SEQUENCE LISTING

<110> Janssen Vaccines & Prevention B.V.
Bunnik, Evelien Margaretha
Custers, Jerome Hubertina Henricus Victor
Scheper, Gerrit Christiaan
Oosterhuis, Koen
Uil, Taco Gilles
Khan, Selina

<120> Therapeutic HPV18 vaccines

<130> 0260 WO 00 ORD

<150> EP15181791
<151> 2015-08-20

<150> EP16156334
<151> 2016-02-18

<160> 24

<170> PatentIn version 3.5

<210> 1
<211> 328
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<213> Artificial Sequence

<220>
<223> HPV16-E6E7SH designer polypeptide

<400> 1

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Arg Lys Leu Pro Gln Leu Cys Thr Glu Leu Gln Thr Thr Ile His Asp
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Ile Ile Leu Glu Cys Val Tyr Cys Lys Gln Gln Leu Glu Asp Glu Ile
        35                  40                  45


Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp Arg Ala His Tyr Asn Ile
    50                  55                  60


Val Thr Phe Cys Cys Lys Cys Asp Ser Thr Leu Arg Leu Cys Val Gln
65                  70                  75                  80


Ser Thr His Val Asp Ile Arg Thr Leu Glu Asp Leu Leu Met Gly Thr
                85                  90                  95


Leu Gly Ile Val Cys Pro Ile Cys Ser Gln Lys Pro Gly Thr Thr Leu
            100                 105                 110


Glu Gln Gln Tyr Asn Lys Pro Leu Cys Asp Leu Leu Ile Arg Cys Ile
        115                 120                 125
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Asn Cys Gln Lys Pro Leu Cys Pro Glu Glu Lys Gln Arg His Leu Asp
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Lys Lys Gln Arg Phe His Asn Ile Arg Gly Arg Trp Thr Gly Arg Cys
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Met Ser Cys Cys Arg Ser Ser Arg Thr Arg Arg Glu Thr Gln Met His
                165                 170                 175

Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln Pro Glu
            180                 185                 190

Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser Glu Glu
        195                 200                 205

Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp Arg Ala
    210                 215                 220

His Tyr Asn Ile Val Thr Phe Cys Cys Gln Leu Cys Thr Glu Leu Gln
225                 230                 235                 240

Thr Thr Ile His Asp Ile Ile Leu Glu Cys Val Tyr Cys Lys Gln Gln
                245                 250                 255

Leu Leu Arg Arg Glu Val Tyr Asp Phe Ala Phe Arg Asp Leu Cys Ile
            260                 265                 270

Val Tyr Arg Asp Gly Asn Pro Tyr Ala Val Cys Asp Lys Cys Leu Lys
        275                 280                 285

Phe Tyr Ser Lys Ile Ser Glu Tyr Arg His Tyr Cys Tyr Ser Leu Tyr
    290                 295                 300

Gly Thr Thr Leu Glu Gln Gln Tyr Asn Lys Pro Leu Cys Asp Leu Leu
305                 310                 315                 320

Ile Arg Cys Ile Asn Cys Gln Lys
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aagcagcagc tggaagatga gatcgacggc cctgctggcc aggccgaacc cgacagagcc 180

cactacaata tcgtgacctt ctgctgcaag tgcgacagca ccctgcggct gtgcgtgcag 240

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tgcgacctgc tgatccggtg catcaactgc cagaaacccc tgtgccccga ggaaaagcag 420

cggcacctgg acaagaagca gcggttccac aacatccggg gcagatggac aggcagatgc 480

atgagctgct gcagaagcag ccggaccaga cgggaaaccc agatgcacgg cgacaccccc 540

accctgcacg agtacatgct ggacctgcag cccgagacaa ccgacctgta ctgctacgag 600

cagctgaacg acagcagcga ggaagaggac gagattgacg gacccgctgg acaggccgag 660

cctgaccggg ctcactataa catcgtgaca ttttgctgtc agctctgtac tgaactccag 720

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gaggtgtacg acttcgcctt ccgggacctc tgcatcgtgt atcgggacgg caacccctac 840

gccgtgtgcg acaagtgcct gaagttctac agcaagatca gcgagtaccg gcactactgc 900

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attcgctgta tcaattgtca gaagtgataa 990

<210> 3
<211> 693
<212> PRT
<213> Artificial Sequence

<220>
<223> HPV16 E2E6E7SH designer polypeptide

<400> 3

Met Glu Thr Leu Cys Gln Arg Leu Asn Val Cys Gln Asp Lys Ile Leu
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Thr His Tyr Glu Asn Asp Ser Thr Asp Leu Arg Asp His Ile Asp Tyr
20 25 30

Trp Lys His Met Arg Leu Glu Cys Ala Ile Tyr Tyr Lys Ala Arg Glu
35 40 45

Met Gly Phe Lys His Ile Asn His Gln Val Val Pro Thr Leu Ala Val
50 55 60

Ser Lys Asn Lys Ala Leu Gln Ala Ile Glu Leu Gln Leu Thr Leu Glu
65 70 75 80

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Thr Ile Tyr Asn Ser Gln Tyr Ser Asn Glu Lys Trp Thr Leu Gln Asp
                85                  90                  95

Val Ser Leu Glu Val Tyr Leu Thr Ala Pro Thr Gly Cys Ile Lys Lys
            100                 105                 110

His Gly Tyr Thr Val Glu Val Gln Phe Asp Gly Asp Ile Cys Asn Thr
        115                 120                 125

