

LISTADO DE SECUENCIAS

<110> Astellas Pharma Inc.
Modalis Therapeutics Corporation

<120> Método para tratar distrofia muscular por direccionamiento del gen DMPK
<130> 093012

<150> US62/853,373
<151> 2019-05-28

<150> US63/025,417
<151> 2020-05-15

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<170> Patente en versión 3.5

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 ggcctgggaa acgtggtcct gggcagttct gataatttaa aaaacaccga ggactttgat 300
 gaggggccct ggctgcgggc aggatgctct tctccccaag agggtcctgc tccagccgct 360
 ggt 363

<210> 138
 <211> 19
 <212> ARN
 <213> Francisella novicid

<220>
 <221> misc_feature
 <222> (1)..(19)
 <223> 5'-manejo de ARNcr

<400> 138
 aauuucuacu guuguagau

19

<210> 139
 <211> 1053
 <212> PRT
 <213> Staphylococcus aureus

<220>
 <221> VARIANTE
 <222> (10)..(10)
 <223> conversión de residuo Asp en residuo Ala

<220>
 <221> VARIANTE
 <222> (580)..(580)
 <223> conversión de residuo Asn en residuo Ala

<400> 139

Met Lys Arg Asn Tyr Ile Leu Gly Leu Ala Ile Gly Ile Thr Ser Val
 1 5 10 15

Gly Tyr Gly Ile Ile Asp Tyr Glu Thr Arg Asp Val Ile Asp Ala Gly
 20 25 30

Val Arg Leu Phe Lys Glu Ala Asn Val Glu Asn Asn Glu Gly Arg Arg
 35 40 45

Ser Lys Arg Gly Ala Arg Arg Leu Lys Arg Arg Arg Arg His Arg Ile
 50 55 60

Gln Arg Val Lys Lys Leu Leu Phe Asp Tyr Asn Leu Leu Thr Asp His
65 70 75 80

Ser Glu Leu Ser Gly Ile Asn Pro Tyr Glu Ala Arg Val Lys Gly Leu
85 90 95

Ser Gln Lys Leu Ser Glu Glu Glu Phe Ser Ala Ala Leu Leu His Leu
100 105 110

Ala Lys Arg Arg Gly Val His Asn Val Asn Glu Val Glu Glu Asp Thr
115 120 125

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

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

Asp Gly Glu Val Arg Gly Ser Ile Asn Arg Phe Lys Thr Ser Asp Tyr
165 170 175

Val Lys Glu Ala Lys Gln Leu Leu Lys Val Gln Lys Ala Tyr His Gln
180 185 190

Leu Asp Gln Ser Phe Ile Asp Thr Tyr Ile Asp Leu Leu Glu Thr Arg
195 200 205

Arg Thr Tyr Tyr Glu Gly Pro Gly Glu Gly Ser Pro Phe Gly Trp Lys
210 215 220

Asp Ile Lys Glu Trp Tyr Glu Met Leu Met Gly His Cys Thr Tyr Phe
225 230 235 240

Pro Glu Glu Leu Arg Ser Val Lys Tyr Ala Tyr Asn Ala Asp Leu Tyr
245 250 255

Asn Ala Leu Asn Asp Leu Asn Asn Leu Val Ile Thr Arg Asp Glu Asn

260

265

270

Glu Lys Leu Glu Tyr Tyr Glu Lys Phe Gln Ile Ile Glu Asn Val Phe
 275 280 285

Lys Gln Lys Lys Lys Pro Thr Leu Lys Gln Ile Ala Lys Glu Ile Leu
 290 295 300

Val Asn Glu Glu Asp Ile Lys Gly Tyr Arg Val Thr Ser Thr Gly Lys
 305 310 315 320

Pro Glu Phe Thr Asn Leu Lys Val Tyr His Asp Ile Lys Asp Ile Thr
 325 330 335

Ala Arg Lys Glu Ile Ile Glu Asn Ala Glu Leu Leu Asp Gln Ile Ala
 340 345 350

Lys Ile Leu Thr Ile Tyr Gln Ser Ser Glu Asp Ile Gln Glu Glu Leu
 355 360 365

Thr Asn Leu Asn Ser Glu Leu Thr Gln Glu Glu Ile Glu Gln Ile Ser
 370 375 380

Asn Leu Lys Gly Tyr Thr Gly Thr His Asn Leu Ser Leu Lys Ala Ile
 385 390 395 400

Asn Leu Ile Leu Asp Glu Leu Trp His Thr Asn Asp Asn Gln Ile Ala
 405 410 415

Ile Phe Asn Arg Leu Lys Leu Val Pro Lys Lys Val Asp Leu Ser Gln
 420 425 430

Gln Lys Glu Ile Pro Thr Thr Leu Val Asp Asp Phe Ile Leu Ser Pro
 435 440 445

Val Val Lys Arg Ser Phe Ile Gln Ser Ile Lys Val Ile Asn Ala Ile
 450 455 460

Ile Lys Lys Tyr Gly Leu Pro Asn Asp Ile Ile Ile Glu Leu Ala Arg
465 470 475 480

Glu Lys Asn Ser Lys Asp Ala Gln Lys Met Ile Asn Glu Met Gln Lys
485 490 495

Arg Asn Arg Gln Thr Asn Glu Arg Ile Glu Glu Ile Ile Arg Thr Thr
500 505 510

Gly Lys Glu Asn Ala Lys Tyr Leu Ile Glu Lys Ile Lys Leu His Asp
515 520 525

Met Gln Glu Gly Lys Cys Leu Tyr Ser Leu Glu Ala Ile Pro Leu Glu
530 535 540

Asp Leu Leu Asn Asn Pro Phe Asn Tyr Glu Val Asp His Ile Ile Pro
545 550 555 560

Arg Ser Val Ser Phe Asp Asn Ser Phe Asn Asn Lys Val Leu Val Lys
565 570 575

Gln Glu Glu Ala Ser Lys Lys Gly Asn Arg Thr Pro Phe Gln Tyr Leu
580 585 590

Ser Ser Ser Asp Ser Lys Ile Ser Tyr Glu Thr Phe Lys Lys His Ile
595 600 605

Leu Asn Leu Ala Lys Gly Lys Gly Arg Ile Ser Lys Thr Lys Lys Glu
610 615 620

Tyr Leu Leu Glu Glu Arg Asp Ile Asn Arg Phe Ser Val Gln Lys Asp
625 630 635 640

Phe Ile Asn Arg Asn Leu Val Asp Thr Arg Tyr Ala Thr Arg Gly Leu
645 650 655

Met Asn Leu Leu Arg Ser Tyr Phe Arg Val Asn Asn Leu Asp Val Lys

660

665

670

Val Lys Ser Ile Asn Gly Gly Phe Thr Ser Phe Leu Arg Arg Lys Trp
 675 680 685

Lys Phe Lys Lys Glu Arg Asn Lys Gly Tyr Lys His His Ala Glu Asp
 690 695 700

Ala Leu Ile Ile Ala Asn Ala Asp Phe Ile Phe Lys Glu Trp Lys Lys
 705 710 715 720

Leu Asp Lys Ala Lys Lys Val Met Glu Asn Gln Met Phe Glu Glu Lys
 725 730 735

Gln Ala Glu Ser Met Pro Glu Ile Glu Thr Glu Gln Glu Tyr Lys Glu
 740 745 750

Ile Phe Ile Thr Pro His Gln Ile Lys His Ile Lys Asp Phe Lys Asp
 755 760 765

Tyr Lys Tyr Ser His Arg Val Asp Lys Lys Pro Asn Arg Glu Leu Ile
 770 775 780

Asn Asp Thr Leu Tyr Ser Thr Arg Lys Asp Asp Lys Gly Asn Thr Leu
 785 790 795 800

Ile Val Asn Asn Leu Asn Gly Leu Tyr Asp Lys Asp Asn Asp Lys Leu
 805 810 815

Lys Lys Leu Ile Asn Lys Ser Pro Glu Lys Leu Leu Met Tyr His His
 820 825 830

Asp Pro Gln Thr Tyr Gln Lys Leu Lys Leu Ile Met Glu Gln Tyr Gly
 835 840 845

Asp Glu Lys Asn Pro Leu Tyr Lys Tyr Tyr Glu Glu Thr Gly Asn Tyr
 850 855 860

Leu Thr Lys Tyr Ser Lys Lys Asp Asn Gly Pro Val Ile Lys Lys Ile
865 870 875 880

Lys Tyr Tyr Gly Asn Lys Leu Asn Ala His Leu Asp Ile Thr Asp Asp
885 890 895

Tyr Pro Asn Ser Arg Asn Lys Val Val Lys Leu Ser Leu Lys Pro Tyr
900 905 910

Arg Phe Asp Val Tyr Leu Asp Asn Gly Val Tyr Lys Phe Val Thr Val
915 920 925

Lys Asn Leu Asp Val Ile Lys Lys Glu Asn Tyr Tyr Glu Val Asn Ser
930 935 940

Lys Cys Tyr Glu Glu Ala Lys Lys Leu Lys Lys Ile Ser Asn Gln Ala
945 950 955 960

Glu Phe Ile Ala Ser Phe Tyr Asn Asn Asp Leu Ile Lys Ile Asn Gly
965 970 975

Glu Leu Tyr Arg Val Ile Gly Val Asn Asn Asp Leu Leu Asn Arg Ile
980 985 990

Glu Val Asn Met Ile Asp Ile Thr Tyr Arg Glu Tyr Leu Glu Asn Met
995 1000 1005

Asn Asp Lys Arg Pro Pro Arg Ile Ile Lys Thr Ile Ala Ser Lys
1010 1015 1020

Thr Gln Ser Ile Lys Lys Tyr Ser Thr Asp Ile Leu Gly Asn Leu
1025 1030 1035

Tyr Glu Val Lys Ser Lys Lys His Pro Gln Ile Ile Lys Lys Gly
1040 1045 1050

<210> 140

<211> 1053
<212> PRT
<213> Staphylococcus aureus

<220>
<221> VARIANTE
<222> (10)..(10)
<223> conversión de residuo Asp en residuo Ala

<220>
<221> VARIANTE
<222> (557)..(557)
<223> conversión de residuo His en residuo Ala

