

SEQUENCE LISTING

<110> Oxford Genetics Limited
Oxford University Innovation Limited

<120> METHOD OF MAKING RECOMBINANT AAVS

<130> 489.150421/01

<160> 30

<170> PatentIn version 3.5

<210> 1

<211> 2211

<212> DNA

<213> Artificial Sequence

<220>

<223> AAV1 - Capsid Nucleotide Sequence (AF063497.1)

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<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> AAV1 - Capsid Protein Sequence

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35 40 45

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

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

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

Asp Ala Glu Phe Gln Glu Arg Leu Gln 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 Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
 145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
 180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
 195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
 210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
 225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
 260 265 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
 275 280 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
 290 295 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
 305 310 315 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
 325 330 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
 340 345 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
 355 360 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
 370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
 385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
435 440 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

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

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

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

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

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<211> 2208
<212> DNA
<213> adeno-associated virus 2

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 <211> 735
 <212> PRT
 <213> adeno-associated virus 2

<400> 4

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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 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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270

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

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
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 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
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 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
 580 585 590
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

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

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

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<212> DNA
<213> adeno-associated virus 3

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<210> 6
 <211> 736
 <212> PRT
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<400> 6

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Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly 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

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

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

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

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

Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145 150 155 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
 180 185 190
 Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
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 Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
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 Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
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 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
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 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
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Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
435 440 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
450 455 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
485 490 495

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565 570 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
580 585 590

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595 600 605

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

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

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

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

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 7
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<213> adeno-associated virus 4

<400> 7
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tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120
gctcggggtc ttgtgcttcc gggttataaa tacctcggac ccggcaacgg actcgacaag 180
ggggaacccg tcaacgcagc ggagcgggca gccctcgagc acgacaaggc ctacgaccag 240
cagctcaagg ccgggtgaaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300
cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360
aaaaagaggg ttcttgaacc tcttggctctg gttgagcaag cgggtgagac ggctcctgga 420
aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480
aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540
ggaccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600
gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gaggggtaa tgcctcgggt 660
gattggcatt gcgattccac ctggctctgag ggccacgtca cgaccaccag caccagaacc 720
tgggtcttgc ccacctataa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780
aacacctaca acggattctc cccccctgg ggatactttg acttcaaccg cttccactgc 840
cacttctcac cacgtgactg gcagcgactc atcaacaaca actggggcat gcgacccaaa 900
gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960
acaacggtgg ctaataacct taccagcacg gttcagatct ttgcggactc gtcgtacgaa 1020
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tttatggtgc ccagtagcg ctactgtgga ctggtagacc gcaacacttc gcagcaacag 1140
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aacaactttg aaattacgta cagttttgag aagggtgcctt tccactcgat gtacgcgcac 1260
agccagagcc tggaccggct gatgaacctt ctcatcgacc agtacctgtg gggactgcaa 1320
tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380
cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440
cagggcttct caaagactgc caatcaaac tacaagatcc ctgccaccgg gtcagacagt 1500
ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgcctt gacccccgga 1560
cctccaatgg ccacggctgg acctgcggac agcaagtcca gcaacagcca gctcatcttt 1620
gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgccacc gatacggaca tgtggggcaa cctacctggc 1740
ggtgaccaga gcaacagcaa cctgccgacc gtggacagac tgacagcctt gggagccgtg 1800
cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860
cctcataccg atggacactt tcacccctca ccgctgattg gtgggttttg gctgaaacac 1920
ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc aacgaccttc 1980
agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag 2040
attgactggg agatccagaa ggagcgggcc aaacgctgga accccgaggt ccagtttacc 2100
tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160
gagcctaggg ctatcgggtac ccgctacctc acccaccacc tgtaa 2205

<210> 8
<211> 734
<212> PRT
<213> adeno-associated virus 4

<400> 8

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

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

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

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

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

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

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

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

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145 150 155 160

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

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

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
 195 200 205

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

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
 225 230 235 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
 245 250 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly 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 Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
 290 295 300