Met His Tyr Thr Asn Trp Thr His Ile Tyr Ile Cys Glu Glu Ala Ser
    130                 135                 140

Val Thr Val Val Glu Gly Gln Val Asp Tyr Tyr Gly Leu Tyr Tyr Val
145                 150                 155                 160

His Glu Gly Ile Arg Thr Tyr Phe Val Gln Phe Lys Asp Asp Ala Glu
                165                 170                 175

Lys Tyr Ser Lys Asn Lys Val Trp Glu Val His Ala Gly Gly Gln Val
            180                 185                 190

Ile Leu Cys Pro Thr Ser Val Phe Ser Ser Asn Glu Val Ser Ser Pro
        195                 200                 205

Glu Ile Ile Arg Gln His Leu Ala Asn His Pro Ala Ala Thr His Thr
    210                 215                 220

Lys Ala Val Ala Leu Gly Thr Glu Glu Thr Gln Thr Thr Ile Gln Arg
225                 230                 235                 240

Pro Arg Ser Glu Pro Asp Thr Gly Asn Pro Cys His Thr Thr Lys Leu
                245                 250                 255

Leu His Arg Asp Ser Val Asp Ser Ala Pro Ile Leu Thr Ala Phe Asn
            260                 265                 270

Ser Ser His Lys Gly Arg Ile Asn Cys Asn Ser Asn Thr Thr Pro Ile
        275                 280                 285

Val His Leu Lys Val Asp Ala Asn Thr Leu Met Arg Leu Arg Tyr Arg
    290                 295                 300

Phe Lys Lys His Cys Thr Leu Tyr Thr Ala Val Ser Ser Thr Trp His
305                 310                 315                 320

Trp Thr Gly His Asn Val Lys His Lys Ser Ala Ile Val Thr Leu Thr
                325                 330                 335
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Tyr Asp Ser Glu Trp Gln Arg Asp Gln Phe Leu Ser Gln Val Lys Ile
            340                 345                 350

Pro Lys Thr Ile Thr Val Ser Thr Gly Phe Met Ser Ile Met His Gln
        355                 360                 365

Lys Arg Thr Ala Met Phe Gln Asp Pro Gln Glu Arg Pro Arg Lys Leu
    370                 375                 380

Pro Gln Leu Cys Thr Glu Leu Gln Thr Thr Ile His Asp Ile Ile Leu
385                 390                 395                 400

Glu Cys Val Tyr Cys Lys Gln Gln Leu Glu Asp Glu Ile Asp Gly Pro
                405                 410                 415

Ala Gly Gln Ala Glu Pro Asp Arg Ala His Tyr Asn Ile Val Thr Phe
            420                 425                 430

Cys Cys Lys Cys Asp Ser Thr Leu Arg Leu Cys Val Gln Ser Thr His
        435                 440                 445

Val Asp Ile Arg Thr Leu Glu Asp Leu Leu Met Gly Thr Leu Gly Ile
    450                 455                 460

Val Cys Pro Ile Cys Ser Gln Lys Pro Gly Thr Thr Leu Glu Gln Gln
465                 470                 475                 480

Tyr Asn Lys Pro Leu Cys Asp Leu Leu Ile Arg Cys Ile Asn Cys Gln
                485                 490                 495

Lys Pro Leu Cys Pro Glu Glu Lys Gln Arg His Leu Asp Lys Lys Gln
            500                 505                 510

Arg Phe His Asn Ile Arg Gly Arg Trp Thr Gly Arg Cys Met Ser Cys
        515                 520                 525

Cys Arg Ser Ser Arg Thr Arg Arg Glu Thr Gln Met His Gly Asp Thr
    530                 535                 540

Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln Pro Glu Thr Thr Asp
545                 550                 555                 560

Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser Glu Glu Glu Asp Glu
                565                 570                 575

Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp Arg Ala His Tyr Asn
            580                 585                 590
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Ile Val Thr Phe Cys Cys Gln Leu Cys Thr Glu Leu Gln Thr Thr Ile
        595                 600                 605

His Asp Ile Ile Leu Glu Cys Val Tyr Cys Lys Gln Gln Leu Leu Arg
    610                 615                 620

Arg Glu Val Tyr Asp Phe Ala Phe Arg Asp Leu Cys Ile Val Tyr Arg
625                 630                 635                 640

Asp Gly Asn Pro Tyr Ala Val Cys Asp Lys Cys Leu Lys Phe Tyr Ser
                645                 650                 655

Lys Ile Ser Glu Tyr Arg His Tyr Cys Tyr Ser Leu Tyr Gly Thr Thr
            660                 665                 670

Leu Glu Gln Gln Tyr Asn Lys Pro Leu Cys Asp Leu Leu Ile Arg Cys
        675                 680                 685

Ile Asn Cys Gln Lys
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<210> 4
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<212> DNA
<213> Artificial Sequence

