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<151> 2009-09-24

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<151> 2009-09-24

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Asp Val Phe Ser Leu Ala Met Thr Ala Phe Ala Arg Glu Ile Asp Pro
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His Thr Asn Tyr Leu Ser Pro Arg Asn Thr Glu Gln Phe Asn Thr Glu
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Lys Ser Leu Ser Ala Leu Val Val Pro Val Gly Ser Leu Glu Asp Pro
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Gly Ser Lys Lys Tyr Pro Gln Ala Asp Ser Leu Ala Glu Tyr Leu Lys
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Met His Gly Gly Ser His Asn Ala Ser Thr Ala Pro Tyr Arg Thr Ala
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Phe Tyr Leu Glu Val Glu Asn Asp Ala Leu Pro Gly Ala Val Asp Arg
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ggcctggcta atcgcgatca ggttgtggcg gcaattttta gctatctcaa tctgttacgt 1140

gaaaaaggca ttgataaaca atacttcgat gaactggcga atgtgctgga tatcgacttc 1200

cgttatccgt cgatcacccg tgatatggat tacgtcgaat ggctggcaga taccatgatt 1260

cgcgttcctg ttgagcatac gctggatgca gtcaatattg ccgatcggta cgatgctaaa 1320

gcagtaaagg aacgtctggc gatgatgacg ccgcagaatg cgcgtatctg gtatatcagc 1380

ccgaaagagc cgcacaacaa aacggcttac tttgtcgatg cgccgtatca ggtcgataaa 1440

atcagcgcac aaactttcgc cgactggcag aaaaaagccg ccgacattgc gctctctttg 1500

ccagagctta acccttatat tcctgatgat ttctcgctga ttaagtcaga gaagaaatac 1560

gaccatccag agctgattgt tgatgagtcg aatctgcgcg tggtgtatgc gccaagccgt 1620

tattttgcca gcgagcccaa agctgatgtc agcctgattt tgcgtaatcc gaaagccatg 1680

gacagcgccc gcaatcaggt gatgtttgcg ctcaatgatt atctcgcagg gctggcgctt 1740

gatcagttaa gcaaccaggc gtcggttggt ggcataagtt tttccaccaa cgctaacaac 1800

ggccttatgg ttaatgctaa tggttacacc cagcgtctgc cgcagctgtt ccaggcattg 1860

ctcgaggggt actttagcta taccgctacg gaagatcagc ttgagcaggc gaagtcctgg 1920

tataaccaga tgatggattc cgcagaaaag ggtaaagcgt ttgagcaggc gattatgccc 1980

gcgcagatgc tctcgcaagt gccgtacttc tcgcgagatg aacggcgtaa aattttgccc 2040

tccattacgt tgaaagaggt gctggcctat cgcgacgcct taaaatcagg ggctcgacca 2100

gagtttatgg ttatcggcaa catgaccgag gcccaggcaa caacgctggc acgcgatgtg 2160

caaaaacagt tgggcgctga tggttcagag tggtgtcgaa acaaagatgt agtggtcgat 2220

aaaaaacaat ccgtcatctt tgaaaaagcc ggtaacagca ccgactccgc actggcagcg 2280

gtatttgtac cgactggcta cgatgaatac accagctcag cctatagctc tctgttgggg 2340

cagatcgtac agccgtggtt ctacaatcag ttgcgtaccg aagaacaatt gggctatgcc 2400

gtgtttgcgt ttccaatgag cgtggggcgt cagtggggca tgggcttcct tttgcaaagc 2460

aatgataaac agccttcatt cttgtgggag cgttacaagg cgtttttccc aaccgcagag 2520

gcaaaattgc gagcgatgaa gccagatgag tttgcgcaaa tccagcaggc ggtaattacc 2580

cagatgctgc aggcaccgca aacgctcggc gaagaagcat cgaagttaag taaagatttc 2640

gatcgcggca atatgcgctt cgattcgcgt gataaaatcg tggcccagat aaaactgctg 2700

acgccgcaaa aacttgctga tttcttccat caggcggtgg tcgagccgca aggcatggct 2760

attctgtcgc agatttccgg cagccagaac gggaaagccg aatatgtaca ccctgaaggc 2820

tggaaagtgt gggagaacgt cagcgcgttg cagcaaacaa tgcccctgat gagtgaaaag 2880

aatgagtgat gtcgccgaga cactagatcc tttgc 2915

<210> 7
<211> 1425
<212> DNA
<213> E. coli

<400> 7
atgaaaaaaa ccacattagc actgagtgca ctggctctga gtttaggttt ggcgttatct 60

ccgctctctg caacggcggc tgagacttct tcagcaacga cagcccagca gatgccaagc 120

cttgcaccga tgctcgaaaa ggtgatgcct tcagtggtca gcattaacgt agaaggtagc 180

acaaccgtta atacgccgcg tatgccgcgt aatttccagc agttcttcgg tgatgattct 240

ccgttctgcc aggaaggttc tccgttccag agctctccgt tctgccaggg tggccagggc 300

ggtaatggtg gcggccagca acagaaattc atggcgctgg gttccggcgt catcattgat 360

gccgataaag gctatgtcgt caccaacaac cacgttgttg ataacgcgac ggtcattaaa 420

gttcaactga gcgatggccg taagttcgac gcgaagatgg ttggcaaaga tccgcgctct 480

gatatcgcgc tgatccaaat ccagaacccg aaaaacctga ccgcaattaa gatggcggat 540

tctgatgcac tgcgcgtggg tgattacacc gtagcgattg gtaacccgtt tggtctgggc 600

gagacggtaa cttccgggat tgtctctgcg ctggggcgta gcggcctgaa tgccgaaaac 660

tacgaaaact tcatccagac cgatgcagcg atcaaccgtg gtaactccgg tggtgcgctg 720

gttaacctga acggcgaact gatcggtatc aacaccgcga tcctcgcacc ggacggcggc 780

aacatcggta tcggttttgc tatcccgagt aacatggtga aaaacctgac ctcgcagatg 840

gtggaatacg gccaggtgaa acgcggtgag ctgggtatta tggggactga gctgaactcc 900

gaactggcga aagcgatgaa agttgacgcc cagcgcggtg ctttcgtaag ccaggttctg 960

cctaattcct ccgctgcaaa agcgggcatt aaagcgggtg atgtgatcac ctcactgaac 1020

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agcaaactga ccctgggctt actgcgcgac ggtaagcagg ttaacgtgaa cctggaactg 1140

cagcagagca gccagaatca ggttgattcc agctccatct tcaacggcat tgaaggcgct 1200

gagatgagca acaaaggcaa agatcagggc gtggtagtga acaacgtgaa aacgggcact 1260

ccggctgcgc agatcggcct gaagaaaggt gatgtgatta ttggcgcgaa ccagcaggca 1320

gtgaaaaaca tcgctgaact gcgtaaagtt ctcgacagca aaccgtctgt gctggcactc 1380

aacattcagc gcggcgacag caccatctac ctgttaatgc agtaa 1425

<210> 8
<211> 474
<212> PRT
<213> E. coli

<400> 8

