SEQUENCE LISTING

<110> UCB Pharma, S.A.

<120> BACTERIAL HOST STRAIN EXPRESSING RECOMBINANT ANTIBODY FRAGMENT

<130> G0157 WO

<150> EP11173880.3
<151> 2011-07-13

<160> 52

<170> PatentIn version 3.5

<210> 1
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 342 CDR-H1

<400> 1

Gly Phe Ser Ser Thr Asn Tyr His Val His
1 5 10

<210> 2
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 342 CDR-H2

<400> 2

Val Ile Trp Gly Asp Gly Asp Thr Ser Tyr Asn Ser Val Leu Lys Ser
1 5 10 15

<210> 3
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 342 CDR-H3

<400> 3

Gln Leu Thr His Tyr Tyr Val Leu Ala Ala
1 5 10

<210> 4
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 342 CDR-L1

<400> 4

Arg Ala Ser Glu Asp Leu Tyr Tyr Asn Leu Ala
1 5 10

<210> 5
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 342 CDR-L2

<400> 5

Asp Thr Tyr Arg Leu Ala Asp
1 5

<210> 6
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 342 CDR-L3

<400> 6

Gln Gln Tyr Tyr Lys Phe Pro Phe Thr
1 5

<210> 7
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 342 variable light chain (gL4)

<220>
<221> sig_peptide
<222> (1)..(63)

<220>
<221> CDS
<222> (64)..(384)

<400> 7
atgaaaaaga cagctatcgc aattgcagtg gccttggctg gtttcgctac cgtagcgcaa 60

gct gat atc cag atg acc cag agt cca agc agt ctc tcc gcc agc gta 108
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

ggc gat cgt gtg act att acc tgt cgt gcc agt gag gac ctc tat tac 156
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Leu Tyr Tyr

```
                20                  25                  30

aac ctg gcc tgg tat cag cgt aaa ccg ggc aaa gcc ccg aag ctg ctc        204
Asn Leu Ala Trp Tyr Gln Arg Lys Pro Gly Lys Ala Pro Lys Leu Leu
            35                  40                  45

atc tat gat acg tac cgc ctg gct gac ggt gtg cca agc cgt ttc agt        252
Ile Tyr Asp Thr Tyr Arg Leu Ala Asp Gly Val Pro Ser Arg Phe Ser
        50                  55                  60

ggc agt ggc agc ggt act gac tat acc ctc aca att tcg tct ctc cag        300
Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln
    65                  70                  75

ccg gaa gat ttc gcc tct tac tat tgt cag caa tat tac aag ttc cct        348
Pro Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Tyr Tyr Lys Phe Pro
80                  85                  90                  95

ttc acc ttc ggt cag ggc act aaa gta gaa atc aaa                       384
Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
                100                 105


<210>  8
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  8

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Leu Tyr Tyr Asn
            20                  25                  30


Leu Ala Trp Tyr Gln Arg Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Thr Tyr Arg Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Tyr Tyr Lys Phe Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105


<210>  9
<211>  351
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 342 variable heavy chain (gH1)

<220>
<221> CDS
<222> (1)..(351)

<400> 9

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gag gtg cag ctg gtc gag tct gga ggc ggg ctt gtc cag cct ggt ggg          48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15

agc ctg cgt ctc tct tgt gca gtg agc ggc ttc agc tct acc aat tac          96
Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ser Ser Thr Asn Tyr
            20                  25                  30

cat gtg cac tgg gtg cgt cag gca cct ggg aag ggc ctg gag tgg atg         144
His Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
        35                  40                  45

ggt gtt att tgg ggc gac ggc gat aca tcc tac aac tcc gtc ctg aag         192
Gly Val Ile Trp Gly Asp Gly Asp Thr Ser Tyr Asn Ser Val Leu Lys
    50                  55                  60

agc cgt ttc acc att tcc cgt gac acc tca aag aat acc gtt tac ctc         240
Ser Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Val Tyr Leu
65                  70                  75                  80

cag atg aac tct ctc cgc gca gag gac aca gca gtc tat tac tgt gca         288
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

cgt caa ctg acc cac tat tac gtt ttg gca gcc tgg ggt caa ggg act         336
Arg Gln Leu Thr His Tyr Tyr Val Leu Ala Ala Trp Gly Gln Gly Thr
            100                 105                 110

ctg gtc aca gtc tcg                                                    351
Leu Val Thr Val Ser
        115
```

<210> 10
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 10

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ser Ser Thr Asn Tyr
            20                  25                  30
```

```
His Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
        35                  40                  45

Gly Val Ile Trp Gly Asp Gly Asp Thr Ser Tyr Asn Ser Val Leu Lys
    50                  55                  60

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

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Gln Leu Thr His Tyr Tyr Val Leu Ala Ala Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser
        115
```

<210> 11
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 342 gL4 (V+C)

<220>
<221> CDS
<222> (64)..(705)

<400> 11

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atgaaaaaga cagctatcgc aattgcagtg gccttggctg gtttcgctac cgtagcgcaa       60

gct gat atc cag atg acc cag agt cca agc agt ctc tcc gcc agc gta        108
    Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
    1               5                   10                  15

ggc gat cgt gtg act att acc tgt cgt gcc agt gag gac ctc tat tac        156
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Leu Tyr Tyr
                20                  25                  30

aac ctg gcc tgg tat cag cgt aaa ccg ggc aaa gcc ccg aag ctg ctc        204
Asn Leu Ala Trp Tyr Gln Arg Lys Pro Gly Lys Ala Pro Lys Leu Leu
            35                  40                  45

atc tat gat acg tac cgc ctg gct gac ggt gtg cca agc cgt ttc agt        252
Ile Tyr Asp Thr Tyr Arg Leu Ala Asp Gly Val Pro Ser Arg Phe Ser
        50                  55                  60

ggc agt ggc agc ggt act gac tat acc ctc aca att tcg tct ctc cag        300
Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln
    65                  70                  75

ccg gaa gat ttc gcc tct tac tat tgt cag caa tat tac aag ttc cct        348
Pro Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Tyr Tyr Lys Phe Pro
```

80 85 90 95

ttc acc ttc ggt cag ggc act aaa gta gaa atc aaa cgt acg gta gcg 396
Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100 105 110

gcc cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct 444
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag 492
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc 540
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155

cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc 588
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
160 165 170 175

agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc 636
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

tac gcc tgc gaa gtc acc cat cag ggc ctg agc tca cca gta aca aaa 684
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

agt ttt aat aga ggg gag tgt 705
Ser Phe Asn Arg Gly Glu Cys
210

<210> 12
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 12

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Leu Tyr Tyr Asn
20 25 30

Leu Ala Trp Tyr Gln Arg Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Thr Tyr Arg Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

```
Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Tyr Tyr Lys Phe Pro Phe
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 13
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 342 gH1 Fab (no hinge) HC with constant region

<220>
<221> CDS
<222> (64)..(726)

<400> 13

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atgaagaaga ctgctatagc aattgcagtg gcgctagctg gtttcgccac cgtggcgcaa       60

gct gag gtt cag ctg gtc gag tct gga ggc ggg ctt gtc cag cct ggt         108
    Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
    1               5                   10                  15

ggg agc ctg cgt ctc tct tgt gca gtg agc ggc ttc agc tct acc aat         156
Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ser Ser Thr Asn
                20                  25                  30
```

```
tac cat gtg cac tgg gtg cgt cag gca cct ggg aag ggc ctg gag tgg          204
Tyr His Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
            35                  40                  45

atg ggt gtt att tgg ggc gac ggc gat aca tcc tac aac tcc gtc ctg          252
Met Gly Val Ile Trp Gly Asp Gly Asp Thr Ser Tyr Asn Ser Val Leu
        50                  55                  60

aag agc cgt ttc acc att tcc cgt gac acc tca aag aat acc gtt tac          300
Lys Ser Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Val Tyr
    65                  70                  75

ctc cag atg aac tct ctc cgc gca gag gac aca gca gtc tat tac tgt          348
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
80                  85                  90                  95

gca cgt caa ctg acc cac tat tac gtt ttg gca gcc tgg ggt caa ggg          396
Ala Arg Gln Leu Thr His Tyr Tyr Val Leu Ala Ala Trp Gly Gln Gly
                100                 105                 110

act ctg gtc aca gtc tcg agc gct tct aca aag ggc cca tcg gtc ttc          444
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
            115                 120                 125

ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg          492
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
        130                 135                 140

ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg          540
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
    145                 150                 155

aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta          588
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
160                 165                 170                 175

cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc          636
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
                180                 185                 190

agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc          684
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
            195                 200                 205

agc aac acc aag gtc gac aag aaa gtt gag ccc aaa tct tgt                  726
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
        210                 215                 220
```

<210> 14
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 14

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ser Ser Thr Asn Tyr
            20                  25                  30

His Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
        35                  40                  45

Gly Val Ile Trp Gly Asp Gly Asp Thr Ser Tyr Asn Ser Val Leu Lys
    50                  55                  60

