

SEQUENCE LISTING

<110> Crucell Holland B.V.
 Bavarian Nordic A/S
 BUNNIK, Evelien M
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 KHAN, Selina
 KALLA, Markus
 WEIDNER, Katrin

<120> Therapeutic HPV Vaccine Combinations

<130> 0269 US P00 PRO

<160> 33

<170> PatentIn version 3.5

<210> 1

<211> 328

<212> PRT

<213> Artificial Sequence

<220>

<223> HPV16-E6E7SH designer polypeptide

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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

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

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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<210> 2
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> nt sequence encoding HPV16-E6E7SH designer polypeptide

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<210> 3

<211> 693

<212> PRT

<213> Artificial Sequence

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<223> HPV16 E2E6E7SH designer polypeptide

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1           5           10          15

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Thr His Tyr Glu Asn Asp Ser Thr Asp Leu Arg Asp His Ile Asp Tyr
20          25          30

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

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

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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

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

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

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

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

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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

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

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
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Leu Glu Gln Gln Tyr Asn Lys Pro Leu Cys Asp Leu Leu Ile Arg Cys
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Ile Asn Cys Gln Lys
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<210> 4

<211> 2085



<212> DNA

<213> Artificial Sequence

<220>

<223> nt sequence encoding HPV16 E2E6E7SH designer polypeptide

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accatctaca acagccagta cagcaacgag aagtggaccc tgcaggacgt gtccctggaa	300
gtgtacctga ccgctcccac cggctgcatc aagaaacacg gctacaccgt ggaagtgcag	360
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taccggcact actgctacag cctgtacgga acaacactcg aacagcagta taacaaacca 2040
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<210> 5
<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

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

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

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<210> 7



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

<220>
<223> IgE leader peptide

<400> 7

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
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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

<400> 10
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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
aacaacaga caatctggc tgtttgta 28

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

<220>
<223> CMV promoter

<400> 13
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tcgtttagtg aaccgtcaga tcgcctggag acgccatcca cgctgttttg acctccatag 780
aagacaccgg gaccgatcca gcctccgagg ccgggaacgg tgcattgga 829

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<212> DNA
<213> Artificial Sequence

<220>
<223> nt sequence encoding TetR polypeptide

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ttgtattggc atgtaaaaa taagcgggct ttgtcgcac ccttagccat tgagatgtta 180



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ttaggtacac ggcttacaga aaaacagtat gaaactctcg aaaatcaatt agccttttta      360
tgccaacaag gtttttcact agagaatgca ttatatgcac tcagcgctgt ggggcatttt      420
actttaggtt gcgtattgga agatcaagag catcaagtcg ctaaagaaga aagggaacaa      480
cctactactg atagtatgcc gccattatta cgacaagcta tcgaattatt tgatcaccaa      540
ggtgcagagc cagccttctt attcggcctt gaattgatca tatgcggatt agaaaaacaa      600
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<210> 15

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> TetR polypeptide

<400> 15

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

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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
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 cctggagctg caggcgtaag cagaggagcc caatctcatc actttccgac caagctggag 180
 cttttgctgg ctaccttcga atggctgtac gagcagatca cggaaggag 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 cagaggggttg gcagttaggt ccccttggca 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 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
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ctgctgtgcc acgagcagct gtccgactcc gaggaagaaa acgacgagat cgacggcgtg 180
aaccatcagc atctgcccgc cagacggggc gagccccaga gacacacat gctgtgcatg 240
tgctgcaagt gcgaggcccc gattgagctg gtggtggaaa gcagcgccga cgacctgcgg 300
gccttcagc 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 gtcataaaca gtcagcgac agcgaagagg aaaatgacga aattgacggg 720
gtcaaccctg acctctgtac cgaactcaat accagtctcc aggatatcga aattacctgt 780



