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PETIT, Robert

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cgagaaagct atataaaggc gctgacagct tcgtttaatt tagaacgtac atttattcaa 6840

gaaactctaa acaaattggc agaacgcccc aaaacggacc cacaactcga tttgtttagc 6900

tacgatacag gctgaaaata aaacccgcac tatgccatta catttatatc tatgatacgt 6960

gtttgttttt ctttgctggc tagcttaatt gcttatattt acctgcaata aaggatttct 7020

tacttccatt atactcccat tttccaaaaa catacgggga acacgggaac ttattgtaca 7080

ggccacctca tagttaatgg tttcgagcct tcctgcaatc tcatccatgg aaatatattc 7140

atccccctgc cggcctatta atgtgacttt tgtgcccggc ggatattcct gatccagctc 7200

caccataaat tggtccatgc aaattcggcc ggcaattttc aggcgttttc ccttcacaag 7260

gatgtcggtc cctttcaatt ttcggagcca gccgtccgca tagcctacag gcaccgtccc 7320

gatccatgtg tctttttccg ctgtgtactc ggctccgtag ctgacgctct cgccttttct 7380

gatcagtttg acatgtgaca gtgtcgaatg cagggtaaat gccggacgca gctgaaacgg 7440

tatctcgtcc gacatgtcag cagacgggcg aaggccatac atgccgatgc cgaatctgac 7500

tgcattaaaa aagccttttt tcagccggag tccagcggcg ctgttcgcgc agtggaccat 7560

tagattcttt aacggcagcg gagcaatcag ctctttaaag cgctcaaact gcattaagaa 7620

atagcctctt tctttttcat ccgctgtcgc aaaatgggta aataccccct tgcactttaa 7680

acgagggttg cggtcaagaa ttgccatcac gttctgaact tcttcctctg tttttacacc 7740

aagtctgttc atccccgtat cgaccttcag atgaaaatga agagaacctt ttttcgtgtg 7800

gcgggctgcc tcctgaagcc attcaacaga ataacctgtt aaggtcacgt catactcagc 7860

agcgattgcc acatactccg ggggaaccgc gccaagcacc aatataggcg ccttcaatcc 7920

ctttttgcgc agtgaaatcg cttcatccaa aatggccacg gccaagcatg aagcacctgc 7980

gtcaagagca gcctttgctg tttctgcatc accatgcccg taggcgtttg ctttcacaac 8040

tgccatcaag tggacatgtt caccgatatg ttttttcata ttgctgacat tttcctttat 8100

cacggacaag tcaatttccg cccacgtatc tctgtaaaaa ggttttgtgc tcatggaaaa 8160

ctcctctctt ttttcagaaa atcccagtac gtaattaagt atttgagaat taattttata 8220

ttgattaata ctaagtttac ccagttttca cctaaaaaac aaatgatgag ataatagctc 8280

caaaggctaa agaggactat accaactatt tgttaat 8317

<210> 3

<211> 306
<212> DNA
<213> Human papillomavirus type 16

<400> 3
ctcgagcatg gagatacacc tacattgcat gaatatatgt tagatttgca accagagaca 60

actgatctct actgttatga gcaattaaat gacagctcag aggaggagga tgaaatagat 120

ggtccagctg gacaagcaga accggacaga gcccattaca atattgtaac cttttgttgc 180

aagtgtgact ctacgcttcg gttgtgcgta caaagcacac acgtagacat tcgtactttg 240

gaagacctgt taatgggcac actaggaatt gtgtgcccca tctgttctca gaaaccataa 300

actagt 306

<210> 4
<211> 1297
<212> DNA
<213> Artificial Sequence

<220>
<223> chimeric Her2-neu

<400> 4
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ctgtgtcacc agctgcaccg tggatgtcag gcagatgccc agaaggcggg agacatatgg 120