<400> 140

Met Lys Arg Asn Tyr Ile Leu Gly Leu Ala Ile Gly Ile Thr Ser Val
1 5 10 15

Gly Tyr Gly Ile Ile Asp Tyr Glu Thr Arg Asp Val Ile Asp Ala Gly
20 25 30

Val Arg Leu Phe Lys Glu Ala Asn Val Glu Asn Asn Glu Gly Arg Arg
35 40 45

Ser Lys Arg Gly Ala Arg Arg Leu Lys Arg Arg Arg Arg His Arg Ile
50 55 60

Gln Arg Val Lys Lys Leu Leu Phe Asp Tyr Asn Leu Leu Thr Asp His
65 70 75 80

Ser Glu Leu Ser Gly Ile Asn Pro Tyr Glu Ala Arg Val Lys Gly Leu
85 90 95

Ser Gln Lys Leu Ser Glu Glu Glu Phe Ser Ala Ala Leu Leu His Leu
100 105 110

Ala Lys Arg Arg Gly Val His Asn Val Asn Glu Val Glu Glu Asp Thr
115 120 125

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

130

135

140

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

Asp Gly Glu Val Arg Gly Ser Ile Asn Arg Phe Lys Thr Ser Asp Tyr
 165 170 175

Val Lys Glu Ala Lys Gln Leu Leu Lys Val Gln Lys Ala Tyr His Gln
 180 185 190

Leu Asp Gln Ser Phe Ile Asp Thr Tyr Ile Asp Leu Leu Glu Thr Arg
 195 200 205

Arg Thr Tyr Tyr Glu Gly Pro Gly Glu Gly Ser Pro Phe Gly Trp Lys
 210 215 220

Asp Ile Lys Glu Trp Tyr Glu Met Leu Met Gly His Cys Thr Tyr Phe
 225 230 235 240

Pro Glu Glu Leu Arg Ser Val Lys Tyr Ala Tyr Asn Ala Asp Leu Tyr
 245 250 255

Asn Ala Leu Asn Asp Leu Asn Asn Leu Val Ile Thr Arg Asp Glu Asn
 260 265 270

Glu Lys Leu Glu Tyr Tyr Glu Lys Phe Gln Ile Ile Glu Asn Val Phe
 275 280 285

Lys Gln Lys Lys Lys Pro Thr Leu Lys Gln Ile Ala Lys Glu Ile Leu
 290 295 300

Val Asn Glu Glu Asp Ile Lys Gly Tyr Arg Val Thr Ser Thr Gly Lys
 305 310 315 320

Pro Glu Phe Thr Asn Leu Lys Val Tyr His Asp Ile Lys Asp Ile Thr
 325 330 335

Ala Arg Lys Glu Ile Ile Glu Asn Ala Glu Leu Leu Asp Gln Ile Ala
340 345 350

Lys Ile Leu Thr Ile Tyr Gln Ser Ser Glu Asp Ile Gln Glu Glu Leu
355 360 365

Thr Asn Leu Asn Ser Glu Leu Thr Gln Glu Glu Ile Glu Gln Ile Ser
370 375 380

Asn Leu Lys Gly Tyr Thr Gly Thr His Asn Leu Ser Leu Lys Ala Ile
385 390 395 400

Asn Leu Ile Leu Asp Glu Leu Trp His Thr Asn Asp Asn Gln Ile Ala
405 410 415

Ile Phe Asn Arg Leu Lys Leu Val Pro Lys Lys Val Asp Leu Ser Gln
420 425 430

Gln Lys Glu Ile Pro Thr Thr Leu Val Asp Asp Phe Ile Leu Ser Pro
435 440 445

Val Val Lys Arg Ser Phe Ile Gln Ser Ile Lys Val Ile Asn Ala Ile
450 455 460

Ile Lys Lys Tyr Gly Leu Pro Asn Asp Ile Ile Ile Glu Leu Ala Arg
465 470 475 480

Glu Lys Asn Ser Lys Asp Ala Gln Lys Met Ile Asn Glu Met Gln Lys
485 490 495

Arg Asn Arg Gln Thr Asn Glu Arg Ile Glu Glu Ile Ile Arg Thr Thr
500 505 510

Gly Lys Glu Asn Ala Lys Tyr Leu Ile Glu Lys Ile Lys Leu His Asp
515 520 525

Met Gln Glu Gly Lys Cys Leu Tyr Ser Leu Glu Ala Ile Pro Leu Glu

530

535

540

Asp Leu Leu Asn Asn Pro Phe Asn Tyr Glu Val Asp Ala Ile Ile Pro
 545 550 555 560

Arg Ser Val Ser Phe Asp Asn Ser Phe Asn Asn Lys Val Leu Val Lys
 565 570 575

Gln Glu Glu Asn Ser Lys Lys Gly Asn Arg Thr Pro Phe Gln Tyr Leu
 580 585 590

Ser Ser Ser Asp Ser Lys Ile Ser Tyr Glu Thr Phe Lys Lys His Ile
 595 600 605

Leu Asn Leu Ala Lys Gly Lys Gly Arg Ile Ser Lys Thr Lys Lys Glu
 610 615 620

Tyr Leu Leu Glu Glu Arg Asp Ile Asn Arg Phe Ser Val Gln Lys Asp
 625 630 635 640

Phe Ile Asn Arg Asn Leu Val Asp Thr Arg Tyr Ala Thr Arg Gly Leu
 645 650 655

Met Asn Leu Leu Arg Ser Tyr Phe Arg Val Asn Asn Leu Asp Val Lys
 660 665 670

Val Lys Ser Ile Asn Gly Gly Phe Thr Ser Phe Leu Arg Arg Lys Trp
 675 680 685

Lys Phe Lys Lys Glu Arg Asn Lys Gly Tyr Lys His His Ala Glu Asp
 690 695 700

Ala Leu Ile Ile Ala Asn Ala Asp Phe Ile Phe Lys Glu Trp Lys Lys
 705 710 715 720

Leu Asp Lys Ala Lys Lys Val Met Glu Asn Gln Met Phe Glu Glu Lys
 725 730 735

Gln Ala Glu Ser Met Pro Glu Ile Glu Thr Glu Gln Glu Tyr Lys Glu
740 745 750

Ile Phe Ile Thr Pro His Gln Ile Lys His Ile Lys Asp Phe Lys Asp
755 760 765

Tyr Lys Tyr Ser His Arg Val Asp Lys Lys Pro Asn Arg Glu Leu Ile
770 775 780

Asn Asp Thr Leu Tyr Ser Thr Arg Lys Asp Asp Lys Gly Asn Thr Leu
785 790 795 800

Ile Val Asn Asn Leu Asn Gly Leu Tyr Asp Lys Asp Asn Asp Lys Leu
805 810 815

Lys Lys Leu Ile Asn Lys Ser Pro Glu Lys Leu Leu Met Tyr His His
820 825 830

Asp Pro Gln Thr Tyr Gln Lys Leu Lys Leu Ile Met Glu Gln Tyr Gly
835 840 845

Asp Glu Lys Asn Pro Leu Tyr Lys Tyr Tyr Glu Glu Thr Gly Asn Tyr
850 855 860

Leu Thr Lys Tyr Ser Lys Lys Asp Asn Gly Pro Val Ile Lys Lys Ile
865 870 875 880

Lys Tyr Tyr Gly Asn Lys Leu Asn Ala His Leu Asp Ile Thr Asp Asp
885 890 895

Tyr Pro Asn Ser Arg Asn Lys Val Val Lys Leu Ser Leu Lys Pro Tyr
900 905 910

Arg Phe Asp Val Tyr Leu Asp Asn Gly Val Tyr Lys Phe Val Thr Val
915 920 925

Lys Asn Leu Asp Val Ile Lys Lys Glu Asn Tyr Tyr Glu Val Asn Ser

930

935

940

Lys Cys Tyr Glu Glu Ala Lys Lys Leu Lys Lys Ile Ser Asn Gln Ala
 945 950 955 960

Glu Phe Ile Ala Ser Phe Tyr Asn Asn Asp Leu Ile Lys Ile Asn Gly
 965 970 975

Glu Leu Tyr Arg Val Ile Gly Val Asn Asn Asp Leu Leu Asn Arg Ile
 980 985 990

Glu Val Asn Met Ile Asp Ile Thr Tyr Arg Glu Tyr Leu Glu Asn Met
 995 1000 1005

Asn Asp Lys Arg Pro Pro Arg Ile Ile Lys Thr Ile Ala Ser Lys
 1010 1015 1020

Thr Gln Ser Ile Lys Lys Tyr Ser Thr Asp Ile Leu Gly Asn Leu
 1025 1030 1035

Tyr Glu Val Lys Ser Lys Lys His Pro Gln Ile Ile Lys Lys Gly
 1040 1045 1050

<210> 141

<211> 1028

<212> PRT

<213> Secuencia artificial

<220>

<223> residuos de amino ácido (721 a 745 residuos de amino ácido
 dSaCas9) delección mutante

<220>

<221> VARIANTE

<222> (10)..(10)

<223> conversión de residuo Asp en residuo Ala

<220>

<221> VARIANTE

<222> (580)..(580)