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gtctactgta aaaccgtcct cgagctgacc gaggtgttcg agttcgcctt caaggacctg      840
tttgtggtgt acagagacag catccccac gccgcctgcc acaagtgcac cgacttctac      900
agccggatca gagagctgcg gcactactcc gattctgtgt atggcgacac actcgagaag      960
ctcacaaca caggactgta caatctgctc atctgataa                               999

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

 <220>
 <223> HPV18-E2E6E7SH designer sequence

 <400> 22

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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

```

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

```

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

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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 encoding HPV18-E2E6E7SH designer sequence

<400> 23

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60



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cagggtggtgc ccgctacaa 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
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aacgacagca tgtgcagcac cagcgacgac accgtgtccg ccaccagct ggtgaaacag	660
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ggccagacca gcgccgccac cagacctgga cactgtggcc tggccgagaa gcagcactgc	780
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ctgtgcagcg gcaacaccac ccccatcatc cacctgaagg tggaccggaa cagcctgatg	900
cggctgcggt acagactgcg gaagcacagc gaccactacc gggacatcag cagcacctgg	960
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aagaccgtgc tggacctgtg gtgccacgag cagctgtccg actccgagga agaaaacgac	1260
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gccgacgacc tgcgggcctt ccagcagctc tttctgaata ccctgagctt cgtgtgccct	1440
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aataccggcc tgtataacct gctgatccgg tgcctgcggt gccagaagcc cctgaatccc	1560
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gaaacatgc acggacccaa ggccaccctc caggacattg tcctgcacct ggaaccccag	1740
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gacgaaattg acggggtcaa ccctgacctc tgtaccgaac tcaataccag tctccaggat	1860
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tgcatcgact tctacagccg gatcagagag ctgcggcact actccgattc tgtgtatggc	2040
gacacactcg agaagctcac aaacacagga ctgtacaatc tgctcatctg ataa	2094



<210> 24
<211> 2085
<212> DNA
<213> Artificial Sequence

<220>

<223> nt sequence encoding HPV16 E2E6E7SH designer polypeptide

<400> 24

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gctatctatt ataaggctcg cgaaatgggt ttcaaacata tcaatcatca ggctgtccct      180
accctcgccg tcagcaaaaa caaagctctg caggctattg aactccagct caccctcgag      240
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cacgaaggga tcagaacata ctttgtccag tttaaggatg atgctgagaa gtattctaag      540
aacaaagttt gggaaagtcca tgccgggtgga caagtgattc tgtgtcctac ctccgtgttc      600
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gctacacata ccaaggctgt ggctctggga acagaagaga cacagacaac aatccagagg      720
cctcggagcg agcctgatac aggcaaccct tgtcacacaa caaaactgct gcacagagac      780
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<210> 25
 <211> 2094
 <212> DNA
 <213> Artificial Sequence

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

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caagtgggtcc cagcctacaa tatctccaag tccaaagccc acaaagctat cgaactccaa 240
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gtctactata tgacagatgc tgggacgtgg gataagacag ccacatgcgt cagccacaga 480
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ctccagcata caccatctcc ctactcctcc actgtgtccg tgggaacagc caaacatat 720
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agactgagat accggctgag aaagcactcc gatcactaca gagatatcag ctctacttgg 960
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gccgacgatc tgagagcttt tcagcaactg tttctcaaca ccctgtcctt tgtctgtcct 1440
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aacacgggac tgtataatct gtcacatccgc tgtctgagat gccagaaacc tctgaatcct      1560
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cgaggccagt gtcactcctg ctgtaacaga gctcggcaag agagactgca gagaaggcgc      1680
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tgtatcgatt tttactctcg catcagagaa ctgcggcact actctgactc agtgtatggc      2040
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<210> 26
 <211> 124
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PrMVA Promoter

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<400> 26
taaaaataga aactataatc atataatagt gtaggttggt agtattgctc ttgtgactag      60
agactttagt taaggctactg taaaataga aactataatc atataatagt gtaggttggt      120
agta          124

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<210> 27
 <211> 227
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PrHyb Promoter