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

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Gln Leu Thr His Tyr Tyr Val Leu Ala Ala Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220
```

<210> 15
<211> 750
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 342 gH1 Fab' HC with constant region

<220>

<221> CDS
<222> (64)..(750)

<400> 15
atgaagaaga ctgctatagc aattgcagtg gcgctagctg gtttcgccac cgtggcgcaa 60

gct gag gtt cag ctg gtc gag tct gga ggc ggg ctt gtc cag cct ggt 108
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15

ggg agc ctg cgt ctc tct tgt gca gtg agc ggc ttc agc tct acc aat 156
Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ser Ser Thr Asn
20 25 30

tac cat gtg cac tgg gtg cgt cag gca cct ggg aag ggc ctg gag tgg 204
Tyr His Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
35 40 45

atg ggt gtt att tgg ggc gac ggc gat aca tcc tac aac tcc gtc ctg 252
Met Gly Val Ile Trp Gly Asp Gly Asp Thr Ser Tyr Asn Ser Val Leu
50 55 60

aag agc cgt ttc acc att tcc cgt gac acc tca aag aat acc gtt tac 300
Lys Ser Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Val Tyr
65 70 75

ctc cag atg aac tct ctc cgc gca gag gac aca gca gtc tat tac tgt 348
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
80 85 90 95

gca cgt caa ctg acc cac tat tac gtt ttg gca gcc tgg ggt caa ggg 396
Ala Arg Gln Leu Thr His Tyr Tyr Val Leu Ala Ala Trp Gly Gln Gly
100 105 110

act ctg gtc aca gtc tcg agc gct tct aca aag ggc cca tcg gtc ttc 444
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg 492
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg 540
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155

aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta 588
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
160 165 170 175

cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc 636
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc 684
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

agc aac acc aag gtc gac aag aaa gtt gag ccc aaa tct tgt gac aaa 732
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

act cac aca tgc gcc gcg 750

Thr His Thr Cys Ala Ala
225

<210> 16
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ser Ser Thr Asn Tyr
20 25 30

His Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Trp Gly Asp Gly Asp Thr Ser Tyr Asn Ser Val Leu Lys
50 55 60

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

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gln Leu Thr His Tyr Tyr Val Leu Ala Ala Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser

195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Ala Ala
225

<210> 17
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: hu342 kappa LC

<220>
<221> CDS
<222> (1)..(711)

<400> 17

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atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg cta ctc tgg          48
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1               5                   10                  15

ctc cga ggt gcc aga tgt gat atc cag atg acc cag agt cca agc agt          96
Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
            20                  25                  30

ctc tcc gcc agc gta ggc gat cgt gtg act att acc tgt cgt gcc agt         144
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
        35                  40                  45

gag gac ctc tat tac aac ctg gcc tgg tat cag cgt aaa ccg ggc aaa         192
Glu Asp Leu Tyr Tyr Asn Leu Ala Trp Tyr Gln Arg Lys Pro Gly Lys
    50                  55                  60

gcc ccg aag ctg ctc atc tat gat acg tac cgc ctg gct gac ggt gtg         240
Ala Pro Lys Leu Leu Ile Tyr Asp Thr Tyr Arg Leu Ala Asp Gly Val
65                  70                  75                  80

cca agc cgt ttc agt ggc agt ggc agc ggt act gac tat acc ctc aca         288
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr
                85                  90                  95

att tcg tct ctc cag ccg gaa gat ttc gcc tct tac tat tgt cag caa         336
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln
            100                 105                 110

tat tac aag ttc cct ttc acc ttc ggt cag ggc act aaa gta gaa atc         384
Tyr Tyr Lys Phe Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
        115                 120                 125

aaa cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat         432
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
    130                 135                 140

gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac         480
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
```

```
145                 150                 155                 160

ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc        528
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
                165                 170                 175

caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac        576
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180                 185                 190

agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac        624
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
        195                 200                 205

gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc        672
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
    210                 215                 220

tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag                    711
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 18
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 18

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Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1               5                   10                  15

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
            20                  25                  30

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

Glu Asp Leu Tyr Tyr Asn Leu Ala Trp Tyr Gln Arg Lys Pro Gly Lys
    50                  55                  60

Ala Pro Lys Leu Leu Ile Tyr Asp Thr Tyr Arg Leu Ala Asp Gly Val
65                  70                  75                  80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr
                85                  90                  95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln
            100                 105                 110

Tyr Tyr Lys Phe Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
        115                 120                 125
```

```
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
    130                 135                 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145                 150                 155                 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
                165                 170                 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180                 185                 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
        195                 200                 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
    210                 215                 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 19
<211> 1392
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: hu342 aglyP-huIgG4 HC

<220>
<221> CDS
<222> (1)..(1392)

<400> 19

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atg gac tgg acc tgg agg gtc ttc tgc ttg ctg gct gta gca cca ggt          48
Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
1               5                   10                  15

gcc cac tcc gaa gta caa ttg gtc gag tct gga ggc ggg ctt gtc cag          96
Ala His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
            20                  25                  30

cct ggt ggg agc ctg cgt ctc tct tgt gca gtg agc ggc ttc agc tct         144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ser Ser
        35                  40                  45

acc aat tac cat gtg cac tgg gtg cgt cag gca cct ggg aag ggc ctg         192
Thr Asn Tyr His Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

gag tgg atg ggt gtt att tgg ggc gac ggc gat aca tcc tac aac tcc         240
Glu Trp Met Gly Val Ile Trp Gly Asp Gly Asp Thr Ser Tyr Asn Ser
65                  70                  75                  80
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gtc ctg aag agc cgt ttc acc att tcc cgt gac acc tca aag aat acc        288
Val Leu Lys Ser Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr
                85                  90                  95

gtt tac ctc cag atg aac tct ctc cgc gca gag gac aca gca gtc tat        336
Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
            100                 105                 110

tac tgt gca cgt caa ctg acc cac tat tac gtt ttg gca gcc tgg ggt        384
Tyr Cys Ala Arg Gln Leu Thr His Tyr Tyr Val Leu Ala Ala Trp Gly
        115                 120                 125

caa ggg act ctg gtc aca gtc tcg agc gct tca acc aag ggc cca tcc        432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gcg ccc tgc tcc aga tct acc tcc gag agc aca gcc        480
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg        528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct        576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg        624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acg aag acc tac acc tgc aac gta gat cac        672
Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag tcc aaa tat ggt        720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
225                 230                 235                 240

ccc cca tgc cca ccg tgc cca gca cct gag ttc ctg ggg gga cca tca        768
Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser
                245                 250                 255

gtc ttc ctg ttc ccc cca aaa ccc aag gac act ctc atg atc tcc cgg        816
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
            260                 265                 270

acc cct gag gtc acg tgc gtg gtg gtg gac gtg agc cag gaa gac ccc        864
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
        275                 280                 285

gag gtc cag ttc aac tgg tac gtg gat ggc gtg gag gtg cat aat gcc        912
Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
    290                 295                 300

aag aca aag ccg cgg gag gag cag ttc aac agc gcg tac cgt gtg gtc        960
Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Ala Tyr Arg Val Val
305                 310                 315                 320

agc gtc ctc acc gtc ctg cac cag gac tgg ctg aac ggc aag gag tac       1008
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
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                325                 330                 335

aag tgc aag gtc tcc aac aaa ggc ctc ccg tcc tcc atc gag aaa acc        1056
Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
            340                 345                 350

atc tcc aaa gcc aaa ggg cag ccc cga gag cca caa gtg tac acc ctg        1104
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
        355                 360                 365

ccc cca tcc cag gag gag atg acc aag aac cag gtc agc ctg acc tgc        1152
Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
    370                 375                 380

ctg gtc aaa ggc ttc tac ccc agc gac atc gcc gtg gag tgg gag agc        1200
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
385                 390                 395                 400

aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtc ctc gat        1248
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
                405                 410                 415

tcc gac ggc tcc ttc ttc ctc tac agc agg cta acc gtg gac aag agc        1296
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser
            420                 425                 430

agg tgg cag gag ggg aat gtc ttc tca tgc tcc gtg atg cat gag gct        1344
Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
        435                 440                 445

ctg cac aac cac tac aca cag aag agc ctc tcc ctg tct ctg ggt tga        1392
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
    450                 455                 460
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<210> 20
<211> 463
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 20

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Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
1               5                   10                  15

Ala His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
            20                  25                  30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ser Ser
        35                  40                  45

Thr Asn Tyr His Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Met Gly Val Ile Trp Gly Asp Gly Asp Thr Ser Tyr Asn Ser
65                  70                  75                  80
```

```
Val Leu Lys Ser Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr
                85                  90                  95

Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
            100                 105                 110

Tyr Cys Ala Arg Gln Leu Thr His Tyr Tyr Val Leu Ala Ala Trp Gly
        115                 120                 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
145                 150                 155                 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His
    210                 215                 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
225                 230                 235                 240

Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser
                245                 250                 255

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
            260                 265                 270

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
        275                 280                 285

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
    290                 295                 300

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Ala Tyr Arg Val Val
305                 310                 315                 320

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
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325 330 335

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
340 345 350

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
355 360 365

Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
370 375 380

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
385 390 395 400

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
405 410 415

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser
420 425 430

Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
435 440 445

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
450 455 460

<210> 21
<211> 1438
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 342 gL4gH1 VH3 (V+C) Fab (no hinge) vector DNA

<400> 21
atgaaaaaga cagctatcgc aattgcagtg gccttggctg gtttcgctac cgtagcgcaa 60

gctgatatcc agatgaccca gagtccaagc agtctctccg ccagcgtagg cgatcgtgtg 120

actattacct gtcgtgccag tgaggacctc tattacaacc tggcctggta tcagcgtaaa 180

ccgggcaaag ccccgaagct gctcatctat gatacgtacc gcctggctga cggtgtgcca 240

agccgtttca gtggcagtgg cagcggtact gactataccc tcacaatttc gtctctccag 300

ccggaagatt tcgcctctta ctattgtcag caatattaca agttcccttt caccttcggt 360

cagggcacta aagtagaaat caaacgtacg gtagcggccc catctgtctt catcttcccg 420

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 480

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 540

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 600

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 660

ggcctgagct caccagtaac aaaaagtttt aatagagggg agtgttaaaa tgaagaagac 720

tgctatagca attgcagtgg cgctagctgg tttcgccacc gtggcgcaag ctgaggttca 780

gctggtcgag tctggaggcg ggcttgtcca gcctggtggg agcctgcgtc tctcttgtgc 840

agtgagcggc ttcagctcta ccaattacca tgtgcactgg gtgcgtcagg cacctgggaa 900

gggcctggag tggatgggtg ttatttgggg cgacggcgat acatcctaca actccgtcct 960

gaagagccgt ttcaccattt cccgtgacac ctcaaagaat accgtttacc tccagatgaa 1020

ctctctccgc gcagaggaca cagcagtcta ttactgtgca cgtcaactga cccactatta 1080

cgttttggca gcctggggtc aagggactct ggtcacagtc tcgagcgctt ctacaaaggg 1140

cccatcggtc ttcccctgg caccctcctc caagagcacc tctgggggca cagcggccct 1200

gggctgcctg gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc 1260

cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactccct 1320

cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt 1380

gaatcacaag cccagcaaca ccaaggtcga caagaaagtt gagcccaaat cttgttaa 1438

<210> 22
<211> 1459
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 342 gL4gH1 VH3 (V+C) Fab' vector DNA

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gctgatatcc agatgaccca gagtccaagc agtctctccg ccagcgtagg cgatcgtgtg 120

actattacct gtcgtgccag tgaggacctc tattacaacc tggcctggta tcagcgtaaa 180

ccgggcaaag ccccgaagct gctcatctat gatacgtacc gcctggctga cggtgtgcca 240

agccgtttca gtggcagtgg cagcggtact gactataccc tcacaatttc gtctctccag 300

ccggaagatt tcgcctctta ctattgtcag caatattaca agttcccttt caccttcggt 360

cagggcacta aagtagaaat caaacgtacg gtagcggccc catctgtctt catcttcccg 420

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 480

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 540

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 600

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 660

ggcctgagct caccagtaac aaaaagtttt aatagagggg agtgttaaaa tgaagaagac 720

tgctatagca attgcagtgg cgctagctgg tttcgccacc gtggcgcaag ctgaggttca 780

gctggtcgag tctggaggcg ggcttgtcca gcctggtggg agcctgcgtc tctcttgtgc 840

agtgagcggc ttcagctcta ccaattacca tgtgcactgg gtgcgtcagg cacctgggaa 900

gggcctggag tggatgggtg ttatttgggg cgacggcgat acatcctaca actccgtcct 960

gaagagccgt ttcaccattt cccgtgacac ctcaaagaat accgtttacc tccagatgaa 1020

ctctctccgc gcagaggaca cagcagtcta ttactgtgca cgtcaactga cccactatta 1080

cgttttggca gcctggggtc aagggactct ggtcacagtc tcgagcgctt ctacaaaggg 1140

cccatcggtc ttcccctgg caccctcctc caagagcacc tctgggggca cagcggccct 1200

gggctgcctg gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc 1260

cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactccct 1320

cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt 1380

gaatcacaag cccagcaaca ccaaggtcga caagaaagtt gagcccaaat cttgtgacaa 1440

aactcacaca tgcgccgcg 1459

<210> 23
<211> 986
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (379)..(945)

<300>
<308> GenBank / D86610
<309> 2009-01-10
<313> (1)..(986)

<400> 23
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tctctaagta aatgaatgga ttgcatgcgt ttcactcaat tgtactttaa ttgaccaacc 120

ccgcttatta actttctgta tcacttttttc ttataaaaaa tcatgtaaaa ccgctcgcca 180

agaccgcacc aatcgggtaa tctcgaactc gttttgcctc ggcggtagat tatcctcaca 240

gcatataatt ttgtgcgtta gtccacagat ttggccttaa ggaattgttt caacatgccc 300

aggtaattag tctcgtgtcg cttggcattt ttttataacg atatttgtcg ttaaggactt 360

caagggaaaa caaacaac atg gtc aaa tct caa ccg att ttg aga tat atc 411
Met Val Lys Ser Gln Pro Ile Leu Arg Tyr Ile
1 5 10

ttg cgc ggg att ccc gcg att gca gta gcg gtt ctg ctt tct gca tgt 459
Leu Arg Gly Ile Pro Ala Ile Ala Val Ala Val Leu Leu Ser Ala Cys

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            15                  20                  25

agt gca aat aac acc gca aag aat atg cat cct gag aca cgt gca gtg        507
Ser Ala Asn Asn Thr Ala Lys Asn Met His Pro Glu Thr Arg Ala Val
        30                  35                  40

ggt agt gaa aca tca tca ctg caa gct tct cag gat gaa ttt gaa aac        555
Gly Ser Glu Thr Ser Ser Leu Gln Ala Ser Gln Asp Glu Phe Glu Asn
    45                  50                  55

ctg gtt cgt aat gtc gac gta aaa tcg cga att atg gat cag tat gct        603
Leu Val Arg Asn Val Asp Val Lys Ser Arg Ile Met Asp Gln Tyr Ala
60                  65                  70                  75

gac tgg aaa ggc gta cgt tat cgt ctg ggc ggc agc act aaa aaa ggt        651
Asp Trp Lys Gly Val Arg Tyr Arg Leu Gly Gly Ser Thr Lys Lys Gly
                80                  85                  90

atc gat tgt tct ggt ttc gta cag cgt aca ttc cgt gag caa ttt ggc        699
Ile Asp Cys Ser Gly Phe Val Gln Arg Thr Phe Arg Glu Gln Phe Gly
            95                  100                 105

tta gaa ctt ccg cgt tcg act tac gaa cag cag gaa atg ggt aaa tct        747
Leu Glu Leu Pro Arg Ser Thr Tyr Glu Gln Gln Glu Met Gly Lys Ser
        110                 115                 120

gtt tcc cgc agt aat ttg cgt acg ggt gat tta gtt ctg ttc cgt gcc        795
Val Ser Arg Ser Asn Leu Arg Thr Gly Asp Leu Val Leu Phe Arg Ala
    125                 130                 135

ggt tca acg gga cgc cat gtc ggt att tat atc ggc aac aat cag ttt        843
Gly Ser Thr Gly Arg His Val Gly Ile Tyr Ile Gly Asn Asn Gln Phe
140                 145                 150                 155

gtc cat gct tcc acc agc agt ggt gtt att att tcc agc atg aat gaa        891
Val His Ala Ser Thr Ser Ser Gly Val Ile Ile Ser Ser Met Asn Glu
                160                 165                 170

ccg tac tgg aag aag cgt tac aac gaa gca cgc cgg gtt ctc agc cgc        939
Pro Tyr Trp Lys Lys Arg Tyr Asn Glu Ala Arg Arg Val Leu Ser Arg
            175                 180                 185

agc taa taaaccgttt ggatgcaatc ccttggctat cctgacgagt t                986
Ser
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<210> 24
<211> 188
<212> PRT
<213> Escherichia coli

<400> 24

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Met Val Lys Ser Gln Pro Ile Leu Arg Tyr Ile Leu Arg Gly Ile Pro
1               5                   10                  15

Ala Ile Ala Val Ala Val Leu Leu Ser Ala Cys Ser Ala Asn Asn Thr
            20                  25                  30

Ala Lys Asn Met His Pro Glu Thr Arg Ala Val Gly Ser Glu Thr Ser
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35 40 45

Ser Leu Gln Ala Ser Gln Asp Glu Phe Glu Asn Leu Val Arg Asn Val
50 55 60

Asp Val Lys Ser Arg Ile Met Asp Gln Tyr Ala Asp Trp Lys Gly Val
65 70 75 80

Arg Tyr Arg Leu Gly Gly Ser Thr Lys Lys Gly Ile Asp Cys Ser Gly
85 90 95

Phe Val Gln Arg Thr Phe Arg Glu Gln Phe Gly Leu Glu Leu Pro Arg
100 105 110

Ser Thr Tyr Glu Gln Gln Glu Met Gly Lys Ser Val Ser Arg Ser Asn
115 120 125

Leu Arg Thr Gly Asp Leu Val Leu Phe Arg Ala Gly Ser Thr Gly Arg
130 135 140

His Val Gly Ile Tyr Ile Gly Asn Asn Gln Phe Val His Ala Ser Thr
145 150 155 160

Ser Ser Gly Val Ile Ile Ser Ser Met Asn Glu Pro Tyr Trp Lys Lys
165 170 175

Arg Tyr Asn Glu Ala Arg Arg Val Leu Ser Arg Ser
180 185

<210> 25
<211> 2196
<212> DNA
<213> Escherichia coli

<220>
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<222> (69)..(2117)

<220>
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<222> (69)..(134)

<300>
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<309> 1993-04-26
<313> (1)..(2196)

<400> 25
gaattcgggt atgtctttga ttgtgcgcgc agaacacctg gtgttctgaa acggaggccg 60

ggccaggc atg aac atg ttt ttt agg ctt acc gcg tta gct ggc ctg ctt 110
Met Asn Met Phe Phe Arg Leu Thr Ala Leu Ala Gly Leu Leu

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          1               5                  10

gca ata gca ggc cag acc ttc gct gta gaa gat atc acg cgt gct gat        158
Ala Ile Ala Gly Gln Thr Phe Ala Val Glu Asp Ile Thr Arg Ala Asp
15                  20                  25                  30

caa att ccg gta tta aag gaa gag acg cag cat gcg acg gta agt gag        206
Gln Ile Pro Val Leu Lys Glu Glu Thr Gln His Ala Thr Val Ser Glu
                35                  40                  45

cgc gta acg tcg cgc ttc acc cgt tct cat tat cgc cag ttc gac ctc        254
Arg Val Thr Ser Arg Phe Thr Arg Ser His Tyr Arg Gln Phe Asp Leu
            50                  55                  60

gat cag gca ttt tcg gcc aaa atc ttt gac cgc tac ctg aat ctg ctc        302
Asp Gln Ala Phe Ser Ala Lys Ile Phe Asp Arg Tyr Leu Asn Leu Leu
        65                  70                  75

gat tac agc cac aac gtg ctg ctg gca agc gat gtt gaa cag ttc gcg        350
Asp Tyr Ser His Asn Val Leu Leu Ala Ser Asp Val Glu Gln Phe Ala
    80                  85                  90

aaa aag aaa acc gag tta ggc gat gaa ctg cgt tca ggc aaa ctc gac        398
Lys Lys Lys Thr Glu Leu Gly Asp Glu Leu Arg Ser Gly Lys Leu Asp
95                  100                 105                 110

gtt ttc tac gat ctc tac aat ctg gcg caa aag cgc cgt ttt gag cgt        446
Val Phe Tyr Asp Leu Tyr Asn Leu Ala Gln Lys Arg Arg Phe Glu Arg
                115                 120                 125

tac cag tac gct ttg tcg gta ctg gaa aag ccg atg gat ttc acc ggc        494
Tyr Gln Tyr Ala Leu Ser Val Leu Glu Lys Pro Met Asp Phe Thr Gly
            130                 135                 140

aac gac act tat aac ctt gac cgc agc aaa gcg ccc tgg ccg aaa aac        542
Asn Asp Thr Tyr Asn Leu Asp Arg Ser Lys Ala Pro Trp Pro Lys Asn
        145                 150                 155

gag gct gag ttg aac gcg ctg tgg gac agt aaa gtc aaa ttc gac gag        590
Glu Ala Glu Leu Asn Ala Leu Trp Asp Ser Lys Val Lys Phe Asp Glu
    160                 165                 170

tta agc ctg aag ctg aca gga aaa acg gat aaa gaa att cgt gaa acc        638
Leu Ser Leu Lys Leu Thr Gly Lys Thr Asp Lys Glu Ile Arg Glu Thr
175                 180                 185                 190

ctg act cgc cgc tac aaa ttt gcc att cgt cgt ctg gcg caa acc aac        686
Leu Thr Arg Arg Tyr Lys Phe Ala Ile Arg Arg Leu Ala Gln Thr Asn
                195                 200                 205

agc gaa gat gtt ttc tcg ctg gca atg acg gcg ttt gcg cgt gaa atc        734
Ser Glu Asp Val Phe Ser Leu Ala Met Thr Ala Phe Ala Arg Glu Ile
            210                 215                 220

gac ccg cat acc aac tat ctt tcc ccg cgt aat acc gaa cag ttc aac        782
Asp Pro His Thr Asn Tyr Leu Ser Pro Arg Asn Thr Glu Gln Phe Asn
        225                 230                 235

act gaa atg agt ttg tcg ctg gaa ggt att ggc gca gtg ctg caa atg        830
Thr Glu Met Ser Leu Ser Leu Glu Gly Ile Gly Ala Val Leu Gln Met
    240                 245                 250

gat gat gac tac acc gtt atc aat tcg atg gtg gca ggt ggt ccg gca        878
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Asp Asp Asp Tyr Thr Val Ile Asn Ser Met Val Ala Gly Gly Pro Ala
255                 260                 265                 270

gcg aag agt aaa gct atc agc gtt ggt gac aaa att gtc ggt gtt ggt        926
Ala Lys Ser Lys Ala Ile Ser Val Gly Asp Lys Ile Val Gly Val Gly
                275                 280                 285

caa aca ggc aag ccg atg gtt gac gtg att ggc tgg cgt ctt gat gat        974
Gln Thr Gly Lys Pro Met Val Asp Val Ile Gly Trp Arg Leu Asp Asp
            290                 295                 300

gtg gtt gcc tta att aaa ggg ccg aag ggc agt aaa gtt cgt ctg gaa       1022
Val Val Ala Leu Ile Lys Gly Pro Lys Gly Ser Lys Val Arg Leu Glu
        305                 310                 315

att tta cct gct ggt aaa ggg acc aag acc cgt act gta acg ttg acc       1070
Ile Leu Pro Ala Gly Lys Gly Thr Lys Thr Arg Thr Val Thr Leu Thr
    320                 325                 330

cgt gaa cgt att cgt ctc gaa gac cgc gcg gtt aaa atg tcg gtg aag       1118
Arg Glu Arg Ile Arg Leu Glu Asp Arg Ala Val Lys Met Ser Val Lys
335                 340                 345                 350

acc gtc ggt aaa gag aaa gtc ggc gtg ctg gat att ccg ggc ttc tat       1166
Thr Val Gly Lys Glu Lys Val Gly Val Leu Asp Ile Pro Gly Phe Tyr
                355                 360                 365

gtg ggt ttg aca gac gat gtc aaa gtg caa ctg cag aaa ctg gaa aaa       1214
Val Gly Leu Thr Asp Asp Val Lys Val Gln Leu Gln Lys Leu Glu Lys
            370                 375                 380

cag aat gtc agc agc gtc atc atc gac ctg cgt agc aat ggc ggt ggg       1262
Gln Asn Val Ser Ser Val Ile Ile Asp Leu Arg Ser Asn Gly Gly Gly
        385                 390                 395

gcg tta act gaa gcc gta tcg ctc tcc ggt ctg ttt att cct gcg ggt       1310
Ala Leu Thr Glu Ala Val Ser Leu Ser Gly Leu Phe Ile Pro Ala Gly
    400                 405                 410

ccc att gtt cag gtc cgc gat aac aac ggc aag gtt cgt gaa gat agc       1358
Pro Ile Val Gln Val Arg Asp Asn Asn Gly Lys Val Arg Glu Asp Ser
415                 420                 425                 430

gat acc gac gga cag gtt ttc tat aaa ggc ccg ctg gtg gtg ctg gtt       1406
Asp Thr Asp Gly Gln Val Phe Tyr Lys Gly Pro Leu Val Val Leu Val
                435                 440                 445

gac cgc ttc agt gct tcg gct tca gaa atc ttt gcc gcg gca atg cag       1454
Asp Arg Phe Ser Ala Ser Ala Ser Glu Ile Phe Ala Ala Ala Met Gln
            450                 455                 460

gat tac ggt cgt gcg ctg gtt gtg ggt gaa ccg acg ttt ggt aaa ggc       1502
Asp Tyr Gly Arg Ala Leu Val Val Gly Glu Pro Thr Phe Gly Lys Gly
        465                 470                 475

acc gtt cag caa tac cgt tca ttg aac cgt att tac gat cag atg tta       1550
Thr Val Gln Gln Tyr Arg Ser Leu Asn Arg Ile Tyr Asp Gln Met Leu
    480                 485                 490

cgt cct gaa tgg cca gcg ctg ggt tct gtg cag tac acg atc cag aaa       1598
Arg Pro Glu Trp Pro Ala Leu Gly Ser Val Gln Tyr Thr Ile Gln Lys
495                 500                 505                 510
```

```
ttc tat cgc gtt aac ggc ggc agt acg caa cgt aaa ggc gta acg cca        1646
Phe Tyr Arg Val Asn Gly Gly Ser Thr Gln Arg Lys Gly Val Thr Pro
                515                 520                 525

gac atc atc atg ccg acg ggt aat gaa gaa acg gaa acg ggt gag aaa        1694
Asp Ile Ile Met Pro Thr Gly Asn Glu Glu Thr Glu Thr Gly Glu Lys
            530                 535                 540

ttc gaa gat aac gcg ctg ccg tgg gat agc att gat gcc gcg act tat        1742
Phe Glu Asp Asn Ala Leu Pro Trp Asp Ser Ile Asp Ala Ala Thr Tyr
        545                 550                 555

gtg aaa tca gga gat tta acg gcc ttt gaa ccg gag ctg ctg aag gaa        1790
Val Lys Ser Gly Asp Leu Thr Ala Phe Glu Pro Glu Leu Leu Lys Glu
    560                 565                 570

cat aat gcg cgt atc gcg aaa gat cct gag ttc cag aac atc atg aag        1838
His Asn Ala Arg Ile Ala Lys Asp Pro Glu Phe Gln Asn Ile Met Lys
575                 580                 585                 590

gat atc gcg cgc ttc aac gct atg aag gac aag cgc aat atc gtt tct        1886
Asp Ile Ala Arg Phe Asn Ala Met Lys Asp Lys Arg Asn Ile Val Ser
                595                 600                 605

ctg aat tac gct gtg cgt gag aaa gag aat aat gaa gat gat gcg acg        1934
Leu Asn Tyr Ala Val Arg Glu Lys Glu Asn Asn Glu Asp Asp Ala Thr
            610                 615                 620

cgt ctg gcg cgt ttg aac gaa cgc ttt aaa cgc gaa ggt aaa ccg gag        1982
Arg Leu Ala Arg Leu Asn Glu Arg Phe Lys Arg Glu Gly Lys Pro Glu
        625                 630                 635

ttg aag aaa ctg gat gat cta ccg aaa gat tac cag gag ccg gat cct        2030
Leu Lys Lys Leu Asp Asp Leu Pro Lys Asp Tyr Gln Glu Pro Asp Pro
    640                 645                 650

tat ctg gat gag acg gtg aat atc gca ctc gat ctg gcg aag ctt gaa        2078
Tyr Leu Asp Glu Thr Val Asn Ile Ala Leu Asp Leu Ala Lys Leu Glu
655                 660                 665                 670

aaa gcc aga ccc gcg gaa caa ccc gct ccc gtc aag taa tatcaatcag        2127
Lys Ala Arg Pro Ala Glu Gln Pro Ala Pro Val Lys
                675                 680

gcacaagaaa ttgtgcctga ttttttaaca gcgacaagat gccgtaaatc agatgctaca     2187

aaatgtaaa                                                            2196
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<210> 26
<211> 682
<212> PRT
<213> Escherichia coli

<400> 26

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Met Asn Met Phe Phe Arg Leu Thr Ala Leu Ala Gly Leu Leu Ala Ile
1               5                   10                  15

Ala Gly Gln Thr Phe Ala Val Glu Asp Ile Thr Arg Ala Asp Gln Ile
            20                  25                  30
```

```
Pro Val Leu Lys Glu Glu Thr Gln His Ala Thr Val Ser Glu Arg Val
        35                  40                  45

Thr Ser Arg Phe Thr Arg Ser His Tyr Arg Gln Phe Asp Leu Asp Gln
    50                  55                  60

Ala Phe Ser Ala Lys Ile Phe Asp Arg Tyr Leu Asn Leu Leu Asp Tyr
65                  70                  75                  80

Ser His Asn Val Leu Leu Ala Ser Asp Val Glu Gln Phe Ala Lys Lys
                85                  90                  95

Lys Thr Glu Leu Gly Asp Glu Leu Arg Ser Gly Lys Leu Asp Val Phe
            100                 105                 110

Tyr Asp Leu Tyr Asn Leu Ala Gln Lys Arg Arg Phe Glu Arg Tyr Gln
        115                 120                 125

Tyr Ala Leu Ser Val Leu Glu Lys Pro Met Asp Phe Thr Gly Asn Asp
    130                 135                 140

Thr Tyr Asn Leu Asp Arg Ser Lys Ala Pro Trp Pro Lys Asn Glu Ala
145                 150                 155                 160

Glu Leu Asn Ala Leu Trp Asp Ser Lys Val Lys Phe Asp Glu Leu Ser
                165                 170                 175

Leu Lys Leu Thr Gly Lys Thr Asp Lys Glu Ile Arg Glu Thr Leu Thr
            180                 185                 190

Arg Arg Tyr Lys Phe Ala Ile Arg Arg Leu Ala Gln Thr Asn Ser Glu
        195                 200                 205

Asp Val Phe Ser Leu Ala Met Thr Ala Phe Ala Arg Glu Ile Asp Pro
    210                 215                 220

His Thr Asn Tyr Leu Ser Pro Arg Asn Thr Glu Gln Phe Asn Thr Glu
225                 230                 235                 240

Met Ser Leu Ser Leu Glu Gly Ile Gly Ala Val Leu Gln Met Asp Asp
                245                 250                 255

Asp Tyr Thr Val Ile Asn Ser Met Val Ala Gly Gly Pro Ala Ala Lys
            260                 265                 270

Ser Lys Ala Ile Ser Val Gly Asp Lys Ile Val Gly Val Gly Gln Thr
        275                 280                 285
```

```
Gly Lys Pro Met Val Asp Val Ile Gly Trp Arg Leu Asp Asp Val Val
    290                 295                 300

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

Pro Ala Gly Lys Gly Thr Lys Thr Arg Thr Val Thr Leu Thr Arg Glu
                325                 330                 335

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

Gly Lys Glu Lys Val Gly Val Leu Asp Ile Pro Gly Phe Tyr Val Gly
        355                 360                 365

Leu Thr Asp Asp Val Lys Val Gln Leu Gln Lys Leu Glu Lys Gln Asn
    370                 375                 380

Val Ser Ser Val Ile Ile Asp Leu Arg Ser Asn Gly Gly Gly Ala Leu
385                 390                 395                 400

Thr Glu Ala Val Ser Leu Ser Gly Leu Phe Ile Pro Ala Gly Pro Ile
                405                 410                 415

Val Gln Val Arg Asp Asn Asn Gly Lys Val Arg Glu Asp Ser Asp Thr
            420                 425                 430

Asp Gly Gln Val Phe Tyr Lys Gly Pro Leu Val Val Leu Val Asp Arg
        435                 440                 445

Phe Ser Ala Ser Ala Ser Glu Ile Phe Ala Ala Ala Met Gln Asp Tyr
    450                 455                 460

Gly Arg Ala Leu Val Val Gly Glu Pro Thr Phe Gly Lys Gly Thr Val
465                 470                 475                 480

Gln Gln Tyr Arg Ser Leu Asn Arg Ile Tyr Asp Gln Met Leu Arg Pro
                485                 490                 495

Glu Trp Pro Ala Leu Gly Ser Val Gln Tyr Thr Ile Gln Lys Phe Tyr
            500                 505                 510

Arg Val Asn Gly Gly Ser Thr Gln Arg Lys Gly Val Thr Pro Asp Ile
        515                 520                 525

Ile Met Pro Thr Gly Asn Glu Glu Thr Glu Thr Gly Glu Lys Phe Glu
```