<223> conversión de residuo Asn en residuo Ala

<400> 141

Met Lys Arg Asn Tyr Ile Leu Gly Leu Ala Ile Gly Ile Thr Ser Val
1 5 10 15

Gly Tyr Gly Ile Ile Asp Tyr Glu Thr Arg Asp Val Ile Asp Ala Gly
20 25 30

Val Arg Leu Phe Lys Glu Ala Asn Val Glu Asn Asn Glu Gly Arg Arg
35 40 45

Ser Lys Arg Gly Ala Arg Arg Leu Lys Arg Arg Arg Arg His Arg Ile
50 55 60

Gln Arg Val Lys Lys Leu Leu Phe Asp Tyr Asn Leu Leu Thr Asp His
65 70 75 80

Ser Glu Leu Ser Gly Ile Asn Pro Tyr Glu Ala Arg Val Lys Gly Leu
85 90 95

Ser Gln Lys Leu Ser Glu Glu Glu Phe Ser Ala Ala Leu Leu His Leu
100 105 110

Ala Lys Arg Arg Gly Val His Asn Val Asn Glu Val Glu Glu Asp Thr
115 120 125

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

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

Asp Gly Glu Val Arg Gly Ser Ile Asn Arg Phe Lys Thr Ser Asp Tyr
165 170 175

Val Lys Glu Ala Lys Gln Leu Leu Lys Val Gln Lys Ala Tyr His Gln
180 185 190

Leu Asp Gln Ser Phe Ile Asp Thr Tyr Ile Asp Leu Leu Glu Thr Arg
195 200 205

Arg Thr Tyr Tyr Glu Gly Pro Gly Glu Gly Ser Pro Phe Gly Trp Lys
210 215 220

Asp Ile Lys Glu Trp Tyr Glu Met Leu Met Gly His Cys Thr Tyr Phe
225 230 235 240

Pro Glu Glu Leu Arg Ser Val Lys Tyr Ala Tyr Asn Ala Asp Leu Tyr
245 250 255

Asn Ala Leu Asn Asp Leu Asn Asn Leu Val Ile Thr Arg Asp Glu Asn
260 265 270

Glu Lys Leu Glu Tyr Tyr Glu Lys Phe Gln Ile Ile Glu Asn Val Phe
275 280 285

Lys Gln Lys Lys Lys Pro Thr Leu Lys Gln Ile Ala Lys Glu Ile Leu
290 295 300

Val Asn Glu Glu Asp Ile Lys Gly Tyr Arg Val Thr Ser Thr Gly Lys
305 310 315 320

Pro Glu Phe Thr Asn Leu Lys Val Tyr His Asp Ile Lys Asp Ile Thr
325 330 335

Ala Arg Lys Glu Ile Ile Glu Asn Ala Glu Leu Leu Asp Gln Ile Ala
340 345 350

Lys Ile Leu Thr Ile Tyr Gln Ser Ser Glu Asp Ile Gln Glu Glu Leu
355 360 365

Thr Asn Leu Asn Ser Glu Leu Thr Gln Glu Glu Ile Glu Gln Ile Ser
370 375 380

Asn Leu Lys Gly Tyr Thr Gly Thr His Asn Leu Ser Leu Lys Ala Ile

385 390 395 400

Asn Leu Ile Leu Asp Glu Leu Trp His Thr Asn Asp Asn Gln Ile Ala
405 410 415

Ile Phe Asn Arg Leu Lys Leu Val Pro Lys Lys Val Asp Leu Ser Gln
420 425 430

Gln Lys Glu Ile Pro Thr Thr Leu Val Asp Asp Phe Ile Leu Ser Pro
435 440 445

Val Val Lys Arg Ser Phe Ile Gln Ser Ile Lys Val Ile Asn Ala Ile
450 455 460

Ile Lys Lys Tyr Gly Leu Pro Asn Asp Ile Ile Ile Glu Leu Ala Arg
465 470 475 480

Glu Lys Asn Ser Lys Asp Ala Gln Lys Met Ile Asn Glu Met Gln Lys
485 490 495

Arg Asn Arg Gln Thr Asn Glu Arg Ile Glu Glu Ile Ile Arg Thr Thr
500 505 510

Gly Lys Glu Asn Ala Lys Tyr Leu Ile Glu Lys Ile Lys Leu His Asp
515 520 525

Met Gln Glu Gly Lys Cys Leu Tyr Ser Leu Glu Ala Ile Pro Leu Glu
530 535 540

Asp Leu Leu Asn Asn Pro Phe Asn Tyr Glu Val Asp His Ile Ile Pro
545 550 555 560

Arg Ser Val Ser Phe Asp Asn Ser Phe Asn Asn Lys Val Leu Val Lys
565 570 575

Gln Glu Glu Ala Ser Lys Lys Gly Asn Arg Thr Pro Phe Gln Tyr Leu
580 585 590

Ser Ser Ser Asp Ser Lys Ile Ser Tyr Glu Thr Phe Lys Lys His Ile
595 600 605

Leu Asn Leu Ala Lys Gly Lys Gly Arg Ile Ser Lys Thr Lys Lys Glu
610 615 620

Tyr Leu Leu Glu Glu Arg Asp Ile Asn Arg Phe Ser Val Gln Lys Asp
625 630 635 640

Phe Ile Asn Arg Asn Leu Val Asp Thr Arg Tyr Ala Thr Arg Gly Leu
645 650 655

Met Asn Leu Leu Arg Ser Tyr Phe Arg Val Asn Asn Leu Asp Val Lys
660 665 670

Val Lys Ser Ile Asn Gly Gly Phe Thr Ser Phe Leu Arg Arg Lys Trp
675 680 685

Lys Phe Lys Lys Glu Arg Asn Lys Gly Tyr Lys His His Ala Glu Asp
690 695 700

Ala Leu Ile Ile Ala Asn Ala Asp Phe Ile Phe Lys Glu Trp Lys Lys
705 710 715 720

Thr Glu Gln Glu Tyr Lys Glu Ile Phe Ile Thr Pro His Gln Ile Lys
725 730 735

His Ile Lys Asp Phe Lys Asp Tyr Lys Tyr Ser His Arg Val Asp Lys
740 745 750

Lys Pro Asn Arg Glu Leu Ile Asn Asp Thr Leu Tyr Ser Thr Arg Lys
755 760 765

Asp Asp Lys Gly Asn Thr Leu Ile Val Asn Asn Leu Asn Gly Leu Tyr
770 775 780

Asp Lys Asp Asn Asp Lys Leu Lys Lys Leu Ile Asn Lys Ser Pro Glu

785				790				795				800				
Lys	Leu	Leu	Met	Tyr	His	His	Asp	Pro	Gln	Thr	Tyr	Gln	Lys	Leu	Lys	
				805					810					815		
Leu	Ile	Met	Glu	Gln	Tyr	Gly	Asp	Glu	Lys	Asn	Pro	Leu	Tyr	Lys	Tyr	
				820					825					830		
Tyr	Glu	Glu	Thr	Gly	Asn	Tyr	Leu	Thr	Lys	Tyr	Ser	Lys	Lys	Asp	Asn	
				835					840					845		
Gly	Pro	Val	Ile	Lys	Lys	Ile	Lys	Tyr	Tyr	Gly	Asn	Lys	Leu	Asn	Ala	
				850					855					860		
His	Leu	Asp	Ile	Thr	Asp	Asp	Tyr	Pro	Asn	Ser	Arg	Asn	Lys	Val	Val	
				865					870					875		
Lys	Leu	Ser	Leu	Lys	Pro	Tyr	Arg	Phe	Asp	Val	Tyr	Leu	Asp	Asn	Gly	
				885					890					895		
Val	Tyr	Lys	Phe	Val	Thr	Val	Lys	Asn	Leu	Asp	Val	Ile	Lys	Lys	Glu	
				900					905					910		
Asn	Tyr	Tyr	Glu	Val	Asn	Ser	Lys	Cys	Tyr	Glu	Glu	Ala	Lys	Lys	Leu	
				915					920					925		
Lys	Lys	Ile	Ser	Asn	Gln	Ala	Glu	Phe	Ile	Ala	Ser	Phe	Tyr	Asn	Asn	
				930					935					940		
Asp	Leu	Ile	Lys	Ile	Asn	Gly	Glu	Leu	Tyr	Arg	Val	Ile	Gly	Val	Asn	
				945					950					955		
Asn	Asp	Leu	Leu	Asn	Arg	Ile	Glu	Val	Asn	Met	Ile	Asp	Ile	Thr	Tyr	
				965					970					975		
Arg	Glu	Tyr	Leu	Glu	Asn	Met	Asn	Asp	Lys	Arg	Pro	Pro	Arg	Ile	Ile	
				980					985					990		

Lys Thr Ile Ala Ser Lys Thr Gln Ser Ile Lys Lys Tyr Ser Thr Asp
995 1000 1005

Ile Leu Gly Asn Leu Tyr Glu Val Lys Ser Lys Lys His Pro Gln
1010 1015 1020

Ile Ile Lys Lys Gly
1025

<210> 142
<211> 6
<212> PRT
<213> Secuencia artificial

<220>
<223> enlazador GGS GGS

<400> 142

Gly Gly Ser Gly Gly Ser
1 5

<210> 143
<211> 1034
<212> PRT
<213> Secuencia artificial

<220>
<223> residuos de amino ácido (721 a 745 residuos de amino ácido de
ddSaCas9) deleción mutante con enlazador GGS GGS

<220>
<221> VARIANTE
<222> (10)..(10)
<223> conversión de residuo Asp en residuo Ala

<220>
<221> VARIANTE
<222> (580)..(580)
<223> conversión de residuo Asn en residuo Ala

<220>
<221> MISC_FEATURE
<222> (721)..(726)

