

LISTADO DE SECUENCIAS

<110> REGENERON PHARMACEUTICALS, INC.
SABIN, LEAH
KYRATSOUS, CHRISTOS
MOLLER-TANK, SVEN

<120> Partículas virales modificadas y usos de estas

<130> 10364W001

<150> 62/852,791

<151> 2019-05-24

<160> 73

<170> PatentIn versión 3.5

<210> 1

<211> 2190

<212> ADN

<213> Secuencia artificial

<220>

<223> Cap AAV2 VP1 AAV VP2 VP3

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<223> Cap AAV2 VP1 AAV VP2 VP3

<400> 2

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Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Gly Thr Gly Glu Lys
130 135 140

Arg Pro Glu Arg Val Asp Asp Phe Phe Pro Lys Lys Lys Lys Ala Lys
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Thr Glu Gln Gly Lys Ala Pro Ala Gln Thr Gly Glu Asp Pro Gly Glu
165 170 175

Gly Thr Ser Ser Asn Ala Gly Ser Ser Ala Pro Ser Ser Val Gly Ser
180 185 190

Ser Val Met Ala Glu Gly Gly Gly Gly Pro Met Gly Asp Ala Gly Gln
195 200 205

Gly Ala Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser
210 215 220

Gln Trp Leu Asp Asn Gly Val Val Thr Arg Thr Thr Arg Thr Trp Val
225 230 235 240

Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Ile Gln Gly Pro Gly
245 250 255

Gly Thr Asp Pro Asn Asn Lys Phe Phe Gly Phe Ser Thr Pro Trp Gly
260 265 270

Tyr Phe Asp Tyr Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
275 280 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Ala Met Arg
290 295 300

Phe Arg Leu Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305 310 315 320

Asn Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ala
325 330 335

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

Thr Phe Pro Pro Phe Pro Ala Asp Ile Tyr Thr Ile Pro Gln Tyr Gly
355 360 365

Tyr Cys Thr Leu Asn Tyr Asn Asn Glu Ala Val Asp Arg Ser Ala Phe
370 375 380

Tyr Cys Leu Asp Tyr Phe Pro Ser Asp Met Leu Arg Thr Gly Asn Asn
385 390 395 400

Phe Glu Phe Thr Tyr Thr Phe Glu Asp Val Pro Phe His Ser Met Phe
405 410 415

Ala His Asn Gln Thr Leu Asp Arg Leu Met Asn Pro Leu Val Asp Gln
420 425 430

Tyr Leu Trp Ala Phe Ser Ser Val Ser Gln Thr Gly Ser Ser Gly Arg
435 440 445

Ala Leu Asn Tyr Ser Arg Ala Thr Lys Thr Asn Met Ala Thr Gln Tyr
450 455 460

Arg Asn Trp Leu Pro Gly Pro Phe Val Arg Asp Gln Gln Ile Phe Thr
465 470 475 480

Gly Ala Ser Asn Ile Thr Gln Asn Asn Val Phe Asn Val Trp Asp Lys
485 490 495

Gly Lys Gln Trp Val Ile Asp Asn Arg Ile Asn Met Met Gln Pro Gly
500 505 510

Pro Ala Ala Ala Thr Thr Phe Ser Gly Glu Pro Asp Arg Gln Ala Met
515 520 525

Gln Asn Thr Leu Ala Phe Ser Arg Thr Val Tyr Asp Gln Thr Thr Ser
530 535 540

Thr Thr Asp Arg Asn Gln Leu Leu Ile Thr Asn Glu Asp Glu Ile Arg
545 550 555 560

Pro Thr Asn Ser Val Gly Ile Asp Thr Trp Gly Val Val Pro Asn Asn
565 570 575

Asn Gln Ser Lys Val Thr Ala Gly Thr Arg Ala Ala Ile Asn Asn Gln
580 585 590

Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Ile Tyr Leu Gln
595 600 605

Gly Pro Ile Trp Ala Lys Ile Pro Asp Thr Asp Asn His Phe His Pro
610 615 620

Ser Pro Leu Ile Gly Gly Phe Gly Cys Lys His Pro Pro Pro Gln Ile
625 630 635 640

Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Glu Thr Phe Gln
645 650 655

Thr Ala Lys Val Ala Ser Phe Ile Asn Gln Tyr Ser Thr Gly Gln Cys
660 665 670

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

Asn Pro Glu Ile Gln Phe Thr Ser Asn Phe Gly Asn Ala Ala Asp Ile
690 695 700

Gln Phe Ala Val Ser Asp Thr Gly Ser Tyr Ser Glu Pro Arg Pro Ile
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Gly Thr Arg Tyr Leu Thr Arg Pro Leu
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<210> 3
<211> 2145
<212> ADN
<213> Secuencia artificial

<220>
<223> Cap AAV2 VP1 de lobo marino VP2 VP3

<400> 3
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cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
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gaaccaaggg tgattggcac cagatacctg actcgtatac tataa	2145

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<211> 714
<212> PRT
<213> Secuencia artificial

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<223> Cap AAV2 VP1 Sea Lion VP2 VP3

<400> 4

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Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Ser Gln Pro Asp Ser Ser Ser Asp Asn
130 135 140

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

Gln Ser Pro Asp Val Ser Ser Ser Thr Gly Gly Gly Ile Ala Asp Val
165 170 175

Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly Gly Ala Pro Gly
180 185 190

Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser Ser Gly Asn Trp
195 200 205

His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg Thr Thr Ser Thr
210 215 220

Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Leu
225 230 235 240

Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
245 250 255

Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe Ser Pro Arg Asn
260 265 270

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Arg Leu
275 280 285

Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Glu Gly
290 295 300

Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe
305 310 315 320

Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp Ala Gly His Glu
325 330 335

Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met Ile Pro Gln Tyr
340 345 350

Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala Gln Ser Asp Leu
355 360 365

Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
370 375 380

Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp Val Pro Phe His
385 390 395 400

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
405 410 415

Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly Asn Pro Thr Gly
420 425 430

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

Ala His Tyr Gly Lys Asn Trp Leu Pro Gly Pro Phe Ile Arg Gln Gln
450 455 460

Gly Trp Thr Thr Gln Asn Ile Asn Asn Ser Val Val Asn Phe Asn Asp
465 470 475 480

Met Leu Gly Lys Asn Ser Thr Phe Thr Leu Asp Thr Arg Trp Ser Ser
485 490 495

Leu Ala Pro Gly Pro Cys Met Gly Asp Asp Gly Arg Thr Pro Ser Thr
500 505 510

Thr Lys Phe Ser Asn Ala Gln Leu Met Phe Gly Ser Gly Thr Gln Pro
515 520 525

Thr Glu Gly Gly Glu Asp Ala Val His Ile Thr Ser Glu Ser Glu Val
530 535 540

Lys Ala Thr Asn Pro Thr Ala Ile Asp Glu Tyr Gly Arg Val Ala Asp
545 550 555 560

Asn Thr Gln Asn Ala Thr Thr Ala Pro Thr Thr Val Gly Asn Ala Ala
565 570 575

Met Gly Ala Met Pro Gly Met Val Trp Gln Asp Arg Asp Ile Tyr Leu
580 585 590

Gln Gly Pro Ile Trp Gly Lys Ile Pro His Thr Asp Gly His Phe His
595 600 605

Pro Ser Pro Leu Met Gly Gly Phe Gly Tyr Arg Lys Pro Pro Pro Gln
610 615 620

Ile Phe Ile Lys Asn Thr Pro Val Pro Gly Asn Pro Ala Thr Thr Phe
625 630 635 640

Ser Pro Asn Arg Ile Asn Asn Phe Ile Thr Gln Tyr Ser Thr Gly Gln
645 650 655

Val Thr Val Thr Ile Asp Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg
660 665 670

Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Phe Gly Thr Val Asp Ser
675 680 685

Leu Asn Trp Ala Pro Asp Asn Ala Gly Asn Tyr Lys Glu Pro Arg Val
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Ile Gly Thr Arg Tyr Leu Thr Arg Ile Leu
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<210> 5
<211> 2187
<212> ADN
<213> Secuencia artificial

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<223> Cap AAV2 VP1 de dragón VP2 VP3

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2187

<210> 6

<211> 728

<212> PRT

<213> Secuencia artificial

<220>

<223> Cap AAV2 VP1 de dragón VP2 VP3

<400> 6

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Glu Lys Arg Lys Thr
130 135 140

Pro Glu Glu Trp Leu Ala Gln Glu Lys Thr Pro Thr Lys Gln Arg Phe
145 150 155 160

Gln Ile Pro Ala Pro Gly Gln Ser Gly Ser Asp Ser Pro Ser Thr Ser
165 170 175

Gly Ser Gly Gly Thr Ala Gly Ser Ser Ser Ser Ala Ser Asn Thr Met
180 185 190

Ala Gln Gly Gly Gly Gly Pro Met Ala Asp Asp Asn Gln Gly Ala Glu
195 200 205

Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Thr Gln Trp Leu
210 215 220

Gly Asp His Val Ile Thr Lys Ser Thr Arg Thr Trp Val Leu Pro Ser
225 230 235 240

Tyr Gly Asn His Leu Tyr Ser Pro Ile Asn Phe Asp Gly Thr Thr Gly
245 250 255

Asn Gly Thr Gln Ala Ala Tyr Cys Gly Tyr Ala Thr Pro Trp Ala Tyr
260 265 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
275 280 285

Arg Leu Ile Asn Asn His Thr Gly Ile Arg Pro Val Gly Leu Lys Phe
290 295 300

Lys Leu Phe Asn Ile Gln Val Lys Glu Ile Thr Val Gln Asp Ser Thr
305 310 315 320

Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ala Asp
325 330 335

Thr Glu His Gln Leu Pro Tyr Val Leu Gly Asn Ala Thr Gln Gly Thr
340 345 350

Phe Pro Pro Phe Pro Ala Glu Val Phe Gln Leu Pro Gln Tyr Gly Tyr
355 360 365

Cys Thr Ile Gln Gly Pro Gln Gly Lys Phe Thr Asp Arg Ser Ala Phe
370 375 380

Tyr Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn Asn
385 390 395 400

Phe Glu Phe Thr Tyr Lys Phe Glu Lys Val Pro Phe His Ser Gly Trp
405 410 415

Ala Gln Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Pro Gln
420 425 430

Tyr Leu Leu Ala Asp Tyr Gly Thr Thr Ala Ser Ser Ala Ile Thr Tyr
435 440 445

Tyr Arg Pro Asn Ser Thr Asp Leu Ser Trp Tyr Phe Lys Asn Trp Leu
450 455 460

Pro Gly Pro Val Glu Arg Arg Gln Gln Ile Asn Ser Glu Asp Ser Thr
465 470 475 480

Lys Asn His Ala Asn Leu Asn Gly Asn Ala His Thr Asn Lys Tyr Ser
485 490 495

Ile Gln His Arg Gln Thr Lys Met Met Pro Gly Val Ala Leu Ser Ser
500 505 510

Lys Tyr Thr Gly Ala Ala Glu Gly Thr Ser Leu Leu Asn Gly Val Leu
515 520 525

Thr Phe Asp Lys Ile Ala Asn Asp Asn Thr Asn Ile Thr Asp Thr Asn
530 535 540

Asn Val Asn Arg Thr Ile Glu Asp Glu Ile Gln Gly Thr Asn Pro Tyr
545 550 555 560

Gly Asn Asp Val Pro Ile Thr Val Ala Val Asn Thr Gln Asn Ala Thr
565 570 575

Thr Ser Pro Thr Met Gln Asn Ser Ser Thr Tyr Glu Leu Leu Pro Gly
580 585 590

Ala Val Trp Ser Asn Arg Asp Ile Tyr Leu Gln Gly Pro Ile Trp Ala
595 600 605

Lys Ile Pro Asp Thr Asp Gly His Phe His Pro Ser Pro Gln Met Gly
610 615 620

Gly Phe Gly Leu Lys Asn Pro Pro Pro Met Ile Leu Ile Lys Asn Thr
625 630 635 640

Pro Val Pro Ala Asp Pro Pro Thr Thr Phe Lys Pro Thr Pro Met Asn
645 650 655

Ser Phe Ile Ser Glu Tyr Ser Thr Gly Gln Val Thr Val Glu Met Leu
660 665 670

Trp Glu Val Arg Lys Glu Asp Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Phe Thr Ser Asn Phe Gly Leu Ser Asp Pro Gln Ile Asp Gly Ile Pro
690 695 700

Phe Gly Ile Thr Lys Leu Gly Asn Tyr Glu Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg His Leu
725

<210> 7
<211> 2265
<212> ADN
<213> Secuencia artificial

<220>
<223> Cap AAV2 VP1 AAV VP2 VP3 G444 enlazador6 SpyTag

<400> 7
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtctttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggccggg	420
accggggaga agcgtcccga acgcgtcgac gactttttcc cgaaaaagaa gaaggccaag	480
accgagcaag gcaaagcccc tgctcaaacg ggcgaagacc ccggagaagg aacctcttcc	540
aacgctggat caagcgcccc ctctagtgtg ggatcatctg tcatggctga aggaggtggc	600
ggtccaatgg gcgatgcagg ccaaggtgcc gacggagtgg gcaattcctc gggaaattgg	660
cattgcgatt cccaatggct ggacaacgga gtcgttacc gaaccactcg aacctgggtc	720
ctgcccagct acaacaacca cttgtacaag cggtaccaag gaccgggagg aaccgacccc	780
aacaataaat tctttggatt cagcaccccc tgggggtact ttgactacaa ccgattccac	840
tgccacttct ccccccgaga ctggcaacga ctcatcaaca acaactgggg catccgaccc	900
aaagcgatgc gctttagact ctttaacatc cagggttaaag aagtcactgt ccaagactcc	960
aacaccacca tcgccaacaa cctcaccagc acggtccaag tctttgcgga caaggactac	1020
cagctgccgt acgtcctcgg atcggctaca gagggcacct tcccgccgtt ccagcggat	1080
atctacacga tcccgagta tggttactgc acgctaaact acaacaacga ggcggtggat	1140
cgttcggcct tctactgtct agactatttc ccctcagaca tgctgcggac aggaaataac	1200
tttgaattca cttacacgtt cgaggacgtt cttttcata gcatgtttgc tcacaaccag	1260
acgctagacc ggctgatgaa tcctctcgtc gatcagtacc tgtgggcttt cagttccgtc	1320
agccaaacag gcggcctgag cggcagcggc gccacatcg tgatggtgga cgcctacaag	1380
ccgacgaagg gcctgagcgg cagcggctcg tctggacggg cactcaatta ttcacgcgcg	1440
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gcgaccacct ttagcggaga acccgaccgt caagccatgc aaaacacgct ggcctttagt	1680
cggacggtct acgaccagac aaccagtacg accgatcgta accagttgct cattaccaac	1740
gaagatgaaa tcagaccac caactcggtc ggcacgaca cgtggggagt agttcccaac	1800
aacaaccagt ccaaggtgac cgccggcact cgcgcggcca tcaacaacca aggggcgctt	1860
cccgggatgg tgtggcaaaa cagagacatt tacctccaag gaccatttg ggcaaaaatc	1920

cccgacacag acaatcactt ccatccgtcc ccgcttattg gcgggtttgg ctgcaagcat 1980
 cccctccccc agattttcat taaaaacaca cccgtcccgg ccaacccttc ggaaacgttc 2040
 cagacggcca aggtggcctc cttcatcaac cagtactcga ccggacagtg caccgtcgaa 2100
 atcttttggg aactcaagaa ggaaacctcc aagcgttgga accccgaaat ccagttcacc 2160
 tccaactttg gcaacgcggc cgacatccag tttgctgtct ccgacaccgg atcctattcc 2220
 gaacctcgtc ccattggcac cagatacctg actcgtcctc tgtaa 2265

<210> 8
 <211> 754
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Cap AAV2 VP1 AAV VP2 VP3 G444 enlazador6 SpyTag

<400> 8

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

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Gly Thr Gly Glu Lys
130 135 140

Arg Pro Glu Arg Val Asp Asp Phe Phe Pro Lys Lys Lys Lys Ala Lys
145 150 155 160

Thr Glu Gln Gly Lys Ala Pro Ala Gln Thr Gly Glu Asp Pro Gly Glu
165 170 175

Gly Thr Ser Ser Asn Ala Gly Ser Ser Ala Pro Ser Ser Val Gly Ser
180 185 190

Ser Val Met Ala Glu Gly Gly Gly Gly Pro Met Gly Asp Ala Gly Gln
195 200 205

Gly Ala Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser
210 215 220

Gln Trp Leu Asp Asn Gly Val Val Thr Arg Thr Thr Arg Thr Trp Val
225 230 235 240

Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Ile Gln Gly Pro Gly
245 250 255

Gly Thr Asp Pro Asn Asn Lys Phe Phe Gly Phe Ser Thr Pro Trp Gly
260 265 270

Tyr Phe Asp Tyr Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
275 280 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Ala Met Arg
290 295 300

Phe Arg Leu Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305 310 315 320

Asn Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ala
325 330 335

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

Thr Phe Pro Pro Phe Pro Ala Asp Ile Tyr Thr Ile Pro Gln Tyr Gly
355 360 365

Tyr Cys Thr Leu Asn Tyr Asn Asn Glu Ala Val Asp Arg Ser Ala Phe
370 375 380

Tyr Cys Leu Asp Tyr Phe Pro Ser Asp Met Leu Arg Thr Gly Asn Asn
385 390 395 400

Phe Glu Phe Thr Tyr Thr Phe Glu Asp Val Pro Phe His Ser Met Phe
405 410 415

Ala His Asn Gln Thr Leu Asp Arg Leu Met Asn Pro Leu Val Asp Gln
420 425 430

Tyr Leu Trp Ala Phe Ser Ser Val Ser Gln Thr Gly Gly Leu Ser Gly
435 440 445

Ser Gly Ala His Ile Val Met Val Asp Ala Tyr Lys Pro Thr Lys Gly
450 455 460

Leu Ser Gly Ser Gly Ser Ser Gly Arg Ala Leu Asn Tyr Ser Arg Ala
465 470 475 480

Thr Lys Thr Asn Met Ala Thr Gln Tyr Arg Asn Trp Leu Pro Gly Pro
485 490 495

Phe Val Arg Asp Gln Gln Ile Phe Thr Gly Ala Ser Asn Ile Thr Gln
500 505 510

Asn Asn Val Phe Asn Val Trp Asp Lys Gly Lys Gln Trp Val Ile Asp
515 520 525

Asn Arg Ile Asn Met Met Gln Pro Gly Pro Ala Ala Ala Thr Thr Phe
530 535 540

Ser Gly Glu Pro Asp Arg Gln Ala Met Gln Asn Thr Leu Ala Phe Ser
545 550 555 560

Arg Thr Val Tyr Asp Gln Thr Thr Ser Thr Thr Asp Arg Asn Gln Leu
565 570 575

Leu Ile Thr Asn Glu Asp Glu Ile Arg Pro Thr Asn Ser Val Gly Ile
580 585 590

Asp Thr Trp Gly Val Val Pro Asn Asn Asn Gln Ser Lys Val Thr Ala
595 600 605

Gly Thr Arg Ala Ala Ile Asn Asn Gln Gly Ala Leu Pro Gly Met Val
610 615 620

Trp Gln Asn Arg Asp Ile Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
625 630 635 640

Pro Asp Thr Asp Asn His Phe His Pro Ser Pro Leu Ile Gly Gly Phe
645 650 655

Gly Cys Lys His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val
660 665 670

Pro Ala Asn Pro Ser Glu Thr Phe Gln Thr Ala Lys Val Ala Ser Phe
675 680 685

Ile Asn Gln Tyr Ser Thr Gly Gln Cys Thr Val Glu Ile Phe Trp Glu
690 695 700

Leu Lys Lys Glu Thr Ser Lys Arg Trp Asn Pro Glu Ile Gln Phe Thr
705 710 715 720

Ser Asn Phe Gly Asn Ala Ala Asp Ile Gln Phe Ala Val Ser Asp Thr
725 730 735

Gly Ser Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
740 745 750

Pro Leu

<210> 9
<211> 2265
<212> ADN
<213> Secuencia artificial

<220>

<223> Cap AAV2 VP1 AAV VP2 VP3 K580 enlazador6 SpyTag

<400> 9

atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga	60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac	120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac	180
aaggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac	240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggccggg	420
accggggaga agcgtcccga acgcgtcgac gactttttcc cgaaaaagaa gaaggccaag	480
accgagcaag gcaaagcccc tgctcaaacg ggcgaagacc ccggagaagg aacctcttcc	540
aacgctggat caagcgcgcc ctctagtgtg ggatcatctg tcatggctga aggaggtggc	600
ggtccaatgg gcgatgcagg ccaaggtgcc gacggagtgg gcaattcctc gggaaattgg	660
cattgcgatt cccaatggct ggacaacgga gtcgttacc gaaccactcg aacctgggtc	720
ctgcccagct acaacaacca cttgtacaag cggatccaag gaccgggagg aaccgacccc	780
aacaataaat tctttggatt cagcaccccc tgggggtact ttgactacaa ccgattccac	840
tgccacttct ccccccgaga ctggcaacga ctcatcaaca acaactgggg catccgaccc	900
aaagcgatgc gctttagact ctttaacatc caggttaaag aagtcactgt ccaagactcc	960
aacaccacca tcgccaacaa cctcaccagc acgggtccaag tctttgcgga caaggactac	1020
cagctgccgt acgtcctcgg atcggctaca gagggcacct tcccgccgtt ccagcggat	1080
atctacacga tcccgcagta tggttactgc acgctaaact acaacaacga ggcggtggat	1140
cgttcggcct tctactgtct agactatttc ccctcagaca tgctgcggac aggaaataac	1200
tttgaattca ctacacgtt cgaggacgtt cttttcata gcatgtttgc tcacaaccag	1260
acgctagacc ggctgatgaa tcctctcgtc gatcagtacc tgtgggcttt cagttccgtc	1320
agccaaacag gctcgtctgg acgggcactc aattattcac gcgcgaccaa aaccaatatg	1380

gcaacccagt acagaaactg gttacctgga cccttcgtcc gggatcagca aatcttttacg 1440
ggggctagca acatcaccca aaacaacgtg ttcaacgttt gggataaagg caagcagtgg 1500
gtgatagaca atcggatcaa tatgatgcag cccggccctg cagcagcgac caccttttagc 1560
ggagaacccg accgtcaagc catgcaaaac acgctggcct ttagtcggac ggtctacgac 1620
cagacaacca gtacgaccga tcgtaaccag ttgctcatta ccaacgaaga tgaaatcaga 1680
cccaccaact cggtcggcat cgacacgtgg ggagtagttc ccaacaacaa ccagtccaag 1740
ggcctgagcg gcagcggcgc ccacatcgtg atgggtggacg cctacaagcc gacgaagggc 1800
ctgagcggca gcggcgtgac cgccggcact cgcgcggcca tcaacaacca aggggcgctt 1860
cccgggatgg tgtggcaaaa cagagacatt tacctccaag gaccatttg ggccaaaatc 1920
cccgacacag acaatcactt ccatccgtcc ccgcttattg gcgggtttgg ctgcaagcat 1980
ccccctccc agattttcat taaaaacaca cccgtcccgg ccaacccttc ggaaacgttc 2040
cagacggcca aggtggcctc cttcatcaac cagtactcga ccggacagtg caccgtcgaa 2100
atcttttggg aactcaagaa ggaaacctcc aagcgctgga accccgaaat ccagttcacc 2160
tccaactttg gcaacgcggc cgacatccag tttgctgtct ccgacaccgg atcctattcc 2220
gaacctcgtc ccattggcac cagatacctg actcgtcctc tgtaa 2265

<210> 10
<211> 754
<212> PRT
<213> Secuencia artificial

<220>
<223> Cap AAV2 VP1 AAV VP2 VP3 K580 enlazador6 SpyTag

<400> 10

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

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Gly Thr Gly Glu Lys
130 135 140