530 535 540

Asp Asn Ala Leu Pro Trp Asp Ser Ile Asp Ala Ala Thr Tyr Val Lys
545 550 555 560

Ser Gly Asp Leu Thr Ala Phe Glu Pro Glu Leu Leu Lys Glu His Asn
565 570 575

Ala Arg Ile Ala Lys Asp Pro Glu Phe Gln Asn Ile Met Lys Asp Ile
580 585 590

Ala Arg Phe Asn Ala Met Lys Asp Lys Arg Asn Ile Val Ser Leu Asn
595 600 605

Tyr Ala Val Arg Glu Lys Glu Asn Asn Glu Asp Asp Ala Thr Arg Leu
610 615 620

Ala Arg Leu Asn Glu Arg Phe Lys Arg Glu Gly Lys Pro Glu Leu Lys
625 630 635 640

Lys Leu Asp Asp Leu Pro Lys Asp Tyr Gln Glu Pro Asp Pro Tyr Leu
645 650 655

Asp Glu Thr Val Asn Ile Ala Leu Asp Leu Ala Lys Leu Glu Lys Ala
660 665 670

Arg Pro Ala Glu Gln Pro Ala Pro Val Lys
675 680

<210> 27
<211> 236
<212> PRT
<213> Escherichia coli

<300>
<308> NCBI Reference Sequence / AP_003452
<309> 2011-06-21
<313> (1)..(236)

<400> 27

Met Lys Lys Gly Phe Met Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly
1 5 10 15

Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met
20 25 30

Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys
35 40 45

Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys
50 55 60

His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val
65 70 75 80

Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys
85 90 95

Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val
100 105 110

Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met
115 120 125

Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro
130 135 140

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

Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys
165 170 175

Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala
180 185 190

Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser
195 200 205

Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
210 215 220

Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys
225 230 235

<210> 28
<211> 2048
<212> DNA
<213> Artificial Sequence

<220>
<223> knockout mutated Tsp gene

<400> 28
atgaattcgt ttttaggctt accgcgttag ctggcctgct tgcaatagca ggccagacat 60

taattgtaga agatatcacg cgtgctgatc aaattccggt attaaaggaa gagacgcagc 120

atgcgacggt aagtgagcgc gtaacgtcgc gcttcacccg ttctcattat cgccagttcg 180

acctcgatca ggcattttcg gccaaaatct ttgaccgcta cctgaatctg ctcgattaca 240

gccacaacgt gctgctggca agcgatgttg aacagttcgc gaaaaagaaa accgagttag 300

gcgatgaact gcgttcaggc aaactcgacg ttttctacga tctctacaat ctggcgcaaa 360

agcgccgttt tgagcgttac cagtacgctt tgtcggtact ggaaaagccg atggatttca 420

ccggcaacga cacttataac cttgaccgca gcaaagcgcc ctggccgaaa aacgaggctg 480

agttgaacgc gctgtgggac agtaaagtca aattcgacga gttaagcctg aagctgacag 540

gaaaaacgga taaagaaatt cgtgaaaccc tgactcgccg ctacaaattt gccattcgtc 600

gtctggcgca aaccaacagc gaagatgttt tctcgctggc aatgacggcg tttgcgcgtg 660

aaatcgaccc gcataccaac tatctttccc cgcgtaatac cgaacagttc aacactgaaa 720

tgagtttgtc gctggaaggt attggcgcag tgctgcaaat ggatgatgac tacaccgtta 780

tcaattcgat ggtggcaggt ggtccggcag cgaagagtaa agctatcagc gttggtgaca 840

aaattgtcgg tgttggtcaa acaggcaagc cgatggttga cgtgattggc tggcgtcttg 900

atgatgtggt tgccttaatt aaagggccga agggcagtaa agttcgtctg gaaattttac 960

ctgctggtaa agggaccaag acccgtactg taacgttgac ccgtgaacgt attcgtctcg 1020

aagaccgcgc ggttaaaatg tcggtgaaga ccgtcggtaa agagaaagtc ggcgtgctgg 1080

atattccggg cttctatgtg ggtttgacag acgatgtcaa agtgcaactg cagaaactgg 1140

aaaaacagaa tgtcagcagc gtcatcatcg acctgcgtag caatggcggt ggggcgttaa 1200

ctgaagccgt atcgctctcc ggtctgttta ttcctgcggg tcccattgtt caggtccgcg 1260

ataacaacgg caaggttcgt gaagatagcg ataccgacgg acaggttttc tataaaggcc 1320

cgctggtggt gctggttgac cgcttcagtg cttcggcttc agaaatcttt gccgcggcaa 1380

tgcaggatta cggtcgtgcg ctggttgtgg gtgaaccgac gtttggtaaa ggcaccgttc 1440

agcaataccg ttcattgaac cgtatttacg atcagatgtt acgtcctgaa tggccagcgc 1500

tgggttctgt gcagtacacg atccagaaat tctatcgcgt taacggcggc agtacgcaac 1560

gtaaaggcgt aacgccagac atcatcatgc cgacgggtaa tgaagaaacg gaaacgggtg 1620

agaaattcga agataacgcg ctgccgtggg atagcattga tgccgcgact tatgtgaaat 1680

caggagattt aacggccttt gaaccggagc tgctgaagga acataatgcg cgtatcgcga 1740

aagatcctga gttccagaac atcatgaagg atatcgcgcg cttcaacgct atgaaggaca 1800

agcgcaatat cgtttctctg aattacgctg tgcgtgagaa agagaataat gaagatgatg 1860

cgacgcgtct ggcgcgtttg aacgaacgct ttaaacgcga aggtaaaccg gagttgaaga 1920

aactggatga tctaccgaaa gattaccagg agccggatcc ttatctggat gagacggtga 1980

atatcgcact cgatctggcg aagcttgaaa aagccagacc cgcggaacaa cccgctcccg 2040

tcaagtaa 2048

<210> 29
<211> 1425
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(1425)