ggagcccaca ccagccatca cgtatgcttc gtctaagatt tctttgttgg ctttggggga 180

tgtgttttcc ctcaacactt tgatggccac tggaattttc acattctccc catcagggat 240

ccagatgccc ttgtagactg tgccaaaagc gccagatcca agcaccttca ccttcctcag 300

ctccgtctct ttcaggatcc gcatctgcgc ctggttgggc atcgctccgc taggtgtcag 360

cggctccacc agctccgttt cctgcagcag tctccgcatc gtgtacttcc ggatcttctg 420

ctgccctcgg gcgcacagct ggtggcaggc caggccctcg cccacacact cgtcctctgg 480

ccggttggca gtgtggagca gagcttggtg cgggttccga aagagctggt cccagggcac 540

cgtgtgcacg aagcagaggt gggtgttatg gtggatgagg gccagtccac tgcccagttc 600

cctcagtgag cgcagcccca gccagctgat gcccagccct tgcagggtca gcgagtaggc 660

gccattgtgc agaattcgtc cccggattac ttgcaggttc tggaagacgc tgaggtcagg 720

caggctgtcc ggccatgctg agatgtatag gtaacctgtg atctcttcca gagtctcaaa 780

cacttggagc tgctctggct ggagcggggc agtgttggag gctgggtccc catcaaagct 840

ctccggcaga aatgccaggc tcccaaagat cttcttgcag ccagcaaact cctggatatt 900

cttccacaaa atcgtgtcct ggtagcagag ctgggggttc cgctggatca agacccctcc 960

tttcaagatc tctgtgaggc ttcgaagctg cagctcccgc aggcctcctg gggaggcccc 1020

tgtgacaggg gtggtattgt tcagcgggtc tccattgtct agcacggcca gggcatagtt 1080

gtcctcaaag agctgggtgc ctcgcacaat ccgcagcctc tgcagtggga cctgcctcac 1140

ttggttgtga gcgatgagca cgtagccctg cacctcctgg atatcctgca ggaaggacag 1200

gctggcattg gtgggcaggt aggtgagttc caggtttccc tgcaccacct ggcagccctg 1260

gtagaggtgg cggagcatgt ccaggtgggt tctagat 1297

<210> 5
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> Listeriolysin-O

<400> 5
atgaaaaaaa taatgctagt ttttattaca cttatattag ttagtctacc aattgcgcaa 60

caaactgaag caaaggatgc atctgcattc aataaagaaa attcaatttc atccatggca 120

ccaccagcat ctccgcctgc aagtcctaag acgccaatcg aaaagaaaca cgcggatgaa 180

atcgataagt atatacaagg attggattac aataaaaaca atgtattagt ataccacgga 240

gatgcagtga caaatgtgcc gccaagaaaa ggttacaaag atggaaatga atatattgtt 300

gtggagaaaa agaagaaatc catcaatcaa aataatgcag acattcaagt tgtgaatgca 360

atttcgagcc taacctatcc aggtgctctc gtaaaagcga attcggaatt agtagaaaat 420

caaccagatg ttctccctgt aaaacgtgat tcattaacac tcagcattga tttgccaggt 480

atgactaatc aagacaataa aatagttgta aaaaatgcca ctaaatcaaa cgttaacaac 540

gcagtaaata cattagtgga aagatggaat gaaaaatatg ctcaagctta tccaaatgta 600

agtgcaaaaa ttgattatga tgacgaaatg gcttacagtg aatcacaatt aattgcgaaa 660

tttggtacag catttaaagc tgtaaataat agcttgaatg taaacttcgg cgcaatcagt 720

gaagggaaaa tgcaagaaga agtcattagt tttaaacaaa tttactataa cgtgaatgtt 780

aatgaaccta caagaccttc cagatttttc ggcaaagctg ttactaaaga gcagttgcaa 840

gcgcttggag tgaatgcaga aaatcctcct gcatatatct caagtgtggc gtatggccgt 900

caagtttatt tgaaattatc aactaattcc catagtacta aagtaaaagc tgcttttgat 960

gctgccgtaa gcggaaaatc tgtctcaggt gatgtagaac taacaaatat catcaaaaat 1020

tcttccttca aagccgtaat ttacggaggt tccgcaaaag atgaagttca aatcatcgac 1080

ggcaacctcg gagacttacg cgatattttg aaaaaaggcg ctacttttaa tcgagaaaca 1140

ccaggagttc ccattgctta tacaacaaac ttcctaaaag acaatgaatt agctgttatt 1200

aaaaacaact cagaatatat tgaaacaact tcaaaagctt atacagatgg aaaaattaac 1260

atcgatcact ctggaggata cgttgctcaa ttcaacattt cttgggatga agtaaattat 1320

gatctcgag 1329

<210> 6
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> Listeriolysin-O

<400> 6

```
Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1               5                  10                  15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
            20                  25                  30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
        35                  40                  45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Glu Ile Asp Lys Tyr
    50                  55                  60

Ile Gln Gly Leu Asp Tyr Asn Lys Asn Asn Val Leu Val Tyr His Gly
65                  70                  75                  80

Asp Ala Val Thr Asn Val Pro Pro Arg Lys Gly Tyr Lys Asp Gly Asn
                85                  90                  95

Glu Tyr Ile Val Val Glu Lys Lys Lys Lys Ser Ile Asn Gln Asn Asn
            100                 105                 110

Ala Asp Ile Gln Val Val Asn Ala Ile Ser Ser Leu Thr Tyr Pro Gly
        115                 120                 125

Ala Leu Val Lys Ala Asn Ser Glu Leu Val Glu Asn Gln Pro Asp Val
    130                 135                 140

Leu Pro Val Lys Arg Asp Ser Leu Thr Leu Ser Ile Asp Leu Pro Gly
145                 150                 155                 160

Met Thr Asn Gln Asp Asn Lys Ile Val Val Lys Asn Ala Thr Lys Ser
                165                 170                 175

Asn Val Asn Asn Ala Val Asn Thr Leu Val Glu Arg Trp Asn Glu Lys
            180                 185                 190

Tyr Ala Gln Ala Tyr Pro Asn Val Ser Ala Lys Ile Asp Tyr Asp Asp
        195                 200                 205

Glu Met Ala Tyr Ser Glu Ser Gln Leu Ile Ala Lys Phe Gly Thr Ala
    210                 215                 220

Phe Lys Ala Val Asn Asn Ser Leu Asn Val Asn Phe Gly Ala Ile Ser
225                 230                 235                 240

Glu Gly Lys Met Gln Glu Glu Val Ile Ser Phe Lys Gln Ile Tyr Tyr
                245                 250                 255

Asn Val Asn Val Asn Glu Pro Thr Arg Pro Ser Arg Phe Phe Gly Lys
            260                 265                 270
```

```
Ala Val Thr Lys Glu Gln Leu Gln Ala Leu Gly Val Asn Ala Glu Asn
        275                 280                 285

Pro Pro Ala Tyr Ile Ser Ser Val Ala Tyr Gly Arg Gln Val Tyr Leu
    290                 295                 300

Lys Leu Ser Thr Asn Ser His Ser Thr Lys Val Lys Ala Ala Phe Asp
305                 310                 315                 320

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

Ile Ile Lys Asn Ser Ser Phe Lys Ala Val Ile Tyr Gly Gly Ser Ala
            340                 345                 350

Lys Asp Glu Val Gln Ile Ile Asp Gly Asn Leu Gly Asp Leu Arg Asp
        355                 360                 365

Ile Leu Lys Lys Gly Ala Thr Phe Asn Arg Glu Thr Pro Gly Val Pro
    370                 375                 380

Ile Ala Tyr Thr Thr Asn Phe Leu Lys Asp Asn Glu Leu Ala Val Ile
385                 390                 395                 400

Lys Asn Asn Ser Glu Tyr Ile Glu Thr Thr Ser Lys Ala Tyr Thr Asp
                405                 410                 415

Gly Lys Ile Asn Ile Asp His Ser Gly Gly Tyr Val Ala Gln Phe Asn
            420                 425                 430

Ile Ser Trp Asp Glu Val Asn Tyr Asp Leu
        435                 440


<210>  7
<211>  390
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  actA

<400>  7

Met Arg Ala Met Met Val Val Phe Ile Thr Ala Asn Cys Ile Thr Ile
1               5                   10                  15

Asn Pro Asp Ile Ile Phe Ala Ala Thr Asp Ser Glu Asp Ser Ser Leu
            20                  25                  30

Asn Thr Asp Glu Trp Glu Glu Glu Lys Thr Glu Glu Gln Pro Ser Glu
        35                  40                  45
```

```
Val Asn Thr Gly Pro Arg Tyr Glu Thr Ala Arg Glu Val Ser Ser Arg
    50                  55                  60

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

Ala Asp Leu Ile Ala Met Leu Lys Glu Lys Ala Glu Lys Gly Pro Asn
                85                  90                  95

Ile Asn Asn Asn Asn Ser Glu Gln Thr Glu Asn Ala Ala Ile Asn Glu
            100                 105                 110

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

Pro Gly Leu Pro Ser Asp Ser Ala Ala Glu Ile Lys Lys Arg Arg Lys
    130                 135                 140

Ala Ile Ala Ser Ser Asp Ser Glu Leu Glu Ser Leu Thr Tyr Pro Asp
145                 150                 155                 160

Lys Pro Thr Lys Val Asn Lys Lys Lys Val Ala Lys Glu Ser Val Ala
                165                 170                 175

Asp Ala Ser Glu Ser Asp Leu Asp Ser Ser Met Gln Ser Ala Asp Glu
            180                 185                 190

Ser Ser Pro Gln Pro Leu Lys Ala Asn Gln Gln Pro Phe Phe Pro Lys
        195                 200                 205

Val Phe Lys Lys Ile Lys Asp Ala Gly Lys Trp Val Arg Asp Lys Ile
    210                 215                 220

Asp Glu Asn Pro Glu Val Lys Lys Ala Ile Val Asp Lys Ser Ala Gly
225                 230                 235                 240

Leu Ile Asp Gln Leu Leu Thr Lys Lys Lys Ser Glu Glu Val Asn Ala
                245                 250                 255

Ser Asp Phe Pro Pro Pro Pro Thr Asp Glu Glu Leu Arg Leu Ala Leu
            260                 265                 270

Pro Glu Thr Pro Met Leu Leu Gly Phe Asn Ala Pro Ala Thr Ser Glu
        275                 280                 285

Pro Ser Ser Phe Glu Phe Pro Pro Pro Pro Thr Asp Glu Glu Leu Arg
    290                 295                 300

Leu Ala Leu Pro Glu Thr Pro Met Leu Leu Gly Phe Asn Ala Pro Ala
305                 310                 315                 320
```

```
Thr Ser Glu Pro Ser Ser Phe Glu Phe Pro Pro Pro Thr Glu Asp
                325                 330                 335

Glu Leu Glu Ile Ile Arg Glu Thr Ala Ser Ser Leu Asp Ser Ser Phe
            340                 345                 350

Thr Arg Gly Asp Leu Ala Ser Leu Arg Asn Ala Ile Asn Arg His Ser
        355                 360                 365

Gln Asn Phe Ser Asp Phe Pro Pro Ile Pro Thr Glu Glu Glu Leu Asn
    370                 375                 380

Gly Arg Gly Gly Arg Pro
385                 390


<210>  8
<211>  1170
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  actA

<400>  8

Ala Thr Gly Cys Gly Thr Gly Cys Gly Ala Thr Gly Ala Thr Gly Gly
1               5                   10                  15

Thr Gly Gly Thr Thr Thr Thr Cys Ala Thr Thr Ala Cys Thr Gly Cys
            20                  25                  30

Cys Ala Ala Thr Thr Gly Cys Ala Thr Thr Ala Cys Gly Ala Thr Thr
        35                  40                  45

Ala Ala Cys Cys Cys Cys Gly Ala Cys Ala Thr Ala Ala Thr Ala Thr
    50                  55                  60

Thr Thr Gly Cys Ala Gly Cys Gly Ala Cys Ala Gly Ala Thr Ala Gly
65                  70                  75                  80

Cys Gly Ala Ala Gly Ala Thr Thr Cys Thr Ala Gly Thr Cys Thr Ala
                85                  90                  95

Ala Ala Cys Ala Cys Ala Gly Ala Thr Gly Ala Ala Thr Gly Gly Gly
            100                 105                 110

Ala Ala Gly Ala Ala Gly Ala Ala Ala Ala Ala Ala Cys Ala Gly Ala
        115                 120                 125

Ala Gly Ala Gly Cys Ala Ala Cys Cys Ala Ala Gly Cys Gly Ala Gly
    130                 135                 140

Gly Thr Ala Ala Ala Thr Ala Cys Gly Gly Gly Ala Cys Cys Ala Ala
145                 150                 155                 160
```

```
Gly Ala Thr Ala Cys Gly Ala Ala Ala Cys Thr Gly Cys Ala Cys Gly
                165                 170                 175

Thr Gly Ala Ala Gly Thr Ala Ala Gly Thr Thr Cys Ala Cys Gly Thr
            180                 185                 190

Gly Ala Thr Ala Thr Thr Ala Ala Ala Gly Ala Ala Cys Thr Ala Gly
        195                 200                 205

Ala Ala Ala Ala Ala Thr Cys Gly Ala Ala Thr Ala Ala Ala Gly Thr
    210                 215                 220

Gly Ala Gly Ala Ala Ala Thr Ala Cys Gly Ala Ala Cys Ala Ala Ala
225                 230                 235                 240

Gly Cys Ala Gly Ala Cys Cys Thr Ala Ala Thr Ala Gly Cys Ala Ala
                245                 250                 255

Thr Gly Thr Thr Gly Ala Ala Ala Gly Ala Ala Ala Ala Ala Gly Cys
            260                 265                 270

Ala Gly Ala Ala Ala Ala Ala Gly Gly Thr Cys Cys Ala Ala Ala Thr
        275                 280                 285

Ala Thr Cys Ala Ala Thr Ala Ala Thr Ala Ala Cys Ala Ala Cys Ala
    290                 295                 300

Gly Thr Gly Ala Ala Cys Ala Ala Ala Cys Thr Gly Ala Gly Ala Ala
305                 310                 315                 320

Thr Gly Cys Gly Gly Cys Thr Ala Thr Ala Ala Ala Thr Gly Ala Ala
                325                 330                 335

Gly Ala Gly Gly Cys Thr Thr Cys Ala Gly Gly Ala Gly Cys Cys Gly
            340                 345                 350

Ala Cys Cys Gly Ala Cys Cys Ala Gly Cys Thr Ala Thr Ala Cys Ala
        355                 360                 365

Ala Gly Thr Gly Gly Ala Gly Cys Gly Thr Cys Gly Thr Cys Ala Thr
    370                 375                 380

Cys Cys Ala Gly Gly Ala Thr Thr Gly Cys Cys Ala Thr Cys Gly Gly
385                 390                 395                 400

Ala Thr Ala Gly Cys Gly Cys Ala Gly Cys Gly Gly Ala Ala Ala Thr
                405                 410                 415

Thr Ala Ala Ala Ala Ala Ala Ala Gly Ala Ala Gly Gly Ala Ala Ala
            420                 425                 430
```

