SEQUENCE LISTING

<110> Oxford Genetic Limited
Oxford University Innovation Limited

<120> DNA AMPLIFICATION METHOD

<130> 489.147163/01

<160> 14

<170> PatentIn version 3.5

<210> 1
<211> 1866
<212> DNA
<213> Rep nucleotide sequence (adeno-associated virus 2)

<400> 1
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ggcatttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120

tctgacatgg atctgaatct gattgagcag gcacccctga 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 tttgccaaac tggttcgcgg tcacaaagac cagaaatggc 420

gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctccccaaa 480

acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgcctgtttg 540

aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600

gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggtgatcag atcaaaaact 660

tcagccaggt acatggagct ggtcgggtgg ctcgtggaca aggggattac ctcggagaag 720

cagtggatcc aggaggacca ggcctcatac atctccttca atgcggcctc caactcgcgg 780

tcccaaatca aggctgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840

cccgactacc tggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900

attttggaac taaacgggta cgatccccaa 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

aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggaggaag caaggtgcgc 1200

gtggaccaga aatgcaagtc ctcggcccag atagacccga ctcccgtgat cgtcacctcc 1260

aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320

ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag 1380

gtcaccaagc aggaagtcaa agacttttc cggtgggcaa aggatcacgt ggttgaggtg 1440

gagcatgaat tctacgtcaa aaagggtgga gccaagaaaa gacccgcccc cagtgacgca 1500

gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560

gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg 1620

aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 1680

ttcactcacg gacagaaaga ctgtttagag tgctttcccg tgtcagaatc tcaacccgtt 1740

tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaaggtg 1800

ccagacgctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa 1860

caatag 1866

<210> 2
<211> 2559
<212> DNA
<213> Cap nucleotide sequence (adeno-associated virus 2)