<220>
<223> nt sequence encoding HPV16 E2E6E7SH designer polypeptide

<400> 4

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gccatctact acaaggccag agagatgggc ttcaagcaca tcaaccacca ggtggtgccc      180

accctggccg tgtccaagaa caaggccctg caggccatcg agctgcagct gaccctggaa      240

accatctaca acagccagta cagcaacgag aagtggaccc tgcaggacgt gtccctggaa      300

gtgtacctga ccgctcccac cggctgcatc aagaaacacg gctacaccgt ggaagtgcag      360

ttcgacggcg acatctgcaa caccatgcac tacaccaact ggacccacat ctacatctgc      420

gaagaggcca gcgtgaccgt ggtggaaggc caggtggact actacggcct gtactacgtg      480

cacgagggca tccggaccta cttcgtgcag ttcaaggacg acgccgagaa gtacagcaag      540

aacaaagtgt gggaggtgca cgctggcggc caggtcatcc tgtgccccac cagcgtgttc      600

agcagcaacg aggtgtccag ccccgagatc atccggcagc acctggccaa tcaccctgcc      660

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cccagaagcg agcccgacac cggcaatccc tgccacacca ccaagctgct gcaccgggac      780

agcgtggaca gcgcccctat cctgaccgcc ttcaacagca gccacaaggg ccggatcaac      840
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tggaccggcc acaacgtgaa gcacaagagc gccatcgtga ccctgaccta cgacagcgag 1020

tggcagcggg accagttcct gagccaggtc aaaatcccca agaccatcac cgtgtccacc 1080

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cccagaaagc tgccccagct gtgcaccgag ctgcagacca ccatccacga catcatcctg 1200

gaatgcgtgt actgcaagca gcagctggaa gatgagatcg acggccctgc tggccaggcc 1260

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cggctgtgcg tgcagagcac ccacgtggac atccggaccc tggaagatct gctgatgggc 1380

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cagctcctgc ggagagaggt gtacgacttc gccttccggg acctctgcat cgtgtatcgg 1920

gacggcaacc cctacgccgt gtgcgacaag tgcctgaagt tctacagcaa gatcagcgag 1980

taccggcact actgctacag cctgtacgga acaacactcg aacagcagta taacaaacca 2040

ctctgtgatc tgctgattcg ctgtatcaat tgtcagaagt gataa 2085

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<211> 693
<212> PRT
<213> Artificial Sequence

<220>
<223> HPV16 E6E7E2SH designer polypeptide

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Arg Lys Leu Pro Gln Leu Cys Thr Glu Leu Gln Thr Thr Ile His Asp
20 25 30