Gly Cys Cys Ala Thr Ala Gly Cys Ala Thr Cys Ala Thr Cys Gly Gly
435 440 445

Ala Thr Ala Gly Thr Gly Ala Gly Cys Thr Thr Gly Ala Ala Ala Gly
450 455 460

Cys Cys Thr Thr Ala Cys Thr Thr Ala Thr Cys Cys Gly Gly Ala Thr
465 470 475 480

Ala Ala Ala Cys Cys Ala Ala Cys Ala Ala Ala Ala Gly Thr Ala Ala
485 490 495

Ala Thr Ala Ala Gly Ala Ala Ala Ala Ala Ala Gly Thr Gly Gly Cys
500 505 510

Gly Ala Ala Ala Gly Ala Gly Thr Cys Ala Gly Thr Thr Gly Cys Gly
515 520 525

Gly Ala Thr Gly Cys Thr Thr Cys Thr Gly Ala Ala Ala Gly Thr Gly
530 535 540

Ala Cys Thr Thr Ala Gly Ala Thr Thr Cys Thr Ala Gly Cys Ala Thr
545 550 555 560

Gly Cys Ala Gly Thr Cys Ala Gly Cys Ala Gly Ala Thr Gly Ala Gly
565 570 575

Thr Cys Thr Thr Cys Ala Cys Cys Ala Cys Ala Ala Cys Cys Thr Thr
580 585 590

Thr Ala Ala Ala Ala Gly Cys Ala Ala Ala Cys Cys Ala Ala Cys Ala
595 600 605

Ala Cys Cys Ala Thr Thr Thr Thr Thr Cys Cys Cys Thr Ala Ala Ala
610 615 620

Gly Thr Ala Thr Thr Thr Ala Ala Ala Ala Ala Ala Ala Thr Ala Ala
625 630 635 640

Ala Ala Gly Ala Thr Gly Cys Gly Gly Gly Gly Ala Ala Ala Thr Gly
645 650 655

Gly Gly Thr Ala Cys Gly Thr Gly Ala Thr Ala Ala Ala Ala Thr Cys
660 665 670

Gly Ala Cys Gly Ala Ala Ala Ala Thr Cys Cys Thr Gly Ala Ala Gly
675 680 685

Thr Ala Ala Ala Gly Ala Ala Ala Gly Cys Gly Ala Thr Thr Gly Thr
690 695 700

```
Thr Gly Ala Thr Ala Ala Ala Ala Gly Thr Gly Cys Ala Gly Gly Gly
705                 710                 715                 720

Thr Thr Ala Ala Thr Thr Gly Ala Cys Cys Ala Ala Thr Thr Ala Thr
                725                 730                 735

Thr Ala Ala Cys Cys Ala Ala Ala Ala Ala Gly Ala Ala Ala Ala Gly
            740                 745                 750

Thr Gly Ala Ala Gly Ala Gly Gly Thr Ala Ala Ala Thr Gly Cys Thr
        755                 760                 765

Thr Cys Gly Gly Ala Cys Thr Thr Cys Cys Cys Gly Cys Cys Ala Cys
    770                 775                 780

Cys Ala Cys Cys Thr Ala Cys Gly Gly Ala Thr Gly Ala Ala Gly Ala
785                 790                 795                 800

Gly Thr Thr Ala Ala Gly Ala Cys Thr Thr Gly Cys Thr Thr Thr Gly
                805                 810                 815

Cys Cys Ala Gly Ala Gly Ala Cys Ala Cys Cys Ala Ala Thr Gly Cys
            820                 825                 830

Thr Thr Cys Thr Thr Gly Gly Thr Thr Thr Thr Ala Ala Thr Gly Cys
        835                 840                 845

Thr Cys Cys Thr Gly Cys Thr Ala Cys Ala Thr Cys Ala Gly Ala Ala
    850                 855                 860

Cys Cys Gly Ala Gly Cys Thr Cys Ala Thr Thr Cys Gly Ala Ala Thr
865                 870                 875                 880

Thr Thr Cys Cys Ala Cys Cys Ala Cys Cys Ala Cys Cys Thr Ala Cys
                885                 890                 895

Gly Gly Ala Thr Gly Ala Ala Gly Ala Gly Thr Thr Ala Ala Gly Ala
            900                 905                 910

Cys Thr Thr Gly Cys Thr Thr Thr Gly Cys Cys Ala Gly Ala Gly Ala
        915                 920                 925

Cys Gly Cys Cys Ala Ala Thr Gly Cys Thr Thr Cys Thr Thr Gly Gly
    930                 935                 940

Thr Thr Thr Thr Ala Ala Thr Gly Cys Thr Cys Cys Thr Gly Cys Thr
945                 950                 955                 960

Ala Cys Ala Thr Cys Gly Gly Ala Ala Cys Cys Gly Ala Gly Cys Thr
                965                 970                 975
```

```
Cys Gly Thr Thr Cys Gly Ala Ala Thr Thr Thr Cys Cys Ala Cys Cys
            980                 985                 990

Gly Cys Cys Thr Cys Cys Ala Ala  Cys Ala Gly Ala Ala  Gly Ala Thr
        995                 1000                1005

Gly Ala  Ala Cys Thr Ala Gly  Ala Ala Ala Thr Cys  Ala Thr Cys
    1010                1015                1020

Cys Gly  Gly Gly Ala Ala Ala  Cys Ala Gly Cys Ala  Thr Cys Cys
    1025                1030                1035

Thr Cys  Gly Cys Thr Ala Gly  Ala Thr Thr Cys Thr  Ala Gly Thr
    1040                1045                1050

Thr Thr  Thr Ala Cys Ala Ala  Gly Ala Gly Gly Gly  Gly Ala Thr
    1055                1060                1065

Thr Thr  Ala Gly Cys Thr Ala  Gly Thr Thr Thr Gly  Ala Gly Ala
    1070                1075                1080

Ala Ala  Thr Gly Cys Thr Ala  Thr Thr Ala Ala Thr  Cys Gly Cys
    1085                1090                1095

Cys Ala  Thr Ala Gly Thr Cys  Ala Ala Ala Ala Thr  Thr Thr Cys
    1100                1105                1110

Thr Cys  Thr Gly Ala Thr Thr  Thr Cys Cys Cys Ala  Cys Cys Ala
    1115                1120                1125

Ala Thr  Cys Cys Cys Ala Ala  Cys Ala Gly Ala Ala  Gly Ala Ala
    1130                1135                1140

Gly Ala  Gly Thr Thr Gly Ala  Ala Cys Gly Gly Gly  Ala Gly Ala
    1145                1150                1155

Gly Gly  Cys Gly Gly Thr Ala  Gly Ala Cys Cys Ala
    1160                1165                1170
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<210> 9
<211> 669
<212> DNA
<213> Artificial Sequence

<220>
<223> actA

<400> 9
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ttttgattt gcttttaaag gttgtggtgt agactcgtct gctgactgca tgctagaatc 120

taagtcactt tcagaagcat ccacaactga ctctttcgcc acttttctct tatttgcttt 180

tgttggttta tctggataag taaggctttc aagctcacta tccgacgacg ctatggcttt 240

tcttcttttt ttaatttccg ctgcgctatc cgatgacaga cctggatgac gacgctccac 300

ttgcagagtt ggtcggtcga ctcctgaagc ctcttcattt atagccacat ttcctgtttg 360

ctcaccgttg ttattattgt tattcggacc tttctctgct tttgctttca acattgctat 420

taggtctgct ttgttcgtat ttttcacttt attcgatttt tctagttcct caatatcacg 480

tgaacttact tcacgtgcag tttcgtatct tggtcccgta tttacctcgc ttggctgctc 540

ttctgttttt tcttcttccc attcatctgt gtttagactg gaatcttcgc tatctgtcgc 600

tgcaaatatt atgtcggggt taatcgtaat gcagttggca gtaatgaaaa ctaccatcat 660

cgcacgcat 669

<210> 10
<211> 390
<212> PRT
<213> Artificial Sequence

<220>
<223> actA

<400> 10

Met Arg Ala Met Met Val Val Phe Ile Thr Ala Asn Cys Ile Thr Ile
1 5 10 15

Asn Pro Asp Ile Ile Phe Ala Ala Thr Asp Ser Glu Asp Ser Ser Leu
20 25 30

Asn Thr Asp Glu Trp Glu Glu Glu Lys Thr Glu Glu Gln Pro Ser Glu
35 40 45

Val Asn Thr Gly Pro Arg Tyr Glu Thr Ala Arg Glu Val Ser Ser Arg
50 55 60

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

Ala Asp Leu Ile Ala Met Leu Lys Glu Lys Ala Glu Lys Gly Pro Asn
85 90 95

Ile Asn Asn Asn Asn Ser Glu Gln Thr Glu Asn Ala Ala Ile Asn Glu
100 105 110

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

Pro Gly Leu Pro Ser Asp Ser Ala Ala Glu Ile Lys Lys Arg Arg Lys
130 135 140

Ala Ile Ala Ser Ser Asp Ser Glu Leu Glu Ser Leu Thr Tyr Pro Asp
145 150 155 160

```
Lys Pro Thr Lys Val Asn Lys Lys Lys Val Ala Lys Glu Ser Val Ala
                165                 170                 175

Asp Ala Ser Glu Ser Asp Leu Asp Ser Ser Met Gln Ser Ala Asp Glu
            180                 185                 190

Ser Ser Pro Gln Pro Leu Lys Ala Asn Gln Gln Pro Phe Phe Pro Lys
        195                 200                 205

Val Phe Lys Lys Ile Lys Asp Ala Gly Lys Trp Val Arg Asp Lys Ile
    210                 215                 220

Asp Glu Asn Pro Glu Val Lys Lys Ala Ile Val Asp Lys Ser Ala Gly
225                 230                 235                 240

Leu Ile Asp Gln Leu Leu Thr Lys Lys Lys Ser Glu Glu Val Asn Ala
                245                 250                 255

Ser Asp Phe Pro Pro Pro Pro Thr Asp Glu Glu Leu Arg Leu Ala Leu
            260                 265                 270

Pro Glu Thr Pro Met Leu Leu Gly Phe Asn Ala Pro Ala Thr Ser Glu
        275                 280                 285

Pro Ser Ser Phe Glu Phe Pro Pro Pro Pro Thr Asp Glu Glu Leu Arg
    290                 295                 300

Leu Ala Leu Pro Glu Thr Pro Met Leu Leu Gly Phe Asn Ala Pro Ala
305                 310                 315                 320

Thr Ser Glu Pro Ser Ser Phe Glu Phe Pro Pro Pro Pro Thr Glu Asp
                325                 330                 335

Glu Leu Glu Ile Ile Arg Glu Thr Ala Ser Ser Leu Asp Ser Ser Phe
            340                 345                 350

Thr Arg Gly Asp Leu Ala Ser Leu Arg Asn Ala Ile Asn Arg His Ser
        355                 360                 365

Gln Asn Phe Ser Asp Phe Pro Pro Ile Pro Thr Glu Glu Glu Leu Asn
    370                 375                 380

Gly Arg Gly Gly Arg Pro
385                 390
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<210> 11
<211> 1170
<212> DNA
<213> Artificial Sequence

<220>

<223> actA

<400> 11

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atatttgcag cgacagatag cgaagattct agtctaaaca cagatgaatg ggaagaagaa 120

aaaacagaag agcaaccaag cgaggtaaat acgggaccaa gatacgaaac tgcacgtgaa 180

gtaagttcac gtgatattaa agaactagaa aaatcgaata aagtgagaaa tacgaacaaa 240

gcagacctaa tagcaatgtt gaaagaaaaa gcagaaaaag gtccaaatat caataataac 300

aacagtgaac aaactgagaa tgcggctata aatgaagagg cttcaggagc cgaccgacca 360

gctatacaag tggagcgtcg tcatccagga ttgccatcgg atagcgcagc ggaaattaaa 420

aaaagaagga aagccatagc atcatcggat agtgagcttg aaagccttac ttatccggat 480

aaaccaacaa aagtaaataa gaaaaaagtg gcgaaagagt cagttgcgga tgcttctgaa 540

agtgacttag attctagcat gcagtcagca gatgagtctt caccacaacc tttaaaagca 600

aaccaacaac catttttccc taaagtattt aaaaaaataa aagatgcggg gaaatgggta 660

cgtgataaaa tcgacgaaaa tcctgaagta aagaaagcga ttgttgataa aagtgcaggg 720

ttaattgacc aattattaac caaaaagaaa agtgaagagg taaatgcttc ggacttcccg 780

ccaccaccta cggatgaaga gttaagactt gctttgccag agacaccaat gcttcttggt 840

tttaatgctc ctgctacatc agaaccgagc tcattcgaat ttccaccacc acctacggat 900

gaagagttaa gacttgcttt gccagagacg ccaatgcttc ttggttttaa tgctcctgct 960

acatcggaac cgagctcgtt cgaatttcca ccgcctccaa cagaagatga actagaaatc 1020

atccgggaaa cagcatcctc gctagattct agttttacaa gaggggattt agctagtttg 1080

agaaatgcta ttaatcgcca tagtcaaaat ttctctgatt tcccaccaat cccaacagaa 1140

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<210> 12
<211> 32
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<213> Listeria monocytogenes

<400> 12

Lys Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala
1 5 10 15

Ser Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Glu Ile Asp Lys
20 25 30

<210> 13
<211> 19
<212> PRT
<213> Listeria monocytogenes

<400> 13

Lys Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala
1 5 10 15

Ser Pro Lys

<210> 14
<211> 14
<212> PRT
<213> Listeria monocytogenes

<400> 14

Lys Thr Glu Glu Gln Pro Ser Glu Val Asn Thr Gly Pro Arg
1 5 10

<210> 15
<211> 28
<212> PRT
<213> Listeria monocytogenes

<400> 15

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

Gln Ser Ala Asp Glu Ser Thr Pro Gln Pro Leu Lys
20 25

<210> 16
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<212> PRT
<213> Listeria monocytogenes

<400> 16

Lys Asn Glu Glu Val Asn Ala Ser Asp Phe Pro Pro Pro Pro Thr Asp
1 5 10 15

Glu Glu Leu Arg
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<210> 17
<211> 33
<212> PRT
<213> Listeria monocytogenes

<400> 17

Arg Gly Gly Ile Pro Thr Ser Glu Glu Phe Ser Ser Leu Asn Ser Gly
1 5 10 15

Asp Phe Thr Asp Asp Glu Asn Ser Glu Thr Thr Glu Glu Glu Ile Asp
20 25 30

Arg

<210> 18
<211> 28

<212> PRT
<213> Listeria monocytogenes

<400> 18

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

Gln Ser Ala Asp Glu Ser Thr Pro Gln Pro Leu Lys
20 25

<210> 19
<211> 20
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<213> Listeria monocytogenes

<400> 19

Lys Ser Glu Glu Val Asn Ala Ser Asp Phe Pro Pro Pro Pro Thr Asp
1 5 10 15

Glu Glu Leu Arg
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<210> 20
<211> 33
<212> PRT
<213> Listeria monocytogenes

<400> 20

Arg Gly Gly Arg Pro Thr Ser Glu Glu Phe Ser Ser Leu Asn Ser Gly
1 5 10 15

Asp Phe Thr Asp Asp Glu Asn Ser Glu Thr Thr Glu Glu Glu Ile Asp
20 25 30

Arg

<210> 21
<211> 19
<212> PRT
<213> Listeria monocytogenes

<400> 21

Arg Ser Glu Val Thr Ile Ser Pro Ala Glu Thr Pro Glu Ser Pro Pro
1 5 10 15

Ala Thr Pro

<210> 22
<211> 17
<212> PRT
<213> Streptococcus pyogenes

<400> 22

Lys Gln Asn Thr Ala Ser Thr Glu Thr Thr Thr Asn Glu Gln Pro
1 5 10 15

Lys

<210> 23
<211> 17
<212> PRT
<213> Streptococcus equisimilis

<400> 23

Lys Gln Asn Thr Ala Asn Thr Glu Thr Thr Thr Asn Glu Gln Pro
1 5 10 15

Lys

<210> 24
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> E7 primer sequence