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<400> 27
gttttgaaaa tttttttata ataaatatcc ggtaaaaatt gaaaaactat tctaatttat      60
tgcacgggcc ggtaaaaatt gaaaaactat tctaatttat tgcacgggcc ggtaaaaatt      120
gaaaaactat tctaatttat tgcacgggcc ggtaaaaatt gaaaaactat tctaatttat      180
tgcacgggcc ggtaaaaatt gaaaaactat tctaatttat tgcacggg          227

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<210> 28
 <211> 365
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HPV 16 E2 fragment

<400> 28

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Met Glu Thr Leu Cys Gln Arg Leu Asn Val Cys Gln Asp Lys Ile Leu
1           5           10          15

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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

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

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
355 360 365

<210> 29
<211> 1095
<212> DNA
<213> Artificial Sequence

<220>
<223> nt sequence encoding HPV 16 E2 fragment

<400> 29
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aacgacagca ccgacctgcg ggaccacatc gactactgga agcacatgcg gctggaatgc 120
gccatctact acaaggccag agagatgggc ttcaagcaca tcaaccacca ggtggtgccc 180
accctggcgg tgtccaagaa caaggccctg caggccatcg agctgcagct gaccctggaa 240
accatctaca acagccagta cagcaacgag aagtggaccc tgcaggacgt gtccctggaa 300
gtgtacctga ccgctccac cggtgcac aagaaacacg gctacaccgt ggaagtgcag 360
ttcgacggcg acatctgcaa caccatgcac tacaccaact ggaccacat ctacatctgc 420
gaagaggcca gcgtgaccgt ggtggaaggc caggtggact actacggcct gtactacgtg 480
cacgagggca tccggaccta cttcgtgcag ttcaaggacg acgccgagaa gtacagcaag 540
aacaagtgt gggagggtgca cgctggcggc caggtcatcc tgtgccccac cagcgtgttc 600
agcagcaacg aggtgtccag ccccgagatc atccggcagc acctggccaa tcaccctgcc 660
gccaccacaa caaaggccgt ggccctgggc accgaggaaa ccagaccac catccagcgg 720
cccagaagcg agcccgacac cggcaatccc tgccacacca ccaagctgct gcaccgggac 780
agcgtggaca gcgcccctat cctgaccgcc ttcaacagca gccacaaggc ccgatcaac 840
tgcaacagca acaccacccc catcgtgcac ctgaaggtgg acgccaacac cctgatgcgg 900
ctgcgggtaca gattcaagaa gactgcacc ctgtacaccg ccgtgtcctc cacctggcac 960
tggaccggcc acaacgtgaa gcacaagagc gccatcgtga ccctgaccta cgacagcgag 1020
tggcagcggg accagttcct gagccaggtc aaaatcccca agaccatcac cgtgtccacc 1080
ggcttcatga gcatc 1095

<210> 30



<211> 1095
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence encoding HPV 16 E2 fragment

<400> 30
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 gctatctatt ataaggctcg cgaaatgggt ttcaaacata tcaatcatca ggctgtccct 180
 accctcgccg tcagcaaaaa caaagctctg caggctattg aactccagct caccctcgag 240
 acaatctaca attcccagta ctccaatgag aaatggacgc tccaggatgt gtctctcgag 300
 gtctacctga cagctctac aggatgtatt aagaacacg ggtacacggt ggaagtccag 360
 tttgatggcg atatatgtaa taccatgcat tatacgaatt ggacgcatat ctatatttgt 420
 gaagaggcct ctgtgacagt ggtcgaggga caggctgact attatgggct gtattatgtg 480
 cacgaaggga tcagaacata ctttgtccag tttaaggatg atgctgagaa gtattctaag 540
 aacaaagttt gggaagtcca tgccgggtgga caagtgattc tgtgtcctac ctccgtgttc 600
 agctctaag aggtgtcctc tccagagatc attagacagc atctggccaa ccatcctgct 660
 gctacacata ccaaggctgt ggctctggga acagaagaga cacagacaac aatccagagg 720
 cctcggagcg agcctgatac aggcaaccct tgtcacacaa caaaactgct gcacagagac 780
 tccgtggact ccgctcctat tctgacagcc tttaactcct cccacaaagg gagaatcaat 840
 tgcaattcca ataccagcc gatcgccac ctcaaagtgg atgctaatac tctcatgcgg 900
 ctccgctacc gcttcaagaa aactgtaca ctgtatacag ctgtgtccag cacatggcat 960
 tggacgggac acaatgtgaa acataagtcc gccatcgta cgctcacata cgattccgag 1020
 tggcagagag atcagtttct gtcccaagtc aagattccga aaacgatcac cgtcagcacc 1080
 ggctttatgt ctatt 1095