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

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

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

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
 355 360 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
 370 375 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
 385 390 395 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
 405 410 415

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

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
 435 440 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
 450 455 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
 465 470 475 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
 485 490 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
 500 505 510

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

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
 530 535 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
 545 550 555 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
 565 570 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
 580 585 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
 595 600 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
 610 615 620

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

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

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
 660 665 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
 675 680 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
 690 695 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
 705 710 715 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730

<210> 9
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> AAV5 - Capsid Nucleotide Sequence (AF085716.1)

<400> 9
atgtcttttg ttgatcacc tccagattgg ttggaagaag ttggtgaagg tcttcgag 60
tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120
gcccgtgggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180
ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240
cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300
gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360
aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420
ggaaagcgga tagacgacca ctttcaaaa agaaagaagg ctcggaccga agaggactcc 480
aagccttcca cctcgtcaga cgccgaagct ggaccagcg gatccagca gctgcaaadc 540
ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600
ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660
gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720
agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780
aacgcctact ttggatacag cacccttggt ggggtactttg actttaaccg cttccacagc 840
cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccg 900
tccctcagag tcaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960
accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020
ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080
tttacgtgc cgagtagcg ttacgcgacg ctgaaccgca acaacacaga aaatcccacc 1140
gagaggagca gcttcttctg cctagagtac tttccagca agatgctgag aacgggcaac 1200
aactttgagt ttacctaaa ctttgaggag gtgcccttc actccagctt cgctcccagt 1260
cagaacctgt tcaagctggc caaccgctg gtggaccagt acttgtagcg cttcgtgagc 1320
acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380
tacaaaaact ggttcccggg gcccatgggc cgaaccagg gctggaacct gggctccggg 1440
gtcaaccgca ccagtgtcag gccttcgcc acgaccaata ggatggagct cgagggcgcg 1500
agttaccagg tgccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560
tatgccctgg agaacactat gatcttcaac agccagccgg cgaaccggg caccaccgcc 1620
acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgcccc 1740
gcgaccggca cgtacaacct ccaggaaatc gtgcccgga gcgtgtggat ggagaggga 1800
gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcga ctttcacccc 1860
tctccggcca tgggcggatt cggactcaaa caccaccgc ccatgatgct catcaagaac 1920
acgcctgtgc ccgaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980
cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040
aagaggtgga acccagagat ccagtacaca aacaactaca acgacccca gtttgtggac 2100
tttgcgccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160
acccgacccc tttaa 2175

<210> 10
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> AAV5 - Capsid Protein Sequence

<400> 10

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

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

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

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

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

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145 150 155 160

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

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
 180 185 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
 195 200 205

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

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

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
 245 250 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
 260 265 270

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

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
 290 295 300

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

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

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
 340 345 350

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

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

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

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
 405 410 415

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

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln

435

440

445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
 450 455 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
 465 470 475 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
 485 490 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
 500 505 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
 515 520 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
 530 535 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
 545 550 555 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
 565 570 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
 580 585 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
 595 600 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
 610 615 620

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

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
 645 650 655

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

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

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
 690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
 705 710 715 720

Thr Arg Pro Leu

<210> 11
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> AAV6 - Capsid Nucleotide Sequence (AF028704.1)

