcgg	cgctgcctgac	aacctgagca	tggccgaccc	taacatcaga	660
	ttcctggaca	agctgcctca	gcagaccggc	gaccacgccg	gcatcaagga	cagagtgtac	720
	agcaacagca	tctacgagct	gctggagaac	ggccagagag	ccggcacctg	ctgtctggag	780
	tacgccaccc	ctctgcagac	cctgttcgcc	atgagccagt	acagccaggc	cggcttcagc	840
	agagaggaca	ccctggagca	ggccaagctg	ttctgcagaa	ccctggagga	catcctggcc	900
	gacgccccctg	agagccagaa	caactgcaga	ctgatcgctt	accaggagcc	tgccgacgac	960
	agcagcttca	gcctgagcca	ggaggtgtct	agacacctga	gacaggagga	gaaggaggag	1020
	gtgaccgtgg	gcagcctgaa	gaccagcgcc	gtgcctagca	ccagcaccat	gagccaggag	1080
	cctgagctgc	tgatcagcgg	catggagaag	cctctgcctc	tgagaaccga	cttcagc	1137

<210> 141
 <211> 1137
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Sintético: hu STING (R284M); sin etiqueta de epítipo; secuencia de nucleótidos

<400> 141	atgccccaca	gcagcctgca	cccctccatc	ccctgtccca	gaggccacgg	cgcccagaag	60
	gccgccctgg	tgctgctgag	cgctgcctg	gtgaccttat	ggggcctggg	cgagcccccc	120
	gagcacaccc	tgagatacct	ggtcctgcac	ctggccagcc	tccagctggg	cctgctgctc	180
	aacggcgtgt	gtagcctggc	cgaggagctg	agacacatcc	acagcagata	cagaggcagc	240
	tactggagaa	ccgtgagagc	ctgcctgggt	tgccactga	gaagaggagc	tctgctgctg	300
	ctgagcatct	acttctacta	ctcgtgccc	aacgtgtgtg	gccccccctt	cacctggatg	360
	ctggccctgc	tgggtctgag	ccaggccctg	aacatcctcc	tgggcctgaa	gggcctggcc	420
	cccgccgaga	taagcgccgt	ttgcgagaag	ggcaacttca	acgtggccca	tggcctggcc	480
	tggagctact	acatcggcta	cttacgcctg	atcctgcccg	agctgcaggc	cagaatcaga	540
	acctacaacc	agcattacaa	caacctgctg	agaggcgccg	tgagccagag	actgtatatc	600
	ctgctgcccc	tggactgcgg	cgctgcccgc	aacctgagca	tggccgaccc	caacatcaga	660
	ttcctggaca	agctccccca	gcagaccggc	gaccacgccg	gaatcaaaga	cagagtgtat	720
	agcaacagca	tctacgagct	gctggagaac	ggccagagag	ccggcacctg	ctgactggag	780
	tacgccaccc	ccttgagac	cctgtttgcc	atgagccagt	acagccaggc	cggcttcagc	840
	agagaggaca	tgctggagca	ggccaagctg	ttctgcagaa	ccctggagga	catcctggcc	900

gacgccccg agagccagaa caactgcaga ctgatcgct accaagagcc cgccgacgac 960
 agcagcttca gcttaagcca ggaggtgctg agacatctga gacaggagga gaaggaggag 1020
 gtgaccgtgg gcagcctcaa gaccagcgt gtgccctcta ccagcaccat gagccaggag 1080
 cccgagctgc tgatcagcgg catggagaag cccctgcccc tgagaacaga cttcagc 1137

<210> 142
 <211> 1137
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Sintético: Hu STING (R284K); sin etiqueta de epítipo; secuencia de nucleótidos

<400> 142
 atgccccata gcagcctgca cccagcatc ccctgcccc gagggcacgg cgcccagaag 60
 gccgccctgg tcctgctgag cgcctgcctg gtcaccctgt ggggcctggg cgagcccccc 120
 gagcacaccc tgagatacct ggtgctgcac ctgccagcc tgagctggg cctgctgctg 180
 aacggcgtgt gcagcctggc cgaggagctg agacacatcc acagcagata tagaggcagc 240
 tactggagaa ccgtgagagc ttgcctcggc tgccccctga gaagaggcgc cctgctgctg 300
 ctgagcatct acttttacta cagcctgccc aacgctgtgg gcccccttt cacgtggatg 360
 ctgccctgc tgggactgag ccaggccctg aacatcctgc tgggccttaa gggcctagcc 420
 cccgccgaga tcagcgccgt gtgcgagaag ggcaacttca atgtggcca cggcctggcc 480
 tggagctact acatcggcta cctgagactg atcctgccc agctgcaggc cagaatcaga 540
 acctacaatc agcactacaa caacctgctg agaggcgccg tgagccagag actgtacatc 600
 ctgctgcccc tggactgcgg cgtgcccgc aacctcagca tggccgacct caacatcaga 660
 ttcttgagaa agctgcccc gcagaccggc gaccacgccc gcatcaagga tcgctgttac 720
 agcaacagca tctacgagct gctggaaaac ggccagagag ccggaacctg cgtgctggag 780
 tacgccacac ccctgcagac cctgttcgcc atgagccagt acagccaggc cggcttcagc 840
 agagaggaca agctggagca ggccaagctg ttctgcagaa ccctggagga tatcctcgcc 900
 gacgccccg agagccagaa caactgcagg ctgatcgct accaggagcc cgctgacgac 960
 agcagcttca gcctgagcca ggaggtgctg agacatctgc gtcaagagga aaaggaggag 1020
 gtgaccgtgg gctccctgaa gaccagcgc gtgccagca ccagcaccat gagccaggag 1080
 cccgagctgc tgatcagcgg catggagaag cactgcccc tcagaaccga cttcagc 1137

<210> 143
 <211> 1137
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Sintético: Hu STING(N154S); sin etiqueta de epítipo; secuencia de nucleótidos

<400> 143
 atgcctcaca gcagcctgca ccctagcatc ccttgcccta gagggcacgg cgcccagaag 60
 gccgccctgg tgctgctgag gcctgcctg gtgaccctgt ggggcctggg cgagcctcct 120
 gagcacaccc tgagatacct ggtgctgcac ctggccagcc tgagctggg cctgctgctg 180
 aacggcgtgt gcagcctggc cgaggagctg agacacatcc acagcagata cagaggcagc 240
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<210> 144
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 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Sintético: Hu STING(V147L); sin etiqueta de epítipo; secuencia de nucleótidos

<400> 144
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<210> 145
 <211> 1137
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Sintético: Hu STING (E315Q); sin etiqueta de epítipo; secuencia de nucleótidos

<400> 145
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<210> 146
 <211> 1137
 <212> ADN
 <213> Secuencia artificial

<220>

<223> Sintético: Hu STING (R375A); sin etiqueta de epítipo; secuencia de nucleótidos

<400> 146

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gagcacaccc tgagatacct ggtgctgcac ctggccagcc tgcagctggg cctgctgctg	180
aacggcgtgt gcagcctggc cgaggagctg agacacatcc acagcagata cagaggcagc	240
tactggagaa ccgtgagagc ctgcctgggc tgccctctga gaagaggcgc cctgctgctg	300
ctgagcatct acttctacta cagcctgcct aacgccgtgg gccctccttt cacctggatg	360
ctggccctgc tgggcctgag ccaggccctg aacatcctgc tgggcctgaa gggcctggcc	420
cctgccgaga tcagcgccgt gtgcgagaag ggcaacttca acgtggcca cggcctggcc	480
tggagctact acatcggcta cctgagactg atcctgcctg agctgcaggc cagaatcaga	540
acctacaacc agcactacaa caacctgctg agaggcgccg tgagccagag actgtacatc	600
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<210> 147

<211> 1137

<212> ADN

<213> Secuencia artificial

<220>

<223> Sintético: Hu STING(V147L/N154S/V155M); sin etiqueta de epítipo; secuencia de nucleótidos

<400> 147

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aacggcgtgt gcagcctggc cgaggagctg agacacatcc acagcagata cagaggcagc	240
tactggagaa ccgtgagagc ctgcctgggc tgccctctga gaagaggcgc cctgctgctg	300
ctgagcatct acttctacta cagcctgcct aacgccgtgg gccctccttt cacctggatg	360
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<210> 148

<211> 1137

<212> ADN

<213> Secuencia artificial

<220>

<223> Sintético: Hu STING(R284M/V147L/N154S/V155M); sin etiqueta de epítipo; secuencia de nucleótidos de nucleótidos

<400> 148

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<210> 149
<211> 141
<212> ADN
<213> Secuencia artificial

<220>
<223> Sintético: 3 UTR utilizada en la construcción de STING V155M, que contiene el sitio de union a miR122

<400> 149
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ctcctcccct tcctgcaccc gtacccccca aacaccattg tcacactcca gtggtctttg 120
aataaagtct gagtgggcgg c 141

<210> 150
<211> 1257
<212> ADN
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(1257)
<223> superratón IRF3 S396D; sin etiqueta de epítipo

<400> 150
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ctggagggcg tagcctggct ggacgagagc agaaccagat tcagaatccc ctggaagcac 120
ggcctgagac aagacgccc gatggccgac ttcggcatct tccaggcctg ggccgaggcc 180
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gtgcccacct gcctgaaaga gctgctggag atggccagag agggcgggcg cagctccctg 1140

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aaaaccgtgg acctgcacat tgacaacagc cagcccatca gcctgaccag cgaccagtac 1200

aaggcctacc tgcaggacct ggtggaggac atggacttcc aggccaccgg caacatc 1257

<210> 151
<211> 1281
<212> ADN
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(1281)
<223> superhumano IRF3 S396D; sin etiqueta de epítipo

<400> 151
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ctggagggag tggcctgggt gaacaagagc agaaccagat tcagaatccc ctggaagcac 120
ggcctcagac aggacgccc gcaggaggac ttcggcattt ttcaggcttg ggccgaggcc 180
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<210> 152
<211> 1509
<212> ADN
<213> Secuencia artificial

<220>
<223> Sintético: isoforma A de Hu IRF7 de tipo salvaje; P037 sin etiqueta de epítipo

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cagcccgcc 1509
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<210> 153
 <211> 1509
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Sintético: Hu IRF7 constitutivamente activo S477D/S479D; P033 sin etiqueta de epítipo

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ggcagacca aggagaagag tctggtcctc gtgaagctgg agccctggct gtgcagagtg 1380
cacctggagg gcacccagcg tgaaggcgtg agcagcctgg attcaagcga cctggacctt 1440
tgcctaagca gcgctaactc actgtacgac gatatcgaat gcttcctgat ggaactggag 1500
cagcctgcc 1509
```

<210> 154
 <211> 1509
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Sintético: Hu IRF7 constitutivamente activo S475D/S477D/L480D; P034 sin etiqueta de epítipo

```
<400> 154
atggcccttg caccgagag ggccgcccc aggggtgctct tcggcgagtg gttactaggc 60
gaaattagca gcggctgcta tgaaggcctt cagtggctgg acgaggccag aacctgcttt 120
agagttcctt ggaagcattt cgccggaaa gatctctctg aagccgacgc cagaatattc 180
aaggcctggg ctgtcgccag gggcagggtg ccacctcca gccgagggtg cgccctccc 240
cctgaggctg agactgcgga aagggcgggc tggaagacca atttcagatg cgctctgaga 300
agcaccagac gttttgtgat gctaagagac aatagcggcg atcccgccga ccccataag 360
```

```

gtatacgcac tgagccgaga gctctgttgg agagaaggcc ccggcaccga ccagaccgag      420
gctgaagccc ctgcagccgt gccccccct caaggcgggc ccccgggccc cttcctggcc      480
catacccatg caggggttaca agcaccggg cccttgcccg cccagcggg agacaagggc      540
gacctcttac tgcaggccgt gcaacaaagt tgtctggcgg accacctgct gaccgcatca      600
tggggcgcg atcctgtgcc caccaaggca cccggcgaag gccaggagg cctgcccttg      660
accggcgcc ctgcctggcg acccggccta cctgctggcg aactgtatgg ctgggccgta      720
gagacgactc ccagccctgg ccacaaacc gcggcttga ccaccggcg agccgccgcc      780
cccagctctc cgcaccaggc cgagccttac ctacagccaa gccctagcgc ctgcaccgcc      840
gtgcaagaac ctagccccgg agccctggat gtgacaatca tgtacaagg tagaaccgta      900
ctgcaaaagg tgggtgggtca tcccagctgc acctttcttt acggcccacc cgaccctgcc      960
gtgagagcca cagaccaca acaggctgcc ttcccaagcc ccgccgaact gcccgatcag     1020
aaacagctga gatatacaga ggagcttctg cggcacgtag ctcccgccct acatctcgag     1080
ctgagggggc cacaactgtg ggccagacgc atgggcaaata gcaaggctta ctgggaagtg     1140
ggaggcccc ccggcagcgc atctcccagc acggccgcgt gcctgctgcc tagaaattgc     1200
gacaccccc tctttgactt ccgggtattc ttccaggagc tggtagagtt cagagccagg     1260
cagcggaggg gctccccag atacacaatc tacctgggct tcggacagga cctgtccgcc     1320
ggccgcccc agggaaagag cctggtgctg gtgaagctgg agccctggct gtgtagggtg     1380
cacctcgaag gcaccagag agaaggagt agctcgcttg atgacagcga tctgtcggat     1440
tgccttagca gcgccaacag cctgtatgat gatatcgagt gcttccttat ggaactggag     1500
cagcccgcc                                     1509

```

```

<210> 155
<211> 1509
<212> ADN
<213> Secuencia artificial

```

```

<220>
<223> Sintético: Hu IRF7 constitutivamente activo S475D/S476D/S477D/S479D/S483D/S487D; P035 sin etiqueta de epítipo

```