<400> 2
cagttgcgca gccatcgacg tcagacgcgg aagcttcgat caactacgca gacaggtacc 60

aaaacaaatg ttctcgtcac gtgggcatga atctgatgct gtttccctgc agacaatgcg 120

agagaatgaa tcagaattca aatatctgct tcactcacgg acagaaagac tgtttagagt 180

gctttcccgt gtcagaatct caacccgttt ctgtcgtcaa aaaggcgtat cagaaactgt 240

gctacattca tcatatcatg ggaaaggtgc cagacgcttg cactgcctgc gatctggtca 300

atgtggattt ggatgactgc atctttgaac aataaatgat ttaaatcagg tatggctgcc 360

gatggttatc ttccagattg gctcgaggac actctctctg aaggaataag acagtggtgg 420

aagctcaaac ctggcccacc accaccaaag cccgcagagc ggcataagga cgacagcagg 480

ggtcttgtgc ttcctgggta caagtacctc ggacccttca acggactcga caagggagag 540

ccggtcaacg aggcagacgc cgcggccctc gagcacgaca aagcctacga ccggcagctc 600

gacagcggag acaacccgta cctcaagtac aaccacgccg acgcggagtt tcaggagcgc 660

cttaaagaag atacgtcttt tgggggcaac ctcggacgag cagtcttcca ggcgaaaaag 720

agggttcttg aacctctggg cctggttgag gaacctgtta agacggctcc gggaaaaaag 780

aggccggtag agcactctcc tgtggagcca gactcctcct cgggaaccgg aaaggcgggc 840

cagcagcctg caagaaaaag attgaatttt ggtcagactg gagacgcaga ctcagtacct 900

gacccccagc ctctcggaca gccaccagca gccccctctg gtctgggaac taatacgatg 960

gctacaggca gtggcgcacc aatggcagac aataacgagg gcgccgacgg agtgggtaat 1020

tcctcgggaa attggcattg cgattccaca tggatgggcg acagagtcat caccaccagc 1080

acccgaacct gggccctgcc cacctacaac aaccacctct acaaacaaat ttccagccaa 1140

tcaggagcct cgaacgacaa tcactacttt ggctacagca ccccttgggg gtattttgac 1200

ttcaacagat tccactgcca cttttcacca cgtgactggc aaagactcat caacaacaac 1260

tggggattcc gacccaagag actcaacttc aagctcttta acattcaagt caaagaggtc 1320

acgcagaatg acggtacgac gacgattgcc aataacctta ccagcacggt tcaggtgttt 1380

actgactcgg agtaccagct cccgtacgtc ctcggctcgg cgcatcaagg atgcctcccg 1440

ccgttcccag cagacgtctt catggtgcca cagtatggat acctcaccct gaacaacggg 1500

agtcaggcag taggacgctc ttcattttac tgcctggagt actttccttc tcagatgctg 1560

cgtaccggaa acaactttac cttcagctac acttttgagg acgttccttt ccacagcagc 1620

tacgctcaca gccagagtct ggaccgtctc atgaatcctc tcatcgacca gtacctgtat 1680

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gcaagccaca aggacgatga agaaaagttt tttcctcaga gcggggttct catctttggg 1980

aagcaaggct cagagaaaac aaatgtggac attgaaaagg tcatgattac agacgaagag 2040

gaaatcagga caaccaatcc cgtggctacg gagcagtatg gttctgtatc taccaacctc 2100

cagagaggca acagacaagc agctaccgca gatgtcaaca cacaaggcgt tcttccaggc 2160

atggtctggc aggacagaga tgtgtacctt caggggccca tctgggcaaa gattccacac 2220

acggacggac attttcaccc ctctcccctc atgggtggat tcggacttaa acaccctcct 2280

ccacagattc tcatcaagaa caccccggta cctgcgaatc cttcgaccac cttcagtgcg 2340

gcaaagtttg cttccttcat cacacagtac tccacgggac aggtcagcgt ggagatcgag 2400

tgggagctgc agaaggaaaa cagcaaacgc tggaatcccg aaattcagta cacttccaac 2460

tacaacaagt ctgttaatgt ggactttact gtggacacta atggcgtgta ttcagagcct 2520

cgccccattg gcaccagata cctgactcgt aatctgtaa 2559

<210> 3
<211> 735
<212> PRT
<213> Cap amino acid sequence (adeno-associated virus 2)

<400> 3

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

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
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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
            500                 505                 510

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
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560
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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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<210> 4
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Rep binding site (RBS)

<400> 4
gcccgagtga gcacgc 16

<210> 5
<211> 350
<212> DNA
<213> CARE element (adeno-associated virus 2)

<400> 5
gtcctgtatt agaggtcacg tgagtgtttt gcgacatttt gcgacaccat gtggtcacgc 60

tgggtattta agcccgagtg agcacgcagg gtctccattt tgaagcggga ggtttgaacg 120

cgcagccgcc atgccggggt tttacgagat tgtgattaag gtccccagcg accttgacga 180

gcatctgccc ggcatttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt 240

gccgccagat tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga 300

gaagctgcag cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc 350

<210> 6
<211> 137
<212> PRT
<213> Artificial Sequence

<220>
<223> L4 22K (Human adenovirus D serotype 9 (HAdV-9))

<400> 6

Met Pro Arg Lys Lys Gln Glu Pro Leu Val Glu Glu Met Glu Glu Glu
1 5 10 15

Trp Asp Ser Gln Ala Glu Glu Asp Glu Trp Glu Glu Glu Thr Glu Glu
20 25 30

Glu Glu Leu Glu Glu Val Glu Glu Glu Gln Ala Thr Glu Gln Pro Val
35 40 45

Ala Ala Pro Ser Ala Pro Ala Ala Pro Ala Val Thr Asp Thr Thr Ser
50 55 60

Ala Ala Pro Ala Lys Pro Pro Arg Arg Trp Asp Arg Val Lys Gly Asp
65 70 75 80

Gly Lys His Glu Arg Gln Gly Tyr Arg Ser Trp Arg Ala His Lys Ala
85 90 95

Ala Ile Ile Ala Cys Leu Gln Asp Cys Gly Gly Asn Ile Ala Phe Ala
100 105 110

Arg Arg Tyr Leu Leu Phe His Arg Gly Val Asn Ile Pro Arg Asn Val
115 120 125

Leu His Tyr Tyr Arg His Leu His Ser
130 135

<210> 7
<211> 585
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad 5 L4 22K