<400> 11
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
gagtgggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120
gacggccggg gtctgggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaagaaga gggttctcga accttttggg ctggttgagg aagtgctaa gacggctcct 420
ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480
aagacaggcc agcagccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540
tcagtccccg acccacaacc tctcggagaa cctccagcaa ccccgctgc tgtgggacct 600
actacaatgg cttcaggcgg tggcgacca atggcagaca ataacgaagg cgccgacgga 660
gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcac 720
accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaadc 780
tccagtgttt caacgggggc cagcaacgac aaccactact tcggctacag cccccctgg 840
gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900
atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960
gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020
gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080
ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgagctacgg ctacctaacg 1140
ctcaacaatg gcagccaggc agtgggacgg tcacaccttt actgcctgga atatttccca 1200
tcgcagatgc tgagaacggg caataacttt accttcagct acaccttcga ggacgtgcct 1260
ttccacagca gctacgcga cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320
cagtacctgt attacctgaa cagaactcag aatcagtcg gaagtgccca aaacaaggac 1380
ttgtgttta gccgggggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440
ggacctgtt accggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500
tttacctgga ctggtgtctt aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560
ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcgggtgc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680
 acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740
 gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800
 gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860
 aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920
 aagcaccgcg ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980
 gagttttcgg ctacaaagtt tgcttcattc atcaccaggt attccacagg acaagtgagc 2040
 gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100
 tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160
 tatactgagc ctcgccccat tggcaccctg tacctcaccg gtcccctgta a 2211

<210> 12
 <211> 736
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AAV6 - Capsid Protein Sequence

<400> 12

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

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30

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

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

Asp Ala Glu Phe Gln Glu Arg Leu Gln 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

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

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
 145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
 180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
 195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
 210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
 225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
 260 265 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
 275 280 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
 290 295 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
 305 310 315 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
 325 330 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
 340 345 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
 355 360 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
 370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
 385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
 405 410 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
 420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
 435 440 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
 450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
 465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
 485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
 500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
 515 520 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
 530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
 545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
 565 570 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
 580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
 595 600 605

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

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

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
 645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
 660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
 690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 13
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> AAV7 - Capsid Nucleotide Sequence (AF513851.1)

<400> 13
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
gagtgggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120
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agcaactttg ctggactgg tgccacaaa tatcacctga acggcagaaa ctcgttgggt 1560

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cttaaacatc cgcctcctca gatcctgata aagaacactc ccgttcccgc taatcctccg      1980
gaggtgttta ctctgcaa gtttgcttcg ttcacacac agtacagcac cggacaagtc      2040
agcgtggaaa tcgagtggga gctgcagaag gaaaacagca agcgtggaa cccggagatt      2100
cagtacacct ccaactttga aaagcagact ggtgtggact ttgccgttga cagccagggt      2160
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```

```

<210> 14
<211> 737
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> AAV7 - Capsid Protein Sequence

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<400> 14

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

```

```

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
          20          25          30