Arg Pro Glu Arg Val Asp Asp Phe Phe Pro Lys Lys Lys Lys Ala Lys
145 150 155 160

Thr Glu Gln Gly Lys Ala Pro Ala Gln Thr Gly Glu Asp Pro Gly Glu
165 170 175

Gly Thr Ser Ser Asn Ala Gly Ser Ser Ala Pro Ser Ser Val Gly Ser
180 185 190

Ser Val Met Ala Glu Gly Gly Gly Gly Pro Met Gly Asp Ala Gly Gln
195 200 205

Gly Ala Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser
210 215 220

Gln Trp Leu Asp Asn Gly Val Val Thr Arg Thr Thr Arg Thr Trp Val
225 230 235 240

Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Ile Gln Gly Pro Gly
245 250 255

Gly Thr Asp Pro Asn Asn Lys Phe Phe Gly Phe Ser Thr Pro Trp Gly
260 265 270

Tyr Phe Asp Tyr Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
275 280 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Ala Met Arg
290 295 300

Phe Arg Leu Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305 310 315 320

Asn Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ala
325 330 335

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

Thr Phe Pro Pro Phe Pro Ala Asp Ile Tyr Thr Ile Pro Gln Tyr Gly
355 360 365

Tyr Cys Thr Leu Asn Tyr Asn Asn Glu Ala Val Asp Arg Ser Ala Phe
370 375 380

Tyr Cys Leu Asp Tyr Phe Pro Ser Asp Met Leu Arg Thr Gly Asn Asn
385 390 395 400

Phe Glu Phe Thr Tyr Thr Phe Glu Asp Val Pro Phe His Ser Met Phe
405 410 415

Ala His Asn Gln Thr Leu Asp Arg Leu Met Asn Pro Leu Val Asp Gln
420 425 430

Tyr Leu Trp Ala Phe Ser Ser Val Ser Gln Thr Gly Ser Ser Gly Arg
435 440 445

Ala Leu Asn Tyr Ser Arg Ala Thr Lys Thr Asn Met Ala Thr Gln Tyr
450 455 460

Arg Asn Trp Leu Pro Gly Pro Phe Val Arg Asp Gln Gln Ile Phe Thr
465 470 475 480

Gly Ala Ser Asn Ile Thr Gln Asn Asn Val Phe Asn Val Trp Asp Lys
485 490 495

Gly Lys Gln Trp Val Ile Asp Asn Arg Ile Asn Met Met Gln Pro Gly
500 505 510

Pro Ala Ala Ala Thr Thr Phe Ser Gly Glu Pro Asp Arg Gln Ala Met
515 520 525

Gln Asn Thr Leu Ala Phe Ser Arg Thr Val Tyr Asp Gln Thr Thr Ser
530 535 540

Thr Thr Asp Arg Asn Gln Leu Leu Ile Thr Asn Glu Asp Glu Ile Arg
545 550 555 560

Pro Thr Asn Ser Val Gly Ile Asp Thr Trp Gly Val Val Pro Asn Asn
565 570 575

Asn Gln Ser Lys Gly Leu Ser Gly Ser Gly Ala His Ile Val Met Val
580 585 590

Asp Ala Tyr Lys Pro Thr Lys Gly Leu Ser Gly Ser Gly Val Thr Ala
595 600 605

Gly Thr Arg Ala Ala Ile Asn Asn Gln Gly Ala Leu Pro Gly Met Val
610 615 620

Trp Gln Asn Arg Asp Ile Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
625 630 635 640

Pro Asp Thr Asp Asn His Phe His Pro Ser Pro Leu Ile Gly Gly Phe
645 650 655

Gly Cys Lys His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val
660 665 670

Pro Ala Asn Pro Ser Glu Thr Phe Gln Thr Ala Lys Val Ala Ser Phe
675 680 685

Ile Asn Gln Tyr Ser Thr Gly Gln Cys Thr Val Glu Ile Phe Trp Glu
690 695 700

Leu Lys Lys Glu Thr Ser Lys Arg Trp Asn Pro Glu Ile Gln Phe Thr
705 710 715 720

Ser Asn Phe Gly Asn Ala Ala Asp Ile Gln Phe Ala Val Ser Asp Thr
725 730 735

Gly Ser Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
740 745 750

Pro Leu

<210> 11
<211> 2220
<212> ADN
<213> Secuencia artificial

<220>
<223> Cap AAV2 VP1 de lobo marino VP2 VP3 G432 enlazador6 SpyTag

<400> 11
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cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aaccctctca gccagattcg 420
tcctcggaca acacggcgcc acccgtgaaa aagtcccgtc tcgaagaagc ccagcccatt 480
caaagtccag acgtttccag cagcactggc ggaggaattg ccgacgtcat gtctggagat 540
gctgaaatgg ctgcagtggg cgggggagca ccgggcgtcg acggccaggg tgccgaggga 600
gtgggtactt cctcgggtaa ttggcattgc gattcccagt ggtcagaagg acacgtcaga 660
accaccagca ccagaacctg ggtgttggcc agctacaaca accacctgta taaacggctt 720
ggaagtagcg cacaatccaa tacctacaac ggattctcca cccctggggg atacctcgac 780
ttcaatagat ggcactgtca cttcagtcct cggaactggc aacgtctcat caacaacaac 840

tggggcatca gacaaaaag acttaatggtt aaattgttca acatacaagt caaagaggctc	900
acgacggaag gggggacgac gaccgtcgcc aataacctta ccagcacgat tcaggtgttt	960
gcggaacaac cgtacgaact cccgtatggtt gtcgacgcgg gtcacgaggg ggcattgccg	1020
ccgttcccaa acgacgtggtt tatgattccc caatacggat actgcgggct ggtgtctggt	1080
caaagtcagg ctgagtcgga cttgtgttcg ttttattgcc tggagtattt tccatcccag	1140
atgctgagaa caggaaacaa ttttgaaatg aatttcaggt ttgaagacgt tccatttcac	1200
tccatgtacg cccacagcca gtctctagac aggctcatga atcctttaat tgatcagtat	1260
ctgtggagtc taaaacaaac aggaaacccg actggaggcc tgagcggcag cggcgccac	1320
atcgtgatgg tggacgccta caagccgacg aagggcctga gcggcagcgg ctcaacaacg	1380
agagacttaa aatttatcaa gaacaaagtt cccaattttg cacattatgg aaaaaattgg	1440
cttcctggac cttttattag acaacagggg tggacaacac aaaatattaa taatagtgtt	1500
gttaatttta atgacatgct gggaaaaaat tcgacattta ctttggacac tagatggagt	1560
tcattagcgc ctggtccgtg tatgggggat gacggacgaa ctccatccac caccaagttc	1620
tcaaatgctc agctcatggt tggatctgga acacaacca ccgaaggcgg tgaagatgct	1680
gtacatatta catccgagtc ggaggtcaag gcaaccaacc caactgcaat cgatgaatac	1740
ggacgagtgg ccgataatac gcaaaatgca acaaccgccc caaccacagt gggaaatgct	1800
gcaatggggg ccatgcctgg gatggtgtgg caagataggg atatctatct tcaaggaccc	1860
atctggggaa aaatacccca tacagacgga cattttcatc cgtctcctct catggggggg	1920
tttgataca gaaaaccccc tccgcaaatt tttattaaaa acaccccgt tcctggaaat	1980
ccggcaacta cattttctcc aaatagaata aacaatttca ttactcaata ctcaacggga	2040
caagtgaccg ttactattga ctgggagctg caaaaggaaa actcaaagag atggaacca	2100
gaagtacaat ttacatcaaa ttttggcacg gtcgattcac taaactgggc accggacaac	2160
gcgggaaact acaaagaacc aagggtgatt ggcaccagat acctgactcg tatactataa	2220

<210> 12
 <211> 739
 <212> PRT
 <213> Secuencia artificial

 <220>

<223> Cap AAV2 VP1 de lobo marino VP2 VP3 G432 enlazador6 SpyTag

<400> 12

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

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Ser Gln Pro Asp Ser Ser Ser Asp Asn
130 135 140

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

Gln Ser Pro Asp Val Ser Ser Ser Thr Gly Gly Gly Ile Ala Asp Val
165 170 175

Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly Gly Ala Pro Gly
180 185 190

Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser Ser Gly Asn Trp
195 200 205

His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg Thr Thr Ser Thr
210 215 220

Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Leu
225 230 235 240

Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
245 250 255

Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe Ser Pro Arg Asn
260 265 270

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Arg Leu
275 280 285

Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Glu Gly
290 295 300

Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe
305 310 315 320

Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp Ala Gly His Glu
325 330 335

Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met Ile Pro Gln Tyr
340 345 350

Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala Gln Ser Asp Leu
355 360 365

Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
370 375 380

Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp Val Pro Phe His
385 390 395 400

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
405 410 415

Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly Asn Pro Thr Gly
420 425 430

Gly Leu Ser Gly Ser Gly Ala His Ile Val Met Val Asp Ala Tyr Lys
435 440 445

Pro Thr Lys Gly Leu Ser Gly Ser Gly Ser Thr Thr Arg Asp Leu Lys
450 455 460

Phe Ile Lys Asn Lys Val Pro Asn Phe Ala His Tyr Gly Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Phe Ile Arg Gln Gln Gly Trp Thr Thr Gln Asn Ile
485 490 495

Asn Asn Ser Val Val Asn Phe Asn Asp Met Leu Gly Lys Asn Ser Thr
500 505 510

Phe Thr Leu Asp Thr Arg Trp Ser Ser Leu Ala Pro Gly Pro Cys Met
515 520 525

Gly Asp Asp Gly Arg Thr Pro Ser Thr Thr Lys Phe Ser Asn Ala Gln
530 535 540

Leu Met Phe Gly Ser Gly Thr Gln Pro Thr Glu Gly Gly Glu Asp Ala
545 550 555 560

Val His Ile Thr Ser Glu Ser Glu Val Lys Ala Thr Asn Pro Thr Ala
565 570 575

Ile Asp Glu Tyr Gly Arg Val Ala Asp Asn Thr Gln Asn Ala Thr Thr
580 585 590

Ala Pro Thr Thr Val Gly Asn Ala Ala Met Gly Ala Met Pro Gly Met
595 600 605

Val Trp Gln Asp Arg Asp Ile Tyr Leu Gln Gly Pro Ile Trp Gly Lys
610 615 620

Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly
625 630 635 640

Phe Gly Tyr Arg Lys Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro
645 650 655

Val Pro Gly Asn Pro Ala Thr Thr Phe Ser Pro Asn Arg Ile Asn Asn
660 665 670

Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Thr Ile Asp Trp
675 680 685

Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Phe
690 695 700

Thr Ser Asn Phe Gly Thr Val Asp Ser Leu Asn Trp Ala Pro Asp Asn
705 710 715 720

Ala Gly Asn Tyr Lys Glu Pro Arg Val Ile Gly Thr Arg Tyr Leu Thr
725 730 735

Arg Ile Leu

<210> 13
<211> 2220
<212> ADN
<213> Secuencia artificial

<220>
<223> Cap AAV2 VP1 de lobo marino VP2 VP3 A565 enlazador6 SpyTag

<400> 13
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aaccctctca gccagattcg 420
tcctcggaca acacggcgcc acccgtgaaa aagtcccgtc tcgaagaagc ccagcccatt 480

caaagtccag acgtttccag cagcactggc ggaggaattg cgcacgtcat gtctggagat	540
gctgaaatgg ctgcagtggg cgggggagca ccgggcgtcg acggccaggg tgccgaggga	600
gtgggtactt cctcgggtaa ttggcattgc gattcccagt ggtcagaagg acacgtcaga	660
accaccagca ccagaacctg ggtgttgccc agctacaaca accacctgta taaacggctt	720
ggaagtagcg cacaatccaa tacctacaac ggattctcca ccccctgggg atacctcgac	780
ttcaatagat ggcactgtca cttcagtcct cggaactggc aacgtctcat caacaacaac	840
tggggcatca gacaaaaag acttaatgtt aaattgttca acatacaagt caaagaggtc	900
acgacggaag gggggacgac gaccgtcgcc aataacctta ccagcacgat tcaggtgttt	960
gcggacaacg cgtacgaact cccgtatgtt gtcgacgcgg gtcacgaggg ggcattgccg	1020
ccgttcccaa acgacgtgtt tatgattccc caatacggat actgcgggct ggtgtctggt	1080
caaagtcagg ctcagtcgga cttgtgttcg ttttattgcc tggagtattt tccatcccag	1140
atgctgagaa caggaaacaa ttttgaaatg aatttcaggt ttgaagacgt tccatttcac	1200
tccatgtacg cccacagcca gtctctagac aggctcatga atcctttaat tgatcagtat	1260
ctgtggagtc taaaacaaac aggaaacccg actggatcaa caacgagaga cttaaaattt	1320
atcaagaaca aagttcccaa ttttgcacat tatggaaaaa attggcttcc tggacctttt	1380
attagacaac aggggtggac aacacaaaat attaataata gtgttggttaa ttttaatgac	1440
atgctgggaa aaaattcgac atttactttg gacactagat ggagttcatt agcgcctggt	1500
ccgtgtatgg gggatgacgg acgaactcca tccaccacca agttctcaaa tgctcagctc	1560
atgtttggat ctggaacaca acccaccgaa ggcggtgaag atgctgtaca tattacatcc	1620
gagtcggagg tcaaggcaac caaccgaact gcaatcgatg aatacggacg agtggccgat	1680
aatacgcaaa atgcaggcct gagcggcagc ggcgcccaca tcgtgatggt ggacgcctac	1740
aagccgacga agggcctgag cggcagcggc acaaccgccc caaccacagt gggaaatgct	1800
gcaatggggg ccatgcctgg gatggtgtgg caagataggg atatctatct tcaaggaccc	1860
atctggggaa aaatacccca tacagacgga cattttcatc cgtctcctct catggggggg	1920
tttgataca gaaaacccc tccgcaaatt tttattaaaa acaccccgt tcctggaaat	1980
ccggcaacta cattttctcc aaatagaata aacaatttca ttactcaata ctcaacggga	2040
caagtgaccg ttactattga ctgggagctg caaaaggaaa actcaaagag atggaaccca	2100

gaagtacaat ttacatcaaa ttttggcacg gtcgattcac taaactgggc accggacaac 2160

gcgggaaact acaaagaacc aagggtgatt ggcaccagat acctgactcg tatactataa 2220

<210> 14

<211> 739

<212> PRT

<213> Secuencia artificial

<220>

<223> Cap AAV2 VP1 de lobo marino VP2 VP3 A565 enlazador6 SpyTag

<400> 14

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

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Ser Gln Pro Asp Ser Ser Ser Asp Asn
130 135 140

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

Gln Ser Pro Asp Val Ser Ser Ser Thr Gly Gly Gly Ile Ala Asp Val
165 170 175

Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly Gly Ala Pro Gly
180 185 190

Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser Ser Gly Asn Trp
195 200 205

His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg Thr Thr Ser Thr
210 215 220

Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Leu
225 230 235 240

Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
245 250 255

Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe Ser Pro Arg Asn
260 265 270

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Arg Leu
275 280 285

Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Glu Gly
290 295 300

Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe
305 310 315 320

Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp Ala Gly His Glu
325 330 335

Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met Ile Pro Gln Tyr
340 345 350

Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala Gln Ser Asp Leu
355 360 365

Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
370 375 380

Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp Val Pro Phe His
385 390 395 400

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
405 410 415

Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly Asn Pro Thr Gly
420 425 430

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

Ala His Tyr Gly Lys Asn Trp Leu Pro Gly Pro Phe Ile Arg Gln Gln
450 455 460

Gly Trp Thr Thr Gln Asn Ile Asn Asn Ser Val Val Asn Phe Asn Asp
465 470 475 480

Met Leu Gly Lys Asn Ser Thr Phe Thr Leu Asp Thr Arg Trp Ser Ser
485 490 495

Leu Ala Pro Gly Pro Cys Met Gly Asp Asp Gly Arg Thr Pro Ser Thr
500 505 510

Thr Lys Phe Ser Asn Ala Gln Leu Met Phe Gly Ser Gly Thr Gln Pro
515 520 525

Thr Glu Gly Gly Glu Asp Ala Val His Ile Thr Ser Glu Ser Glu Val
530 535 540

Lys Ala Thr Asn Pro Thr Ala Ile Asp Glu Tyr Gly Arg Val Ala Asp
545 550 555 560

Asn Thr Gln Asn Ala Gly Leu Ser Gly Ser Gly Ala His Ile Val Met
565 570 575

Val Asp Ala Tyr Lys Pro Thr Lys Gly Leu Ser Gly Ser Gly Thr Thr
580 585 590

Ala Pro Thr Thr Val Gly Asn Ala Ala Met Gly Ala Met Pro Gly Met
595 600 605

Val Trp Gln Asp Arg Asp Ile Tyr Leu Gln Gly Pro Ile Trp Gly Lys
610 615 620

Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly
625 630 635 640

Phe Gly Tyr Arg Lys Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro
645 650 655

Val Pro Gly Asn Pro Ala Thr Thr Phe Ser Pro Asn Arg Ile Asn Asn
660 665 670

Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Thr Ile Asp Trp
675 680 685

Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Phe
690 695 700

Thr Ser Asn Phe Gly Thr Val Asp Ser Leu Asn Trp Ala Pro Asp Asn
705 710 715 720

Ala Gly Asn Tyr Lys Glu Pro Arg Val Ile Gly Thr Arg Tyr Leu Thr
725 730 735

Arg Ile Leu

<210> 15
<211> 2220
<212> ADN
<213> Secuencia artificial

<220>
<223> Cap AAV2 VP1 de lobo marino VP2 VP3 N429 enlazador6 SpyTag

<400> 15
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgttgga agctcaaacc tggcccacca ccaccaaagc cgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac	180
aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac	240
cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aaccctctca gccagattcg	420
tcctcggaca acacggcgcc acccgtgaaa aagtcccgtc tcgaagaagc ccagcccatt	480
caaagtccag acgtttccag cagcactggc ggaggaattg ccgacgtcat gtctggagat	540
gctgaaatgg ctgcagtggg cgggggagca ccgggcgtcg acggccaggg tgccgaggga	600
gtgggtactt cctcgggtaa ttggcattgc gattcccagt ggtcagaagg acacgtcaga	660
accaccagca ccagaacctg ggtgttgccc agctacaaca accacctgta taaacggctt	720
ggaagtagcg cacaatcaa tacctacaac ggattctcca cccctgggg atacctcgac	780
ttcaatagat ggcactgtca cttcagtcct cggaactggc aacgtctcat caacaacaac	840
tggggcatca gacaaaaag acttaatgtt aaattgttca acatacaagt caaagaggtc	900
acgacggaag gggggacgac gaccgtcgcc aataacctta ccagcacgat tcaggtgttt	960
gcggacaacg cgtacgaact cccgtatgtt gtcgacgcgg gtcacgaggg ggcattgccg	1020
ccgttcccaa acgacgtgtt tatgattccc caatacggat actgcgggct ggtgtctggt	1080
caaagtcagg ctcagtcgga cttgtgttcg ttttattgcc tggagtattt tccatcccag	1140
atgctgagaa caggaaacaa ttttgaaatg aatttcaggt ttgaagacgt tccatttcac	1200
tccatgtacg cccacagcca gtctctagac aggctcatga atcctttaat tgatcagtat	1260
ctgtggagtc taaaacaaac aggaaacggc ctgagcggca gcggcgcca catcgtgatg	1320
gtggacgcct acaagccgac gaagggcctg agcggcagcg gcccgactgg atcaacaacg	1380
agagacttaa aatttatcaa gaacaaagt ccgaattttg cacattatgg aaaaaattgg	1440
cttcctggac cttttattag acaacagggg tggacaacac aaaatattaa taatagtgtt	1500
gttaatttta atgacatgct gggaaaaaat tcgacattta ctttggacac tagatggagt	1560
tcattagcgc ctggtccgtg tatgggggat gacggacgaa ctccatccac caccaagttc	1620
tcaaagtctc agctcatgtt tggatctgga acacaacca ccgaaggcgg tgaagatgct	1680
gtacatatta catccgagtc ggaggtcaag gcaaccaacc caactgcaat cgatgaatac	1740

ggacgagtgg ccgataatac gcaaaatgca acaaccgccc caaccacagt gggaaatgct 1800
 gcaatggggg ccatgcctgg gatggtgtgg caagataggg atatctatct tcaaggaccc 1860
 atctgggggaa aaatacccca tacagacgga cattttcatc cgtctcctct catggggggg 1920
 tttggataca gaaaaccccc tccgcaaatt tttattaaaa acacccccgt tcctggaaat 1980
 ccggcaacta cattttctcc aaatagaata aacaatttca ttactcaata ctcaacggga 2040
 caagtgaccg ttactattga ctgggagctg caaaaggaaa actcaaagag atggaaccca 2100
 gaagtacaat ttacatcaaa ttttggcacg gtcgattcac taaactgggc accggacaac 2160
 gcgggaaact acaaagaacc aagggtgatt ggcaccagat acctgactcg tatactataa 2220

<210> 16
 <211> 739
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Cap AAV2 VP1 de lobo marino VP2 VP3 N429 enlazador6 SpyTag

<400> 16

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

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Ser Gln Pro Asp Ser Ser Ser Asp Asn
130 135 140

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

Gln Ser Pro Asp Val Ser Ser Ser Thr Gly Gly Gly Ile Ala Asp Val
165 170 175

Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly Gly Ala Pro Gly
180 185 190

Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser Ser Gly Asn Trp
195 200 205

His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg Thr Thr Ser Thr
210 215 220

Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Leu
225 230 235 240

Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
245 250 255

Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe Ser Pro Arg Asn
260 265 270

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Arg Leu
275 280 285

Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Glu Gly
290 295 300

Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe
305 310 315 320

Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp Ala Gly His Glu
325 330 335

Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met Ile Pro Gln Tyr
340 345 350

Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala Gln Ser Asp Leu
355 360 365

Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
370 375 380

Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp Val Pro Phe His
385 390 395 400

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
405 410 415

Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly Asn Gly Leu Ser
420 425 430

Gly Ser Gly Ala His Ile Val Met Val Asp Ala Tyr Lys Pro Thr Lys
435 440 445

Gly Leu Ser Gly Ser Gly Pro Thr Gly Ser Thr Thr Arg Asp Leu Lys
450 455 460

Phe Ile Lys Asn Lys Val Pro Asn Phe Ala His Tyr Gly Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Phe Ile Arg Gln Gln Gly Trp Thr Thr Gln Asn Ile
485 490 495

Asn Asn Ser Val Val Asn Phe Asn Asp Met Leu Gly Lys Asn Ser Thr
500 505 510

Phe Thr Leu Asp Thr Arg Trp Ser Ser Leu Ala Pro Gly Pro Cys Met
515 520 525

Gly Asp Asp Gly Arg Thr Pro Ser Thr Thr Lys Phe Ser Asn Ala Gln
530 535 540

Leu Met Phe Gly Ser Gly Thr Gln Pro Thr Glu Gly Gly Glu Asp Ala
545 550 555 560

Val His Ile Thr Ser Glu Ser Glu Val Lys Ala Thr Asn Pro Thr Ala
565 570 575

Ile Asp Glu Tyr Gly Arg Val Ala Asp Asn Thr Gln Asn Ala Thr Thr
580 585 590

Ala Pro Thr Thr Val Gly Asn Ala Ala Met Gly Ala Met Pro Gly Met
595 600 605

Val Trp Gln Asp Arg Asp Ile Tyr Leu Gln Gly Pro Ile Trp Gly Lys
610 615 620

Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly
625 630 635 640

Phe Gly Tyr Arg Lys Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro
645 650 655