```

<400> 155
atggccctag cccccgaaag agcagctccc agagtgtgtg tcggcgaatg gctgcttggc      60
gagatcagca gcggctgcta cgaaggcctg cagtggctgg acgaagccc cacctgtttc     120
agagtgcctt ggaagcactt cgctagaaag gatttgagcg aggtgatgc tagaatcttt     180
aaggcttggg ctgtggcaag aggcagatgg ccgcctagta gcagaggggg cgacacctcc     240
cccagggctg agaccgctga gagagcaggg tggaaaacca acttcagatg cgcgctgaga     300
agcaccgcaa gattcgtgat gctacgtgac aatagcggcg acccgccga cccccacaaa     360
gtgtacgccc tgtcccgaga actttgctgg agagagggac ccggcaccga tcaaacagag     420
gctgagggcc cggccgctgt acccccgccc caaggaggcc cccagggccc ctttctggct     480
catacacatg ccggcctgca ggcaccggg cccctcccgg ctctgcccgg cgacaagggc     540
gatctccttc tccaggccgt gcagcagagc tgcctggccg atcacctgct gaccgcctcg     600
tggggcgccg acccgtgcc caccaaagcc ccgggtgaag gccaagagg gctcccttta     660
accggagcat gcgccggagg ccccgccctg ccagccggcg agttatatg ctgggctgtg     720
gagaccacac cctcccccg ccctcaacc gctgccctga ccaccggtga ggccgccgcc     780
cccagagacc cacaccaggc cgaaccctac ctgagcccta gccctagcgc ctgcaccgcc     840
gtgcaagaac ccagccccgg agccctggat gtgaccatta tgtacaagg ccggacagtg     900
ctgcaaaagg ttgtgggaca cccgagctgc acctttctgt acggtccgcc tgaccccgcc     960
gtgagagcca cggaccgca gcagggtggc ttccctcac ccgcggagct gcccgaccaa     1020
aagcaactca gatacacaga agaactattg cgtcacgtcg cggccggcct gcatctggag     1080
ctgagaggcc ccagctctg ggccagaagg atgggcaaata gcaagggtga ctgggagggtg     1140
ggaggcccc ccggcagcgc cagccccagc actcccgct gcctgctgcc cagaaattgc     1200
gacactccca tcttcgattt cagggtgttc ttccaggagc tgggtggagt cagagccagg     1260
cagagaaggg gtagccccag atacacaatc tatctaggct ttggacaaga tctgagcgcc     1320
ggccggccta agggaaaaag cctggtgctg gtaaagctgg agccgtggct ttgtagagtg     1380
cacctggagg ggacgcagcg agaggcgctg agcagcttag acgacgatga cttggatctg     1440
tgtctcgaca gcgccaacga cttgtacgac gacatcgagt gcttcctgat ggaactggag     1500
cagcccgcc                                     1509

```

<210> 156
 <211> 846
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Sintético: Hu IRF7 truncado constitutivamente activo 1-246 + 468-503; P032 sin etiqueta de epítipo

<400> 156
 atggccctgg cccccgagag agccgcccc agagtgtctt tcggcgagt gctgctgggc 60
 gagataagca gcggctgcta cgaaggctct cagtggctag acgaggccag aacctgtttt 120
 agagtgccct ggaagcactt cgctcgaaag gacctgtccg aggccgatgc tagaattttt 180
 aaggcttggg ccgtcgctag gggaagatgg cccctagca gtagaggcg cgccccct 240
 cccgaagccg agacggccga gagggccggc tggaaaacca atttcagatg cgccctgagg 300
 agcaccgcga gggtcgtaat gctgcgagac aatagcggcg atcctgcgga tcctcacaag 360
 gtttacgcct tgagtagaga actgtgtctg cgggagggcc ccggaaccga ccagacggag 420
 gcagaggcac ccgtgacctg gccccccct caaggaggac cccctggacc ctttctggcc 480
 cacaccacg ctggtctgca ggccccaggc ccactgcccg cccagcggg cgataagggt 540
 gacctgtcc tacaggcgtt gcaacagagc tgtctggccg accacctgtt gaccgccagc 600
 tggggggccg acccggtgcc caccaaagct cccggagagg gccaagaagg cctcccacta 660
 actggcgctt gcgcggggg cccgggatta cccgccggcg agctgtatgg ctgggccgtg 720
 gagaccacgc ccagccccga ggcgtgtctg tccctggaca gcagcagcct gacgtgtgc 780
 ctgagctccg ccaacagcct gtatgacgac atcgagtgtt tcctgatgga gctggaacaa 840
 cccgcc 846

<210> 157
 <211> 846
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Sintético: Hu IRF7 truncado constitutivamente activo 1-246 + 468-503 más S475D/S476D/S477D/S479D/S483D/S487D; P036 sin etiqueta de epítipo

<400> 157
 atggcactgg cgcctgaaag agccgctccg cgtgtgtctt tcggcgagt gctgctgggc 60
 gagatcagct ccggctgcta cgagggctta cagtggctgg acgaggccag aacctgtttt 120
 agagtgccct ggaagcactt cgcgagaaag gacctgagcg aggccgacgc cagaatcttc 180
 aaagcctggg cagtggctag gggcagatgg cctcccagca gccggggcg cgccccacc 240
 cccgaggccg aaaccgcca aagagctggc tggaaagacca acttcagatg cgccctgaga 300
 agcaccagaa gatttgtcat gctgagagat aattcaggag accccgccga ccctcacaag 360
 gtgtacgccc tgtccagaga gctgtgttgg agagagggcc ccggaaccga ccagaccgag 420
 gccgaggctc cagctgacct gccaccccc caaggcggac caccggccc cttcttggca 480
 catacgacg ccggcctcca ggctcccggc cctctgcccg cccctgtgtg tgacaaaggc 540
 gatctgtgct tgcaagccgt ccagcaatcc tgcttggctg accacctgtt gaccgctagc 600
 tggggagccg accccgttcc caccaaggct cccggagaag gacaggagg cctgcccctt 660
 accggcgctt gcgcggggg ccctggcttg cctgccggcg aactgtacgg ctgggccgtg 720
 gagaccacgc cttccccga ggcgtgtcc agcctggacg atgatgacct ggatctgtgc 780
 ctggacagcg ccaacgacct gtacgatgac atcgagtgtt ttttgatgga gctggagcag 840
 cccgcc 846

<210> 158
 <211> 1224
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Sintético: Hu IRF7 truncado 1-151 + 247-503; P038 sin etiqueta de epítipo; mutación nula

<400> 158
 atggccctgg cccccgagag agccgcgccc agagtgtgtt tcggcgaatg gctgctgggc 60
 gagatcagca gcggctgcta tgaggcctg cagtggctcg acgaagccag gacgtgcttc 120
 agatccccct ggaagcactt cgccagaaag gatctgagcg aggtgacgc cagaatcttc 180
 aaggcctggg cagttgctcg tgggagatgg cccccagct cgcgggggcg cgtcccccc 240
 cctgaggccg agaccgcca aagagccgga tggaaaacca actttcgatg cgccctcaga 300
 agcaccagac ggtttgtgat gctgagagat aacagcggcg accctgcaga ccccataaa 360

```

gtgtatgccc tgagcagaga gctgtgttgg cgagagggcc ccggaaccga ccaaaccgag 420
gccgagggcc ccgcccgtt acccccccct caaggccccc agcctgctgc tctgaccacg 480
ggagaagccg ccgctcctga gagccccac caagccgagc cctatctgag ccctagcccc 540
agcgctgca ccgccgtgca ggagccctca ccgggcgccc tagacgtgac catcatgtac 600
aaggggca cgggtgctga aaaggtggtg ggccaccca gctgcacctt cctgtacggc 660
cccccgacc ctgccgtgag agccaccgac cccagcaag tcgccttccc cagccccgcc 720
gagctgccc accagaagca gctgaggtac accgaggagt tgctgagaca tgtggcccc 780
ggcttgacc tcgagctgag agggccgag ctctgggcca gaagaatggg caagtgaag 840
gtgtactggg aggtgggagg cccccccggc agcgcgagcc caagcaccgc ggctgcctg 900
ctgcctagaa actgcgacac ccctatcttc gacttcagag tttttttcca ggagctggtc 960
gagttcagg ccagacagcg tagaggcagc cccagataca ccatctacct tggattcggc 1020
caggacctga gcgcccggc agccaaagag aagtccttgg tactggtgaa gctagagccc 1080
tggctgtgta ggggtgcatct ggaaggcacc caaagagagg gcgtaagctc gcttgacagc 1140
agcagcctca gcctgtgcct gagcagcgct aacagcttat acgacgacat cgagtgcctc 1200
ctgatggagc tggaacaacc cgcc 1224

```

```

<210> 159
<211> 1059
<212> ADN
<213> Secuencia artificial

```

```

<220>
<223> Sintético: Hu IRF7 truncado 152-503; P039 sin etiqueta de epítipo; mutación nula

```

```

<400> 159
atgggcggcc ctcccgggccc ttccctggcc catacacacg ccggcctaca ggctcctggc 60
cctctgcccg ccccgggcgg cgacaagggc gacctcctgc tgcaggccgt gcagcagtcc 120
tgtctggccg accacctgct gactgctagc tggggcgccg atcccgtgcc caccaaggcc 180
ccaggagagg ggcaagaggg cctgcctcta accggcgcat gcgcagggtg accaggcctc 240
ccgcccggcg agctgtatgg ttgggcccgtg gagacaaccc ccagccccgg cccgcagcct 300
gctgcgctga ccacaggcga ggccgctgcc cctgagagcc cccaccaagc tgaaccctac 360
ctgagcccca gccctctgc ctgcacagcg gtgcaggagc ccagtcccgg cgcttgagc 420
gtgaccatca tgtataaggg caggactgtg ttacaaaagg tagtgggcca cccaagtgtg 480
acctttctgt acggggcccc cgaccagcc gtgcgcgcca ccgaccccca gcagggtggc 540
ttcccagcc ccgctgagtt gcccgatcag aaacaactcc ggtacaccga ggaattactt 600
agacatgtgg ctcccggcct gcactgtgag cttagaggtc cacagtgtgt ggccagaaga 660
atgggcaagt gcaaggttta ttgggagggtc ggaggccccc cgggcagcgc cagccccagc 720
acccccgcct gtcttctgcc cagaaactgc gacaccccaa tcttcgattt cagagtgttt 780
ttccaggaac tgggtggagtt cagagcaagg caaagaagag gcagccctag atacaccatc 840
tacctgggct ttggccaaga cctgagcgcc ggccagacca aggaataatc cctggctcctg 900
gtgaaactgg agccctggct gtgcagagtc cacctggagg gcaccagag agagggcgctg 960
agcagcctgg actcgagcag cctgtccctg tgtctgagca gcgcgaattc gctatatgac 1020
gacatcgaat gctttctgat ggagctggaa cagcccgc 1059

```

```

<210> 160
<211> 1269
<212> ADN
<213> Secuencia artificial

```

```

<220>
<223> Sintético: KRAS(G12D)25mer_nt.STING(V155M)

```

```

<400> 160
atgcctcaca gcagcctcca ccctagcatc ccttgcccta gaggccacgg cggccagaag 60
gccgccctcg tgcttttaag cgctgtcttg gtgacctttt ggggcttggg cgagcctcca 120
gagcacacct tgagatattt ggtgtccac ctggccagcc ttcagctggg cttgttactc 180
aacggcggtg gcagcctggc cgaggagctg agacacatcc acagcagata cagaggcagc 240
tactggagaa ccgtgagagc gtgtctgggc tgccctctga gaagaggcgc cttgcttctt 300
ctcagtatct acttctacta ctccctgcct aacgccgtgg gccctccttt cacctggatg 360
ctggcactgc tcggcctcag ccaggccctg aacatcttgt tgggcttgaa gggcctggcc 420
cctgccgaga tcagcgccgt gtgcgagaag ggcaacttca acatggcca cggattggct 480
tggagctact acatcggcta cctgagactg atcctgcctg agctgcaggc cagaatcaga 540

```

```

acctacaacc agcactacaa caacctgctg cgcgggcgag tgagccagag actgtatat 600
ctgctgcctc tggactgcgg cgtgcctgac aacctgagca tggccgaccc taacatcaga 660
ttcctggaca agctgcctca gcagaccggc gaccacgccg gcatcaagga cagagtgtac 720
agcaacagca tctatgagct gctcgagaat ggccagagag ccggcacctg cgtgctggag 780
tacgccaccc ctctgcagac cctgttcgcc atgagccagt atagtcaagc tggcttcagc 840
agagaggaca gactggagca ggccaagctg ttctgcagaa ccctggagga cattctggct 900
gacgcccctg agagccagaa caactgccga ctgatcgct accaggaacc agccgacgac 960
agcagcttca gtctttctca ggaggttctt cgccacttgc gccaggagga gaaggaggag 1020
gtgaccgtgg gcagcctgaa gacctccgca gtccctagca ccagcaccat gagtccaggag 1080
ccggagctat taatcagcgg catggagaag cctcttccac tccgaaccga cttcagcgcc 1140
accaacttca gcctgctgaa gcaggcaggt gacgttgagg agaatccggg acctatgacc 1200
gagtacaagc tgggtggtgt gggcgccgac ggcgtgggca agagcgccct gaccatccag 1260
ctgatccag 1269

```