```

```

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

```

```

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

```

```

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

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```

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

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```

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

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Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
 180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly
 195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
 210 215 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255

Leu Tyr Lys Gln Ile Ser Ser Glu Thr Ala Gly Ser Thr Asn Asp Asn
 260 265 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
 305 310 315 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
 325 330 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
 340 345 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
 355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
 370 375 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser
 405 410 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu

420

425

430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
 435 440 445

Arg Thr Gln Ser Asn Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
 450 455 460

Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
 465 470 475 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
 485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
 530 535 540

Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
 545 550 555 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
 565 570 575

Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
 580 585 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
 595 600 605

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

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

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
 645 650 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
 660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
 675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
 690 695 700

Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705 710 715 720

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

Leu

<210> 15
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> AAV8 - Capsid Nucleotide Sequence (AF513852.1)

<400> 15
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gagtgggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120
gacggccggg gtctgggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggccggacgca gcggccctcg agcacgacaa ggcctacgac 240
cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420
ggaaagaaga gaccggtaga gccatcacc cagcgttctc cagactcctc tacgggcatc 480
ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540
gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tgggtgtggga 600
cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660
ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720
atcaccacca gacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780
atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840
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cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960
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cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440
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 atgctcacca gcgaggaaga aatcaaaacc actaacctg tggctacaga ggaatacggc 1740
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 ggctgaaac atcctccgcc tcagatcctg atcaagaaca cgctgtacc tgcggatcct 1980
 ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040
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 atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160
 ggctgtact ctgaaccccg cccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 16
 <211> 738
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AAV8 - Capsid Protein Sequence

<400> 16

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

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

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

Asp Ala Glu Phe Gln Glu Arg Leu Gln 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 Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
 180 185 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
 195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
 260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
 450 455 460
 Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
 530 535 540
 Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
 580 585 590
 Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
 660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 17
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> AAV9 - Capsid Nucleotide Sequence (AY530556.1)

<400> 17
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gacggccggg gtctgggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacggcaa ggcctacgac 240
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caggagcgctc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420
ggaaagaaga gaccggtaga gccatcacc cagcgttctc cagactcctc tacgggcatc 480
ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540
gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tgggtgtggga 600
cctaatacaa tggctgcagg cgggtggcgca ccaatggcag acaataacga aggcgcccgc 660
ggagtgggta attcctcggg aaattggcat tgcgattcca catggctggg ggacagagtc 720
atcaccacca gcacccgaac ctgggcattg cccacctaca acaaccacct ctacaagcaa 780
atctccaatg gaacatcggg aggaagcacc aacgacaaca cctactttgg ctacagcacc 840
ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900
cgactcatca acaacaactg gggattccgg ccaaagagac tcaacttcaa gctgttcaac 960
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ttcccttctc agatgctgag aaccggcaac aactttcagt tcagctacac tttcgaggac	1260
gtgcctttcc acagcagcta cgcacacagc cagagtctag atcgactgat gaacccctc	1320
atcgaccagt acctatacta cctggtcaga acacagacaa ctggaactgg gggaactcaa	1380
actttggcat tcagccaagc aggccctagc tcaatggcca atcaggctag aaactgggta	1440
cccgggcctt gctaccgtca gcagcgcgtc tccacaacca ccaacaaaa taacaacagc	1500
aactttgcgt ggacgggagc tgctaaattc aagctgaacg ggagagactc gctaatgaat	1560
cctggcgtgg ctatggcatc gcacaaagac gacgaggacc gcttctttcc atcaagtggc	1620
gttctcatat ttggcaagca aggagccggg aacgatggag tcgactacag ccaggtgctg	1680
attacagatg aggaagaaat taaagccacc aaccctgtag ccacagagga atacggagca	1740
gtggccatca acaaccaggc cgctaacacg caggcgcaaa ctggacttgt gcataaccag	1800
ggagtatttc ctggtatggt ctggcagaac cgggacgtgt acctgcaggg ccctatttgg	1860
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ctgaaacacc cacctccaca gattctaatt aaaaatacac cagtgccggc agatcctcct	1980
cttaccttca atcaagccaa gctgaactct ttcacacgc agtacagcac gggacaagtc	2040
agcgtggaaa tcgagtggga gctgcagaaa gaaaacagca agcgctggaa tccagagatc	2100
cagtatactt caaactacta caaatctaca aatgtggact ttgctgtcaa taccgaaggt	2160
gtttactctg agcctcgccc catttggtact cgttacctca cccgtaattt gtaa	2214

<210> 18
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AAV9 - Capsid Protein Sequence

<400> 18

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

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

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