<223> enlazador GSGGS

<400> 143

Met Lys Arg Asn Tyr Ile Leu Gly Leu Ala Ile Gly Ile Thr Ser Val
1 5 10 15

Gly Tyr Gly Ile Ile Asp Tyr Glu Thr Arg Asp Val Ile Asp Ala Gly
20 25 30

Val Arg Leu Phe Lys Glu Ala Asn Val Glu Asn Asn Glu Gly Arg Arg
35 40 45

Ser Lys Arg Gly Ala Arg Arg Leu Lys Arg Arg Arg Arg His Arg Ile
50 55 60

Gln Arg Val Lys Lys Leu Leu Phe Asp Tyr Asn Leu Leu Thr Asp His
65 70 75 80

Ser Glu Leu Ser Gly Ile Asn Pro Tyr Glu Ala Arg Val Lys Gly Leu
85 90 95

Ser Gln Lys Leu Ser Glu Glu Glu Phe Ser Ala Ala Leu Leu His Leu
100 105 110

Ala Lys Arg Arg Gly Val His Asn Val Asn Glu Val Glu Glu Asp Thr
115 120 125

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

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

Asp Gly Glu Val Arg Gly Ser Ile Asn Arg Phe Lys Thr Ser Asp Tyr
165 170 175

Val Lys Glu Ala Lys Gln Leu Leu Lys Val Gln Lys Ala Tyr His Gln
180 185 190

Leu Asp Gln Ser Phe Ile Asp Thr Tyr Ile Asp Leu Leu Glu Thr Arg
195 200 205

Arg Thr Tyr Tyr Glu Gly Pro Gly Glu Gly Ser Pro Phe Gly Trp Lys
210 215 220

Asp Ile Lys Glu Trp Tyr Glu Met Leu Met Gly His Cys Thr Tyr Phe
225 230 235 240

Pro Glu Glu Leu Arg Ser Val Lys Tyr Ala Tyr Asn Ala Asp Leu Tyr
245 250 255

Asn Ala Leu Asn Asp Leu Asn Asn Leu Val Ile Thr Arg Asp Glu Asn
260 265 270

Glu Lys Leu Glu Tyr Tyr Glu Lys Phe Gln Ile Ile Glu Asn Val Phe
275 280 285

Lys Gln Lys Lys Lys Pro Thr Leu Lys Gln Ile Ala Lys Glu Ile Leu
290 295 300

Val Asn Glu Glu Asp Ile Lys Gly Tyr Arg Val Thr Ser Thr Gly Lys
305 310 315 320

Pro Glu Phe Thr Asn Leu Lys Val Tyr His Asp Ile Lys Asp Ile Thr
325 330 335

Ala Arg Lys Glu Ile Ile Glu Asn Ala Glu Leu Leu Asp Gln Ile Ala
340 345 350

Lys Ile Leu Thr Ile Tyr Gln Ser Ser Glu Asp Ile Gln Glu Glu Leu
355 360 365

Thr Asn Leu Asn Ser Glu Leu Thr Gln Glu Glu Ile Glu Gln Ile Ser
370 375 380

Asn Leu Lys Gly Tyr Thr Gly Thr His Asn Leu Ser Leu Lys Ala Ile
385 390 395 400

Asn Leu Ile Leu Asp Glu Leu Trp His Thr Asn Asp Asn Gln Ile Ala
405 410 415

Ile Phe Asn Arg Leu Lys Leu Val Pro Lys Lys Val Asp Leu Ser Gln
420 425 430

Gln Lys Glu Ile Pro Thr Thr Leu Val Asp Asp Phe Ile Leu Ser Pro
435 440 445

Val Val Lys Arg Ser Phe Ile Gln Ser Ile Lys Val Ile Asn Ala Ile
450 455 460

Ile Lys Lys Tyr Gly Leu Pro Asn Asp Ile Ile Ile Glu Leu Ala Arg
465 470 475 480

Glu Lys Asn Ser Lys Asp Ala Gln Lys Met Ile Asn Glu Met Gln Lys
485 490 495

Arg Asn Arg Gln Thr Asn Glu Arg Ile Glu Glu Ile Ile Arg Thr Thr
500 505 510

Gly Lys Glu Asn Ala Lys Tyr Leu Ile Glu Lys Ile Lys Leu His Asp
515 520 525

Met Gln Glu Gly Lys Cys Leu Tyr Ser Leu Glu Ala Ile Pro Leu Glu
530 535 540

Asp Leu Leu Asn Asn Pro Phe Asn Tyr Glu Val Asp His Ile Ile Pro
545 550 555 560

Arg Ser Val Ser Phe Asp Asn Ser Phe Asn Asn Lys Val Leu Val Lys
565 570 575

Gln Glu Glu Ala Ser Lys Lys Gly Asn Arg Thr Pro Phe Gln Tyr Leu
580 585 590

Ser Ser Ser Asp Ser Lys Ile Ser Tyr Glu Thr Phe Lys Lys His Ile
595 600 605

Leu Asn Leu Ala Lys Gly Lys Gly Arg Ile Ser Lys Thr Lys Lys Glu
610 615 620

Tyr Leu Leu Glu Glu Arg Asp Ile Asn Arg Phe Ser Val Gln Lys Asp
625 630 635 640

Phe Ile Asn Arg Asn Leu Val Asp Thr Arg Tyr Ala Thr Arg Gly Leu
645 650 655

Met Asn Leu Leu Arg Ser Tyr Phe Arg Val Asn Asn Leu Asp Val Lys
660 665 670

Val Lys Ser Ile Asn Gly Gly Phe Thr Ser Phe Leu Arg Arg Lys Trp
675 680 685

Lys Phe Lys Lys Glu Arg Asn Lys Gly Tyr Lys His His Ala Glu Asp
690 695 700

Ala Leu Ile Ile Ala Asn Ala Asp Phe Ile Phe Lys Glu Trp Lys Lys
705 710 715 720

Gly Gly Ser Gly Gly Ser Thr Glu Gln Glu Tyr Lys Glu Ile Phe Ile
725 730 735

Thr Pro His Gln Ile Lys His Ile Lys Asp Phe Lys Asp Tyr Lys Tyr
740 745 750

Ser His Arg Val Asp Lys Lys Pro Asn Arg Glu Leu Ile Asn Asp Thr
755 760 765

Leu Tyr Ser Thr Arg Lys Asp Asp Lys Gly Asn Thr Leu Ile Val Asn
770 775 780

Asn Leu Asn Gly Leu Tyr Asp Lys Asp Asn Asp Lys Leu Lys Lys Leu
785 790 795 800

Ile Asn Lys Ser Pro Glu Lys Leu Leu Met Tyr His His Asp Pro Gln
805 810 815

Thr Tyr Gln Lys Leu Lys Leu Ile Met Glu Gln Tyr Gly Asp Glu Lys
820 825 830

Asn Pro Leu Tyr Lys Tyr Tyr Glu Glu Thr Gly Asn Tyr Leu Thr Lys
835 840 845

Tyr Ser Lys Lys Asp Asn Gly Pro Val Ile Lys Lys Ile Lys Tyr Tyr
850 855 860

Gly Asn Lys Leu Asn Ala His Leu Asp Ile Thr Asp Asp Tyr Pro Asn
865 870 875 880

Ser Arg Asn Lys Val Val Lys Leu Ser Leu Lys Pro Tyr Arg Phe Asp
885 890 895

Val Tyr Leu Asp Asn Gly Val Tyr Lys Phe Val Thr Val Lys Asn Leu
900 905 910

Asp Val Ile Lys Lys Glu Asn Tyr Tyr Glu Val Asn Ser Lys Cys Tyr
915 920 925

Glu Glu Ala Lys Lys Leu Lys Lys Ile Ser Asn Gln Ala Glu Phe Ile
930 935 940

Ala Ser Phe Tyr Asn Asn Asp Leu Ile Lys Ile Asn Gly Glu Leu Tyr
945 950 955 960

Arg Val Ile Gly Val Asn Asn Asp Leu Leu Asn Arg Ile Glu Val Asn
965 970 975

Met Ile Asp Ile Thr Tyr Arg Glu Tyr Leu Glu Asn Met Asn Asp Lys
980 985 990

Arg Pro Pro Arg Ile Ile Lys Thr Ile Ala Ser Lys Thr Gln Ser Ile
995 1000 1005

Lys Lys Tyr Ser Thr Asp Ile Leu Gly Asn Leu Tyr Glu Val Lys
1010 1015 1020

Ser Lys Lys His Pro Gln Ile Ile Lys Lys Gly
1025 1030

<210> 144

<211> 886

<212> PRT

<213> Secuencia artificial

<220>

<223> residuos de amino ácido (482 a 648 residuos de amino ácido de
dSaCas9) delección mutante

<220>

<221> VARIANTE

<222> (10)..(10)