Ile Ile Leu Glu Cys Val Tyr Cys Lys Gln Gln Leu Glu Asp Glu Ile
35 40 45

```
Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp Arg Ala His Tyr Asn Ile
    50                  55                  60

Val Thr Phe Cys Cys Lys Cys Asp Ser Thr Leu Arg Leu Cys Val Gln
65                  70                  75                  80

Ser Thr His Val Asp Ile Arg Thr Leu Glu Asp Leu Leu Met Gly Thr
                85                  90                  95

Leu Gly Ile Val Cys Pro Ile Cys Ser Gln Lys Pro Gly Thr Thr Leu
            100                 105                 110

Glu Gln Gln Tyr Asn Lys Pro Leu Cys Asp Leu Leu Ile Arg Cys Ile
        115                 120                 125

Asn Cys Gln Lys Pro Leu Cys Pro Glu Glu Lys Gln Arg His Leu Asp
    130                 135                 140

Lys Lys Gln Arg Phe His Asn Ile Arg Gly Arg Trp Thr Gly Arg Cys
145                 150                 155                 160

Met Ser Cys Cys Arg Ser Ser Arg Thr Arg Arg Glu Thr Gln Met His
                165                 170                 175

Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln Pro Glu
            180                 185                 190

Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser Glu Glu
        195                 200                 205

Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp Arg Ala
    210                 215                 220

His Tyr Asn Ile Val Thr Phe Cys Cys Gln Leu Cys Thr Glu Leu Gln
225                 230                 235                 240

Thr Thr Ile His Asp Ile Ile Leu Glu Cys Val Tyr Cys Lys Gln Gln
                245                 250                 255

Leu Leu Arg Arg Glu Val Tyr Asp Phe Ala Phe Arg Asp Leu Cys Ile
            260                 265                 270

Val Tyr Arg Asp Gly Asn Pro Tyr Ala Val Cys Asp Lys Cys Leu Lys
        275                 280                 285

Phe Tyr Ser Lys Ile Ser Glu Tyr Arg His Tyr Cys Tyr Ser Leu Tyr
    290                 295                 300
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```
Gly Thr Thr Leu Glu Gln Gln Tyr Asn Lys Pro Leu Cys Asp Leu Leu
305                 310                 315                 320

Ile Arg Cys Ile Asn Cys Gln Lys Met Glu Thr Leu Cys Gln Arg Leu
                325                 330                 335

Asn Val Cys Gln Asp Lys Ile Leu Thr His Tyr Glu Asn Asp Ser Thr
            340                 345                 350

Asp Leu Arg Asp His Ile Asp Tyr Trp Lys His Met Arg Leu Glu Cys
        355                 360                 365

Ala Ile Tyr Tyr Lys Ala Arg Glu Met Gly Phe Lys His Ile Asn His
    370                 375                 380

Gln Val Val Pro Thr Leu Ala Val Ser Lys Asn Lys Ala Leu Gln Ala
385                 390                 395                 400

Ile Glu Leu Gln Leu Thr Leu Glu Thr Ile Tyr Asn Ser Gln Tyr Ser
                405                 410                 415

Asn Glu Lys Trp Thr Leu Gln Asp Val Ser Leu Glu Val Tyr Leu Thr
            420                 425                 430

Ala Pro Thr Gly Cys Ile Lys Lys His Gly Tyr Thr Val Glu Val Gln
        435                 440                 445

Phe Asp Gly Asp Ile Cys Asn Thr Met His Tyr Thr Asn Trp Thr His
    450                 455                 460

Ile Tyr Ile Cys Glu Glu Ala Ser Val Thr Val Val Glu Gly Gln Val
465                 470                 475                 480

Asp Tyr Tyr Gly Leu Tyr Tyr Val His Glu Gly Ile Arg Thr Tyr Phe
                485                 490                 495

Val Gln Phe Lys Asp Asp Ala Glu Lys Tyr Ser Lys Asn Lys Val Trp
            500                 505                 510

Glu Val His Ala Gly Gly Gln Val Ile Leu Cys Pro Thr Ser Val Phe
        515                 520                 525

Ser Ser Asn Glu Val Ser Ser Pro Glu Ile Ile Arg Gln His Leu Ala
    530                 535                 540

Asn His Pro Ala Ala Thr His Thr Lys Ala Val Ala Leu Gly Thr Glu
545                 550                 555                 560
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Glu Thr Gln Thr Thr Ile Gln Arg Pro Arg Ser Glu Pro Asp Thr Gly
                565                 570                 575

Asn Pro Cys His Thr Thr Lys Leu Leu His Arg Asp Ser Val Asp Ser
            580                 585                 590

Ala Pro Ile Leu Thr Ala Phe Asn Ser Ser His Lys Gly Arg Ile Asn
        595                 600                 605

Cys Asn Ser Asn Thr Thr Pro Ile Val His Leu Lys Val Asp Ala Asn
    610                 615                 620

Thr Leu Met Arg Leu Arg Tyr Arg Phe Lys Lys His Cys Thr Leu Tyr
625                 630                 635                 640

Thr Ala Val Ser Ser Thr Trp His Trp Thr Gly His Asn Val Lys His
                645                 650                 655

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

Gln Phe Leu Ser Gln Val Lys Ile Pro Lys Thr Ile Thr Val Ser Thr
        675                 680                 685

Gly Phe Met Ser Ile
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<210> 6
<211> 2085
<212> DNA
<213> Artificial Sequence

<220>
<223> nt sequence encoding HPV16 E6E7E2SH designer polypeptide

<400> 6

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cactacaata tcgtgacctt ctgctgcaag tgcgacagca ccctgcggct gtgcgtgcag      240

agcacccacg tggacatccg gaccctggaa gatctgctga tgggcaccct gggcatcgtg      300

tgccccatct gcagccagaa gcccggcacc accctggaac agcagtacaa caagcccctg      360

tgcgacctgc tgatccggtg catcaactgc cagaaacccc tgtgccccga ggaaaagcag      420

cggcacctgg acaagaagca gcggttccac aacatccggg gcagatggac aggcagatgc      480

atgagctgct gcagaagcag ccggaccaga cgggaaaccc agatgcacgg cgacaccccc      540
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cagctgaacg acagcagcga ggaagaggac gagattgacg gacccgctgg acaggccgag 660

cctgaccggg ctcactataa catcgtgaca ttttgctgtc agctctgtac tgaactccag 720

acaacaattc acgatattat tctcgaatgt gtgtattgta aacagcagct cctgcggaga 780

gaggtgtacg acttcgcctt ccgggacctc tgcatcgtgt atcgggacgg caacccctac 840

gccgtgtgcg acaagtgcct gaagttctac agcaagatca gcgagtaccg gcactactgc 900

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gaaacccaga ccaccatcca gcggcccaga agcgagcccg acaccggcaa tccctgccac 1740

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<210> 7
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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His Ser

<210> 8
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> nt sequence encoding IgE leader peptide

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<210> 9
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> HAVT20 leader peptide

<400> 9

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1 5 10 15

Glu Phe Ser Met Ala
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<210> 10
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> nt sequence encoding HAVT20 leader peptide

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gcc 63

<210> 11
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> 2xTetO-containing sequence

<400> 11
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<210> 12
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> 2xCuO-containing sequence

<400> 12
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<212> DNA
<213> Artificial Sequence

<220>
<223> CMV promoter

<400> 13
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aacattaccg ccatgttgac attgattatt gactagttat taatagtaat caattacggg 180

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caatgggagt ttgttttggc accaaaatca acgggacttt ccaaaatgtc gtaacaactc 660

cgccccattg acgcaaatgg gcggtaggcg tgtacggtgg gaggtctata taagcagagc 720

tcgtttagtg aaccgtcaga tcgcctggag acgccatcca cgctgttttg acctccatag 780

aagacaccgg gaccgatcca gcctccgcgg ccgggaacgg tgcattgga 829

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<211> 657
<212> DNA
<213> Artificial Sequence

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<223> nt sequence encoding TetR polypeptide

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ttgtattggc atgtaaaaaa taagcgggct ttgctcgacg ccttagccat tgagatgtta 180

gataggcacc atactcactt ttgcccttta gaaggggaaa gctggcaaga ttttttacgt 240

aataacgcta aaagttttag atgtgcttta ctaagtcatc gcgatggagc aaaagtacat 300

ttaggtacac ggcctacaga aaaacagtat gaaactctcg aaaatcaatt agccttttta 360

tgccaacaag gtttttcact agagaatgca ttatatgcac tcagcgctgt ggggcatttt 420

actttaggtt gcgtattgga agatcaagag catcaagtcg ctaaagaaga aagggaaaca 480

cctactactg atagtatgcc gccattatta cgacaagcta tcgaattatt tgatcaccaa 540

ggtgcagagc cagccttctt attcggcctt gaattgatca tatgcggatt agaaaaacaa 600

cttaaatgtg aaagtgggtc cgcgtacagc ggatcccggg aattcagatc ttattaa 657

<210> 15
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> TetR polypeptide

<400> 15

Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
1 5 10 15

Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
20 25 30

Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
35 40 45

Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
50 55 60

Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
65 70 75 80

Asn Asn Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly
85 90 95

Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
100 105 110

Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
115 120 125

Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
130 135 140

