SEQUENCE LISTING

<110> Bayer BioScience N.V.
D'Halluin, Kathleen

<120> Methods and means to modify a plant genome at a nucleotide sequence commonly used in plant genome engineering

<130> BCS 10-2010

<160> 18

<170> PatentIn version 3.5

<210> 1
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Recognition site for BAY39/40

<400> 1
gacgaggtcg tccgtccact cc 22

<210> 2
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Complement of the recognition site for BAY39/40

<400> 2
ggagtggacg gacgacctcg tc 22

<210> 3
<211> 552
<212> DNA
<213> Artificial

<220>
<223> Coding region of the phosphinotricin actelyltransferase gene derived from S. hygroscopicus (bar)

<400> 3
atgagcccag aacgacgccc ggccgacatc cgccgtgcca ccgaggcgga catgccggcg 60

gtctgcacca tcgtcaacca ctacatcgag acaagcacgg tcaacttccg taccgagccg 120

caggaaccgc aggagtggac ggacgacctc gtccgtctgc gggagcgcta tccctggctc 180

gtcgccgagg tggacggcga ggtcgccggc atcgcctacg cgggcccctg gaaggcacgc 240

aacgcctacg actggacggc cgagtcgacc gtgtacgtct ccccccgcca ccagcggacg 300

ggactgggct ccacgctcta cacccacctg ctgaagtccc tggaggcaca gggcttcaag 360

agcgtggtcg ctgtcatcgg gctgcccaac gacccgagcg tgcgcatgca cgaggcgctc 420

ggatatgccc cccgcggcat gctgcgggcg gccggcttca agcacgggaa ctggcatgac 480

gtgggtttct ggcagctgga cttcagcctg ccggtaccgc cccgtccggt cctgcccgtc 540

accgagatct ga 552

<210> 4
<211> 6234
<212> DNA
<213> Artificial

<220>
<223> Plasmid pCV177

<220>
<221> CDS
<222> (2004)..(2522)

<220>
<221> CDS
<222> (4885)..(5403)