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

Asp Ala Glu Phe Gln Glu Arg Leu Gln 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 Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
 180 185 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
 195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
 210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
 305 310 315 320

Ile Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335

Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365

Pro Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn

36/49

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

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly
705 710 715 720

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

Leu

<210> 19
<211> 1866
<212> DNA
<213> adeno-associated virus 2

<400> 19
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tctgacatgg atctgaatct gattgagcag gcaccctga ccgtggccga gaagctgcag 180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360
taccgcggga tcgagccgac tttgcaaac tggttcgcg tcacaaagac cagaaatggc 420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gtccccaaa 480
accagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgcctgtttg 540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660
tcagccaggt acatggagct ggtcgggtgg ctctgggaca aggggattac ctcggagaag 720
cagtggatcc agggaggacca ggcctcatat atctccttca atgcggcctc caactcgcg 780
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cccgactacc tgggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900
attttgaac taaacgggta cgatcccaa tatgcggtt ccgtctttct gggatgggcc 960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc 1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140

aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggaggaag caaggtgcgc	1200
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ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttggaag	1380
gtcaccaagc aggaagtcaa agactttttc cgggtgggcaa aggatcacgt ggttgaggtg	1440
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gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg	1560
gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg	1620
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc	1680
ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccggtt	1740
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaagggtg	1800
ccagacgctt gactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa	1860
caatag	1866

<210> 20
 <211> 1866
 <212> DNA
 <213> adeno-associated virus 2

<400> 20	
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tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag	180
cgcgactttc tgacggaatg ggcgcgtgtg agtaaggccc cggaggccct tttctttgtg	240
caatttgaga agggagagag ctacttcac atgcacgtgc tcgtggaaac caccggggtg	300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt	360
taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc	420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaa	480
accagcctg agctccagtg ggcgtggact aatatggaac agtacctcag cgcctgtttg	540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag	600
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cagtggatcc aggaggacca ggcctcatac atctccttca atgcggcctc caactcgcgg	780
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cccgactacc tgggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa	900
atthtgaac taaacgggta cgatcccaa tatgcggctt ccgtctttct gggatgggcc	960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcaac taccgggaag	1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc	1080

aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140
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ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttggaag 1380
gtcaccaagc aggaagtcaa agactttttc cggtgggcaa aggatcacgt ggttgaggtg 1440
gagcatgaat tctacgtcaa aaaggggtgga gccaagaaaa gacccgcccc cagtgcgca 1500
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560
gaagcttcga tcaactacgc agacaggtag caaaacaaat gttctcgtca cgtgggcatg 1620
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ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaacccgtt 1740
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaagggtg 1800
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caatag 1866

<210> 21
<211> 621
<212> PRT
<213> adeno-associated virus 2

<400> 21

Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1 5 10 15

Gly His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35 40 45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50 55 60

Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65 70 75 80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85 90 95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105 110

Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130 135 140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175

Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180 185 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195 200 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210 215 220

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 235 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275 280 285

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305 310 315 320

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325 330 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340 345 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355 360 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370 375 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val

	405		410		415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser	420		425		430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe	435		440		445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln	450		455		460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val	465		470		480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala	485		490		495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val	500		505		510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp	515		520		525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu	530		535		540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys	545		550		560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu	565		570		575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr	580		585		590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp	595		600		605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln	610		615		620

<210> 22
 <211> 1589
 <212> DNA
 <213> adeno-associated virus 2

<400> 22	
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tctgacatgg atctgaatct gattgagcag gcaccctga ccgtggccga gaagctgcag	180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg	240

caatttgaga agggagagag ctactttcac atgcacgtgc tcgtggaaac caccggggtg	300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt	360
taccgcggga tcgagccgac tttgccaac tggttcgchg tcacaaagac cagaaatggc	420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaa	480
accagcctg agctccagtg ggcgtggact aatatggaac agtacctcag cgcctgtttg	540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag	600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggtgatcag atcaaaaact	660
tcagccaggt acatggagct ggtcgggtgg ctctgtggaca aggggattac ctcggagaag	720
cagtggatcc aggaggacca ggcctcatac atctccttca atgcggcctc caactcgcgg	780