<400> 7

atggcaccca aaaagaagct gcagctgccg ccgccaccca cggacgagga ggaatactgg 60

gacagtcagg cagaggaggt tttggacgag gaggaggagg acatgatgga agactgggag 120

agcctagacg aggaagcttc cgaggtcgaa gaggtgtcag acgaaacacc gtcaccctcg 180

gtcgcattcc cctcgccggc gccccagaaa tcggcaaccg gttccagcat ggctacaacc 240

tccgctcctc aggcgccgcc ggcactgccc gttcgccgac ccaaccgtag atgggacacc 300

actggaacca gggccggtaa gtccaagcag ccgccgccgt tagcccaaga gcaacaacag 360

cgccaaggct accgctcatg gcgcgggcac aagaacgcca tagttgcttg cttgcaagac 420

tgtgggggca acatctcctt cgcccgccgc tttcttctct accatcacgg cgtggccttc 480

ccccgtaaca tcctgcatta ctaccgtcat ctctacagcc catactgcac cggcggcagc 540

ggcagcaaca gcagcggcca cacagaagca aaggcgaccg gatag 585

<210> 8
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad 5 L4 22K

<400> 8

Met Ala Pro Lys Lys Lys Leu Gln Leu Pro Pro Pro Pro Thr Asp Glu
1 5 10 15

Glu Glu Tyr Trp Asp Ser Gln Ala Glu Glu Val Leu Asp Glu Glu Glu
20 25 30

Glu Asp Met Met Glu Asp Trp Glu Ser Leu Asp Glu Glu Ala Ser Glu
35 40 45

Val Glu Glu Val Ser Asp Glu Thr Pro Ser Pro Ser Val Ala Phe Pro
50 55 60

Ser Pro Ala Pro Gln Lys Ser Ala Thr Gly Ser Ser Met Ala Thr Thr
65 70 75 80

Ser Ala Pro Gln Ala Pro Pro Ala Leu Pro Val Arg Arg Pro Asn Arg
85 90 95

Arg Trp Asp Thr Thr Gly Thr Arg Ala Gly Lys Ser Lys Gln Pro Pro
100 105 110

Pro Leu Ala Gln Glu Gln Gln Gln Arg Gln Gly Tyr Arg Ser Trp Arg
115 120 125

Gly His Lys Asn Ala Ile Val Ala Cys Leu Gln Asp Cys Gly Gly Asn
130 135 140

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Ile Ser Phe Ala Arg Arg Phe Leu Leu Tyr His His Gly Val Ala Phe
145                 150                 155                 160

Pro Arg Asn Ile Leu His Tyr Tyr Arg His Leu Tyr Ser Pro Tyr Cys
                165                 170                 175

Thr Gly Gly Ser Gly Ser Asn Ser Ser Gly His Thr Glu Ala Lys Ala
            180                 185                 190