Val Pro Gly Asn Pro Ala Thr Thr Phe Ser Pro Asn Arg Ile Asn Asn
660 665 670

Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Thr Ile Asp Trp
675 680 685

Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Phe
690 695 700

Thr Ser Asn Phe Gly Thr Val Asp Ser Leu Asn Trp Ala Pro Asp Asn
705 710 715 720

Ala Gly Asn Tyr Lys Glu Pro Arg Val Ile Gly Thr Arg Tyr Leu Thr
725 730 735

Arg Ile Leu

<210> 17
<211> 2220
<212> ADN
<213> Secuencia artificial

<220>

<223> Cap AAV2 VP1 de lobo marino VP2 VP3 P430 enlazador6 SpyTag

<400> 17

atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga	60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac	120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac	180
aaggagagc cggatcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac	240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aaccctctca gccagattcg	420
tcctcggaca acacggcgcc acccgtgaaa aagtcccgtc tcgaagaagc ccagcccatt	480
caaagtccag acgtttccag cagcactggc ggaggaattg ccgacgtcat gtctggagat	540
gctgaaatgg ctgcagtggg cgggggagca ccgggcgtcg acggccaggg tgccgaggga	600
gtgggtactt cctcgggtaa ttggcattgc gattcccagt ggtcagaagg acacgtcaga	660
accaccagca ccagaacctg ggtgttggcc agctacaaca accacctgta taaacggctt	720
ggaagtagcg cacaatcaa tacctacaac ggattctcca cccctgggg atacctcgac	780
ttcaatagat ggcactgtca cttcagtcct cggaactggc aacgttcat caacaacaac	840
tggggcatca gacaaaaag acttaatgtt aaattgttca acatacaagt caaagaggtc	900
acgacggaag gggggacgac gaccgtcgcc aataacctta ccagcacgat tcaggtgttt	960
gcggacaacg cgtacgaact cccgtatgtt gtcgacgcgg gtcacgaggg ggcattgccg	1020
ccgttcccaa acgacgtgtt tatgattccc caatacggat actgcgggct ggtgtctggt	1080
caaagtcagg ctcagtcgga cttgtgttcg ttttattgcc tggagtattt tccatcccag	1140
atgctgagaa caggaaacaa ttttgaaatg aatttcaggt ttgaagacgt tccatttcac	1200
tccatgtacg cccacagcca gtctctagac aggctcatga atcctttaat tgatcagtat	1260
ctgtggagtc taaaacaaac aggaaacccg ggcctgagcg gcagcggcgc ccacatcgtg	1320
atggtggacg cctacaagcc gacgaagggc ctgagcggca gcggcactgg atcaacaacg	1380

agagacttaa aatttatcaa gaacaaagtt cccaattttg cacattatgg aaaaaattgg 1440
 cttcctggac cttttattag acaacagggg tggacaacac aaaatattaa taatagtgtt 1500
 gttaatttta atgacatgct gggaaaaaat tcgacattta ctttggacac tagatggagt 1560
 tcattagcgc ctggtccgtg tatgggggat gacggacgaa ctccatccac caccaagttc 1620
 tcaaatgctc agctcatgtt tggatctgga acacaacca ccgaaggcgg tgaagatgct 1680
 gtacatatta catccgagtc ggaggtcaag gcaaccaacc caactgcaat cgatgaatac 1740
 ggacgagtgg ccgataatac gcaaaatgca acaaccgcc caaccacagt gggaaatgct 1800
 gcaatggggg ccatgcctgg gatggtgtgg caagataggg atatctatct tcaaggaccc 1860
 atctggggaa aaatacccca tacagacgga cattttcatc cgtctcctct catggggggg 1920
 tttggataca gaaaaccccc tccgcaaatt ttatttaaaa acacccccgt tcctggaaat 1980
 ccggcaacta cattttctcc aaatagaata aacaatttca ttactcaata ctcaacggga 2040
 caagtgaccg ttactattga ctgggagctg caaaaggaaa actcaaagag atggaacca 2100
 gaagtacaat ttacatcaaa ttttggcacg gtcgattcac taaactgggc accggacaac 2160
 gcgggaaact acaaagaacc aagggtgatt ggcaccagat acctgactcg tatactataa 2220

<210> 18
 <211> 739
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Cap AAV2 VP1 de lobo marino VP2 VP3 P430 enlazador6 SpyTag

<400> 18

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

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Ser Gln Pro Asp Ser Ser Ser Asp Asn
130 135 140

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

Gln Ser Pro Asp Val Ser Ser Ser Thr Gly Gly Gly Ile Ala Asp Val
165 170 175

Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly Gly Ala Pro Gly
180 185 190

Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser Ser Gly Asn Trp
195 200 205

His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg Thr Thr Ser Thr
210 215 220

Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Leu
225 230 235 240

Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
245 250 255

Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe Ser Pro Arg Asn
260 265 270

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Arg Leu
275 280 285

Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Glu Gly
290 295 300

Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe
305 310 315 320

Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp Ala Gly His Glu
325 330 335

Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met Ile Pro Gln Tyr
340 345 350

Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala Gln Ser Asp Leu
355 360 365

Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
370 375 380

Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp Val Pro Phe His
385 390 395 400

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
405 410 415

Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly Asn Pro Gly Leu
420 425 430

Ser Gly Ser Gly Ala His Ile Val Met Val Asp Ala Tyr Lys Pro Thr
435 440 445

Lys Gly Leu Ser Gly Ser Gly Thr Gly Ser Thr Thr Arg Asp Leu Lys
450 455 460

Phe Ile Lys Asn Lys Val Pro Asn Phe Ala His Tyr Gly Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Phe Ile Arg Gln Gln Gly Trp Thr Thr Gln Asn Ile
485 490 495

Asn Asn Ser Val Val Asn Phe Asn Asp Met Leu Gly Lys Asn Ser Thr
500 505 510

Phe Thr Leu Asp Thr Arg Trp Ser Ser Leu Ala Pro Gly Pro Cys Met
515 520 525

Gly Asp Asp Gly Arg Thr Pro Ser Thr Thr Lys Phe Ser Asn Ala Gln
530 535 540

Leu Met Phe Gly Ser Gly Thr Gln Pro Thr Glu Gly Gly Glu Asp Ala
545 550 555 560

Val His Ile Thr Ser Glu Ser Glu Val Lys Ala Thr Asn Pro Thr Ala
565 570 575

Ile Asp Glu Tyr Gly Arg Val Ala Asp Asn Thr Gln Asn Ala Thr Thr
580 585 590

Ala Pro Thr Thr Val Gly Asn Ala Ala Met Gly Ala Met Pro Gly Met
595 600 605

Val Trp Gln Asp Arg Asp Ile Tyr Leu Gln Gly Pro Ile Trp Gly Lys
610 615 620

Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly
625 630 635 640

Phe Gly Tyr Arg Lys Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro
645 650 655

Val Pro Gly Asn Pro Ala Thr Thr Phe Ser Pro Asn Arg Ile Asn Asn
660 665 670

Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Thr Ile Asp Trp
675 680 685

Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Phe
690 695 700

Thr Ser Asn Phe Gly Thr Val Asp Ser Leu Asn Trp Ala Pro Asp Asn
 705 710 715 720

Ala Gly Asn Tyr Lys Glu Pro Arg Val Ile Gly Thr Arg Tyr Leu Thr
 725 730 735

Arg Ile Leu

<210> 19
 <211> 2220
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Cap AAV2 VP1 de lobo marino VP2 VP3 T431 enlazador6 SpyTag

<400> 19
 atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
 cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
 gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
 aaggagagc cggatcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
 cggcagctcg acagcggaga caacccttac ctcaagtaca accacgccga cgcggagttt 300
 caggagcgcc tttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
 gcgaaaaaga gggttcttga acctctgggc ctggttgagg aaccctctca gccagattcg 420
 tcctcggaca acacggcgcc acccgtgaaa aagtcccgtc tcgaagaagc ccagcccatt 480
 caaagtccag acgtttccag cagcactggc ggaggaattg ccgacgtcat gtctggagat 540
 gctgaaatgg ctgcagtggg cgggggagca ccgggcgtcg acggccaggg tgccgaggga 600
 gtgggtactt cctcgggtaa ttggcattgc gattcccagt ggtcagaagg acacgtcaga 660
 accaccagca ccagaacctg ggtgttgccc agctacaaca accacctgta taaacggctt 720
 ggaagtagcg cacaatcaa tacctacaac ggattctcca cccctgggg atacctcgac 780
 ttcaatagat ggcactgtca cttcagtcct cggaactggc aacgtctcat caacaacaac 840
 tggggcatca gacaaaaag acttaatgtt aaattgttca acatacaagt caaagaggtc 900
 acgacggaag gggggacgac gaccgtcgcc aataacctta ccagcacgat tcaggtgttt 960
 gcggacaacg cgtacgaact cccgtatgtt gtcgacgcgg gtcacgaggg ggcattgccg 1020

ccgttcccaa acgacgtgtt tatgattccc caatacggat actgcgggct ggtgtctggt 1080
 caaagtcagg ctgagtcgga cttgtgttcg ttttattgcc tggagtattt tccatcccag 1140
 atgctgagaa caggaaacaa ttttgaaatg aatttcaggt ttgaagacgt tccatttcac 1200
 tccatgtacg cccacagcca gtctctagac aggctcatga atcctttaat tgatcagtat 1260
 ctgtggagtc taaaacaaac aggaaacccg actggcctga gcggcagcgg cgccccacatc 1320
 gtgatggtgg acgcctacaa gccgacgaag ggcctgagcg gcagcggcgg atcaacaacg 1380
 agagacttaa aatttatcaa gaacaaagtt cccaattttg cacattatgg aaaaaattgg 1440
 cttcctggac cttttattag acaacagggg tggacaacac aaaatattaa taatagtgtt 1500
 gttaatttta atgacatgct gggaaaaaat tcgacattta ctttggacac tagatggagt 1560
 tcattagcgc ctggtccgtg tatgggggat gacggacgaa ctccatccac caccaagttc 1620
 tcaaagtctc agctcatgtt tggatctgga acacaacca ccgaaggcgg tgaagatgct 1680
 gtacatatta catccgagtc ggaggtcaag gcaaccaacc caactgcaat cgatgaatac 1740
 ggacgagtgg ccgataatac gcaaaatgca acaaccgccc caaccacagt gggaaatgct 1800
 gcaatggggg ccatgcctgg gatggtgtgg caagataggg atatctatct tcaaggaccc 1860
 atctggggaa aaatacccca tacagacgga cattttcatc cgtctcctct catggggggg 1920
 tttggataca gaaaaccccc tccgcaaatt tttattaaaa acacccccgt tcctggaaat 1980
 ccggcaacta cattttctcc aaatagaata aacaatttca ttactcaata ctcaacggga 2040
 caagtgaccg ttactattga ctgggagctg caaaaggaaa actcaaagag atggaacca 2100
 gaagtacaat ttacatcaaa ttttggcacg gtcgattcac taaactgggc accggacaac 2160
 gcgggaaact acaaagaacc aagggtgatt ggcaccagat acctgactcg tatactataa 2220

<210> 20
 <211> 739
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Cap AAV2 VP1 de lobo marino VP2 VP3 T431 enlazador6 SpyTag

<400> 20

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

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Ser Gln Pro Asp Ser Ser Ser Asp Asn
130 135 140

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

Gln Ser Pro Asp Val Ser Ser Ser Thr Gly Gly Gly Ile Ala Asp Val
165 170 175

Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly Gly Ala Pro Gly
180 185 190

Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser Ser Gly Asn Trp
195 200 205

His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg Thr Thr Ser Thr
210 215 220

Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Leu
225 230 235 240

Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
245 250 255

Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe Ser Pro Arg Asn
260 265 270

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Arg Leu
275 280 285

Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Glu Gly
290 295 300

Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe
305 310 315 320

Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp Ala Gly His Glu
325 330 335

Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met Ile Pro Gln Tyr
340 345 350

Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala Gln Ser Asp Leu
355 360 365

Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
370 375 380

Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp Val Pro Phe His
385 390 395 400

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
405 410 415

Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly Asn Pro Thr Gly
420 425 430

Leu Ser Gly Ser Gly Ala His Ile Val Met Val Asp Ala Tyr Lys Pro
435 440 445

Thr Lys Gly Leu Ser Gly Ser Gly Gly Ser Thr Thr Arg Asp Leu Lys
450 455 460

Phe Ile Lys Asn Lys Val Pro Asn Phe Ala His Tyr Gly Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Phe Ile Arg Gln Gln Gly Trp Thr Thr Gln Asn Ile
485 490 495

Asn Asn Ser Val Val Asn Phe Asn Asp Met Leu Gly Lys Asn Ser Thr
500 505 510

Phe Thr Leu Asp Thr Arg Trp Ser Ser Leu Ala Pro Gly Pro Cys Met
515 520 525

Gly Asp Asp Gly Arg Thr Pro Ser Thr Thr Lys Phe Ser Asn Ala Gln
530 535 540

Leu Met Phe Gly Ser Gly Thr Gln Pro Thr Glu Gly Gly Glu Asp Ala
545 550 555 560

Val His Ile Thr Ser Glu Ser Glu Val Lys Ala Thr Asn Pro Thr Ala
565 570 575

Ile Asp Glu Tyr Gly Arg Val Ala Asp Asn Thr Gln Asn Ala Thr Thr
580 585 590

Ala Pro Thr Thr Val Gly Asn Ala Ala Met Gly Ala Met Pro Gly Met
595 600 605

Val Trp Gln Asp Arg Asp Ile Tyr Leu Gln Gly Pro Ile Trp Gly Lys
610 615 620

Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly
625 630 635 640

Phe Gly Tyr Arg Lys Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro
645 650 655

Val Pro Gly Asn Pro Ala Thr Thr Phe Ser Pro Asn Arg Ile Asn Asn
660 665 670

Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Thr Ile Asp Trp
675 680 685

Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Phe
690 695 700

Thr Ser Asn Phe Gly Thr Val Asp Ser Leu Asn Trp Ala Pro Asp Asn
705 710 715 720

Ala Gly Asn Tyr Lys Glu Pro Arg Val Ile Gly Thr Arg Tyr Leu Thr
725 730 735

Arg Ile Leu

<210> 21
<211> 2220
<212> ADN
<213> Secuencia artificial

<220>
<223> Cap AAV2 VP1 de lobo marino VP2 VP3 S433 enlazador6 SpyTag

<400> 21
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aaccctctca gccagattcg 420
tcctcggaca acacggcgcc acccgtgaaa aagtcccgtc tcgaagaagc ccagcccatt 480
caaagtccag acgtttccag cagcactggc ggaggaattg ccgacgtcat gtctggagat 540
gctgaaatgg ctgcagtggg cgggggagca ccgggcgtcg acggccaggg tgccgaggga 600
gtgggtactt cctcgggtaa ttggcattgc gattcccagt ggtcagaagg acacgtcaga 660

accaccagca ccagaacctg ggtgttgccc agctacaaca accacctgta taaacggctt	720
ggaagtagcg cacaatccaa tacctacaac ggattctcca cccctggggg atacctcgac	780
ttcaatagat ggcactgtca cttcagtcct cggaactggc aacgtctcat caacaacaac	840
tggggcatca gacaaaaag acttaatgtt aaattgttca acatacaagt caaagaggtc	900
acgacggaag gggggacgac gaccgtcgcc aataacctta ccagcacgat tcaggtgttt	960
gcggacaacg cgtacgaact cccgtatgtt gtcgacgcgg gtcacgaggg ggcattgccg	1020
ccgttcccaa acgacgtgtt tatgattccc caatacggat actgcgggct ggtgtctggt	1080
caaagtcagg ctcagtcgga cttgtgttcg ttttattgcc tggagtattt tccatcccag	1140
atgctgagaa caggaaacaa ttttgaaatg aatttcaggt ttgaagacgt tccatttcac	1200
tccatgtacg cccacagcca gtctctagac aggctcatga atcctttaat tgatcagtat	1260
ctgtggagtc taaaacaaac aggaaacccg actggatcag gcctgagcgg cagcggcgcc	1320
cacatcgtga tgggtggacgc ctacaagccg acgaagggcc tgagcggcag cggcacaacg	1380
agagacttaa aatttatcaa gaacaaagtt cccaattttg cacattatgg aaaaaattgg	1440
cttcctggac cttttattag acaacagggg tggacaacac aaaatattaa taatagtgtt	1500
gttaatttta atgacatgct gggaaaaaat tcgacattta ctttggacac tagatggagt	1560
tcattagcgc ctggtccgtg tatgggggat gacggacgaa ctccatccac caccaagttc	1620
tcaaagtctc agctcatgtt tggatctgga acacaacca ccgaaggcgg tgaagatgct	1680
gtacatatta catccgagtc ggaggtcaag gcaaccaacc caactgcaat cgatgaatac	1740
ggacgagtgg ccgataatac gcaaaatgca acaaccgccc caaccacagt gggaaatgct	1800
gcaatggggg ccatgcctgg gatggtgtgg caagataggg atatctatct tcaaggaccc	1860
atctggggaa aaatacccca tacagacgga ctttttcatc cgtctcctct catggggggg	1920
tttgataca gaaaaccccc tccgcaaatt tttattaaaa acacccccgt tcctggaaat	1980
ccggcaacta ctttttctcc aaatagaata aacaatttca ttactcaata ctcaacggga	2040
caagtgaccg ttactattga ctgggagctg caaaaggaaa actcaaagag atggaacca	2100
gaagtacaat ttacatcaaa ttttggcacg gtcgattcac taaactgggc accggacaac	2160
gcgggaaact acaaagaacc aagggtgatt ggcaccagat acctgactcg tatactataa	2220

<210> 22
<211> 739
<212> PRT
<213> Secuencia artificial

<220>

<223> Cap AAV2 VP1 de lobo marino VP2 VP3 S433 enlazador6 SpyTag

<400> 22

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

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Ser Gln Pro Asp Ser Ser Ser Asp Asn
130 135 140

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

Gln Ser Pro Asp Val Ser Ser Ser Thr Gly Gly Gly Ile Ala Asp Val
165 170 175

Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly Gly Ala Pro Gly
180 185 190

Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser Ser Gly Asn Trp
195 200 205

His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg Thr Thr Ser Thr
210 215 220

Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Leu
225 230 235 240

Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
245 250 255

Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe Ser Pro Arg Asn
260 265 270

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Arg Leu
275 280 285

Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Glu Gly
290 295 300

Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe
305 310 315 320

Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp Ala Gly His Glu
325 330 335

Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met Ile Pro Gln Tyr
340 345 350

Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala Gln Ser Asp Leu
355 360 365

Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
370 375 380

Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp Val Pro Phe His
385 390 395 400

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
405 410 415

Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly Asn Pro Thr Gly
420 425 430

Ser Gly Leu Ser Gly Ser Gly Ala His Ile Val Met Val Asp Ala Tyr
435 440 445

Lys Pro Thr Lys Gly Leu Ser Gly Ser Gly Thr Thr Arg Asp Leu Lys
450 455 460

Phe Ile Lys Asn Lys Val Pro Asn Phe Ala His Tyr Gly Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Phe Ile Arg Gln Gln Gly Trp Thr Thr Gln Asn Ile
485 490 495

Asn Asn Ser Val Val Asn Phe Asn Asp Met Leu Gly Lys Asn Ser Thr
500 505 510

Phe Thr Leu Asp Thr Arg Trp Ser Ser Leu Ala Pro Gly Pro Cys Met
515 520 525

Gly Asp Asp Gly Arg Thr Pro Ser Thr Thr Lys Phe Ser Asn Ala Gln
530 535 540

Leu Met Phe Gly Ser Gly Thr Gln Pro Thr Glu Gly Gly Glu Asp Ala
545 550 555 560

Val His Ile Thr Ser Glu Ser Glu Val Lys Ala Thr Asn Pro Thr Ala
565 570 575

Ile Asp Glu Tyr Gly Arg Val Ala Asp Asn Thr Gln Asn Ala Thr Thr
580 585 590

Ala Pro Thr Thr Val Gly Asn Ala Ala Met Gly Ala Met Pro Gly Met
595 600 605

Val Trp Gln Asp Arg Asp Ile Tyr Leu Gln Gly Pro Ile Trp Gly Lys
610 615 620

Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly
625 630 635 640

Phe Gly Tyr Arg Lys Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro
645 650 655

Val Pro Gly Asn Pro Ala Thr Thr Phe Ser Pro Asn Arg Ile Asn Asn
660 665 670

Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Thr Ile Asp Trp
675 680 685

Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Phe
690 695 700

Thr Ser Asn Phe Gly Thr Val Asp Ser Leu Asn Trp Ala Pro Asp Asn
705 710 715 720

Ala Gly Asn Tyr Lys Glu Pro Arg Val Ile Gly Thr Arg Tyr Leu Thr
725 730 735

Arg Ile Leu

<210> 23
<211> 2220
<212> ADN
<213> Secuencia artificial

<220>
<223> Cap AAV2 VP1 de lobo marino VP2 VP3 T434 enlazador6 SpyTag

<400> 23
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aaccctctca gccagattcg	420
tcctcggaca acacggcgcc acccgtgaaa aagtcccgtc tcgaagaagc ccagcccatt	480
caaagtccag acgtttccag cagcactggc ggaggaattg ccgacgtcat gtctggagat	540
gctgaaatgg ctgcagtggg cgggggagca ccgggcgtcg acggccaggg tgccgaggga	600
gtgggtactt cctcgggtaa ttggcattgc gattcccagt ggtcagaagg acacgtcaga	660
accaccagca ccagaacctg ggtgttgccc agctacaaca accacctgta taaacggctt	720
ggaagtagcg cacaatccaa tacctacaac ggattctcca cccctgggg atacctcgac	780
ttcaatagat ggactgtca cttcagtcct cggaactggc aacgtctcat caacaacaac	840
tggggcatca gacaaaaag acttaatgtt aaattgttca acatacaagt caaagaggtc	900
acgacggaag gggggacgac gaccgtcgcc aataacctta ccagcacgat tcaggtgttt	960
gcggacaacg cgtacgaact cccgtatgtt gtcgacgcgg gtcacgaggg ggcattgccg	1020
ccgttcccaa acgacgtgtt tatgattccc caatacggat actgcgggct ggtgtctggt	1080
caaagtcagg ctcagtcgga cttgtgttcg ttttattgcc tggagtattt tccatcccag	1140
atgctgagaa caggaaacaa ttttgaaatg aatttcaggt ttgaagacgt tccatttcac	1200
tccatgtacg cccacagcca gtctctagac aggctcatga atcctttaat tgatcagtat	1260
ctgtggagtc taaaacaaac aggaaacccg actggatcaa caggcctgag cggcagcggc	1320
gcccacatcg tgatggtgga cgcctacaag ccgacgaagg gcctgagcgg cagcggcacg	1380
agagacttaa aatttatcaa gaacaaagt cccaattttg cacattatgg aaaaaattgg	1440
cttcctggac cttttattag acaacagggg tggacaacac aaaatattaa taatagtgtt	1500
gttaatttta atgacatgct gggaaaaaat tcgacattta ctttggacac tagatggagt	1560
tcattagcgc ctggtccgtg tatgggggat gacggacgaa ctccatccac caccaagttc	1620
tcaaagtctc agctcatgtt tggatctgga acacaacca ccgaaggcgg tgaagatgct	1680
gtacatatta catccgagtc ggaggtcaag gcaaccaacc caactgcaat cgatgaatac	1740
ggacgagtgg ccgataatac gcaaaatgca acaaccgcc caaccacagt gggaaatgct	1800
gcaatggggg ccatgcctgg gatggtgtgg caagataggg atatctatct tcaaggaccc	1860
atctggggaa aaatacccca tacagacgga cattttcatc cgtctcctct catggggggg	1920

tttgataca gaaaaccccc tccgcaaatt tttattaaaa acacccccgt tcctggaaat	1980
ccggcaacta cattttctcc aaatagaata aacaatttca ttactcaata ctcaacggga	2040
caagtgaccg ttactattga ctgggagctg caaaaggaaa actcaaagag atggaacca	2100
gaagtacaat ttacatcaaa ttttggcacg gtcgattcac taaactgggc accggacaac	2160
gcgggaaact acaaagaacc aagggtgatt ggcaccagat acctgactcg tatactataa	2220

<210> 24
 <211> 739
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Cap AAV2 VP1 de lobo marino VP2 VP3 T434 enlazador6 SpyTag

<400> 24

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

Glu	Gly	Ile	Arg	Gln	Trp	Trp	Lys	Leu	Lys	Pro	Gly	Pro	Pro	Pro	Pro
			20					25					30		

Lys	Pro	Ala	Glu	Arg	His	Lys	Asp	Asp	Ser	Arg	Gly	Leu	Val	Leu	Pro
		35					40					45			

Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro
	50					55					60				

Val	Asn	Glu	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp
65					70					75					80

Arg	Gln	Leu	Asp	Ser	Gly	Asp	Asn	Pro	Tyr	Leu	Lys	Tyr	Asn	His	Ala
			85						90					95	

Asp	Ala	Glu	Phe	Gln	Glu	Arg	Leu	Lys	Glu	Asp	Thr	Ser	Phe	Gly	Gly
			100					105					110		

Asn	Leu	Gly	Arg	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Val	Leu	Glu	Pro
		115					120					125			