```
Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
145                 150                 155                 160

Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
                165                 170                 175

Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
            180                 185                 190

Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
        195                 200                 205

Tyr Ser Gly Ser Arg Glu Phe Arg Ser Tyr
    210                 215
```

<210> 16
<211> 612
<212> DNA
<213> Artificial Sequence

<220>
<223> nt sequence encoding CymR polypeptide

<400> 16
atgtctccca aacgacggac tcaagcggaa agggcaatgg aaactcaggg taagctgatt 60

gccgcggctc tgggagtgct gcgagagaaa gggtatgccg ggtttcgcat agccgacgtt 120

cctggagctg caggcgtaag cagaggagcc caatctcatc actttccgac caagctggag 180

cttttgctgg ctaccttcga atggctgtac gagcagatca cggaaaggag tcgtgctagg 240

ctggccaagc tgaaacccga ggatgatgtc attcagcaga tgctggacga tgcagccgag 300

ttcttcctgg acgacgactt cagcatcagt ctcgacctca tcgtagccgc agatcgcgat 360

ccagctttgc gcgagggcat acagagaaca gtcgagcgga atcggtttgt ggtggaggac 420

atgtggcttg gtgttctggt gagcagaggc ctctcacggg atgatgccga ggacatcctg 480

tggctgatct ttaactccgt cagagggttg gcagtgaggt ccctttggca gaaggacaaa 540

gaacggtttg aacgtgtgcg aaactcaaca ctcgagattg ctagggaacg ctacgccaag 600

ttcaagagat ga 612

<210> 17
<211> 203
<212> PRT
<213> Artificial Sequence

<220>
<223> CymR polypeptide

<400> 17

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

```
Gly Lys Leu Ile Ala Ala Ala Leu Gly Val Leu Arg Glu Lys Gly Tyr
            20                  25                  30

Ala Gly Phe Arg Ile Ala Asp Val Pro Gly Ala Ala Gly Val Ser Arg
        35                  40                  45

Gly Ala Gln Ser His His Phe Pro Thr Lys Leu Glu Leu Leu Leu Ala
    50                  55                  60

Thr Phe Glu Trp Leu Tyr Glu Gln Ile Thr Glu Arg Ser Arg Ala Arg
65                  70                  75                  80

Leu Ala Lys Leu Lys Pro Glu Asp Asp Val Ile Gln Gln Met Leu Asp
                85                  90                  95

Asp Ala Ala Glu Phe Phe Leu Asp Asp Asp Phe Ser Ile Ser Leu Asp
            100                 105                 110

Leu Ile Val Ala Ala Asp Arg Asp Pro Ala Leu Arg Glu Gly Ile Gln
        115                 120                 125

Arg Thr Val Glu Arg Asn Arg Phe Val Val Glu Asp Met Trp Leu Gly
    130                 135                 140

Val Leu Val Ser Arg Gly Leu Ser Arg Asp Asp Ala Glu Asp Ile Leu
145                 150                 155                 160

Trp Leu Ile Phe Asn Ser Val Arg Gly Leu Ala Val Arg Ser Leu Trp
                165                 170                 175

Gln Lys Asp Lys Glu Arg Phe Glu Arg Val Arg Asn Ser Thr Leu Glu
            180                 185                 190

Ile Ala Arg Glu Arg Tyr Ala Lys Phe Lys Arg
        195                 200


<210>  18
<211>  25
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HPV16 E6 aa41-65

<400>  18

Lys Gln Gln Leu Leu Arg Arg Glu Val Tyr Asp Phe Ala Phe Arg Asp
1               5                   10                  15
```

```
Leu Cys Ile Val Tyr Arg Asp Gly Asn
            20                  25


<210>  19
<211>  35
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HPV16 E7 aa43-77

<400>  19

Gly Gln Ala Glu Pro Asp Arg Ala His Tyr Asn Ile Val Thr Phe Cys
1               5                   10                  15


Cys Lys Cys Asp Ser Thr Leu Arg Leu Cys Val Gln Ser Thr His Val
            20                  25                  30


Asp Ile Arg
        35


<210>  20
<211>  331
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HPV18-E6E7SH designer polypeptide

<400>  20

Met Ala Arg Phe Glu Asp Pro Thr Arg Arg Pro Tyr Lys Leu Pro Asp
1               5                   10                  15


Leu Cys Thr Glu Leu Asn Thr Ser Leu Gln Asp Ile Glu Ile Thr Cys
            20                  25                  30


Val Tyr Cys Lys Thr Val Leu Asp Leu Leu Cys His Glu Gln Leu Ser
        35                  40                  45


Asp Ser Glu Glu Glu Asn Asp Glu Ile Asp Gly Val Asn His Gln His
    50                  55                  60


Leu Pro Ala Arg Arg Ala Glu Pro Gln Arg His Thr Met Leu Cys Met
65                  70                  75                  80


Cys Cys Lys Cys Glu Ala Arg Ile Glu Leu Val Val Glu Ser Ser Ala
                85                  90                  95