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
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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> 9
<211> 1425
<212> DNA
<213> E. coli

<400> 9
atgaaaaaaa ccacattagc actgagtgca ctggctctga gtttaggttt ggcgttatct 60

ccgctctctg caacggcggc tgagacttct tcagcaacga cagcccagca gatgccaagc 120

cttgcaccga tgctcgaaaa ggtgatgcct tcagtggtca gcattaacgt agaaggtagc 180

acaaccgtta atacgccgcg tatgccgcgt aatttccagc agttcttcgg tgatgattct 240

ccgttctgcc aggaaggttc tccgttccag agctctccgt tctgccaggg tggccagggc 300

ggtaatggtg gcggccagca acagaaattc atggcgctgg gttccggcgt catcattgat 360

gccgataaag gctatgtcgt caccaacaac cacgttgttg ataacgcgac ggtcattaaa 420

gttcaactga gcgatggccg taagttcgac gcgaagatgg ttggcaaaga tccgcgctct 480

gatatcgcgc tgatccaaat ccagaacccg aaaaacctga ccgcaattaa gatggcggat 540

tctgatgcac tgcgcgtggg tgattacacc gtagcgattg gtaacccgtt tggtctgggc 600

gagacggtaa cttccgggat tgtctctgcg ctggggcgta gcggcctgaa tgccgaaaac 660

tacgaaaact tcatccagac cgatgcagcg attaatcgtg gtaacgccgg tggtgcgctg 720

gttaacctga acggcgaact gatcggtatc aacaccgcga tcctcgcacc ggacggcggc 780

aacatcggta tcggttttgc tatcccgagt aacatggtga aaaacctgac ctcgcagatg 840

gtggaatacg gccaggtgaa acgcggtgag ctgggtatta tggggactga gctgaactcc 900

gaactggcga aagcgatgaa agttgacgcc cagcgcggtg ctttcgtaag ccaggttctg 960

cctaattcct ccgctgcaaa agcgggcatt aaagcgggtg atgtgatcac ctcactgaac 1020

ggtaagccga tcagcagctt tgccgcactg cgtgctcagg tgggtactat gccggtaggc 1080

agcaaactga ccctgggctt actgcgcgac ggtaagcagg ttaacgtgaa cctggaactg 1140

cagcagagca gccagaatca ggttgattcc agctccatct tcaacggcat tgaaggcgct 1200

gagatgagca acaaaggcaa agatcagggc gtggtagtga acaacgtgaa aacgggcact 1260

ccggctgcgc agatcggcct gaagaaaggt gatgtgatta ttggcgcgaa ccagcaggca 1320

gtgaaaaaca tcgctgaact gcgtaaagtt ctcgacagca aaccgtctgt gctggcactc 1380

aacattcagc gcggcgacag caccatctac ctgttaatgc agtaa 1425

<210> 10
<211> 474
<212> PRT
<213> E. coli

<400> 10

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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
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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
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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> 11
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> hTNF40-gL1

<400> 11

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 Lys Ala Ser Gln Asn Val Gly Thr Asn
20 25 30

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
85 90 95

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

<210> 12
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> gh3h TNF40.4

<400> 12

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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 Ala Ser Gly Tyr Val Phe Thr Asp Tyr
            20                  25                  30

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

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
65                  70                  75                  80

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

Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115
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<210> 13
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Grafted Light Chain

<400> 13

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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 Lys Ala Ser Gln Asn Val Gly Thr Asn
            20                  25                  30

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
                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
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<210> 14
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Grafted Heavy Chain

<400> 14

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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 Ala Ser Gly Tyr Val Phe Thr Asp Tyr
            20                  25                  30

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

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
65                  70                  75                  80

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

Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110
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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> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 15
gcatcataat tttcttttta cctc 24

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 16
gggaaatgaa cctgagcaaa acgc 24

<210> 17
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 17
gtgccaggag atgcagcagc ttgc 24

<210> 18
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 18
tttgcagcca gtcagaaagt g 21

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 19
ctgcctgcga ttttcgccgg aacg 24

<210> 20
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide primer

<400> 20
cgcatggtac gtgccacgat atcc 24