Leu Gly Leu Val Glu Glu Pro Ser Gln Pro Asp Ser Ser Ser Asp Asn
130 135 140

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

Gln Ser Pro Asp Val Ser Ser Ser Thr Gly Gly Gly Ile Ala Asp Val
165 170 175

Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly Gly Ala Pro Gly
180 185 190

Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser Ser Gly Asn Trp
195 200 205

His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg Thr Thr Ser Thr
210 215 220

Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Leu
225 230 235 240

Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
245 250 255

Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe Ser Pro Arg Asn
260 265 270

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Arg Leu
275 280 285

Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Glu Gly
290 295 300

Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe
305 310 315 320

Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp Ala Gly His Glu
325 330 335

Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met Ile Pro Gln Tyr
340 345 350

Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala Gln Ser Asp Leu
355 360 365

Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
370 375 380

Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp Val Pro Phe His
385 390 395 400

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
405 410 415

Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly Asn Pro Thr Gly
420 425 430

Ser Thr Gly Leu Ser Gly Ser Gly Ala His Ile Val Met Val Asp Ala
435 440 445

Tyr Lys Pro Thr Lys Gly Leu Ser Gly Ser Gly Thr Arg Asp Leu Lys
450 455 460

Phe Ile Lys Asn Lys Val Pro Asn Phe Ala His Tyr Gly Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Phe Ile Arg Gln Gln Gly Trp Thr Thr Gln Asn Ile
485 490 495

Asn Asn Ser Val Val Asn Phe Asn Asp Met Leu Gly Lys Asn Ser Thr
500 505 510

Phe Thr Leu Asp Thr Arg Trp Ser Ser Leu Ala Pro Gly Pro Cys Met
515 520 525

Gly Asp Asp Gly Arg Thr Pro Ser Thr Thr Lys Phe Ser Asn Ala Gln
530 535 540

Leu Met Phe Gly Ser Gly Thr Gln Pro Thr Glu Gly Gly Glu Asp Ala
545 550 555 560

Val His Ile Thr Ser Glu Ser Glu Val Lys Ala Thr Asn Pro Thr Ala
565 570 575

Ile Asp Glu Tyr Gly Arg Val Ala Asp Asn Thr Gln Asn Ala Thr Thr
580 585 590

Ala Pro Thr Thr Val Gly Asn Ala Ala Met Gly Ala Met Pro Gly Met
595 600 605

Val Trp Gln Asp Arg Asp Ile Tyr Leu Gln Gly Pro Ile Trp Gly Lys
610 615 620

Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly
625 630 635 640

Phe Gly Tyr Arg Lys Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro
645 650 655

Val Pro Gly Asn Pro Ala Thr Thr Phe Ser Pro Asn Arg Ile Asn Asn
660 665 670

Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Thr Ile Asp Trp
675 680 685

Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Phe
690 695 700

Thr Ser Asn Phe Gly Thr Val Asp Ser Leu Asn Trp Ala Pro Asp Asn
705 710 715 720

Ala Gly Asn Tyr Lys Glu Pro Arg Val Ile Gly Thr Arg Tyr Leu Thr
725 730 735

Arg Ile Leu

<210> 25

<211> 2220

<212> ADN

<213> Secuencia artificial

<220>

<223> Cap AAV2 VP1 de lobo marino VP2 VP3 T435 enlazador6 SpyTag

<400> 25

atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga	60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac	120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac	180
aaggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac	240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aaccctctca gccagattcg	420
tcctcggaca acacggcgcc acccgtgaaa aagtcccgtc tcgaagaagc ccagcccatt	480
caaagtccag acgtttccag cagcactggc ggaggaattg ccgacgtcat gtctggagat	540
gctgaaatgg ctgcagtggg cgggggagca ccgggcgtcg acggccaggg tgccgaggga	600
gtgggtactt cctcgggtaa ttggcattgc gattcccagt ggtcagaagg acacgtcaga	660
accaccagca ccagaacctg ggtgttgccc agctacaaca accacctgta taaacggctt	720
ggaagtagcg cacaatcaa tacctacaac ggattctcca cccctgggg atacctcgac	780
ttcaatagat ggcactgtca cttcagtcct cggaactggc aacgtctcat caacaacaac	840
tggggcatca gacaaaaag acttaatgtt aaattgttca acatacaagt caaagaggtc	900
acgacggaag gggggacgac gaccgtcgcc aataacctta ccagcacgat tcaggtgttt	960
gcggacaacg cgtacgaact cccgtatgtt gtcgacgcgg gtcacgaggg ggcattgccg	1020
ccgttcccaa acgacgtgtt tatgattccc caatacggat actgcgggct ggtgtctggt	1080
caaagtcagg ctcagtcgga cttgtgttcg ttttattgcc tggagtattt tccatcccag	1140
atgctgagaa caggaaacaa ttttgaaatg aatttcaggt ttgaagacgt tccatttcac	1200
tccatgtacg cccacagcca gtctctagac aggctcatga atcctttaat tgatcagtat	1260
ctgtggagtc taaaacaaac aggaaacccg actggatcaa caacgggcct gagcggcagc	1320
ggcgcccaca tcgtgatggt ggacgcctac aagccgacga agggcctgag cggcagcggc	1380
agagacttaa aatttatcaa gaacaaagtt cccaattttg cacattatgg aaaaaattgg	1440
cttcctggac cttttattag acaacagggg tggacaacac aaaatattaa taatagtgtt	1500
gttaatttta atgacatgct gggaaaaaat tcgacattta ctttggacac tagatggagt	1560

tcattagcgc ctggtccgtg tatgggggat gacggacgaa ctccatccac caccaagttc	1620
tcaaattgctc agctcatgtt tggatctgga acacaaccca ccgaaggcgg tgaagatgct	1680
gtacatatta catccgagtc ggaggtcaag gcaaccaacc caactgcaat cgatgaatac	1740
ggacgagtgg ccgataatac gcaaaatgca acaaccgccc caaccacagt gggaaatgct	1800
gcaatggggg ccatgcctgg gatggtgtgg caagataggg atatctatct tcaaggaccc	1860
atctggggaa aaatacccca tacagacgga ctttttcatt cgtctcctct catggggggg	1920
tttgataca gaaaaccccc tccgcaaatt ttattataaa acacccccgt tcctggaaat	1980
ccggcaacta ctttttctcc aaatagaata aacaatttca ttactcaata ctcaacggga	2040
caagtgaccg ttactattga ctgggagctg caaaaggaaa actcaaagag atggaaccca	2100
gaagtacaat ttacatcaaa ttttggcacg gtcgattcac taaactgggc accggacaac	2160
gcgggaaact acaaagaacc aagggtgatt ggcaccagat acctgactcg tatactataa	2220

<210> 26
 <211> 739
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Cap AAV2 VP1 de lobo marino VP2 VP3 T435 enlazador6 SpyTag
 <400> 26

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

Glu	Gly	Ile	Arg	Gln	Trp	Trp	Lys	Leu	Lys	Pro	Gly	Pro	Pro	Pro	Pro
			20					25					30		

Lys	Pro	Ala	Glu	Arg	His	Lys	Asp	Asp	Ser	Arg	Gly	Leu	Val	Leu	Pro
		35					40					45			

Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro
	50					55					60				

Val	Asn	Glu	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp
65					70					75					80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Ser Gln Pro Asp Ser Ser Ser Asp Asn
130 135 140

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

Gln Ser Pro Asp Val Ser Ser Ser Thr Gly Gly Gly Ile Ala Asp Val
165 170 175

Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly Gly Ala Pro Gly
180 185 190

Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser Ser Gly Asn Trp
195 200 205

His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg Thr Thr Ser Thr
210 215 220

Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Leu
225 230 235 240

Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
245 250 255

Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe Ser Pro Arg Asn
260 265 270

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Arg Leu
275 280 285

Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Glu Gly
290 295 300

Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe
305 310 315 320

Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp Ala Gly His Glu
325 330 335

Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met Ile Pro Gln Tyr
340 345 350

Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala Gln Ser Asp Leu
355 360 365

Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
370 375 380

Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp Val Pro Phe His
385 390 395 400

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
405 410 415

Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly Asn Pro Thr Gly
420 425 430

Ser Thr Thr Gly Leu Ser Gly Ser Gly Ala His Ile Val Met Val Asp
435 440 445

Ala Tyr Lys Pro Thr Lys Gly Leu Ser Gly Ser Gly Arg Asp Leu Lys
450 455 460

Phe Ile Lys Asn Lys Val Pro Asn Phe Ala His Tyr Gly Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Phe Ile Arg Gln Gln Gly Trp Thr Thr Gln Asn Ile
485 490 495

Asn Asn Ser Val Val Asn Phe Asn Asp Met Leu Gly Lys Asn Ser Thr
500 505 510

Phe Thr Leu Asp Thr Arg Trp Ser Ser Leu Ala Pro Gly Pro Cys Met
515 520 525

Gly Asp Asp Gly Arg Thr Pro Ser Thr Thr Lys Phe Ser Asn Ala Gln
530 535 540

Leu Met Phe Gly Ser Gly Thr Gln Pro Thr Glu Gly Gly Glu Asp Ala
545 550 555 560

Val His Ile Thr Ser Glu Ser Glu Val Lys Ala Thr Asn Pro Thr Ala
565 570 575

Ile Asp Glu Tyr Gly Arg Val Ala Asp Asn Thr Gln Asn Ala Thr Thr
580 585 590

Ala Pro Thr Thr Val Gly Asn Ala Ala Met Gly Ala Met Pro Gly Met
595 600 605

Val Trp Gln Asp Arg Asp Ile Tyr Leu Gln Gly Pro Ile Trp Gly Lys
610 615 620

Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly
625 630 635 640

Phe Gly Tyr Arg Lys Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro
645 650 655

Val Pro Gly Asn Pro Ala Thr Thr Phe Ser Pro Asn Arg Ile Asn Asn
660 665 670

Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Thr Ile Asp Trp
675 680 685

Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Phe
690 695 700

Thr Ser Asn Phe Gly Thr Val Asp Ser Leu Asn Trp Ala Pro Asp Asn
705 710 715 720

Ala Gly Asn Tyr Lys Glu Pro Arg Val Ile Gly Thr Arg Tyr Leu Thr
725 730 735

Arg Ile Leu

<210> 27
<211> 2220
<212> ADN
<213> Secuencia artificial

<220>
<223> Cap AAV2 VP1 de lobo marino VP2 VP3 R436 enlazador6 SpyTag

<400> 27
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aaggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aaccctctca gccagattcg 420
tcctcggaac acacggcgcc acccgtgaaa aagtcccgtc tcgaagaagc ccagcccatt 480
caaagtccag acgtttccag cagcactggc ggaggaattg ccgacgtcat gtctggagat 540
gctgaaatgg ctgcagtggg cgggggagca ccgggcgtcg acggccaggg tgccgaggga 600
gtgggtactt cctcgggtaa ttggcattgc gattcccagt ggtcagaagg acacgtcaga 660
accaccagca ccagaacctg ggtgttggcc agctacaaca accacctgta taaacggctt 720
ggaagtagcg cacaatcaa tacctacaac ggattctcca cccctggggg atacctcgac 780
ttcaatagat ggcactgtca cttcagtcct cggaactggc aacgtctcat caacaacaac 840
tggggcatca gacaaaaag acttaatgtt aaattgttca acatacaagt caaagaggtc 900
acgacggaag gggggacgac gaccgtcgcc aataacctta ccagcacgat tcaggtgttt 960
gcggacaacg cgtacgaact cccgtatgtt gtcgacgcgg gtcacgaggg ggcattgccg 1020
ccgttcccaa acgacgtgtt tatgattccc caatacggat actgcgggct ggtgtctggt 1080
caaagtcagg ctcagtcgga cttgtgttcg ttttattgcc tggagtattt tccatcccag 1140
atgctgagaa caggaaacaa ttttgaaatg aatttcaggt ttgaagacgt tccatttcac 1200

tccatgtacg cccacagcca gtctctagac aggctcatga atcctttaat tgatcagtat	1260
ctgtggagtc taaaacaaac aggaaacccg actggatcaa caacgagagg cctgagcggc	1320
agcggcgccc acatcgtgat ggtggacgcc tacaagccga cgaagggcct gagcggcagc	1380
ggcgacttaa aatttatcaa gaacaaagtt cccaattttg cacattatgg aaaaaattgg	1440
cttcctggac cttttattag acaacagggg tggacaacac aaaatattaa taatagtgtt	1500
gttaatttta atgacatgct gggaaaaaat tcgacattta ctttggacac tagatggagt	1560
tcattagcgc ctgggtccgtg tatgggggat gacggacgaa ctccatccac caccaagttc	1620
tcaaatgctc agctcatggt tggatctgga acacaacca ccgaaggcgg tgaagatgct	1680
gtacatatta catccgagtc ggaggtcaag gcaaccaacc caactgcaat cgatgaatac	1740
ggacgagtgg ccgataatac gcaaaatgca acaaccgccc caaccacagt gggaaatgct	1800
gcaatggggg ccatgcctgg gatggtgtgg caagataggg atatctatct tcaaggaccc	1860
atctggggaa aaatacccca tacagacgga cttttcatc cgtctcctct catggggggg	1920
tttgataca gaaaaccccc tccgcaaatt tttattaaaa acacccccgt tcctggaaat	1980
ccggcaacta cttttctcc aaatagaata aacaatttca ttactcaata ctcaacggga	2040
caagtgaccg ttactattga ctgggagctg caaaaggaaa actcaaagag atggaacca	2100
gaagtacaat ttacatcaaa ttttggcacg gtcgattcac taaactgggc accggacaac	2160
gcgggaaact acaaagaacc aagggtgatt ggcaccagat acctgactcg tatactataa	2220

<210> 28
 <211> 739
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Cap AAV2 VP1 de lobo marino VP2 VP3 R436 enlazador6 SpyTag

<400> 28

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

Glu	Gly	Ile	Arg	Gln	Trp	Trp	Lys	Leu	Lys	Pro	Gly	Pro	Pro	Pro	Pro
			20					25					30		

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Ser Gln Pro Asp Ser Ser Ser Asp Asn
130 135 140

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

Gln Ser Pro Asp Val Ser Ser Ser Thr Gly Gly Gly Ile Ala Asp Val
165 170 175

Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly Gly Ala Pro Gly
180 185 190

Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser Ser Gly Asn Trp
195 200 205

His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg Thr Thr Ser Thr
210 215 220

Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Leu
225 230 235 240

Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
245 250 255

Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe Ser Pro Arg Asn
260 265 270

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Arg Leu
275 280 285

Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Glu Gly
290 295 300

Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe
305 310 315 320

Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp Ala Gly His Glu
325 330 335

Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met Ile Pro Gln Tyr
340 345 350

Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala Gln Ser Asp Leu
355 360 365

Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
370 375 380

Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp Val Pro Phe His
385 390 395 400

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
405 410 415

Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly Asn Pro Thr Gly
420 425 430

Ser Thr Thr Arg Gly Leu Ser Gly Ser Gly Ala His Ile Val Met Val
435 440 445

Asp Ala Tyr Lys Pro Thr Lys Gly Leu Ser Gly Ser Gly Asp Leu Lys
450 455 460

Phe Ile Lys Asn Lys Val Pro Asn Phe Ala His Tyr Gly Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Phe Ile Arg Gln Gln Gly Trp Thr Thr Gln Asn Ile
485 490 495

Asn Asn Ser Val Val Asn Phe Asn Asp Met Leu Gly Lys Asn Ser Thr
500 505 510

Phe Thr Leu Asp Thr Arg Trp Ser Ser Leu Ala Pro Gly Pro Cys Met
515 520 525

Gly Asp Asp Gly Arg Thr Pro Ser Thr Thr Lys Phe Ser Asn Ala Gln
530 535 540

Leu Met Phe Gly Ser Gly Thr Gln Pro Thr Glu Gly Gly Glu Asp Ala
545 550 555 560

Val His Ile Thr Ser Glu Ser Glu Val Lys Ala Thr Asn Pro Thr Ala
565 570 575

Ile Asp Glu Tyr Gly Arg Val Ala Asp Asn Thr Gln Asn Ala Thr Thr
580 585 590

Ala Pro Thr Thr Val Gly Asn Ala Ala Met Gly Ala Met Pro Gly Met
595 600 605

Val Trp Gln Asp Arg Asp Ile Tyr Leu Gln Gly Pro Ile Trp Gly Lys
610 615 620

Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly
625 630 635 640

Phe Gly Tyr Arg Lys Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro
645 650 655

Val Pro Gly Asn Pro Ala Thr Thr Phe Ser Pro Asn Arg Ile Asn Asn
660 665 670

Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Thr Ile Asp Trp
675 680 685

Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Phe
690 695 700

Thr Ser Asn Phe Gly Thr Val Asp Ser Leu Asn Trp Ala Pro Asp Asn
705 710 715 720

Ala Gly Asn Tyr Lys Glu Pro Arg Val Ile Gly Thr Arg Tyr Leu Thr
725 730 735

Arg Ile Leu

<210> 29
<211> 2220
<212> ADN
<213> Secuencia artificial

<220>
<223> Cap AAV2 VP1 de lobo marino VP2 VP3 D437 enlazador6 SpyTag

<400> 29
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cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aaccctctca gccagattcg 420
tcctcggaca acacggcgcc acccgtgaaa aagtcccgtc tcgaagaagc ccagcccatt 480
caaagtccag acgtttccag cagcactggc ggaggaattg ccgacgtcat gtctggagat 540
gctgaaatgg ctgcagtggg cgggggagca ccgggcgtcg acggccaggg tgccgaggga 600
gtgggtactt cctcgggtaa ttggcattgc gattcccagt ggtcagaagg acacgtcaga 660
accaccagca ccagaacctg ggtgttgccc agctacaaca accacctgta taaacggctt 720
ggaagtagcg cacaatcaa tacctacaac ggattctcca cccctgggg atacctcgac 780
ttcaatagat ggcactgtca cttcagtcct cggaactggc aacgtctcat caacaacaac 840

tggggcatca gacaaaaag acttaatggtt aaattgttca acatacaagt caaagaggctc	900
acgacggaag gggggacgac gaccgtcgcc aataacctta ccagcacgat tcaggtgttt	960
gcggaacaac cgtacgaact cccgtatggt gtcgacgcgg gtcacgaggg ggcattgccg	1020
ccgttcccaa acgacgtggt tatgattccc caatacggat actgcgggct ggtgtctggt	1080
caaagtcagg ctgagtcgga cttgtgttcg ttttattgcc tggagtattt tccatcccag	1140
atgctgagaa caggaaacaa ttttgaaatg aatttcaggt ttgaagacgt tccatttcac	1200
tccatgtacg cccacagcca gtctctagac aggctcatga atcctttaat tgatcagtat	1260
ctgtggagtc taaaacaaac aggaacccg actggatcaa caacgagaga cggcctgagc	1320
ggcagcggcg cccacatcgt gatggtggac gcctacaagc cgacgaaggg cctgagcggc	1380
agcggcttaa aatttatcaa gaacaaagt cccaattttg cacattatgg aaaaaattgg	1440
cttcctggac cttttattag acaacagggg tggacaacac aaaatattaa taatagtgtt	1500
gttaatttta atgacatgct gggaaaaaat tcgacattta ctttggacac tagatggagt	1560
tcattagcgc ctggtccgtg tatgggggat gacggacgaa ctccatccac caccaagttc	1620
tcaaatgctc agctcatggt tggatctgga acacaacca ccgaaggcgg tgaagatgct	1680
gtacatatta catccgagtc ggaggtcaag gcaaccaacc caactgcaat cgatgaatac	1740
ggacgagtgg ccgataatac gcaaaatgca acaaccgcc caaccacagt gggaaatgct	1800
gcaatggggg ccatgcctgg gatggtgtgg caagataggg atatctatct tcaaggaccc	1860
atctggggaa aaatacccca tacagacgga cttttcatc cgtctcctct catggggggg	1920
tttgataca gaaaacccc tccgcaaatt tttattaaaa acaccccgt tcctggaaat	1980
ccggcaacta cttttctcc aaatagaata aacaatttca ttactcaata ctcaacggga	2040
caagtgaccg ttactattga ctgggagctg caaaaggaaa actcaaagag atggaacca	2100
gaagtacaat ttacatcaaa ttttggcacg gtcgattcac taaactgggc accggacaac	2160
gcgggaaact acaaagaacc aagggtgatt ggcaccagat acctgactcg tatactataa	2220

<210> 30

<211> 739

<212> PRT

<213> Secuencia artificial

<220>

<223> Cap AAV2 VP1 de lobo marino VP2 VP3 D437 enlazador6 SpyTag

<400> 30

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

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Ser Gln Pro Asp Ser Ser Ser Asp Asn
130 135 140

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

Gln Ser Pro Asp Val Ser Ser Ser Thr Gly Gly Gly Ile Ala Asp Val
165 170 175

Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly Gly Ala Pro Gly
180 185 190

Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser Ser Gly Asn Trp
195 200 205

His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg Thr Thr Ser Thr
210 215 220

Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Leu
225 230 235 240

Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
245 250 255

Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe Ser Pro Arg Asn
260 265 270

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Arg Leu
275 280 285

Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Glu Gly
290 295 300

Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe
305 310 315 320

Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp Ala Gly His Glu
325 330 335

Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met Ile Pro Gln Tyr
340 345 350

Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala Gln Ser Asp Leu
355 360 365

Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
370 375 380

Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp Val Pro Phe His
385 390 395 400

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
405 410 415

Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly Asn Pro Thr Gly
420 425 430

Ser Thr Thr Arg Asp Gly Leu Ser Gly Ser Gly Ala His Ile Val Met
435 440 445

Val Asp Ala Tyr Lys Pro Thr Lys Gly Leu Ser Gly Ser Gly Leu Lys
450 455 460

Phe Ile Lys Asn Lys Val Pro Asn Phe Ala His Tyr Gly Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Phe Ile Arg Gln Gln Gly Trp Thr Thr Gln Asn Ile
485 490 495

Asn Asn Ser Val Val Asn Phe Asn Asp Met Leu Gly Lys Asn Ser Thr
500 505 510

Phe Thr Leu Asp Thr Arg Trp Ser Ser Leu Ala Pro Gly Pro Cys Met
515 520 525

Gly Asp Asp Gly Arg Thr Pro Ser Thr Thr Lys Phe Ser Asn Ala Gln
530 535 540

Leu Met Phe Gly Ser Gly Thr Gln Pro Thr Glu Gly Gly Glu Asp Ala
545 550 555 560

Val His Ile Thr Ser Glu Ser Glu Val Lys Ala Thr Asn Pro Thr Ala
565 570 575

Ile Asp Glu Tyr Gly Arg Val Ala Asp Asn Thr Gln Asn Ala Thr Thr
580 585 590

Ala Pro Thr Thr Val Gly Asn Ala Ala Met Gly Ala Met Pro Gly Met
595 600 605

Val Trp Gln Asp Arg Asp Ile Tyr Leu Gln Gly Pro Ile Trp Gly Lys
610 615 620

Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly
625 630 635 640

Phe Gly Tyr Arg Lys Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro
645 650 655