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

```
Val Cys Pro Trp Cys Ala Ser Gln His Tyr Ser Asp Ser Val Tyr Gly
        115                 120                 125

Asp Thr Leu Glu Lys Leu Thr Asn Thr Gly Leu Tyr Asn Leu Leu Ile
    130                 135                 140

Arg Cys Leu Arg Cys Gln Lys Pro Leu Asn Pro Ala Glu Lys Leu Arg
145                 150                 155                 160

His Leu Asn Glu Lys Arg Arg Phe His Asn Ile Ala Gly His Tyr Arg
                165                 170                 175

Gly Gln Cys His Ser Cys Cys Asn Arg Ala Arg Gln Glu Arg Leu Gln
            180                 185                 190

Arg Arg Arg Glu Thr Met His Gly Pro Lys Ala Thr Leu Gln Asp Ile
        195                 200                 205

Val Leu His Leu Glu Pro Gln Asn Glu Ile Pro Val Asp Leu Leu Cys
    210                 215                 220

His Glu Gln Leu Ser Asp Ser Glu Glu Glu Asn Asp Glu Ile Asp Gly
225                 230                 235                 240

Val Asn Pro Asp Leu Cys Thr Glu Leu Asn Thr Ser Leu Gln Asp Ile
                245                 250                 255

Glu Ile Thr Cys Val Tyr Cys Lys Thr Val Leu Glu Leu Thr Glu Val
            260                 265                 270

Phe Glu Phe Ala Phe Lys Asp Leu Phe Val Val Tyr Arg Asp Ser Ile
        275                 280                 285

Pro His Ala Ala Cys His Lys Cys Ile Asp Phe Tyr Ser Arg Ile Arg
    290                 295                 300

Glu Leu Arg His Tyr Ser Asp Ser Val Tyr Gly Asp Thr Leu Glu Lys
305                 310                 315                 320

Leu Thr Asn Thr Gly Leu Tyr Asn Leu Leu Ile
                325                 330
```