<210> 31
 <211> 365
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HPV 18 E2 fragment

<400> 31

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
 355 360 365

<210> 32
 <211> 1095
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence encoding HPV 18 E2 fragment

<400> 32
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 gaccactacg agaacgacag caaggacatc gacagccaga tccagtactg gcagctgatc 120
 agatggggaga acgccatctt cttcgccgcc agagagcacg gcatccagac cctgaaccac 180
 caggtggtgc cgcctacaa 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
 ggccctgtact acgtgaaaga gggctacaac accttctaca tcgagttcaa gagcgagtgc 540
 gagaagtacg gcaacaccgg cacatgggag gtgcacttcg gcaacaacgt gatcgactgc 600
 aacgacagca tgtgcagcac cagcgacgac accgtgtccg ccaccagct 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 ggcacacctga ccgtgaccta ccacagcgaa 1020
 acccagcgga ccaagttcct gaacaccgtg gccatccccg acagcgtgca gatcctggtg 1080
 ggatatatga ccatg 1095

<210> 33
 <211> 1095
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence encoding HPV 18 E2 fragment

<400> 33
 atgcagacgc cgaaagaaac cctgtccgag agactgagcg ctctccaaga taagattatt 60



gatcactatg agaatgactc caaggacatt gattcccaga ttcagtattg gcaacttatt	120
cgctgggaaa atgccatctt ctttgccgct cggaacacg ggattcagac actgaatcat	180
caagtgggcc cagcctacaa tatctccaag tccaaagccc acaaagctat cgaactcaa	240
atggctctcc agggactggc tcagtccgct tataagacag aagattggac actccaggac	300
acgtgtgaag aactctggaa taccgaaccg acgcactgtt ttaagaaggg tggacagaca	360
gttcaagtct actttgatgg gaacaaagat aattgcatga catatgtcgc ttgggattcc	420
gtctactata tgacagatgc tgggacgtgg gataagacag ccacatgcgt cagccacaga	480
gggctgtact atgtcaaaga aggggtataat acgttctata tcgagtttaa gtctgaatgc	540
gagaaatatg ggaatacggg aacctgggaa gtgcattttg ggaacaatgt catcgattgc	600
aatgactcca tgtgctccac ctccgatgac acagtcagcg ccacacagct cgtgaaacag	660
ctccagcata caccatctcc ctactcctcc actgtgtccg tgggaacagc caaacatat	720
ggacagacct ccgctgccac acggcctggc cattgcggac tggccgagaa acagcattgt	780
ggaccagtca accctctgct gggagctgct actccaacag ggaacaacaa gaggcggaaa	840
ctgtgttccg gcaatacgac acctatcatt cacctcaagg tcgacagaaa ctccctgatg	900
agactgagat accggctgag aaagcactcc gatcactaca gagatatcag ctctacttgg	960
cattggacag gtgctggaaa cgaaaagaca gggatcctga cagtgcgta tcactccgag	1020
actcagcgca ccaaatttct caatactgtg gccattcccg attccgtgca gattcttgtc	1080
ggatatatga cgatg	1095