Val Pro Gly Asn Pro Ala Thr Thr Phe Ser Pro Asn Arg Ile Asn Asn
660 665 670

Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Thr Ile Asp Trp
675 680 685

Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Phe
690 695 700

Thr Ser Asn Phe Gly Thr Val Asp Ser Leu Asn Trp Ala Pro Asp Asn
705 710 715 720

Ala Gly Asn Tyr Lys Glu Pro Arg Val Ile Gly Thr Arg Tyr Leu Thr
725 730 735

Arg Ile Leu

<210> 31
<211> 2244
<212> ADN
<213> Secuencia artificial

<220>
<223> Cap AAV2 VP1 de lobo marino VP2 VP3 G432 enlazador10 SpyTag

<400> 31
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aaccctctca gccagattcg 420
tcctcggaca acacggcgcc acccgtgaaa aagtcccgtc tcgaagaagc ccagcccatt 480

caaagtccag acgtttccag cagcactggc ggaggaattg cgcacgtcat gtctggagat	540
gctgaaatgg ctgcagtggg cgggggagca ccgggcgtcg acggccaggg tgccgaggga	600
gtgggtactt cctcgggtaa ttggcattgc gattcccagt ggtcagaagg acacgtcaga	660
accaccagca ccagaacctg ggtgttgccc agctacaaca accacctgta taaacggctt	720
ggaagtagcg cacaatccaa tacctacaac ggattctcca cccctggggg atacctcgac	780
ttcaatagat ggcaactgtca cttcagtcct cggaactggc aacgtctcat caacaacaac	840
tggggcatca gacaaaaag acttaatgtt aaattgttca acatacaagt caaagaggtc	900
acgacggaag gggggacgac gaccgtcgcc aataacctta ccagcacgat tcaggtgttt	960
gcggacaacg cgtacgaact cccgtatgtt gtcgacgcgg gtcacgaggg ggcattgccg	1020
ccgttcccaa acgacgtgtt tatgattccc caatacggat actgcgggct ggtgtctggt	1080
caaagtcagg ctgagtcgga cttgtgttcg ttttattgcc tggagtattt tccatcccag	1140
atgctgagaa caggaaacaa ttttgaaatg aatttcaggt ttgaagacgt tccatttcac	1200
tccatgtacg cccacagcca gtctctagac aggctcatga atcctttaat tgatcagtat	1260
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tttactttgg aactagatg gagttcatta gcgcctggtc cgtgtatggg ggatgacgga	1620
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cccaccgaag gcggtgaaga tgctgtacat attacatccg agtcggaggt caaggcaacc	1740
aaccaactg caatcgatga atacggacga gtggccgata atacgcaaaa tgcaacaacc	1800
gccccaacca cagtgggaaa tgctgcaatg ggggccatgc ctgggatggt gtggcaagat	1860
agggatatct atcttcaagg acccatctgg gaaaaatac ccatacaga cggacatttt	1920
catccgtctc ctctcatggg ggggtttgga tacagaaaac cccctccgca aatttttatt	1980
aaaaacaccc ccgttcctgg aaatccggca actacatttt ctccaaatag aataaacaat	2040
ttcattactc aatactcaac gggacaagt accgttacta ttgactggga gctgcaaaag	2100

gaaaactcaa agagatggaa cccagaagta caattttacat caaatttttgg cacggtcgat 2160
 tcactaaact gggcaccgga caacgcggga aactacaaag aaccaagggt gattggcacc 2220
 agatacctga ctcgtatact ataa 2244

<210> 32
 <211> 747
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Cap AAV2 VP1 de lobo marino VP2 VP3 G432 enlazador10 SpyTag

<400> 32

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

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125

Leu Gly Leu Val Glu Glu Pro Ser Gln Pro Asp Ser Ser Ser Asp Asn
 130 135 140

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

Gln Ser Pro Asp Val Ser Ser Ser Thr Gly Gly Gly Ile Ala Asp Val
165 170 175

Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly Gly Ala Pro Gly
180 185 190

Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser Ser Gly Asn Trp
195 200 205

His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg Thr Thr Ser Thr
210 215 220

Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Leu
225 230 235 240

Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
245 250 255

Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe Ser Pro Arg Asn
260 265 270

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Arg Leu
275 280 285

Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Glu Gly
290 295 300

Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe
305 310 315 320

Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp Ala Gly His Glu
325 330 335

Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met Ile Pro Gln Tyr
340 345 350

Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala Gln Ser Asp Leu
355 360 365

Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
370 375 380

Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp Val Pro Phe His
385 390 395 400

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
405 410 415

Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly Asn Pro Thr Gly
420 425 430

Gly Leu Gly Ser Gly Gly Gly Leu Ser Gly Ala His Ile Val Met Val
435 440 445

Asp Ala Tyr Lys Pro Thr Lys Gly Leu Ser Gly Gly Ser Gly Leu Gly
450 455 460

Gly Ser Thr Thr Arg Asp Leu Lys Phe Ile Lys Asn Lys Val Pro Asn
465 470 475 480

Phe Ala His Tyr Gly Lys Asn Trp Leu Pro Gly Pro Phe Ile Arg Gln
485 490 495

Gln Gly Trp Thr Thr Gln Asn Ile Asn Asn Ser Val Val Asn Phe Asn
500 505 510

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

Ser Leu Ala Pro Gly Pro Cys Met Gly Asp Asp Gly Arg Thr Pro Ser
530 535 540

Thr Thr Lys Phe Ser Asn Ala Gln Leu Met Phe Gly Ser Gly Thr Gln
545 550 555 560

Pro Thr Glu Gly Gly Glu Asp Ala Val His Ile Thr Ser Glu Ser Glu
565 570 575

Val Lys Ala Thr Asn Pro Thr Ala Ile Asp Glu Tyr Gly Arg Val Ala
580 585 590

Asp Asn Thr Gln Asn Ala Thr Thr Ala Pro Thr Thr Val Gly Asn Ala
595 600 605

Ala Met Gly Ala Met Pro Gly Met Val Trp Gln Asp Arg Asp Ile Tyr
610 615 620

Leu Gln Gly Pro Ile Trp Gly Lys Ile Pro His Thr Asp Gly His Phe
625 630 635 640

His Pro Ser Pro Leu Met Gly Gly Phe Gly Tyr Arg Lys Pro Pro Pro
645 650 655

Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Gly Asn Pro Ala Thr Thr
660 665 670

Phe Ser Pro Asn Arg Ile Asn Asn Phe Ile Thr Gln Tyr Ser Thr Gly
675 680 685

Gln Val Thr Val Thr Ile Asp Trp Glu Leu Gln Lys Glu Asn Ser Lys
690 695 700

Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Phe Gly Thr Val Asp
705 710 715 720

Ser Leu Asn Trp Ala Pro Asp Asn Ala Gly Asn Tyr Lys Glu Pro Arg
725 730 735

Val Ile Gly Thr Arg Tyr Leu Thr Arg Ile Leu
740 745

<210> 33

<211> 2262

<212> ADN

<213> Secuencia artificial

<220>

<223> Cap AAV2 VP1 de dragón VP2 VP3 G436 enlazador6 SpyTag

<400> 33

atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga

cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac	120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac	180
aaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgaca agcctacgac	240
cggcagctcg acagcggaga caaccctac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggccgaa	420
aagcgaaaga caccgaaga gtggttagct caagaaaaga ctccaaccaa acaaaggttc	480
cagataccag ctccaggaca atctggatca gattctcctt ccacctcagg atccggcggc	540
actgcaggct ccagttctag cgcacaaat acaatggctc aaggaggtgg cggaccaatg	600
gcagacgata accaaggcgc cgaggagtg ggtaatgcct cgggagattg gcattgcgat	660
acccaatggc tgggcgacca cgtcattaca aaatctacca gaacttgggt tctgccctct	720
tacgggaatc atcttactc gcccatcaac tttgatggaa ccacaggga cggaaaccaa	780
gccgcttact gcggatacgc taccctctgg gcctactttg actttaaccg attccactgc	840
cacttttccc cccgagactg gcaaagactc attaacaacc ataccggaat acgaccagtc	900
ggactcaaat tcaagctgtt caacatccag gtcaaggaaa tcacagtaca agattcgacc	960
aaaacgatcg ccaacaatct caccagcacc gtacaggtct ttgcggacac ggagcaccag	1020
ctcccgtacg tattaggaaa tgccacgcag ggcacgtttc ctccctttcc ggctgaagtc	1080
tttcagttgc ctcagtagg ctactgtacc atccaaggcc ctcagggtaa gtttaccgac	1140
agaagtgcct tctactgctt ggagtacttt cttccaaga tgctgagaac ggggaataac	1200
tttgaattta cttacaagtt cgagaagggt cccttcatt ctggctgggc tcaaagccag	1260
tcgttggatc gattgatgaa tcccttgatc ccacagtacc tgttggccga ttatggtggc	1320
ctgagcggca gcggcgccca catcgtgatg gtggacgcct acaagccgac gaagggcctg	1380
agcggcagcg gcacgaccgc cagtagtgcc ataacatact atcgccaaa cagcacagac	1440
ttgagctggc actttaaaaa ctggctgcct gggccagtgg aaaggcgaca gcaaatcaat	1500
tctgaagact cgacgaaaaa ccatgccaat ttgaacggga atgcacacac caacaatac	1560
agcatccagc acagacaaac caagatgatg ccagggtgg ctctcagtag taaatacaca	1620
ggtgctgctg aaggaacgtc gttactgaac ggggtattga ctttgataa gatcgccaat	1680

gacaatacta acatcacgga tacaaataat gtcaatcgga cgatcgaaga tgaaattcaa	1740
ggtaccaatc cttatggaaa cgacgtaccc attaccgtcg ctgtcaatac acaaaacgcg	1800
accacttctc ctaccatgca aaacagcagc acgtatgaac tattacctgg tgctgtctgg	1860
tccaacagag atattttacct gcaaggtccc atctgggcta aaataccga taccgatgga	1920
cactttcacc cgtctccaca aatgggtggt ttcggactta aaaaccacc accgatgatc	1980
ctcatcaaaa acacaccgt tcccgccgat ccaccaacga cttcaaacc gactccgatg	2040
aacagcttca tcagcgaata cagtaccggt caggtgactg tagagatgct gtgggaggtc	2100
cggaaagaag actccaagag atggaacccg gaaatccagt ttacctcaa ttttgattg	2160
tccgatcctc agatcgacgg tatacccttt ggtattacca aattgggtaa ttacgaggaa	2220
ccacgtccta ttggcaccag atacctgact cgtcatttgt aa	2262

<210> 34
 <211> 753
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Cap AAV2 VP1 de dragón VP2 VP3 G436 enlazador6 SpyTag

<400> 34

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

Glu	Gly	Ile	Arg	Gln	Trp	Trp	Lys	Leu	Lys	Pro	Gly	Pro	Pro	Pro	Pro
			20					25					30		

Lys	Pro	Ala	Glu	Arg	His	Lys	Asp	Asp	Ser	Arg	Gly	Leu	Val	Leu	Pro
		35					40					45			

Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro
	50					55					60				

Val	Asn	Glu	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp
65					70					75					80

Arg	Gln	Leu	Asp	Ser	Gly	Asp	Asn	Pro	Tyr	Leu	Lys	Tyr	Asn	His	Ala
				85					90					95	

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Glu Lys Arg Lys Thr
130 135 140

Pro Glu Glu Trp Leu Ala Gln Glu Lys Thr Pro Thr Lys Gln Arg Phe
145 150 155 160

Gln Ile Pro Ala Pro Gly Gln Ser Gly Ser Asp Ser Pro Ser Thr Ser
165 170 175

Gly Ser Gly Gly Thr Ala Gly Ser Ser Ser Ser Ala Ser Asn Thr Met
180 185 190

Ala Gln Gly Gly Gly Gly Pro Met Ala Asp Asp Asn Gln Gly Ala Glu
195 200 205

Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Thr Gln Trp Leu
210 215 220

Gly Asp His Val Ile Thr Lys Ser Thr Arg Thr Trp Val Leu Pro Ser
225 230 235 240

Tyr Gly Asn His Leu Tyr Ser Pro Ile Asn Phe Asp Gly Thr Thr Gly
245 250 255

Asn Gly Thr Gln Ala Ala Tyr Cys Gly Tyr Ala Thr Pro Trp Ala Tyr
260 265 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
275 280 285

Arg Leu Ile Asn Asn His Thr Gly Ile Arg Pro Val Gly Leu Lys Phe
290 295 300

Lys Leu Phe Asn Ile Gln Val Lys Glu Ile Thr Val Gln Asp Ser Thr
305 310 315 320

Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ala Asp
325 330 335

Thr Glu His Gln Leu Pro Tyr Val Leu Gly Asn Ala Thr Gln Gly Thr
340 345 350

Phe Pro Pro Phe Pro Ala Glu Val Phe Gln Leu Pro Gln Tyr Gly Tyr
355 360 365

Cys Thr Ile Gln Gly Pro Gln Gly Lys Phe Thr Asp Arg Ser Ala Phe
370 375 380

Tyr Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn Asn
385 390 395 400

Phe Glu Phe Thr Tyr Lys Phe Glu Lys Val Pro Phe His Ser Gly Trp
405 410 415

Ala Gln Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Pro Gln
420 425 430

Tyr Leu Leu Ala Asp Tyr Gly Gly Leu Ser Gly Ser Gly Ala His Ile
435 440 445

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

Thr Thr Ala Ser Ser Ala Ile Thr Tyr Tyr Arg Pro Asn Ser Thr Asp
465 470 475 480

Leu Ser Trp Tyr Phe Lys Asn Trp Leu Pro Gly Pro Val Glu Arg Arg
485 490 495

Gln Gln Ile Asn Ser Glu Asp Ser Thr Lys Asn His Ala Asn Leu Asn
500 505 510

Gly Asn Ala His Thr Asn Lys Tyr Ser Ile Gln His Arg Gln Thr Lys
515 520 525

Met Met Pro Gly Val Ala Leu Ser Ser Lys Tyr Thr Gly Ala Ala Glu
530 535 540

Gly Thr Ser Leu Leu Asn Gly Val Leu Thr Phe Asp Lys Ile Ala Asn
545 550 555 560

Asp Asn Thr Asn Ile Thr Asp Thr Asn Asn Val Asn Arg Thr Ile Glu
565 570 575

Asp Glu Ile Gln Gly Thr Asn Pro Tyr Gly Asn Asp Val Pro Ile Thr
580 585 590

Val Ala Val Asn Thr Gln Asn Ala Thr Thr Ser Pro Thr Met Gln Asn
595 600 605

Ser Ser Thr Tyr Glu Leu Leu Pro Gly Ala Val Trp Ser Asn Arg Asp
610 615 620

Ile Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Asp Thr Asp Gly
625 630 635 640

His Phe His Pro Ser Pro Gln Met Gly Gly Phe Gly Leu Lys Asn Pro
645 650 655

Pro Pro Met Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro
660 665 670

Thr Thr Phe Lys Pro Thr Pro Met Asn Ser Phe Ile Ser Glu Tyr Ser
675 680 685

Thr Gly Gln Val Thr Val Glu Met Leu Trp Glu Val Arg Lys Glu Asp
690 695 700

Ser Lys Arg Trp Asn Pro Glu Ile Gln Phe Thr Ser Asn Phe Gly Leu
705 710 715 720

Ser Asp Pro Gln Ile Asp Gly Ile Pro Phe Gly Ile Thr Lys Leu Gly
725 730 735

Asn Tyr Glu Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg His
740 745 750

Leu

<210> 35
<211> 2262
<212> ADN
<213> Secuencia artificial

<220>
<223> Cap AAV2 VP1 de dragón VP2 VP3 T573 enlazador6 SpyTag

<400> 35
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cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggccgaa 420
aagcgaaaga caccgaaga gtggttagct caagaaaaga ctccaaccaa acaaaggttc 480
cagataccag ctccaggaca atctggatca gattctcctt ccacctcagg atccggcggt 540
actgcaggct ccagttctag cgcacaaat acaatggctc aaggaggtgg cggaccaatg 600
gcagacgata accaaggcgc cgagggagtg ggtaatgcct cgggagattg gcattgcgat 660
acccaatggc tgggcgacca cgtcattaca aaatctacca gaacttgggt tctgccctct 720
tacgggaatc atctctactc gccatcaac tttgatggaa ccacaggga cggaaaccaa 780
gccgcttact gcggatacgc taccctctgg gcctactttg actttaaccg attccactgc 840
cacttttccc cccgagactg gcaaagactc attaacaacc ataccggaat acgaccagtc 900
ggactcaaat tcaagctggt caacatccag gtcaaggaaa tcacagtaca agattcgacc 960
aaaacgatcg ccaacaatct caccagcacc gtacaggtct ttgcggacac ggagcaccag 1020
ctcccgtacg tattaggaaa tgccacgcag ggcacgtttc ctccctttcc ggctgaagtc 1080
tttcagttgc ctcagtacgg ctactgtacc atccaaggcc ctcagggtaa gtttaccgac 1140

agaagtcct tctactgctt ggagtacttt cttccaaga tgctgagaac ggggaataac	1200
tttgaattta cttacaagtt cgagaagggt cccttccatt ctggctgggc tcaaagccag	1260
tcgttggatc gattgatgaa tcccttgatc ccacagtacc tgttggccga ttatggtacg	1320
accgccagta gtgccataac atactatcgg ccaaacagca cagacttgag ctggtacttt	1380
aaaaactggc tgcctgggcc agtggaaagg cgacagcaaa tcaattctga agactcgacg	1440
aaaaaccatg ccaatttgaa cggaatgca cacaccaaca aatacagcat ccagcacaga	1500
caaaccaaga tgatgccagg ggtggctctc agtagtaa atacaggtgc tgctgaagga	1560
acgtcgttac tgaacggggt attgaccttt gataagatcg ccaatgacaa tactaacatc	1620
acggatacaa ataatgtcaa tcggacgatc gaagatgaaa ttcaaggtag caatccttat	1680
ggaaacgacg taccattac cgtcgtgtc aatacacaaa acgcgaccgg cctgagcggc	1740
agcggcgccc acatcgtgat ggtggacgcc tacaagccga cgaagggcct gagcggcagc	1800
ggcacttctc ctacatgca aaacagcagc acgtatgaac tattacctgg tgctgtctgg	1860
tccaacagag atatttacct gcaagggtccc atctgggcta aaatacccga taccgatgga	1920
cactttcacc cgtctccaca aatgggtgggt ttcggactta aaaaccacc accgatgatc	1980
ctcatcaaaa acacaccgt tcccgccgat ccaccaacga cttcaaacc gactccgatg	2040
aacagcttca tcagcgaata cagtaccggg caggtgactg tagagatgct gtgggaggtc	2100
cggaaagaag actccaagag atggaacccg gaaatccagt ttacctcaa ttttgattg	2160
tccgatcctc agatcgacgg tatacccttt ggtattacca aattgggtaa ttacgaggaa	2220
ccacgtccta ttggcaccag atacctgact cgtcatttgt aa	2262

<210> 36
 <211> 753
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Cap AAV2 VP1 de dragón VP2 VP3 T573 enlazador6 SpyTag

<400> 36

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

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Glu Lys Arg Lys Thr
130 135 140

Pro Glu Glu Trp Leu Ala Gln Glu Lys Thr Pro Thr Lys Gln Arg Phe
145 150 155 160

Gln Ile Pro Ala Pro Gly Gln Ser Gly Ser Asp Ser Pro Ser Thr Ser
165 170 175

Gly Ser Gly Gly Thr Ala Gly Ser Ser Ser Ser Ala Ser Asn Thr Met
180 185 190

Ala Gln Gly Gly Gly Gly Pro Met Ala Asp Asp Asn Gln Gly Ala Glu
195 200 205

Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Thr Gln Trp Leu
210 215 220

Gly Asp His Val Ile Thr Lys Ser Thr Arg Thr Trp Val Leu Pro Ser
225 230 235 240

Tyr Gly Asn His Leu Tyr Ser Pro Ile Asn Phe Asp Gly Thr Thr Gly
245 250 255

Asn Gly Thr Gln Ala Ala Tyr Cys Gly Tyr Ala Thr Pro Trp Ala Tyr
260 265 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
275 280 285

Arg Leu Ile Asn Asn His Thr Gly Ile Arg Pro Val Gly Leu Lys Phe
290 295 300

Lys Leu Phe Asn Ile Gln Val Lys Glu Ile Thr Val Gln Asp Ser Thr
305 310 315 320

Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ala Asp
325 330 335

Thr Glu His Gln Leu Pro Tyr Val Leu Gly Asn Ala Thr Gln Gly Thr
340 345 350

Phe Pro Pro Phe Pro Ala Glu Val Phe Gln Leu Pro Gln Tyr Gly Tyr
355 360 365

Cys Thr Ile Gln Gly Pro Gln Gly Lys Phe Thr Asp Arg Ser Ala Phe
370 375 380

Tyr Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn Asn
385 390 395 400

Phe Glu Phe Thr Tyr Lys Phe Glu Lys Val Pro Phe His Ser Gly Trp
405 410 415

Ala Gln Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Pro Gln
420 425 430

Tyr Leu Leu Ala Asp Tyr Gly Thr Thr Ala Ser Ser Ala Ile Thr Tyr
435 440 445

Tyr Arg Pro Asn Ser Thr Asp Leu Ser Trp Tyr Phe Lys Asn Trp Leu
450 455 460

Pro Gly Pro Val Glu Arg Arg Gln Gln Ile Asn Ser Glu Asp Ser Thr
465 470 475 480

Lys Asn His Ala Asn Leu Asn Gly Asn Ala His Thr Asn Lys Tyr Ser
485 490 495

Ile Gln His Arg Gln Thr Lys Met Met Pro Gly Val Ala Leu Ser Ser
500 505 510

Lys Tyr Thr Gly Ala Ala Glu Gly Thr Ser Leu Leu Asn Gly Val Leu
515 520 525

Thr Phe Asp Lys Ile Ala Asn Asp Asn Thr Asn Ile Thr Asp Thr Asn
530 535 540

Asn Val Asn Arg Thr Ile Glu Asp Glu Ile Gln Gly Thr Asn Pro Tyr
545 550 555 560

Gly Asn Asp Val Pro Ile Thr Val Ala Val Asn Thr Gln Asn Ala Thr
565 570 575

Gly Leu Ser Gly Ser Gly Ala His Ile Val Met Val Asp Ala Tyr Lys
580 585 590

Pro Thr Lys Gly Leu Ser Gly Ser Gly Thr Ser Pro Thr Met Gln Asn
595 600 605

Ser Ser Thr Tyr Glu Leu Leu Pro Gly Ala Val Trp Ser Asn Arg Asp
610 615 620

Ile Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Asp Thr Asp Gly
625 630 635 640

His Phe His Pro Ser Pro Gln Met Gly Gly Phe Gly Leu Lys Asn Pro
645 650 655

Pro Pro Met Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro
660 665 670

Thr Thr Phe Lys Pro Thr Pro Met Asn Ser Phe Ile Ser Glu Tyr Ser
675 680 685

Thr Gly Gln Val Thr Val Glu Met Leu Trp Glu Val Arg Lys Glu Asp
690 695 700

Ser Lys Arg Trp Asn Pro Glu Ile Gln Phe Thr Ser Asn Phe Gly Leu
705 710 715 720

Ser Asp Pro Gln Ile Asp Gly Ile Pro Phe Gly Ile Thr Lys Leu Gly
725 730 735

Asn Tyr Glu Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg His
740 745 750

Leu

<210> 37
<211> 4
<212> PRT
<213> Secuencia artificial

<220>
<223> 4 enlazador

<400> 37

Gly Leu Ser Gly
1

<210> 38
<211> 6
<212> PRT
<213> Secuencia artificial

<220>
<223> 6 enlazador

<400> 38

Gly Leu Ser Gly Ser Gly
1 5

<210> 39
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> 8 enlazador

<400> 39

Gly Leu Ser Gly Leu Ser Gly Ser
1 5

<210> 40
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> 10 enlazador

<400> 40

Gly Leu Ser Gly Leu Ser Gly Leu Ser Gly
1 5 10

<210> 41
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> 10 enlazador

<400> 41

Gly Leu Ser Gly Gly Ser Gly Leu Ser Gly
1 5 10

<210> 42
<211> 13
<212> PRT
<213> Secuencia artificial

<220>
<223> SpyTag

<400> 42

Ala His Ile Val Met Val Asp Ala Tyr Lys Pro Thr Lys
1 5 10

<210> 43
<211> 113
<212> PRT
<213> Secuencia artificial

<220>
<223> Spycatcher

<400> 43

Val Asp Thr Leu Ser Gly Leu Ser Ser Glu Gln Gly Gln Ser Gly Asp
1 5 10 15

Met Thr Ile Glu Glu Asp Ser Ala Thr His Ile Lys Phe Ser Lys Arg
20 25 30

Asp Glu Asp Gly Lys Glu Leu Ala Gly Ala Thr Met Glu Leu Arg Asp
35 40 45

Ser Ser Gly Lys Thr Ile Ser Thr Trp Ile Ser Asp Gly Gln Val Lys
50 55 60

Asp Phe Tyr Leu Tyr Pro Gly Lys Tyr Thr Phe Val Glu Thr Ala Ala
65 70 75 80

Pro Asp Gly Tyr Glu Val Ala Thr Ala Ile Thr Phe Thr Val Asn Glu
85 90 95

Gln Gly Gln Val Thr Val Asn Gly Lys Ala Thr Lys Gly Asp Ala His
100 105 110

Ile

<210> 44
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> c-myc

<400> 44

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 45
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> B1