<210> 21
<211> 999
<212> DNA
<213> Artificial Sequence

<220>
<223> nt sequence of HPV18-E6E7SH designer sequence

<400> 21
atggccagat tcgaggaccc caccagacgg ccctacaagc tgcccgacct gtgcaccgag 60

ctgaacacat ctctgcagga catcgagatc acatgcgtgt actgcaagac cgtgctggac 120

ctgctgtgcc acgagcagct gtccgactcc gaggaagaaa acgacgagat cgacggcgtg 180

aaccatcagc atctgcccgc cagacgggcc gagccccaga gacacaccat gctgtgcatg 240

tgctgcaagt gcgaggcccg gattgagctg gtggtggaaa gcagcgccga cgacctgcgg 300

gccttccagc agctctttct gaataccctg agcttcgtgt gcccttggtg cgccagccag 360

cactacagcg actccgtgta cggcgatacc ctggaaaagc tgaccaatac cggcctgtat 420

aacctgctga tccggtgcct gcggtgccag aagcccctga atcccgccga gaaactgaga 480

cacctgaacg agaagcggcg gttccacaat atcgccggcc actacagagg ccagtgccac 540

agctgctgca accgggccag acaggaacgg ctgcagcgga ggcgggaaac catgcacgga 600

cccaaggcca ccctccagga cattgtcctg cacctggaac cccagaacga gatccccgtc 660

gatctgctgt gtcatgaaca gctcagcgac agcgaagagg aaaatgacga aattgacggg 720

gtcaaccctg acctctgtac cgaactcaat accagtctcc aggatatcga aattacctgt 780

gtctactgta aaaccgtcct cgagctgacc gaggtgttcg agttcgcctt caaggacctg 840

tttgtggtgt acagagacag catcccccac gccgcctgcc acaagtgcat cgacttctac 900

agccggatca gagagctgcg gcactactcc gattctgtgt atggcgacac actcgagaag 960

ctcacaaaca caggactgta caatctgctc atctgataa 999

<210> 22
<211> 696
<212> PRT
<213> Artificial Sequence

<220>
<223> HPV18-E2E6E7SH designer sequence

<400> 22

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

Asp Lys Ile Ile Asp His Tyr Glu Asn Asp Ser Lys Asp Ile Asp Ser
20 25 30

Gln Ile Gln Tyr Trp Gln Leu Ile Arg Trp Glu Asn Ala Ile Phe Phe
35 40 45

Ala Ala Arg Glu His Gly Ile Gln Thr Leu Asn His Gln Val Val Pro
50 55 60

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

```
Met Ala Leu Gln Gly Leu Ala Gln Ser Ala Tyr Lys Thr Glu Asp Trp
                85                  90                  95

Thr Leu Gln Asp Thr Cys Glu Glu Leu Trp Asn Thr Glu Pro Thr His
            100                 105                 110

Cys Phe Lys Lys Gly Gly Gln Thr Val Gln Val Tyr Phe Asp Gly Asn
        115                 120                 125

Lys Asp Asn Cys Met Thr Tyr Val Ala Trp Asp Ser Val Tyr Tyr Met
    130                 135                 140

Thr Asp Ala Gly Thr Trp Asp Lys Thr Ala Thr Cys Val Ser His Arg
145                 150                 155                 160

Gly Leu Tyr Tyr Val Lys Glu Gly Tyr Asn Thr Phe Tyr Ile Glu Phe
                165                 170                 175

Lys Ser Glu Cys Glu Lys Tyr Gly Asn Thr Gly Thr Trp Glu Val His
            180                 185                 190

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

Asp Asp Thr Val Ser Ala Thr Gln Leu Val Lys Gln Leu Gln His Thr
    210                 215                 220

Pro Ser Pro Tyr Ser Ser Thr Val Ser Val Gly Thr Ala Lys Thr Tyr
225                 230                 235                 240

Gly Gln Thr Ser Ala Ala Thr Arg Pro Gly His Cys Gly Leu Ala Glu
                245                 250                 255

Lys Gln His Cys Gly Pro Val Asn Pro Leu Leu Gly Ala Ala Thr Pro
            260                 265                 270

Thr Gly Asn Asn Lys Arg Arg Lys Leu Cys Ser Gly Asn Thr Thr Pro
        275                 280                 285

Ile Ile His Leu Lys Val Asp Arg Asn Ser Leu Met Arg Leu Arg Tyr
    290                 295                 300

Arg Leu Arg Lys His Ser Asp His Tyr Arg Asp Ile Ser Ser Thr Trp
305                 310                 315                 320

His Trp Thr Gly Ala Gly Asn Glu Lys Thr Gly Ile Leu Thr Val Thr
                325                 330                 335
```

```
Tyr His Ser Glu Thr Gln Arg Thr Lys Phe Leu Asn Thr Val Ala Ile
            340                 345                 350

Pro Asp Ser Val Gln Ile Leu Val Gly Tyr Met Thr Met Met Ala Arg
        355                 360                 365

Phe Glu Asp Pro Thr Arg Arg Pro Tyr Lys Leu Pro Asp Leu Cys Thr
    370                 375                 380

Glu Leu Asn Thr Ser Leu Gln Asp Ile Glu Ile Thr Cys Val Tyr Cys
385                 390                 395                 400

Lys Thr Val Leu Asp Leu Leu Cys His Glu Gln Leu Ser Asp Ser Glu
                405                 410                 415

Glu Glu Asn Asp Glu Ile Asp Gly Val Asn His Gln His Leu Pro Ala
            420                 425                 430

Arg Arg Ala Glu Pro Gln Arg His Thr Met Leu Cys Met Cys Cys Lys
        435                 440                 445

Cys Glu Ala Arg Ile Glu Leu Val Val Glu Ser Ser Ala Asp Asp Leu
    450                 455                 460

Arg Ala Phe Gln Gln Leu Phe Leu Asn Thr Leu Ser Phe Val Cys Pro
465                 470                 475                 480

Trp Cys Ala Ser Gln His Tyr Ser Asp Ser Val Tyr Gly Asp Thr Leu
                485                 490                 495

Glu Lys Leu Thr Asn Thr Gly Leu Tyr Asn Leu Leu Ile Arg Cys Leu
            500                 505                 510

Arg Cys Gln Lys Pro Leu Asn Pro Ala Glu Lys Leu Arg His Leu Asn
        515                 520                 525

Glu Lys Arg Arg Phe His Asn Ile Ala Gly His Tyr Arg Gly Gln Cys
    530                 535                 540

His Ser Cys Cys Asn Arg Ala Arg Gln Glu Arg Leu Gln Arg Arg Arg
545                 550                 555                 560

Glu Thr Met His Gly Pro Lys Ala Thr Leu Gln Asp Ile Val Leu His
                565                 570                 575

Leu Glu Pro Gln Asn Glu Ile Pro Val Asp Leu Leu Cys His Glu Gln
            580                 585                 590
```

```
Leu Ser Asp Ser Glu Glu Glu Asn Asp Glu Ile Asp Gly Val Asn Pro
        595                 600                 605

Asp Leu Cys Thr Glu Leu Asn Thr Ser Leu Gln Asp Ile Glu Ile Thr
    610                 615                 620

Cys Val Tyr Cys Lys Thr Val Leu Glu Leu Thr Glu Val Phe Glu Phe
625                 630                 635                 640

Ala Phe Lys Asp Leu Phe Val Val Tyr Arg Asp Ser Ile Pro His Ala
                645                 650                 655

Ala Cys His Lys Cys Ile Asp Phe Tyr Ser Arg Ile Arg Glu Leu Arg
            660                 665                 670

His Tyr Ser Asp Ser Val Tyr Gly Asp Thr Leu Glu Lys Leu Thr Asn
        675                 680                 685

Thr Gly Leu Tyr Asn Leu Leu Ile
    690                 695
```

<210> 23
<211> 2094
<212> DNA
<213> Artificial Sequence

<220>
<223> nt sequence of HPV18-E2E6E7SH designer sequence

<400> 23

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atgcagaccc ccaaagagac actgagcgag cggctgagcg ccctgcagga caagatcatc       60