```

<210> 161
<211> 1269
<212> ADN
<213> Secuencia artificial

```

```

<220>
<223> Sintético: KRAS(G12D)25mer_ct.STING(V155M)

```

```

<400> 161
atgaccgagt acaagctagt agtcgtgggc gccgacggcg tgggcaagag cgccctcacc 60
atccagctaa tccaggccac caacttcagc ttgctcaagc aggccggcga cgtggaggag 120
aaccaggcc ctatgcctca cagcagcctt caccctagca tcccttgccc tagaggccac 180
ggcgcccaga aggcggccct ggtgctgctg agcgctgcc tggtgaccct gtggggcctg 240
ggcgagcctc ctgagcacac cctgagatat ctggtgcttc acctggccag ttacagctg 300
ggcctgcttc ttaacggcgt gtgcagcctg gccgaggagc tgagacacat ccacagcaga 360
tacagaggca gctactggag aaccgtgaga gcctgcctag gctgccctct gagaagaggc 420
gctctgttgc tactttccat ctacttctac tactccctgc ctaacgccgt gggccctcct 480
ttcacttga tgctggcgtt gctgggtctg agccaggccc tgaacatcct tctcggctctg 540
aaggccctgg cccctgccga gatcagcgcc gtgtgcgaga agggcaactt caacatggcc 600
cacggactcg cctggagcta ctacatcggc tacctgagac tgatcctgcc tgagctgcag 660
gccagaatca gaacctacaa ccagcactac aacaacctgc tgcgggggcg cgtgagccag 720
agactgtata tacttcttcc tctggactgc ggcgtgcctg acaacctgag catggccgac 780
cctaacatca gattcctgga caagctgcct cagcagaccg gcgaccacgc cggcatcaag 840
gacagagtgt acagcaactc catatatgag ctgctcgaga atggccagag agccggcacc 900
tgctgtctgg agtacgccac ccctctgcag accctgttcg ccatgagcca gtacagtcag 960
gctggattca gcagagagga cagactggag caggccaagc tgttctgcag gacttgag 1020
gacatactag cagacgcccc tgagagccag aacaactgca gactgattgc ctaccaggag 1080
cctgcgagac acagctcctt cagtctgagt caggaggtgt tgcggcactt acgccaagaa 1140
gagaaggagg aggtgaccgt gggcagcctg aagactagcg ctgtgcctag caccagcaca 1200
atgtcacagg agccggaatt gctaatacag ggcattggaga agcctctccc attacgtacc 1260
gacttcagc 1269

```

```

<210> 162
<211> 1419
<212> ADN
<213> Secuencia artificial

```

```

<220>
<223> Sintético: KRAS(G12D)25mer^3_nt.STING(V155M)

```

```

<400> 162
atgcctcaca gcagccttca ccctagcctc ccttgcccta gaggccacgg cgcccagaag 60
gccgccttag tgctccttag cgctgcctc gtgacctat ggggcttagg cgagcctcca 120
gagcacacct tgagatacct cgtcctccac ctggctagtc tacagctggg cttctcctc 180
aacggcgtgt gcagcctggc cgaggagctg agacacatcc acagcagata cagaggcagc 240
tactggagaa ccgtgagagc gtgcctgggc tgccctctga gaagaggcgc actgctgtta 300
ctcagcatct acttctacta ctacttgcca aacgccgtgg gccctcctt cacctggatg 360

```

```

ctggccttgc tcggattgag ccaggccctg aacattttac tgggattgaa gggcctggcc 420
cctgccgaga tcagcgccgt gtgcgagaag ggcaacttca acatggccca cggcctagct 480
tggagctact acatcggcta cctgagactg atcctgcctg agctgcaggc cagaatcaga 540
acctacaacc agcactacaa caacctgctg cgtggagcgg tgagccagag actgtatatc 600
ctcctgcctc tggactgcgg agtgcctgac aacctgagca tggccgaccc taacatcaga 660
ttcctggaca agctgcctca gcagaccggc gaccacgccg gcatcaagga cagagtgtac 720
agcaactcaa tctacgagct gttggagaat ggccagagag ccggcacctg cgtgctggag 780
tacgccaccc ctctgcagac cctgttcgcc atgagccagt actctcaggc aggttcagc 840
agagaggaca gactggagca ggccaagctg ttctgcagaa ccctggagga catcctggcg 900
gacgccccctg agagccagaa caactgccgg cttatcgctt accaggagcc agcagacgac 960
agcagcttct ctctctcaca agaggtagct cgccatcttc gccaggagga gaaggaggag 1020
gtgaccgtgg gcagcctgaa gacatccgcc gtacctagca ccagcaccat gtctcaggaa 1080
ccggaactgt tgatcagcgg catggagaag cctctgccac tgcgcaccga cttcagcgcc 1140
accaacttct ccctactgaa gcaagccggt gacgttgaag agaaccctgg ccctatgacc 1200
gagtacaagc tggtagtagt aggcgccgac ggcgtgggca agagcgccct gaccatccag 1260
ctgatccaga tgactgaata taagcttgtc gtcgtgggcg cagatggcgt tggtaagagc 1320
gcacttacaa ttcaactcat tcagatgacg gagtataagc tgggtggtggt cggagctgac 1380
ggcgtaggca agagtgcctt tactattcag ctaattcag 1419

```

```

<210> 163
<211> 1419
<212> ADN
<213> Secuencia artificial

```

```

<220>
<223> Sintético: KRAS(G12D)25mer^3_ct.STING(V155M)

```

```

<400> 163
atgaccgagt acaagcttgt ggtggttggc gccgacggcg tgggcaagag cgccttaacc 60
atccagctta tccagatgac agagtataag ctagtggtgg tcggcgagca cggagtggga 120
aagagtgcac taactattca actcatccaa atgaccgaat acaagctagt agttgtgggt 180
gcagatggcg tcggcaagtc tgcactgaca attcagctca tccaggccac caacttcagc 240
ctgctgaagc aggccggcga cgtggaggag aaccctggcc ctatgcctca cagcagcctg 300
caccctagca tcccttgccc tagaggccac ggcgcccaga aggccgccct ggtgctgctg 360
agcgctgcc tggtagacct gtggggcctg ggcgagcctc ctgagcacac cctgagatac 420
ctagttttgc acctggcttc tctgcagctg ggcctactgc tcaacggcgt gtgcagcctg 480
gccgaggagc tgagacacat ccacagcaga tacagaggca gctactggag aaccgtgaga 540
gcatgcttag gctgccctct gagaagaggc gctctgctcc tcttgtccat ctacttctac 600
tactcgctac ctaacgccgt gggccctcct ttcacctgga tgctggccct cttgggatta 660
agccaggccc tgaacatctt gctgggactg aagggcctgg cccctgccga gatcagcgcc 720
gtgtgcgaga agggcaactt caacatggcc cacggactcg cttggagcta ctacatcggc 780
tacctgagac tgatcctgcc tgagctgcag gccagaatca gaacctacaa ccagcactac 840
aacaacctgc tgcggggagc agtgagccag agactgtata ttctgctccc tctggactgc 900
ggcgtgcctg acaacctgag catggccgac cctaacatca gattcctgga caagctgcct 960
cagcagaccg gcgaccacgc cggcatcaag gacagagtgt acagcaacag catttacgag 1020
ctgctggaga acggccagag agccggcacc tgcgtgctgg agtacgccac ccctctgcag 1080
accctgttcg ccatgagcca gtactcccag gcaggattca gcagagagga cagactggag 1140
caggccaagc tgttctgccg tactcttgag gacatccttg cagacgcccc tgagagccag 1200
aacaactgcc ggttgattgc ctaccaggaa ccggcagacg acagctcatt ctccttgtct 1260
caggaggtcc ttagacacct gcggcaggag gagaaggagg aggtgaccgt gggcagcctg 1320
aagacatccg ccgtgcctag cacgtctacc atgtcccagg agccggaact gctaatacagc 1380
ggcatggaga agcctctgcc tctcaggacc gacttcagc 1419

```

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<210> 164
<211> 380
<212> PRT
<213> Secuencia artificial

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<220>
<223> Sintético: Hu STING (R284K) var; sin etiqueta de epítipo

```

<400> 164

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
1 5 10 15

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
20 25 30

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
35 40 45

Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
50 55 60

Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65 70 75 80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
85 90 95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
100 105 110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
115 120 125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
130 135 140

Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala
145 150 155 160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
165 170 175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
180 185 190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
195 200 205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
210 215 220

Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
225 230 235 240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
245 250 255

Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
260 265 270

Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Lys Leu Glu Gln Ala
275 280 285

Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
290 295 300

Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305 310 315 320

Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
325 330 335

Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
340 345 350

Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
355 360 365

Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser Thr
370 375 380

<210> 165

<211> 1140

<212> ADN

<213> Secuencia artificial

<220>

<223> Sintético: Hu STING (R284K) var; sin etiqueta de epítipo

<400> 165

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atgcccata gcagcctgca cccagcatc ccctgcccc gaggccacgg cgcccagaag      60
gccgccctgg tcctgctgag cgcagcctg gtcaccctgt ggggcctggg cgagcccccc    120
gagcacaccc tgagatacct ggtgctgcac ctcgccagcc tgcagctggg cctgctgctg    180
aacggcgtgt gcagcctggc cgaggagctg agacacatcc acagcagata tagaggcagc    240
tactggagaa ccgtgagagc ttgcctcggc tgccccctga gaagaggcgc cctgctgctg    300
ctgagcatct acttttacta cagcctgccc aacgctgtgg gcccccttt cacgtggatg    360
ctcgccctgc tgggactgag ccaggccctg aacatcctgc tgggccttaa gggcctagcc    420
cccgccgaga tcagcgccgt gtgcgagaag ggcaacttca atgtggccca cggcctggcc    480
tggagctact acatcggcta cctgagactg atcctgcccg agctgcaggc cagaatcaga    540
acctacaatc agcactacaa caacctgctg agaggcgccg tgagccagag actgtacatc    600
ctgctgcccc tggactgcgg cgtgcccgc aacctcagca tggccgaccc caacatcaga    660
ttcctggaca agctgcccc gcagaccggc gaccacgccg gcatcaagga tcgctgttac    720
agcaacagca tctacgagct gctggaaaac ggccagagag ccggaacctg cgtgctggag    780
tacgccacac ccctgcagac cctgttcgcc atgagccagt acagccaggc cggcttcagc    840
agagaggaca agctggagca ggccaagctg ttctgcagaa ccctggagga tatcctcgcc    900
gacgcccccg agagccagaa caactgcagg ctgatcgct accaggagcc cgctgacgac    960
agcagcttta gcctgagcca ggaggtgctg agacatctgc gtcaagagga aaaggaggag   1020
gtgaccgtgg gctccctgaa gaccagcgcc gtgccagca ccagcaccat gagccaggag   1080
cccagctgc tgatcagcgg catggagaag cactgcccc tcagaaccga cttcagcacc   1140

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<210> 166

<211> 186

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(186)

<223> Human KRAS sp/P01116[1-186]

<400> 166

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

Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
      20      25      30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
      35      40      45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
      50      55      60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
65      70      75      80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His His Tyr
      85      90      95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Glu Asp Val Pro Met Val
      100     105     110

Leu Val Gly Asn Lys Cys Asp Leu Pro Ser Arg Thr Val Asp Thr Lys
      115     120     125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Phe Ile Glu Thr
      130     135     140

Ser Ala Lys Thr Arg Gln Arg Val Glu Asp Ala Phe Tyr Thr Leu Val
145     150     155     160

Arg Glu Ile Arg Gln Tyr Arg Leu Lys Lys Ile Ser Lys Glu Glu Lys
      165     170     175

Thr Pro Gly Cys Val Lys Ile Lys Lys Cys
      180     185

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<210> 167
 <211> 570
 <212> ARN
 <213> Secuencia artificial

<220>
 <223> Sintético

<220>
 <221> misc_feature
 <223> 5' 7 MeGpppG 2'Ome - OH 3'; donde: A,C G y U = AMP, CMP, GMP y N1-psi-UMP, respectivamente; Me = metilo; p = fosfato inorgánico (secuencia de ARNm de concatémoro de KRAS; CX-012908)

<400> 167
 ggaaauaaga gagaaaagaa gaguaagaag aaauauaaga gccaccauga ccgaguacaa 60
 gcucgugguc gucggcgccg acgggguagg caaguccgcu cugaccuuc agcucaucca 120
 gaugacggag uacaaacucg ugguaugggg agccgugggu gugggcaaga gcgcgucac 180
 cauccaacuc auccaaauga ccgaauauaa acucgucgug gugggagccg gcgacguggg 240
 aaagagcgcc cuuaccuucc aguuaaucca gaugacagaa uacaagcugg ugguggucgg 300
 ugccugcggc guggguaagu ccgcccugac aauccagcug auccagugau aaugggcugg 360
 agccucggug gccaugcuuc uugcccuug gccuccccc cagcccccucc ucccuuccu 420
 gcacccguac ccccgugguc uuugaauaaa gucugagugg gcggcaaaaa aaaaaaaaaa 480
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 540
 aaaaaaaaaa aaaaaaaaaa aaaaaucuaag 570

<210> 168
 <211> 1429
 <212> ARN
 <213> Secuencia artificial

<220>
 <223> Sintético

<220>
 <221> misc_feature
 <223> 5' 7 MeGpppG 2'Ome - OH 3'; donde: A,C G y U = AMP, CMP, GMP y N1-psi-UMP, respectivamente; Me = metilo; p = fosfato inorgánico; subrayado = sitio de unión a miR-122 (secuencia de ARNm de STING; CX-012871)

<400> 168
 ggaaauaaga gagaaaagaa gaguaagaag aaauauaaga gccaccaugc cccacaguag 60
 ccuccacccc agcaucccu gccccagagg ccacggcgca cagaaggccg ccuggugcu 120
 gcugagcgcc ugucugguga ccugugggg ucugggcgag ccccccagc acaccugcg 180
 guaccucgug cugcaucugg ccagccugca gcugggccug cugcugaacg gcgugucag 240
 ccuggccgaa gagcugagac acauccacag cagauacaga ggcuccuacu ggagaaccgu 300
 cagagccugc cucggcuguc ccugagaag aggcgccug cugcuccuga gcaucuacuu 360
 cuacuacagc cugcccaacg ccguggggcc cccuucacc uggaugcugg cccugcuggg 420
 ccugagccag gcccugaaca uccugcuggg ccugaagggc uuggccccc ccgagaucuc 480
 cgccgugugc gagaagggca acuuaacau ggcccauggc cuugccuggu ccuacuacau 540
 cggcuaccug agacugauc ugcccagcu gcaggccaga aucagaaccu acaaccagca 600
 cuacaacaac cugcugagag gcgccgugag ccaaagacug uacaucugc ugcccugga 660
 cugcggcgug cccgacaacc uuagcauggc cgacccaac aucagauucc uggacaagcu 720
 gcccagcag accggcgacc acgccggcau caaggacaga guguacagca acagcaucua 780
 cgagcugcug gagaacggcc agagagccgg caccugcug cuggaguacg ccacccccu 840
 gcagaccug uucgccauga gccaguacag ccaggccggc uucagcagag aggacagacu 900
 ggagcaagcc aagcuguucu gcagaaccu ggaggacau cuggcggacg ccccgagag 960
 ccaaaacaac ugcagacuga ucgccuacca ggagcccgcc gacgacagca gcuucagccu 1020
 gagccaggaa gucgugagac accugagaca ggaagagaag gaggagguga ccgugggaag 1080
 ccugaagacc agcgccgugc ccagcaccag caccaugagc caggagccc agcugcugau 1140
 cagcggcaug gagaagcccc ugcccugag aaccgacuuc agcugauau aggcuggagc 1200
 cucgguggcc uagcuucuug cccuugggc cccccccag cccuccucc ccuuccugca 1260
 cccguacccc ccaaacacca uugucacacu ccaguggucu uugaauaaag ucugaguggg 1320
 cggcaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1380
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaucuaag 1429