<400> 24
ggctcgagca tggagataca cc 22

<210> 25
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> E7 primer sequence

<400> 25
ggggactagt ttatggtttc tgagaaca 28

<210> 26
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> hly promoter and gene fragment F primer

<400> 26
gggggctagc cctcctttga ttagtatatt c 31

<210> 27
<211> 28
<212> DNA
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<220>
<223> hly promoter and gene fragment R primer

<400> 27
ctccctcgag atcataattt acttcatc 28

<210> 28
<211> 55
<212> DNA
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<220>
<223> prfA gene amplification F primer

<400> 28
gactacaagg acgatgaccg acaagtgata acccgggatc taaataaatc cgttt 55

<210> 29
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<400> 29
cccgtcgacc agctcttctt ggtgaag 27

<210> 30
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<220>
<223> E7 F primer sequence

<400> 30
gcggatccca tggagataca cctac 25

<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> E7 R primer sequence

<400> 31
gctctagatt atggtttctg ag 22

<210> 32
<211> 9
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<213> Artificial Sequence

<220>
<223> (PE)-conjugated E7 peptide

<400> 32

Arg Ala His Tyr Asn Ile Val Thr Phe
1 5

<210> 33
<211> 31

<212> DNA
<213> Artificial Sequence

<220>
<223> hly promoter and gene fragment F primer

<400> 33
ggggtctaga cctcctttga ttagtatatt c 31

<210> 34
<211> 45
<212> DNA
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<220>
<223> hly promoter and gene fragment R primer

<400> 34
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<210> 35
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> ActA gene amplification F primer

<400> 35
gcgcaacaaa ctgaagcagc ggccgcggcg acagatagcg aagat 45

<210> 36
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> ActA gene amplification R primer

<400> 36
tgtaggtgta tctccatgct cgagagctag gcgatcaatt tc 42

<210> 37
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> E7 F primer sequence

<400> 37
ggaattgatc gcctagctct cgagcatgga gatacaccta ca 42

<210> 38
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> E7 R primer sequence

<400> 38
aaacggattt atttagatcc cgggttatgg tttctgagaa ca 42

<210> 39
<211> 42
<212> DNA
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<220>
<223> prfA gene amplification F primer

<400> 39
tgttctcaga aaccataacc cgggatctaa ataaatccgt tt 42

<210> 40
<211> 28
<212> DNA
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<220>
<223> prfA gene amplification R primer

<400> 40
gggggtcgac cagctcttct tggtgaag 28

<210> 41
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> dal gene forward primer

<400> 41
ccatggtgac aggctggcat c 21

<210> 42
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> dal gene reverse primer

<400> 42
gctagcctaa tggatgtatt ttctagg 27

<210> 43
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> minimal p60 promoter sequence forward primer

<400> 43
ttaattaaca aatagttggt atagtcc 27

<210> 44
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> minimal p60 promoter sequence forward primer

<400> 44
gacgatgcca gcctgtcacc atggaaaact cctctc 36

<210> 45
<211> 156
<212> DNA
<213> Artificial Sequence

<220>
<223> truncated p60 promoter

<400> 45
caaatagttg gtatagtcct ctttagcctt tggagtatta tctcatcatt tgttttttag 60

gtgaaaactg ggtaaactta gtattatcaa tataaaatta attctcaaat acttaattac 120

gtactgggat tttctgaaaa aagagaggag ttttcc 156

<210> 46
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oriRep forward primer

<400> 46
ggcgccacta actcaacgct agtag 25

<210> 47
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> oriRep reverse primer

<400> 47
gctagccagc aaagaaaaac aaacacg 27

<210> 48
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> oriRep forward primer

<400> 48
gtcgacggtc accggcgcca ctaactcaac gctagtag 38

<210> 49
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> oriRep reverse primer

<400> 49
ttaattaagc tagccagcaa agaaaaacaa acacg 35

<210> 50
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> LLO-E7 gene forward amplification primer

<400> 50
atgaaaaaaa taatgctagt ttttattac 29

<210> 51
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> LLO-E7 gene reverse amplification primer

<400> 51
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<210> 52
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Taqman primer-probe sets

<400> 52
gcaagtgtga ctctacgctt cg 22

<210> 53
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Taqman primer-probe sets

<400> 53
tgcccattaa caggtcttcc a 21

<210> 54
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Taqman primer-probe sets

<400> 54
tgcgtacaaa gcacacacgt agacattcgt ac 32

<210> 55
<211> 24
<212> DNA
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<220>

<223> Taqman primer-probe sets

<400> 55
tgacatcgtt tgtgtttgag ctag 24

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Taqman primer-probe sets

<400> 56
gcagcgctct ctataccagg tac 23

<210> 57
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Taqman primer-probe sets

<400> 57
ttaatgtcca tgttatgtct ccgttatagc tcatcgta 38

<210> 58
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer to verify deletion of ActA

<400> 58
tgggatggcc aagaaattc 19

<210> 59
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer to verify deletion of ActA

<400> 59
ctaccatgtc ttccgttgct tg 22

<210> 60
<211> 1256
<212> DNA
<213> Artificial Sequence

<220>
<223> Lm-dd actA

<400> 60
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ataagaagca ttaaagatcc tgacaaatat aatcaagcgg ctcatatgaa agattacgaa 120

tcgcttccac tcacagagga aggcgactgg ggcggagttc attataatag tggtatcccg 180

aataaagcag cctataatac tatcactaaa cttggaaaag aaaaaacaga acagctttat 240

tttcgcgcct taaagtacta tttaacgaaa aaatcccagt ttaccgatgc gaaaaaagcg 300

cttcaacaag cagcgaaaga tttatatggt gaagatgctt ctaaaaaagt tgctgaagct 360

tgggaagcag ttggggttaa ctgattaaca aatgttagag aaaaattaat tctccaagtg 420

atattcttaa aataattcat gaatattttt tcttatatta gctaattaag aagataacta 480

actgctaatc caatttttaa cggaacaaat tagtgaaaat gaaggccgaa ttttccttgt 540

tctaaaaagg ttgtattagc gtatcacgag gagggagtat aagtgggatt aaacagattt 600

atgcgtgcga tgatggtggt tttcattact gccaattgca ttacgattaa ccccgacgtc 660

gacccatacg acgttaattc ttgcaatgtt agctattggc gtgttctctt taggggcgtt 720

tatcaaaatt attcaattaa gaaaaaataa ttaaaaacac agaacgaaag aaaaagtgag 780

gtgaatgata tgaaattcaa aaaggtggtt ctaggtatgt gcttgatcgc aagtgttcta 840

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gctccgcatg atattgacag caaattacca cataaactta gttggtccgc ggataacccg 960

acaaatactg acgtaaatac gcactattgg ctttttaaac aagcggaaaa aatactagct 1020

aaagatgtaa atcatatgcg agctaattta atgaatgaac ttaaaaaatt cgataaacaa 1080

atagctcaag gaatatatga tgcggatcat aaaaatccat attatgatac tagtacattt 1140

ttatctcatt tttataatcc tgatagagat aatacttatt tgccgggttt tgctaatgcg 1200

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<210> 61
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Her-2-Chimera (F) primer

<400> 61
tgatctcgag acccacctgg acatgctc 28

<210> 62
<211> 49
<212> DNA
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<220>
<223> HerEC1-EC2F primer

<400> 62
ctaccaggac acgattttgt ggaagaatat ccaggagttt gctggctgc 49

<210> 63
<211> 49
<212> DNA
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<223> HerEC1-EC2R primer

<400> 63
gcagccagca aactcctgga tattcttcca caaaatcgtg tcctggtag 49

<210> 64
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<212> DNA
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<223> HerEC2-ICIF primer

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ctgccaccag ctgtgcgccc gagggcagca gaagatccgg aagtacacga 50

<210> 65
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<210> 66
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<223> Her-2-Chimera (R) primer

<400> 66
gtggcccggg tctagattag tctaagaggc agccatagg 39

<210> 67
<211> 28
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<400> 67
ccgcctcgag gccgcgagca cccaagtg 28

<210> 68
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<212> DNA
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<400> 68
cgcgactagt ttaatcctct gctgtcacct c 31

<210> 69
<211> 28

<212> DNA
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<400> 69
ccgcctcgag tacctttcta cggacgtg 28

<210> 70
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<212> DNA
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<400> 70
cgcgactagt ttactctggc cggttggcag 30

<210> 71
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<400> 71
ccgcctcgag cagcagaaga tccggaagta c 31

<210> 72
<211> 30
<212> DNA
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<220>
<223> Her-2-IC1(R) primer

<400> 72
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<210> 73
<211> 7075
<212> DNA
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<220>
<223> pAdv164 sequence

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tggcaggaga aaaaaggctg caccggtgcg tcagcagaat atgtgataca ggatatattc 120

cgcttcctcg ctcactgact cgctacgctc ggtcgttcga ctgcggcgag cggaaatggc 180

ttacgaacgg ggcggagatt tcctggaaga tgccaggaag atacttaaca gggaagtgag 240

agggccgcgg caaagccgtt tttccatagg ctccgccccc ctgacaagca tcacgaaatc 300

tgacgctcaa atcagtggtg gcgaaacccg acaggactat aaagatacca ggcgtttccc 360

cctggcggct ccctcgtgcg ctctcctgtt cctgcctttc ggtttaccgg tgtcattccg 420

ctgttatggc cgcgtttgtc tcattccacg cctgacactc agttccgggt aggcagttcg 480

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taactatcgt cttgagtcca acccggaaag acatgcaaaa gcaccactgg cagcagccac 600

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atcactacca agccaggtaa aagtaaaggg gctatttttg cgtatcgctc aaaaaaaagc 4320

atgattggcg gacgtggcgt tgttctgact tccgaagaag cgattcacga aaatcaagat 4380

acatttacgc attggacacc aaacgtttat cgttatggta cgtatgcaga cgaaaaccgt 4440

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tttgatattc acacggaaaa agaaactatt tcagcaagcg atattttaac aacagctatt 4560
gatttaggtt ttatgcctac gttaattatc aaatctgata aaggttatca agcatatttt 4620
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gacattttcc tttatcgcgg acaagtcaat ttccgcccac gtatctctgt aaaaaggttt 6900

tgtgctcatg gaaaactcct ctcttttttc agaaaatccc agtacgtaat taagtatttg 6960

agaattaatt ttatattgat taatactaag tttacccagt tttcacctaa aaaacaaatg 7020

atgagataat agctccaaag gctaaagagg actataccaa ctatttgtta attaa 7075

<210> 74
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A2 restricted epitopes

<400> 74

His Leu Tyr Gln Gly Cys Gln Val Val
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<210> 75
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A2 restricted epitopes

<400> 75

Lys Ile Phe Gly Ser Leu Ala Phe Leu
1 5

<210> 76
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A2 restricted epitopes

<400> 76

Arg Leu Leu Gln Glu Thr Glu Leu Val
1 5

<210> 77
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> forward amplification primer actA promoter region

<400> 77
atcccgggtg aagcttggga agcagttggg 30

<210> 78
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse amplification primer actA promoter region

<400> 78
attctagatt tatcacgtac ccatttcccc gc 32

<210> 79
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> chimera Her2/neu amplification F primer

<400> 79
attctagaac ccacctggac atgctccgcc ac 32

<210> 80
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> chimera Her2/neu amplification R primer

