

LISTADO DE SECUENCIAS

<110> Astellas Pharma Inc.

Modalis Therapeutics Corporation

<120> MÉTODO PARA TRATAR DISTROFIA MUSCULAR POR DIRECCIONAMIENTO DEL GEN DMPK

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<150> US62/853,373

<151> 2019-05-28

<150> US63/025,417

<151> 2020-05-15

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<170> PatentIn versión 3.5

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35 40 45

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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 de
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
865 870 875 880

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
945 950 955 960

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 GGSGGS

<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
dSaCas9) delección mutante con enlazador GGSGGS

<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> SITE

<222> (721)..(726)

<223> enlazador GGS GGS

<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 GGSGGS

<220>

<221> VARIANTE

<222> (10)..(10)

<223> conversión de residuo Asp en resiudo Ala

<220>

<221> SITE

<222> (482)..(487)

<223> enlazador GGSGGS

<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> crARN 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 novicida

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

<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 gcgagatddd 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 tctggaacaa 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 aagaagaagc gaaggtcggg atccacggag tcccagcagc caagcggaac 60

tacatcctgg gcttgccat cggcatcacc agcgtgggct acggcatcat cgactacgag 120

acacgggacg tgatcgatgc cggcgtgcgg ctgttcaaag aggccaacgt ggaaaacaac 180

gagggcaggc ggagcaagag aggcgccaga aggtgaagc ggcggaggcg gcatagaatc 240

cagagagtga agaagctgct gttcgactac aacctgctga ccgaccacag cgagctgagc 300

ggcatcaacc cctacaggc 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 aagaagcaa acagctgctg 600

aaggtgcaga aggcctacca ccagctggac cagagcttca tcgacaccta catcgacctg	660
ctggaaaccc ggcggaccta ctatgagggg cctggcgagg gcagcccctt cggttggaag	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 ctgaccagcagg aagagatcga gcagatctct	1200
aatctgaagg gctataccgg caccacaaac ctgagcctga aggccatcaa cctgatcctg	1260
gacgagctgt ggcacaccaa cgacaaccag atcgctatct tcaaccggct gaagctggtg	1320
ccaagaagg tggacctgtc ccagcagaaa gagatcccca ccacctggt 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

gatctgctga acaaccctt caactatgag gtggaccaca tcatcccag aagcgtgtcc	1740
ttcgacaaca gcttcaaca caagtgctc gtgaagcagg aagaagccag caagaagggc	1800
aaccggaccc cattccagta cctgagcagc agcgacagca agatcagcta cgaaaccttc	1860
aagaagcaca tcttgaatct ggccaagggc aagggcagaa tcagcaagac caagaaagag	1920
tatctgctgg aagaacggga catcaacagg ttctccgtgc agaaagactt catcaaccgg	1980
aacctggtgg ataccagata cgccaccaga ggcctgatga acctgctgcg gagctacttc	2040
agagtgaaca acctggacgt gaaagtgaag tccatcaatg gcggcttcac cagctttctg	2100
cggcggaagt ggaagtttaa gaaagagcgg aacaaggggt acaagcacca cgccgaggac	2160
gcctgatca ttgccaacgc cgatttcac ttcaaagagt ggaagaaact ggacaaggcc	2220
aaaaaagtga tggaaaacca gatgttcgag gaaaagcagg ccgagagcat gcccgagatc	2280
gaaaccgagc aggagtacaa agagatcttc atcaccccc accagatcaa gcacattaag	2340
gacttcaagg actacaagta cagccaccgg gtggacaaga agcctaatag agagctgatt	2400
aacgacaccc tgtactccac ccggaaggac gacaagggca acacctgat cgtgaacaat	2460
ctgaacggcc tgtacgacaa ggacaatgac aagctgaaaa agctgatcaa caagagcccc	2520
gaaaagctgc tgatgtacca ccacgacccc cagacctacc agaaactgaa gctgattatg	2580
gaacagtacg gcgacgagaa gaatcccctg tacaagtact acgaggaaac cgggaactac	2640
ctgaccaagt actcaaaaa ggacaacggc cccgtgatca agaagattaa gtattacggc	2700
aacaaactga acgcccattt ggacatcacc gacgactacc ccaacagcag aaacaaggtc	2760

gtgaagctgt ccctgaagcc ctacagattc gacgtgtacc tggacaatgg cgtgtacaag	2820
ttcgtgaccg tgaagaatct ggatgtgata aaaaaagaaa actactacga agtgaatagc	2880
aagtgttatg aggaagctaa gaagctgaag aagatcagca accaggccga gtttatcgcc	2940
tccttctaca acaacgatct gatcaagatc aacggcgagc tgtatagagt gatcggcgtg	3000
aacaacgacc tgctgaaccg gatcgaagtg aacatgatcg acatcaccta ccgcgagtac	3060
ctggaaaaca tgaacgacaa gagggccccc aggatcatta agacaatcgc ctccaagacc	3120
cagagcatta agaagtacag cacagacatt ctgggcaacc tgtatgaagt gaaatctaag	3180
aagcaccctc agatcatcaa aaagggcaaa aggccggcgg ccacgaaaaa ggccggccag	3240
gcaaaaaaga aaaagggatc catggatgct aagtcactaa ctgcctgggc ccggacactg	3300
gtgaccttca aggatgtatt tgtggacttc accaggggagg agtggaaagt 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
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