Thr Gly
```

<210> 9
<211> 1590
<212> DNA
<213> Artificial Sequence

<220>
<223> E2A polypeptide nucleotide sequence (Adenovirus type 5)

<400> 9

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atggccagtc gggaagagga gcagcgcgaa accacccccg agcgcggacg cggtgcggcg       60

cgacgtcccc caaccatgga ggacgtgtcg tccccgtccc cgtcgccgcc gcctccccgg      120

gcgcccccaa aaaagcggat gaggcggcgt atcgagtccg aggacgagga agactcatca      180

caagacgcgc tggtgccgcg cacacccagc ccgcggccat cgacctcggc ggcggatttg      240

gccattgcgc ccaagaagaa aaagaagcgc ccttctccca agcccgagcg cccgccatca      300

ccagaggtaa tcgtggacag cgaggaagaa agagaagatg tggcgctaca aatggtgggt      360

ttcagcaacc caccggtgct aatcaagcat ggcaaaggag gtaagcgcac agtgcggcgg      420

ctgaatgaag acgacccagt ggcgcgtggt atgcggacgc aagaggaaga ggaagagccc      480

agcgaagcgg aaagtgaaat tacggtgatg aacccgctga gtgtgccgat cgtgtctgcg      540

tgggagaagg gcatggaggc tgcgcgcgcg ctgatggaca agtaccacgt ggataacgat      600

ctaaaggcga acttcaaact actgcctgac caagtggaag ctctggcggc cgtatgcaag      660

acctggctga acgaggagca ccgcgggttg cagctgacct tcaccagcaa caagaccttt      720

gtgacgatga tggggcgatt cctgcaggcg tacctgcagt cgtttgcaga ggtgacctac      780

aagcatcacg agcccacggg ctgcgcgttg tggctgcacc gctgcgctga gatcgaaggc      840

gagcttaagt gtctacacgg aagcattatg ataaataagg agcacgtgat tgaaatggat      900

gtgacgagcg aaaacgggca gcgcgcgctg aaggagcagt ctagcaaggc caagatcgtg      960

aagaaccggt ggggccgaaa tgtggtgcag atctccaaca ccgacgcaag gtgctgcgtg     1020

cacgacgcgg cctgtccggc caatcagttt tccggcaagt cttgcggcat gttcttctct     1080

gaaggcgcaa aggctcaggt ggcttttaag cagatcaagg cttttatgca ggcgctgtat     1140
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cctaacgccc agaccgggca cggtcacctt ttgatgccac tacggtgcga gtgcaactca 1200

aagcctgggc acgcgccctt tttgggaagg cagctaccaa agttgactcc gttcgccctg 1260

agcaacgcgg aggacctgga cgcggatctg atctccgaca agagcgtgct ggccagcgtg 1320

caccacccgg cgctgatagt gttccagtgc tgcaaccctg tgtatcgcaa ctcgcgcgcg 1380

cagggcggag gccccaactg cgacttcaag atatcggcgc ccgacctgct aaacgcgttg 1440

gtgatggtgc gcagcctgtg gagtgaaaac ttcaccgagc tgccgcggat ggttgtgcct 1500

gagtttaagt ggagcactaa acaccagtat cgcaacgtgt ccctgccagt ggcgcatagc 1560

gatgcgcggc agaacccctt tgatttttaa 1590

<210> 10
<211> 529
<212> PRT
<213> Artificial Sequence

<220>
<223> E2A polypeptide amino acid sequence (Adenovirus type 5)

<400> 10

Met Ala Ser Arg Glu Glu Glu Gln Arg Glu Thr Thr Pro Glu Arg Gly
1 5 10 15

Arg Gly Ala Ala Arg Arg Pro Pro Thr Met Glu Asp Val Ser Ser Pro
20 25 30

Ser Pro Ser Pro Pro Pro Pro Arg Ala Pro Pro Lys Lys Arg Met Arg
35 40 45

Arg Arg Ile Glu Ser Glu Asp Glu Glu Asp Ser Ser Gln Asp Ala Leu
50 55 60

Val Pro Arg Thr Pro Ser Pro Arg Pro Ser Thr Ser Ala Ala Asp Leu
65 70 75 80

Ala Ile Ala Pro Lys Lys Lys Lys Lys Arg Pro Ser Pro Lys Pro Glu
85 90 95

Arg Pro Pro Ser Pro Glu Val Ile Val Asp Ser Glu Glu Glu Arg Glu
100 105 110

Asp Val Ala Leu Gln Met Val Gly Phe Ser Asn Pro Pro Val Leu Ile
115 120 125

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

Asp Pro Val Ala Arg Gly Met Arg Thr Gln Glu Glu Glu Glu Glu Pro
145 150 155 160

```
Ser Glu Ala Glu Ser Glu Ile Thr Val Met Asn Pro Leu Ser Val Pro
                165                 170                 175

Ile Val Ser Ala Trp Glu Lys Gly Met Glu Ala Ala Arg Ala Leu Met
            180                 185                 190