gaccactacg agaacgacag caaggacatc gacagccaga tccagtactg gcagctgatc      120

agatgggaga acgccatctt cttcgccgcc agagagcacg gcatccagac cctgaaccac      180

caggtggtgc ccgcctacaa catcagcaag agcaaggccc acaaggctat cgagctgcag      240

atggccctgc agggactggc ccagagcgcc tacaagaccg aggactggac cctgcaggat      300

acctgcgagg aactgtggaa caccgagccc acccactgct tcaagaaagg cggccagacc      360

gtgcaggtgt acttcgacgg caacaaggac aactgcatga cctacgtggc ctgggacagc      420

gtgtactaca tgaccgacgc cggcacctgg gacaagaccg ccacctgtgt gtcccaccgg      480

ggcctgtact acgtgaaaga gggctacaac accttctaca tcgagttcaa gagcgagtgc      540

gagaagtacg gcaacaccgg cacatgggag gtgcacttcg gcaacaacgt gatcgactgc      600

aacgacagca tgtgcagcac cagcgacgac accgtgtccg ccacccagct ggtgaaacag      660

ctgcagcaca cccccagccc ctacagcagc accgtgtctg tgggcaccgc caagacctac      720

ggccagacca gcgccgccac cagacctgga cactgtggcc tggccgagaa gcagcactgc      780
```

ggccctgtga accctctgct gggagccgcc acccccaccg gcaacaacaa gcggagaaag 840

ctgtgcagcg gcaacaccac ccccatcatc cacctgaagg tggaccggaa cagcctgatg 900

cggctgcggt acagactgcg gaagcacagc gaccactacc gggacatcag cagcacctgg 960

cactggaccg gcgctggcaa cgagaaaacc ggcatcctga ccgtgaccta ccacagcgaa 1020

acccagcgga ccaagttcct gaacaccgtg gccatccccg acagcgtgca gatcctggtg 1080

ggatatatga ccatgatggc cagattcgag gaccccacca gacggcccta caagctgccc 1140

gacctgtgca ccgagctgaa cacatctctg caggacatcg agatcacatg cgtgtactgc 1200

aagaccgtgc tggacctgct gtgccacgag cagctgtccg actccgagga agaaaacgac 1260

gagatcgacg gcgtgaacca tcagcatctg cccgccagac gggccgagcc ccagagacac 1320

accatgctgt gcatgtgctg caagtgcgag gcccggattg agctggtggt ggaaagcagc 1380

gccgacgacc tgcgggcctt ccagcagctc tttctgaata ccctgagctt cgtgtgccct 1440

tggtgcgcca gccagcacta cagcgactcc gtgtacggcg ataccctgga aaagctgacc 1500

aataccggcc tgtataacct gctgatccgg tgcctgcggt gccagaagcc cctgaatccc 1560

gccgagaaac tgagacacct gaacgagaag cggcggttcc acaatatcgc cggccactac 1620

agaggccagt gccacagctg ctgcaaccgg gccagacagg aacggctgca gcggaggcgg 1680

gaaaccatgc acggacccaa ggccaccctc caggacattg tcctgcacct ggaaccccag 1740

aacgagatcc ccgtcgatct gctgtgtcat gaacagctca gcgacagcga agaggaaaat 1800

gacgaaattg acggggtcaa ccctgacctc tgtaccgaac tcaataccag tctccaggat 1860

atcgaaatta cctgtgtcta ctgtaaaacc gtcctcgagc tgaccgaggt gttcgagttc 1920

gccttcaagg acctgtttgt ggtgtacaga gacagcatcc cccacgccgc ctgccacaag 1980

tgcatcgact tctacagccg gatcagagag ctgcggcact actccgattc tgtgtatggc 2040

gacacactcg agaagctcac aaacacagga ctgtacaatc tgctcatctg ataa 2094

<210> 24
<211> 338
<212> PRT
<213> Artificial Sequence

<220>
<223> HPV18DS2 amino acid sequence

<400> 24

Met His Gly Pro Lys Ala Thr Leu Gln Asp Ile Val Leu His Leu Glu
1 5 10 15

Pro Gln Asn Glu Ile Pro Val Asp Leu Leu Cys His Glu Gln Leu Ser
20 25 30

```
Asp Ser Glu Glu Glu Asn Asp Glu Ile Asp Gly Val Asn His Gln His
        35                  40                  45

Leu Pro Ala Arg Arg Ala Glu Pro Gln Arg His Thr Ser Leu Gln Asp
    50                  55                  60

Ile Glu Ile Thr Cys Val Tyr Cys Lys Thr Val Leu Glu Leu Thr Glu
65                  70                  75                  80

Val Phe Glu Phe Ala Phe Lys Asp Leu Phe Val Val Tyr Arg Asp Ser
                85                  90                  95

Ile Pro His Ala Ala Cys His Lys Cys Ile Asp Phe Tyr Ser Arg Ile
            100                 105                 110

Arg Glu Leu Arg His Tyr Ser Asp Ser Val Tyr Gly Asp Thr Leu Glu
        115                 120                 125

Lys Leu Thr Asn Thr Gly Leu Tyr Asn Leu Leu Ile Arg Cys Leu Gln
    130                 135                 140

Arg Phe Glu Asp Pro Thr Arg Arg Pro Tyr Lys Leu Pro Asp Leu Cys
145                 150                 155                 160

Thr Glu Leu Asn Thr Ser Leu Gln Asp Ile Glu Ile Thr Cys Val Tyr
                165                 170                 175

Cys Lys Thr Val Leu Glu Leu Thr Glu Val Phe Glu Phe Ala Asp Ser
            180                 185                 190

Glu Glu Glu Asn Asp Glu Ile Asp Gly Val Asn His Gln His Leu Pro
        195                 200                 205

Ala Arg Arg Ala Glu Pro Gln Arg His Thr Met Leu Cys Met Cys Cys
    210                 215                 220

Lys Cys Glu Ala Arg Ile Glu Leu Val Val Glu Ser Ser Ala Asp Asp
225                 230                 235                 240

Leu Arg Ala Phe Gln Gln Leu Phe Leu Asn Thr Leu Ser Phe Val Cys
                245                 250                 255

Pro Trp Cys Ala Ser Gln Ser Asp Ser Val Tyr Gly Asp Thr Leu Glu
            260                 265                 270

Lys Leu Thr Asn Thr Gly Leu Tyr Asn Leu Leu Ile Arg Cys Leu Arg
        275                 280                 285
```

```
Cys Gln Lys Pro Leu Asn Pro Ala Glu Lys Leu Arg His Leu Asn Glu
    290                 295                 300

Lys Arg Arg Phe His Asn Ile Ala Gly His Tyr Arg Gly Gln Cys His
305                 310                 315                 320

Ser Cys Cys Asn Arg Ala Arg Gln Glu Arg Leu Gln Arg Arg Arg Glu
                325                 330                 335

Thr Gln
```