<400> 29

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atg aaa aaa acc aca tta gca ctg agt gca ctg gct ctg agt tta ggt          48
Met Lys Lys Thr Thr Leu Ala Leu Ser Ala Leu Ala Leu Ser Leu Gly
1               5                  10                  15

ttg gcg tta tct ccg ctc tct gca acg gcg gct gag act tct tca gca          96
Leu Ala Leu Ser Pro Leu Ser Ala Thr Ala Ala Glu Thr Ser Ser Ala
            20                  25                  30

acg aca gcc cag cag atg cca agc ctt gca ccg atg ctc gaa aag gtg         144
Thr Thr Ala Gln Gln Met Pro Ser Leu Ala Pro Met Leu Glu Lys Val
        35                  40                  45

atg cct tca gtg gtc agc att aac gta gaa ggt agc aca acc gtt aat         192
Met Pro Ser Val Val Ser Ile Asn Val Glu Gly Ser Thr Thr Val Asn
    50                  55                  60

acg ccg cgt atg ccg cgt aat ttc cag cag ttc ttc ggt gat gat tct         240
Thr Pro Arg Met Pro Arg Asn Phe Gln Gln Phe Phe Gly Asp Asp Ser
65                  70                  75                  80

ccg ttc tgc cag gaa ggt tct ccg ttc cag agc tct ccg ttc tgc cag         288
Pro Phe Cys Gln Glu Gly Ser Pro Phe Gln Ser Ser Pro Phe Cys Gln
                85                  90                  95

ggt ggc cag ggc ggt aat ggt ggc ggc cag caa cag aaa ttc atg gcg         336
Gly Gly Gln Gly Gly Asn Gly Gly Gly Gln Gln Gln Lys Phe Met Ala
            100                 105                 110

ctg ggt tcc ggc gtc atc att gat gcc gat aaa ggc tat gtc gtc acc         384
Leu Gly Ser Gly Val Ile Ile Asp Ala Asp Lys Gly Tyr Val Val Thr
        115                 120                 125

aac aac cac gtt gtt gat aac gcg acg gtc att aaa gtt caa ctg agc         432
Asn Asn His Val Val Asp Asn Ala Thr Val Ile Lys Val Gln Leu Ser
    130                 135                 140

gat ggc cgt aag ttc gac gcg aag atg gtt ggc aaa gat ccg cgc tct         480
Asp Gly Arg Lys Phe Asp Ala Lys Met Val Gly Lys Asp Pro Arg Ser
145                 150                 155                 160

gat atc gcg ctg atc caa atc cag aac ccg aaa aac ctg acc gca att         528
Asp Ile Ala Leu Ile Gln Ile Gln Asn Pro Lys Asn Leu Thr Ala Ile
                165                 170                 175

aag atg gcg gat tct gat gca ctg cgc gtg ggt gat tac acc gta gcg         576
Lys Met Ala Asp Ser Asp Ala Leu Arg Val Gly Asp Tyr Thr Val Ala
            180                 185                 190

att ggt aac ccg ttt ggt ctg ggc gag acg gta act tcc ggg att gtc         624
Ile Gly Asn Pro Phe Gly Leu Gly Glu Thr Val Thr Ser Gly Ile Val
```

```
        195                 200                 205

tct gcg ctg ggg cgt agc ggc ctg aat gcc gaa aac tac gaa aac ttc        672
Ser Ala Leu Gly Arg Ser Gly Leu Asn Ala Glu Asn Tyr Glu Asn Phe
    210                 215                 220

atc cag acc gat gca gcg atc aac cgt ggt aac tcc ggt ggt gcg ctg        720
Ile Gln Thr Asp Ala Ala Ile Asn Arg Gly Asn Ser Gly Gly Ala Leu
225                 230                 235                 240

gtt aac ctg aac ggc gaa ctg atc ggt atc aac acc gcg atc ctc gca        768
Val Asn Leu Asn Gly Glu Leu Ile Gly Ile Asn Thr Ala Ile Leu Ala
                245                 250                 255

ccg gac ggc ggc aac atc ggt atc ggt ttt gct atc ccg agt aac atg        816
Pro Asp Gly Gly Asn Ile Gly Ile Gly Phe Ala Ile Pro Ser Asn Met
            260                 265                 270

gtg aaa aac ctg acc tcg cag atg gtg gaa tac ggc cag gtg aaa cgc        864
Val Lys Asn Leu Thr Ser Gln Met Val Glu Tyr Gly Gln Val Lys Arg
        275                 280                 285

ggt gag ctg ggt att atg ggg act gag ctg aac tcc gaa ctg gcg aaa        912
Gly Glu Leu Gly Ile Met Gly Thr Glu Leu Asn Ser Glu Leu Ala Lys
    290                 295                 300

gcg atg aaa gtt gac gcc cag cgc ggt gct ttc gta agc cag gtt ctg        960
Ala Met Lys Val Asp Ala Gln Arg Gly Ala Phe Val Ser Gln Val Leu
305                 310                 315                 320

cct aat tcc tcc gct gca aaa gcg ggc att aaa gcg ggt gat gtg atc       1008
Pro Asn Ser Ser Ala Ala Lys Ala Gly Ile Lys Ala Gly Asp Val Ile
                325                 330                 335

acc tca ctg aac ggt aag ccg atc agc agc ttt gcc gca ctg cgt gct       1056
Thr Ser Leu Asn Gly Lys Pro Ile Ser Ser Phe Ala Ala Leu Arg Ala
            340                 345                 350

cag gtg ggt act atg ccg gta ggc agc aaa ctg acc ctg ggc tta ctg       1104
Gln Val Gly Thr Met Pro Val Gly Ser Lys Leu Thr Leu Gly Leu Leu
        355                 360                 365

cgc gac ggt aag cag gtt aac gtg aac ctg gaa ctg cag cag agc agc       1152
Arg Asp Gly Lys Gln Val Asn Val Asn Leu Glu Leu Gln Gln Ser Ser
    370                 375                 380

cag aat cag gtt gat tcc agc tcc atc ttc aac ggc att gaa ggc gct       1200
Gln Asn Gln Val Asp Ser Ser Ser Ile Phe Asn Gly Ile Glu Gly Ala
385                 390                 395                 400

gag atg agc aac aaa ggc aaa gat cag ggc gtg gta gtg aac aac gtg       1248
Glu Met Ser Asn Lys Gly Lys Asp Gln Gly Val Val Val Asn Asn Val
                405                 410                 415

aaa acg ggc act ccg gct gcg cag atc ggc ctg aag aaa ggt gat gtg       1296
Lys Thr Gly Thr Pro Ala Ala Gln Ile Gly Leu Lys Lys Gly Asp Val
            420                 425                 430

att att ggc gcg aac cag cag gca gtg aaa aac atc gct gaa ctg cgt       1344
Ile Ile Gly Ala Asn Gln Gln Ala Val Lys Asn Ile Ala Glu Leu Arg
        435                 440                 445

aaa gtt ctc gac agc aaa ccg tct gtg ctg gca ctc aac att cag cgc       1392
```

```
Lys Val Leu Asp Ser Lys Pro Ser Val Leu Ala Leu Asn Ile Gln Arg
    450                 455                 460

ggc gac agc acc atc tac ctg tta atg cag taa                          1425
Gly Asp Ser Thr Ile Tyr Leu Leu Met Gln
465                 470
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<210> 30
<211> 474
<212> PRT
<213> Escherichia coli

<400> 30

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Met Lys Lys Thr Thr Leu Ala Leu Ser Ala Leu Ala Leu Ser Leu Gly
1               5                  10                  15

Leu Ala Leu Ser Pro Leu Ser Ala Thr Ala Ala Glu Thr Ser Ser Ala
            20                  25                  30

Thr Thr Ala Gln Gln Met Pro Ser Leu Ala Pro Met Leu Glu Lys Val
        35                  40                  45

Met Pro Ser Val Val Ser Ile Asn Val Glu Gly Ser Thr Thr Val Asn
    50                  55                  60

Thr Pro Arg Met Pro Arg Asn Phe Gln Gln Phe Phe Gly Asp Asp Ser
65                  70                  75                  80

Pro Phe Cys Gln Glu Gly Ser Pro Phe Gln Ser Ser Pro Phe Cys Gln
                85                  90                  95

Gly Gly Gln Gly Gly Asn Gly Gly Gly Gln Gln Gln Lys Phe Met Ala
            100                 105                 110

Leu Gly Ser Gly Val Ile Ile Asp Ala Asp Lys Gly Tyr Val Val Thr
        115                 120                 125

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

Asp Gly Arg Lys Phe Asp Ala Lys Met Val Gly Lys Asp Pro Arg Ser
145                 150                 155                 160

Asp Ile Ala Leu Ile Gln Ile Gln Asn Pro Lys Asn Leu Thr Ala Ile
                165                 170                 175

Lys Met Ala Asp Ser Asp Ala Leu Arg Val Gly Asp Tyr Thr Val Ala
            180                 185                 190
```

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

Ser Ala Leu Gly Arg Ser Gly Leu Asn Ala Glu Asn Tyr Glu Asn Phe
210 215 220

Ile Gln Thr Asp Ala Ala Ile Asn Arg Gly Asn Ser Gly Gly Ala Leu
225 230 235 240

Val Asn Leu Asn Gly Glu Leu Ile Gly Ile Asn Thr Ala Ile Leu Ala
245 250 255

Pro Asp Gly Gly Asn Ile Gly Ile Gly Phe Ala Ile Pro Ser Asn Met
260 265 270

Val Lys Asn Leu Thr Ser Gln Met Val Glu Tyr Gly Gln Val Lys Arg
275 280 285

Gly Glu Leu Gly Ile Met Gly Thr Glu Leu Asn Ser Glu Leu Ala Lys
290 295 300

Ala Met Lys Val Asp Ala Gln Arg Gly Ala Phe Val Ser Gln Val Leu
305 310 315 320

Pro Asn Ser Ser Ala Ala Lys Ala Gly Ile Lys Ala Gly Asp Val Ile
325 330 335

Thr Ser Leu Asn Gly Lys Pro Ile Ser Ser Phe Ala Ala Leu Arg Ala
340 345 350

Gln Val Gly Thr Met Pro Val Gly Ser Lys Leu Thr Leu Gly Leu Leu
355 360 365

Arg Asp Gly Lys Gln Val Asn Val Asn Leu Glu Leu Gln Gln Ser Ser
370 375 380

Gln Asn Gln Val Asp Ser Ser Ser Ile Phe Asn Gly Ile Glu Gly Ala
385 390 395 400

Glu Met Ser Asn Lys Gly Lys Asp Gln Gly Val Val Val Asn Asn Val
405 410 415

Lys Thr Gly Thr Pro Ala Ala Gln Ile Gly Leu Lys Lys Gly Asp Val
420 425 430

Ile Ile Gly Ala Asn Gln Gln Ala Val Lys Asn Ile Ala Glu Leu Arg
435 440 445

```
Lys Val Leu Asp Ser Lys Pro Ser Val Leu Ala Leu Asn Ile Gln Arg
    450                 455                 460

Gly Asp Ser Thr Ile Tyr Leu Leu Met Gln
465                 470
```

<210> 31
<211> 1425
<212> DNA
<213> Artificial Sequence

<220>
<223> mutated DegP gene comprising the mutation S210A and an Ase I restriction marker

<220>
<221> CDS
<222> (1)..(1425)

<400> 31

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atg aaa aaa acc aca tta gca ctg agt gca ctg gct ctg agt tta ggt          48
Met Lys Lys Thr Thr Leu Ala Leu Ser Ala Leu Ala Leu Ser Leu Gly
1               5                   10                  15

ttg gcg tta tct ccg ctc tct gca acg gcg gct gag act tct tca gca          96
Leu Ala Leu Ser Pro Leu Ser Ala Thr Ala Ala Glu Thr Ser Ser Ala
            20                  25                  30

acg aca gcc cag cag atg cca agc ctt gca ccg atg ctc gaa aag gtg         144
Thr Thr Ala Gln Gln Met Pro Ser Leu Ala Pro Met Leu Glu Lys Val
        35                  40                  45

atg cct tca gtg gtc agc att aac gta gaa ggt agc aca acc gtt aat         192
Met Pro Ser Val Val Ser Ile Asn Val Glu Gly Ser Thr Thr Val Asn
    50                  55                  60

acg ccg cgt atg ccg cgt aat ttc cag cag ttc ttc ggt gat gat tct         240
Thr Pro Arg Met Pro Arg Asn Phe Gln Gln Phe Phe Gly Asp Asp Ser
65                  70                  75                  80

ccg ttc tgc cag gaa ggt tct ccg ttc cag agc tct ccg ttc tgc cag         288
Pro Phe Cys Gln Glu Gly Ser Pro Phe Gln Ser Ser Pro Phe Cys Gln
                85                  90                  95

ggt ggc cag ggc ggt aat ggt ggc ggc cag caa cag aaa ttc atg gcg         336
Gly Gly Gln Gly Gly Asn Gly Gly Gly Gln Gln Gln Lys Phe Met Ala
            100                 105                 110

ctg ggt tcc ggc gtc atc att gat gcc gat aaa ggc tat gtc gtc acc         384
Leu Gly Ser Gly Val Ile Ile Asp Ala Asp Lys Gly Tyr Val Val Thr
        115                 120                 125

aac aac cac gtt gtt gat aac gcg acg gtc att aaa gtt caa ctg agc         432
Asn Asn His Val Val Asp Asn Ala Thr Val Ile Lys Val Gln Leu Ser
    130                 135                 140

gat ggc cgt aag ttc gac gcg aag atg gtt ggc aaa gat ccg cgc tct         480
Asp Gly Arg Lys Phe Asp Ala Lys Met Val Gly Lys Asp Pro Arg Ser
145                 150                 155                 160
```

```
gat atc gcg ctg atc caa atc cag aac ccg aaa aac ctg acc gca att          528
Asp Ile Ala Leu Ile Gln Ile Gln Asn Pro Lys Asn Leu Thr Ala Ile
                165                 170                 175

aag atg gcg gat tct gat gca ctg cgc gtg ggt gat tac acc gta gcg          576
Lys Met Ala Asp Ser Asp Ala Leu Arg Val Gly Asp Tyr Thr Val Ala
            180                 185                 190

att ggt aac ccg ttt ggt ctg ggc gag acg gta act tcc ggg att gtc          624
Ile Gly Asn Pro Phe Gly Leu Gly Glu Thr Val Thr Ser Gly Ile Val
        195                 200                 205

tct gcg ctg ggg cgt agc ggc ctg aat gcc gaa aac tac gaa aac ttc          672
Ser Ala Leu Gly Arg Ser Gly Leu Asn Ala Glu Asn Tyr Glu Asn Phe
    210                 215                 220

atc cag acc gat gca gcg att aat cgt ggt aac gcc ggt ggt gcg ctg          720
Ile Gln Thr Asp Ala Ala Ile Asn Arg Gly Asn Ala Gly Gly Ala Leu
225                 230                 235                 240

gtt aac ctg aac ggc gaa ctg atc ggt atc aac acc gcg atc ctc gca          768
Val Asn Leu Asn Gly Glu Leu Ile Gly Ile Asn Thr Ala Ile Leu Ala
                245                 250                 255

ccg gac ggc ggc aac atc ggt atc ggt ttt gct atc ccg agt aac atg          816
Pro Asp Gly Gly Asn Ile Gly Ile Gly Phe Ala Ile Pro Ser Asn Met
            260                 265                 270

gtg aaa aac ctg acc tcg cag atg gtg gaa tac ggc cag gtg aaa cgc          864
Val Lys Asn Leu Thr Ser Gln Met Val Glu Tyr Gly Gln Val Lys Arg
        275                 280                 285

ggt gag ctg ggt att atg ggg act gag ctg aac tcc gaa ctg gcg aaa          912
Gly Glu Leu Gly Ile Met Gly Thr Glu Leu Asn Ser Glu Leu Ala Lys
    290                 295                 300

gcg atg aaa gtt gac gcc cag cgc ggt gct ttc gta agc cag gtt ctg          960
Ala Met Lys Val Asp Ala Gln Arg Gly Ala Phe Val Ser Gln Val Leu
305                 310                 315                 320

cct aat tcc tcc gct gca aaa gcg ggc att aaa gcg ggt gat gtg atc         1008
Pro Asn Ser Ser Ala Ala Lys Ala Gly Ile Lys Ala Gly Asp Val Ile
                325                 330                 335

acc tca ctg aac ggt aag ccg atc agc agc ttt gcc gca ctg cgt gct         1056
Thr Ser Leu Asn Gly Lys Pro Ile Ser Ser Phe Ala Ala Leu Arg Ala
            340                 345                 350

cag gtg ggt act atg ccg gta ggc agc aaa ctg acc ctg ggc tta ctg         1104
Gln Val Gly Thr Met Pro Val Gly Ser Lys Leu Thr Leu Gly Leu Leu
        355                 360                 365

cgc gac ggt aag cag gtt aac gtg aac ctg gaa ctg cag cag agc agc         1152
Arg Asp Gly Lys Gln Val Asn Val Asn Leu Glu Leu Gln Gln Ser Ser
    370                 375                 380

cag aat cag gtt gat tcc agc tcc atc ttc aac ggc att gaa ggc gct         1200
Gln Asn Gln Val Asp Ser Ser Ser Ile Phe Asn Gly Ile Glu Gly Ala
385                 390                 395                 400

gag atg agc aac aaa ggc aaa gat cag ggc gtg gta gtg aac aac gtg         1248
Glu Met Ser Asn Lys Gly Lys Asp Gln Gly Val Val Val Asn Asn Val
```