<223> conversión de residuo Asp en residuo Ala

<400> 144

Met Lys Arg Asn Tyr Ile Leu Gly Leu Ala Ile Gly Ile Thr Ser Val
1 5 10 15

Gly Tyr Gly Ile Ile Asp Tyr Glu Thr Arg Asp Val Ile Asp Ala Gly
20 25 30

Val Arg Leu Phe Lys Glu Ala Asn Val Glu Asn Asn Glu Gly Arg Arg
35 40 45

Ser Lys Arg Gly Ala Arg Arg Leu Lys Arg Arg Arg Arg His Arg Ile
50 55 60

Gln Arg Val Lys Lys Leu Leu Phe Asp Tyr Asn Leu Leu Thr Asp His
65 70 75 80

Ser Glu Leu Ser Gly Ile Asn Pro Tyr Glu Ala Arg Val Lys Gly Leu
85 90 95

Ser Gln Lys Leu Ser Glu Glu Glu Phe Ser Ala Ala Leu Leu His Leu
100 105 110

Ala Lys Arg Arg Gly Val His Asn Val Asn Glu Val Glu Glu Asp Thr
115 120 125

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

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

Asp Gly Glu Val Arg Gly Ser Ile Asn Arg Phe Lys Thr Ser Asp Tyr
165 170 175

Val Lys Glu Ala Lys Gln Leu Leu Lys Val Gln Lys Ala Tyr His Gln
180 185 190

Leu Asp Gln Ser Phe Ile Asp Thr Tyr Ile Asp Leu Leu Glu Thr Arg
195 200 205

Arg Thr Tyr Tyr Glu Gly Pro Gly Glu Gly Ser Pro Phe Gly Trp Lys
210 215 220

Asp Ile Lys Glu Trp Tyr Glu Met Leu Met Gly His Cys Thr Tyr Phe
225 230 235 240

Pro Glu Glu Leu Arg Ser Val Lys Tyr Ala Tyr Asn Ala Asp Leu Tyr
245 250 255

Asn Ala Leu Asn Asp Leu Asn Asn Leu Val Ile Thr Arg Asp Glu Asn
260 265 270

Glu Lys Leu Glu Tyr Tyr Glu Lys Phe Gln Ile Ile Glu Asn Val Phe

275

280

285

Lys Gln Lys Lys Lys Pro Thr Leu Lys Gln Ile Ala Lys Glu Ile Leu
290 295 300

Val Asn Glu Glu Asp Ile Lys Gly Tyr Arg Val Thr Ser Thr Gly Lys
305 310 315 320

Pro Glu Phe Thr Asn Leu Lys Val Tyr His Asp Ile Lys Asp Ile Thr
325 330 335

Ala Arg Lys Glu Ile Ile Glu Asn Ala Glu Leu Leu Asp Gln Ile Ala
340 345 350

Lys Ile Leu Thr Ile Tyr Gln Ser Ser Glu Asp Ile Gln Glu Glu Leu
355 360 365

Thr Asn Leu Asn Ser Glu Leu Thr Gln Glu Glu Ile Glu Gln Ile Ser
370 375 380

Asn Leu Lys Gly Tyr Thr Gly Thr His Asn Leu Ser Leu Lys Ala Ile
385 390 395 400

Asn Leu Ile Leu Asp Glu Leu Trp His Thr Asn Asp Asn Gln Ile Ala
405 410 415

Ile Phe Asn Arg Leu Lys Leu Val Pro Lys Lys Val Asp Leu Ser Gln
420 425 430

Gln Lys Glu Ile Pro Thr Thr Leu Val Asp Asp Phe Ile Leu Ser Pro
435 440 445

Val Val Lys Arg Ser Phe Ile Gln Ser Ile Lys Val Ile Asn Ala Ile
450 455 460

Ile Lys Lys Tyr Gly Leu Pro Asn Asp Ile Ile Ile Glu Leu Ala Arg
465 470 475 480

Glu Thr Arg Tyr Ala Thr Arg Gly Leu Met Asn Leu Leu Arg Ser Tyr
485 490 495

Phe Arg Val Asn Asn Leu Asp Val Lys Val Lys Ser Ile Asn Gly Gly
500 505 510

Phe Thr Ser Phe Leu Arg Arg Lys Trp Lys Phe Lys Lys Glu Arg Asn
515 520 525

Lys Gly Tyr Lys His His Ala Glu Asp Ala Leu Ile Ile Ala Asn Ala
530 535 540

Asp Phe Ile Phe Lys Glu Trp Lys Lys Leu Asp Lys Ala Lys Lys Val
545 550 555 560

Met Glu Asn Gln Met Phe Glu Glu Lys Gln Ala Glu Ser Met Pro Glu
565 570 575

Ile Glu Thr Glu Gln Glu Tyr Lys Glu Ile Phe Ile Thr Pro His Gln
580 585 590

Ile Lys His Ile Lys Asp Phe Lys Asp Tyr Lys Tyr Ser His Arg Val
595 600 605

Asp Lys Lys Pro Asn Arg Glu Leu Ile Asn Asp Thr Leu Tyr Ser Thr
610 615 620

Arg Lys Asp Asp Lys Gly Asn Thr Leu Ile Val Asn Asn Leu Asn Gly
625 630 635 640

Leu Tyr Asp Lys Asp Asn Asp Lys Leu Lys Lys Leu Ile Asn Lys Ser
645 650 655

Pro Glu Lys Leu Leu Met Tyr His His Asp Pro Gln Thr Tyr Gln Lys
660 665 670

Leu Lys Leu Ile Met Glu Gln Tyr Gly Asp Glu Lys Asn Pro Leu Tyr

675

680

685

Lys Tyr Tyr Glu Glu Thr Gly Asn Tyr Leu Thr Lys Tyr Ser Lys Lys
 690 695 700

Asp Asn Gly Pro Val Ile Lys Lys Ile Lys Tyr Tyr Gly Asn Lys Leu
 705 710 715 720

Asn Ala His Leu Asp Ile Thr Asp Asp Tyr Pro Asn Ser Arg Asn Lys
 725 730 735

Val Val Lys Leu Ser Leu Lys Pro Tyr Arg Phe Asp Val Tyr Leu Asp
 740 745 750

Asn Gly Val Tyr Lys Phe Val Thr Val Lys Asn Leu Asp Val Ile Lys
 755 760 765

Lys Glu Asn Tyr Tyr Glu Val Asn Ser Lys Cys Tyr Glu Glu Ala Lys
 770 775 780

Lys Leu Lys Lys Ile Ser Asn Gln Ala Glu Phe Ile Ala Ser Phe Tyr
 785 790 795 800

Asn Asn Asp Leu Ile Lys Ile Asn Gly Glu Leu Tyr Arg Val Ile Gly
 805 810 815

Val Asn Asn Asp Leu Leu Asn Arg Ile Glu Val Asn Met Ile Asp Ile
 820 825 830

Thr Tyr Arg Glu Tyr Leu Glu Asn Met Asn Asp Lys Arg Pro Pro Arg
 835 840 845

Ile Ile Lys Thr Ile Ala Ser Lys Thr Gln Ser Ile Lys Lys Tyr Ser
 850 855 860

Thr Asp Ile Leu Gly Asn Leu Tyr Glu Val Lys Ser Lys Lys His Pro
 865 870 875 880

Gln Ile Ile Lys Lys Gly
885

<210> 145
<211> 892
<212> PRT
<213> Secuencia artificial

<220>
<223> residuos de amino ácido (482 a 648 residuos de amino ácido de
dSaCas9) delección mutante con enlazador GGS GGS

<220>
<221> VARIANTE
<222> (10)..(10)
<223> conversión de residuo Asp en resiudo Ala

<220>
<221> MISC_FEATURE
<222> (482)..(487)
<223> enlazador GGS GGS

<400> 145

Met Lys Arg Asn Tyr Ile Leu Gly Leu Ala Ile Gly Ile Thr Ser Val
1 5 10 15

Gly Tyr Gly Ile Ile Asp Tyr Glu Thr Arg Asp Val Ile Asp Ala Gly
20 25 30

Val Arg Leu Phe Lys Glu Ala Asn Val Glu Asn Asn Glu Gly Arg Arg
35 40 45

Ser Lys Arg Gly Ala Arg Arg Leu Lys Arg Arg Arg Arg His Arg Ile
50 55 60

Gln Arg Val Lys Lys Leu Leu Phe Asp Tyr Asn Leu Leu Thr Asp His
65 70 75 80

Ser Glu Leu Ser Gly Ile Asn Pro Tyr Glu Ala Arg Val Lys Gly Leu
85 90 95

Ser Gln Lys Leu Ser Glu Glu Glu Phe Ser Ala Ala Leu Leu His Leu
100 105 110

Ala Lys Arg Arg Gly Val His Asn Val Asn Glu Val Glu Glu Asp Thr
115 120 125

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

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

Asp Gly Glu Val Arg Gly Ser Ile Asn Arg Phe Lys Thr Ser Asp Tyr
165 170 175

Val Lys Glu Ala Lys Gln Leu Leu Lys Val Gln Lys Ala Tyr His Gln
180 185 190

Leu Asp Gln Ser Phe Ile Asp Thr Tyr Ile Asp Leu Leu Glu Thr Arg
195 200 205

Arg Thr Tyr Tyr Glu Gly Pro Gly Glu Gly Ser Pro Phe Gly Trp Lys
210 215 220

Asp Ile Lys Glu Trp Tyr Glu Met Leu Met Gly His Cys Thr Tyr Phe
225 230 235 240

Pro Glu Glu Leu Arg Ser Val Lys Tyr Ala Tyr Asn Ala Asp Leu Tyr
245 250 255

Asn Ala Leu Asn Asp Leu Asn Asn Leu Val Ile Thr Arg Asp Glu Asn
260 265 270

Glu Lys Leu Glu Tyr Tyr Glu Lys Phe Gln Ile Ile Glu Asn Val Phe
275 280 285

Lys Gln Lys Lys Lys Pro Thr Leu Lys Gln Ile Ala Lys Glu Ile Leu

290

295

300

Val Asn Glu Glu Asp Ile Lys Gly Tyr Arg Val Thr Ser Thr Gly Lys
 305 310 315 320

Pro Glu Phe Thr Asn Leu Lys Val Tyr His Asp Ile Lys Asp Ile Thr
 325 330 335

Ala Arg Lys Glu Ile Ile Glu Asn Ala Glu Leu Leu Asp Gln Ile Ala
 340 345 350

Lys Ile Leu Thr Ile Tyr Gln Ser Ser Glu Asp Ile Gln Glu Glu Leu
 355 360 365

Thr Asn Leu Asn Ser Glu Leu Thr Gln Glu Glu Ile Glu Gln Ile Ser
 370 375 380

Asn Leu Lys Gly Tyr Thr Gly Thr His Asn Leu Ser Leu Lys Ala Ile
 385 390 395 400

Asn Leu Ile Leu Asp Glu Leu Trp His Thr Asn Asp Asn Gln Ile Ala
 405 410 415

Ile Phe Asn Arg Leu Lys Leu Val Pro Lys Lys Val Asp Leu Ser Gln
 420 425 430

Gln Lys Glu Ile Pro Thr Thr Leu Val Asp Asp Phe Ile Leu Ser Pro
 435 440 445

Val Val Lys Arg Ser Phe Ile Gln Ser Ile Lys Val Ile Asn Ala Ile
 450 455 460

Ile Lys Lys Tyr Gly Leu Pro Asn Asp Ile Ile Ile Glu Leu Ala Arg
 465 470 475 480

Glu Gly Gly Ser Gly Gly Ser Thr Arg Tyr Ala Thr Arg Gly Leu Met
 485 490 495

Asn Leu Leu Arg Ser Tyr Phe Arg Val Asn Asn Leu Asp Val Lys Val
500 505 510

Lys Ser Ile Asn Gly Gly Phe Thr Ser Phe Leu Arg Arg Lys Trp Lys
515 520 525

Phe Lys Lys Glu Arg Asn Lys Gly Tyr Lys His His Ala Glu Asp Ala
530 535 540

Leu Ile Ile Ala Asn Ala Asp Phe Ile Phe Lys Glu Trp Lys Lys Leu
545 550 555 560

Asp Lys Ala Lys Lys Val Met Glu Asn Gln Met Phe Glu Glu Lys Gln
565 570 575

Ala Glu Ser Met Pro Glu Ile Glu Thr Glu Gln Glu Tyr Lys Glu Ile
580 585 590

Phe Ile Thr Pro His Gln Ile Lys His Ile Lys Asp Phe Lys Asp Tyr
595 600 605

Lys Tyr Ser His Arg Val Asp Lys Lys Pro Asn Arg Glu Leu Ile Asn
610 615 620

Asp Thr Leu Tyr Ser Thr Arg Lys Asp Asp Lys Gly Asn Thr Leu Ile
625 630 635 640

Val Asn Asn Leu Asn Gly Leu Tyr Asp Lys Asp Asn Asp Lys Leu Lys
645 650 655

Lys Leu Ile Asn Lys Ser Pro Glu Lys Leu Leu Met Tyr His His Asp
660 665 670

Pro Gln Thr Tyr Gln Lys Leu Lys Leu Ile Met Glu Gln Tyr Gly Asp
675 680 685

Glu Lys Asn Pro Leu Tyr Lys Tyr Tyr Glu Glu Thr Gly Asn Tyr Leu

690

695

700

Thr Lys Tyr Ser Lys Lys Asp Asn Gly Pro Val Ile Lys Lys Ile Lys
 705 710 715 720

Tyr Tyr Gly Asn Lys Leu Asn Ala His Leu Asp Ile Thr Asp Asp Tyr
 725 730 735

Pro Asn Ser Arg Asn Lys Val Val Lys Leu Ser Leu Lys Pro Tyr Arg
 740 745 750

Phe Asp Val Tyr Leu Asp Asn Gly Val Tyr Lys Phe Val Thr Val Lys
 755 760 765

Asn Leu Asp Val Ile Lys Lys Glu Asn Tyr Tyr Glu Val Asn Ser Lys
 770 775 780

Cys Tyr Glu Glu Ala Lys Lys Leu Lys Lys Ile Ser Asn Gln Ala Glu
 785 790 795 800

Phe Ile Ala Ser Phe Tyr Asn Asn Asp Leu Ile Lys Ile Asn Gly Glu
 805 810 815

Leu Tyr Arg Val Ile Gly Val Asn Asn Asp Leu Leu Asn Arg Ile Glu
 820 825 830

Val Asn Met Ile Asp Ile Thr Tyr Arg Glu Tyr Leu Glu Asn Met Asn
 835 840 845

Asp Lys Arg Pro Pro Arg Ile Ile Lys Thr Ile Ala Ser Lys Thr Gln
 850 855 860

Ser Ile Lys Lys Tyr Ser Thr Asp Ile Leu Gly Asn Leu Tyr Glu Val
 865 870 875 880

Lys Ser Lys Lys His Pro Gln Ile Ile Lys Lys Gly
 885 890

<210> 146
<211> 21
<212> ARN
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(21)
<223> ARNcr correspondiente a la secuencia diana (SEQ ID NO:5)