<400> 4
gacgaaaggg cctcgtgata cgcctatttt tataggttaa tgtcatgata ataatggttt 60
cttagacgtc aggtggcact tttcggggaa atgtgcgcgg aacccctatt tgtttatttt 120
tctaaataca ttcaaatatg tatccgctca tgagacaata accctgataa atgcttcaat 180
aatattgaaa aaggaagagt atgagtattc aacatttccg tgtcgccctt attccctttt 240
ttgcggcatt ttgccttcct gtttttgctc acccagaaac gctggtgaaa gtaaaagatg 300
ctgaagatca gttgggtgca cgagtgggtt acatcgaact ggatctcaac agcggtaaga 360
tccttgagag ttttcgcccc gaagaacgtt ttccaatgat gagcactttt aaagttctgc 420
tatgtggcgc ggtattatcc cgtattgacg ccgggcaaga gcaactcggt cgccgcatac 480
actattctca gaatgacttg gttgagtact caccagtcac agaaaagcat cttacggatg 540
gcatgacagt aagagaatta tgcagtgctg ccataaccat gagtgataac actgcggcca 600
acttacttct gacaacgatc ggaggaccga aggagctaac cgcttttttg cacaacatgg 660
gggatcatgt aactcgcctt gatcgttggg aaccggagct gaatgaagcc ataccaaacg 720
acgagcgtga caccacgatg cctgtagcaa tggcaacaac gttgcgcaaa ctattaactg 780
gcgaactact tactctagct tcccggcaac aattaataga ctggatggag gcggataaag 840
ttgcaggacc acttctgcgc tcggcccttc cggctggctg gtttattgct gataaatctg 900
gagccggtga gcgtgggtct cgcggtatca ttgcagcact ggggccagat ggtaagccct 960
cccgtatcgt agttatctac acgacgggga gtcaggcaac tatggatgaa cgaaatagac 1020
agatcgctga gataggtgcc tcactgatta agcattggta actgtcagac caagtttact 1080
catatatact ttagattgat ttaaaacttc atttttaatt taaaaggatc taggtgaaga 1140
tccttttttgc tagcgagagg cggtttgcgt attggctaga gcagcttgcc aacatggtgg 1200
agcacgacac tctcgtctac tccaagaata tcaaagatac agtctcagaa gaccaaaggg 1260
ctattgagac ttttcaacaa agggtaatat cgggaaacct cctcggattc cattgcccag 1320
ctatctgtca cttcatcaaa aggacagtag aaaaggaagg tggcacctac aaatgccatc 1380
attgcgataa aggaaaggct atcgttcaag atgcctctgc cgacagtggt cccaaagatg 1440
gacccccacc cacgaggagc atcgtggaaa aagaagacgt tccaaccacg tcttcaaagc 1500
aagtggattg atgtgaacat ggtggagcac gacactctcg tctactccaa gaatatcaaa 1560
gatacagtct cagaagacca aagggctatt gagacttttc aacaaagggt aatatcggga 1620
aacctcctcg gattccattg cccagctatc tgtcacttca tcaaaaggac agtagaaaag 1680
gaaggtggca cctacaaatg ccatcattgc gataaaggaa aggctatcgt tcaagatgcc 1740
tctgccgaca gtggtcccaa agatggaccc ccacccacga ggagcatcgt ggaaaaagaa 1800
gacgttccaa ccacgtcttc aaagcaagtg gattgatgtg atatctccac tgacgtaagg 1860
gatgacgcac aatcccacta tccttcgcaa gacccttcct ctatataagg aagttcattt 1920
catttggaga ggacacgctg aaatcaccag tctctctcta caaatctatc tctctcgagc 1980

```
tttcgcagat ctgtcgaacc acc atg gca ccg aag aag aag cgc aag gtg cat      2033
                          Met Ala Pro Lys Lys Lys Arg Lys Val His
                          1               5                   10

atg aac acc aag tac aac aag aag ttc ctg ctc tac ctg gcg ggc ttc      2081
Met Asn Thr Lys Tyr Asn Lys Lys Phe Leu Leu Tyr Leu Ala Gly Phe
                15                  20                  25

gtg gac ggg gac ggc tcc atc atc gcc tcc atc tcc ccg aac cag tcc      2129
Val Asp Gly Asp Gly Ser Ile Ile Ala Ser Ile Ser Pro Asn Gln Ser
            30                  35                  40

cgc aag ttc aag cat cag ctg cgc ctc acc ttc acc gtc acc cag aag      2177
Arg Lys Phe Lys His Gln Leu Arg Leu Thr Phe Thr Val Thr Gln Lys
        45                  50                  55

aca cag cgc cgt tgg ttc ctc gac aag ctg gtg gac aag atc ggg gtg      2225
Thr Gln Arg Arg Trp Phe Leu Asp Lys Leu Val Asp Lys Ile Gly Val
    60                  65                  70

ggc aag gtg cgc gac cgc ggc agc gtc tcc gac tac cgc ctg tcc cag      2273
Gly Lys Val Arg Asp Arg Gly Ser Val Ser Asp Tyr Arg Leu Ser Gln
75                  80                  85                  90

atc aag cct ctg cac aac ttc ctg acc cag ctc cag ccc ttc ctg aag      2321
Ile Lys Pro Leu His Asn Phe Leu Thr Gln Leu Gln Pro Phe Leu Lys
                95                  100                 105

ctc aag cag aag cag gcc aac ctc gtg ctg aag atc atc gag cag ctg      2369
Leu Lys Gln Lys Gln Ala Asn Leu Val Leu Lys Ile Ile Glu Gln Leu
            110                 115                 120

ccc tcc gcc aag gaa tcc ccg gac aag ttc ctg gag gtg tgc acc tgg      2417
Pro Ser Ala Lys Glu Ser Pro Asp Lys Phe Leu Glu Val Cys Thr Trp
        125                 130                 135

gtg gac cag atc gcc gct ctg aac gac tcc aag acc cgc aag acc act      2465
Val Asp Gln Ile Ala Ala Leu Asn Asp Ser Lys Thr Arg Lys Thr Thr
    140                 145                 150

tcc gag acc gtc cgc gcc gtt cta gac agt ctc tcc gag aag aag aag      2513
Ser Glu Thr Val Arg Ala Val Leu Asp Ser Leu Ser Glu Lys Lys Lys