405 410 415

aaa acg ggc act ccg gct gcg cag atc ggc ctg aag aaa ggt gat gtg 1296
Lys Thr Gly Thr Pro Ala Ala Gln Ile Gly Leu Lys Lys Gly Asp Val
420 425 430

att att ggc gcg aac cag cag gca gtg aaa aac atc gct gaa ctg cgt 1344
Ile Ile Gly Ala Asn Gln Gln Ala Val Lys Asn Ile Ala Glu Leu Arg
435 440 445

aaa gtt ctc gac agc aaa ccg tct gtg ctg gca ctc aac att cag cgc 1392
Lys Val Leu Asp Ser Lys Pro Ser Val Leu Ala Leu Asn Ile Gln Arg
450 455 460

ggc gac agc acc atc tac ctg tta atg cag taa 1425
Gly Asp Ser Thr Ile Tyr Leu Leu Met Gln
465 470

<210> 32
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 32

Met Lys Lys Thr Thr Leu Ala Leu Ser Ala Leu Ala Leu Ser Leu Gly
1 5 10 15

Leu Ala Leu Ser Pro Leu Ser Ala Thr Ala Ala Glu Thr Ser Ser Ala
20 25 30

Thr Thr Ala Gln Gln Met Pro Ser Leu Ala Pro Met Leu Glu Lys Val
35 40 45

Met Pro Ser Val Val Ser Ile Asn Val Glu Gly Ser Thr Thr Val Asn
50 55 60

Thr Pro Arg Met Pro Arg Asn Phe Gln Gln Phe Phe Gly Asp Asp Ser
65 70 75 80

Pro Phe Cys Gln Glu Gly Ser Pro Phe Gln Ser Ser Pro Phe Cys Gln
85 90 95

Gly Gly Gln Gly Gly Asn Gly Gly Gly Gln Gln Gln Lys Phe Met Ala
100 105 110

Leu Gly Ser Gly Val Ile Ile Asp Ala Asp Lys Gly Tyr Val Val Thr
115 120 125

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

Asp Gly Arg Lys Phe Asp Ala Lys Met Val Gly Lys Asp Pro Arg Ser
145 150 155 160

Asp Ile Ala Leu Ile Gln Ile Gln Asn Pro Lys Asn Leu Thr Ala Ile
165 170 175

Lys Met Ala Asp Ser Asp Ala Leu Arg Val Gly Asp Tyr Thr Val Ala
180 185 190

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

Ser Ala Leu Gly Arg Ser Gly Leu Asn Ala Glu Asn Tyr Glu Asn Phe
210 215 220

Ile Gln Thr Asp Ala Ala Ile Asn Arg Gly Asn Ala Gly Gly Ala Leu
225 230 235 240

Val Asn Leu Asn Gly Glu Leu Ile Gly Ile Asn Thr Ala Ile Leu Ala
245 250 255

Pro Asp Gly Gly Asn Ile Gly Ile Gly Phe Ala Ile Pro Ser Asn Met
260 265 270

Val Lys Asn Leu Thr Ser Gln Met Val Glu Tyr Gly Gln Val Lys Arg
275 280 285

Gly Glu Leu Gly Ile Met Gly Thr Glu Leu Asn Ser Glu Leu Ala Lys
290 295 300

Ala Met Lys Val Asp Ala Gln Arg Gly Ala Phe Val Ser Gln Val Leu
305 310 315 320

Pro Asn Ser Ser Ala Ala Lys Ala Gly Ile Lys Ala Gly Asp Val Ile
325 330 335

Thr Ser Leu Asn Gly Lys Pro Ile Ser Ser Phe Ala Ala Leu Arg Ala
340 345 350

Gln Val Gly Thr Met Pro Val Gly Ser Lys Leu Thr Leu Gly Leu Leu
355 360 365

Arg Asp Gly Lys Gln Val Asn Val Asn Leu Glu Leu Gln Gln Ser Ser
370 375 380

Gln Asn Gln Val Asp Ser Ser Ser Ile Phe Asn Gly Ile Glu Gly Ala

385 390 395 400

Glu Met Ser Asn Lys Gly Lys Asp Gln Gly Val Val Val Asn Asn Val
405 410 415

Lys Thr Gly Thr Pro Ala Ala Gln Ile Gly Leu Lys Lys Gly Asp Val
420 425 430

Ile Ile Gly Ala Asn Gln Gln Ala Val Lys Asn Ile Ala Glu Leu Arg
435 440 445

Lys Val Leu Asp Ser Lys Pro Ser Val Leu Ala Leu Asn Ile Gln Arg
450 455 460

Gly Asp Ser Thr Ile Tyr Leu Leu Met Gln
465 470

<210> 33
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> IGS cassette-1

<400> 33
gagctcacca gtaacaaaaa gttttaatag aggagagtgt taatgaagaa gactgctata 60

gcaattg 67

<210> 34
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> IGS cassette-2

<400> 34
gagctcacca gtaacaaaaa gttttaatag aggggagtgt taaaatgaag aagactgcta 60

tagcaattg 69

<210> 35
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> IGS cassette-3

<400> 35
gagctcacca gtaacaaaaa gctttaatag aggagagtgt tgaggaggaa aaaaaaatga 60

agaaaactgc tatagcaatt g 81

<210> 36
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> IGS cassette-4

<400> 36
gagctcacca gtaacaaaaa gttttaatag aggagagtgt tgacgaggat tatataatga 60

agaaaactgc tatagcaatt g 81

<210> 37
<211> 954
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(954)

<400> 37
atg cgg gcg aaa ctt ctg gga ata gtc ctg aca acc cct att gcg atc 48
Met Arg Ala Lys Leu Leu Gly Ile Val Leu Thr Thr Pro Ile Ala Ile
1 5 10 15

agc tct ttt gct tct acc gag act tta tcg ttt act cct gac aac ata 96
Ser Ser Phe Ala Ser Thr Glu Thr Leu Ser Phe Thr Pro Asp Asn Ile
20 25 30

aat gcg gac att agt ctt gga act ctg agc gga aaa aca aaa gag cgt 144
Asn Ala Asp Ile Ser Leu Gly Thr Leu Ser Gly Lys Thr Lys Glu Arg
35 40 45

gtt tat cta gcc gaa gaa gga ggc cga aaa gtc agt caa ctc gac tgg 192
Val Tyr Leu Ala Glu Glu Gly Gly Arg Lys Val Ser Gln Leu Asp Trp
50 55 60

aaa ttc aat aac gct gca att att aaa ggt gca att aat tgg gat ttg 240
Lys Phe Asn Asn Ala Ala Ile Ile Lys Gly Ala Ile Asn Trp Asp Leu
65 70 75 80

atg ccc cag ata tct atc ggg gct gct ggc tgg aca act ctc ggc agc 288
Met Pro Gln Ile Ser Ile Gly Ala Ala Gly Trp Thr Thr Leu Gly Ser
85 90 95

cga ggt ggc aat atg gtc gat cag gac tgg atg gat tcc agt aac ccc 336
Arg Gly Gly Asn Met Val Asp Gln Asp Trp Met Asp Ser Ser Asn Pro
100 105 110

gga acc tgg acg gat gaa agt aga cac cct gat aca caa ctc aat tat 384
Gly Thr Trp Thr Asp Glu Ser Arg His Pro Asp Thr Gln Leu Asn Tyr
115 120 125

gcc aac gaa ttt gat ctg aat atc aaa ggc tgg ctc ctc aac gaa ccc 432
Ala Asn Glu Phe Asp Leu Asn Ile Lys Gly Trp Leu Leu Asn Glu Pro
130 135 140

```
aat tac cgc ctg gga ctc atg gcc gga tat cag gaa agc cgt tat agc          480
Asn Tyr Arg Leu Gly Leu Met Ala Gly Tyr Gln Glu Ser Arg Tyr Ser
145                 150                 155                 160

ttt aca gcc aga ggt ggt tcc tat atc tac agt tct gag gag gga ttc          528
Phe Thr Ala Arg Gly Gly Ser Tyr Ile Tyr Ser Ser Glu Glu Gly Phe
                165                 170                 175

aga gat gat atc ggc tcc ttc ccg aat gga gaa aga gca atc ggc tac          576
Arg Asp Asp Ile Gly Ser Phe Pro Asn Gly Glu Arg Ala Ile Gly Tyr
            180                 185                 190

aaa caa cgt ttt aaa atg ccc tac att ggc ttg act gga agt tat cgt          624
Lys Gln Arg Phe Lys Met Pro Tyr Ile Gly Leu Thr Gly Ser Tyr Arg
        195                 200                 205

tat gaa gat ttt gaa ctc ggt ggc aca ttt aaa tac agc ggc tgg gtg          672
Tyr Glu Asp Phe Glu Leu Gly Gly Thr Phe Lys Tyr Ser Gly Trp Val
    210                 215                 220

gaa tca tct gat aac gat gaa cac tat gac ccg gga aaa aga atc act          720
Glu Ser Ser Asp Asn Asp Glu His Tyr Asp Pro Gly Lys Arg Ile Thr
225                 230                 235                 240

tat cgc agt aag gtc aaa gac caa aat tac tat tct gtt gca gtc aat          768
Tyr Arg Ser Lys Val Lys Asp Gln Asn Tyr Tyr Ser Val Ala Val Asn
                245                 250                 255

gca ggt tat tac gtc aca cct aac gca aaa gtt tat gtt gaa ggc gca          816
Ala Gly Tyr Tyr Val Thr Pro Asn Ala Lys Val Tyr Val Glu Gly Ala
            260                 265                 270

tgg aat cgg gtt acg aat aaa aaa ggt aat act tca ctt tat gat cac          864
Trp Asn Arg Val Thr Asn Lys Lys Gly Asn Thr Ser Leu Tyr Asp His
        275                 280                 285

aat aat aac act tca gac tac agc aaa aat gga gca ggt ata gaa aac          912
Asn Asn Asn Thr Ser Asp Tyr Ser Lys Asn Gly Ala Gly Ile Glu Asn
    290                 295                 300

tat aac ttc atc act act gct ggt ctt aag tac aca ttt taa                  954
Tyr Asn Phe Ile Thr Thr Ala Gly Leu Lys Tyr Thr Phe
305                 310                 315
```