<400> 146
cccagucgag gccaaagaag a 21

<210> 147
<211> 21
<212> ADN
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(21)
<223> secuencia complementaria a la secuencia diana (SEQ ID
No:5)

<400> 147
tcttcttttg cctcgactgg g 21

<210> 148
<211> 19
<212> ADN
<213> Francisella novicid

<220>
<221> misc_feature
<223> 5'-manejo de ARNcr

<400> 148
aatttctact gttgtagat 19

<210> 149
<211> 83
<212> ADN
<213> Staphylococcus aureus

<220>
<221> misc_feature
<222> (1)..(83)
<223> secuencia que codifica tracrARN

<400> 149
gttttagtac tctggaaaca gaatctacta aaacaaggca aaatgccgtg tttatctcgt 60
caacttggtg gcgagatttt ttt 83

<210> 150
<211> 76
<212> ADN
<213> Staphylococcus aureus

<220>
<221> misc_feature
<222> (1)..(76)
<223> secuencia de andamio SaCas9 gARN

<400> 150
gttttagtac tctggaaaca gaatctacta aaacaaggca aaatgccgtg tttatctcgt 60
caacttggtg gcgaga 76

<210> 151
<211> 3477
<212> ADN
<213> Secuencia artificial

<220>
<223> dSaCas9 fusionada con KRAB (ADN)

<400> 151
atggcccca aaagaagcg gaaggtcgg atccacggag tcccagcagc caagcggaac 60
tacatcctgg gcctggccat cggcatcacc agcgtgggct acggcatcat cgactacgag 120
acacgggacg tgatcgatgc cggcgtgcgg ctgttcaaag aggccaacgt ggaaaacaac 180
gagggcaggc ggagcaagag aggcgccaga aggctgaagc ggcggaggcg gcatagaatc 240
cagagagtga agaagctgct gttcgactac aacctgctga ccgaccacag cgagctgagc 300
ggcatcaacc cctacgaggc cagagtgaag ggcctgagcc agaagctgag cgaggaagag 360

ttctctgccg ccctgctgca cctggccaag agaagaggcg tgcacaacgt gaacgaggtg	420
gaagaggaca ccggcaacga gctgtccacc aaagagcaga tcagccggaa cagcaaggcc	480
ctggaagaga aatacgtggc cgaactgcag ctggaacggc tgaagaaaga cggcgaagtg	540
cggggcagca tcaacagatt caagaccagc gactacgtga aagaagccaa acagctgctg	600
aaggtgcaga aggcctacca ccagctggac cagagcttca tcgacaccta catcgacctg	660
ctggaaaccc ggcggaacct ctatgaggga cctggcgagg gcagcccctt cggctggaag	720
gacatcaaag aatggtacga gatgctgatg ggccactgca cctacttccc cgaggaactg	780
cggagcgtga agtacgccta caacgccgac ctgtacaacg ccctgaacga cctgaacaat	840
ctcgtgatca ccagggacga gaacgagaag ctggaatatt acgagaagtt ccagatcatc	900
gagaacgtgt tcaagcagaa gaagaagccc accctgaagc agatcgccaa agaaatcctc	960
gtgaacgaag aggatattaa gggctacaga gtgaccagca ccggcaagcc cgagtccacc	1020
aacctgaagg tgtaccacga catcaaggac attaccgccc ggaaagagat tattgagaac	1080
gccgagctgc tggatcagat tgccaagatc ctgaccatct accagagcag cgaggacatc	1140
caggaagaac tgaccaatct gaactccgag ctgaccagga aagagatcga gcagatctct	1200
aatctgaagg gctataccgg caccacaac ctgagcctga aggccatcaa cctgatcctg	1260
gacgagctgt ggcacaccaa cgacaaccag atcgctatct tcaaccggct gaagctgggtg	1320
cccaagaagg tggacctgtc ccagcagaaa gagatcccca ccaccctggt ggacgacttc	1380
atcctgagcc ccgtcgtgaa gagaagcttc atccagagca tcaaagtgat caacgccatc	1440
atcaagaagt acggcctgcc caacgacatc attatcgagc tggcccgca gaagaactcc	1500
aaggacgccc agaaaatgat caacgagatg cagaagcgga accggcagac caacgagcgg	1560
atcgaggaaa tcatccggac caccggcaaa gagaacgcca agtacctgat cgagaagatc	1620
aagctgcacg acatgcagga aggcaagtgc ctgtacagcc tggaaagccat ccctctggaa	1680
gatctgtgta acaaccccct caactatgag gtggaccaca tcatccccag aagcgtgtcc	1740
ttcgacaaca gcttcaacaa caaggtgctc gtgaagcagg aagaagccag caagaagggc	1800
aaccggaccc cattccagta cctgagcagc agcgacagca agatcagcta cgaaaccttc	1860

aagaagcaca	tcctgaatct	ggccaagggc	aagggcagaa	tcagcaagac	caagaaagag	1920
tatctgctgg	aagaacggga	catcaacagg	ttctccgtgc	agaaagactt	catcaaccgg	1980
aacctggtgg	ataccagata	cgccaccaga	ggcctgatga	acctgctgcg	gagctacttc	2040
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cggcggaagt	ggaagtttaa	gaaagagcgg	aacaaggggt	acaagcacca	cgccgaggac	2160
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aaaaaagtga	tggaaaacca	gatgttcgag	gaaaagcagg	ccgagagcat	gcccgagatc	2280
gaaaccgagc	aggagtacaa	agagatcttc	atcaccccc	accagatcaa	gcacattaag	2340
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aacgacaccc	tgtactccac	ccggaaggac	gacaagggca	acaccctgat	cgtgaacaat	2460
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gaaaagctgc	tgatgtacca	ccacgacccc	cagacctacc	agaaactgaa	gctgattatg	2580
gaacagtacg	gcgacgagaa	gaatccccctg	tacaagtact	acgaggaaac	cgggaactac	2640
ctgaccaagt	actccaaaaa	ggacaacggc	cccgtgatca	agaagattaa	gtattacggc	2700
aacaaactga	acgcccattct	ggacatcacc	gacgactacc	ccaacagcag	aaacaaggtc	2760
gtgaagctgt	ccctgaagcc	ctacagattc	gacgtgtacc	tggacaatgg	cgtgtacaag	2820
ttcgtgaccg	tgaagaatct	ggatgtgatc	aaaaaagaaa	actactacga	agtgaatagc	2880
aagtgctatg	aggaagctaa	gaagctgaag	aagatcagca	accaggccga	gtttatcgcc	2940
tccttctaca	acaacgatct	gatcaagatc	aacggcgagc	tgtatagagt	gatcggcgtg	3000
aacaacgacc	tgctgaaccg	gatcgaagtg	aacatgatcg	acatcaccta	ccgcgagtac	3060
ctggaaaaca	tgaacgacaa	gaggcccccc	aggatcatta	agacaatcgc	ctccaagacc	3120
cagagcatta	agaagtacag	cacagacatt	ctgggcaacc	tgtatgaagt	gaaatctaag	3180
aagcacccctc	agatcatcaa	aaagggcaaa	aggccggcgg	ccacgaaaaa	ggccggccag	3240
gcaaaaaaga	aaaagggatc	catggatgct	aagtcactaa	ctgcctgggtc	ccggacactg	3300
gtgaccttca	aggatgtatt	tgtggacttc	accagggagg	agtggaagct	gctggacact	3360

gctcagcaga tcgtgtacag aaatgtgatg ctggagaact ataagaacct ggtttccttg 3420

ggttatcagc ttactaagcc agatgtgatc ctccggttgg agaagggaga agagccc 3477

<210> 152

<211> 1159

<212> PRT

<213> Secuencia artificial

<220>

<223> dSaCas9 fusionada con KRAB (Proteína)