<210> 169
 <211> 300

<212> ARN
 <213> Secuencia artificial
 <220>
 <223> Sintético: sec. nt. KRAS(G12D G12V G13D G12C) 100mer 4MUT
 <400> 169
 augaccgagu acaagcucgu ggucgucggc gccgacgggg uaggcaaguc cgcucugacc 60
 auucagcuca uccagaugac ggaguacaaa cucgugguag ugggagccgu gggugugggc 120
 aagagcgcgc ucaccaucca acucauccaa augaccgaau auaaacucgu cgugguggga 180
 gccggcgacg ugggaaagag cgcuccuacc auccaguuaa uccagaugac agaauacaag 240
 cugguggugg ucggugccug cggcgugggu aaguccgccc ugacaaucca gcugauccag 300
 <210> 170
 <211> 1137
 <212> ARN
 <213> Secuencia artificial
 <220>
 <223> Sintético: huSTING(V155M); sin etiqueta de epítipo; secuencia de nucleótidos
 <400> 170
 augccccaca guagccucca ccccgagcauc ccugcccca gagggcacgg cgcacagaag 60
 gccgcccugg ugcugcugag cgccugucug gugaccugug ggggucuggg cgagcccccc 120
 gagcacaccc ugcgguaccu cgugcugcau cuggccagcc ugcagcuggg ccugcugcug 180
 aacggcgugu gcagccuggc cgaagagcug agacacauc acagcagaua cagaggcucc 240
 uacuggagaa ccgucagagc cugccucggc ugucuccuga gaagaggcg ccugcugcuc 300
 cugagcaucu acuucuaa cagccugccc aacgccgugg gccccccuu caccuggaug 360
 cuggcccugc ugggcccugag ccaggcccug acauccugc ugggcccuga gggcuuggcc 420
 cccgccgaga ucuccgccgu gugcgagaag ggcaacuua acauggcca ugcccuugcc 480
 ugguccuacu acaucggcu ccugagacug auccugccc agcugcaggc cagaauca 540
 accuacaacc agcacuacaa caaccugcug agaggcgccg ugagccaaag acuguacau 600
 cugcugcccc uggacugcgg cgugcccagc aaccuuagca uggccgaccc caacaucaga 660
 uuccuggaca agcugccca gcagaccggc gaccacgccg gcaucaagga cagaguguac 720
 agcaacagca ucuacgagcu gcuggagaac ggccagagag ccggcaccug cgugcuggag 780
 uacgccaccc ccugcagac ccuguucgcc augagccagu acagccaggc cggcuucagc 840
 agagaggaca gacuggagca agccaagcug uucugcagaa ccuggagga cauccuggcg 900
 gacgcccccg agagccaaaa caacugcaga cugaucgccu accaggagcc cgccgacgac 960
 agcagcuua gccugagcca ggaagugcug agacaccuga gacaggaaga gaaggaggag 1020
 gugaccgugg gaagccuga gaccagcgcc gugcccagca ccagcaccu gagccaggag 1080
 cccgagcugc ugaucagcgg cauggagaag cccugcccc ugagaaccga cuucagc 1137
 <210> 171
 <211> 85
 <212> ARN
 <213> Secuencia artificial
 <220>
 <223> Sintético: mir-122
 <400> 171
 ccuagcaga gcuguggagu gugacaaugg uguuuguguc uaaacuaa aacgccauua 60
 ucacacuaaa uagcuacugc uaggc 85
 <210> 172
 <211> 22
 <212> ARN
 <213> Secuencia artificial
 <220>
 <223> Sintético: mir-122-3p_
 <400> 172
 aacgccauua ucacacuaaa ua 22
 <210> 173
 <211> 22
 <212> ARN
 <213> Secuencia artificial
 <220>
 <223> Sintético: mir-122-3p binding site
 <400> 173
 uauuuagugu gauaauggcg uu 22

<210> 174
 <211> 22
 <212> ARN
 <213> Secuencia artificial

 <220>
 <223> Sintético: mir-122-5p

 <400> 174
 uggaguguga caaugguguu ug 22

 <210> 175
 <211> 22
 <212> ARN
 <213> Secuencia artificial

 <220>
 <223> Sintético: sitio de unión a mir-122-5p

 <400> 175
 caaacacc au ugucacacuc ca 22

 <210> 176
 <211> 46
 <212> ARN
 <213> Secuencia artificial

 <220>
 <223> Sintético: 5 UTR

 <400> 176
 ggaaauaaga gagaaaagaa gaguaagaag aaauauaaga gccacc 46

 <210> 177
 <211> 12
 <212> ADN
 <213> Secuencia artificial

 <220>
 <223> Sintético: elemento de ARN rico en GC

 <400> 177
 ccgccgccgc cg 12

 <210> 178
 <211> 15
 <212> ADN
 <213> Secuencia artificial

 <220>
 <223> Sintético: elemento de ARN rico en GC

 <400> 178
 ccgccgccgc cgccg 15

 <210> 179
 <211> 10
 <212> ADN
 <213> Secuencia artificial

 <220>
 <223> Sintético: V1 - elemento de ARN rico en GC

 <400> 179
 ccccgccgcc 10

 <210> 180
 <211> 41
 <212> ADN
 <213> Secuencia artificial

 <220>
 <223> Sintético: 5UTR

 <400> 180
 gggaaataag agagaaaaga agagtaagaa gaaatataag a 41

 <210> 181
 <211> 57
 <212> ADN
 <213> Secuencia artificial

 <220>
 <223> Sintético: V1-UTR

 <400> 181
 gggaaataag agagaaaaga agagtaagaa gaaatataag accccggcgc cgccacc 57

 <210> 182
 <211> 54
 <212> ADN
 <213> Secuencia artificial

 <220>

<223> Sintético: V2-UTR

<400> 182
gggaaataag agagaaaaga agagtaagaa gaaatataag accccggcgc cacc 54

<210> 183
<211> 45
<212> PRT
<213> Secuencia artificial

<220>
<223> Sintético: KRAS G12C 15mer^3

<400> 183
Met Lys Leu Val Val Val Gly Ala Cys Gly Val Gly Lys Ser Ala Met
1 5 10 15

Lys Leu Val Val Val Gly Ala Cys Gly Val Gly Lys Ser Ala Met Lys
20 25 30

Leu Val Val Val Gly Ala Cys Gly Val Gly Lys Ser Ala
35 40 45

<210> 184
<211> 225
<212> ADN
<213> Secuencia artificial

<220>
<223> Sintético: secuencia de nucleótidos de KRAS G12C 25mer^3

<400> 184
atgaccgagt acaagctcgt ggttggtggc gcctgcggcg tgggcaagag cgccctcacc 60
atccagctca tccagatgac agagtataag ttagtcgttg tcggagcttg cggagttgga 120
aagtcggcgc tcaccattca actcatacaa atgacagaat ataagttagt ggtggtgggt 180
gcgtgtggcg ttggcaagag tgcgcttact atccagctca ttcag 225

<210> 185
<211> 92
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: 5 UTR

<400> 185
ucaagcuuuu ggaccucgu acagaagcua auacgacuca cuauaggga auaagagaga 60
aaagaagagu aagaagaaau auaagagcca cc 92

<210> 186
<211> 119
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: 3 UTR

<400> 186
ugauaaauagg cuggagccuc gguggccaug cuucuugccc cuugggccuc ccccagccc 60
cuccucccu uccugcacc guacccccgu ggucuuugaa uaaagucuga gugggcggc 119

<210> 187
<211> 164
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: 3 UTR con sitios mi-122 y mi-142.3p

<400> 187
ugauaaauagg cuggagccuc gguggccaug cuucuugccc cuugggccca aacaccauug 60
ucacacucca uccccccagc ccuccuccc cuuccuccau aaaguaggaa acacuacaug 120
cacccguacc ccguggucu uugaauaaag ucugaguggg cggc 164

<210> 188
<211> 66
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: Secuencia de nucleótidos que codifica el péptido 2A

<400> 188
ggaagcggag cuacuaacuu cagccugcug aagcaggcug gagacgugga ggagaacccu 60
ggaccu 66

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<210> 189
<211> 108
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: Secuencia de nucleótidos que codifica el péptido 2A

<400> 189
uccggacuca gaucgggga ucuaaaauu gucgcuccug ucaaacaac ucuuaacuuu    60
gauuuacuca aacuggcugg ggauguagaa agcaauccag guccacuc                108

<210> 190
<211> 75
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: secuencia de nucleótidos de KRAS G12D 25mer

<400> 190
augaccgagu acaagcuggu gguggugggc gccgacggcg ugggcaagag cgcccugacc    60
auccagcuga uccag                                                    75

<210> 191
<211> 75
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: secuencia de nucleótidos de KRAS G12V 25mer

<400> 191
augaccgagu acaagcuggu gguggugggc gccgugggcg ugggcaagag cgcccugacc    60
auccagcuga uccag                                                    75

<210> 192
<211> 75
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: secuencia de nucleótidos de KRAS G13D 25mer

<400> 192
augaccgagu acaagcuggu gguggugggc gccggcgacg ugggcaagag cgcccugacc    60
auccagcuga uccag                                                    75

<210> 193
<211> 225
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: secuencia de nucleótidos de KRAS G12D 25mer^3

<400> 193
augaccgagu acaaguuagu gguugugggc gccgacggcg ugggcaagag cgcccucacc    60
auccagcuua uccagaugac ggaauauaag uuaguaguag ugggagccga cggugucggc    120
aaguccgcuu ugaccauuca acuuauucag augacagagu auaagcuggu cguuguaggc    180
gcagacggcg uuggaaaguc ggcacugacg auccaguuga uccag                225

<210> 194
<211> 225
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: secuencia de nucleótidos de KRAS G12V 25mer^3

<400> 194
augaccgagu acaagcucgu cguggugggc gccgugggcg ugggcaagag cgcccuaacc    60
auccaguuga uccagaugac cgaauauaag cucgugguag ugggagcggg gggcguuggc    120
aagucagcgc uaacaauaca acuaauccaa augaccgaau acaagcuagu uguagucggg    180
gccgucggcg uuggaaaguc agcccuuaca auccagcuca uucag                225

<210> 195
<211> 225
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: secuencia de nucleótidos de KRAS G13D 25mer^3

<400> 195
augaccgagu acaagcucgu agugguuggc gccggcgacg ugggcaagag cgcccuaacc    60

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auccagcuca uccagaugac agaauuaag cuugugguug ugggagcagg agacguggga 120
aagagugcgu ugacgauuca acucauacag augaccgaau acaaguuggu gguggucggc 180
gcaggugacg uugguaaguc ugcacuaacu auacaacuga uccag 225

<210> 196
<211> 75
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: secuencia de nucleótidos de KRAS G12C 25mer

<400> 196
augaccgagu acaagcuggu gguggugggc gccugcggcg ugggcaagag cgcccugacc 60
auccagcuga uccag 75

<210> 197
<211> 225
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: secuencia de nucleótidos de KRAS G12C 25mer^3

<400> 197
augaccgagu acaagcucgu gguuguuggc gccugcggcg ugggcaagag cgcccucacc 60
auccagcuca uccagaugac agaguuaag uuagucguug ucggagcuug cggaguugga 120
aagucggcg ucaccauua acucauacaa augacagaau auaaguugu gguggugggg 180
gcuugugcg ugggcaagag ugcgcuuacu auccagcuca uucag 225

<210> 198
<211> 75
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: secuencia de nucleótidos de KRAS WT 25mer

<400> 198
augaccgagu acaagcuggu gguggugggc gccggcggcg ugggcaagag cgcccugacc 60
auccagcuga uccag 75

<210> 199
<211> 47
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: Secuencia 5 UTR; sin promotor

<400> 199
gggaaauaag agagaaaaga agaguaagaa gaaauuaag agccacc 47

<210> 200
<211> 225
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: sec. nt. KRAS(G12D G12V G13D) 75mer 3MUT

<400> 200
augaccgagu acaagcucgu uguagucggc gccgacggcg ugggcaagag cgccuugacc 60
auccaguuga uccagaugac cgaauuaag uuggugugg uaggcgagc gggaguuggc 120
aagucagcac ucacaauuca gcucauuaa augacagaau acaaguugu cguuguagga 180
gcaggcgacg ucggcaagag ugccuuaacc auucaacuaa uccag 225

<210> 201
<211> 1137
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: Hu STING(R284T); sin etiqueta de epítipo; secuencia de nucleótidos

<400> 201
augccucaca gcagccugca cccuagcauc ccuugcccua gaggccacgg cgcccagaag 60
gccgcccugg ugcugcugag cgccugccug gugaccuggu ggggcccugg cgagccuccu 120
gagcacaccc ugagauaccu ggugcugcac cuggccagcc ugagcuggg ccugcugcug 180
aacggcgugu gcagccuggc cgaggagcug agacacauc acagcagaua cagaggcagc 240
uacuggagaa ccgugagagc cugccugggc ugcccucuga gaagaggcg ccugcugcug 300

cugagcaucu	acuucuacua	cagccugccu	aacgccgugg	gccuccuuu	caccuggaug	360
cuggcccugc	ugggccugag	ccaggcccug	aacauccugc	ugggccugaa	gggccuggcc	420
ccugccgaga	ucagcgccgu	gugcgagaag	ggcaacuuca	acguggcca	cggccuggcc	480
uggagcuacu	acaucggcua	ccugagacug	auccugccug	agcugcaggc	cagaauca	540
accuacaacc	agcacuacaa	caaccugcug	agaggcgccg	ugagccagag	acuguacauc	600
cugcugccuc	uggacugcgg	cgugccugac	aaccugagca	uggccgaccc	uaacaucaga	660
uuccuggaca	agcugccuca	gcagaccggc	gaccacgccg	gcaucaagga	cagaguguac	720
agcaacagca	ucuacgagcu	gcuggagaa	ggccagagag	ccggcaccug	cgugcuggag	780
uacgccaccc	cucugcagac	ccuguucgcc	augagccagu	acagccaggc	cggcuucagc	840
agagaggaca	cccuggagca	ggccaagcug	uucugcagaa	cccuggagga	cauccuggcc	900
gacgccccug	agagccagaa	caacugcaga	cugaucgccu	accaggagcc	ugccgacgac	960
agcagcuuca	gccugagcca	ggaggugcug	agacaccuga	gacaggagga	gaaggaggag	1020
gugaccgugg	gcagccugaa	gaccagcgcc	gugccuagca	ccagcaccu	gagccaggag	1080
ccugagcugc	ugaucagcgg	cauggagaag	ccucugccuc	ugagaaccga	cuucagc	1137