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cccgactacc tggtagggcca gcagcccgtg gaggacatct ccagcaatcg gatttataaa	900
attttgaac taaacgggta cgatcccaa tatgcggctt ccgtctttct gggatgggcc	960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcaac taccgggaag	1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc	1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctgggt ggaggagggg	1140
aagatgaccg ccaaggctgt ggagtcggcc aaagccattc tcggaggaag caaggtgcgc	1200
gtggaccaga aatgcaagtc ctcggcccag atagaccga ctcccgtgat cgtcacctcc	1260
aacaccaaca tgtgcgccgt gattgacggg aactcaacga ctttgaaca ccagcagccg	1320
ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag	1380
gtcaccaagc aggaagtcaa agactttttc cggtgggcaa aggatcacgt ggttgaggtg	1440
gagcatgaat tctacgtcaa aaagggtgga gccaagaaaa gacccgcccc cagtgcgca	1500
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg	1560
gaagcttcga tcaactacgc agacagtag	1589

<210> 23
 <211> 528
 <212> PRT
 <213> adeno-associated virus 2
 <400> 23

Met	Pro	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
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Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20						25					30		

Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			

Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				

Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
 65 70 75 80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
 85 90 95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
 100 105 110

Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
 115 120 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
 130 135 140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
 145 150 155 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
 165 170 175

Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
 180 185 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
 195 200 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
 210 215 220

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 225 230 235 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 245 250 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 260 265 270

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 275 280 285

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 290 295 300

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 305 310 315 320

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
 325 330 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
 340 345 350
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
 355 360 365
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
 370 375 380
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
 385 390 395 400
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
 405 410 415
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
 420 425 430
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
 435 440 445
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
 450 455 460
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
 465 470 475 480
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
 485 490 495
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
 500 505 510
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
 515 520 525

<210> 24
 <211> 1195
 <212> DNA
 <213> adeno-associated virus 2

<400> 24
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 ggctgccttg gacaatgcgg gaaagattat gagcctgact aaaaccgccc ccgactacct 180
 ggtgggccag cagcccgtgg aggacatttc cagcaatcgg atttataaaa ttttggaact 240
 aaacgggtac gatccccaat atgcggcttc cgtctttctg ggatgggcca cgaaaaagtt 300
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 ggaggccata gccacactg tgcccttcta cggggtgcgta aactggacca atgagaactt 420
 tcccttcaac gactgtgtcg acaagatggt gatctggtgg gaggagggga agatgaccgc 480

caaggtcgtg gagtcggcca aagccattct cggaggaagc aaggtgctcg tggaccagaa 540
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 gtgcgccgtg attgacggga actcaacgac cttcgaacac cagcagccgt tgcaagaccg 660
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 gcccaaacgg gtgcgcgagt cagttgcgca gccatcgacg tcagacgcgg aagcttcgat 900
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 aaaggcgtat cagaaactgt gctacattca tcatatcatg ggaaagggtgc cagacgcttg 1140
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<210> 25
 <211> 397
 <212> PRT
 <213> adeno-associated virus 2

<400> 25

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20 25 30

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35 40 45

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

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65 70 75 80

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85 90 95

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
 100 105 110

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
 115 120 125

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
 130 135 140

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 160

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210 215 220

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225 230 235 240

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275 280 285

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305 310 315 320

Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325 330 335

Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340 345 350

Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365

Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370 375 380

Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385 390 395

<210> 26

<211> 939

<212> DNA

<213> adeno-associated virus 2

<400> 26
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gctgccttgg acaatgcggg aaagattatg agcctgacta aaaccgcccc cgactacctg 180
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gaagtcaaag actttttccg gtgggcaaag gatcacgtgg ttgaggtgga gcatgaattc 780
tacgtcaaaa aggttgagc caagaaaaga cccgccccca gtgacgcaga tataagttag 840
cccaaacggg tgcgcgagtc agttgcgcag ccatcgacgt cagacgcgga agcttcgatc 900
aactacgcag acagattggc tcgaggacac tctctctag 939

<210> 27
<211> 312
<212> PRT
<213> adeno-associated virus 2

<400> 27

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1 5 10 15

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20 25 30

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40 45

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

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100 105 110

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120 125

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 160

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210 215 220

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225 230 235 240

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275 280 285

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300

Arg Leu Ala Arg Gly His Ser Leu
305 310

<210> 28
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> TetR binding site

<400> 28
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19

<210> 29
<211> 107
<212> DNA
<213> Artificial Sequence

<220>

<223> Modified MLP

<400> 29

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ttcctgaagg ggggctataa aaggcccta tcagtgatag agactca 107

<210> 30

<211> 107

<212> DNA

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