Asp Lys Tyr His Val Asp Asn Asp Leu Lys Ala Asn Phe Lys Leu Leu
        195                 200                 205

Pro Asp Gln Val Glu Ala Leu Ala Ala Val Cys Lys Thr Trp Leu Asn
    210                 215                 220

Glu Glu His Arg Gly Leu Gln Leu Thr Phe Thr Ser Asn Lys Thr Phe
225                 230                 235                 240

Val Thr Met Met Gly Arg Phe Leu Gln Ala Tyr Leu Gln Ser Phe Ala
                245                 250                 255

Glu Val Thr Tyr Lys His His Glu Pro Thr Gly Cys Ala Leu Trp Leu
            260                 265                 270

His Arg Cys Ala Glu Ile Glu Gly Glu Leu Lys Cys Leu His Gly Ser
        275                 280                 285

Ile Met Ile Asn Lys Glu His Val Ile Glu Met Asp Val Thr Ser Glu
    290                 295                 300

Asn Gly Gln Arg Ala Leu Lys Glu Gln Ser Ser Lys Ala Lys Ile Val
305                 310                 315                 320

Lys Asn Arg Trp Gly Arg Asn Val Val Gln Ile Ser Asn Thr Asp Ala
                325                 330                 335

Arg Cys Cys Val His Asp Ala Ala Cys Pro Ala Asn Gln Phe Ser Gly
            340                 345                 350

Lys Ser Cys Gly Met Phe Phe Ser Glu Gly Ala Lys Ala Gln Val Ala
        355                 360                 365

Phe Lys Gln Ile Lys Ala Phe Met Gln Ala Leu Tyr Pro Asn Ala Gln
    370                 375                 380

Thr Gly His Gly His Leu Leu Met Pro Leu Arg Cys Glu Cys Asn Ser
385                 390                 395                 400

Lys Pro Gly His Ala Pro Phe Leu Gly Arg Gln Leu Pro Lys Leu Thr
                405                 410                 415
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```
Pro Phe Ala Leu Ser Asn Ala Glu Asp Leu Asp Ala Asp Leu Ile Ser
            420                 425                 430

Asp Lys Ser Val Leu Ala Ser Val His His Pro Ala Leu Ile Val Phe
        435                 440                 445

Gln Cys Cys Asn Pro Val Tyr Arg Asn Ser Arg Ala Gln Gly Gly Gly
    450                 455                 460

Pro Asn Cys Asp Phe Lys Ile Ser Ala Pro Asp Leu Leu Asn Ala Leu
465                 470                 475                 480

Val Met Val Arg Ser Leu Trp Ser Glu Asn Phe Thr Glu Leu Pro Arg
                485                 490                 495

Met Val Val Pro Glu Phe Lys Trp Ser Thr Lys His Gln Tyr Arg Asn
            500                 505                 510

Val Ser Leu Pro Val Ala His Ser Asp Ala Arg Gln Asn Pro Phe Asp
        515                 520                 525

Phe
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<210> 11
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> TetR binding site

<400> 11
tccctatcag tgatagaga 19

<210> 12
<211> 107
<212> DNA
<213> Artificial Sequence

<220>
<223> Modified MLP

<400> 12
cgccctcttc ggcatcaagg aaggtgattg gtttgtaggt gtaggccacg tgaccgggtg 60

ttcctgaagg ggggctataa aaggtcccta tcagtgatag agactca 107

<210> 13
<211> 107
<212> DNA
<213> Artificial Sequence

<220>

<223> Modified MLP

<400> 13
cgccctcttc ggcatcaagg aaggtgattg gtttgtaggt gtaggccacg tgactcccta 60

tcagtgatag agaactataa aaggtcccta tcagtgatag agactca 107

<210> 14
<211> 107
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of the wild-type Ad5 MLP

<400> 14
cgccctcttc ggcatcaagg aaggtgattg gtttgtaggt gtaggccacg tgaccgggtg 60

ttcctgaagg ggggctataa aaggggggtgg gggcgcgttc gtcctca 107