<210> 202
 <211> 1137
 <212> ARN
 <213> Secuencia artificial

<220>
 <223> Sintético: hu STING (R284M); sin etiqueta de epítipo; secuencia de nucleótidos

<400> 202	
augccccaca	gcagccugca cccuccauc cccuguccca gaggccacgg cgcccagaag 60
gccgcccugg	ugcugcugag cgccugccug gugaccuuau ggggccuggg cgagcccccc 120
gagcacaccc	ugagauaccu gguccugcac cuggccagcc uccagcuggg ccugcugcuc 180
aacggcgugu	guagccuggc cgaggagcug agacacaucc acagcagaua cagaggcagc 240
uacuggagaa	ccgugagagc cugccugggu ugcccacuga gaagaggagc ucugcugcug 300
cugagcaucu	acuucuacua cucgcugccc aacgcugugg gccccccuu caccuggaug 360
cuggcccugc	ugggucugag ccaggcccug aacauccucc ugggccugaa gggccuggcc 420
cccgccgaga	uaagcgccgu uugcgagaag ggcaacuuca acguggcca uggccuggcc 480
uggagcuacu	acaucggcua cuuacgccug auccugcccg agcugcaggc cagaauca 540
accuacaacc	agcauuacaa caaccugcug agaggcgccg ugagccagag acuguauauc 600
cugcugcccc	uggacugcgg cgugcccagc aaccugagca uggccgaccc caacaucaga 660
uuccuggaca	agcuccccca gcagaccggc gaccacgccg gaaucaaga cagaguguau 720
agcaacagca	ucuacgagcu gcuggagaa ggccagagag ccggcaccug cguacuggag 780
uacgccaccc	ccuugcagac ccuguuugcc augagccagu acagccaggc cggcuucagc 840
agagaggaca	ugcuggagca ggccaagcug uucugcagaa cccuggagga cauccuggcc 900
gacgcccccg	agagccagaa caacugcaga cugaucgccu accaagagcc cgccgacgac 960
agcagcuuca	gcuaaagcca ggaggugcug agacaucuga gacaggagga gaaggaggag 1020
gugaccgugg	gcagccucaa gaccagcgcu gugcccucua ccagcaccu gagccaggag 1080
cccagcugc	ugaucagcgg cauggagaag cccugcccc ugagaacaga cuucagc 1137

<210> 203
 <211> 1137
 <212> ARN
 <213> Secuencia artificial

<220>
 <223> Sintético: Hu STING (R284K); sin etiqueta de epítipo; secuencia de nucleótidos

<400> 203	
augccccaua	gcagccugca ccccagcauc cccugcccca gaggccacgg cgcccagaag 60
gccgcccugg	uccugcugag cgcaugccug gucaccuugu ggggccuggg cgagcccccc 120
gagcacaccc	ugagauaccu ggugcugcac cucgccagcc ugagcuggg ccugcugcug 180
aacggcgugu	gcagccuggc cgaggagcug agacacaucc acagcagaua uagaggcagc 240
uacuggagaa	ccgugagagc uugccucggc ugccccuga gaagaggcgc ccugcugcug 300
cugagcaucu	acuuuacua cagccugccc aacgcugugg gccccccuu caguggaug 360
cucgcccugc	ugggacugag ccaggcccug aacauccugc ugggccuuaa gggccuagcc 420
cccgccgaga	ucagcgccgu gugcgagaag ggcaacuuca auguggcca cggccuggcc 480
uggagcuacu	acaucggcua ccugagacug auccugcccg agcugcaggc cagaauca 540

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accuacaauc agcacuacaa caaccugcug agaggcgccg ugagccagag acuguacauc      600
cugcugcccc uggacugcgg cgugcccgac aaccucagca uggccgaccc caacaucaga      660
uuccuggaca agcugcccca gcagaccggc gaccacgccg gcaucaagga ucgcguguac      720
agcaacagca ucuacgagcu gcuggaaaac ggccagagag ccggaaccug cgugcuggag      780
uacgccacac ccugcagac ccuguucgcc augagccagu acagccaggc cggcuucagc      840
agagaggaca agcuggagca ggccaagcug uucugcagaa ccuggagga uaucucgcc      900
gacgcccccg agagccagaa caacugcagg cugaucgcu accaggagcc cgugacgac      960
agcaguuua gccugagcca ggaggugcug agacaucugc gucaagagga aaaggaggag     1020
gugaccgugg gcuccugaa gaccagcgcc gugccagca ccagcaccu gagccaggag     1080
cccgagcugc ugaucagcgg cauggagaag ccacugcccc ucagaaccga cuucagc      1137

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<210> 204
<211> 1137
<212> ARN
<213> Secuencia artificial

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<220>
<223> Sintético: Hu STING(N154S); sin etiqueta de epítipo; secuencia de nucleótidos

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<400> 204
augccucaca gcagccugca ccuagcauc ccuugcccua gaggccacgg cgcccagaag      60
gccgcccugg ugcugcugag cgccugccug gugaccugug ggggcccugg cgagccuccu     120
gagcacaccc ugagauaccu ggugcugcac cuggccagcc ugcagcuggg ccugcugcug     180
aacggcgugu gcagccuggc cgaggagcug agacacauc acagcagaua cagaggcagc     240
uacuggagaa ccgugagagc cugccugggc ugcccucuga gaagaggcgc ccugcugcug     300
cugagcaucu acuucuacua cagccugccu aacgccgugg gccuccuuu caccuggaug     360
cuggcccugc ugggcccugag ccaggcccug acauccugc ugggcccugaa gggccuggcc     420
ccugccgaga ucagcgccgu gugcgagaag ggcaacuua gcguggccca cggccuggcc     480
uggagcuacu acaucggcu ccugagacug auccugccug agcugcaggc cagaaucaga     540
accuacaacc agcacuacaa caaccugcug agaggcgccg ugagccagag acuguacauc     600
cugcugccuc uggacugcgg cgugccugac aaccugagca uggccgaccc uaacaucaga     660
uuccuggaca agcugccuca gcagaccggc gaccacgccg gcaucaagga cagaguguac     720
agcaacagca ucuacgagcu gcuggagaac ggccagagag ccggcaccug cgugcuggag     780
uacgccaccc cucugcagac ccuguucgcc augagccagu acagccaggc cggcuucagc     840
agagaggaca gacuggagca ggccaagcug uucugcagaa ccuggagga cauccuggcc     900
gacgccccug agagccagaa caacugcaga cugaucgcu accaggagcc ugccgacgac     960
agcagcuua gccugagcca ggaggugcug agacaccuga gacaggagga gaaggaggag     1020
gugaccgugg gcagccugaa gaccagcgcc gugccuagca ccagcaccu gagccaggag     1080
ccugagcugc ugaucagcgg cauggagaag ccucugccuc ugagaaccga cuucagc      1137

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<210> 205
<211> 1137
<212> ARN
<213> Secuencia artificial

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<220>
<223> Sintético: Hu STING(V147L); sin etiqueta de epítipo; secuencia de nucleótidos

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```

<400> 205
augccucaca gcagccugca ccuagcauc ccuugcccua gaggccacgg cgcccagaag      60
gccgcccugg ugcugcugag cgccugccug gugaccugug ggggcccugg cgagccuccu     120
gagcacaccc ugagauaccu ggugcugcac cuggccagcc ugcagcuggg ccugcugcug     180
aacggcgugu gcagccuggc cgaggagcug agacacauc acagcagaua cagaggcagc     240
uacuggagaa ccgugagagc cugccugggc ugcccucuga gaagaggcgc ccugcugcug     300
cugagcaucu acuucuacua cagccugccu aacgccgugg gccuccuuu caccuggaug     360
cuggcccugc ugggcccugag ccaggcccug acauccugc ugggcccugaa gggccuggcc     420
ccugccgaga ucagcgcccu gugcgagaag ggcaacuua acguggccca cggccuggcc     480
uggagcuacu acaucggcu ccugagacug auccugccug agcugcaggc cagaaucaga     540
accuacaacc agcacuacaa caaccugcug agaggcgccg ugagccagag acuguacauc     600
cugcugccuc uggacugcgg cgugccugac aaccugagca uggccgaccc uaacaucaga     660
uuccuggaca agcugccuca gcagaccggc gaccacgccg gcaucaagga cagaguguac     720

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agcaacagca	ucuacgagcu	gcuggagaa	ggccagagag	ccggcaccug	cgugcuggag	780
uacgccaccc	cucugcagac	ccuguucgcc	augagccagu	acagccaggc	cgguucagc	840
agagaggaca	gacuggagca	ggccaagcug	uucugcagaa	cccuggagga	cauccuggcc	900
gacgccccug	agagccagaa	caacugcaga	cugaucgccu	accaggagcc	ugccgacgac	960
agcagcuuca	gccugagcca	ggaggugcug	agacaccuga	gacaggagga	gaaggaggag	1020
gugaccgugg	gcagccugaa	gaccagcgcc	gugccuagca	ccagcaccu	gagccaggag	1080
ccugagcugc	ugaucagcgg	cauggagaag	ccucugccuc	ugagaaccga	cuucagc	1137

<210> 206
 <211> 1137
 <212> ARN
 <213> Secuencia artificial

<220>
 <223> Sintético: Hu STING (E315Q); sin etiqueta de epítipo; secuencia de nucleótidos

<400> 206						
augccucaca	gcagccugca	cccuagcauc	ccuugcccua	gaggccacgg	cgcccagaag	60
gccgcccugg	ugcugcugag	cgccugccug	gugacccugu	ggggccuggg	cgagccuccu	120
gagcacaccc	ugagauaccu	ggugcugcac	cuggccagcc	ugcagcuggg	ccugcugcug	180
aacggcgugu	gcagccuggc	cgaggagcug	agacacauc	acagcagaua	cagaggcagc	240
uacuggagaa	ccgugagagc	cugccugggc	ugcccucuga	gaagaggcgc	ccugcugcug	300
cugagcaucu	acuucuacua	cagccugccu	aacgccgugg	gccuccuuu	caccuggaug	360
cuggcccugc	ugggcccugag	ccaggcccug	aacaucugc	ugggcccugaa	gggcccuggcc	420
ccugccgaga	ucagcgccgu	gugcgagaag	ggcaacuua	acguggccca	cgcccuggcc	480
uggagcuacu	acaucggcua	ccugagacug	auccugccug	agcugcaggc	cagaauca	540
accuacaacc	agcacuacaa	caaccugcug	agaggcgccg	ugagccagag	acuguacauc	600
cugcugccuc	uggacugcgg	cgugccugac	aaccugagca	uggccgaccc	uaacaucaga	660
uuccuggaca	agcugccuca	gcagaccggc	gaccacgccg	gcaucaagga	cagaguguac	720
agcaacagca	ucuacgagcu	gcuggagaa	ggccagagag	ccggcaccug	cgugcuggag	780
uacgccaccc	cucugcagac	ccuguucgcc	augagccagu	acagccaggc	cgguucagc	840
agagaggaca	gacuggagca	ggccaagcug	uucugcagaa	cccuggagga	cauccuggcc	900
gacgccccug	agagccagaa	caacugcaga	cugaucgccu	accaggagcc	ugccgacgac	960
agcagcuuca	gccugagcca	ggaggugcug	agacaccuga	gacaggagga	gaaggaggag	1020
gugaccgugg	gcagccugaa	gaccagcgcc	gugccuagca	ccagcaccu	gagccaggag	1080
ccugagcugc	ugaucagcgg	cauggagaag	ccucugccuc	ugagaaccga	cuucagc	1137

<210> 207
 <211> 1137
 <212> ARN
 <213> Secuencia artificial

<220>
 <223> Sintético: Hu STING (R375A); sin etiqueta de epítipo; secuencia de nucleótidos

<400> 207						
augccucaca	gcagccugca	cccuagcauc	ccuugcccua	gaggccacgg	cgcccagaag	60
gccgcccugg	ugcugcugag	cgccugccug	gugacccugu	ggggccuggg	cgagccuccu	120
gagcacaccc	ugagauaccu	ggugcugcac	cuggccagcc	ugcagcuggg	ccugcugcug	180
aacggcgugu	gcagccuggc	cgaggagcug	agacacauc	acagcagaua	cagaggcagc	240
uacuggagaa	ccgugagagc	cugccugggc	ugcccucuga	gaagaggcgc	ccugcugcug	300
cugagcaucu	acuucuacua	cagccugccu	aacgccgugg	gccuccuuu	caccuggaug	360
cuggcccugc	ugggcccugag	ccaggcccug	aacaucugc	ugggcccugaa	gggcccuggcc	420
ccugccgaga	ucagcgccgu	gugcgagaag	ggcaacuua	acguggccca	cgcccuggcc	480
uggagcuacu	acaucggcua	ccugagacug	auccugccug	agcugcaggc	cagaauca	540
accuacaacc	agcacuacaa	caaccugcug	agaggcgccg	ugagccagag	acuguacauc	600
cugcugccuc	uggacugcgg	cgugccugac	aaccugagca	uggccgaccc	uaacaucaga	660
uuccuggaca	agcugccuca	gcagaccggc	gaccacgccg	gcaucaagga	cagaguguac	720
agcaacagca	ucuacgagcu	gcuggagaa	ggccagagag	ccggcaccug	cgugcuggag	780
uacgccaccc	cucugcagac	ccuguucgcc	augagccagu	acagccaggc	cgguucagc	840
agagaggaca	gacuggagca	ggccaagcug	uucugcagaa	cccuggagga	cauccuggcc	900
gacgccccug	agagccagaa	caacugcaga	cugaucgccu	accaggagcc	ugccgacgac	960