<210> 38
<211> 317
<212> PRT
<213> Escherichia coli

<400> 38

```
Met Arg Ala Lys Leu Leu Gly Ile Val Leu Thr Thr Pro Ile Ala Ile
1               5                   10                  15

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

Asn Ala Asp Ile Ser Leu Gly Thr Leu Ser Gly Lys Thr Lys Glu Arg
        35                  40                  45
```

```
Val Tyr Leu Ala Glu Glu Gly Gly Arg Lys Val Ser Gln Leu Asp Trp
 50                  55                  60

Lys Phe Asn Asn Ala Ala Ile Ile Lys Gly Ala Ile Asn Trp Asp Leu
65                  70                  75                  80

Met Pro Gln Ile Ser Ile Gly Ala Ala Gly Trp Thr Thr Leu Gly Ser
                85                  90                  95

Arg Gly Gly Asn Met Val Asp Gln Asp Trp Met Asp Ser Ser Asn Pro
            100                 105                 110

Gly Thr Trp Thr Asp Glu Ser Arg His Pro Asp Thr Gln Leu Asn Tyr
        115                 120                 125

Ala Asn Glu Phe Asp Leu Asn Ile Lys Gly Trp Leu Leu Asn Glu Pro
    130                 135                 140

Asn Tyr Arg Leu Gly Leu Met Ala Gly Tyr Gln Glu Ser Arg Tyr Ser
145                 150                 155                 160

Phe Thr Ala Arg Gly Gly Ser Tyr Ile Tyr Ser Ser Glu Glu Gly Phe
                165                 170                 175

Arg Asp Asp Ile Gly Ser Phe Pro Asn Gly Glu Arg Ala Ile Gly Tyr
            180                 185                 190

Lys Gln Arg Phe Lys Met Pro Tyr Ile Gly Leu Thr Gly Ser Tyr Arg
        195                 200                 205

Tyr Glu Asp Phe Glu Leu Gly Gly Thr Phe Lys Tyr Ser Gly Trp Val
    210                 215                 220

Glu Ser Ser Asp Asn Asp Glu His Tyr Asp Pro Gly Lys Arg Ile Thr
225                 230                 235                 240

Tyr Arg Ser Lys Val Lys Asp Gln Asn Tyr Tyr Ser Val Ala Val Asn
                245                 250                 255

Ala Gly Tyr Tyr Val Thr Pro Asn Ala Lys Val Tyr Val Glu Gly Ala
            260                 265                 270

Trp Asn Arg Val Thr Asn Lys Lys Gly Asn Thr Ser Leu Tyr Asp His
        275                 280                 285

Asn Asn Asn Thr Ser Asp Tyr Ser Lys Asn Gly Ala Gly Ile Glu Asn
    290                 295                 300
```

```
Tyr Asn Phe Ile Thr Thr Ala Gly Leu Lys Tyr Thr Phe
305                 310                 315


<210>  39
<211>  954
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  knock-out mutant OmpT gene


<220>
<221>  CDS
<222>  (1)..(954)

<400>  39
att cgg gcg aaa ctt ctg gga ata gtc ctg aca acc cct att gcg atc          48
Ile Arg Ala Lys Leu Leu Gly Ile Val Leu Thr Thr Pro Ile Ala Ile
1               5                   10                  15

agc tct ttt gct tct acc gag act tta tcg ttt act cct gac aac ata          96
Ser Ser Phe Ala Ser Thr Glu Thr Leu Ser Phe Thr Pro Asp Asn Ile
            20                  25                  30

aat gcg gac att agt ctt gga act ctg agc gga aaa aca aaa gag cgt         144
Asn Ala Asp Ile Ser Leu Gly Thr Leu Ser Gly Lys Thr Lys Glu Arg
        35                  40                  45

gtt tat cta gcc gaa gaa gga ggc cga aaa gtc agt caa ctc gac tgg         192
Val Tyr Leu Ala Glu Glu Gly Gly Arg Lys Val Ser Gln Leu Asp Trp
    50                  55                  60

aaa ttc aat aac gct gca att att aaa ggt gca att aat tgg gat ttg         240
Lys Phe Asn Asn Ala Ala Ile Ile Lys Gly Ala Ile Asn Trp Asp Leu
65                  70                  75                  80

atg ccc cag ata tct atc ggg gct gct ggc tgg aca act ctc ggc agc         288
Met Pro Gln Ile Ser Ile Gly Ala Ala Gly Trp Thr Thr Leu Gly Ser
                85                  90                  95

cga ggt ggc aat atg gtc gat cag gac tgg atg gat tcc agt aac ccc         336
Arg Gly Gly Asn Met Val Asp Gln Asp Trp Met Asp Ser Ser Asn Pro
            100                 105                 110

gga acc tgg acg gat gaa agt aga cac cct gat aca caa ctc aat tat         384
Gly Thr Trp Thr Asp Glu Ser Arg His Pro Asp Thr Gln Leu Asn Tyr
        115                 120                 125

gcc aac gaa ttt gat ctg aat atc aaa ggc tgg ctc ctc aac gaa ccc         432
Ala Asn Glu Phe Asp Leu Asn Ile Lys Gly Trp Leu Leu Asn Glu Pro
    130                 135                 140

aat tac cgc ctg gga ctc atg gcc gga tat cag gaa agc cgt tat agc         480
Asn Tyr Arg Leu Gly Leu Met Ala Gly Tyr Gln Glu Ser Arg Tyr Ser
145                 150                 155                 160

ttt aca gcc aga ggt ggt tcc tat atc tac agt tct gag gag gga ttc         528
Phe Thr Ala Arg Gly Gly Ser Tyr Ile Tyr Ser Ser Glu Glu Gly Phe
                165                 170                 175
```

```
aga gat gat atc ggc tcc ttc ccg aat gga gaa aga gca atc ggc tac          576
Arg Asp Asp Ile Gly Ser Phe Pro Asn Gly Glu Arg Ala Ile Gly Tyr
            180                 185                 190

aaa caa cgt ttt aaa atg ccc tac att ggc ttg act gga agt tat cgt          624
Lys Gln Arg Phe Lys Met Pro Tyr Ile Gly Leu Thr Gly Ser Tyr Arg
        195                 200                 205

tat gaa gat ttt gaa ctc ggt ggc aca ttt aaa tac agc ggc tgg gtg          672
Tyr Glu Asp Phe Glu Leu Gly Gly Thr Phe Lys Tyr Ser Gly Trp Val
    210                 215                 220

gaa tca tct gat aac gat gaa cac tat gac ccg gga aaa aga atc act          720
Glu Ser Ser Asp Asn Asp Glu His Tyr Asp Pro Gly Lys Arg Ile Thr
225                 230                 235                 240

tat cgc agt aag gtc aaa gac caa aat tac tat tct gtt gca gtc aat          768
Tyr Arg Ser Lys Val Lys Asp Gln Asn Tyr Tyr Ser Val Ala Val Asn
                245                 250                 255

gca ggt tat tac gtc aca cct aac gca aaa gtt tat gtt gaa ggc gca          816
Ala Gly Tyr Tyr Val Thr Pro Asn Ala Lys Val Tyr Val Glu Gly Ala
            260                 265                 270

tgg aat cgg gtt acg aat aaa aaa ggt aat act tca ctt tat gat cac          864
Trp Asn Arg Val Thr Asn Lys Lys Gly Asn Thr Ser Leu Tyr Asp His
        275                 280                 285

aat aat aac act tca gac tac agc aaa aat gga gca ggt ata gaa aac          912
Asn Asn Asn Thr Ser Asp Tyr Ser Lys Asn Gly Ala Gly Ile Glu Asn
    290                 295                 300

tat aac ttc atc act act gct ggt ctt aag tac aca ttt taa                  954
Tyr Asn Phe Ile Thr Thr Ala Gly Leu Lys Tyr Thr Phe
305                 310                 315
```

<210> 40
<211> 317
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 40

```
Ile Arg Ala Lys Leu Leu Gly Ile Val Leu Thr Thr Pro Ile Ala Ile
1               5                   10                  15

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

Asn Ala Asp Ile Ser Leu Gly Thr Leu Ser Gly Lys Thr Lys Glu Arg
        35                  40                  45

Val Tyr Leu Ala Glu Glu Gly Gly Arg Lys Val Ser Gln Leu Asp Trp
    50                  55                  60
```

```
Lys Phe Asn Asn Ala Ala Ile Ile Lys Gly Ala Ile Asn Trp Asp Leu
65                  70                  75                  80

Met Pro Gln Ile Ser Ile Gly Ala Ala Gly Trp Thr Thr Leu Gly Ser
                85                  90                  95

Arg Gly Gly Asn Met Val Asp Gln Asp Trp Met Asp Ser Ser Asn Pro
            100                 105                 110

Gly Thr Trp Thr Asp Glu Ser Arg His Pro Asp Thr Gln Leu Asn Tyr
        115                 120                 125

Ala Asn Glu Phe Asp Leu Asn Ile Lys Gly Trp Leu Leu Asn Glu Pro
    130                 135                 140

Asn Tyr Arg Leu Gly Leu Met Ala Gly Tyr Gln Glu Ser Arg Tyr Ser
145                 150                 155                 160

Phe Thr Ala Arg Gly Gly Ser Tyr Ile Tyr Ser Ser Glu Glu Gly Phe
                165                 170                 175

Arg Asp Asp Ile Gly Ser Phe Pro Asn Gly Glu Arg Ala Ile Gly Tyr
            180                 185                 190

Lys Gln Arg Phe Lys Met Pro Tyr Ile Gly Leu Thr Gly Ser Tyr Arg
        195                 200                 205

Tyr Glu Asp Phe Glu Leu Gly Gly Thr Phe Lys Tyr Ser Gly Trp Val
    210                 215                 220

Glu Ser Ser Asp Asn Asp Glu His Tyr Asp Pro Gly Lys Arg Ile Thr
225                 230                 235                 240

Tyr Arg Ser Lys Val Lys Asp Gln Asn Tyr Tyr Ser Val Ala Val Asn
                245                 250                 255

Ala Gly Tyr Tyr Val Thr Pro Asn Ala Lys Val Tyr Val Glu Gly Ala
            260                 265                 270

Trp Asn Arg Val Thr Asn Lys Lys Gly Asn Thr Ser Leu Tyr Asp His
        275                 280                 285

Asn Asn Asn Thr Ser Asp Tyr Ser Lys Asn Gly Ala Gly Ile Glu Asn
    290                 295                 300

Tyr Asn Phe Ile Thr Thr Ala Gly Leu Lys Tyr Thr Phe
305                 310                 315
```

<210> 41
<211> 954
<212> DNA
<213> Artificial Sequence

<220>
<223> mutated OmpT gene encoding the protein with the point mutations D210A and H212A

<220>
<221> CDS
<222> (1)..(954)

<400> 41

```
atg cgg gcg aaa ctt ctg gga ata gtc ctg aca acc cct att gcg atc          48
Met Arg Ala Lys Leu Leu Gly Ile Val Leu Thr Thr Pro Ile Ala Ile
1               5                  10                  15

agc tct ttt gct tct acc gag act tta tcg ttt act cct gac aac ata          96
Ser Ser Phe Ala Ser Thr Glu Thr Leu Ser Phe Thr Pro Asp Asn Ile
            20                  25                  30

aat gcg gac att agt ctt gga act ctg agc gga aaa aca aaa gag cgt         144
Asn Ala Asp Ile Ser Leu Gly Thr Leu Ser Gly Lys Thr Lys Glu Arg
        35                  40                  45

gtt tat cta gcc gaa gaa gga ggc cga aaa gtc agt caa ctc gac tgg         192
Val Tyr Leu Ala Glu Glu Gly Gly Arg Lys Val Ser Gln Leu Asp Trp
    50                  55                  60

aaa ttc aat aac gct gca att att aaa ggt gca att aat tgg gat ttg         240
Lys Phe Asn Asn Ala Ala Ile Ile Lys Gly Ala Ile Asn Trp Asp Leu
65                  70                  75                  80

atg ccc cag ata tct atc ggg gct gct ggc tgg aca act ctc ggc agc         288
Met Pro Gln Ile Ser Ile Gly Ala Ala Gly Trp Thr Thr Leu Gly Ser
                85                  90                  95

cga ggt ggc aat atg gtc gat cag gac tgg atg gat tcc agt aac ccc         336
Arg Gly Gly Asn Met Val Asp Gln Asp Trp Met Asp Ser Ser Asn Pro
            100                 105                 110

gga acc tgg acg gat gaa agt aga cac cct gat aca caa ctc aat tat         384
Gly Thr Trp Thr Asp Glu Ser Arg His Pro Asp Thr Gln Leu Asn Tyr
        115                 120                 125

gcc aac gaa ttt gat ctg aat atc aaa ggc tgg ctc ctc aac gaa ccc         432
Ala Asn Glu Phe Asp Leu Asn Ile Lys Gly Trp Leu Leu Asn Glu Pro
    130                 135                 140

aat tac cgc ctg gga ctc atg gcc gga tat cag gaa agc cgt tat agc         480
Asn Tyr Arg Leu Gly Leu Met Ala Gly Tyr Gln Glu Ser Arg Tyr Ser
145                 150                 155                 160

ttt aca gcc aga ggt ggt tcc tat atc tac agt tct gag gag gga ttc         528
Phe Thr Ala Arg Gly Gly Ser Tyr Ile Tyr Ser Ser Glu Glu Gly Phe
                165                 170                 175

aga gat gat atc ggc tcc ttc ccg aat gga gaa aga gca atc ggc tac         576
Arg Asp Asp Ile Gly Ser Phe Pro Asn Gly Glu Arg Ala Ile Gly Tyr
```

```
            180                 185                 190

aaa caa cgt ttt aaa atg ccc tac att ggc ttg act gga agt tat cgt        624
Lys Gln Arg Phe Lys Met Pro Tyr Ile Gly Leu Thr Gly Ser Tyr Arg
        195                 200                 205

tat gaa gat ttt gaa ctc ggt ggc aca ttt aaa tac agc ggc tgg gtg        672
Tyr Glu Asp Phe Glu Leu Gly Gly Thr Phe Lys Tyr Ser Gly Trp Val
    210                 215                 220

gaa tca tct gat aac gct gaa gct tat gac ccg gga aaa aga atc act        720
Glu Ser Ser Asp Asn Ala Glu Ala Tyr Asp Pro Gly Lys Arg Ile Thr
225                 230                 235                 240

tat cgc agt aag gtc aaa gac caa aat tac tat tct gtt gca gtc aat        768
Tyr Arg Ser Lys Val Lys Asp Gln Asn Tyr Tyr Ser Val Ala Val Asn
                245                 250                 255

gca ggt tat tac gtc aca cct aac gca aaa gtt tat gtt gaa ggc gca        816
Ala Gly Tyr Tyr Val Thr Pro Asn Ala Lys Val Tyr Val Glu Gly Ala
            260                 265                 270

tgg aat cgg gtt acg aat aaa aaa ggt aat act tca ctt tat gat cac        864
Trp Asn Arg Val Thr Asn Lys Lys Gly Asn Thr Ser Leu Tyr Asp His
        275                 280                 285

aat aat aac act tca gac tac agc aaa aat gga gca ggt ata gaa aac        912
Asn Asn Asn Thr Ser Asp Tyr Ser Lys Asn Gly Ala Gly Ile Glu Asn
    290                 295                 300

tat aac ttc atc act act gct ggt ctt aag tac aca ttt taa                954
Tyr Asn Phe Ile Thr Thr Ala Gly Leu Lys Tyr Thr Phe
305                 310                 315
```

<210> 42
<211> 317
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 42

```
Met Arg Ala Lys Leu Leu Gly Ile Val Leu Thr Thr Pro Ile Ala Ile
1               5                   10                  15

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

Asn Ala Asp Ile Ser Leu Gly Thr Leu Ser Gly Lys Thr Lys Glu Arg
        35                  40                  45

Val Tyr Leu Ala Glu Glu Gly Gly Arg Lys Val Ser Gln Leu Asp Trp
    50                  55                  60

Lys Phe Asn Asn Ala Ala Ile Ile Lys Gly Ala Ile Asn Trp Asp Leu
65                  70                  75                  80
```

Met Pro Gln Ile Ser Ile Gly Ala Ala Gly Trp Thr Thr Leu Gly Ser
85 90 95

Arg Gly Gly Asn Met Val Asp Gln Asp Trp Met Asp Ser Ser Asn Pro
100 105 110

Gly Thr Trp Thr Asp Glu Ser Arg His Pro Asp Thr Gln Leu Asn Tyr
115 120 125

Ala Asn Glu Phe Asp Leu Asn Ile Lys Gly Trp Leu Leu Asn Glu Pro
130 135 140

Asn Tyr Arg Leu Gly Leu Met Ala Gly Tyr Gln Glu Ser Arg Tyr Ser
145 150 155 160

Phe Thr Ala Arg Gly Gly Ser Tyr Ile Tyr Ser Ser Glu Glu Gly Phe
165 170 175

Arg Asp Asp Ile Gly Ser Phe Pro Asn Gly Glu Arg Ala Ile Gly Tyr
180 185 190

Lys Gln Arg Phe Lys Met Pro Tyr Ile Gly Leu Thr Gly Ser Tyr Arg
195 200 205

Tyr Glu Asp Phe Glu Leu Gly Gly Thr Phe Lys Tyr Ser Gly Trp Val
210 215 220

Glu Ser Ser Asp Asn Ala Glu Ala Tyr Asp Pro Gly Lys Arg Ile Thr
225 230 235 240

Tyr Arg Ser Lys Val Lys Asp Gln Asn Tyr Tyr Ser Val Ala Val Asn
245 250 255

Ala Gly Tyr Tyr Val Thr Pro Asn Ala Lys Val Tyr Val Glu Gly Ala
260 265 270

Trp Asn Arg Val Thr Asn Lys Lys Gly Asn Thr Ser Leu Tyr Asp His
275 280 285

Asn Asn Asn Thr Ser Asp Tyr Ser Lys Asn Gly Ala Gly Ile Glu Asn
290 295 300

Tyr Asn Phe Ile Thr Thr Ala Gly Leu Lys Tyr Thr Phe
305 310 315

<210> 43

<211> 711
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(711)

