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<151> 2010-01-14

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Phe Tyr Leu Glu Val Glu Asn Asp Ala Leu Pro Gly Ala Val Asp Arg
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Leu Ala Asp Ala Ile Ala Glu Pro Leu Leu Asp Lys Lys Tyr Ala Glu
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Arg Glu Arg Asn Ala Val Asn Ala Glu Leu Thr Met Ala Arg Thr Arg
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Ala Gln Lys Gly Ile Ile Ile His Tyr Val Pro Ala Leu Pro Arg Lys
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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

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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

ggtaagccga tcagcagctt tgccgcactg cgtgctcagg tgggtactat gccggtaggc 1080

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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

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
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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

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> 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

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

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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
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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> 14
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Grafted Heavy Chain

<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 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 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

<210> 21
<211> 188
<212> PRT
<213> Escherichia coli

<400> 21

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
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> 22
<211> 162
<212> PRT
<213> Escherichia coli

<400> 22

Cys Ser Ala Asn Asn Thr Ala Lys Asn Met His Pro Glu Thr Arg Ala
1 5 10 15

Val Gly Ser Glu Thr Ser Ser Leu Gln Ala Ser Gln Asp Glu Phe Glu
20 25 30

Asn Leu Val Arg Asn Val Asp Val Lys Ser Arg Ile Met Asp Gln Tyr
35 40 45

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

Gly Ile Asp Cys Ser Gly Phe Val Gln Arg Thr Phe Arg Glu Gln Phe
65 70 75 80

Gly Leu Glu Leu Pro Arg Ser Thr Tyr Glu Gln Gln Glu Met Gly Lys
85 90 95

Ser Val Ser Arg Ser Asn Leu Arg Thr Gly Asp Leu Val Leu Phe Arg
100 105 110

Ala Gly Ser Thr Gly Arg His Val Gly Ile Tyr Ile Gly Asn Asn Gln
115 120 125

Phe Val His Ala Ser Thr Ser Ser Gly Val Ile Ile Ser Ser Met Asn
130 135 140

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

Arg Ser

<210> 23
<211> 951
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutated OmpT sequence

<400> 23
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tctaccgaga ctttatcgtt tactcctgac aacataaatg cggacattag tcttggaact 120

ctgagcggaa aaacaaaaga gcgtgtttat ctagccgaag aaggaggccg aaaagtcagt 180

caactcgact ggaaattcaa taacgctgca attattaaag gtgcaattaa ttgggatttg 240

atgccccaga tatctatcgg ggctgctggc tggacaactc tcggcagccg aggtggcaat 300

atggtcgatc aggactggat ggattccagt aaccccggaa cctggacgga tgaaagtaga 360

caccctgata cacaactcaa ttatgccaac gaatttgatc tgaatatcaa aggctggctc 420

ctcaacgaac ccaattaccg cctgggactc atggccggat atcaggaaag ccgttatagc 480

tttacagcca gaggtggttc ctatatctac agttctgagg agggattcag agatgatatc 540

ggctccttcc cgaatggaga aagagcaatc ggctacaaac aacgttttaa aatgccctac 600

attggcttga ctggaagtta tcgttatgaa gattttgaac tcggtggcac atttaaatac 660

agcggctggg tggaatcatc tgataacgct gaagcttatg acccgggaaa aagaatcact 720

tatcgcagta aggtcaaaga ccaaaattac tattctgttg cagtcaatgc aggttattac 780

gtcacaccta acgcaaaagt ttatgttgaa ggcgcatgga atcgggttac gaataaaaaa 840

ggtaatactt cactttatga tcacaataat aacacttcag actacagcaa aaatggagca 900

ggtatagaaa actataactt catcactact gctggtctta agtacacatt t 951

<210> 24
<211> 317
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutated OmpT sequence