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agcagcuuca gccugagcca ggaggugcug agacaccuga gacaggagga gaaggaggag      1020
gugaccgugg gcagccugaa gaccagcgcc gugccuagca ccagcaccuau gagccaggag      1080
ccugagcugc ugaucagcgg cauggagaag ccucugccuc uggccaccga cuucagc        1137

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<210> 208
<211> 1137
<212> ARN
<213> Secuencia artificial

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<220>
<223> Sintético: Hu STING(V147L/N154S/V155M); sin etiqueta de epítipo; secuencia de nucleótidos

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<400> 208
augccucaca gcagccugca cccuagcauc ccuugcccua gagggcacgg cgcccagaag      60
gccgcccugg ugcugcugag cgccugccug gugaccuugu gggggccuggg cgagccuccu    120
gagcacaccc ugagauaccu ggugcugcac cuggccagcc ugcagcuggg ccugcugcug      180
aacggcgugu gcagccuggc cgaggagcug agacacaucc acagcagaua cagaggcagc      240
uacuggagaa ccgugagagc cugccugggc ugcccucuga gaagaggcgc ccugcugcug      300
cugagcaucu acuucuacua cagccugccu aacgccgugg gccuccuuu caccuggaug      360
cuggcccugc ugggcccugag ccaggcccug acauccugc ugggcccugaa gggccuggcc      420
ccugccgaga ucagcgcccu gugcgagaag ggcaacuua gcauggcca cggccuggcc      480
uggagcuacu acaucggcuu ccugagacug auccugccug agcugcaggc cagaaucaga      540
accuacaacc agcacuacaa caaccugcug agaggcgccg ugagccagag acuguacauc      600
cugcugccuc uggacugcgg cgugccugac aaccugagca uggccgaccc uaacaucaga      660
uuccuggaca agcugccuca gcagaccggc gaccacgccg gcaucaagga cagaguguac      720
agcaacagca ucuacgagcu gcuggagaac ggccagagag ccggcaccug cgugcuggag      780
uacgccaccc cucugcagac ccuguucgcc augagccagu acagccaggc cggcuucagc      840
agagaggaca gacuggagca ggccaagcug uucugcagaa cccuggagga cauccuggcc      900
gacgccccug agagccagaa caacugcaga cugaucgccu accaggagcc ugccgacgac      960
agcagcuuca gccugagcca ggaggugcug agacaccuga gacaggagga gaaggaggag     1020
gugaccgugg gcagccugaa gaccagcgcc gugccuagca ccagcaccuau gagccaggag     1080
ccugagcugc ugaucagcgg cauggagaag ccucugccuc ugagaaccga cuucagc       1137

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<210> 209
<211> 1137
<212> ARN
<213> Secuencia artificial

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<220>
<223> Sintético: Hu STING(R284M/V147L/N154S/V155M); sin etiqueta de epítipo; secuencia de nucleótidos

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<400> 209
augccucaca gcagccugca cccuagcauc ccuugcccua gagggcacgg cgcccagaag      60
gccgcccugg ugcugcugag cgccugccug gugaccuugu gggggccuggg cgagccuccu    120
gagcacaccc ugagauaccu ggugcugcac cuggccagcc ugcagcuggg ccugcugcug      180
aacggcgugu gcagccuggc cgaggagcug agacacaucc acagcagaua cagaggcagc      240
uacuggagaa ccgugagagc cugccugggc ugcccucuga gaagaggcgc ccugcugcug      300
cugagcaucu acuucuacua cagccugccu aacgccgugg gccuccuuu caccuggaug      360
cuggcccugc ugggcccugag ccaggcccug acauccugc ugggcccugaa gggccuggcc      420
ccugccgaga ucagcgcccu gugcgagaag ggcaacuua gcauggcca cggccuggcc      480
uggagcuacu acaucggcuu ccugagacug auccugccug agcugcaggc cagaaucaga      540
accuacaacc agcacuacaa caaccugcug agaggcgccg ugagccagag acuguacauc      600
cugcugccuc uggacugcgg cgugccugac aaccugagca uggccgaccc uaacaucaga      660
uuccuggaca agcugccuca gcagaccggc gaccacgccg gcaucaagga cagaguguac      720
agcaacagca ucuacgagcu gcuggagaac ggccagagag ccggcaccug cgugcuggag      780
uacgccaccc cucugcagac ccuguucgcc augagccagu acagccaggc cggcuucagc      840
agagaggaca ugcuggagca ggccaagcug uucugcagaa cccuggagga cauccuggcc      900
gacgccccug agagccagaa caacugcaga cugaucgccu accaggagcc ugccgacgac      960
agcagcuuca gccugagcca ggaggugcug agacaccuga gacaggagga gaaggaggag     1020
gugaccgugg gcagccugaa gaccagcgcc gugccuagca ccagcaccuau gagccaggag     1080
ccugagcugc ugaucagcgg cauggagaag ccucugccuc ugagaaccga cuucagc       1137

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<210> 210
 <211> 141
 <212> ARN
 <213> Secuencia artificial

<220>
 <223> Sintético: 3 UTR utilizada en la construcción de STING V155M, que contiene el sitio de unión a miR122

<400> 210
 ugauaaauagg cuggagccuc gguggccuag cuucuugccc cuugggccuc cccccagccc 60
 cuccuccccu uccugcacc guacccccca aacaccauug ucacacucca guggucuuug 120
 aaauaaagucu gagugggcgg c 141

<210> 211
 <211> 1257
 <212> ARN
 <213> Mus musculus

<220>
 <221> misc_feature
 <222> (1)..(1257)
 <223> superratón IRF3 S396D; sin etiqueta de epítipo

<400> 211
 auggagaccc ccaagccuag aauccugccc uggcugguga gccagcugga ccugggccag 60
 cuggagggcg uagccuggcu ggacgagagc agaaccagau ucagaauccc cuggaagcac 120
 ggccugagac aagacgccc gauggccgac uucggcaucu uccaggccug ggccgaggcc 180
 agcggcgccu acacccucgg caaggauaag cccgauguga gcaccuggaa gagaaacuuc 240
 agaagcggcc ugaacagaaa ggaggugcug agacuggccg ccgacaauag caaggacccc 300
 uacgaccccc acaaggugua cgaguucguu acccccggcg ccagggacuu cgugcaccug 360
 ggccgacgcc ccgacaccaa cggcaagagc agccugcccc acagccagga gaaccugccc 420
 aagcuguucg auggccugau ccugggcccc cugaaggacg agggcagcag cgaccuggcc 480
 aucgugagcg acccuagcca gcagcugccc uccccaacg ugaacaacuu ccugaacccc 540
 gccccccagg agaaccccu gaagcaacug cuggccgagg agcaguggga guucgaggug 600
 accgccuucu acagaggcag acagguguuc cagcagacc uguucugccc cggcggccug 660
 agacugguag gcagcaccgc ugacaugacc cugccucggc agcccugac ccugcccgac 720
 cccgaaggcu uucugaccga caagcuggug aaggaguacg ucggccaagu gcugaagggc 780
 cugggcaacg gccuggcccu guggcaggcc ggccagugcc ugugggcca gagacucggc 840
 cacagccacg ccuucugggc ccugggcgag gaacuccugc ccgauagcgg cagaggcccc 900
 gacggcgagg ugcacaagga caaggacggc gccguguucg accugcgccc cuucguggcc 960
 gaccugaucg ccuucaugga gggcagcggc cacagcccca gauauacccu gugguucugc 1020
 augggcgaga uguggcccca ggaccagccc ugggugaaga gacuggugau ggugaaggug 1080
 gugcccaccu gccugaaaga gcugcuggag auggccagag agggcgggcg cagcucccug 1140
 aaaaccgugg accugcacau ugacaacagc cagcccauca gccugaccag cgaccaguac 1200
 aaggccuacc ugcaggaccu gguggaggac auggacuucc aggccaccgg caacauc 1257

<210> 212
 <211> 1281
 <212> ARN
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(1281)
 <223> superhumano IRF3 S396D; sin etiqueta de epítipo

<400> 212
 augggcaccc ccaagcccag aauccugccc uggcugguga gccagcugga ccugggccag 60
 cuggagggag uggccugggu gaacaagagc agaaccagau ucagaauccc cuggaagcac 120
 ggccucagac aggacgccc gcaggaggac uucggcauuu uucaggcuug ggccgaggcc 180
 accggcgccu acgugcccgg cagagacaag cccgaccugc ccaccuggaa aagaaacuuc 240
 agaagcggcu ugaauagaaa ggagggccug agacuggccg aggacagaag caaggacccc 300
 cacgaccuc acaagaucua cgaguucgug aauagcggcg ugggcgacuu uagccagccc 360
 gacaccagcc ccgacaccaa cggcgggcggc agcaccagcg acacgcagga ggacaucug 420
 gaugaacugc ugggcaacau ggugcuggcc cccugcccg aucccgccc cccuucgcuu 480
 gccguggccc ccgagcccug cccccagccc cugagaagcc ccucucugga uaaccacc 540
 cccuucccca accugggccc cagcgagaau ccacugaaga gacuucuggu ccccgcgag 600

```

gagugggagu ucgaggugac cgccuucua acaggcagac agguuguuca gcagaccauc      660
agcugccccg aaggccugag auuagugggc agcgaagugg gcgacaggac ccugcccggg      720
uggcccguaga cccugcccga ucccggcaug agccugaccg acagaggugu gaugagcuac      780
gugagacacg ugcugagcug ccuggggcggc ggccuggcac uguggagagc cggccagugg      840
cuguggggcc agagacuggg ccacugccac accuacuggg ccgugagcga ggagcugcug      900
cccaacagcg gccacggccc cgacggcgag gugcccaagg acaaggaagg gggcguguuc      960
gaccuggggc ccuucaucgu agaccugauc accuuuaccg agggcagcgg caggagcccc     1020
agauacgccc ugugguucug cguggggcga agcuggcccc aggaccagcc cuggaccaag     1080
agacugguga uggugaaggu agugcccacc ugccugagag ccuuagugga gauggccaga     1140
gugggcgggg ccagcagccu ggagaacacc guggaucuuc acaucgaca cagccacccc     1200
cugagccuga ccagcgacca guacaaggcc uaccugcagg accuggugga gggcauggac     1260
uuccagggcc ccggcgagac c                                     1281

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<210> 213
<211> 1509
<212> ARN
<213> Secuencia artificial

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<220>
<223> Sintético: isoforma A de Hu IRF7 de tipo salvaje; P037 sin etiqueta de epítipo

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<400> 213
auggcgucgg cccccgaaag agccgcccc agaguccucu ucggcgaaug gcuccuuggc      60
gaaauuucgu cgggcugcua cgagggcuua caauggcugg augaggcgag aaccuguuuc     120
agggucccuu ggaaacacuu cgccagaaag gaucuaagcg aagcagaugc uagaauuuuu     180
aaggcuuggg ccguggccag gggaagaugg cccccucga gcagaggcgg cggccuuccc     240
cccaggcgag aaacggccga gagagccgga uggaaaacca auuucagaug cgccugaga     300
ucuacaagaa gauucgugau gcuuagagac aacagcggag aucccgccga ucccuaaag     360
guguauggcc ugucccgga gcugugcugg agggaagggc cuggcacuga ccagaccgaa     420
gccgaagccc ccgcgccgu gcccgccc caaggaggcc caccaggccc uuuccucgu     480
cacaccacg ccggucugca agccccggga ccucuaccug cccugccgg cgauaaaggc     540
gaccuguugc ugcaggccgu ccaacagagc ugccuggccg aucaucugcu cacagccagc     600
uggggcgug accccgucac aacaaaggcc cccggugagg gccaagaagg ccugccucug     660
accggcgccu gugccggcg cccuggccug ccugcuggcg agcuguacgg augggcuguc     720
gaaaccacuc ccuuccccgg ccccaaccu gcgggccuga caaccggcg ggcagccgca     780
cccgaagccc cccaccaggc cgaaccuac cucaguccca gcccuccgc cugcaccgcu     840
gugcaggagc ccagccccgg ugcucuggac guaacaauca uguacaaagg cagaaccgug     900
cuucagaagg uggauugga cccuccugu acuuuucucu acggcccccc cgaccucgccc     960
gugagagcua ccgaccgca acagguggcc uuuccucgc ccgccgaacu gcccgaucua     1020
aaacagcuga gauacaccga ggagcugcug agacacugg cgccgggcuu acaccuagag     1080
uugagaggcc cccaacucug ggccagacgc augggcaagu guaaggugua cugggagguc     1140
ggggggccuc ccggcucugc cagccccagc acccugcuu gucucuugcc cagaaacugu     1200
gauaccccca ucuucgacuu ccguguauuu uuccaggaac uggucgagu uagagccaga     1260
cagagacgag gcagccccag auauacaauc uaccucggcu ucggccagga ccugagugcc     1320
ggcagaccua aggagaaguc gcugguccua gugaaguua agccugggcu auguagagug     1380
caccuggagg gcaccagag agaaggagug agcagccugg acagcagcag ccugagucug     1440
ugccugagcu ccgccaacuc gcuguaugau gacaucgagu guuuccuau ggagcuggag     1500
cagcccgcc                                     1509

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<210> 214
<211> 1509
<212> ARN
<213> Secuencia artificial

```

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<220>
<223> Sintético: Hu IRF7 constitutivamente activo S477D/S479D; P033 sin etiqueta de epítipo

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```

<400> 214
auggccuug cccugagcg ggccgcccc agaguguuau ucggcgagug gcugcugggc      60
gagauagca gcggcugcua cgagggacug caguggcugg acgaggcuag aaccugcuuc     120
agagugcccu ggaagcauu cgccagaaaa gaccugagcg aggcugaugc uagaauuuc     180