155                 160                 165                 170

tcg tcc ccc tagcatgccg ttcaaacatt tggcaataaa gtttcttaag              2562
Ser Ser Pro

attgaatcct gttgccggtc ttgcgatgat tatcatataa tttctgttga attacgttaa    2622

gcatgtaata attaacatgt aatgcatgac gttatttatg agatgggttt ttatgattag    2682

agtcccgcaa ttatacattt aatacgcgat agaaaacaaa atatagcgcg caaactagga    2742

taaattatcg cgcgcggtgt catctatgtt actagatcgg gcccgggaat aaaatatctt    2802

tattttcatt acatctgtgt gttggttttt tgtgtgaatc gatagtacta acatacgctc    2862

tccatcaaaa caaaacgaaa caaaacaaac tagcaaaata ggctgtcccc agtgcaagtg    2922

caggtgccag aacatttctc tgctagcctc atgaccaaaa tcccttaacg tgagttttcg    2982

ttccactgag cgtcagaccc cgtagaaaag atcaaaggat cttcttgaga tccttttttt    3042

ctgcgcgtaa tctgctgctt gcaaacaaaa aaaccaccgc taccagcggt ggtttgtttg    3102

ccggatcaag agctaccaac tctttttccg aaggtaactg gcttcagcag agcgcagata    3162

ccaaatactg ttcttctagt gtagccgtag ttaggccacc acttcaagaa ctctgtagca    3222

ccgcctacat acctcgctct gctaatcctg ttaccagtgg ctgctgccag tggcgataag    3282

tcgtgtctta ccgggttgga ctcaagacga tagttaccgg ataaggcgca gcggtcgggc    3342

tgaacggggg gttcgtgcac acagcccagc ttggagcgaa cgacctacac cgaactgaga    3402
```

```
tacctacagc gtgagctatg agaaagcgcc acgcttcccg aagggagaaa ggcggacagg      3462

tatccggtaa gcggcagggt cggaacagga gagcgcacga gggagcttcc agggggaaac      3522

gcctggtatc tttatagtcc tgtcgggttt cgccacctct gacttgagcg tcgatttttg      3582

tgatgctcgt caggggggcg gagcctatgg aaaaacgcca gcaacgcggc ctttttacgg      3642

ttcctggcct tttgctggcc ttttgctcac atgttctttc ctgcgttatc ccctgattct      3702

gtggataacc gtattaccgc ctttgagtga gctgataccg ctcgccgcag ccgaacgacc      3762

gagcgcagcg agtcagtgag cgaggaagcg gaagagcgcc caatacgcaa accgcctctc      3822

cccgcgcgtt ggccgattca ttaatgcagc tggcacgaca ggtttcccga ctggaaagcg      3882

ggcagtgagc gcaacgcaat taatgtgagt tagctcactc attaggcacc ccaggcttta      3942

cactttatgc ttccggctcg tatgttgtgt ggaattgtga gcggataaca atttcacaca      4002

ggaaacagct atgaccatga ttacgccaag cttgagaggc ggtttgcgta ttggctagag      4062

cagcttgcca acatggtgga gcacgacact ctcgtctact ccaagaatat caaagataca      4122

gtctcagaag accaaagggc tattgagact tttcaacaaa gggtaatatc gggaaacctc      4182

ctcggattcc attgcccagc tatctgtcac ttcatcaaaa ggacagtaga aaaggaaggt      4242

ggcacctaca aatgccatca ttgcgataaa ggaaaggcta tcgttcaaga tgcctctgcc      4302

gacagtggtc ccaaagatgg acccccaccc acgaggagca tcgtggaaaa agaagacgtt      4362

ccaaccacgt cttcaaagca agtggattga tgtgaacatg gtggagcacg acactctcgt      4422

ctactccaag aatatcaaag atacagtctc agaagaccaa agggctattg agacttttca      4482

acaaagggta atatcgggaa acctcctcgg attccattgc ccagctatct gtcacttcat      4542

caaaaggaca gtagaaaagg aaggtggcac ctacaaatgc catcattgcg ataaaggaaa      4602

ggctatcgtt caagatgcct ctgccgacag tggtcccaaa gatggacccc cacccacgag      4662

gagcatcgtg gaaaaagaag acgttccaac cacgtcttca aagcaagtgg attgatgtga      4722

tatctccact gacgtaaggg atgacgcaca atcccactat ccttcgcaag acccttcctc      4782

tatataagga agttcatttc atttggagag gacacgctga aatcaccagt ctctctctac      4842

aaatctatct ctctcgagct ttcgcagatc tgtcgaacca cc atg gca ccg aag          4896
                                                Met Ala Pro Lys
                                                    175

aag aag cgc aag gtg cat atg aac acc aag tac aac gag gag ttc ctg          4944
Lys Lys Arg Lys Val His Met Asn Thr Lys Tyr Asn Glu Glu Phe Leu
        180                 185                 190

ctc tac ctg gcg ggc ttc gtg gac ggg gac ggc tcc atc atc gcc tcc          4992
Leu Tyr Leu Ala Gly Phe Val Asp Gly Asp Gly Ser Ile Ile Ala Ser
    195                 200                 205

atc tcc ccg cgc cag tcc tac aag ttc aag cat gag ctg cgc ctc acc          5040
Ile Ser Pro Arg Gln Ser Tyr Lys Phe Lys His Glu Leu Arg Leu Thr
210                 215                 220                 225

ttc cag gtc acg cag aag aca cag cgc cgt tgg ttc ctc gac gag ctg          5088
Phe Gln Val Thr Gln Lys Thr Gln Arg Arg Trp Phe Leu Asp Glu Leu
                230                 235                 240

gtg gac gag atc ggg gtg ggc aag gtg cgc gac cgc ggc agc gtc tcc          5136
Val Asp Glu Ile Gly Val Gly Lys Val Arg Asp Arg Gly Ser Val Ser
            245                 250                 255

gac tac cgc ctg tcc cag atc aag cct ctg cac aac ttc ctg acc cag          5184
Asp Tyr Arg Leu Ser Gln Ile Lys Pro Leu His Asn Phe Leu Thr Gln
        260                 265                 270
```