<400> 80
gtcgacacta gtctagtggt gatggtgatg atggagctca gatctgtcta agaggcagcc 60

atagggc 67

<210> 81
<211> 2015
<212> DNA
<213> Listeria monocytogenes

<400> 81
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gtacaataaa gttaacttca ttagacaaaa agaaaaaaca aggaagaata gtacatagtt 120

ataaatactt ggagagtgag gtgtaatatg ggggcagctg atttttgggg tttcatatat 180

gtagtttcaa gattagccat tgttgcggca gtagtttact tcttatactt attgagaaaa 240

attgcaaata aatagaaaaa aagccttgtc aaacgaggct ttttttatgc aaaaaatacg 300

acgaatgaag ccatgtgaga caatttggaa tagcagacaa caaggaaggt agaacatgtt 360

ttgaaaaatt tactgatttt cgattattat taacgcttgt taatttaaac atctcttatt 420

tttgctaaca tataagtata caaagggaca taaaaaggtt aacagcgttt gttaaatagg 480

aagtatatga aaatcctctt ttgtgtttct aaatttattt ttaaggagtg gagaatgttg 540

aaaaaaaata attggttaca aaatgcagta atagcaatgc tagtgttaat tgtaggtctg 600

tgcattaata tgggttctgg aacaaaagta caagctgaga gtattcaacg accaacgcct 660

attaaccaag tttttccaga tcccggccta gcgaatgcag tgaaacaaaa tttagggaag 720

caaagtgtta cagaccttgt atcacaaaag gaactatctg gagtacaaaa tttcaatgga 780

gataatagca acattcaatc tcttgcggga atgcaatttt tcactaattt aaaagaactt 840

catctatccc ataatcaaat aagtgacctt agtcctttaa aggatctaac taagttagaa 900

gagctatctg tgaatagaaa cagactgaaa aatttaaacg gaattccaag tgcttgttta 960

tctcgcttgt ttttagataa caacgaactc agagatactg actcgcttat tcatttgaaa 1020

aatctagaaa tcttatctat tcgtaataat aagttaaaaa gtattgtgat gcttggtttt 1080

ttatcaaaac tagaggtatt agatttgcat ggtaatgaaa taacaaatac aggtggacta 1140

actagattga agaaagttaa ctggatagat ttaactggtc agaaatgtgt gaatgaacca 1200

gtaaaatacc aaccagaatt gtatataaca aatactgtca aagacccaga tggaagatgg 1260

atatctccat attacatcag taatggtggg agttatgtag atggttgtgt cctgtgggaa 1320

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actgaggcta tatttgatgg aacagttaca caacctatca agaattagga cttgtgcaca 1440

cctgtatact ttgagctctc gtataatcac gagagctttt taaatatgta agtcttaatt 1500

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tatttacaat tcaccttgac accaaaaact ccatatgata tagtaaataa ggttattaaa 1620

caagaaagaa gaagcaaccc gcttctcgcc tcgttaacac gaacgttttc aggcaaaaaa 1680

ttcaaacttt cgtcgcgtag cttacgcgat tttgaatgtg cgggattgct gaaaagcagc 1740

ccgtttttt atggcctccg aacgaatgag ttagcaggcc gcagatttga acagctattt 1800

tctatcttgt tgtaacaaaa ttaagtggag gtggctcacc attagcaaag acatgttggt 1860

aaacgatggg attcgtgcac gtgaagtaag attgatcgac caagacggtg aacaattagg 1920

cgtgaagagt aaaatcgatg cgcttcaaat tgctgaaaag gctaatcttg atctagtgct 1980

tgttgctcca acagcgaaac cgccagtagc tcgta 2015

<210> 82
<211> 1140
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of DNA that is cloned in the temperature sensitive plasmid, pKSV7 to create inl C deletion mutant

<400> 82
gaattcatgg cgcgggatgg tatactatac aagcgtatgg ttcaaaaaga tactttgaat 60

taagaagtac aataaagtta acttcattag acaaaaagaa aaaacaagga agaatagtac 120

atagttataa atacttggag agtgaggtgt aatatggggg cagctgattt ttggggtttc 180

atatatgtag tttcaagatt agccattgtt gcggcagtag tttacttctt atacttattg 240

agaaaaattg caaataaata gaaaaaaagc cttgtcaaac gaggcttttt ttatgcaaaa 300

aatacgacga atgaagccat gtgagacaat ttggaatagc agacaacaag gaaggtagaa 360

catgttttga aaaatttact gattttcgat tattattaac gcttgttaat ttaaacatct 420

cttatttttg ctaacatata agtatacaaa gggacataaa aaggttaaca gcgtttgtta 480

aataggaagt atatgaaaat cctcttttgt gtttctaaat ttatttttaa ggagtggaga 540

ggatccggac ttgtgcacac ctgtatactt tgagctctcg tataatcacg agagcttttt 600

aaatatgtaa gtcttaatta tctcttgaca aaaagaacgt ttattcgtat aaggttacca 660

agagatgaag aaactatttt atttacaatt caccttgaca ccaaaaactc catatgatat 720

agtaaataag gttattaaac aagaaagaag aagcaacccg cttctcgcct cgttaacacg 780

aacgttttca ggcaaaaaat tcaaactttc gtcgcgtagc ttacgcgatt ttgaatgtgc 840

gggattgctg aaaagcagcc cgtttttta tggcctccga acgaatgagt tagcaggccg 900

cagatttgaa cagctatttt ctatcttgtt gtaacaaaat taagtggagg tggctcacca 960

ttagcaaaga catgttggta aacgatggga ttcgtgcacg tgaagtaaga ttgatcgacc 1020

aagacggtga acaattaggc gtgaagagta aaatcgatgc gcttcaaatt gctgaaaagg 1080

ctaatcttga tctagtgctt gttgctccaa cagcgaaacc gccagtagct cgtactgcag 1140

<210> 83
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Lm-LLO-ISG15.Forward primer

<400> 83
taatctcgag atggcctggg acctaaag 28

<210> 84
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Lm-LLO-ISG15.Reverse primer

<400> 84
attaactagt ttaggcacac tggtcccc 28

<210> 85
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward primers specific for ISG15

<400> 85
atggcctggg acctaaag 18

<210> 86
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward primers specific for ISG15

<400> 86
ttaggcacac tggtcccc 18

<210> 87
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> 18S rRNA 18SRNA. Forward primer

<400> 87
cggctaccac atccaaggaa 20

<210> 88
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> 18S rRNA 18SRNA. Reverse primer

<400> 88
gctggaatta ccgcggct 18

<210> 89
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> beta-actin ACTIN. Forward primer

<400> 89
gtgggccgct ctaggcacca a 21

<210> 90
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> beta-actin ACTIN. Reverse primer

<400> 90
ctctttgatg tcacgcacga tttc 24

<210> 91
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HIV-gag H-2Kd CTL epitope

<400> 91

Ala Met Gln Met Leu Lys Glu Thr Ile
1 5

<210> 92
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> ISG15 d1 primer

<400> 92

Arg Gly His Ser Asn Ile Tyr Glu Val
1 5

<210> 93
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> ISG15 d2 primer

<400> 93

Leu Gly Pro Ser Ser Thr Val Met Leu
1 5

<210> 94
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Her2/neu-specific H-2Kd epitope peptides Her2-EC1

<400> 94

Pro Tyr Asn Tyr Leu Ser Thr Glu Val
1 5

<210> 95
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Her2-EC2

<400> 95

Leu Phe Arg Asn Pro His Gln Ala Leu Leu
1 5 10

<210> 96
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Her2-IC1

<400> 96

Pro Tyr Val Ser Arg Leu Leu Gly Ile
1 5

<210> 97
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> her-2/neu EC2

<400> 97

Pro Asp Ser Leu Arg Asp Leu Ser Val Phe
1 5 10

<210> 98
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Her-2/neu EC1

<400> 98

Ala Ser Pro Glu Thr His Leu Asp Met Leu
1 5 10

<210> 99
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> her-2/neu IC1

<400> 99

Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys
1 5 10

<210> 100
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Flk-E1

<400> 100

Thr Tyr Gln Ser Ile Met Tyr Ile Val
1 5

<210> 101
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
<223> Flk-E2

<400> 101

Met Phe Ser Asn Ser Thr Asn Asp Ile
1 5

<210> 102
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> FLK-I1 906-915

<400> 102

Pro Gly Gly Pro Leu Met Val Ile Val
1 5

<210> 103
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Flk-I1 839-848

<400> 103

Gly Arg Gly Ala Phe Gly Gln Val Ile
1 5

<210> 104
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Flk-E1 primer (F)

<400> 104
gggctcgagc gtgattctga ggaaagggta tt 32

<210> 105
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Flk-E1 (R)

<400> 105
gggactagtt tacccggttt acaatcttct tat 33

<210> 106
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Flk-E2 (F)

<400> 106
gggctcgagg tgatcagggg tcctgaaatt a 31

<210> 107
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Flk-E2 (R)

<400> 107
gggactagtt tagcctccat cctccttcct 30

<210> 108
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Flk-I1 (F)

<400> 108
gggctcgagg aaggggaact gaagacagcc 30

<210> 109
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Flk-I1 (R)

<400> 109
gggactagtt tatgtgtata ctctgtcaaa aatggtttc 39

<210> 110
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> EC1FP FP =reverse primer RP= reverse primer

<400> 110
agggctgtca ggtagtgc 18

<210> 111
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> EC1RP

<400> 111
tgacctcttg gttattcg 18

<210> 112

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

<220>
<223> EC2FP

<400> 112
acctgcccct acaactac 18

<210> 113
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> EC3 FP

<400> 113
gacgccctct acagttgc 18

<210> 114
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> EC2 RP

<400> 114
gtggattggc tctgattc 18

<210> 115
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> EC3RP

<400> 115
tgagttacag accaagcc 18

<210> 116
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> IC1FP

<400> 116
caaacgaagg agacagaag 19

<210> 117
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> IC1 RP

<400> 117

caccatcaaa cacatcgg 18

<210> 118
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> IC2 FP

<400> 118
cactgctgga agatgatg 18

<210> 119
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> IC2 RP

<400> 119
tttgtggcga tggagacc 18

<210> 120
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CD105A peptide

<400> 120

Ala Gly Pro Arg Thr Val Thr Val Met
1 5

<210> 121
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Cd105B peptide

<400> 121

Ala Tyr Ser Ser Cys Gly Met Lys Val
1 5

<210> 122
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> AH1 peptide

<400> 122

Ser Pro Ser Tyr Val Tyr His Gln Phe
1 5

<210> 123
<211> 529
<212> PRT
<213> Listeria monocytogenes

<400> 123

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Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
            20                  25                  30

Glu Asn Ser Ile Ser Ser Val Ala Pro Pro Ala Ser Pro Pro Ala Ser
        35                  40                  45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Glu Ile Asp Lys Tyr
    50                  55                  60

Ile Gln Gly Leu Asp Tyr Asn Lys Asn Asn Val Leu Val Tyr His Gly
65                  70                  75                  80

Asp Ala Val Thr Asn Val Pro Pro Arg Lys Gly Tyr Lys Asp Gly Asn
                85                  90                  95

Glu Tyr Ile Val Val Glu Lys Lys Lys Lys Ser Ile Asn Gln Asn Asn
            100                 105                 110

Ala Asp Ile Gln Val Val Asn Ala Ile Ser Ser Leu Thr Tyr Pro Gly
        115                 120                 125

Ala Leu Val Lys Ala Asn Ser Glu Leu Val Glu Asn Gln Pro Asp Val
    130                 135                 140

Leu Pro Val Lys Arg Asp Ser Leu Thr Leu Ser Ile Asp Leu Pro Gly
145                 150                 155                 160

Met Thr Asn Gln Asp Asn Lys Ile Val Val Lys Asn Ala Thr Lys Ser
                165                 170                 175