<400> 43

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atg aag aaa ggt ttt atg ttg ttt act ttg tta gcg gcg ttt tca ggc          48
Met Lys Lys Gly Phe Met Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly
1               5                  10                  15

ttt gct cag gct gat gac gcg gca att caa caa acg tta gcc aaa atg          96
Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met
            20                  25                  30

ggc atc aaa agc agc gat att cag ccc gcg cct gta gct ggc atg aag         144
Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys
        35                  40                  45

aca gtt ctg act aac agc ggc gtg ttg tac atc acc gat gat ggt aaa         192
Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys
    50                  55                  60

cat atc att cag ggg cca atg tat gac gtt agt ggc acg gct ccg gtc         240
His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val
65                  70                  75                  80

aat gtc acc aat aag atg ctg tta aag cag ttg aat gcg ctt gaa aaa         288
Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys
                85                  90                  95

gag atg atc gtt tat aaa gcg ccg cag gaa aaa cac gtc atc acc gtg         336
Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val
            100                 105                 110

ttt act gat att acc tgt ggt tac tgc cac aaa ctg cat gag caa atg         384
Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met
        115                 120                 125

gca gac tac aac gcg ctg ggg atc acc gtg cgt tat ctt gct ttc ccg         432
Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro
    130                 135                 140

cgc cag ggg ctg gac agc gat gca gag aaa gaa atg aaa gct atc tgg         480
Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met Lys Ala Ile Trp
145                 150                 155                 160

tgt gcg aaa gat aaa aac aaa gcg ttt gat gat gtg atg gca ggt aaa         528
Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys
                165                 170                 175

agc gtc gca cca gcc agt tgc gac gtg gat att gcc gac cat tac gca         576
Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala
            180                 185                 190

ctt ggc gtc cag ctt ggc gtt agc ggt act ccg gca gtt gtg ctg agc         624
Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser
        195                 200                 205

aat ggc aca ctt gtt ccg ggt tac cag ccg ccg aaa gag atg aaa gaa         672
```

```
Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
    210                 215                 220

ttt ctc gac gaa cac caa aaa atg acc agc ggt aaa taa                 711
Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys
225                 230                 235
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<210> 44
<211> 236
<212> PRT
<213> Escherichia coli

<400> 44

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Met Lys Lys Gly Phe Met Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly
1               5                  10                  15

Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met
            20                  25                  30

Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys
        35                  40                  45

Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys
    50                  55                  60

His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val
65                  70                  75                  80

Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys
                85                  90                  95

Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val
            100                 105                 110

Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met
        115                 120                 125

Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro
    130                 135                 140

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

Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys
                165                 170                 175

Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala
            180                 185                 190
```

```
Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser
        195                 200                 205

Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
    210                 215                 220

Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys
225                 230                 235
```

<210> 45
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> DsbC comprising his-tag and lacking an EcoRI restriction site

<220>
<221> CDS
<222> (1)..(729)

<400> 45

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atg aag aaa ggt ttt atg ttg ttt act ttg tta gcg gcg ttt tca ggc          48
Met Lys Lys Gly Phe Met Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly
1               5                   10                  15

ttt gct cag gct gat gac gcg gca att caa caa acg tta gcc aaa atg          96
Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met
            20                  25                  30

ggc atc aaa agc agc gat att cag ccc gcg cct gta gct ggc atg aag         144
Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys
        35                  40                  45

aca gtt ctg act aac agc ggc gtg ttg tac atc acc gat gat ggt aaa         192
Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys
    50                  55                  60

cat atc att cag ggg cca atg tat gac gtt agt ggc acg gct ccg gtc         240
His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val
65                  70                  75                  80

aat gtc acc aat aag atg ctg tta aag cag ttg aat gcg ctt gaa aaa         288
Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys
                85                  90                  95

gag atg atc gtt tat aaa gcg ccg cag gaa aaa cac gtc atc acc gtg         336
Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val
            100                 105                 110

ttt act gat att acc tgt ggt tac tgc cac aaa ctg cat gag caa atg         384
Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met
        115                 120                 125

gca gac tac aac gcg ctg ggg atc acc gtg cgt tat ctt gct ttc ccg         432
Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro
    130                 135                 140

cgc cag ggg ctg gac agc gat gca gag aaa gaa atg aaa gct atc tgg         480
```

```
Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met Lys Ala Ile Trp
145                 150                 155                 160

tgt gcg aaa gat aaa aac aaa gcg ttt gat gat gtg atg gca ggt aaa        528
Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys
                165                 170                 175

agc gtc gca cca gcc agt tgc gac gtg gat att gcc gac cat tac gca        576
Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala
            180                 185                 190

ctt ggc gtc cag ctt ggc gtt agc ggt act ccg gca gtt gtg ctg agc        624
Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser
        195                 200                 205

aat ggc aca ctt gtt ccg ggt tac cag ccg ccg aaa gag atg aaa gaa        672
Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
    210                 215                 220

ttt ctc gac gaa cac caa aaa atg acc agc ggt aaa cac cat cac cat        720
Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys His His His His
225                 230                 235                 240

cac cac taa                                                           729
His His
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<210> 46
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 46

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Met Lys Lys Gly Phe Met Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly
1               5                   10                  15

Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met
            20                  25                  30

Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys
        35                  40                  45

Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys
    50                  55                  60

His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val
65                  70                  75                  80

Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys
                85                  90                  95

Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val
```

100 105 110

Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met
115 120 125

Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro
130 135 140

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

Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys
165 170 175

Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala
180 185 190

Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser
195 200 205

Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
210 215 220

Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys His His His His
225 230 235 240

His His

<210> 47
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer 6283 Tsp 3'

<400> 47
gcatcataat tttcttttta cctc 24

<210> 48
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer 6283 Tsp 5'

<400> 48
gggaaatgaa cctgagcaaa acgc 24

<210> 49
<211> 3120
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (206)..(3091)
<223> preprotease III (AA -23 to 939)

<220>
<221> sig_peptide
<222> (206)..(274)

<220>
<221> mat_peptide
<222> (275)..(3091)
<223> protease III (AA 1 - 939)

<300>
<308> GenBank / X06227
<309> 2005-04-18
<313> (1)..(3120)

<400> 49
ttaccgctgt ttcgctttaa tcagtcatga gtgctgtata aaaattgcgc aatctatccg 60

cttactttat gatgcgcacc agtcacggac tgatggttat ataaacatag gctgactcct 120

gcagcacaag attaaattct ggcagatgat ttgcgttaac gtgttgaatc tggacagaaa 180

attaagttga ttatgaggtc cgtga atg ccc cgc agc acc tgg ttc aaa gca 232
Met Pro Arg Ser Thr Trp Phe Lys Ala
-20 -15

tta ttg ttg tta gtt gcc ctt tgg gca ccc tta agt cag gca gaa acg 280
Leu Leu Leu Leu Val Ala Leu Trp Ala Pro Leu Ser Gln Ala Glu Thr
-10 -5 -1 1

gga tgg cag ccg att cag gaa acc atc cgt aaa agt gat aaa gat aac 328
Gly Trp Gln Pro Ile Gln Glu Thr Ile Arg Lys Ser Asp Lys Asp Asn
5 10 15

cgc cag tat cag gct ata cgt ctg gat aac ggt atg gtg gtc ttg ctg 376
Arg Gln Tyr Gln Ala Ile Arg Leu Asp Asn Gly Met Val Val Leu Leu
20 25 30

gtt tct gat ccg cag gca gtt aaa tcg ctc tcg gcg ctg gtg gtg ccc 424
Val Ser Asp Pro Gln Ala Val Lys Ser Leu Ser Ala Leu Val Val Pro
35 40 45 50

gtt ggg tcg ctg gaa gat ccc gag gcg tac cag ggg ctg gca cat tac 472
Val Gly Ser Leu Glu Asp Pro Glu Ala Tyr Gln Gly Leu Ala His Tyr
55 60 65

ctt gaa cat atg agt ctg atg ggg tcg aaa aag tac ccg cag gct gac 520
Leu Glu His Met Ser Leu Met Gly Ser Lys Lys Tyr Pro Gln Ala Asp
70 75 80