ctc cag ccc ttc ctg gag ctc aag cag aag cag gcc aac ctc gtg ctg 5232
Leu Gln Pro Phe Leu Glu Leu Lys Gln Lys Gln Ala Asn Leu Val Leu
275 280 285

aag atc atc gag cag ctg ccc tcc gcc aag gaa tcc ccg gac aag ttc 5280
Lys Ile Ile Glu Gln Leu Pro Ser Ala Lys Glu Ser Pro Asp Lys Phe
290 295 300 305

ctg gag gtg tgc acc tgg gtg gac cag atc gcc gct ctg aac gac tcc 5328
Leu Glu Val Cys Thr Trp Val Asp Gln Ile Ala Ala Leu Asn Asp Ser
310 315 320

aag acc cgc aag acc act tcc gag acc gtc cgc gcc gtt cta gac agt 5376
Lys Thr Arg Lys Thr Thr Ser Glu Thr Val Arg Ala Val Leu Asp Ser
325 330 335

ctc tcc gag aag aag aag tcg tcc ccc tagcatgccg ttcaaacatt 5423
Leu Ser Glu Lys Lys Lys Ser Ser Pro
340 345

tggcaataaa gtttcttaag attgaatcct gttgccggtc ttgcgatgat tatcatataa 5483

tttctgttga attacgttaa gcatgtaata attaacatgt aatgcatgac gttatttatg 5543

agatgggttt ttatgattag agtcccgcaa ttatacattt aatacgcgat agaaaacaaa 5603

atatagcgcg caaactagga taaattatcg cgcgcggtgt catctatgtt actagatcgg 5663

gcccgggaat aaaatatctt tattttcatt acatctgtgt gttggttttt tgtgtgaatc 5723

gatagtacta acatacgctc tccatcaaaa caaaacgaaa caaaacaaac tagcaaaata 5783

ggctgtcccc agtgcaagtg caggtgccag aacatttcgg taccgagctc gaattcactg 5843

gccgtcgttt tacaacgtcg tgactgggaa aaccctggcg ttacccaact taatcgcctt 5903

gcagcacatc ccccttcgc cagctggcgt aatagcgaag aggcccgcac cgatcgccct 5963

tcccaacagt tgcgcagcct gaatggcgaa tggcgcctga tgcggtattt tctccttacg 6023

catctgtgcg gtatttcaca ccgcatatgg tgcactctca gtacaatctg ctctgatgcc 6083

gcatagttaa gccagccccg acacccgcca acacccgctg acgcgccctg acgggcttgt 6143

ctgctcccgg catccgctta cagacaagct gtgaccgtct ccgggagctg catgtgtcag 6203

aggttttcac cgtcatcacc gaaacgcgcg a 6234

<210> 5
<211> 173
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 5

Met Ala Pro Lys Lys Lys Arg Lys Val His Met Asn Thr Lys Tyr Asn
1 5 10 15

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

Ile Ile Ala Ser Ile Ser Pro Asn Gln Ser Arg Lys Phe Lys His Gln
35 40 45

Leu Arg Leu Thr Phe Thr Val Thr Gln Lys Thr Gln Arg Arg Trp Phe
50 55 60

Leu Asp Lys Leu Val Asp Lys Ile Gly Val Gly Lys Val Arg Asp Arg
65 70 75 80

Gly Ser Val Ser Asp Tyr Arg Leu Ser Gln Ile Lys Pro Leu His Asn
85 90 95

Phe Leu Thr Gln Leu Gln Pro Phe Leu Lys Leu Lys Gln Lys Gln Ala
100 105 110

Asn Leu Val Leu Lys Ile Ile Glu Gln Leu Pro Ser Ala Lys Glu Ser
115 120 125

Pro Asp Lys Phe Leu Glu Val Cys Thr Trp Val Asp Gln Ile Ala Ala
130 135 140

Leu Asn Asp Ser Lys Thr Arg Lys Thr Thr Ser Glu Thr Val Arg Ala
145 150 155 160

Val Leu Asp Ser Leu Ser Glu Lys Lys Lys Ser Ser Pro
165 170

<210> 6
<211> 173
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 6

Met Ala Pro Lys Lys Lys Arg Lys Val His Met Asn Thr Lys Tyr Asn
1 5 10 15

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

Ile Ile Ala Ser Ile Ser Pro Arg Gln Ser Tyr Lys Phe Lys His Glu
35 40 45

Leu Arg Leu Thr Phe Gln Val Thr Gln Lys Thr Gln Arg Arg Trp Phe
50 55 60

Leu Asp Glu Leu Val Asp Glu Ile Gly Val Gly Lys Val Arg Asp Arg
65 70 75 80

Gly Ser Val Ser Asp Tyr Arg Leu Ser Gln Ile Lys Pro Leu His Asn
85 90 95

Phe Leu Thr Gln Leu Gln Pro Phe Leu Glu Leu Lys Gln Lys Gln Ala
100 105 110

Asn Leu Val Leu Lys Ile Ile Glu Gln Leu Pro Ser Ala Lys Glu Ser
115 120 125

Pro Asp Lys Phe Leu Glu Val Cys Thr Trp Val Asp Gln Ile Ala Ala
130 135 140

Leu Asn Asp Ser Lys Thr Arg Lys Thr Thr Ser Glu Thr Val Arg Ala
145 150 155 160

Val Leu Asp Ser Leu Ser Glu Lys Lys Lys Ser Ser Pro
165 170

<210> 7
<211> 68
<212> DNA
<213> Artificial

<220>
<223> PCR amplicon of bar coding region around the BAY 39/40 recognition site (control)

<400> 7
cggtcaactt ccgtaccgag ccgcaggaac cgcaggagtg gacggacgac ctcgtccgtc 60

tgcgggac 68

<210> 8
<211> 68
<212> DNA
<213> Artificial

<220>
<223> PCR amplicon of bar coding region around the BAY 39/40 recognition site (PPT tolerant plant line1)