Asn Val Asn Asn Ala Val Asn Thr Leu Val Glu Arg Trp Asn Glu Lys
            180                 185                 190

Tyr Ala Gln Ala Tyr Ser Asn Val Ser Ala Lys Ile Asp Tyr Asp Asp
        195                 200                 205

Glu Met Ala Tyr Ser Glu Ser Gln Leu Ile Ala Lys Phe Gly Thr Ala
    210                 215                 220

Phe Lys Ala Val Asn Asn Ser Leu Asn Val Asn Phe Gly Ala Ile Ser
225                 230                 235                 240
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Glu Gly Lys Met Gln Glu Glu Val Ile Ser Phe Lys Gln Ile Tyr Tyr
                245                 250                 255

Asn Val Asn Val Asn Glu Pro Thr Arg Pro Ser Arg Phe Phe Gly Lys
            260                 265                 270

Ala Val Thr Lys Glu Gln Leu Gln Ala Leu Gly Val Asn Ala Glu Asn
        275                 280                 285

Pro Pro Ala Tyr Ile Ser Ser Val Ala Tyr Gly Arg Gln Val Tyr Leu
    290                 295                 300

Lys Leu Ser Thr Asn Ser His Ser Thr Lys Val Lys Ala Ala Phe Asp
305                 310                 315                 320

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

Ile Ile Lys Asn Ser Ser Phe Lys Ala Val Ile Tyr Gly Gly Ser Ala
            340                 345                 350

Lys Asp Glu Val Gln Ile Ile Asp Gly Asn Leu Gly Asp Leu Arg Asp
        355                 360                 365

Ile Leu Lys Lys Gly Ala Thr Phe Asn Arg Glu Thr Pro Gly Val Pro
    370                 375                 380

Ile Ala Tyr Thr Thr Asn Phe Leu Lys Asp Asn Glu Leu Ala Val Ile
385                 390                 395                 400

Lys Asn Asn Ser Glu Tyr Ile Glu Thr Thr Ser Lys Ala Tyr Thr Asp
                405                 410                 415

Gly Lys Ile Asn Ile Asp His Ser Gly Gly Tyr Val Ala Gln Phe Asn
            420                 425                 430

Ile Ser Trp Asp Glu Val Asn Tyr Asp Pro Glu Gly Asn Glu Ile Val
        435                 440                 445

Gln His Lys Asn Trp Ser Glu Asn Asn Lys Ser Lys Leu Ala His Phe
    450                 455                 460

Thr Ser Ser Ile Tyr Leu Pro Gly Asn Ala Arg Asn Ile Asn Val Tyr
465                 470                 475                 480

Ala Lys Glu Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Thr Val Ile
                485                 490                 495

Asp Asp Arg Asn Leu Pro Leu Val Lys Asn Arg Asn Ile Ser Ile Trp
            500                 505                 510
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Gly Thr Thr Leu Tyr Pro Lys Tyr Ser Asn Lys Val Asp Asn Pro Ile
515 520 525

Glu

<210> 124
<211> 535
<212> PRT
<213> Listeria monocytogenes

<400> 124

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
20 25 30

Glu Asn Ser Ile Ser Ser Val Ala Pro Pro Ala Ser Pro Pro Ala Ser
35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Glu Ile Asp Lys Tyr
50 55 60

Ile Gln Gly Leu Asp Tyr Asn Lys Asn Asn Val Leu Val Tyr His Gly
65 70 75 80

Asp Ala Val Thr Asn Val Pro Pro Arg Lys Gly Tyr Lys Asp Gly Asn
85 90 95

Glu Tyr Ile Val Val Glu Lys Lys Lys Ser Ile Asn Gln Asn Asn
100 105 110

Ala Asp Ile Gln Val Val Asn Ala Ile Ser Ser Leu Thr Tyr Pro Gly
115 120 125

Ala Leu Val Lys Ala Asn Ser Glu Leu Val Glu Asn Gln Pro Asp Val
130 135 140

Leu Pro Val Lys Arg Asp Ser Leu Thr Leu Ser Ile Asp Leu Pro Gly
145 150 155 160

Met Thr Asn Gln Asp Asn Lys Ile Val Val Lys Asn Ala Thr Lys Ser
165 170 175

Asn Val Asn Asn Ala Val Asn Thr Leu Val Glu Arg Trp Asn Glu Lys
180 185 190

Tyr Ala Gln Ala Tyr Ser Asn Val Ser Ala Lys Ile Asp Tyr Asp Asp
195 200 205

Glu Met Ala Tyr Ser Glu Ser Gln Leu Ile Ala Lys Phe Gly Thr Ala

210 215 220

Phe Lys Ala Val Asn Asn Ser Leu Asn Val Asn Phe Gly Ala Ile Ser
225 230 235 240

Glu Gly Lys Met Gln Glu Glu Val Ile Ser Phe Lys Gln Ile Tyr Tyr
245 250 255

Asn Val Asn Val Asn Glu Pro Thr Arg Pro Ser Arg Phe Phe Gly Lys
260 265 270

Ala Val Thr Lys Glu Gln Leu Gln Ala Leu Gly Val Asn Ala Glu Asn
275 280 285

Pro Pro Ala Tyr Ile Ser Ser Val Ala Tyr Gly Arg Gln Val Tyr Leu
290 295 300

Lys Leu Ser Thr Asn Ser His Ser Thr Lys Val Lys Ala Ala Phe Asp
305 310 315 320

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

Ile Ile Lys Asn Ser Ser Phe Lys Ala Val Ile Tyr Gly Gly Ser Ala
340 345 350

Lys Asp Glu Val Gln Ile Ile Asp Gly Asn Leu Gly Asp Leu Arg Asp
355 360 365

Ile Leu Lys Lys Gly Ala Thr Phe Asn Arg Glu Thr Pro Gly Val Pro
370 375 380

Ile Ala Tyr Thr Thr Asn Phe Leu Lys Asp Asn Glu Leu Ala Val Ile
385 390 395 400

Lys Asn Asn Ser Glu Tyr Ile Glu Thr Thr Ser Lys Ala Tyr Thr Asp
405 410 415

Gly Lys Ile Asn Ile Asp His Ser Gly Gly Tyr Val Ala Gln Phe Asn
420 425 430

Ile Ser Trp Asp Glu Val Asn Tyr Asp Pro Glu Gly Asn Glu Ile Val
435 440 445

Gln His Lys Asn Trp Ser Glu Asn Asn Lys Ser Lys Leu Ala His Phe
450 455 460

Thr Ser Ser Ile Tyr Leu Pro Gly Asn Ala Arg Asn Ile Asn Val Tyr
465 470 475 480

Ala Lys Glu Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Thr Val Ile

485 490 495

Asp Asp Arg Asn Leu Pro Leu Val Lys Asn Arg Asn Ile Ser Ile Trp
500 505 510

Gly Thr Thr Leu Tyr Pro Lys Tyr Ser Asn Lys Val Asp Asn Pro Ile
515 520 525

Glu His His His His His His
530 535

<210> 125
<211> 1551
<212> DNA
<213> Listeria monocytogenes

<400> 125
catatgaagg atgcatctgc attcaataaa gaaaattcaa tttcatccgt ggcaccacca 60

gcatctccgc ctgcaagtcc taagacgcca atcgaaaaga aacacgcgga tgaaatcgat 120

aagtatatac aaggattgga ttacaataaa aacaatgtat tagtatacca cggagatgca 180

gtgacaaatg tgccgccaag aaaaggttac aaagatggaa atgaatatat tgttgtggag 240

aaaaagaaga aatccatcaa tcaaaataat gcagacattc aagttgtgaa tgcaatttcg 300

agcctaacct atccaggtgc tctcgtaaaa gcgaattcgg aattagtaga aaatcaacca 360

gatgttctcc ctgtaaaacg tgattcatta acactcagca ttgatttgcc aggtatgact 420

aatcaagaca ataaaatagt tgtaaaaaat gccactaaat caaacgttaa caacgcagta 480

aatacattag tggaaagatg gaatgaaaaa tatgctcaag cttattcaaa tgtaagtgca 540

aaaattgatt atgatgacga aatggcttac agtgaatcac aattaattgc gaaatttggt 600

acagcattta aagctgtaaa taatagcttg aatgtaaact tcggcgcaat cagtgaaggg 660

aaaatgcaag aagaagtcat tagttttaaa caaatttact ataacgtgaa tgttaatgaa 720

cctacaagac cttccagatt tttcggcaaa gctgttacta aagagcagtt gcaagcgctt 780

ggagtgaatg cagaaaatcc tcctgcatat atctcaagtg tggcgtatgg ccgtcaagtt 840

tatttgaaat tatcaactaa ttcccatagt actaaagtaa aagctgcttt tgatgctgcc 900

gtaagcggaa aatctgtctc aggtgatgta gaactaacaa atatcatcaa aaattcttcc 960

ttcaaagccg taatttacgg aggttccgca aaagatgaag ttcaaatcat cgacggcaac 1020

ctcggagact tacgcgatat tttgaaaaaa ggcgctactt ttaatcgaga aacaccagga 1080

gttcccattg cttatacaac aaacttccta aaagacaatg aattagctgt tattaaaaac 1140

aactcagaat atattgaaac aacttcaaaa gcttatacag atggaaaaat taacatcgat 1200

cactctggag gatacgttgc tcaattcaac atttcttggg atgaagtaaa ttatgatcct 1260

gaaggtaacg aaattgttca acataaaaac tggagcgaaa acaataaaag caagctagct 1320

catttcacat cgtccatcta tttgcctggt aacgcgagaa atattaatgt ttacgctaaa 1380

gaatgcactg gtttagcttg ggaatggtgg agaacggtaa ttgatgaccg gaacttacca 1440

cttgtgaaaa atagaaatat ctccatctgg ggcaccacgc tttatccgaa atatagtaat 1500

aaagtagata atccaatcga acaccaccac caccaccact aataaggatc c 1551

<210> 126
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 126
gctagctcat ttcacatcgt 20

<210> 127
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 127
tcttgcagct tcccaagcta aaccagtcgc ttctttagcg taaacattaa tatt 54

<210> 128
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 128
gaagcgactg gtttagcttg ggaagctgca agaacggtaa ttgatgaccg gaac 54

<210> 129
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 129
ggatccttat tagtggtggt ggtggtggtg ttcgattgg 39

<210> 130
<211> 11
<212> PRT
<213> Listeria monocytogenes

<400> 130

Glu Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg
1 5 10

<210> 131
<211> 11
<212> PRT

<213> Listeria monocytogenes

<400> 131

Glu Ala Thr Gly Leu Ala Trp Glu Ala Ala Arg
1 5 10

<210> 132
<211> 238
<212> DNA
<213> Listeria monocytogenes

<400> 132
gctagctcat ttcacatcgt ccatctattt gcctggtaac gcgagaaata ttaatgttta 60

cgctaaagaa gcgactggtt tagcttggga agctgcaaga acggtaattg atgaccggaa 120

cttaccactt gtgaaaaata gaaatatctc catctggggc accacgcttt atccgaaata 180

tagtaataaa gtagataatc caatcgaaca ccaccaccac caccactaat aaggatcc 238

<210> 133
<211> 11
<212> PRT
<213> Listeria monocytogenes

<400> 133

Glu Ser Leu Leu Met Trp Ile Thr Gln Cys Arg
1 5 10

<210> 134
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 134
tctgcactgg gtgatccaca tcagcaggct ttctttagcg taaacattaa tatt 54

<210> 135
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 135
gaaagcctgc tgatgtggat cacccagtgc agaacggtaa ttgatgaccg gaac 54