<400> 152

Met Ala Pro Lys Lys Lys Arg Lys Val Gly Ile His Gly Val Pro Ala
1 5 10 15

Ala Lys Arg Asn Tyr Ile Leu Gly Leu Ala Ile Gly Ile Thr Ser Val
20 25 30

Gly Tyr Gly Ile Ile Asp Tyr Glu Thr Arg Asp Val Ile Asp Ala Gly
35 40 45

Val Arg Leu Phe Lys Glu Ala Asn Val Glu Asn Asn Glu Gly Arg Arg
50 55 60

Ser Lys Arg Gly Ala Arg Arg Leu Lys Arg Arg Arg Arg His Arg Ile
65 70 75 80

Gln Arg Val Lys Lys Leu Leu Phe Asp Tyr Asn Leu Leu Thr Asp His
85 90 95

Ser Glu Leu Ser Gly Ile Asn Pro Tyr Glu Ala Arg Val Lys Gly Leu
100 105 110

Ser Gln Lys Leu Ser Glu Glu Glu Phe Ser Ala Ala Leu Leu His Leu
115 120 125

Ala Lys Arg Arg Gly Val His Asn Val Asn Glu Val Glu Glu Asp Thr
130 135 140

Gly Asn Glu Leu Ser Thr Lys Glu Gln Ile Ser Arg Asn Ser Lys Ala
145 150 155 160

Leu Glu Glu Lys Tyr Val Ala Glu Leu Gln Leu Glu Arg Leu Lys Lys
165 170 175

Asp Gly Glu Val Arg Gly Ser Ile Asn Arg Phe Lys Thr Ser Asp Tyr
180 185 190

Val Lys Glu Ala Lys Gln Leu Leu Lys Val Gln Lys Ala Tyr His Gln
195 200 205

Leu Asp Gln Ser Phe Ile Asp Thr Tyr Ile Asp Leu Leu Glu Thr Arg
210 215 220

Arg Thr Tyr Tyr Glu Gly Pro Gly Glu Gly Ser Pro Phe Gly Trp Lys
225 230 235 240

Asp Ile Lys Glu Trp Tyr Glu Met Leu Met Gly His Cys Thr Tyr Phe
245 250 255

Pro Glu Glu Leu Arg Ser Val Lys Tyr Ala Tyr Asn Ala Asp Leu Tyr
260 265 270

Asn Ala Leu Asn Asp Leu Asn Asn Leu Val Ile Thr Arg Asp Glu Asn
275 280 285

Glu Lys Leu Glu Tyr Tyr Glu Lys Phe Gln Ile Ile Glu Asn Val Phe
290 295 300

Lys Gln Lys Lys Lys Pro Thr Leu Lys Gln Ile Ala Lys Glu Ile Leu
305 310 315 320

Val Asn Glu Glu Asp Ile Lys Gly Tyr Arg Val Thr Ser Thr Gly Lys
325 330 335

Pro Glu Phe Thr Asn Leu Lys Val Tyr His Asp Ile Lys Asp Ile Thr
340 345 350

Ala Arg Lys Glu Ile Ile Glu Asn Ala Glu Leu Leu Asp Gln Ile Ala
355 360 365

Lys Ile Leu Thr Ile Tyr Gln Ser Ser Glu Asp Ile Gln Glu Glu Leu
370 375 380

Thr Asn Leu Asn Ser Glu Leu Thr Gln Glu Glu Ile Glu Gln Ile Ser
385 390 395 400

Asn Leu Lys Gly Tyr Thr Gly Thr His Asn Leu Ser Leu Lys Ala Ile
405 410 415

Asn Leu Ile Leu Asp Glu Leu Trp His Thr Asn Asp Asn Gln Ile Ala
420 425 430

Ile Phe Asn Arg Leu Lys Leu Val Pro Lys Lys Val Asp Leu Ser Gln
435 440 445

Gln Lys Glu Ile Pro Thr Thr Leu Val Asp Asp Phe Ile Leu Ser Pro
450 455 460

Val Val Lys Arg Ser Phe Ile Gln Ser Ile Lys Val Ile Asn Ala Ile
465 470 475 480

Ile Lys Lys Tyr Gly Leu Pro Asn Asp Ile Ile Ile Glu Leu Ala Arg
485 490 495

Glu Lys Asn Ser Lys Asp Ala Gln Lys Met Ile Asn Glu Met Gln Lys
500 505 510

Arg Asn Arg Gln Thr Asn Glu Arg Ile Glu Glu Ile Ile Arg Thr Thr
515 520 525

Gly Lys Glu Asn Ala Lys Tyr Leu Ile Glu Lys Ile Lys Leu His Asp
530 535 540

Met Gln Glu Gly Lys Cys Leu Tyr Ser Leu Glu Ala Ile Pro Leu Glu
545 550 555 560

Asp Leu Leu Asn Asn Pro Phe Asn Tyr Glu Val Asp His Ile Ile Pro
565 570 575

Arg Ser Val Ser Phe Asp Asn Ser Phe Asn Asn Lys Val Leu Val Lys
580 585 590

Gln Glu Glu Ala Ser Lys Lys Gly Asn Arg Thr Pro Phe Gln Tyr Leu
595 600 605

Ser Ser Ser Asp Ser Lys Ile Ser Tyr Glu Thr Phe Lys Lys His Ile
610 615 620

Leu Asn Leu Ala Lys Gly Lys Gly Arg Ile Ser Lys Thr Lys Lys Glu
625 630 635 640

Tyr Leu Leu Glu Glu Arg Asp Ile Asn Arg Phe Ser Val Gln Lys Asp
645 650 655

Phe Ile Asn Arg Asn Leu Val Asp Thr Arg Tyr Ala Thr Arg Gly Leu
660 665 670

Met Asn Leu Leu Arg Ser Tyr Phe Arg Val Asn Asn Leu Asp Val Lys
675 680 685

Val Lys Ser Ile Asn Gly Gly Phe Thr Ser Phe Leu Arg Arg Lys Trp
690 695 700

Lys Phe Lys Lys Glu Arg Asn Lys Gly Tyr Lys His His Ala Glu Asp
705 710 715 720

Ala Leu Ile Ile Ala Asn Ala Asp Phe Ile Phe Lys Glu Trp Lys Lys
725 730 735

Leu Asp Lys Ala Lys Lys Val Met Glu Asn Gln Met Phe Glu Glu Lys
740 745 750

Gln Ala Glu Ser Met Pro Glu Ile Glu Thr Glu Gln Glu Tyr Lys Glu
755 760 765

Ile Phe Ile Thr Pro His Gln Ile Lys His Ile Lys Asp Phe Lys Asp
770 775 780

Tyr Lys Tyr Ser His Arg Val Asp Lys Lys Pro Asn Arg Glu Leu Ile
785 790 795 800

Asn Asp Thr Leu Tyr Ser Thr Arg Lys Asp Asp Lys Gly Asn Thr Leu
805 810 815

Ile Val Asn Asn Leu Asn Gly Leu Tyr Asp Lys Asp Asn Asp Lys Leu
820 825 830

Lys Lys Leu Ile Asn Lys Ser Pro Glu Lys Leu Leu Met Tyr His His
835 840 845

Asp Pro Gln Thr Tyr Gln Lys Leu Lys Leu Ile Met Glu Gln Tyr Gly
850 855 860

Asp Glu Lys Asn Pro Leu Tyr Lys Tyr Tyr Glu Glu Thr Gly Asn Tyr
865 870 875 880

Leu Thr Lys Tyr Ser Lys Lys Asp Asn Gly Pro Val Ile Lys Lys Ile
885 890 895

Lys Tyr Tyr Gly Asn Lys Leu Asn Ala His Leu Asp Ile Thr Asp Asp
900 905 910

Tyr Pro Asn Ser Arg Asn Lys Val Val Lys Leu Ser Leu Lys Pro Tyr
915 920 925

Arg Phe Asp Val Tyr Leu Asp Asn Gly Val Tyr Lys Phe Val Thr Val
930 935 940

Lys Asn Leu Asp Val Ile Lys Lys Glu Asn Tyr Tyr Glu Val Asn Ser
945 950 955 960

Lys Cys Tyr Glu Glu Ala Lys Lys Leu Lys Lys Ile Ser Asn Gln Ala
965 970 975

Glu Phe Ile Ala Ser Phe Tyr Asn Asn Asp Leu Ile Lys Ile Asn Gly
980 985 990

Glu Leu Tyr Arg Val Ile Gly Val Asn Asn Asp Leu Leu Asn Arg Ile
995 1000 1005

Glu Val Asn Met Ile Asp Ile Thr Tyr Arg Glu Tyr Leu Glu Asn
1010 1015 1020

Met Asn Asp Lys Arg Pro Pro Arg Ile Ile Lys Thr Ile Ala Ser
1025 1030 1035

Lys Thr Gln Ser Ile Lys Lys Tyr Ser Thr Asp Ile Leu Gly Asn
1040 1045 1050

Leu Tyr Glu Val Lys Ser Lys Lys His Pro Gln Ile Ile Lys Lys
1055 1060 1065

Gly Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys
1070 1075 1080

Lys Lys Gly Ser Met Asp Ala Lys Ser Leu Thr Ala Trp Ser Arg
1085 1090 1095

Thr Leu Val Thr Phe Lys Asp Val Phe Val Asp Phe Thr Arg Glu
1100 1105 1110

Glu Trp Lys Leu Leu Asp Thr Ala Gln Gln Ile Val Tyr Arg Asn
1115 1120 1125

Val Met Leu Glu Asn Tyr Lys Asn Leu Val Ser Leu Gly Tyr Gln
 1130 1135 1140

Leu Thr Lys Pro Asp Val Ile Leu Arg Leu Glu Lys Gly Glu Glu
 1145 1150 1155

Pro

<210> 153
 <211> 399
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> cassette blastR (ADN)

<400> 153
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 aacagcatcc ccatctctga agactacagc gtcgccagcg cagctctctc tagcgacggc 120
 cgcattcttca ctgggtgtcaa tgtatatcat ttactgggg gaccttgtgc agaactcgtg 180
 gtgctgggca ctgctgctgc tgcggcagct ggcaacctga cttgtatcgt cgcgatcgga 240
 aatgagaaca ggggcatctt gagcccctgc ggacggtgcc gacaggtgct tctcgatctg 300
 catcctggga tcaaagccat agtgaaggac agtgatggac agccgacggc agttgggatt 360
 cgtgaattgc tgccctctgg ttatgtgtgg gagggctaa 399

<210> 154
 <211> 132
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> cassette blastR (Proteína)

<400> 154

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

Thr Ala Thr Ile Asn Ser Ile Pro Ile Ser Glu Asp Tyr Ser Val Ala
 20 25 30

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

Tyr His Phe Thr Gly Gly Pro Cys Ala Glu Leu Val Val Leu Gly Thr
 50 55 60

Ala Ala Ala Ala Ala Ala Gly Asn Leu Thr Cys Ile Val Ala Ile Gly
 65 70 75 80

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

Leu Leu Asp Leu His Pro Gly Ile Lys Ala Ile Val Lys Asp Ser Asp
 100 105 110

Gly Gln Pro Thr Ala Val Gly Ile Arg Glu Leu Leu Pro Ser Gly Tyr
 115 120 125

Val Trp Glu Gly
 130

<210> 155
 <211> 241
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> promotor U6

<400> 155
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 ataattagaa ttaatttgac tgtaaacaca aagatattag tacaaaatac gtgacgtaga 120
 aagtaataat ttcttgggta gtttgcagtt ttaaaattat gttttaaaat ggactatcat 180
 atgcttaccg taacttgaaa gtatttcgat ttcttggcctt tatatatctt gtggaaagga 240
 c 241