<400> 8
cggtcaactt ccgtaccgag ccgcaggaac cgcaggagtg gacggacgac ctcgtccgtc 60

tgcgggac 68

<210> 9
<211> 67
<212> DNA
<213> Artificial

<220>
<223> PCR amplicon of bar coding region around the BAY 39/40 recognition site (PPT sensitive plant line1 1)

<400> 9
cggtcaactt ccgtaccgag ccgcaggaac cgcaggagtg gacgacgacc tcgtccgtct 60

gcgggac 67

<210> 10
<211> 27
<212> DNA
<213> Artificial

<220>
<223> PCR amplicon of bar coding region around the BAY 39/40 recognition site (PPT sensitive plant line1 2)

<400> 10
cggtcaactt ccgtccgtct gcgggac 27

<210> 11
<211> 61
<212> DNA
<213> Artificial

<220>
<223> PCR amplicon of bar coding region around the BAY 39/40 recognition site (PPT sensitive plant line1 3)

<400> 11
cggtcaactt ccgtaccgag ccgcaggaac cgcaggagtg gacctcgtcc gtctgcggga 60

c 61

<210> 12
<211> 49
<212> DNA
<213> Artificial

<220>
<223> PCR amplicon of bar coding region around the BAY 39/40 recognition site (PPT sensitive plant linel 4)

<400> 12
cggtcaactt ccgtaccgag ccgcaggaac cctcgtccgt ctgcgggac 49

<210> 13
<211> 48
<212> DNA
<213> Artificial

<220>
<223> PCR amplicon of bar coding region around the BAY 39/40 recognition site (PPT sensitive plant linel 5)

<400> 13
cggtcaactt ccgtaccgag ccgcaggaac ctcgtccgtc tgcgggac 48

<210> 14
<211> 56
<212> DNA
<213> Artificial

<220>
<223> PCR amplicon of bar coding region around the BAY 39/40 recognition site (PPT sensitive plant linel 6)

<400> 14
cggtcaactt ccgtaccgag ccgcaggaac cgcacgacct cgtccgtctg cgggac 56

<210> 15
<211> 68
<212> DNA
<213> Artificial

<220>
<223> PCR amplicon of bar coding region around the BAY 39/40 recognition site (PPT sensitive plant linel 7)

<400> 15
cggtcaactt ccgtaccgag ccgcaggaac cgcaggagtg gacggacgac ctcgtccgtc 60

tgcgggac 68

<210> 16
<211> 163
<212> PRT
<213> Artificial

<220>
<223> I-CreI

<400> 16

Met Asn Thr Lys Tyr Asn Lys Glu Phe Leu Leu Tyr Leu Ala Gly Phe
1 5 10 15

Val Asp Gly Asp Gly Ser Ile Ile Ala Gln Ile Lys Pro Asn Gln Ser
20 25 30

Tyr Lys Phe Lys His Gln Leu Ser Leu Thr Phe Gln Val Thr Glu Lys

35 40 45

Thr Gln Arg Arg Trp Phe Leu Asp Lys Leu Val Asp Glu Ile Gly Val
50 55 60

Gly Tyr Val Arg Asp Arg Gly Ser Val Ser Asp Tyr Ile Leu Ser Glu
65 70 75 80

Ile Lys Pro Leu His Asn Phe Leu Thr Gln Leu Gln Pro Phe Leu Lys
85 90 95

Leu Lys Gln Lys Gln Ala Asn Leu Val Leu Lys Ile Ile Glu Gln Leu
100 105 110

Pro Ser Ala Lys Glu Ser Pro Asp Lys Phe Leu Glu Val Cys Thr Trp
115 120 125

Val Asp Gln Ile Ala Ala Leu Asn Asp Ser Lys Thr Arg Lys Thr Thr
130 135 140

Ser Glu Thr Val Arg Ala Val Leu Asp Ser Leu Ser Glu Lys Lys Lys
145 150 155 160

Ser Ser Pro

<210> 17
<211> 4925
<212> DNA
<213> Artificial Sequence

<220>
<223> vector

<220>
<221> CDS
<222> (1267)..(1605)

<220>
<221> CDS
<222> (1795)..(2541)