<210> 136
<211> 238
<212> DNA
<213> Listeria monocytogenes

<400> 136
gctagctcat ttcacatcgt ccatctattt gcctggtaac gcgagaaata ttaatgttta 60

cgctaaagaa agcctgctga tgtggatcac ccagtgcaga acggtaattg atgaccggaa 120

cttaccactt gtgaaaaata gaaatatctc catctggggc accacgcttt atccgaaata 180

tagtaataaa gtagataatc caatcgaaca ccaccaccac caccactaat aaggatcc 238

<210> 137
<211> 1345
<212> PRT
<213> Mus musculus

<400> 137

Met Glu Ser Lys Ala Leu Leu Ala Val Ala Leu Trp Phe Cys Val Glu
1 5 10 15

Thr Arg Ala Ala Ser Val Gly Leu Pro Gly Asp Phe Leu His Pro Pro
20 25 30

Lys Leu Ser Thr Gln Lys Asp Ile Leu Thr Ile Leu Ala Asn Thr Thr
35 40 45

Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro
50 55 60

Asn Ala Gln Arg Asp Ser Glu Glu Arg Val Leu Val Thr Glu Cys Gly
65 70 75 80

Gly Gly Asp Ser Ile Phe Cys Lys Thr Leu Thr Ile Pro Arg Val Val
85 90 95

Gly Asn Asp Thr Gly Ala Tyr Lys Cys Ser Tyr Arg Asp Val Asp Ile
100 105 110

Ala Ser Thr Val Tyr Val Tyr Val Arg Asp Tyr Arg Ser Pro Phe Ile
115 120 125

Ala Ser Val Ser Asp Gln His Gly Ile Val Tyr Ile Thr Glu Asn Lys
130 135 140

Asn Lys Thr Val Val Ile Pro Cys Arg Gly Ser Ile Ser Asn Leu Asn
145 150 155 160

Val Ser Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly
165 170 175

Asn Arg Ile Ser Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr
180 185 190

Met Ile Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp
195 200 205

Glu Thr Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg
210 215 220

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Ile Tyr Asp Val Ile Leu Ser Pro Pro His Glu Ile Glu Leu Ser Ala
225                 230                 235                 240

Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val
                245                 250                 255

Gly Leu Asp Phe Thr Trp His Ser Pro Pro Ser Lys Ser His His Lys
            260                 265                 270

Lys Ile Val Asn Arg Asp Val Lys Pro Phe Pro Gly Thr Val Ala Lys
        275                 280                 285

Met Phe Leu Ser Thr Leu Thr Ile Glu Ser Val Thr Lys Ser Asp Gln
    290                 295                 300

Gly Glu Tyr Thr Cys Val Ala Ser Ser Gly Arg Met Ile Lys Arg Asn
305                 310                 315                 320

Arg Thr Phe Val Arg Val His Thr Lys Pro Phe Ile Ala Phe Gly Ser
                325                 330                 335

Gly Met Lys Ser Leu Val Glu Ala Thr Val Gly Ser Gln Val Arg Ile
            340                 345                 350

Pro Val Lys Tyr Leu Ser Tyr Pro Ala Pro Asp Ile Lys Trp Tyr Arg
        355                 360                 365

Asn Gly Arg Pro Ile Glu Ser Asn Tyr Thr Met Ile Val Gly Asp Glu
    370                 375                 380

Leu Thr Ile Met Glu Val Thr Glu Arg Asp Ala Gly Asn Tyr Thr Val
385                 390                 395                 400

Ile Leu Thr Asn Pro Ile Ser Met Glu Lys Gln Ser His Met Val Ser
                405                 410                 415

Leu Val Val Asn Val Pro Pro Gln Ile Gly Glu Lys Ala Leu Ile Ser
            420                 425                 430

Pro Met Asp Ser Tyr Gln Tyr Gly Thr Met Gln Thr Leu Thr Cys Thr
        435                 440                 445

Val Tyr Ala Asn Pro Pro Leu His His Ile Gln Trp Tyr Trp Gln Leu
    450                 455                 460

Glu Glu Ala Cys Ser Tyr Arg Pro Gly Gln Thr Ser Pro Tyr Ala Cys
465                 470                 475                 480

Lys Glu Trp Arg His Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu
                485                 490                 495
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Val Thr Lys Asn Gln Tyr Ala Leu Ile Glu Gly Lys Asn Lys Thr Val
            500                 505                 510

Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys
        515                 520                 525

Glu Ala Ile Asn Lys Ala Gly Arg Gly Glu Arg Val Ile Ser Phe His
    530                 535                 540

Val Ile Arg Gly Pro Glu Ile Thr Val Gln Pro Ala Ala Gln Pro Thr
545                 550                 555                 560

Glu Gln Glu Ser Val Ser Leu Leu Cys Thr Ala Asp Arg Asn Thr Phe
                565                 570                 575

Glu Asn Leu Thr Trp Tyr Lys Leu Gly Ser Gln Ala Thr Ser Val His
            580                 585                 590

Met Gly Glu Ser Leu Thr Pro Val Cys Lys Asn Leu Asp Ala Leu Trp
        595                 600                 605

Lys Leu Asn Gly Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile
    610                 615                 620

Val Ala Phe Gln Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys
625                 630                 635                 640

Ser Ala Gln Asp Lys Lys Thr Lys Lys Arg His Cys Leu Val Lys Gln
                645                 650                 655

Leu Ile Ile Leu Glu Arg Met Ala Pro Met Ile Thr Gly Asn Leu Glu
            660                 665                 670

Asn Gln Thr Thr Thr Ile Gly Glu Thr Ile Glu Val Thr Cys Pro Ala
        675                 680                 685

Ser Gly Asn Pro Thr Pro His Ile Thr Trp Phe Lys Asp Asn Glu Thr
    690                 695                 700

Leu Val Glu Asp Ser Gly Ile Val Leu Arg Asp Gly Asn Arg Asn Leu
705                 710                 715                 720

Thr Ile Arg Arg Val Arg Lys Glu Asp Gly Gly Leu Tyr Thr Cys Gln
                725                 730                 735

Ala Cys Asn Val Leu Gly Cys Ala Arg Ala Glu Thr Leu Phe Ile Ile
            740                 745                 750

Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Val Ile Ile Leu Val Gly
        755                 760                 765
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Thr Ala Val Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile Val Leu
    770                 775                 780

Arg Thr Val Lys Arg Ala Asn Glu Gly Glu Leu Lys Thr Gly Tyr Leu
785                 790                 795                 800

Ser Ile Val Met Asp Pro Asp Glu Leu Pro Leu Asp Glu Arg Cys Glu
                805                 810                 815

Arg Leu Pro Tyr Asp Ala Ser Lys Trp Glu Phe Pro Arg Asp Arg Leu
            820                 825                 830

Lys Leu Gly Lys Pro Leu Gly Arg Gly Ala Phe Gly Gln Val Ile Glu
        835                 840                 845

Ala Asp Ala Phe Gly Ile Asp Lys Thr Ala Thr Cys Lys Thr Val Ala
    850                 855                 860

Val Lys Met Leu Lys Glu Gly Ala Thr His Ser Glu His Arg Ala Leu
865                 870                 875                 880

Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly His His Leu Asn Val
                885                 890                 895

Val Asn Leu Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu Met Val
            900                 905                 910

Ile Val Glu Phe Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu Arg Gly
        915                 920                 925

Lys Arg Asn Glu Phe Val Pro Tyr Lys Ser Lys Gly Ala Arg Phe Arg
    930                 935                 940

Gln Gly Lys Asp Tyr Val Gly Glu Leu Ser Val Asp Leu Lys Arg Arg
945                 950                 955                 960

Leu Asp Ser Ile Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly Phe Val
                965                 970                 975

Glu Glu Lys Ser Leu Ser Asp Val Glu Glu Glu Glu Ala Ser Glu Glu
            980                 985                 990

Leu Tyr Lys Asp Phe Leu Thr Leu  Glu His Leu Ile Cys  Tyr Ser Phe
        995                 1000                1005

Gln Val  Ala Lys Gly Met Glu  Phe Leu Ala Ser Arg  Lys Cys Ile
    1010                1015                1020

His Arg  Asp Leu Ala Ala Arg  Asn Ile Leu Leu Ser  Glu Lys Asn
    1025                1030                1035
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Val Val  Lys Ile Cys Asp Phe  Gly Leu Ala Arg Asp  Ile Tyr Lys
    1040                1045                1050

Asp Pro  Asp Tyr Val Arg Lys  Gly Asp Ala Arg Leu  Pro Leu Lys
    1055                1060                1065

Trp Met  Ala Pro Glu Thr Ile  Phe Asp Arg Val Tyr  Thr Ile Gln
    1070                1075                1080

Ser Asp  Val Trp Ser Phe Gly  Val Leu Leu Trp Glu  Ile Phe Ser
    1085                1090                1095

Leu Gly  Ala Ser Pro Tyr Pro  Gly Val Lys Ile Asp  Glu Glu Phe
    1100                1105                1110

Cys Arg  Arg Leu Lys Glu Gly  Thr Arg Met Arg Ala  Pro Asp Tyr
    1115                1120                1125

Thr Thr  Pro Glu Met Tyr Gln  Thr Met Leu Asp Cys  Trp His Glu
    1130                1135                1140

Asp Pro  Asn Gln Arg Pro Ser  Phe Ser Glu Leu Val  Glu His Leu
    1145                1150                1155

Gly Asn  Leu Leu Gln Ala Asn  Ala Gln Gln Asp Gly  Lys Asp Tyr
    1160                1165                1170

Ile Val  Leu Pro Met Ser Glu  Thr Leu Ser Met Glu  Glu Asp Ser
    1175                1180                1185

Gly Leu  Ser Leu Pro Thr Ser  Pro Val Ser Cys Met  Glu Glu Glu
    1190                1195                1200

Glu Val  Cys Asp Pro Lys Phe  His Tyr Asp Asn Thr  Ala Gly Ile
    1205                1210                1215

Ser His  Tyr Leu Gln Asn Ser  Lys Arg Lys Ser Arg  Pro Val Ser
    1220                1225                1230

Val Lys  Thr Phe Glu Asp Ile  Pro Leu Glu Glu Pro  Glu Val Lys
    1235                1240                1245

Val Ile  Pro Asp Asp Ser Gln  Thr Asp Ser Gly Met  Val Leu Ala
    1250                1255                1260

Ser Glu  Glu Leu Lys Thr Leu  Glu Asp Arg Asn Lys  Leu Ser Pro
    1265                1270                1275