<210> 156
<211> 82
<212> ARN
<213> Staphylococcus aureus

<220>
<221> misc_feature
<222> (1)..(82)
<223> tracrARN

<400> 156
guuuuaguac ucuggaaaca gaauacuacua aaacaaggca aaaugccgug uuuaucacgu 60

caacuuguug gcgagauuuu uu 82

<210> 157
<211> 19
<212> ARN
<213> Homo sapiens

<400> 157
gugguggggg aaaagaacc 19

<210> 158
<211> 21
<212> ARN
<213> Homo sapiens

<400> 158
agagagaagg ggagacagac a 21

<210> 159
<211> 21
<212> ARN
<213> Homo sapiens

<400> 159
gggugugcag gaugguuagg g 21

<210> 160
<211> 21
<212> ARN
<213> Homo sapiens

<400> 160
aaguggaggc aggauggaga g 21

<210> 161
<211> 21
<212> ARN
<213> Homo sapiens

<400> 161
ggaggcagga uggagagagg g 21

<210> 162
<211> 21
<212> ARN
<213> Homo sapiens

<400> 162
gcaggguaaa cugagaccgg g 21

<210> 163
<211> 21
<212> ARN
<213> Homo sapiens

<400> 163
gacauaugag ggccagaggg g 21

<210> 164
<211> 21
<212> ARN
<213> Homo sapiens

<400> 164
agaaaccagu gaccagugag c 21

<210> 165
<211> 21
<212> ARN
<213> Homo sapiens

<400> 165
gccuggggcc agggcuggaa g 21

<210> 166
<211> 21
<212> ARN
<213> Homo sapiens

<400> 166
ucagccacca uucccgccac c 21

<210> 167
<211> 21
<212> ARN
<213> Homo sapiens

<400> 167
gucucgguuc cuaugagccg u 21

<210> 168
<211> 21
<212> ARN
<213> Homo sapiens

<400> 168
ugugacucag agccauggcu u 21

<210> 169
<211> 21
<212> ARN
<213> Homo sapiens

<400> 169
ugugacuccu aagccauggc u 21

<210> 170
<211> 19
<212> ARN
<213> Homo sapiens

<400> 170
ugacucagag ccauggcuu 19

<210> 171
<211> 21
<212> ARN
<213> Homo sapiens

<400> 171
cagaguaagg ucagcagagg c 21

<210> 172
<211> 19
<212> ARN
<213> Homo sapiens

<400> 172
gggcuccugc agauggggu 19

<210> 173
<211> 21
<212> ARN
<213> Homo sapiens

<400> 173
uggccgacuu cuugcagugg g 21

<210> 174
<211> 21
<212> ARN
<213> Homo sapiens

<400> 174
ggggcuccag ccccaggaag c 21

<210> 175
<211> 21
<212> ARN
<213> Homo sapiens

<400> 175
auuuccccua cucuagcacu g 21

<210> 176
<211> 21
<212> ARN
<213> Homo sapiens

<400> 176
agcuucuugg gugacucaga g 21

<210> 177

<211>	21	
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<213>	Homo sapiens	
<400>	177	
cugagggcua	aauuuacug u	21
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<212>	ARN	
<213>	Homo sapiens	
<400>	178	
ggucaccccu	guucaggcuc u	21
<210>	179	
<211>	21	
<212>	ARN	
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<400>	179	
guuucuaauc	ccagccuggg c	21
<210>	180	
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<212>	ARN	
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auuagaaaca	gaaacauuuc g	21
<210>	181	
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<212>	ARN	
<213>	Homo sapiens	
<400>	181	
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<210>	182	
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<400>	182	

ccugcggcuc cgagagccaa g 21

<210> 183
<211> 21
<212> ARN
<213> Homo sapiens

<400> 183
gaaacuagga ggcaaggacc g 21

<210> 184
<211> 21
<212> ARN
<213> Homo sapiens

<400> 184
gcaggaugcu cuucucccca a 21

<210> 185
<211> 21
<212> ARN
<213> Homo sapiens

<400> 185
acagacaaua gcaagggcag c 21

<210> 186
<211> 21
<212> ARN
<213> Homo sapiens

<400> 186
ucacaugcug gggacaggga u 21

<210> 187
<211> 450
<212> ADN
<213> Secuencia artificial

<220>
<223> promotor CK8

<400> 187
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tataattaac ccagacatgt ggctgcccc cccccccaa cacctgctgc ctctaaaaat	120
aaccctgcat gccatgttcc cggcgaaggg ccagctgtcc cccgccagct agactcagca	180
cttagtttag gaaccagtga gcaagtcagc ctttggggca gcccatacaa ggccatgggg	240
ctgggcaagc tgcacgcctg ggtccggggg gggcacgggtg cccgggcaac gagctgaaag	300
ctcatctgct ctcaggggcc cctccctggg gacagcccct cctggctagt cacaccctgt	360
aggctcctct atataacca ggggcacagg ggctgccctc attctaccac cacctccaca	420
gcacagacag acactcagga gccagccagc	450

<210> 188
 <211> 16
 <212> PRT
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 <220>
 <223> Señal de localización nuclear

 <400> 188

Ala	Pro	Lys	Lys	Lys	Arg	Lys	Val	Gly	Ile	His	Gly	Val	Pro	Ala	Ala
1				5					10					15	

<210> 189
 <211> 48
 <212> ADN
 <213> Secuencia artificial

 <220>
 <223> secuencia de ADN que codifica NLS de SEQ ID NO 188

 <400> 189
 gccccaaaga agaagcggaa ggtcgggtatc cacggagtcc cagcagcc

48

<210> 190
 <211> 16
 <212> PRT
 <213> Secuencia artificial

 <220>
 <223> Señal de localización nuclear

 <400> 190

Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys Lys
 1 5 10 15

<210> 191
 <211> 48
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Secuencia de ADN que codifica NLS de SEQ ID NO 190

<400> 191
 aaaaggccgg cggccacgaa aaaggccggc caggcaaaaa agaaaaag 48

<210> 192
 <211> 20
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> DMD exón 78 cebador directo

<400> 192
 ttagaggagg tgatggagca 20

<210> 193
 <211> 20
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> DMD exón 78 cebador reverso

<400> 193
 gataactaagg actccatcgc 20

<210> 194
 <211> 21
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> MBNL1 exón 7 cebador directo

<400> 194

gctgcccatt accaggtcaa c 21

<210> 195

<211> 22

<212> ADN

<213> Secuencia artificial

<220>

<223> MBNL1 exon 7 cebador reverso

<400> 195

tggtgggaga aatgctgtat gc 22

<210> 196

<211> 23

<212> ADN

<213> Secuencia artificial

<220>

<223> KIF13A exón 21 cebador directo

<400> 196

acctgtgcag cattcaggga cac 23

<210> 197

<211> 24

<212> ADN

<213> Secuencia artificial

<220>

<223> KIF13A exón 21 cebador reverso

<400> 197

ctcgtcgttt aatgagtgca tctg 24

<210> 198

<211> 24

<212> ADN

<213> Secuencia artificial

<220>

<223> TNNT2 exón 5 cebador directo

<400> 198

atagaagagg tggtggaaga gtac 24

<210> 199
<211> 24
<212> ADN
<213> Secuencia artificial

<220>
<223> TNNT2 exón 5 cebador reverso

<400> 199
gtctcagcct ctgcttcagc atcc 24

<210> 200
<211> 3480
<212> ADN
<213> Secuencia artificial

<220>
<223> dSaCas9 fusionado a KRAB (ADN) con codón de parada terminal

<400> 200
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tacatcctgg gcctggccat cggcatcacc agcgtgggct acggcatcat cgactacgag 120
acacgggacg tgatcgatgc cggcgtgcgg ctgttcaaag aggccaacgt ggaaaacaac 180
gagggcaggc ggagcaagag aggcgccaga aggctgaagc ggaggaggcg gcatagaatc 240
cagagagtga agaagctgct gttcgactac aacctgctga ccgaccacag cgagctgagc 300
ggcatcaacc cctacgaggc cagagtgaag ggctgagcc agaagctgag cgaggaagag 360
ttctctgccg ccctgctgca cctggccaag agaagaggcg tgcacaacgt gaacgaggtg 420
gaagaggaca ccggcaacga gctgtccacc aaagagcaga tcagccggaa cagcaaggcc 480
ctggaagaga aatactggc cgaactgcag ctggaacggc tgaagaaaga cggcgaagtg 540
cggggcagca tcaacagatt caagaccagc gactacgtga aagaagccaa acagctgctg 600
aaggtgcaga aggcctacca ccagctggac cagagcttca tcgacaccta catcgacctg 660
ctggaaaccc ggaggaccta ctatgaggga cctggcgagg gcagcccctt cggctggaag 720
gacatcaaag aatggtacga gatgctgatg ggccactgca cctacttccc cgaggaactg 780
cggagcgtga agtacgccta caacgccgac ctgtacaacg ccctgaacga cctgaacaat 840

ctcgtgatca ccagggacga gaacgagaag ctggaatatt acgagaagtt ccagatcatc	900
gagaacgtgt tcaagcagaa gaagaagccc accctgaagc agatcgccaa agaaatcctc	960
gtgaacgaag aggatattaa gggctacaga gtgaccagca ccggcaagcc cgagttcacc	1020
aacctgaagg tgtaccacga catcaaggac attaccgccc ggaaagagat tattgagaac	1080
gccgagctgc tggatcagat tgccaagatc ctgaccatct accagagcag cgaggacatc	1140
caggaagaac tgaccaatct gaactccgag ctgacccagg aagagatcga gcagatctct	1200
aatctgaagg gctataccgg caccacaaac ctgagcctga aggccatcaa cctgatcctg	1260
gacgagctgt ggcacaccaa cgacaaccag atcgctatct tcaaccggct gaagctgggtg	1320
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<211> 208

<212> ADN

<213> Secuencia artificial

<220>

<223> secuencia bGlobin polyA

<400> 201

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tgagtaggtg tcattctatt ctgggggggtg ggggtggggca ggacagcaag ggggaggatt	180
gggaagagaa tagcaggcat gctgggga	208

<210> 202
 <211> 242
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> polímero U6

<400> 202	
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aagtaataat ttcttgggta gtttgcagtt ttaaaattat gttttaaaat ggactatcat	180
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cg	242

<210> 203
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 <213> Secuencia artificial

<220>
 <223> pED0001

<400> 203	
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gccggatcaa gagctaccaa ctctttttcc gaaggtaact ggcttcagca gagcgcagat	240
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ctgaacgggg ggttcgtgca cacagcccag cttggagcga acgacctaca ccgaactgag	480
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tcatagccca tatatggagt tccgcgttac ataacttacg gtaaatggcc cgcttggtg	1020
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