<400> 17
ctaaattgta agcgttaata ttttgttaaa attcgcgtta aatttttgtt aaatcagctc 60

atttttttaac caataggccg aaatcggcaa aatcccttat aaatcaaaag aatagaccga 120

gatagggttg agtgttgttc agtttggaa caagagtcca ctattaaaga acgtggactc 180

caacgtcaaa gggcgaaaaa ccgtctatca gggcgatggc ccactacgtg aaccatcacc 240

ctaatcaagt tttttggggt cgaggtgccg taaagcacta aatcggaacc ctaaagggag 300

cccccgattt agagcttgac ggggaaagcc ggcgaacgtg gcgagaaagg aagggaagaa 360

agcgaaagga gcgggcgcta gggcgctggc aagtgtagcg gtcacgctgc gcgtaaccac 420

cacacccgcc gcgcttaatg cgccgctaca gggcgcgtcc cattcgccat tcaggctgcg 480

caactgttgg gaagggcgat cggtgcgggc ctcttcgcta ttacgccagc tggcgaaagg 540

gggatgtgct gcaaggcgat taagttgggt aacgccaggg ttttcccagt cacgacgttg 600

taaaacgacg gccagtgagc gcgcgtaata cgactcacta tagggcgaat tgggtacggc 660

cgtcaaggcc aagcttcccg tgggggatcc accatacatg gagtcaaaaa ttcagatcga 720

ggatctaaca gaactcgccg tgaagactgg cgaacagttc atacagagtc ttttacgact 780

caatgacaag aagaaaatct tcgtcaacat ggtggagcac gacactctcg tctactccaa 840

gaatatcaaa gatacagtct cagaagacca aagggctatt gagacttttc aacaaagggt 900

aatatcggga aacctcctcg gattccattg cccagctatc tgtcacttca tcaaaaggac 960

agtagaaaag gaaggtggca cctacaaatg ccatcattgc gataaaggaa aggctatcgt 1020

tcaagatgcc tctgccgaca gtggtcccaa agatggaccc ccacccacga ggagcatcgt 1080

ggaaaaagaa gacgttccaa ccacgtcttc aaagcaagtg gattgatgtg atatctccac 1140

tgacgtaagg gatgacgcac aatcccacta tccttcgcaa gacccttcct ctatataagg 1200

aagttcattt catttggaga ggactcgaga attaagcaaa agaagaagaa gaagaagtcc 1260

aaaacc atg gct aaa ccg cct aag aaa aag cgg aag gtt cat atg aat 1308
Met Ala Lys Pro Pro Lys Lys Lys Arg Lys Val His Met Asn
1 5 10

acc aaa tac aac aaa gaa ttc ctt ctc tac cta gct ggt ttc gta gac 1356
Thr Lys Tyr Asn Lys Glu Phe Leu Leu Tyr Leu Ala Gly Phe Val Asp
15 20 25 30

gga gat gga tct att atc gca tca att agc cct cgg caa tcg tac aaa 1404
Gly Asp Gly Ser Ile Ile Ala Ser Ile Ser Pro Arg Gln Ser Tyr Lys
35 40 45

ttc aag cat gaa ctg cga ctt act ttc caa gtg aca cag aaa acc caa 1452
Phe Lys His Glu Leu Arg Leu Thr Phe Gln Val Thr Gln Lys Thr Gln
50 55 60

agg aga tgg ttc ctt gat aaa ctc gtg gac gaa atc ggc gtt gga aag 1500
Arg Arg Trp Phe Leu Asp Lys Leu Val Asp Glu Ile Gly Val Gly Lys
65 70 75

gtc aga gat aga ggg tcg gtg tcc gac tat agg ctc agt cag att aaa 1548
Val Arg Asp Arg Gly Ser Val Ser Asp Tyr Arg Leu Ser Gln Ile Lys
80 85 90

cct ttg cat aac ttc cta act caa ctt caa cca ttt ctg aaa ttg aag 1596
Pro Leu His Asn Phe Leu Thr Gln Leu Gln Pro Phe Leu Lys Leu Lys
95 100 105 110

cag aag cag gtaagtttct gcttctacct ttgatatata tataataatt 1645
Gln Lys Gln

atcattaatt agtagtaata taatatttca aatatttttt tcaaaataaa agaatgtagt 1705

atatagcaat tgcttttctg tagtttataa gtgtgtatat tttaatttat aacttttcta 1765

atatatgacc aaaacatggt gatgtgcag gca aat ctg gtt ctc aag ata ata 1818
Ala Asn Leu Val Leu Lys Ile Ile
115 120

gag caa cta cca agc gca aag gaa tct cca gac aag ttt ttg gaa gtg 1866
Glu Gln Leu Pro Ser Ala Lys Glu Ser Pro Asp Lys Phe Leu Glu Val
125 130 135

tgt acc tgg gtt gac caa atc gca gct ttg aat gat tcc aag aca cga 1914
Cys Thr Trp Val Asp Gln Ile Ala Ala Leu Asn Asp Ser Lys Thr Arg
140 145 150

aag aca act tct gag act gtg aga gca gtc ctt gat tca tta ccc ggt 1962
Lys Thr Thr Ser Glu Thr Val Arg Ala Val Leu Asp Ser Leu Pro Gly
155 160 165

tcg gtt ggt ggc tta agc cct agt cag gct agt tct gcc gct agt tct 2010
Ser Val Gly Gly Leu Ser Pro Ser Gln Ala Ser Ser Ala Ala Ser Ser
170 175 180 185