Ser Phe  Gly Gly Met Met Pro  Ser Lys Ser Arg Glu  Ser Val Ala
    1280                1285                1290
```

Ser Glu Gly Ser Asn Gln Thr Ser Gly Tyr Gln Ser Gly Tyr His
1295 1300 1305

Ser Asp Asp Thr Asp Thr Thr Val Tyr Ser Ser Asp Glu Ala Gly
1310 1315 1320

Leu Leu Lys Met Val Asp Ala Ala Val His Ala Asp Ser Gly Thr
1325 1330 1335

Thr Leu Arg Ser Pro Pro Val
1340 1345

<210> 138
<211> 210
<212> PRT
<213> Artificial Sequence

<220>
<223> VEGFR2 protein fragment

<400> 138

Arg Asp Ser Glu Glu Arg Val Leu Val Thr Glu Cys Gly Gly Gly Asp
1 5 10 15

Ser Ile Phe Cys Lys Thr Leu Thr Ile Pro Arg Val Val Gly Asn Asp
20 25 30

Thr Gly Ala Tyr Lys Cys Ser Tyr Arg Asp Val Asp Ile Ala Ser Thr
35 40 45

Val Tyr Val Tyr Val Arg Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val
50 55 60

Ser Asp Gln His Gly Ile Val Tyr Ile Thr Glu Asn Lys Asn Lys Thr
65 70 75 80

Val Val Ile Pro Cys Arg Gly Ser Ile Ser Asn Leu Asn Val Ser Leu
85 90 95

Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg Ile
100 105 110

Ser Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr Met Ile Ser
115 120 125

Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Thr Tyr
130 135 140

Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr Asp
145 150 155 160

Val Ile Leu Ser Pro Pro His Glu Ile Glu Leu Ser Ala Gly Glu Lys
165 170 175

Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Leu Asp
180 185 190

Phe Thr Trp His Ser Pro Pro Ser Lys Ser His His Lys Lys Ile Val
195 200 205

Asn Arg
210

<210> 139
<211> 186
<212> PRT
<213> Artificial Sequence

<220>
<223> VEGFR2 protein fragment

<400> 139

Val Ile Arg Gly Pro Glu Ile Thr Val Gln Pro Ala Ala Gln Pro Thr
1 5 10 15

Glu Gln Glu Ser Val Ser Leu Leu Cys Thr Ala Asp Arg Asn Thr Phe
20 25 30

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

Met Gly Glu Ser Leu Thr Pro Val Cys Lys Asn Leu Asp Ala Leu Trp
50 55 60

Lys Leu Asn Gly Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile
65 70 75 80

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

Ser Ala Gln Asp Lys Lys Thr Lys Lys Arg His Cys Leu Val Lys Gln
100 105 110

Leu Ile Ile Leu Glu Arg Met Ala Pro Met Ile Thr Gly Asn Leu Glu
115 120 125

Asn Gln Thr Thr Thr Ile Gly Glu Thr Ile Glu Val Thr Cys Pro Ala
130 135 140

Ser Gly Asn Pro Thr Pro His Ile Thr Trp Phe Lys Asp Asn Glu Thr
145 150 155 160

Leu Val Glu Asp Ser Gly Ile Val Leu Arg Asp Gly Asn Arg Asn Leu
165 170 175

Thr Ile Arg Arg Val Arg Lys Glu Asp Gly
180 185

<210> 140
<211> 290
<212> PRT
<213> Artificial Sequence

<220>
<223> VEGFR2 protein fragment

<400> 140

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

Glu Leu Pro Leu Asp Glu Arg Cys Glu Arg Leu Pro Tyr Asp Ala Ser
20 25 30

Lys Trp Glu Phe Pro Arg Asp Arg Leu Lys Leu Gly Lys Pro Leu Gly
35 40 45

Arg Gly Ala Phe Gly Gln Val Ile Glu Ala Asp Ala Phe Gly Ile Asp
50 55 60

Lys Thr Ala Thr Cys Lys Thr Val Ala Val Lys Met Leu Lys Glu Gly
65 70 75 80

Ala Thr His Ser Glu His Arg Ala Leu Met Ser Glu Leu Lys Ile Leu
85 90 95

Ile His Ile Gly His His Leu Asn Val Val Asn Leu Leu Gly Ala Cys
100 105 110

Thr Lys Pro Gly Gly Pro Leu Met Val Ile Val Glu Phe Cys Lys Phe
115 120 125

Gly Asn Leu Ser Thr Tyr Leu Arg Gly Lys Arg Asn Glu Phe Val Pro
130 135 140

Tyr Lys Ser Lys Gly Ala Arg Phe Arg Gln Gly Lys Asp Tyr Val Gly
145 150 155 160

Glu Leu Ser Val Asp Leu Lys Arg Arg Leu Asp Ser Ile Thr Ser Ser
165 170 175

Gln Ser Ser Ala Ser Ser Gly Phe Val Glu Glu Lys Ser Leu Ser Asp
180 185 190

Val Glu Glu Glu Glu Ala Ser Glu Glu Leu Tyr Lys Asp Phe Leu Thr
195 200 205

Leu Glu His Leu Ile Cys Tyr Ser Phe Gln Val Ala Lys Gly Met Glu
210 215 220

Phe Leu Ala Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn
225 230 235 240

Ile Leu Leu Ser Glu Lys Asn Val Val Lys Ile Cys Asp Phe Gly Leu
245 250 255

Ala Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly Asp Ala
260 265 270

Arg Leu Pro Leu Lys Trp Met Ala Pro Glu Thr Ile Phe Asp Arg Val
275 280 285

Tyr Thr
290

<210> 141
<211> 156
<212> PRT
<213> Artificial Sequence

<220>
<223> VEGFR2 protein

<400> 141

Ile Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe
1 5 10 15

Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Lys Ile Asp Glu Glu Phe
20 25 30

Cys Arg Arg Leu Lys Glu Gly Thr Arg Met Arg Ala Pro Asp Tyr Thr
35 40 45

Thr Pro Glu Met Tyr Gln Thr Met Leu Asp Cys Trp His Glu Asp Pro
50 55 60

Asn Gln Arg Pro Ser Phe Ser Glu Leu Val Glu His Leu Gly Asn Leu
65 70 75 80

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

Met Ser Glu Thr Leu Ser Met Glu Glu Asp Ser Gly Leu Ser Leu Pro
100 105 110

Thr Ser Pro Val Ser Cys Met Glu Glu Glu Glu Val Cys Asp Pro Lys
115 120 125

Phe His Tyr Asp Asn Thr Ala Gly Ile Ser His Tyr Leu Gln Asn Ser
130 135 140

Lys Arg Lys Ser Arg Pro Val Ser Val Lys Thr Phe
145 150 155

<210> 142
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> VEGFR2 fragment

<400> 142

Ile Ile Leu Val Gly Thr Ala Val Ile
1 5

<210> 143
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> VEGFR2 fragment

<400> 143

Leu Leu Val Ile Ile Leu Arg Thr Val
1 5

<210> 144
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> VEGFR2 fragment

<400> 144

Ile Leu Leu Ser Glu Lys Asn Val Val
1 5

<210> 145
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> VEGFR2 fragment

<400> 145

Thr Ile Phe Asp Arg Val Tyr Thr Ile
1 5

<210> 146
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> VEGFR2 fragment

<400> 146

Val Leu Leu Trp Glu Ile Phe Ser Leu
1 5

<210> 147
<211> 654
<212> PRT
<213> Mus musculus

<400> 147

Met Asp Arg Gly Val Leu Pro Leu Pro Ile Thr Leu Leu Leu Phe Glu
1 5 10 15

Ile Tyr Ser Phe Glu Pro Thr Thr Gly Leu Ala Glu Arg Val Gly Cys
20 25 30

Asp Leu Gln Pro Val Asp Pro Thr Arg Gly Glu Val Thr Phe Thr Thr
35 40 45

Ser Gln Val Ser Glu Gly Cys Val Ala Gln Ala Ala Asn Ala Val Arg
50 55 60

Glu Val His Val Leu Phe Leu Asp Phe Pro Gly Met Leu Ser His Leu
65 70 75 80

Glu Leu Thr Leu Gln Ala Ser Lys Gln Asn Gly Thr Glu Thr Arg Glu
85 90 95

Val Phe Leu Val Leu Val Ser Asn Lys Asn Val Phe Val Lys Phe Gln
100 105 110

Ala Pro Glu Ile Pro Leu His Leu Ala Tyr Asp Ser Ser Leu Val Ile
115 120 125

Phe Gln Gly Gln Pro Arg Val Asn Ile Thr Val Leu Pro Ser Leu Thr
130 135 140

Ser Arg Lys Gln Ile Leu Asp Trp Ala Ala Thr Lys Gly Ala Ile Thr
145 150 155 160

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

Gln Asp Pro Lys Ala Pro Phe Leu Cys Leu Pro Glu Ala His Lys Asp
180 185 190

Met Gly Ala Thr Leu Glu Trp Gln Pro Arg Ala Gln Thr Pro Val Gln
195 200 205

Ser Cys Arg Leu Glu Gly Val Ser Gly His Lys Glu Ala Tyr Ile Leu
210 215 220

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Arg Ile Leu Pro Gly Ser Glu Ala Gly Pro Arg Thr Val Thr Val Met
225                 230                 235                 240

Met Glu Leu Ser Cys Thr Ser Gly Asp Ala Ile Leu Ile Leu His Gly
                245                 250                 255

Pro Pro Tyr Val Ser Trp Phe Ile Asp Ile Asn His Ser Met Gln Ile
            260                 265                 270

Leu Thr Thr Gly Glu Tyr Ser Val Lys Ile Phe Pro Gly Ser Lys Val
        275                 280                 285

Lys Gly Val Glu Leu Pro Asp Thr Pro Gln Gly Leu Ile Ala Glu Ala
    290                 295                 300

Arg Lys Leu Asn Ala Ser Ile Val Thr Ser Phe Val Glu Leu Pro Leu
305                 310                 315                 320

Val Ser Asn Val Ser Leu Arg Ala Ser Ser Cys Gly Gly Val Phe Gln
                325                 330                 335

Thr Thr Pro Ala Pro Val Val Thr Thr Pro Pro Lys Asp Thr Cys Ser
            340                 345                 350

Pro Val Leu Leu Met Ser Leu Ile Gln Pro Lys Cys Gly Asn Gln Val
        355                 360                 365

Met Thr Leu Ala Leu Asn Lys Lys His Val Gln Thr Leu Gln Cys Thr
    370                 375                 380

Ile Thr Gly Leu Thr Phe Trp Asp Ser Ser Cys Gln Ala Glu Asp Thr
385                 390                 395                 400

Asp Asp His Leu Val Leu Ser Ser Ala Tyr Ser Ser Cys Gly Met Lys
                405                 410                 415

Val Thr Ala His Val Val Ser Asn Glu Val Ile Ile Ser Phe Pro Ser
            420                 425                 430

Gly Ser Pro Pro Leu Arg Lys Lys Val Gln Cys Ile Asp Met Asp Ser
        435                 440                 445

Leu Ser Phe Gln Leu Gly Leu Tyr Leu Ser Pro His Phe Leu Gln Ala
    450                 455                 460

Ser Asn Thr Ile Glu Leu Gly Gln Gln Ala Phe Val Gln Val Ser Val
465                 470                 475                 480

Ser Pro Leu Thr Ser Glu Val Thr Val Gln Leu Asp Ser Cys His Leu
                485                 490                 495
```

```
Asp Leu Gly Pro Glu Gly Asp Met Val Glu Leu Ile Gln Ser Arg Thr
            500                 505                 510

Ala Lys Gly Ser Cys Val Thr Leu Leu Ser Pro Ser Pro Glu Gly Asp
        515                 520                 525

Pro Arg Phe Ser Phe Leu Leu Arg Val Tyr Met Val Pro Thr Pro Thr
    530                 535                 540

Ala Gly Thr Leu Ser Cys Asn Leu Ala Leu Arg Pro Ser Thr Leu Ser
545                 550                 555                 560

Gln Glu Val Tyr Lys Thr Val Ser Met Arg Leu Asn Val Val Ser Pro
                565                 570                 575

Asp Leu Ser Gly Lys Gly Leu Val Leu Pro Ser Val Leu Gly Ile Thr
            580                 585                 590

Phe Gly Ala Phe Leu Ile Gly Ala Leu Leu Thr Ala Ala Leu Trp Tyr
        595                 600                 605

Ile Tyr Ser His Thr Arg Gly Pro Ser Lys Arg Glu Pro Val Val Ala
    610                 615                 620

Val Ala Ala Pro Ala Ser Ser Glu Ser Ser Ser Thr Asn His Ser Ile
625                 630                 635                 640

Gly Ser Thr Gln Ser Thr Pro Cys Ser Thr Ser Ser Met Ala
                645                 650
```