<400> 45

Ile Gly Thr Arg Tyr Leu Thr Arg
1 5

<210> 46
<211> 1341
<212> ADN
<213> Secuencia artificial

<220>
<223> Cadena pesada de IgG4 humana - enlazador - SpyCatcher

<400> 46
gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag 60
agcacagccg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 120
tggaactcag gcgccctgac cagcggcgctg cacaccttcc cggctgtcct acagtcctca 180
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg cacgaagacc 240
tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc 300
aaatatggtc ccccatgccc accctgcccga gcacctgagt tcctgggggg accatcagtc 360
ttcctgttcc ccccaaaacc caaggacact ctcatgatct cccggacccc tgagggtcacg 420
tgcgtgggtgg tggacgtgag ccaggaagac cccgaggtcc agttcaactg gtacgtggat 480
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagttcaa cagcacgtac 540
cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaacggcaa ggagtacaag 600
tgcaagggtct ccaacaaagg cctcccgtcc tccatcgaga aaaccatctc caaagccaaa 660
gggcagcccc gagagccaca ggtgtacacc ctgcccccat cccaggagga gatgaccaag 720
aaccagggtca gcctgacctg cctgggtcaaa ggcttctacc ccagcgacat cgccgtggag 780
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 840

gacggctcct tcttcctcta cagcaggctc accgtggaca agagcaggtg gcaggagggg 900
 aatgtcttct catgctccgt gatgcatgag gctctgcaca accactacac acagaagtcc 960
 ctctccctgt ctctgggtaa aggaagcggc gaaagcggcg tggataccct gtccggactg 1020
 agcagtgagc aaggccagtc cggagatatg acaattgaag aagatagcgc cacccatatt 1080
 aaattctcca aaagatatga ggacggcaaa gagctggctg gagcaacaat ggagctgaga 1140
 gattcctctg gaaagactat tagtacatgg atctctgatg gccaaagtga agatttctat 1200
 ctgtatccag gaaagtacac atttgtcgaa accgctgcac cagacggata tgaggtggct 1260
 acagctatta cctttacagt gaatgagcaa ggacaggtga ctgttaatgg caaagctact 1320
 aaaggagacg ctcatattta a 1341

<210> 47
 <211> 446
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Cadena pesada de IgG4 humana - enlazador - SpyCatcher

<400> 47

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
 65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305 310 315 320

Leu Ser Leu Ser Leu Gly Lys Gly Ser Gly Glu Ser Gly Val Asp Thr
325 330 335

Leu Ser Gly Leu Ser Ser Glu Gln Gly Gln Ser Gly Asp Met Thr Ile
340 345 350

Glu Glu Asp Ser Ala Thr His Ile Lys Phe Ser Lys Arg Asp Glu Asp
355 360 365

Gly Lys Glu Leu Ala Gly Ala Thr Met Glu Leu Arg Asp Ser Ser Gly
370 375 380

Lys Thr Ile Ser Thr Trp Ile Ser Asp Gly Gln Val Lys Asp Phe Tyr
385 390 395 400

Leu Tyr Pro Gly Lys Tyr Thr Phe Val Glu Thr Ala Ala Pro Asp Gly
405 410 415

Tyr Glu Val Ala Thr Ala Ile Thr Phe Thr Val Asn Glu Gln Gly Gln
420 425 430

Val Thr Val Asn Gly Lys Ala Thr Lys Gly Asp Ala His Ile
435 440 445

<210> 48
<211> 18
<212> ADN
<213> Secuencia artificial

<220>
<223> IgG-SpyCatcher enlazador

<400> 48
ggaagcggcg aaagcggc

18

<210> 49
<211> 6
<212> PRT
<213> Secuencia artificial

<220>
<223> IgG-SpyCatcher enlazador

<400> 49

Gly Ser Gly Glu Ser Gly
1 5

<210> 50

<211> 981

<212> ADN

<213> Secuencia artificial

<220>

<223> hIgG4

<400> 50

gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag	60
agcacagccg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg	120
tggaactcag gcgccctgac cagcggcgctg cacaccttcc cggctgtcct acagtcctca	180
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg cacgaagacc	240
tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc	300
aaatatggtc ccccatgccc accctgcccga gcacctgagt tcctggggggg accatcagtc	360
ttcctgttcc ccccaaaacc caaggacact ctcatgatct cccggacccc tgaggtcacg	420
tgcgtgggtg tggacgtgag ccaggaagac cccgaggtcc agttcaactg gtacgtggat	480
ggcgtggagg tgcataatgc caagacaaaag ccgcgggagg agcagttcaa cagcacgtac	540
cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaacggcaa ggagtacaag	600
tgcaagggtct ccaacaaaagg cctcccgtcc tccatcgaga aaaccatctc caaagccaaa	660
gggcagcccc gagagccaca ggtgtacacc ctgcccccat cccaggagga gatgaccaag	720
aaccagggtca gcctgacctg cctgggtcaaa ggcttctacc ccagcgacat cgccgtggag	780
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc	840
gacggctcct tcttcctcta cagcaggctc accgtggaca agagcaggtg gcaggagggg	900
aatgtcttct catgctccgt gatgcatgag gctctgcaca accactacac acagaagtcc	960
ctctccctgt ctctgggtaa a	981

<210> 51

<211> 327

<212> PRT

<213> Secuencia artificial

<220>

<223> hIgG4

<400> 51

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
325

<210> 52
<211> 2145
<212> ADN
<213> Secuencia artificial

<220>
<223> Cap AAV2 VP1 de lobo marino VP2 VP3 Y730F

<400> 52
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aaccctctca gccagattcg	420
tcctcggaca acacggcgcc acccgtgaaa aagtcccgtc tcgaagaagc ccagcccatt	480
caaagtccag acgtttccag cagcactggc ggaggaattg ccgacgtcat gtctggagat	540
gctgaaatgg ctgcagtggg cgggggagca ccgggcgtcg acggccaggg tgccgaggga	600
gtgggtactt cctcgggtaa ttggcattgc gattcccagt ggtcagaagg acacgtcaga	660
accaccagca ccagaacctg ggtgttgccc agctacaaca accacctgta taaacggctt	720
ggaagtagcg cacaatccaa tacctacaac ggattctcca cccctgggg atacctcgac	780
ttcaatagat ggcaactgtca cttcagtcct cggaactggc aacgtctcat caacaacaac	840
tggggcatca gacaaaaag acttaatgtt aaattgttca acatacaagt caaagaggtc	900
acgacggaag gggggacgac gaccgtcgcc aataacctta ccagcacgat tcagggtgtt	960
gcggacaacg cgtacgaact cccgtatgtt gtcgacgcgg gtcacgaggg ggcattgccg	1020
ccgttcccaa acgacgtgtt tatgattccc caatacggat actgcgggct ggtgtctggt	1080
caaagtcagg ctcagtcgga cttgtgttcg ttttattgcc tggagtattt tccatcccag	1140
atgctgagaa caggaaacaa ttttgaaatg aatttcaggt ttgaagacgt tccatttcac	1200
tccatgtacg cccacagcca gtctctagac aggctcatga atcctttaat tgatcagtat	1260
ctgtggagtc taaaacaaac aggaaacccg actggatcaa caacgagaga cttaaaattt	1320
atcaagaaca aagttcccaa ttttgcacat tatggaaaaa attggcttcc tggacctttt	1380
attagacaac aggggtggac aacacaaaat attaataata gtgttggttaa ttttaatgac	1440
atgctgggaa aaaattcgac atttactttg gacactagat ggagttcatt agcgcctggt	1500
ccgtgtatgg gggatgacgg acgaactcca tccaccacca agttctcaaa tgctcagctc	1560
atgtttggat ctggaacaca acccaccgaa ggcggtgaag atgctgtaca tattacatcc	1620
gagtcggagg tcaaggcaac caacccaact gcaatcgatg aatacggacg agtggccgat	1680
aatacgcaaa atgcaacaac cgccccaacc acagtgggaa atgctgcaat gggggccatg	1740
cctgggatgg tgtggcaaga tagggatatc tatcttcaag gaccatctg gggaaaaata	1800
ccccatacag acggacattt tcatccgtct cctctcatgg gggggtttgg atacagaaaa	1860
ccccctccgc aaatttttat taaaaacacc cccgttcctg gaaatccggc aactacattt	1920

tctccaaata gaataaaca tttcattact caataactcaa cgggacaagt gaccgttact	1980
attgactggg agctgcaaaa ggaaaactca aagagatgga acccagaagt acaatttaca	2040
tcaaattttg gcacgggtcga ttcactaaac tgggcaccgg acaacgcggg aaactacaaa	2100
gaaccaaggg tgattggcac cagattcctg actcgtatac tataa	2145

<210> 53
 <211> 714
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Cap AAV2 VP1 de lobo marino VP2 VP3 Y730F

<400> 53

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

Glu	Gly	Ile	Arg	Gln	Trp	Trp	Lys	Leu	Lys	Pro	Gly	Pro	Pro	Pro	Pro
			20					25					30		

Lys	Pro	Ala	Glu	Arg	His	Lys	Asp	Asp	Ser	Arg	Gly	Leu	Val	Leu	Pro
		35					40					45			

Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro
	50					55					60				

Val	Asn	Glu	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp
65					70					75					80

Arg	Gln	Leu	Asp	Ser	Gly	Asp	Asn	Pro	Tyr	Leu	Lys	Tyr	Asn	His	Ala
				85					90					95	

Asp	Ala	Glu	Phe	Gln	Glu	Arg	Leu	Lys	Glu	Asp	Thr	Ser	Phe	Gly	Gly
			100					105						110	

Asn	Leu	Gly	Arg	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Val	Leu	Glu	Pro
		115					120					125			

Leu	Gly	Leu	Val	Glu	Glu	Pro	Ser	Gln	Pro	Asp	Ser	Ser	Ser	Asp	Asn
	130					135					140				

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

Gln Ser Pro Asp Val Ser Ser Ser Thr Gly Gly Gly Ile Ala Asp Val
165 170 175

Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly Gly Ala Pro Gly
180 185 190

Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser Ser Gly Asn Trp
195 200 205

His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg Thr Thr Ser Thr
210 215 220

Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Leu
225 230 235 240

Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
245 250 255

Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe Ser Pro Arg Asn
260 265 270

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Arg Leu
275 280 285

Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Glu Gly
290 295 300

Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe
305 310 315 320

Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp Ala Gly His Glu
325 330 335

Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met Ile Pro Gln Tyr
340 345 350

Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala Gln Ser Asp Leu
355 360 365

Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
370 375 380

Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp Val Pro Phe His
385 390 395 400

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
405 410 415

Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly Asn Pro Thr Gly
420 425 430

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

Ala His Tyr Gly Lys Asn Trp Leu Pro Gly Pro Phe Ile Arg Gln Gln
450 455 460

Gly Trp Thr Thr Gln Asn Ile Asn Asn Ser Val Val Asn Phe Asn Asp
465 470 475 480

Met Leu Gly Lys Asn Ser Thr Phe Thr Leu Asp Thr Arg Trp Ser Ser
485 490 495

Leu Ala Pro Gly Pro Cys Met Gly Asp Asp Gly Arg Thr Pro Ser Thr
500 505 510

Thr Lys Phe Ser Asn Ala Gln Leu Met Phe Gly Ser Gly Thr Gln Pro
515 520 525

Thr Glu Gly Gly Glu Asp Ala Val His Ile Thr Ser Glu Ser Glu Val
530 535 540

Lys Ala Thr Asn Pro Thr Ala Ile Asp Glu Tyr Gly Arg Val Ala Asp
545 550 555 560

Asn Thr Gln Asn Ala Thr Thr Ala Pro Thr Thr Val Gly Asn Ala Ala
565 570 575

Met Gly Ala Met Pro Gly Met Val Trp Gln Asp Arg Asp Ile Tyr Leu
580 585 590

Gln Gly Pro Ile Trp Gly Lys Ile Pro His Thr Asp Gly His Phe His
595 600 605

Pro Ser Pro Leu Met Gly Gly Phe Gly Tyr Arg Lys Pro Pro Pro Gln
610 615 620

Ile Phe Ile Lys Asn Thr Pro Val Pro Gly Asn Pro Ala Thr Thr Phe
625 630 635 640

Ser Pro Asn Arg Ile Asn Asn Phe Ile Thr Gln Tyr Ser Thr Gly Gln
645 650 655

Val Thr Val Thr Ile Asp Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg
660 665 670

Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Phe Gly Thr Val Asp Ser
675 680 685

Leu Asn Trp Ala Pro Asp Asn Ala Gly Asn Tyr Lys Glu Pro Arg Val
690 695 700

Ile Gly Thr Arg Phe Leu Thr Arg Ile Leu
705 710

<210> 54
<211> 2145
<212> ADN
<213> Secuencia artificial

<220>
<223> Cap AAV2 VP1 de lobo marino VP2 VP3 B1 reemplazado

<400> 54
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aaccctctca gccagattcg	420
tcctcggaca acacggcgcc acccgtgaaa aagtcccgtc tcgaagaagc ccagcccatt	480
caaagtccag acgtttccag cagcactggc ggaggaattg ccgacgtcat gtctggagat	540
gctgaaatgg ctgcagtggg cgggggagca ccgggcgtcg acggccaggg tgccgaggga	600
gtgggtactt cctcgggtaa ttggcattgc gattcccagt ggtcagaagg acacgtcaga	660
accaccagca ccagaacctg ggtgttgccc agctacaaca accacctgta taaacggctt	720
ggaagtagcg cacaatcaa tacctacaac ggattctcca cccctggggg atacctcgac	780
ttcaatagat ggcaactgtca cttcagtcct cggaactggc aacgtctcat caacaacaac	840
tggggcatca gacaaaaag acttaatgtt aaattgttca acatacaagt caaagaggtc	900
acgacggaag gggggacgac gaccgtcgcc aataacctta ccagcacgat tcaggtgttt	960
gcggacaacg cgtacgaact cccgtatgtt gtcgacgcgg gtcacgaggg ggcattgccg	1020
ccgttcccaa acgacgtgtt tatgattccc caatacggat actgcgggct ggtgtctggt	1080
caaagtcagg ctcagtcgga cttgtgttcg ttttattgcc tggagtattt tccatcccag	1140
atgctgagaa caggaaacaa ttttgaaatg aatttcaggt ttgaagacgt tccatttcac	1200
tccatgtacg cccacagcca gtctctagac aggctcatga atcctttaat tgatcagtat	1260
ctgtggagtc taaaacaaac aggaaacccg actggatcaa caacgagaga cttaaaattt	1320
atcaagaaca aagttcccaa ttttgcacat tatggaaaaa attggcttcc tggacctttt	1380
attagacaac aggggtggac aacacaaaat attaataata gtgttggttaa ttttaatgac	1440
atgctgggaa aaaattcgac atttactttg gacactagat ggagttcatt agcgcctggt	1500
ccgtgtatgg gggatgacgg acgaactcca tccaccacca agttctcaaa tgctcagctc	1560
atgtttggat ctggaacaca acccaccgaa ggcggtgaag atgctgtaca tattacatcc	1620
gagtcggagg tcaaggcaac caacccaact gcaatcgatg aatacggacg agtggccgat	1680
aatacgcaaa atgcaacaac cgccccaacc acagtgggaa atgctgcaat gggggccatg	1740
cctgggatgg tgtggcaaga tagggatatc tatcttcaag gaccatctg gggaaaaata	1800
ccccatacag acggacattt tcatccgtct cctctcatgg gggggtttgg atacagaaaa	1860

cccctccgc aaatatttat taaaaacacc cccgttcctg gaaatccggc aactacattt 1920
 tctccaaata gaataaacia tttcattact caatactcaa cgggacaagt gaccgttact 1980
 attgactggg agctgcaaaa ggaaaactca aagagatgga acccagaagt acaatttaca 2040
 tcaaattttg gcacggtcga ttcactaaac tgggcaccgg acaacgcggg aaactacaaa 2100
 gaaccaaggg tgggtggggtc tcgattcctt acgcatatac tataa 2145

<210> 55
 <211> 714
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Cap AAV2 VP1 de lobo marino VP2 VP3 B1 reemplazado

<400> 55

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

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125

Leu Gly Leu Val Glu Glu Pro Ser Gln Pro Asp Ser Ser Ser Asp Asn
130 135 140

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

Gln Ser Pro Asp Val Ser Ser Ser Thr Gly Gly Gly Ile Ala Asp Val
165 170 175

Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly Gly Ala Pro Gly
180 185 190

Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser Ser Gly Asn Trp
195 200 205

His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg Thr Thr Ser Thr
210 215 220

Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Leu
225 230 235 240

Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
245 250 255

Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe Ser Pro Arg Asn
260 265 270

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Arg Leu
275 280 285

Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Glu Gly
290 295 300

Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe
305 310 315 320

Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp Ala Gly His Glu
325 330 335

Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met Ile Pro Gln Tyr
340 345 350

Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala Gln Ser Asp Leu
355 360 365

Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
370 375 380

Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp Val Pro Phe His
385 390 395 400

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
405 410 415

Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly Asn Pro Thr Gly
420 425 430

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

Ala His Tyr Gly Lys Asn Trp Leu Pro Gly Pro Phe Ile Arg Gln Gln
450 455 460

Gly Trp Thr Thr Gln Asn Ile Asn Asn Ser Val Val Asn Phe Asn Asp
465 470 475 480

Met Leu Gly Lys Asn Ser Thr Phe Thr Leu Asp Thr Arg Trp Ser Ser
485 490 495

Leu Ala Pro Gly Pro Cys Met Gly Asp Asp Gly Arg Thr Pro Ser Thr
500 505 510

Thr Lys Phe Ser Asn Ala Gln Leu Met Phe Gly Ser Gly Thr Gln Pro
515 520 525

Thr Glu Gly Gly Glu Asp Ala Val His Ile Thr Ser Glu Ser Glu Val
530 535 540

Lys Ala Thr Asn Pro Thr Ala Ile Asp Glu Tyr Gly Arg Val Ala Asp
545 550 555 560

Asn Thr Gln Asn Ala Thr Thr Ala Pro Thr Thr Val Gly Asn Ala Ala
565 570 575

Met Gly Ala Met Pro Gly Met Val Trp Gln Asp Arg Asp Ile Tyr Leu
580 585 590

Gln Gly Pro Ile Trp Gly Lys Ile Pro His Thr Asp Gly His Phe His
595 600 605

Pro Ser Pro Leu Met Gly Gly Phe Gly Tyr Arg Lys Pro Pro Pro Gln
610 615 620

Ile Phe Ile Lys Asn Thr Pro Val Pro Gly Asn Pro Ala Thr Thr Phe
625 630 635 640

Ser Pro Asn Arg Ile Asn Asn Phe Ile Thr Gln Tyr Ser Thr Gly Gln
645 650 655

Val Thr Val Thr Ile Asp Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg
660 665 670

Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Phe Gly Thr Val Asp Ser
675 680 685

Leu Asn Trp Ala Pro Asp Asn Ala Gly Asn Tyr Lys Glu Pro Arg Val
690 695 700

Val Gly Ser Arg Phe Leu Thr His Ile Leu
705 710

<210> 56
<211> 2145
<212> ADN
<213> Secuencia artificial

<220>
<223> Cap AAV2 VP1 de lobo marino VP2 VP3 v2

<400> 56
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac	240
cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt	300
caggagcggc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg	420
ggaaaaaaga ggacggcgcc acccgtgaaa aagtcccgtc tcgaagaagc ccagcccatt	480
caaagtccag acgtttccag cagcactggc ggaggaattg ccgacgtcat gtctggagat	540
gctgaaatgg ctgcagtggg cgggggagca ccgggcgtcg acggccaggg tgccgaggga	600
gtgggtactt cctcgggtaa ttggcattgc gattcccagt ggtcagaagg acacgtcaga	660
accaccagca ccagaacctg ggtgttgccc agctacaaca accacctgta taaacggctt	720
ggaagtagcg cacaatcaa tacctacaac ggattctcca cccctgggg atacctcgac	780
ttcaatagat ggcactgtca cttcagtcct cggaactggc aacgtctcat caacaacaac	840
tggggcatca gacaaaaag acttaatgtt aaattgttca acatacaagt caaagaggtc	900
acgacggaag gggggacgac gaccgtcgcc aataacctta ccagcacgat tcaggtgttt	960
gcggacaacg cgtacgaact cccgtatgtt gtcgacgcgg gtcacgaggg ggcattgccg	1020
ccgttcccaa acgacgtgtt tatgattccc caatacggat actgcgggct ggtgtctggt	1080
caaagtcagg ctcagtcgga cttgtgttcg ttttattgcc tggagtattt tccatcccag	1140
atgctgagaa caggaaacaa ttttgaaatg aatttcaggt ttgaagacgt tccatttcac	1200
tccatgtacg cccacagcca gtctctagac aggctcatga atcctttaat tgatcagtat	1260
ctgtggagtc taaaacaaac aggaaacccg actggatcaa caacgagaga cttaaaattt	1320
atcaagaaca aagttcccaa ttttgcacat tatggaaaaa attggcttcc tggacctttt	1380
attagacaac aggggtggac aacacaaaat attaataata gtgttggttaa ttttaatgac	1440
atgctgggaa aaaattcgac atttactttg gacactagat ggagttcatt agcgcctggt	1500
ccgtgtatgg gggatgacgg acgaactcca tccaccacca agttctcaaa tgctcagctc	1560
atgtttggat ctggaacaca acccaccgaa ggcggtgaag atgctgtaca tattacatcc	1620
gagtcggagg tcaaggcaac caacccaact gcaatcgatg aatacggacg agtggccgat	1680
aatacgcaaa atgcaacaac cgccccaacc acagtgggaa atgctgcaat gggggccatg	1740
cctgggatgg tgtggcaaga tagggatatc tatcttcaag gacccatctg gggaaaaata	1800

ccccatacag acggacattt tcatccgtct cctctcatgg gggggtttgg atacagaaaa	1860
ccccctccgc aaatttttat taaaaacacc cccgttcctg gaaatccggc aactacattt	1920
tctccaaata gaataaacia ttctattact caatactcaa cgggacaagt gaccgttact	1980
attgactggg agctgcaaaa ggaaaactca aagagatgga acccagaagt acaatttaca	2040
tcaaattttg gcacggtcga ttactaaac tgggcaccgg acaacgcggg aaactacaaa	2100
gaaccaaggg tgattggcac cagatacctg actcgataac tataa	2145

<210> 57
 <211> 714
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Cap AAV2 VP1 de lobo marino VP2 VP3 v2

<400> 57

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

Glu	Gly	Ile	Arg	Gln	Trp	Trp	Lys	Leu	Lys	Pro	Gly	Pro	Pro	Pro	Pro
		20					25					30			

Lys	Pro	Ala	Glu	Arg	His	Lys	Asp	Asp	Ser	Arg	Gly	Leu	Val	Leu	Pro
		35					40					45			

Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro
	50					55					60				

Val	Asn	Glu	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp
65					70					75					80

Arg	Gln	Leu	Asp	Ser	Gly	Asp	Asn	Pro	Tyr	Leu	Lys	Tyr	Asn	His	Ala
			85						90					95	

Asp	Ala	Glu	Phe	Gln	Glu	Arg	Leu	Lys	Glu	Asp	Thr	Ser	Phe	Gly	Gly
		100						105					110		

Asn	Leu	Gly	Arg	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Val	Leu	Glu	Pro
		115					120					125			

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

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

Gln Ser Pro Asp Val Ser Ser Ser Thr Gly Gly Gly Ile Ala Asp Val
165 170 175

Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly Gly Ala Pro Gly
180 185 190

Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser Ser Gly Asn Trp
195 200 205

His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg Thr Thr Ser Thr
210 215 220

Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Leu
225 230 235 240

Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
245 250 255

Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe Ser Pro Arg Asn
260 265 270

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Arg Leu
275 280 285

Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Glu Gly
290 295 300

Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe
305 310 315 320

Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp Ala Gly His Glu
325 330 335

Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met Ile Pro Gln Tyr
340 345 350

Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala Gln Ser Asp Leu
355 360 365

Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
370 375 380

Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp Val Pro Phe His
385 390 395 400

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
405 410 415

Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly Asn Pro Thr Gly
420 425 430