agt ctg gcc gaa tat ctc aaa atg cac ggc ggt agt cac aat gcc agc 568
Ser Leu Ala Glu Tyr Leu Lys Met His Gly Gly Ser His Asn Ala Ser
85 90 95

```
act gcg ccg tat cgc acg gct ttc tat ctg gaa gtt gag aac gac gcc        616
Thr Ala Pro Tyr Arg Thr Ala Phe Tyr Leu Glu Val Glu Asn Asp Ala
    100                 105                 110

ttg cct ggt gcg gta gac cgc ctg gcc gat gct att gct gaa cct ttg        664
Leu Pro Gly Ala Val Asp Arg Leu Ala Asp Ala Ile Ala Glu Pro Leu
115                 120                 125                 130

ctc gac aag aaa tat gcc gaa cgt gag cgt aat gcg gtg aac gct gaa        712
Leu Asp Lys Lys Tyr Ala Glu Arg Glu Arg Asn Ala Val Asn Ala Glu
                135                 140                 145

tta acc atg gcg cgt acg cgt gac ggg atg cgc atg gca cag gtc agc        760
Leu Thr Met Ala Arg Thr Arg Asp Gly Met Arg Met Ala Gln Val Ser
            150                 155                 160

gca gaa acc att aac ccg gca cac ccc ggt tca aag ttt tct ggt ggt        808
Ala Glu Thr Ile Asn Pro Ala His Pro Gly Ser Lys Phe Ser Gly Gly
        165                 170                 175

aac ctc gaa act tta agc gac aaa cct ggt aat ccg gtg cag cag gcg        856
Asn Leu Glu Thr Leu Ser Asp Lys Pro Gly Asn Pro Val Gln Gln Ala
    180                 185                 190

ctg aaa gat ttc cac gag aag tac tat tcc gcc aat ttg atg aag gcg        904
Leu Lys Asp Phe His Glu Lys Tyr Tyr Ser Ala Asn Leu Met Lys Ala
195                 200                 205                 210

gtt att tac agt aat aaa ccg ctg ccg gag ttg gca aaa atg gcg gcg        952
Val Ile Tyr Ser Asn Lys Pro Leu Pro Glu Leu Ala Lys Met Ala Ala
                215                 220                 225

gac acc ttt ggt cgc gtg ccg aac aaa gag agc aaa aaa ccg gaa atc       1000
Asp Thr Phe Gly Arg Val Pro Asn Lys Glu Ser Lys Lys Pro Glu Ile
            230                 235                 240

acc gtg ccg gta gtc acc gac gcg caa aag ggc att atc att cat tac       1048
Thr Val Pro Val Val Thr Asp Ala Gln Lys Gly Ile Ile Ile His Tyr
        245                 250                 255

gtc cct gcg ctg ccg cgt aaa gtg ttg cgc gtt gag ttt cgc atc gat       1096
Val Pro Ala Leu Pro Arg Lys Val Leu Arg Val Glu Phe Arg Ile Asp
    260                 265                 270

aac aac tca gcg aag ttc cgt agt aaa acc gat gaa ttg att acc tat       1144
Asn Asn Ser Ala Lys Phe Arg Ser Lys Thr Asp Glu Leu Ile Thr Tyr
275                 280                 285                 290

ctg att ggc aat cgc agc cca ggt aca ctt tct gac tgg ctg caa aag       1192
Leu Ile Gly Asn Arg Ser Pro Gly Thr Leu Ser Asp Trp Leu Gln Lys
                295                 300                 305

cag gga tta gtt gag ggc att agc gcc aac tcc gat cct atc gtc aac       1240
Gln Gly Leu Val Glu Gly Ile Ser Ala Asn Ser Asp Pro Ile Val Asn
            310                 315                 320

ggc aac agc ggc gta tta gcg atc tct gcg tct tta acc gat aaa ggc       1288
Gly Asn Ser Gly Val Leu Ala Ile Ser Ala Ser Leu Thr Asp Lys Gly
        325                 330                 335

ctg gct aat cgc gat cag gtt gtg gcg gca att ttt agc tat ctc aat       1336
Leu Ala Asn Arg Asp Gln Val Val Ala Ala Ile Phe Ser Tyr Leu Asn
```

```
    340                 345                 350

ctg tta cgt gaa aaa ggc att gat aaa caa tac ttc gat gaa ctg gcg        1384
Leu Leu Arg Glu Lys Gly Ile Asp Lys Gln Tyr Phe Asp Glu Leu Ala
355                 360                 365                 370

aat gtg ctg gat atc gac ttc cgt tat ccg tcg atc acc cgt gat atg        1432
Asn Val Leu Asp Ile Asp Phe Arg Tyr Pro Ser Ile Thr Arg Asp Met
                375                 380                 385

gat tac gtc gaa tgg ctg gca gat acc atg att cgc gtt cct gtt gag        1480
Asp Tyr Val Glu Trp Leu Ala Asp Thr Met Ile Arg Val Pro Val Glu
            390                 395                 400

cat acg ctg gat gca gtc aat att gcc gat cgg tac gat gct aaa gca        1528
His Thr Leu Asp Ala Val Asn Ile Ala Asp Arg Tyr Asp Ala Lys Ala
        405                 410                 415

gta aag gaa cgt ctg gcg atg atg acg ccg cag aat gcg cgt atc tgg        1576
Val Lys Glu Arg Leu Ala Met Met Thr Pro Gln Asn Ala Arg Ile Trp
    420                 425                 430

tat atc agc ccg aaa gag ccg cac aac aaa acg gct tac ttt gtc gat        1624
Tyr Ile Ser Pro Lys Glu Pro His Asn Lys Thr Ala Tyr Phe Val Asp
435                 440                 445                 450

gcg ccg tat cag gtc gat aaa atc agc gca caa act ttc gcc gac tgg        1672
Ala Pro Tyr Gln Val Asp Lys Ile Ser Ala Gln Thr Phe Ala Asp Trp
                455                 460                 465

cag aaa aaa gcc gcc gac att gcg ctc tct ttg cca gag ctt aac cct        1720
Gln Lys Lys Ala Ala Asp Ile Ala Leu Ser Leu Pro Glu Leu Asn Pro
            470                 475                 480

tat att cct gat gat ttc tcg ctg att aag tca gag aag aaa tac gac        1768
Tyr Ile Pro Asp Asp Phe Ser Leu Ile Lys Ser Glu Lys Lys Tyr Asp
        485                 490                 495

cat cca gag ctg att gtt gat gag tcg aat ctg cgc gtg gtg tat gcg        1816
His Pro Glu Leu Ile Val Asp Glu Ser Asn Leu Arg Val Val Tyr Ala
    500                 505                 510

cca agc cgt tat ttt gcc agc gag ccc aaa gct gat gtc agc ctg att        1864
Pro Ser Arg Tyr Phe Ala Ser Glu Pro Lys Ala Asp Val Ser Leu Ile
515                 520                 525                 530

ttg cgt aat ccg aaa gcc atg gac agc gcc cgc aat cag gtg atg ttt        1912
Leu Arg Asn Pro Lys Ala Met Asp Ser Ala Arg Asn Gln Val Met Phe
                535                 540                 545

gcg ctc aat gat tat ctc gca ggg ctg gcg ctt gat cag tta agc aac        1960
Ala Leu Asn Asp Tyr Leu Ala Gly Leu Ala Leu Asp Gln Leu Ser Asn
            550                 555                 560

cag gcg tcg gtt ggt ggc ata agt ttt tcc acc aac gct aac aac ggc        2008
Gln Ala Ser Val Gly Gly Ile Ser Phe Ser Thr Asn Ala Asn Asn Gly
        565                 570                 575

ctt atg gtt aat gct aat ggt tac acc cag cgt ctg ccg cag ctg ttc        2056
Leu Met Val Asn Ala Asn Gly Tyr Thr Gln Arg Leu Pro Gln Leu Phe
    580                 585                 590

cag gca ttg ctc gag ggg tac ttt agc tat acc gct acg gaa gat cag        2104
```

```
Gln Ala Leu Leu Glu Gly Tyr Phe Ser Tyr Thr Ala Thr Glu Asp Gln
595                 600                 605                 610

ctt gag cag gcg aag tcc tgg tat aac cag atg atg gat tcc gca gaa      2152
Leu Glu Gln Ala Lys Ser Trp Tyr Asn Gln Met Met Asp Ser Ala Glu
                615                 620                 625

aag ggt aaa gcg ttt gag cag gcg att atg ccc gcg cag atg ctc tcg      2200
Lys Gly Lys Ala Phe Glu Gln Ala Ile Met Pro Ala Gln Met Leu Ser
            630                 635                 640

caa gtg ccg tac ttc tcg cga gat gaa cgg cgt aaa att ttg ccc tcc      2248
Gln Val Pro Tyr Phe Ser Arg Asp Glu Arg Arg Lys Ile Leu Pro Ser
        645                 650                 655

att acg ttg aaa gag gtg ctg gcc tat cgc gac gcc tta aaa tca ggg      2296
Ile Thr Leu Lys Glu Val Leu Ala Tyr Arg Asp Ala Leu Lys Ser Gly
    660                 665                 670

gct cga cca gag ttt atg gtt atc ggc aac atg acc gag gcc cag gca      2344
Ala Arg Pro Glu Phe Met Val Ile Gly Asn Met Thr Glu Ala Gln Ala
675                 680                 685                 690

aca acg ctg gca cgc gat gtg caa aaa cag ttg ggc gct gat ggt tca      2392
Thr Thr Leu Ala Arg Asp Val Gln Lys Gln Leu Gly Ala Asp Gly Ser
                695                 700                 705

gag tgg tgt cga aac aaa gat gta gtg gtc gat aaa aaa caa tcc gtc      2440
Glu Trp Cys Arg Asn Lys Asp Val Val Val Asp Lys Lys Gln Ser Val
            710                 715                 720

atc ttt gaa aaa gcc ggt aac agc acc gac tcc gca ctg gca gcg gta      2488
Ile Phe Glu Lys Ala Gly Asn Ser Thr Asp Ser Ala Leu Ala Ala Val
        725                 730                 735

ttt gta ccg act ggc tac gat gaa tac acc agc tca gcc tat agc tct      2536
Phe Val Pro Thr Gly Tyr Asp Glu Tyr Thr Ser Ser Ala Tyr Ser Ser
    740                 745                 750

ctg ttg ggg cag atc gta cag ccg tgg ttc tac aat cag ttg cgt acc      2584
Leu Leu Gly Gln Ile Val Gln Pro Trp Phe Tyr Asn Gln Leu Arg Thr
755                 760                 765                 770

gaa gaa caa ttg ggc tat gcc gtg ttt gcg ttt cca atg agc gtg ggg      2632
Glu Glu Gln Leu Gly Tyr Ala Val Phe Ala Phe Pro Met Ser Val Gly
                775                 780                 785

cgt cag tgg ggc atg ggc ttc ctt ttg caa agc aat gat aaa cag cct      2680
Arg Gln Trp Gly Met Gly Phe Leu Leu Gln Ser Asn Asp Lys Gln Pro
            790                 795                 800

tca ttc ttg tgg gag cgt tac aag gcg ttt ttc cca acc gca gag gca      2728
Ser Phe Leu Trp Glu Arg Tyr Lys Ala Phe Phe Pro Thr Ala Glu Ala
        805                 810                 815

aaa ttg cga gcg atg aag cca gat gag ttt gcg caa atc cag cag gcg      2776
Lys Leu Arg Ala Met Lys Pro Asp Glu Phe Ala Gln Ile Gln Gln Ala
    820                 825                 830

gta att acc cag atg ctg cag gca ccg caa acg ctc ggc gaa gaa gca      2824
Val Ile Thr Gln Met Leu Gln Ala Pro Gln Thr Leu Gly Glu Glu Ala
835                 840                 845                 850
```

```
tcg aag tta agt aaa gat ttc gat cgc ggc aat atg cgc ttc gat tcg       2872
Ser Lys Leu Ser Lys Asp Phe Asp Arg Gly Asn Met Arg Phe Asp Ser
                855                 860                 865

cgt gat aaa atc gtg gcc cag ata aaa ctg ctg acg ccg caa aaa ctt       2920
Arg Asp Lys Ile Val Ala Gln Ile Lys Leu Leu Thr Pro Gln Lys Leu
            870                 875                 880

gct gat ttc ttc cat cag gcg gtg gtc gag ccg caa ggc atg gct att       2968
Ala Asp Phe Phe His Gln Ala Val Val Glu Pro Gln Gly Met Ala Ile
        885                 890                 895

ctg tcg cag att tcc ggc agc cag aac ggg aaa gcc gaa tat gta cac       3016
Leu Ser Gln Ile Ser Gly Ser Gln Asn Gly Lys Ala Glu Tyr Val His
    900                 905                 910

cct gaa ggc tgg aaa gtg tgg gag aac gtc agc gcg ttg cag caa aca       3064
Pro Glu Gly Trp Lys Val Trp Glu Asn Val Ser Ala Leu Gln Gln Thr
915                 920                 925                 930

atg ccc ctg atg agt gaa aag aat gag tgatgtcgcc gagacactag             3111
Met Pro Leu Met Ser Glu Lys Asn Glu
                935

atcctttgc                                                            3120
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<210> 50
<211> 962
<212> PRT
<213> Escherichia coli

<400> 50

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Met Pro Arg Ser Thr Trp Phe Lys Ala Leu Leu Leu Leu Val Ala Leu
            -20                 -15                 -10

Trp Ala Pro Leu Ser Gln Ala Glu Thr Gly Trp Gln Pro Ile Gln Glu
        -5                  -1  1                   5

Thr Ile Arg Lys Ser Asp Lys Asp Asn Arg Gln Tyr Gln Ala Ile Arg
10                  15                  20                  25

Leu Asp Asn Gly Met Val Val Leu Leu Val Ser Asp Pro Gln Ala Val
                30                  35                  40

Lys Ser Leu Ser Ala Leu Val Val Pro Val Gly Ser Leu Glu Asp Pro
            45                  50                  55

Glu Ala Tyr Gln Gly Leu Ala His Tyr Leu Glu His Met Ser Leu Met
        60                  65                  70

Gly Ser Lys Lys Tyr Pro Gln Ala Asp Ser Leu Ala Glu Tyr Leu Lys
    75                  80                  85

Met His Gly Gly Ser His Asn Ala Ser Thr Ala Pro Tyr Arg Thr Ala
```

```
90                  95                  100                 105

Phe Tyr Leu Glu Val Glu Asn Asp Ala Leu Pro Gly Ala Val Asp Arg
                110                 115                 120

Leu Ala Asp Ala Ile Ala Glu Pro Leu Leu Asp Lys Lys Tyr Ala Glu
            125                 130                 135

Arg Glu Arg Asn Ala Val Asn Ala Glu Leu Thr Met Ala Arg Thr Arg
        140                 145                 150

Asp Gly Met Arg Met Ala Gln Val Ser Ala Glu Thr Ile Asn Pro Ala
    155                 160                 165

His Pro Gly Ser Lys Phe Ser Gly Gly Asn Leu Glu Thr Leu Ser Asp
170                 175                 180                 185

Lys Pro Gly Asn Pro Val Gln Gln Ala Leu Lys Asp Phe His Glu Lys
                190                 195                 200

Tyr Tyr Ser Ala Asn Leu Met Lys Ala Val Ile Tyr Ser Asn Lys Pro
            205                 210                 215

Leu Pro Glu Leu Ala Lys Met Ala Ala Asp Thr Phe Gly Arg Val Pro
        220                 225                 230

Asn Lys Glu Ser Lys Lys Pro Glu Ile Thr Val Pro Val Val Thr Asp
    235                 240                 245

Ala Gln Lys Gly Ile Ile Ile His Tyr Val Pro Ala Leu Pro Arg Lys
250                 255                 260                 265

Val Leu Arg Val Glu Phe Arg Ile Asp Asn Asn Ser Ala Lys Phe Arg
                270                 275                 280

Ser Lys Thr Asp Glu Leu Ile Thr Tyr Leu Ile Gly Asn Arg Ser Pro
            285                 290                 295

Gly Thr Leu Ser Asp Trp Leu Gln Lys Gln Gly Leu Val Glu Gly Ile
        300                 305                 310

Ser Ala Asn Ser Asp Pro Ile Val Asn Gly Asn Ser Gly Val Leu Ala
    315                 320                 325

Ile Ser Ala Ser Leu Thr Asp Lys Gly Leu Ala Asn Arg Asp Gln Val
330                 335                 340                 345
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Val Ala Ala Ile Phe Ser Tyr Leu Asn Leu Leu Arg Glu Lys Gly Ile
350 355 360

Asp Lys Gln Tyr Phe Asp Glu Leu Ala Asn Val Leu Asp Ile Asp Phe
365 370 375

Arg Tyr Pro Ser Ile Thr Arg Asp Met Asp Tyr Val Glu Trp Leu Ala
380 385 390

Asp Thr Met Ile Arg Val Pro Val Glu His Thr Leu Asp Ala Val Asn
395 400 405

Ile Ala Asp Arg Tyr Asp Ala Lys Ala Val Lys Glu Arg Leu Ala Met
410 415 420 425

Met Thr Pro Gln Asn Ala Arg Ile Trp Tyr Ile Ser Pro Lys Glu Pro
430 435 440

His Asn Lys Thr Ala Tyr Phe Val Asp Ala Pro Tyr Gln Val Asp Lys
445 450 455

Ile Ser Ala Gln Thr Phe Ala Asp Trp Gln Lys Lys Ala Ala Asp Ile
460 465 470

Ala Leu Ser Leu Pro Glu Leu Asn Pro Tyr Ile Pro Asp Asp Phe Ser
475 480 485

Leu Ile Lys Ser Glu Lys Lys Tyr Asp His Pro Glu Leu Ile Val Asp
490 495 500 505

Glu Ser Asn Leu Arg Val Val Tyr Ala Pro Ser Arg Tyr Phe Ala Ser
510 515 520

Glu Pro Lys Ala Asp Val Ser Leu Ile Leu Arg Asn Pro Lys Ala Met
525 530 535

Asp Ser Ala Arg Asn Gln Val Met Phe Ala Leu Asn Asp Tyr Leu Ala
540 545 550

Gly Leu Ala Leu Asp Gln Leu Ser Asn Gln Ala Ser Val Gly Gly Ile
555 560 565

Ser Phe Ser Thr Asn Ala Asn Asn Gly Leu Met Val Asn Ala Asn Gly
570 575 580 585

Tyr Thr Gln Arg Leu Pro Gln Leu Phe Gln Ala Leu Leu Glu Gly Tyr
590 595 600

```
Phe Ser Tyr Thr Ala Thr Glu Asp Gln Leu Glu Gln Ala Lys Ser Trp
            605                 610                 615

Tyr Asn Gln Met Met Asp Ser Ala Glu Lys Gly Lys Ala Phe Glu Gln
        620                 625                 630

Ala Ile Met Pro Ala Gln Met Leu Ser Gln Val Pro Tyr Phe Ser Arg
    635                 640                 645

Asp Glu Arg Arg Lys Ile Leu Pro Ser Ile Thr Leu Lys Glu Val Leu
650                 655                 660                 665

Ala Tyr Arg Asp Ala Leu Lys Ser Gly Ala Arg Pro Glu Phe Met Val
                670                 675                 680

Ile Gly Asn Met Thr Glu Ala Gln Ala Thr Thr Leu Ala Arg Asp Val
            685                 690                 695

Gln Lys Gln Leu Gly Ala Asp Gly Ser Glu Trp Cys Arg Asn Lys Asp
        700                 705                 710

Val Val Val Asp Lys Lys Gln Ser Val Ile Phe Glu Lys Ala Gly Asn
    715                 720                 725

Ser Thr Asp Ser Ala Leu Ala Ala Val Phe Val Pro Thr Gly Tyr Asp
730                 735                 740                 745

Glu Tyr Thr Ser Ser Ala Tyr Ser Ser Leu Leu Gly Gln Ile Val Gln
                750                 755                 760

Pro Trp Phe Tyr Asn Gln Leu Arg Thr Glu Glu Gln Leu Gly Tyr Ala
            765                 770                 775

Val Phe Ala Phe Pro Met Ser Val Gly Arg Gln Trp Gly Met Gly Phe
        780                 785                 790

Leu Leu Gln Ser Asn Asp Lys Gln Pro Ser Phe Leu Trp Glu Arg Tyr
    795                 800                 805

Lys Ala Phe Phe Pro Thr Ala Glu Ala Lys Leu Arg Ala Met Lys Pro
810                 815                 820                 825

Asp Glu Phe Ala Gln Ile Gln Gln Ala Val Ile Thr Gln Met Leu Gln
                830                 835                 840

Ala Pro Gln Thr Leu Gly Glu Glu Ala Ser Lys Leu Ser Lys Asp Phe
            845                 850                 855
```

```
Asp Arg Gly Asn Met Arg Phe Asp Ser Arg Asp Lys Ile Val Ala Gln
        860                 865                 870

Ile Lys Leu Leu Thr Pro Gln Lys Leu Ala Asp Phe Phe His Gln Ala
    875                 880                 885

Val Val Glu Pro Gln Gly Met Ala Ile Leu Ser Gln Ile Ser Gly Ser
890                 895                 900                 905

Gln Asn Gly Lys Ala Glu Tyr Val His Pro Glu Gly Trp Lys Val Trp
                910                 915                 920

Glu Asn Val Ser Ala Leu Gln Gln Thr Met Pro Leu Met Ser Glu Lys
            925                 930                 935

Asn Glu
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<222> (1)..(729)

<400> 51

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atg aag aaa ggt ttt atg ttg ttt act ttg tta gcg gcg ttt tca ggc          48
Met Lys Lys Gly Phe Met Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly
1               5                   10                  15

ttt gct cag gct gat gac gcg gca att caa caa acg tta gcc aaa atg          96
Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met
            20                  25                  30

ggc atc aaa agc agc gat att cag ccc gcg cct gta gct ggc atg aag         144
Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys
        35                  40                  45

aca gtt ctg act aac agc ggc gtg ttg tac atc acc gat gat ggt aaa         192
Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys
    50                  55                  60

cat atc att cag ggg cca atg tat gac gtt agt ggc acg gct ccg gtc         240
His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val
65                  70                  75                  80

aat gtc acc aat aag atg ctg tta aag cag ttg aat gcg ctt gaa aaa         288
Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys
                85                  90                  95
```

```
gag atg atc gtt tat aaa gcg ccg cag gaa aaa cac gtc atc acc gtg          336
Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val
            100                 105                 110

ttt act gat att acc tgt ggt tac tgc cac aaa ctg cat gag caa atg          384
Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met
        115                 120                 125

gca gac tac aac gcg ctg ggg atc acc gtg cgt tat ctt gct ttc ccg          432
Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro
    130                 135                 140

cgc cag ggg ctg gac agc gat gca gag aaa gaa atg aaa gct atc tgg          480
Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met Lys Ala Ile Trp
145                 150                 155                 160

tgt gcg aaa gat aaa aac aaa gcg ttt gat gat gtg atg gca ggt aaa          528
Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys
                165                 170                 175

agc gtc gca cca gcc agt tgc gac gtg gat att gcc gac cat tac gca          576
Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala
            180                 185                 190

ctt ggc gtc cag ctt ggc gtt agc ggt act ccg gca gtt gtg ctg agc          624
Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser
        195                 200                 205

aat ggc aca ctt gtt ccg ggt tac cag ccg ccg aaa gag atg aaa gaa          672
Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
    210                 215                 220

ttc ctc gac gaa cac caa aaa atg acc agc ggt aaa cac cat cac cat          720
Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys His His His His
225                 230                 235                 240

cac cac taa                                                             729
His His
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<210> 52
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 52

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Met Lys Lys Gly Phe Met Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly
1               5                   10                  15

Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met
            20                  25                  30

Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys
        35                  40                  45
```

```
Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys
     50                  55                  60

His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val
65                  70                  75                  80

Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys
                85                  90                  95

Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val
            100                 105                 110

Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met
        115                 120                 125

Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro
    130                 135                 140

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

Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys
                165                 170                 175

Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala
            180                 185                 190

Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser
        195                 200                 205

Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
    210                 215                 220

Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys His His His His
225                 230                 235                 240

His His
```