gcc tca agc tct cca ggt tct ggg ata tcc gaa gcc ctt aga gct ggt 2058

```
Ala Ser Ser Ser Pro Gly Ser Gly Ile Ser Glu Ala Leu Arg Ala Gly
                190                 195                 200

gct act aag agc aag gag ttt ctc ctg tat tta gcc gga ttt gtt gat      2106
Ala Thr Lys Ser Lys Glu Phe Leu Leu Tyr Leu Ala Gly Phe Val Asp
            205                 210                 215

ggg gat ggt tca atc att gcc tct atc tca cca aat cag agc cgt aag      2154
Gly Asp Gly Ser Ile Ile Ala Ser Ile Ser Pro Asn Gln Ser Arg Lys
        220                 225                 230

ttt aag cac caa ctg agg ttg aca ttc acc gtg aca cag aag act caa      2202
Phe Lys His Gln Leu Arg Leu Thr Phe Thr Val Thr Gln Lys Thr Gln
    235                 240                 245

aga aga tgg ttt ctg gat aag ctt gtc gat gaa att ggc gtg gga aag      2250
Arg Arg Trp Phe Leu Asp Lys Leu Val Asp Glu Ile Gly Val Gly Lys
250                 255                 260                 265

gtt cgt gat aga gga tct gtt agt gac tat cgc cta tcc cag att aaa      2298
Val Arg Asp Arg Gly Ser Val Ser Asp Tyr Arg Leu Ser Gln Ile Lys
                270                 275                 280

cct ctt cac aac ttc ctg acc cag ctt caa cct ttc ttg aaa tta aag      2346
Pro Leu His Asn Phe Leu Thr Gln Leu Gln Pro Phe Leu Lys Leu Lys
            285                 290                 295

cag aag cag gct aac ctg gtt ctc aaa atc att gag caa ctc cca tca      2394
Gln Lys Gln Ala Asn Leu Val Leu Lys Ile Ile Glu Gln Leu Pro Ser
        300                 305                 310

gca aaa gaa tca ccg gat aaa ttt ctg gag gta tgc act tgg gta gac      2442
Ala Lys Glu Ser Pro Asp Lys Phe Leu Glu Val Cys Thr Trp Val Asp
    315                 320                 325

caa att gct gct ctg aac gat tca aag act cga aaa acc act agt gag      2490
Gln Ile Ala Ala Leu Asn Asp Ser Lys Thr Arg Lys Thr Thr Ser Glu
330                 335                 340                 345

aca gtt cgt gct gtc tta gat tcc ttg tcc gag aaa aag aaa agc tct      2538
Thr Val Arg Ala Val Leu Asp Ser Leu Ser Glu Lys Lys Lys Ser Ser
                350                 355                 360

ccc tgattcccag ataagggaat tagggttcct atagggtttc gctcatgtgt          2591
Pro

tgagcatata agaaaccctt agtatgtatt tgtatttgta aaatacttct atcaataaaa   2651

tttctaattc ctaaaaccaa aatccagcct gcaggtctag ataagtggga tatcacgtga   2711

agcttgcaag ctccagcttt tgttcccttt agtgagggtt aattgcgcgc ttggcgtaat   2771

catggtcata gctgtttcct gtgtgaaatt gttatccgct cacaattcca cacaacatac   2831

gagccggaag cataaagtgt aaagcctggg gtgcctaatg agtgagctaa ctcacattaa   2891

ttgcgttgcg ctcactgccc gctttccagt cgggaaacct gtcgtgccag ctgcattaat   2951

gaatcggcca acgcgcgggg agaggcggtt tgcgtattgg gcgctcttcc gcttcctcgc   3011

tcactgactc gctgcgctcg gtcgttcggc tgcggcgagc ggtatcagct cactcaaagg   3071

cggtaatacg gttatccaca gaatcagggg ataacgcagg aaagaacatg tgagcaaaag   3131

gccagcaaaa ggccaggaac cgtaaaaagg ccgcgttgct ggcgtttttc cataggctcc   3191

gcccccctga cgagcatcac aaaaatcgac gctcaagtca gaggtggcga aacccgacag   3251

gactataaag ataccaggcg tttcccccctg gaagctccct cgtgcgctct cctgttccga  3311

ccctgccgct taccggatac ctgtccgcct ttctcccttc gggaagcgtg gcgctttctc   3371

atagctcacg ctgtaggtat ctcagttcgg tgtaggtcgt tcgctccaag ctgggctgtg   3431

tgcacgaacc ccccgttcag cccgaccgct gcgccttatc cggtaactat cgtcttgagt   3491
```