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

Ala His Tyr Gly Lys Asn Trp Leu Pro Gly Pro Phe Ile Arg Gln Gln
450 455 460

Gly Trp Thr Thr Gln Asn Ile Asn Asn Ser Val Val Asn Phe Asn Asp
465 470 475 480

Met Leu Gly Lys Asn Ser Thr Phe Thr Leu Asp Thr Arg Trp Ser Ser
485 490 495

Leu Ala Pro Gly Pro Cys Met Gly Asp Asp Gly Arg Thr Pro Ser Thr
500 505 510

Thr Lys Phe Ser Asn Ala Gln Leu Met Phe Gly Ser Gly Thr Gln Pro
515 520 525

Thr Glu Gly Gly Glu Asp Ala Val His Ile Thr Ser Glu Ser Glu Val
530 535 540

Lys Ala Thr Asn Pro Thr Ala Ile Asp Glu Tyr Gly Arg Val Ala Asp
545 550 555 560

Asn Thr Gln Asn Ala Thr Thr Ala Pro Thr Thr Val Gly Asn Ala Ala
565 570 575

Met Gly Ala Met Pro Gly Met Val Trp Gln Asp Arg Asp Ile Tyr Leu
580 585 590

Gln Gly Pro Ile Trp Gly Lys Ile Pro His Thr Asp Gly His Phe His
595 600 605

Pro Ser Pro Leu Met Gly Gly Phe Gly Tyr Arg Lys Pro Pro Pro Gln
610 615 620

Ile Phe Ile Lys Asn Thr Pro Val Pro Gly Asn Pro Ala Thr Thr Phe
625 630 635 640

Ser Pro Asn Arg Ile Asn Asn Phe Ile Thr Gln Tyr Ser Thr Gly Gln
645 650 655

Val Thr Val Thr Ile Asp Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg
660 665 670

Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Phe Gly Thr Val Asp Ser
675 680 685

Leu Asn Trp Ala Pro Asp Asn Ala Gly Asn Tyr Lys Glu Pro Arg Val
690 695 700

Ile Gly Thr Arg Tyr Leu Thr Arg Ile Leu
705 710

<210> 58
<211> 2145
<212> ADN
<213> Secuencia artificial

<220>
<223> Cap AAV2 VP1 de lobo marino VP2 VP3 v3

<400> 58
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc cgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac	180
aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac	240
cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg	420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga	480
aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactat gtctggagat	540
gctgaaatgg ctgcagtggg cgggggagca ccgggcgtcg acggccaggg tgccgaggga	600
gtgggtactt cctcgggtaa ttggcattgc gattcccagt ggtcagaagg acacgtcaga	660
accaccagca ccagaacctg ggtgttgccc agctacaaca accacctgta taaacggctt	720
ggaagtagcg cacaatcaa tacctacaac ggattctcca cccctggggg atacctcgac	780
ttcaatagat ggcactgtca cttcagtcct cggaactggc aacgtctcat caacaacaac	840
tggggcatca gacaaaaag acttaatgtt aaattgttca acatacaagt caaagaggtc	900
acgacggaag gggggacgac gaccgtcgcc aataacctta ccagcacgat tcagggtgtt	960
gcggacaacg cgtacgaact cccgtatgtt gtcgacgcgg gtcacgaggg ggcattgccg	1020
ccgttcccaa acgacgtgtt tatgattccc caatacggat actgcgggct ggtgtctggt	1080
caaagtcagg ctcagtcgga cttgtgttcg ttttattgcc tggagtattt tccatcccag	1140
atgctgagaa caggaaacaa ttttgaaatg aatttcaggt ttgaagacgt tccatttcac	1200
tccatgtacg cccacagcca gtctctagac aggctcatga atcctttaat tgatcagtat	1260
ctgtggagtc taaaacaaac aggaaacccg actggatcaa caacgagaga cttaaaattt	1320
atcaagaaca aagttcccaa ttttgcacat tatggaaaaa attggcttcc tggacctttt	1380
attagacaac aggggtggac aacacaaaat attaataata gtgttggttaa ttttaatgac	1440
atgctgggaa aaaattcgac atttactttg gacactagat ggagttcatt agcgcctggt	1500
ccgtgtatgg gggatgacgg acgaactcca tccaccacca agttctcaaa tgctcagctc	1560
atgtttggat ctggaacaca acccaccgaa ggcggtgaag atgctgtaca tattacatcc	1620
gagtcggagg tcaaggcaac caacccaact gcaatcgatg aatacggacg agtggccgat	1680
aatacgcaaa atgcaacaac cgccccaacc acagtgggaa atgctgcaat gggggccatg	1740

cctgggatgg tgtggcaaga tagggatatc tatcttcaag gacccatctg gggaaaaata 1800
 ccccatcacg acggacattt tcatccgtct cctctcatgg gggggtttgg atacagaaaa 1860
 cccctccgc aaatttttat taaaaacacc cccgttcctg gaaatccggc aactacattt 1920
 tctccaaata gaataaaca tttcattact caatactcaa cgggacaagt gaccgttact 1980
 attgactggg agctgcaaaa ggaaaactca aagagatgga acccagaagt acaatttaca 2040
 tcaaattttg gcacggtcga ttactaaac tgggcaccgg acaacgcggg aaactacaaa 2100
 gaaccaaggg tgattggcac cagatacctg actcgatac tataa 2145

<210> 59
 <211> 714
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Cap AAV2 VP1 de lobo marino VP2 VP3 v3

<400> 59

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

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly Gly Ala Pro Gly
180 185 190

Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser Ser Gly Asn Trp
195 200 205

His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg Thr Thr Ser Thr
210 215 220

Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Leu
225 230 235 240

Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
245 250 255

Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe Ser Pro Arg Asn
260 265 270

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Arg Leu
275 280 285

Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Glu Gly
290 295 300

Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe
305 310 315 320

Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp Ala Gly His Glu
325 330 335

Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met Ile Pro Gln Tyr
340 345 350

Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala Gln Ser Asp Leu
355 360 365

Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
370 375 380

Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp Val Pro Phe His
385 390 395 400

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
405 410 415

Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly Asn Pro Thr Gly
420 425 430

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

Ala His Tyr Gly Lys Asn Trp Leu Pro Gly Pro Phe Ile Arg Gln Gln
450 455 460

Gly Trp Thr Thr Gln Asn Ile Asn Asn Ser Val Val Asn Phe Asn Asp
465 470 475 480

Met Leu Gly Lys Asn Ser Thr Phe Thr Leu Asp Thr Arg Trp Ser Ser
485 490 495

Leu Ala Pro Gly Pro Cys Met Gly Asp Asp Gly Arg Thr Pro Ser Thr
500 505 510

Thr Lys Phe Ser Asn Ala Gln Leu Met Phe Gly Ser Gly Thr Gln Pro
515 520 525

Thr Glu Gly Gly Glu Asp Ala Val His Ile Thr Ser Glu Ser Glu Val
530 535 540

Lys Ala Thr Asn Pro Thr Ala Ile Asp Glu Tyr Gly Arg Val Ala Asp
545 550 555 560

Asn Thr Gln Asn Ala Thr Thr Ala Pro Thr Thr Val Gly Asn Ala Ala
565 570 575

Met Gly Ala Met Pro Gly Met Val Trp Gln Asp Arg Asp Ile Tyr Leu
580 585 590

Gln Gly Pro Ile Trp Gly Lys Ile Pro His Thr Asp Gly His Phe His
595 600 605

Pro Ser Pro Leu Met Gly Gly Phe Gly Tyr Arg Lys Pro Pro Pro Gln
610 615 620

Ile Phe Ile Lys Asn Thr Pro Val Pro Gly Asn Pro Ala Thr Thr Phe
625 630 635 640

Ser Pro Asn Arg Ile Asn Asn Phe Ile Thr Gln Tyr Ser Thr Gly Gln
645 650 655

Val Thr Val Thr Ile Asp Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg
660 665 670

Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Phe Gly Thr Val Asp Ser
675 680 685

Leu Asn Trp Ala Pro Asp Asn Ala Gly Asn Tyr Lys Glu Pro Arg Val
690 695 700

Ile Gly Thr Arg Tyr Leu Thr Arg Ile Leu
705 710

<210> 60
<211> 2145
<212> ADN
<213> Secuencia artificial

<220>
<223> Cap AAV2 VP1 de lobo marino VP2 VP3 v4

<400> 60
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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac	180
aaggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac	240
cggcagctcg acagcggaga caacccttac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg	420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctctc gggaaccgga	480
aaggcgggcc agcagcctgc aagaactggc ggaggaattg ccgacgtcat gtctggagat	540
gctgaaatgg ctgcagtggg cgggggagca ccgggcgtcg acggccaggg tgccgaggga	600
gtgggtactt cctcgggtaa ttggcattgc gattcccagt ggtcagaagg acacgtcaga	660
accaccagca ccagaacctg ggtgttgccc agctacaaca accacctgta taaacggctt	720
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tccatgtacg cccacagcca gtctctagac aggctcatga atcctttaat tgatcagtat	1260
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tctccaaata gaataaaciaa tttcattact caatactcaa cgggacaagt gaccgttact	1980
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tcaaattttg gcacggtcga ttcactaaac tgggcaccgg acaacgcggg aaactacaaa	2100
gaaccaaggg tgattggcac cagatacctg actcgtatac tataa	2145

<210> 61
 <211> 714
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Cap AAV2 VP1 de lobo marino VP2 VP3 v4

<400> 61

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

Glu	Gly	Ile	Arg	Gln	Trp	Trp	Lys	Leu	Lys	Pro	Gly	Pro	Pro	Pro	Pro
			20					25					30		

Lys	Pro	Ala	Glu	Arg	His	Lys	Asp	Asp	Ser	Arg	Gly	Leu	Val	Leu	Pro
		35					40					45			

Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro
	50					55					60				

Val	Asn	Glu	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp
65					70					75				80	

Arg	Gln	Leu	Asp	Ser	Gly	Asp	Asn	Pro	Tyr	Leu	Lys	Tyr	Asn	His	Ala
				85					90					95	

Asp	Ala	Glu	Phe	Gln	Glu	Arg	Leu	Lys	Glu	Asp	Thr	Ser	Phe	Gly	Gly
			100					105					110		

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Thr Gly Gly Gly Ile Ala Asp Val
165 170 175

Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly Gly Ala Pro Gly
180 185 190

Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser Ser Gly Asn Trp
195 200 205

His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg Thr Thr Ser Thr
210 215 220

Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Leu
225 230 235 240

Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
245 250 255

Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe Ser Pro Arg Asn
260 265 270

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Arg Leu
275 280 285

Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Glu Gly
290 295 300

Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe
305 310 315 320

Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp Ala Gly His Glu
325 330 335

Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met Ile Pro Gln Tyr
340 345 350

Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala Gln Ser Asp Leu
355 360 365

Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
370 375 380

Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp Val Pro Phe His
385 390 395 400

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
405 410 415

Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly Asn Pro Thr Gly
420 425 430

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

Ala His Tyr Gly Lys Asn Trp Leu Pro Gly Pro Phe Ile Arg Gln Gln
450 455 460

Gly Trp Thr Thr Gln Asn Ile Asn Asn Ser Val Val Asn Phe Asn Asp
465 470 475 480

Met Leu Gly Lys Asn Ser Thr Phe Thr Leu Asp Thr Arg Trp Ser Ser
485 490 495

Leu Ala Pro Gly Pro Cys Met Gly Asp Asp Gly Arg Thr Pro Ser Thr
500 505 510

Thr Lys Phe Ser Asn Ala Gln Leu Met Phe Gly Ser Gly Thr Gln Pro
515 520 525

Thr Glu Gly Gly Glu Asp Ala Val His Ile Thr Ser Glu Ser Glu Val
530 535 540

Lys Ala Thr Asn Pro Thr Ala Ile Asp Glu Tyr Gly Arg Val Ala Asp
545 550 555 560

Asn Thr Gln Asn Ala Thr Thr Ala Pro Thr Thr Val Gly Asn Ala Ala
565 570 575

Met Gly Ala Met Pro Gly Met Val Trp Gln Asp Arg Asp Ile Tyr Leu
580 585 590

Gln Gly Pro Ile Trp Gly Lys Ile Pro His Thr Asp Gly His Phe His
595 600 605

Pro Ser Pro Leu Met Gly Gly Phe Gly Tyr Arg Lys Pro Pro Pro Gln
610 615 620

Ile Phe Ile Lys Asn Thr Pro Val Pro Gly Asn Pro Ala Thr Thr Phe
625 630 635 640

Ser Pro Asn Arg Ile Asn Asn Phe Ile Thr Gln Tyr Ser Thr Gly Gln
645 650 655

Val Thr Val Thr Ile Asp Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg
660 665 670

Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Phe Gly Thr Val Asp Ser
675 680 685

Leu Asn Trp Ala Pro Asp Asn Ala Gly Asn Tyr Lys Glu Pro Arg Val
690 695 700

Ile Gly Thr Arg Tyr Leu Thr Arg Ile Leu
705 710

<210> 62

<211> 2157

<212> ADN

<213> Secuencia artificial

<220>

<223> Cap AAV2 VP1 de lobo marino VP2 VP3 v5

<400> 62

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aaggaggaca	cagccagagg	gctggtcctt	cccggttaca	agtacctcgg	gcccttcaac	180
ggtctagagc	ggggcgagcc	tgtgaatgcc	gcggacgccg	cggcccagcg	acacgaccga	240
cagtacgatc	gtattctaca	acaagggggg	aatccatacc	tcacgtacaa	ccacgccgac	300
cgagagtcc	aggaggagct	ccagtctgac	gagtcttttg	ggggaaatct	tggcaaggct	360
gtgtttcagg	ccaagaagcg	aatcctagag	cccctcggtc	tggttgaaga	ggatccctct	420
cagccagatt	cgtcctcgga	caacacggcg	ccaccctga	aaaagtcccg	tctcgaagaa	480
gcccagccca	ttcaaagtcc	agacgtttcc	agcagcactg	gcggaggaat	tgccgacgtc	540
atgtctggag	atgctgaaat	ggctgcagtg	ggcgggggag	caccgggcgt	cgacggccag	600
ggtgccgagg	gagtgggtac	ttcctcgggt	aattggcatt	gcgattccca	gtggtcagaa	660
ggacacgtca	gaaccaccag	caccagaacc	tgggtgttgc	ccagctacaa	caaccacctg	720
tataaacggc	ttggaagtag	cgcacaatcc	aatactaca	acggattctc	caccccctgg	780
ggatacctcg	acttcaatag	atggcactgt	cacttcagtc	ctcggaactg	gcaacgtctc	840
atcaacaaca	actggggcat	cagaccaaaa	agacttaatg	ttaaattggt	caacatacaa	900
gtcaaagagg	tcacgacgga	agggggggacg	acgaccgtcg	ccaataacct	taccagcacg	960
attcaggtgt	ttgcggacaa	cgcgtacgaa	ctcccgtatg	ttgtcgacgc	gggtcacgag	1020
ggggcattgc	cgccgttccc	aaacgacgtg	tttatgattc	ccaatacgg	atactgcggg	1080
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gacttaaaa	ttatcaagaa	caaagttccc	aattttgcac	attatggaaa	aaattggctt	1380
cctggacctt	ttattagaca	acaggggtgg	acaacacaaa	atattaataa	tagtgttggt	1440
aattttaatg	acatgctggg	aaaaaattcg	acatttactt	tggacactag	atggagttca	1500
ttagcgctg	gtccgtgtat	gggggatgac	ggacgaactc	catccaccac	caagttctca	1560
aatgctcagc	tcatgtttgg	atctggaaca	caaccaccg	aaggcgggtga	agatgctgta	1620

catattacat ccgagtcgga ggtcaaggca accaacccaa ctgcaatcga tgaatacggga 1680
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gtacaattta catcaaattt tggcacggtc gattcactaa actgggcacc ggacaacgcg 2100
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<210> 63
<211> 718
<212> PRT
<213> Secuencia artificial

<220>
<223> Cap AAV2 VP1 de lobo marino VP2 VP3 v5

<400> 63

Met Ser Ser Leu Phe Lys Glu Tyr Leu Gln Ser Thr Gly Leu Val Gly
1 5 10 15

Ile Gln Ser Gly Ala Pro Lys Pro Lys Ala Gly Gln Gln Lys Gln Asp
20 25 30

Thr Gly Ser Phe Glu Trp Lys Lys Lys Glu Asp Thr Ala Arg Gly Leu
35 40 45

Val Leu Pro Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Glu Arg
50 55 60

Gly Glu Pro Val Asn Ala Ala Asp Ala Ala Ala Gln Arg His Asp Arg
65 70 75 80

Gln Tyr Asp Arg Ile Leu Gln Gln Gly Gly Asn Pro Tyr Leu Thr Tyr
85 90 95

Asn His Ala Asp Arg Glu Phe Gln Glu Glu Leu Gln Ser Asp Glu Ser
100 105 110

Phe Gly Gly Asn Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Ile
115 120 125

Leu Glu Pro Leu Gly Leu Val Glu Glu Asp Pro Ser Gln Pro Asp Ser
130 135 140

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

Ala Gln Pro Ile Gln Ser Pro Asp Val Ser Ser Ser Thr Gly Gly Gly
165 170 175

Ile Ala Asp Val Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly
180 185 190

Gly Ala Pro Gly Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser
195 200 205

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg
210 215 220

Thr Thr Ser Thr Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu
225 230 235 240

Tyr Lys Arg Leu Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe
245 250 255

Ser Thr Pro Trp Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe
260 265 270

Ser Pro Arg Asn Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg
275 280 285

Pro Lys Arg Leu Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val
290 295 300

Thr Thr Glu Gly Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr
305 310 315 320

Ile Gln Val Phe Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp
325 330 335

Ala Gly His Glu Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met
340 345 350

Ile Pro Gln Tyr Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala
355 360 365

Gln Ser Asp Leu Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln
370 375 380

Met Leu Arg Thr Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp
385 390 395 400

Val Pro Phe His Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu
405 410 415

Met Asn Pro Leu Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly
420 425 430

Asn Pro Thr Gly Ser Thr Thr Arg Asp Leu Lys Phe Ile Lys Asn Lys
435 440 445

Val Pro Asn Phe Ala His Tyr Gly Lys Asn Trp Leu Pro Gly Pro Phe
450 455 460

Ile Arg Gln Gln Gly Trp Thr Thr Gln Asn Ile Asn Asn Ser Val Val
465 470 475 480

Asn Phe Asn Asp Met Leu Gly Lys Asn Ser Thr Phe Thr Leu Asp Thr
485 490 495

Arg Trp Ser Ser Leu Ala Pro Gly Pro Cys Met Gly Asp Asp Gly Arg
500 505 510

Thr Pro Ser Thr Thr Lys Phe Ser Asn Ala Gln Leu Met Phe Gly Ser
515 520 525

Gly Thr Gln Pro Thr Glu Gly Gly Glu Asp Ala Val His Ile Thr Ser
530 535 540

Glu Ser Glu Val Lys Ala Thr Asn Pro Thr Ala Ile Asp Glu Tyr Gly
545 550 555 560

Arg Val Ala Asp Asn Thr Gln Asn Ala Thr Thr Ala Pro Thr Thr Val
565 570 575

Gly Asn Ala Ala Met Gly Ala Met Pro Gly Met Val Trp Gln Asp Arg
580 585 590

Asp Ile Tyr Leu Gln Gly Pro Ile Trp Gly Lys Ile Pro His Thr Asp
595 600 605

Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Tyr Arg Lys
610 615 620

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Gly Asn Pro
625 630 635 640

Ala Thr Thr Phe Ser Pro Asn Arg Ile Asn Asn Phe Ile Thr Gln Tyr
645 650 655

Ser Thr Gly Gln Val Thr Val Thr Ile Asp Trp Glu Leu Gln Lys Glu
660 665 670

Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Phe Gly
675 680 685

Thr Val Asp Ser Leu Asn Trp Ala Pro Asp Asn Ala Gly Asn Tyr Lys
690 695 700

Glu Pro Arg Val Ile Gly Thr Arg Tyr Leu Thr Arg Ile Leu
705 710 715

<210> 64

<211> 2145

<212> ADN

<213> Secuencia artificial

<220>

<223> Cap AAV2 VP1 de lobo marino VP2 VP3 v2 B1 reemplazado

<400> 64

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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac	180
aaggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac	240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg	420
ggaaaaaaga ggacggcgcc acccgtgaaa aagtcccgtc tcgaagaagc ccagcccatt	480
caaagtccag acgtttccag cagcactggc ggaggaattg ccgacgtcat gtctggagat	540
gctgaaatgg ctgcagtggg cgggggagca ccgggcgtcg acggccaggg tgccgaggga	600
gtgggtactt cctcgggtaa ttggcattgc gattcccagt ggtcagaagg acacgtcaga	660
accaccagca ccagaacctg ggtgttgccc agctacaaca accacctgta taaacggctt	720
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tggggcatca gacaaaaag acttaatgtt aaattgttca acatacaagt caaagaggtc	900
acgacggaag gggggacgac gaccgtcgcc aataacctta ccagcacgat tcaggtgttt	960
gcggacaacg cgtacgaact cccgtatgtt gtcgacgcgg gtcacgaggg ggcattgccg	1020
ccgttcccaa acgacgtgtt tatgattccc caatacggat actgcgggct ggtgtctggt	1080
caaagtcagg ctcagtcgga cttgtgttcg ttttattgcc tggagtattt tccatcccag	1140
atgctgagaa caggaaacaa ttttgaaatg aatttcaggt ttgaagacgt tccatttcac	1200
tccatgtacg cccacagcca gtctctagac aggctcatga atcctttaat tgatcagtat	1260
ctgtggagtc taaaacaaac aggaaacccg actggatcaa caacgagaga cttaaaattt	1320
atcaagaaca aagttcccaa ttttgcacat tatggaaaaa attggcttcc tggacctttt	1380
attagacaac aggggtggac aacacaaaat attaataata gtgttggttaa ttttaatgac	1440
atgctgggaa aaaattcgac atttactttg gacactagat ggagttcatt agcgcctggt	1500
ccgtgtatgg gggatgacgg acgaactcca tccaccacca agttctcaaa tgctcagctc	1560

atgtttggat ctggaacaca acccaccgaa ggcggtgaag atgctgtaca tattacatcc	1620
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aatacgcaaa atgcaacaac cgccccaacc acagtgggaa atgctgcaat gggggccatg	1740
cctgggatgg tgtggcaaga tagggatatc tatcttcaag gacccatctg gggaaaaata	1800
ccccatacag acggacattt tcatccgtct cctctcatgg gggggtttgg atacagaaaa	1860
ccccctccgc aaatttttat taaaaacacc cccgttcctg gaaatccggc aactacattt	1920
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tcaaattttg gcacgggtcga ttcactaaac tgggcaccgg acaacgcggg aaactacaaa	2100
gaaccaaggg tgggtggggtc tcgattcctt acgcatatac tataa	2145

<210> 65
 <211> 714
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Cap AAV2 VP1 Sea Lion VP2 VP3 v2 B1 Replaced

<400> 65

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

Glu	Gly	Ile	Arg	Gln	Trp	Trp	Lys	Leu	Lys	Pro	Gly	Pro	Pro	Pro	Pro
			20					25					30		

Lys	Pro	Ala	Glu	Arg	His	Lys	Asp	Asp	Ser	Arg	Gly	Leu	Val	Leu	Pro
		35					40					45			

Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro
	50					55					60				

Val	Asn	Glu	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp
65					70					75				80	

Arg	Gln	Leu	Asp	Ser	Gly	Asp	Asn	Pro	Tyr	Leu	Lys	Tyr	Asn	His	Ala
				85					90					95	

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

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

Gln Ser Pro Asp Val Ser Ser Ser Thr Gly Gly Gly Ile Ala Asp Val
165 170 175

Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly Gly Ala Pro Gly
180 185 190

Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser Ser Gly Asn Trp
195 200 205

His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg Thr Thr Ser Thr
210 215 220

Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Leu
225 230 235 240

Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
245 250 255

Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe Ser Pro Arg Asn
260 265 270

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Arg Leu
275 280 285

Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Glu Gly
290 295 300

Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe
305 310 315 320

Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp Ala Gly His Glu
325 330 335

Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met Ile Pro Gln Tyr
340 345 350

Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala Gln Ser Asp Leu
355 360 365

Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
370 375 380

Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp Val Pro Phe His
385 390 395 400

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
405 410 415

Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly Asn Pro Thr Gly
420 425 430