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aaagccuggg	cuguggcccc	aggaagaugg	ccccccagca	gcagaggagg	cgccccuccu	240
cccgaggccg	aaaccgcaga	gcgugcuggc	uggaaaacca	acuuuaggug	ugcccugagg	300
agcaccagaa	gauucguuau	gcucagagac	aacagcgggg	accccgccga	cccgcacaa	360
guguacgccu	uaaguaggga	gcugugcugg	agagaggggac	cggggaccga	ccaaaccgag	420
gcugaggcgc	ccgccgccgu	uccaccuccc	cagggugguc	ccccagggcc	cuuucuggca	480
cacaccacg	ccggauuaca	ggcgccaggg	cccuuacccg	cccccgccg	agacaaaggc	540
gaccuccugc	ugcaagccgu	gcaacaaagc	ugccuggccg	aucacuuacu	aaccgcuagc	600
uggggcgccg	auccuguucc	caccaaggcc	cccggugaag	ggcaagaagg	acugcccuua	660
accggcgccu	gugccggagg	cccuggucug	ccagccggcg	agcuguacgg	uugggcuguc	720
gaaacaacac	ccaguccggg	cccacagccu	gccgcucuga	ccaccggcga	agccgccgcc	780
cccgagagcc	cacaccaggc	ugaaccuac	cugagcccca	gccccagcgc	cugcaccgcu	840
gugcaggagc	cuagccccgg	cgcuuugau	gugacaauaa	uguacaagg	caggaccgug	900
cugcaaaagg	ucgugggcca	uccgucgugu	accuuucugu	acggcccucc	agaccccgcg	960
guuagagcca	ccgaccccc	gcaagucgcc	uuccccuccc	ccgccgaacu	gcccgaccaa	1020
aagcagcugc	gguacacaga	agaacuacuu	agacacugg	cccccgguu	gcacuuggag	1080
cugagaggcc	cccagcucug	ggccagaaga	augggcaagu	gcaaagugua	cugggaggug	1140
ggcgggccac	ccggcucagc	uucgcccucc	acaccgcau	gccugcugcc	cagaaaauugc	1200
gacacgcca	ucuucgauuu	uagaguguuc	uuucaggagu	ugguggaguu	cagagccaga	1260
caaagacgcg	gcagccccag	auacaccauu	uaccucggcu	ucggccagga	ccucagcgcu	1320
ggcagacca	aggagaagag	ucugguccuc	gugaagcugg	agccugggcu	gugcagagug	1380
caccuggagg	gcacccagcg	ugaaggcgug	agcagccugg	auucaagcga	ccuggaccua	1440
ugccuaagca	gcgcuaacuc	acuguacgac	gauaucgaau	gcuuccugau	ggaacuggag	1500
cagccugcc						1509

<210> 215
 <211> 1509
 <212> ARN
 <213> Secuencia artificial

<220>
 <223> Sintético: Hu IRF7 constitutivamente activo S475D/S477D/L480D; P034 sin etiqueta de epítopo

<400> 215	
auggcccugg	cacccgagag
gaaauuagca	gcggcugcua
agaguucccu	ggaagcacuu
aaggccuggg	cugucgccag
ccugaggcug	agacugcgga
agcaccagac	guuuugugau
guauacgcac	ugagccgaga
gcugaagccc	cugcagccgu
cauacccaug	caggguuaca
gaccucuuac	ugcaggccgu
uggggcgccg	auccugugcc
accggcgccu	gcgcuggcgg
gagacgacuc	ccagcccugg
cccgagucuc	cgacccaggc
gugcaagaac	cuagccccgg
cugcaaaagg	ugguggguca
gugcgagcca	cagaccaca
aaacagcuga	gauauacaga
cugaggggccc	cacaacugug
ggaggcccc	ccggcagcgc
gacaccccc	ucuugacuu
cagcggagg	gcucacacag
ggccgcccc	aggaaaagag
caccucgaag	gcacccagag

ugccuuagca gcgccaacag ccuguau gauaucgagu gcuuccuuau ggaacuggag 1500
cagcccgcc 1509

<210> 216
<211> 1509
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: Hu IRF7 constitutivamente activo S475D/S476D/S477D/S479D/S483D/S487D; P035 sin etiqueta de epítipo

<400> 216
auggcccuaug cccccgaaag agcagcuccc agagugcugu ucggcgaaug gcugcuuggc 60
gagaucagca gcggcugcua cgaaggccug caguggcugg acgaagccc caccuguuuc 120
agagugcccu ggaagcacuu cgcuaaaaag gauuugagcg aggcugaugc uagaauuuu 180
aaggcuuggg cuguggcaag aggcagaugg ccgccuagua gcagaggggg cggaaccucc 240
cccagggcug agaccgcuga gagagcaggg uggaaaacca acuucagaug cgcgcugaga 300
agcaccgcaa gauucgugau gcuacgugac aaugcggcg accccgccga cccccacaaa 360
guguacgccc ugucccgaga acuuugcugg agagagggac ccggcaccga ucaaacagag 420
gcugagggcc cgccgcugu acccccgccc caaggaggcc cccagggccc cuuucuggcu 480
cauacacaug ccggccugca ggacccggg cccucccg cuccugccgg cgacaagggc 540
gaucuccuuc uccaggccgu gcagcagagc ugccuggccg aucaccugcu gaccgccucg 600
uggggcgccg accccgugcc caccaaagcc ccgggugaag gccaagaggg gcuccuuua 660
accggagcau gcgccggagg ccccgccug ccagccggcg aguuaauagg cugggcugug 720
gagaccacac ccucccccg cccucaacc gcugcccuga ccaccgguga ggccgccgcc 780
cccagagacc cacaccagg cgaaccuac cugagccua gccuagcgc cugcaccgcc 840
gugcaagaac ccagcccg agcccuggau gugaccuua uguacaagg ccggacagug 900
cugcaaaagg uugugggaca cccgagcug accuuucugu acgguccgcc ugaccccgcc 960
gugagagcca cggaccgca gcagguggcc uuccccucac ccgcggagcu gcccagcaa 1020
aagcaacuca gauacacaga agaacuauug cgucacgucg cggccggccu gcaucuggag 1080
cugagaggcc cccagcugc ggccagaagg augggaaaau gcaaggugua cugggaggug 1140
ggaggccccc ccggcagcgc cagccccagc acucccgcu gccugcugcc cagaaauugc 1200
gacacucca ucuucgauu caggguguu uccaggagc ugguggagu cagagccagg 1260
cagagaaggg guagccccag auacacaauc uaucuaggcu uggacaaga ucugagcgcc 1320
ggccggccua aggaaaaaag ccuggugcug guaaagcugg agccguggcu uuguagagug 1380
caccuggagg ggacgcagc agaggcgug agcagcuuag acgacgauga cuuggaucug 1440
ugucucgaca gcgccaacga cuuguacgac gacaucgagu gcuuccugau ggaacuggag 1500
cagcccgcc 1509

<210> 217
<211> 846
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: Hu IRF7 truncado constitutivamente activo 1-246 + 468-503; P032 sin etiqueta de epítipo

<400> 217
auggcccugg cccccgagag agccgcccc agagugcucu ucggcgagug gcugcugggc 60
gagauaagca gcggcugcua cgaaggucug caguggcuag acgaggccag aaccugcuu 120
agagugcccu ggaagcacuu cgcucgaaag gaccuguccg aggcgaguc uagaauuuu 180
aaggcuuggg ccgucgcuag ggaagaugg ccccuagca guagaggcg cgccccccu 240
cccgaagccg agacggccga gagggccggc uggaaaacca auuucagaug cgccugagg 300
agcaccgca gguucguaa gcugcgagac aaugcggcg auccugcgga uccucacaag 360
guuacgcu ugaguagaga acugugcugg cgggagggg ccggaaccga ccagacggag 420
gcagaggcac ccgugccgu gcccccccu caaggaggac cccuggacc cuuucuggcc 480
cacaccacg cuggucugca ggccccagg ccacugccc cccagcggg cgauaaggg 540
gaccugucc uacaggcggu gcaacagagc ugucggccg accaccugu gaccgccagc 600
uggggggccg acccgugcc caccaaagcu cccggagagg gccaagaagg ccuccacua 660
acuggcgccu gcgccgggg cccgggaaua cccgccggcg agcuguaugg cugggccgug 720
gagaccacgc ccagccccga gggcgugucg uccuggaca gcagcagccu gagccuguc 780

cugagcuccg ccaacagccu guaagacgac aucgagugcu uccugaugga gcuggaacia 840

cccgcc 846

<210> 218
<211> 846
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: Hu IRF7 truncado constitutivamente activo 1-246 + 468-503 más S475D/S476D/S477D/S479D/S483D/S487D; P036 sin etiqueta de epítipo

<400> 218
auggcacugg cgccugaaag agccgcuccg cgugugcucu ucggcgagug gcugcugggc 60
gagaucagcu ccggcugcua cgagggucua caguggcugg acgaggccag aaccuguuuu 120
agagugcccu ggaagcacuu cgcgagaaag gaccugagcg aggccgacgc cagaauucuuc 180
aaagccuggg caguggcuag gggcagaugg ccucccagca gccggggcg cgcccaccc 240
cccgaggccg aaaccgccga aagagcuggc uggaagacca acuucagaug cgcccugaga 300
agcaccagaa gauuugucuu gcugagagau aaucaggag accccgccga ccucacaag 360
guguacgccc uguccagaga gcuguguugg agagagggcc ccggaaccga ccagaccgag 420
gccgaggcuc cagcugccgu gccaccccc caaggcggac caccggccc cuucuuggca 480
cauacgcacg ccggccucca ggcucccgcc ccucugccc cccugcugg ugacaaaggc 540
gaucugcugc ugcaagccgu ccagcaaucc ugcugggcug accaccugcu gaccguagc 600
uggggagccg accccguucc caccaaggcu cccggagaag gacaggagg ccugcccuu 660
accggcgcuu gcgcgggggg cccuggcuug ccugccggcg aacugacgg cugggcccug 720
gagaccacgc cuucccccga gggcgugucc agccuggacg augaugaccu ggauugugc 780
cuggacagcg ccaacgaccu guacgaugac aucgagugcu uuuugaugga gcuggagcag 840
cccgcc 846

<210> 219
<211> 1224
<212> ARN
<213> Secuencia artificial

<220>
<223> Sintético: Hu IRF7 truncado 1-151 + 247-503; P038 sin etiqueta de epítipo; mutación nula

<400> 219
auggcccugg ccccgagag agccgcgccc agagugcugu ucggcgaaug gcugcugggc 60
gagaucagca gcggcugcua ugagggccug caguggcucg acgaagccag gacgugcuuc 120
agagucccuu ggaagcacuu cgccagaaag gaucugagcg aggcugacgc cagaauucuuc 180
aaggccuggg caguugcgcg ugaggagaugg ccccccagcu cgcgggggcg cgguccccc 240
ccugaggccg agaccgccga aagagccgga uggaaaacca acuuucgaug cgcccucaga 300
agcaccagac gguuugugau gcugagagau aacagcggcg acccugcaga ccccauaaa 360
guguaugcc ugagcagaga gcuguguugg cgagagggcc ccggaaccga ccaaccgag 420
gccgaggccc ccgcccguu accccccc cuaggcccc agccugcugc ucugaccacg 480
ggagaagccg ccgcuccuga gagccccac caagccgagc ccuauugag ccuagcccc 540
agcgccugca ccgcccugca ggagcccua ccggggcgccc uagacgugac caucauguac 600
aagggcgca cggugcugca aaagguggug ggccaccca gcugcaccuu ccuguacggc 660
cccccgacc cugccgugag agccaccgac cccagcaag ucgcuuccc cagccccgcc 720
gagcugcccg accagaagca gcugagguac accgaggagu ugcugagaca uguggcccc 780
ggcuugcacc ucgagcugag agggccgag cucugggcca gaagauggg caagugcaag 840
guguacuggg agguggggcg ccccccgcc agcgcgagcc caagcacc ccgugccug 900
cugccuagaa acugcgacac ccuauucuuc gacuucagag uauuuuucca ggagcugguc 960
gaguucaggg ccagacagcg uagaggcagc cccagauaca ccaucuaccu uggauucggc 1020
caggaccuga gcgcccggag acccaaagag aagucccugg uacuggugaa gcuagagccc 1080
uggcugugua gggugcaucu ggaaggcacc caaagagagg gcguaagcuc gcuugacagc 1140
agcagccuca gccugugccu gagcagcgcu aacagcuuau acgacgacau cgagugcuuc 1200
cugauggagc uggaacaacc cgcc 1224

<210> 220
<211> 1059
<212> ARN
<213> Secuencia artificial

<220>
 <223> Sintético: Hu IRF7 truncado 152-503; P039 sin etiqueta de epítipo; mutación nula

<400> 220
 augggcgggc cccccgggc uuuccuggcc cauacacacg ccggccuaca ggcuccuggc 60
 ccucugcccg ccccgggcg cgacaagggc gaccuccugc ugcaggccgu gcagcagucc 120
 ugucuggccg accaccugcu gacugcuagc uggggcgccg aucccgugcc caccaaggcc 180
 ccaggagagg ggcaagagg ccugccucua accggcgcau gcgcaggugg accaggccuc 240
 cccgccggcg agcuguaugg uuggggcgug gagacaaccc ccagccccgg cccgcagccu 300
 gcugcgcuga ccacaggcga ggcgcugcc ccugagagcc cccaccaagc ugaacccuac 360
 cugagcccca gcccucugc cugcacagcg gugcaggagc ccagucccg cgccuuggac 420
 gugaccauca uguauaagg caggacugug uuacaaaagg uagugggcca cccaaguugu 480
 accuuucugu acggggcccc cgaccagcc gugcgcgcca ccgaccccca gcagguggcc 540
 uuccccagcc ccgcugagu gcccgaucag aaacaacucc gguacaccga ggaauuacuu 600
 agacauugg cucccgccu gcaucuggag cuuagagguc cacaguugug ggccagaaga 660
 augggcaagu gcaagguua uugggagguc ggaggcccc cgggcagcgc cagccccagc 720
 acccccgccu gucuucugc cagaaacugc gacaccccaa ucuucgauuu cagaguguuu 780
 uuccaggaac ugguggagu cagagcaagg caaagaagag gcagcccuag auacaccauc 840
 uaccugggcu uggccaaga ccugagcgc ggcagacca aggaaaaauc ccugguccug 900
 gugaaacugg agcccuggcu gugcagaguc caccuggagg gcaccagag agagggcgug 960
 agcagccugg acucgagcag ccugucccug ugucugagca gcgcgaauuc gcuauaugac 1020
 gacaucgaau gcuuucugau ggagcuggaa cagcccgc 1059