ccaacccggt aagacacgac ttatcgccac tggcagcagc cactggtaac aggattagca 3551

gagcgaggta tgtaggcggt gctacagagt tcttgaagtg gtggcctaac tacggctaca 3611

ctagaaggac agtatttggt atctgcgctc tgctgaagcc agttaccttc ggaaaaagag 3671

ttggtagctc ttgatccggc aaacaaacca ccgctggtag cggtggtttt tttgtttgca 3731

agcagcagat tacgcgcaga aaaaaaggat ctcaagaaga tcctttgatc ttttctacgg 3791

ggtctgacgc tcagtggaac gaaaactcac gttaagggat tttggtcatg agattatcaa 3851

aaaggatctt cacctagatc cttttaaatt aaaaatgaag ttttaaatca atctaaagta 3911

tatatgagta aacttggtct gacagttacc aatgcttaat cagtgaggca cctatctcag 3971

cgatctgtct atttcgttca tccatagttg cctgactccc cgtcgtgtag ataactacga 4031

tacgggaggg cttaccatct ggccccagtg ctgcaatgat accgcgagat ccacgctcac 4091

cggctccaga tttatcagca ataaaccagc cagccggaag ggccgagcgc agaagtggtc 4151

ctgcaacttt atccgcctcc atccagtcta ttaattgttg ccgggaagct agagtaagta 4211

gttcgccagt taatagtttg cgcaacgttg ttgccattgc tacaggcatc gtggtgtcac 4271

gctcgtcgtt tggtatggct tcattcagct ccggttccca acgatcaagg cgagttacat 4331

gatcccccat gttgtgcaaa aaagcggtta gctccttcgg tcctccgatc gttgtcagaa 4391

gtaagttggc cgcagtgtta tcactcatgg ttatggcagc actgcataat tctcttactg 4451

tcatgccatc cgtaagatgc ttttctgtga ctggtgagta ctcaaccaag tcattctgag 4511

aatagtgtat gcggcgaccg agttgctctt gcccggcgtc aatacgggat aataccgcgc 4571

cacatagcag aactttaaaa gtgctcatca ttggaaaacg ttcttcgggg cgaaaactct 4631

caaggatctt accgctgttg agatccagtt cgatgtaacc cactcgtgca cccaactgat 4691

cttcagcatc ttttactttc accagcgttt ctgggtgagc aaaaacagga aggcaaaatg 4751

ccgcaaaaaa gggaataagg gcgacacgga aatgttgaat actcatactc ttcctttttc 4811

aatattattg aagcatttat cagggttatt gtctcatgag cggatacata tttgaatgta 4871

tttagaaaaa taaacaaata ggggttccgc gcacatttcc ccgaaaagtg ccac 4925

<210> 18
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 18

Met Ala Lys Pro Pro Lys Lys Lys Arg Lys Val His Met Asn Thr Lys
1 5 10 15

Tyr Asn Lys Glu Phe Leu Leu Tyr Leu Ala Gly Phe Val Asp Gly Asp
20 25 30

Gly Ser Ile Ile Ala Ser Ile Ser Pro Arg Gln Ser Tyr Lys Phe Lys
35 40 45

His Glu Leu Arg Leu Thr Phe Gln Val Thr Gln Lys Thr Gln Arg Arg
50 55 60

```
Trp Phe Leu Asp Lys Leu Val Asp Glu Ile Gly Val Gly Lys Val Arg
65                  70                  75                  80

Asp Arg Gly Ser Val Ser Asp Tyr Arg Leu Ser Gln Ile Lys Pro Leu
                85                  90                  95

His Asn Phe Leu Thr Gln Leu Gln Pro Phe Leu Lys Leu Lys Gln Lys
            100                 105                 110

Gln Ala Asn Leu Val Leu Lys Ile Ile Glu Gln Leu Pro Ser Ala Lys
        115                 120                 125

Glu Ser Pro Asp Lys Phe Leu Glu Val Cys Thr Trp Val Asp Gln Ile
    130                 135                 140

Ala Ala Leu Asn Asp Ser Lys Thr Arg Lys Thr Thr Ser Glu Thr Val
145                 150                 155                 160

Arg Ala Val Leu Asp Ser Leu Pro Gly Ser Val Gly Gly Leu Ser Pro
                165                 170                 175

Ser Gln Ala Ser Ser Ala Ala Ser Ser Ala Ser Ser Ser Pro Gly Ser
            180                 185                 190

Gly Ile Ser Glu Ala Leu Arg Ala Gly Ala Thr Lys Ser Lys Glu Phe
        195                 200                 205

Leu Leu Tyr Leu Ala Gly Phe Val Asp Gly Asp Gly Ser Ile Ile Ala
    210                 215                 220

Ser Ile Ser Pro Asn Gln Ser Arg Lys Phe Lys His Gln Leu Arg Leu
225                 230                 235                 240

Thr Phe Thr Val Thr Gln Lys Thr Gln Arg Arg Trp Phe Leu Asp Lys
                245                 250                 255

Leu Val Asp Glu Ile Gly Val Gly Lys Val Arg Asp Arg Gly Ser Val
            260                 265                 270

Ser Asp Tyr Arg Leu Ser Gln Ile Lys Pro Leu His Asn Phe Leu Thr
        275                 280                 285

Gln Leu Gln Pro Phe Leu Lys Leu Lys Gln Lys Gln Ala Asn Leu Val
    290                 295                 300

Leu Lys Ile Ile Glu Gln Leu Pro Ser Ala Lys Glu Ser Pro Asp Lys
305                 310                 315                 320

Phe Leu Glu Val Cys Thr Trp Val Asp Gln Ile Ala Ala Leu Asn Asp
                325                 330                 335

Ser Lys Thr Arg Lys Thr Thr Ser Glu Thr Val Arg Ala Val Leu Asp
            340                 345                 350

Ser Leu Ser Glu Lys Lys Lys Ser Ser Pro
        355                 360
```