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

Ala His Tyr Gly Lys Asn Trp Leu Pro Gly Pro Phe Ile Arg Gln Gln
450 455 460

Gly Trp Thr Thr Gln Asn Ile Asn Asn Ser Val Val Asn Phe Asn Asp
465 470 475 480

Met Leu Gly Lys Asn Ser Thr Phe Thr Leu Asp Thr Arg Trp Ser Ser
485 490 495

Leu Ala Pro Gly Pro Cys Met Gly Asp Asp Gly Arg Thr Pro Ser Thr
500 505 510

Thr Lys Phe Ser Asn Ala Gln Leu Met Phe Gly Ser Gly Thr Gln Pro
515 520 525

Thr Glu Gly Gly Glu Asp Ala Val His Ile Thr Ser Glu Ser Glu Val
530 535 540

Lys Ala Thr Asn Pro Thr Ala Ile Asp Glu Tyr Gly Arg Val Ala Asp
545 550 555 560

Asn Thr Gln Asn Ala Thr Thr Ala Pro Thr Thr Val Gly Asn Ala Ala
565 570 575

Met Gly Ala Met Pro Gly Met Val Trp Gln Asp Arg Asp Ile Tyr Leu
580 585 590

Gln Gly Pro Ile Trp Gly Lys Ile Pro His Thr Asp Gly His Phe His
595 600 605

Pro Ser Pro Leu Met Gly Gly Phe Gly Tyr Arg Lys Pro Pro Pro Gln
610 615 620

Ile Phe Ile Lys Asn Thr Pro Val Pro Gly Asn Pro Ala Thr Thr Phe
625 630 635 640

Ser Pro Asn Arg Ile Asn Asn Phe Ile Thr Gln Tyr Ser Thr Gly Gln
645 650 655

Val Thr Val Thr Ile Asp Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg
660 665 670

Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Phe Gly Thr Val Asp Ser
675 680 685

Leu Asn Trp Ala Pro Asp Asn Ala Gly Asn Tyr Lys Glu Pro Arg Val
690 695 700

Val Gly Ser Arg Phe Leu Thr His Ile Leu
705 710

<210> 66

<211> 2145

<212> ADN

<213> Secuencia artificial

<220>

<223> Cap AAV2 VP1 de lobo marino VP2 VP3 v3 B1 reemplazado

<400> 66

atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga	60
cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac	120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac	180
aaggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac	240
cggcagctcg acagcggaga caacccttac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg	420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga	480
aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactat gtctggagat	540
gctgaaatgg ctgcagtggg cgggggagca ccgggcgtcg acggccaggg tgccgaggga	600
gtgggtactt cctcgggtaa ttggcattgc gattcccagt ggtcagaagg acacgtcaga	660
accaccagca ccagaacctg ggtgttgccc agctacaaca accacctgta taaacggctt	720
ggaagtagcg cacaatccaa tacctacaac ggattctcca cccctggggg atacctcgac	780
ttcaatagat ggcactgtca cttcagtcct cggaactggc aacgtctcat caacaacaac	840
tggggcatca gacaaaaag acttaatgtt aaattgttca acatacaagt caaagaggtc	900
acgacggaag gggggacgac gaccgtcgcc aataacctta ccagcacgat tcaggtgttt	960
gcggacaacg cgtacgaact cccgtatgtt gtcgacgcgg gtcacgaggg ggcattgccg	1020
ccgttcccaa acgacgtgtt tatgattccc caatacggat actgcgggct ggtgtctggt	1080
caaagtcagg ctcagtcgga cttgtgttcg ttttattgcc tggagtattt tccatcccag	1140
atgctgagaa caggaaacaa ttttgaaatg aatttcaggt ttgaagacgt tccatttcac	1200
tccatgtacg cccacagcca gtctctagac aggctcatga atcctttaat tgatcagtat	1260
ctgtggagtc taaaacaaac aggaaacccg actggatcaa caacgagaga cttaaaattt	1320
atcaagaaca aagttcccaa ttttgcacat tatggaaaaa attggcttcc tggacctttt	1380
attagacaac aggggtggac aacacaaaat attaataata gtgttggttaa ttttaatgac	1440
atgctgggaa aaaattcgac atttactttg gacactagat ggagttcatt agcgcctggt	1500

ccgtgtatgg gggatgacgg acgaactcca tccaccacca agtttctcaaa tgctcagctc 1560
atgtttggat ctggaacaca acccaccgaa ggcggtgaag atgctgtaca tattacatcc 1620
gagtcggagg tcaaggcaac caacccaact gcaatcgatg aatacggacg agtggccgat 1680
aatacgcaaa atgcaacaac cgccccaacc acagtgggaa atgctgcaat gggggccatg 1740
cctgggatgg tgtggcaaga tagggatatc tatcttcaag gacccatctg gggaaaaata 1800
ccccatacag acggacattt tcatccgtct cctctcatgg gggggtttgg atacagaaaa 1860
ccccctccgc aaatttttat taaaaacacc cccgttcctg gaaatccggc aactacattt 1920
tctccaaata gaataaaca tttcattact caatactcaa cgggacaagt gaccgttact 1980
attgactggg agctgcaaaa ggaaaactca aagagatgga acccagaagt acaatttaca 2040
tcaaattttg gcacggtcga ttactaaac tgggcaccgg acaacgcggg aaactacaaa 2100
gaaccaaggg tggtgggggtc tcgattcctt acgcatatac tataa 2145

<210> 67
<211> 714
<212> PRT
<213> Secuencia artificial

<220>
<223> Cap AAV2 VP1 de lobo marino VP2 VP3 v3 B1 reemplazado
<400> 67

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

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly Gly Ala Pro Gly
180 185 190

Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser Ser Gly Asn Trp
195 200 205

His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg Thr Thr Ser Thr
210 215 220

Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Leu
225 230 235 240

Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
245 250 255

Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe Ser Pro Arg Asn
260 265 270

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Arg Leu
275 280 285

Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Glu Gly
290 295 300

Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe
305 310 315 320

Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp Ala Gly His Glu
325 330 335

Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met Ile Pro Gln Tyr
340 345 350

Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala Gln Ser Asp Leu
355 360 365

Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
370 375 380

Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp Val Pro Phe His
385 390 395 400

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
405 410 415

Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly Asn Pro Thr Gly
420 425 430

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

Ala His Tyr Gly Lys Asn Trp Leu Pro Gly Pro Phe Ile Arg Gln Gln
450 455 460

Gly Trp Thr Thr Gln Asn Ile Asn Asn Ser Val Val Asn Phe Asn Asp
465 470 475 480

Met Leu Gly Lys Asn Ser Thr Phe Thr Leu Asp Thr Arg Trp Ser Ser
485 490 495

Leu Ala Pro Gly Pro Cys Met Gly Asp Asp Gly Arg Thr Pro Ser Thr
500 505 510

Thr Lys Phe Ser Asn Ala Gln Leu Met Phe Gly Ser Gly Thr Gln Pro
515 520 525

Thr Glu Gly Gly Glu Asp Ala Val His Ile Thr Ser Glu Ser Glu Val
530 535 540

Lys Ala Thr Asn Pro Thr Ala Ile Asp Glu Tyr Gly Arg Val Ala Asp
545 550 555 560

Asn Thr Gln Asn Ala Thr Thr Ala Pro Thr Thr Val Gly Asn Ala Ala
565 570 575

Met Gly Ala Met Pro Gly Met Val Trp Gln Asp Arg Asp Ile Tyr Leu
580 585 590

Gln Gly Pro Ile Trp Gly Lys Ile Pro His Thr Asp Gly His Phe His
595 600 605

Pro Ser Pro Leu Met Gly Gly Phe Gly Tyr Arg Lys Pro Pro Pro Gln
610 615 620

Ile Phe Ile Lys Asn Thr Pro Val Pro Gly Asn Pro Ala Thr Thr Phe
625 630 635 640

Ser Pro Asn Arg Ile Asn Asn Phe Ile Thr Gln Tyr Ser Thr Gly Gln
645 650 655

Val Thr Val Thr Ile Asp Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg
660 665 670

Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Phe Gly Thr Val Asp Ser
675 680 685

Leu Asn Trp Ala Pro Asp Asn Ala Gly Asn Tyr Lys Glu Pro Arg Val
690 695 700

Val Gly Ser Arg Phe Leu Thr His Ile Leu
705 710

<210> 68

<211> 2145

<212> ADN

<213> Secuencia artificial

<220>

<223> Cap AAV2 VP1 de lobo marino VP2 VP3 v4 B1 reemplazado

<400> 68

atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga	60
cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac	120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac	180
aaggagagc cgggtcaacga ggacagcgcc gcggccctcg agcacgacaa agcctacgac	240
cggcagctcg acagcggaga caacccttac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg	420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga	480
aaggcgggcc agcagcctgc aagaactggc ggaggaattg ccgacgtcat gtctggagat	540
gctgaaatgg ctgcagtggg cgggggagca ccgggcgtcg acggccaggg tgccgaggga	600
gtgggtactt cctcgggtaa ttggcattgc gattcccagt ggtcagaagg acacgtcaga	660
accaccagca ccagaacctg ggtgttgccc agctacaaca accacctgta taaacggctt	720
ggaagtagcg cacaatccaa tacctacaac ggattctcca cccctggggg atacctcgac	780
ttcaatagat ggactgtca cttcagtcct cggaactggc aacgtctcat caacaacaac	840
tggggcatca gacaaaaag acttaatgtt aaattgttca acatacaagt caaagaggtc	900
acgacggaag gggggacgac gaccgtcgcc aataacctta ccagcacgat tcaggtgttt	960
gcggacaacg cgtacgaact cccgtatgtt gtcgacgcgg gtcacgaggg ggcattgccg	1020
ccgttcccaa acgacgtgtt tatgattccc caatacggat actgcgggct ggtgtctggt	1080
caaagtcagg ctcagtcgga cttgtgttcg ttttattgcc tggagtattt tccatcccag	1140
atgctgagaa caggaaacaa ttttgaaatg aatttcaggt ttgaagacgt tccatttcac	1200
tccatgtacg cccacagcca gtctctagac aggctcatga atcctttaat tgatcagtat	1260
ctgtggagtc taaaacaaac aggaaacccg actggatcaa caacgagaga cttaaaattt	1320
atcaagaaca aagttcccaa ttttgcacat tatggaaaaa attggcttcc tggacctttt	1380
attagacaac aggggtggac aacacaaaat attaataata gtgttggttaa ttttaatgac	1440

atgctgggaa aaaattcgac atttactttg gacactagat ggagttcatt agcgcctggt	1500
ccgtgtatgg gggatgacgg acgaactcca tccaccacca agttctcaaa tgctcagctc	1560
atgtttggat ctggaacaca acccaccgaa ggcggtgaag atgctgtaca tattacatcc	1620
gagtcggagg tcaaggcaac caacccaact gcaatcgatg aatacggacg agtggccgat	1680
aatacgcaaa atgcaacaac cgccccaacc acagtgggaa atgctgcaat gggggccatg	1740
cctgggatgg tgtggcaaga tagggatatc tatcttcaag gacccatctg gggaaaaata	1800
ccccatacag acggacattt tcatccgtct cctctcatgg gggggtttgg atacagaaaa	1860
ccccctccgc aaatttttat taaaaacacc cccgttcctg gaaatccggc aactacattt	1920
tctccaaata gaataaaca tttcattact caatactcaa cgggacaagt gaccgttact	1980
attgactggg agctgcaaaa ggaaaactca aagagatgga acccagaagt acaatttaca	2040
tcaaattttg gcacggtcga ttcactaaac tgggcaccgg acaacgcggg aaactacaaa	2100
gaaccaaggg tggtgggggtc tcgattcctt acgcatatac tataa	2145

<210> 69
 <211> 714
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Cap AAV2 VP1 de lobo marino VP2 VP3 v4 B1 reemplazado

<400> 69

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

Glu	Gly	Ile	Arg	Gln	Trp	Trp	Lys	Leu	Lys	Pro	Gly	Pro	Pro	Pro	Pro
			20					25					30		

Lys	Pro	Ala	Glu	Arg	His	Lys	Asp	Asp	Ser	Arg	Gly	Leu	Val	Leu	Pro
		35					40					45			

Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro
	50					55					60				

Val	Asn	Glu	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp
65					70					75				80	

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Thr Gly Gly Gly Ile Ala Asp Val
165 170 175

Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly Gly Ala Pro Gly
180 185 190

Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser Ser Gly Asn Trp
195 200 205

His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg Thr Thr Ser Thr
210 215 220

Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu Tyr Lys Arg Leu
225 230 235 240

Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
245 250 255

Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe Ser Pro Arg Asn
260 265 270

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Arg Leu
275 280 285

Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Glu Gly
290 295 300

Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe
305 310 315 320

Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp Ala Gly His Glu
325 330 335

Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met Ile Pro Gln Tyr
340 345 350

Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala Gln Ser Asp Leu
355 360 365

Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
370 375 380

Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp Val Pro Phe His
385 390 395 400

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
405 410 415

Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly Asn Pro Thr Gly
420 425 430

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

Ala His Tyr Gly Lys Asn Trp Leu Pro Gly Pro Phe Ile Arg Gln Gln
450 455 460

Gly Trp Thr Thr Gln Asn Ile Asn Asn Ser Val Val Asn Phe Asn Asp
465 470 475 480

Met Leu Gly Lys Asn Ser Thr Phe Thr Leu Asp Thr Arg Trp Ser Ser
485 490 495

Leu Ala Pro Gly Pro Cys Met Gly Asp Asp Gly Arg Thr Pro Ser Thr
500 505 510

Thr Lys Phe Ser Asn Ala Gln Leu Met Phe Gly Ser Gly Thr Gln Pro
515 520 525

Thr Glu Gly Gly Glu Asp Ala Val His Ile Thr Ser Glu Ser Glu Val
530 535 540

Lys Ala Thr Asn Pro Thr Ala Ile Asp Glu Tyr Gly Arg Val Ala Asp
545 550 555 560

Asn Thr Gln Asn Ala Thr Thr Ala Pro Thr Thr Val Gly Asn Ala Ala
565 570 575

Met Gly Ala Met Pro Gly Met Val Trp Gln Asp Arg Asp Ile Tyr Leu
580 585 590

Gln Gly Pro Ile Trp Gly Lys Ile Pro His Thr Asp Gly His Phe His
595 600 605

Pro Ser Pro Leu Met Gly Gly Phe Gly Tyr Arg Lys Pro Pro Pro Gln
610 615 620

Ile Phe Ile Lys Asn Thr Pro Val Pro Gly Asn Pro Ala Thr Thr Phe
625 630 635 640

Ser Pro Asn Arg Ile Asn Asn Phe Ile Thr Gln Tyr Ser Thr Gly Gln
645 650 655

Val Thr Val Thr Ile Asp Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg
660 665 670

Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Phe Gly Thr Val Asp Ser
675 680 685

Leu Asn Trp Ala Pro Asp Asn Ala Gly Asn Tyr Lys Glu Pro Arg Val
690 695 700

Val Gly Ser Arg Phe Leu Thr His Ile Leu
705 710

<210> 70
<211> 2157
<212> ADN
<213> Secuencia artificial

<220>

<223> Cap AAV2 VP1 de lobo marino VP2 VP3 v5 B1 reemplazado

<400> 70

atgtcttctt tgttttaaaga gtacctgcag agtaccggac tgggtgggtat ccagtcggga	60
gcgccgaagc caaaggccgg ccagcagaag caggatacag ggtcctttga gtggaaaaag	120
aaggaggaca cagccagagg gctggtcctt cccggttaca agtacctcgg gcccttcaac	180
ggtctagagc ggggagagcc tgtgaatgcc gcggacgccg cggcccagcg acacgaccga	240
cagtacgata gtattctaca acaaggggggt aatccatacc tcacgtacaa ccacgccgac	300
cgagagttcc aggaggagct ccagtctgac gagtcttttg ggggaaatct tggcaaggct	360
gtgtttcagg ccaagaagcg aatcctagag cccctcggtc tggttgaaga ggatccctct	420
cagccagatt cgtcctcgga caacacggcg ccacccgtga aaaagtcccg tctcgaagaa	480
gcccagccca ttcaaagtcc agacgtttcc agcagcactg gcggaggaat tgccgacgtc	540
atgtctggag atgctgaaat ggctgcagtg ggcgggggag caccgggcgt cgacggccag	600
ggtgccgagg gagtgggtac ttcctcgggt aattggcatt gcgattcca gtggtcagaa	660
ggacacgtca gaaccaccag caccagaacc tgggtgttgc ccagctacaa caaccacctg	720
tataaacggc ttggaagtag cgcacaatcc aatactaca acggattctc cacccttg	780
ggatactctg acttcaatag atggcactgt cacttcagtc ctcggaactg gcaacgtctc	840
atcaacaaca actggggcat cagacaaaaa agacttaatg tttaaattgtt caacatacaa	900
gtcaaagagg tcacgacgga aggggggacg acgaccgtcg ccaataacct taccagcacg	960
attcaggtgt ttgcggacaa cgcgtacgaa ctcccgtatg ttgtcgacgc gggtcacgag	1020
ggggcattgc cgccgttccc aaacgacgtg tttatgattc cccaatacgg atactgcggg	1080
ctggtgtctg gtcaaagtca ggctcagtcg gacttgtgtt cgttttattg cctggagtat	1140
tttccatccc agatgctgag aacaggaaac aattttgaaa tgaatttcag gtttgaagac	1200
gttccatttc actccatgta cgcccacagc cagtctctag acaggctcat gaatccttta	1260
attgatcagt atctgtggag tctaaaacaa acaggaaacc cgactggatc aacaacgaga	1320
gacttaaaat ttatcaagaa caaagttccc aattttgcac attatggaaa aaattggctt	1380

cctggacctt ttattagaca acaggggtgg acaacacaaa atattaataa tagtgttggt 1440
aattttaatg acatgctggg aaaaaattcg acatttactt tggacactag atggagttca 1500
ttagcgcctg gtccgtgtat ggggggatgac ggacgaactc catccaccac caagtttctca 1560
aatgctcagc tcatgttttg atctggaaca caaccaccg aaggcgggtga agatgctgta 1620
catattacat ccgagtcgga ggtcaaggca accaacccaa ctgcaatcga tgaatacggga 1680
cgagtggccg ataatacgca aaatgcaaca accgccccaa ccacagtggg aaatgctgca 1740
atggggggcca tgcctgggat ggtgtggcaa gatagggata tctatcttca aggacccatc 1800
tgggggaaaaa taccatac agacggacat tttcatccgt ctctctcat ggggggggttt 1860
ggatacagaa aacccctcc gcaaattttt attaaaaaca ccccgttcc tggaaatccg 1920
gcaactacat tttctccaaa tagaataaac aatttcatta ctcaatactc aacgggacaa 1980
gtgaccgtta ctattgactg ggagctgcaa aaggaaaact caaagagatg gaaccagaa 2040
gtacaattta catcaaattt tggcacggtc gattcactaa actgggcacc ggacaacgcg 2100
ggaaactaca aagaaccaag ggtggtgggg tctcgattcc ttacgatat actataa 2157

<210> 71
<211> 718
<212> PRT
<213> Secuencia artificial

<220>
<223> Cap AAV2 VP1 de lobo marino VP2 VP3 v5 B1 reemplazado
<400> 71

Met Ser Ser Leu Phe Lys Glu Tyr Leu Gln Ser Thr Gly Leu Val Gly
1 5 10 15

Ile Gln Ser Gly Ala Pro Lys Pro Lys Ala Gly Gln Gln Lys Gln Asp
20 25 30

Thr Gly Ser Phe Glu Trp Lys Lys Lys Glu Asp Thr Ala Arg Gly Leu
35 40 45

Val Leu Pro Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Glu Arg
50 55 60

Gly Glu Pro Val Asn Ala Ala Asp Ala Ala Ala Gln Arg His Asp Arg
65 70 75 80

Gln Tyr Asp Arg Ile Leu Gln Gln Gly Gly Asn Pro Tyr Leu Thr Tyr
85 90 95

Asn His Ala Asp Arg Glu Phe Gln Glu Glu Leu Gln Ser Asp Glu Ser
100 105 110

Phe Gly Gly Asn Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Ile
115 120 125

Leu Glu Pro Leu Gly Leu Val Glu Glu Asp Pro Ser Gln Pro Asp Ser
130 135 140

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

Ala Gln Pro Ile Gln Ser Pro Asp Val Ser Ser Ser Thr Gly Gly Gly
165 170 175

Ile Ala Asp Val Met Ser Gly Asp Ala Glu Met Ala Ala Val Gly Gly
180 185 190

Gly Ala Pro Gly Val Asp Gly Gln Gly Ala Glu Gly Val Gly Thr Ser
195 200 205

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Ser Glu Gly His Val Arg
210 215 220

Thr Thr Ser Thr Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Leu
225 230 235 240

Tyr Lys Arg Leu Gly Ser Ser Ala Gln Ser Asn Thr Tyr Asn Gly Phe
245 250 255

Ser Thr Pro Trp Gly Tyr Leu Asp Phe Asn Arg Trp His Cys His Phe
260 265 270

Ser Pro Arg Asn Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Ile Arg
275 280 285

Pro Lys Arg Leu Asn Val Lys Leu Phe Asn Ile Gln Val Lys Glu Val
290 295 300

Thr Thr Glu Gly Gly Thr Thr Thr Val Ala Asn Asn Leu Thr Ser Thr
305 310 315 320

Ile Gln Val Phe Ala Asp Asn Ala Tyr Glu Leu Pro Tyr Val Val Asp
325 330 335

Ala Gly His Glu Gly Ala Leu Pro Pro Phe Pro Asn Asp Val Phe Met
340 345 350

Ile Pro Gln Tyr Gly Tyr Cys Gly Leu Val Ser Gly Gln Ser Gln Ala
355 360 365

Gln Ser Asp Leu Cys Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln
370 375 380

Met Leu Arg Thr Gly Asn Asn Phe Glu Met Asn Phe Arg Phe Glu Asp
385 390 395 400

Val Pro Phe His Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu
405 410 415

Met Asn Pro Leu Ile Asp Gln Tyr Leu Trp Ser Leu Lys Gln Thr Gly
420 425 430

Asn Pro Thr Gly Ser Thr Thr Arg Asp Leu Lys Phe Ile Lys Asn Lys
435 440 445

Val Pro Asn Phe Ala His Tyr Gly Lys Asn Trp Leu Pro Gly Pro Phe
450 455 460

Ile Arg Gln Gln Gly Trp Thr Thr Gln Asn Ile Asn Asn Ser Val Val
465 470 475 480

Asn Phe Asn Asp Met Leu Gly Lys Asn Ser Thr Phe Thr Leu Asp Thr
485 490 495

Arg Trp Ser Ser Leu Ala Pro Gly Pro Cys Met Gly Asp Asp Gly Arg
500 505 510

Thr Pro Ser Thr Thr Lys Phe Ser Asn Ala Gln Leu Met Phe Gly Ser
515 520 525

Gly Thr Gln Pro Thr Glu Gly Gly Glu Asp Ala Val His Ile Thr Ser
530 535 540

Glu Ser Glu Val Lys Ala Thr Asn Pro Thr Ala Ile Asp Glu Tyr Gly
545 550 555 560

Arg Val Ala Asp Asn Thr Gln Asn Ala Thr Thr Ala Pro Thr Thr Val
565 570 575

Gly Asn Ala Ala Met Gly Ala Met Pro Gly Met Val Trp Gln Asp Arg
580 585 590

Asp Ile Tyr Leu Gln Gly Pro Ile Trp Gly Lys Ile Pro His Thr Asp
595 600 605

Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Tyr Arg Lys
610 615 620

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Gly Asn Pro
625 630 635 640

Ala Thr Thr Phe Ser Pro Asn Arg Ile Asn Asn Phe Ile Thr Gln Tyr
645 650 655

Ser Thr Gly Gln Val Thr Val Thr Ile Asp Trp Glu Leu Gln Lys Glu
660 665 670

Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Phe Gly
675 680 685

Thr Val Asp Ser Leu Asn Trp Ala Pro Asp Asn Ala Gly Asn Tyr Lys
690 695 700

Glu Pro Arg Val Val Gly Ser Arg Phe Leu Thr His Ile Leu
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Val	Pro	Thr	Ile	Val	Met	Val	Asp	Ala	Tyr	Lys	Arg	Tyr	Lys
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