<210> 221
 <211> 1269
 <212> ARN
 <213> Secuencia artificial

<220>
 <223> Sintético: KRAS(G12D)25mer_nt.STING(V155M)

<400> 221
 augccucaca gcagccucca cccuagcauc ccuugcccua gagggcacgg cgcccagaag 60
 gccgcccucg ugcuuuaag cgccugcuug gugacccuuu ggggcuuggg cgagccucca 120
 gagcacaccu ugagauauuu ggugcuccac cuggccagcc uucagcuggg cuuguuacuc 180
 aacggcgugu gcagccuggc cgaggagcug agacacauc acagcagaua cagaggcagc 240
 uacuggagaa ccgugagagc gugucugggc ugcccucuga gaagaggcgc cuugcuucuu 300
 cucagauacu acuucuacua cucccugccu aacgccgugg gccuccuuu caccuggaug 360
 cuggcacugc ucggccucag ccaggcccug aacaucuuu ugggcuugaa gggccuggcc 420
 ccugccgaga ucagcgccgu gugcgagaag ggcaacuua acauggcca cggauuggcu 480
 uggagcuacu acaucggcu ccugagacug auccugccug agcugcaggc cagaaucaaga 540
 accuacaacc agcacuacaa caaccugcug cgcggcgcag ugagccagag acugauauu 600
 cugcugccuc uggacugcg cgugccugac aaccugagca uggccgacc uaacaucaga 660
 uuccuggaca agcugccua gcagaccggc gaccacgccg gcaucaagga cagaguguac 720
 agcaacagca ucuauagcu gcucgagaau ggccagagag ccggcaccug cgugcuggag 780
 uacgccacc cucugcagac ccuguucgcc augagccagu auagucaagc ugguucagc 840
 agagaggaca gacuggagca ggccaagcug uucugcagaa ccuggagga cauucuggcu 900
 gacgcccug agagccagaa caacugccga cugaucgccu accaggaacc agccgacgac 960
 agcagcuua gcuuucua ggagguucuu cgccacuug gccaggagga gaaggaggag 1020
 gugaccgugg gcagccugaa gaccuccgca gucccuagca ccagcaccu gagucaggag 1080
 ccggagcuau uauacagcg cauggagaag ccucuuccac uccgaaccga cuucagcgcc 1140
 accaacuua gccugcugaa gcaggcaggu gacguugagg agaauccgg accuauagacc 1200
 gaguacaagc uggugguugu gggcgccgac ggcgugggca agagcgccu gaccauccag 1260
 cugauccag 1269

<210> 222
 <211> 1269
 <212> ARN
 <213> Secuencia artificial

<220>
 <223> Sintético: KRAS(G12D)25mer_ct.STING(V155M)

<400> 222
 augaccgagu acaagcuagu agucgugggc gccgacggcg ugggcaagag cgcccucacc 60
 auccagcuua uccaggccac caacuucagc uugcucaagc aggccggcga cguggaggag 120
 aaccagggcc cuaugccuca cagcagccuu caccuagca ucccuugccc uagaggccac 180
 ggcgccaga aggccgccc ggugcugcug agcgcugcc uggugacccu guggggccug 240
 ggcgagccuc cugagcacac ccugagauau cuggugcuuc accuggccag uuuacagcug 300
 ggccugcuuc uuaacggcgu gucgagccug gccgaggagc ugagacacau ccacagcaga 360
 uacagaggca gcuacuggag aaccgugaga gccugccuag gcugcccucu gagaagaggc 420
 gcucuguugc uacuuuccau cuacuucac uacuccugc cuaacgccgu gggcccuccu 480
 uucacuugga ugcuggcguu gcugggucug agccaggccc ugaacauccu ucucggucug 540
 aaggggcugg cccuggccga gaucagcgc gugugcgaga agggcaacu caacauggcc 600
 cacggacucg ccuggagcua cuacaucggc uaccugagac ugauccugcc ugagcugcag 660
 gccagaauca gaaccuacaa ccagcacuac aacaaccugc ugcggggccc cgugagccag 720
 agacuguaua uacuucuucc ucuggacugc ggcgugccug acaaccugag cauggccgac 780
 ccuaacauca gauuccugga caagcugccu cagcagaccg gcgaccacgc cggcaucaag 840
 gacagagugu acagcaacuc cauuuagag cugcucgaga auggccagag agccggcacc 900
 ugcgugcugg aguacgccac cccucugcag acccuguucg ccaugagcca guacagucag 960
 gcuggauuca gcagagagga cagacuggag caggccaagc uguucugcag gacacuggag 1020
 gacauacuag cagacgcccc ugagagccag aacaacugca gacugauugc cuaccaggag 1080
 ccugcggacg acagcuccuu cagucugagu caggaggugu ugcggcacuu acgccaagaa 1140
 gagaaggagg aggugaccgu gggcagccug aagacuagcg cugugccuag caccagcaca 1200
 augucacagg agccggaauu gcuaaucagc ggcauggaga agccucuccc auuacguacc 1260
 gacuucagc 1269

<210> 223
 <211> 1419
 <212> ARN
 <213> Secuencia artificial

<220>
 <223> Sintético: KRAS(G12D)25mer^3_nt.STING(V155M)

<400> 223
 augccucaca gcagccuua cccuagcauc ccuugcccua gagggcacgg cgcccagaag 60
 gccgcccuaug ugcuccuua cgccugccuc gugacccuau ggggcuuagg cgagccucca 120
 gagcacaccu ugagauaccu cguccuccac cuggcuaguc uacagcuggg ccuuccucc 180
 aacggcgugu gcagccuggc cgaggagcug agacacauc acagcagaua cagaggcagc 240
 uacuggagaa ccgugagagc gugccugggc ugcccucuga gaagaggcgc acugcuguua 300
 cucagcaucu acuucuacua cucacugcca aacgccgugg gccuccuuu caccuggaug 360
 cuggccuugc ucggauugag ccaggcccug aacauuuuac ugggauugaa gggccuggcc 420
 ccugccgaga ucagcgccgu gugcgagaag ggcaacuua acauggcca cggccuagcu 480
 uggagcuacu acaucggcua ccugagacug auccugccug agcugcaggc cagaucaga 540
 accuacaacc agcacuacaa caaccugcug cguggagcgg ugagccagag acuguauauc 600
 cuccugccuc uggacugcgg agugccugac aaccugagca uggccgacc uaacaucaga 660
 uuccuggaca agcugccuca gcagaccggc gaccacgccg gcaucaagga cagaguguac 720
 agcaacuaa ucuacgagcu guuggagaau ggccagagag ccggcaccug cgugcuggag 780
 uacgccacc cucugcagac ccuguucgac augagccagu acucucaggc agguucagc 840
 agagaggaca gacuggagca ggccaagcug uucugcagaa ccuggagga cauccuggcg 900
 gacgcccug agagccagaa caacugccg cuuauccgu accaggagcc agcagacgac 960
 agcagcuucu cucucucaca agagguacug cgccauuuc gccaggagga gaaggaggag 1020
 gugaccgugg gcagccugaa gacaucgcc guaccuagca ccagcaccu gucucaggaa 1080
 ccggaacugu ugaucagcg cauggagaag ccucugccac ugcgcaccga cuucagcgcc 1140
 accaacuucu cccuacugaa gcaagccggu gacguugaag agaaccugg cccuauagacc 1200
 gaguacaagc ugguauguu aggcgcccag ggcgugggca agagcgccu gaccauccag 1260
 cugauccaga ugacugaaua uaagcuugc gucgugggag cagauggcgu ugguaagagc 1320
 gcacuuacaa uucaacuca ucagaugagc gaguauaagc uggugguggu cggagcugac 1380
 ggcguaggca agagugcccu uacuauucag cuaauucag 1419

<210> 224
 <211> 1419
 <212> ARN
 <213> Secuencia artificial

<220>
 <223> Sintético: KRAS(G12D)25mer^3_ct.STING(V155M)

<400> 224
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 auccagcuua uccagaugac agaguauaag cuaguggugg ucggcgagaga cggaguggga 120
 aagagugcau uaacuauuca acucauccaa augaccgaau acaagcuagu aguugugggu 180
 gcagauggcg ucggcaaguc ugcacugaca auucagcuca uccaggccac caacuucagc 240
 cugcugaagc aggccggcga cguggaggag aaccugggc cuaugccuca cagcagccug 300
 caccuagca ucccuugccc uagaggccac ggcggccaga aggcggcccu ggugcugcug 360
 agcgccugcc uggugacccu guggggccug ggcgagccuc cugagcacac ccugagauac 420
 cuaguuuugc accuggcuuc ucugcagcug ggccuacugc ucaacggcggu gucagccug 480
 gccgaggagc ugagacacau ccacagcaga uacagaggca gcuacuggag aaccgugaga 540
 gcaugcuuag gcugcccucu gagaagaggc gcucugcucc ucuuguccau cuacuucua 600
 uacucgcuac cuaacgccgu gggccuccu uucaccugga ugcuggcccu cuugggauua 660
 agccaggccc ugaacaucuu gcugggacug aaggggccug cccugccga gaucagcgcc 720
 gugugcgaga agggcaacuu caacauggcc cacggacucg cuuggagcua cuacaucggc 780
 uaccugagac ugaucugcc ugagcugcag gccagaauc gaaccuacaa ccagcacuac 840
 aacaaccugc ugcggggagc agugagccag agacuguaua uucugcuccc ucuggacugc 900
 ggcgugccug acaaccugag cauggccgac ccuaacauca gauuccugga caagcugccu 960
 cagcagaccg gcgaccacgc cggcaucaag gacagagugu acagcaacag cauuuacgag 1020
 cugcuggaga acggccagag agccggcacc ugcgugcugg aguacgccac cccucugcag 1080
 acccuguucg ccaugagcca guacuccag gcaggauuca gcagagagga cagacuggag 1140
 caggccaagc uguucugccg uacucuugag gacauccuug cagacgccc ugagagccag 1200
 aacaacugcc gguugauugc cuaccaggaa cgggcagacg acagcuauu cuccuugucu 1260
 caggaggucc uuagacaccu gcggcaggag gagaaggagg aggugaccgu gggcagccug 1320
 aagacaucg cggugccuag cacgucuacc augucccagg agccggaacu gcuaaucagc 1380
 ggcauggaga agccucugcc ucucaggacc gacuucagc 1419

<210> 225
 <211> 1140
 <212> ARN
 <213> Secuencia artificial

<220>
 <223> Sintético: Hu STING (R284K) var; sin etiqueta de epítipo

<400> 225
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 gccgcccugg uccugcugag cgcaugccug gucaccuugu gggggccugg cgagccccc 120
 gagcacacc ugagauaccu ggugcugcac cucgccagcc ugcagcuggg ccugcugcug 180
 aacggcgugu gcagccuggc cgaggagcug agacacaucc acagcagaua uagaggcagc 240
 uacuggagaa ccgugagagc uugccucggc ugccccuga gaagaggcg ccugcugcug 300
 cugagcaucu acuuuacua cagccugccc aacgcugugg gcccccuuu cacguggaug 360
 cucgcccugc ugggacugag ccaggcccug aacaucugc ugggcuuaa gggccuagcc 420
 cccgcccaga ucagcgccgu gucgagaaag ggcaacuua auguggcca cggccuggcc 480
 uggagcuacu acaucggcu ccugagacug auccugccc agcugcaggc cagaauca 540
 accuacaauc agcacuacaa caaccugcug agaggcgccg ugagccagag acuguacau 600
 cugcugcccc uggacugcgg cgugcccagc aaccucagca uggccgacc caacauca 660
 uuccuggaga agcugccca gcagaccggc gaccagccg gcaucaagga ucgcuguuac 720
 agcaacagca ucuacgagcu gcuggaaaac ggccagagag ccggaaccug cgugcuggag 780
 uacgccacac cccugcagac ccuguucgcc augagccagu acagccaggc cggcuucagc 840
 agagaggaga agcuggagca ggccaagcug uucugcagaa cccuggagga uauccucgcc 900
 gacgccccg agagccagaa caucugcagg cugaucgcu accaggagcc cgcugacgac 960
 agcagcuua gccugagcca ggaggugcug agacaucug gucaagagga aaaggaggag 1020
 gugaccgugg gcuccugaa gaccagcgcc gugcccagca ccagcaccu gagccaggag 1080

cccgagcugc ugaucagcgg cauggagaag ccacugcccc ucagaaccga cuucagcacc 1140

<210> 226
 <211> 9
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: péptido EBV BRLF1

<400> 226

Ala Thr Ile Gly Thr Ala Met Tyr Lys
 1 5

<210> 227
 <211> 9
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: péptido FLU

<400> 227

Ser Ile Ile Pro Ser Gly Pro Leu Lys
 1 5

<210> 228
 <211> 9
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: péptido HIV NEF

<400> 228

Ala Val Asp Leu Ser His Phe Leu Lys
 1 5

<210> 229
 <211> 10
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: péptido EBV

<400> 229

Ala Val Phe Asp Arg Lys Ser Asp Ala Lys
 1 5 10

<210> 230
 <211> 9
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: péptido de antígeno nuclear de HBV
 <400> 230

Tyr Val Asn Val Asn Met Gly Leu Lys
 1 5

<210> 231
 <211> 9
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: péptido HC

<400> 231

Arg Val Cys Glu Lys Met Ala Leu Tyr
 1 5

<210> 232
 <211> 9
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Sintético: péptido CMV

<400> 232

Lys Leu Gly Gly Ala Leu Gln Ala Lys
 1 5