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

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

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

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

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 ccattctctga agactacagc gtcgccagcg cagctctctc tagcgacggc 120

cgcattcttca ctggtgtcaa tgtatatcat ttactgggg gaccttgtgc agaactcgtg 180

gtgctgggca ctgctgctgc tgcggcagct ggcaacctga cttgtatcgt cgcgatcgga 240

aatgagaaca ggggcatctt gagccccctgc ggacgggtgcc 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

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<212> ADN

<213> Secuencia Artificial

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<223> promotor U6

<400> 155

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aagtaataat ttcttgggta gtttgcagtt ttaaaattat gttttaaaat ggactatcat 180

atgcttaccg taacttgaaa gtatttcgat ttcttggcct tatatatctt gtggaaagga 240

c 241

<210> 156

<211> 82

<212> ARN

<213> Staphylococcus aureus

<220>

<221> misc_feature

<222> (1)..(82)

<223> tracrARN

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caacuuguug gcgagauuuu uu 82

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<213> Homo sapiens

<400> 157
gugguggggg aaaagaacc 19

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<400> 158
agagagaagg ggagacagac a 21

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<213> Homo sapiens

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gggugugcag gaugguuagg g 21

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aaguggaggc aggauggaga g

21

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gcaggguaaa cugagaccgg g

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agaaaccagu gaccagugag c

21

<210> 165

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<210> 166

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<400> 166

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<210> 169

<211> 21

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<213> Homo sapiens

<400> 169

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<210> 170

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<400> 170

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<400> 174

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<210> 175

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<210> 176

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<212> ARN

<213> Homo sapiens

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<210> 177

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acagaaacau uucgggggggu g

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<210> 182

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<400> 182

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<400> 183

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21

<210> 185

<211> 21

<212> ARN

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<400> 185

acagacaaua gcaagggcag c

21

<210> 186

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<212> ARN

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ucacaugcug gggacaggga u

21

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120

aaccctgcat gccatgttcc cggcgaaggg ccagctgtcc cccgccagct agactcagca	180
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ctgggcaagc tgcacgcctg ggtccggggg gggcacggtg cccgggcaac gagctgaaag	300
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<210> 189

<211> 48

<212> ADN

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

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48

<210> 190

<211> 16

<212> PRT

<213> Secuencia Artificial

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<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

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

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48

<210> 192

<211> 20

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<213> Secuencia Artificial

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<223> DMD exón 78 cebador directo

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<210> 193

<211> 20

<212> ADN

<213> Secuencia Artificial

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<223> DMD exón 78 cebador reverso

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<210> 194

<211> 21

<212> ADN

<213> Secuencia Artificial

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<223> MBNL1 exón 7 cebador directo

<400> 194

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<210> 195

<211> 22

<212> ADN

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<223> MBNL1 exon 7 cebador reverso

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22

<210> 196

<211> 23

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<223> KIF13A exón 21 cebador directo

<400> 196

acctgtgcag cattcaggga cac

23

<210> 197

<211> 24

<212> ADN

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<223> KIF13A exón 21 cebador reverso

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24

<210> 198

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<223> TNNT2 exón 5 cebador directo

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24

<210> 199

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<223> TNNT2 exón 5 cebador reverso

<400> 199

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24

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<211> 3480

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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 ggctgagcc agaagctgag cgaggaagag	360
ttctctgccg ccctgctgca cctggccaag agaagaggcg tgcacaacgt gaacgaggtg	420
gaagaggaca ccggcaacga gctgtccacc aaagagcaga tcagccggaa cagcaaggcc	480
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cggggcagca tcaacagatt caagaccagc gactacgtga aagaagccaa acagctgctg	600
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cggagcgtga agtacgcta caacccgac ctgtacaacg ccctgaacga cctgaacaat	840
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gagaacgtgt tcaagcagaa gaagaagccc accctgaagc agatcgccaa agaaatcctc	960
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 aagtaataat ttcttgggta gtttgcagtt ttaaaattat gttttaaaat ggactatcat 180

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