<400> 24

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> 25

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

<220>
<223> Mutated OmpT sequence

<400> 25
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tctaccgaga ctttatcgtt tactcctgac aacataaatg cggacattag tcttggaact 120

ctgagcggaa aaacaaaaga gcgtgtttat ctagccgaag aaggaggccg aaaagtcagt 180

caactcgact ggaaattcaa taacgctgca attattaaag gtgcaattaa ttgggatttg 240

atgccccaga tatctatcgg ggctgctggc tggacaactc tcggcagccg aggtggcaat 300

atggtcgatc aggactggat ggattccagt aaccccggaa cctggacgga tgaaagtaga 360

caccctgata cacaactcaa ttatgccaac gaatttgatc tgaatatcaa aggctggctc 420

ctcaacgaac ccaattaccg cctgggactc atggccggat atcaggaaag ccgttatagc 480

tttacagcca gaggtggttc ctatatctac agttctgagg agggattcag agatgatatc 540

ggctccttcc cgaatggaga aagagcaatc ggctacaaac aacgttttaa aatgccctac 600

attggcttga ctggaagtta tcgttatgaa gattttgaac tcggtggcac atttaaatac 660

agcggctggg tggaatcatc tgataacgat gaacactatg acccgggaaa aagaatcact 720

tatcgcagta aggtcaaaga ccaaaattac tattctgttg cagtcaatgc aggttattac 780

gtcacaccta acgcaaaagt ttatgttgaa ggcgcatgga atcgggttac gaataaaaaa 840

ggtaatactt cactttatga tcacaataat aacacttcag actacagcaa aaatggagca 900

ggtatagaaa actataactt catcactact gctggtctta agtacacatt ttaa 954

<210> 26
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutated DsbC sequence

<400> 26
atgaagaaag gttttatgtt gtttactttg ttagcggcgt tttcaggctt tgctcaggct 60

gatgacgcgg caattcaaca aacgttagcc aaaatgggca tcaaaagcag cgatattcag 120

cccgcgcctg tagctggcat gaagacagtt ctgactaaca gcggcgtgtt gtacatcacc 180

gatgatggta aacatatcat tcaggggcca atgtatgacg ttagtggcac ggctccggtc 240

aatgtcacca ataagatgct gttaaagcag ttgaatgcgc ttgaaaaaga gatgatcgtt 300

tataaagcgc cgcaggaaaa acacgtcatc accgtgttta ctgatattac ctgtggttac 360

tgccacaaac tgcatgagca aatggcagac tacaacgcgc tggggatcac cgtgcgttat 420

cttgctttcc cgcgccaggg gctggacagc gatgcagaga aagaaatgaa agctatctgg 480

tgtgcgaaag ataaaaacaa agcgtttgat gatgtgatgg caggtaaaag cgtcgcacca 540

gccagttgcg acgtggatat tgccgaccat tacgcacttg gcgtccagct tggcgttagc 600

ggtactccgg cagttgtgct gagcaatggc acacttgttc cgggttacca gccgccgaaa 660

gagatgaaag aatttctcga cgaacaccaa aaaatgacca gcggtaaaca ccatcaccat 720

caccactaa 729

<210> 27
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutated DsbC sequence

<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

eolf-seql

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> 28
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hTNF40 CDRH1

<400> 28

Asp Tyr Gly Met Asn
1 5

<210> 29
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hTNF40 Human hybrid CDRH2

<400> 29

Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 30
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hTNF40 CDRH3

<400> 30

Gly Tyr Arg Ser Tyr Ala Met Asp Tyr
1 5

<210> 31
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hTNF40 CDRL1

<400> 31

Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala
1 5 10

<210> 32
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hTNF40 CDRL2

<400> 32

Ser Ala Ser Phe Leu Tyr Ser
1 5

<210> 33
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hTNF40 CDRL3

<400> 33

Gln Gln Tyr Asn Ile Tyr Pro Leu Thr
1 5

<210> 34
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hTNF40 CDRH2

<400> 34

Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Val Asp Asp Phe Lys
1 5 10 15

Gly

<210> 35
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> OmpA oligonucleotide adaptor

<400> 35
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cttggctctg acgtacgagt cagg 84

<210> 36

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

<220>
<223> IGS cassette-1

<400> 36
gagctcacca gtaacaaaaa gttttaatag aggagagtgt taatgaagaa gactgctata 60

gcaattg 67

<210> 37
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> IGS cassette-2

<400> 37
gagctcacca gtaacaaaaa gttttaatag aggggagtgt taaaatgaag aagactgcta 60

tagcaattg 69

<210> 38
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> IGS cassette-3

<400> 38
gagctcacca gtaacaaaaa gctttaatag aggagagtgt tgaggaggaa aaaaaaatga 60

agaaaactgc tatagcaatt g 81

<210> 39
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> IGS cassette-4

<400> 39
gagctcacca gtaacaaaaa gttttaatag aggagagtgt tgacgaggat tatataatga 60

agaaaactgc tatagcaatt g 81