SEQUENCE LISTING

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<120> Recombinant Bacterial Host Cell for Protein Expression

<130> G0164-WO

<150> GB1208367.1
<151> 2012-05-14

<160> 82

<170> PatentIn version 3.5

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Phe Tyr Leu Glu Val Glu Asn Asp Ala Leu Pro Gly Ala Val Asp Arg
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Arg Glu Arg Asn Ala Val Asn Ala Glu Leu Thr Met Ala Arg Thr Arg
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195 200 205

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Tyr Tyr Ser Ala Asn Leu Met Lys Ala Val Ile Tyr Ser Asn Lys Pro
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Ala Gln Lys Gly Ile Ile Ile His Tyr Val Pro Ala Leu Pro Arg Lys
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eolf-seql

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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

aatgagtga 2889

<210> 7

<211> 1425
<212> DNA
<213> Escherichia 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

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> Escherichia 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> Artificial Sequence

<220>
<223> mutated DegP

<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> Artificial Sequence

<220>
<223> mutated DegP

<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> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligonucleotide primer for the region of the mutated DegP gene comprising the Ase I restriction site

<400> 11
ctgcctgcga ttttcgccgg aacg 24

<210> 12
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligonucleotide primer for the region of the mutated DegP gene comprising the Ase I restriction site

<400> 12
cgcatggtac gtgccacgat atcc 24

<210> 13
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> the 5' oligonucleotide primer for the region of the mutated Tsp gene comprising the Ase I restriction site

<400> 13
gggaaatgaa cctgagcaaa acgc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligonucleotide primer for the region of the mutated Protease III gene comprising the Ase I restriction site

<400> 14
gggaaaggcg gcggaaccgc ctag 24

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligonucleotide primer for the region of the mutated Protease III gene comprising the Ase I restriction site

<400> 15
ctactgtgcc agcggtggta atgg 24

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

<220>
<223> 3' oligonucleotide primer for the region of the mutated Tsp gene comprising the Ase I restriction site

<400> 16
gcatcataat tttcttttta cctc 24

<210> 17
<211> 564
<212> DNA
<213> Artificial Sequence

<220>
<223> wild-type spr gene

<400> 17
atggtcaaat ctcaaccgat tttgagatat atcttgcgcg ggattcccgc gattgcagta 60

gcggttctgc tttctgcatg tagtgcaaat aacaccgcaa agaatatgca tcctgagaca 120

cgtgcagtgg gtagtgaaac atcatcactg caagcttctc aggatgaatt tgaaaacctg 180

gttcgtaatg tcgacgtaaa atcgcgaatt atggatcagt atgctgactg gaaaggcgta 240

cgttatcgtc tgggcggcag cactaaaaaa ggtatcgatt gttctggttt cgtacagcgt 300

acattccgtg agcaatttgg cttagaactt ccgcgttcga cttacgaaca gcaggaaatg 360

ggtaaatctg tttcccgcag taatttgcgt acgggtgatt tagttctgtt ccgtgccggt 420

tcaacgggac gccatgtcgg tatttatatc ggcaacaatc agtttgtcca tgcttccacc 480

agcagtggtg ttattatttc cagcatgaat gaaccgtact ggaagaagcg ttacaacgaa 540

gcacgccggg ttctcagccg cagc 564

<210> 18
<211> 188
<212> PRT
<213> Escherichia coli

<400> 18

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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
        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> 19
<211> 162
<212> PRT
<213> Escherichia coli

<400> 19

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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> 20
<211> 954
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence of a mutated OmpT sequence comprising D210A and H212A mutations

<400> 20
atgcgggcga aacttctggg aatagtcctg acaaccccta ttgcgatcag ctcttttgct 60

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 ttaa 954

<210> 21
<211> 317
<212> PRT
<213> Artificial Sequence

<220>
<223> mutated OmpT sequence comprising D210A and H212A mutations

<400> 21

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> 22
<211> 954
<212> DNA
<213> Artificial Sequence

<220>
<223> mutated knockout OmpT sequence

<400> 22

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attcgggcga aacttctggg aatagtcctg acaaccccta ttgcgatcag ctcttttgct       60

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
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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> 23
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> OmpA oligonucleotide adapter

<400> 23
cgattgaatg gagaacttga attcgggcga aacttctggg aatag 45

<210> 24
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide cassette encoding intergenic sequence 1 (IGS1) for E. coli Fab expression

<400> 24
aagttttaat agaggagagt gttaatgaag aag 33

<210> 25
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> the oligonucleotide cassette encoding intergenic sequence 2 (IGS2) for E. coli Fab expression.

<400> 25
aagttttaat agaggggagt gttaaaatga agaag 35

<210> 26
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide cassette encoding intergenic sequence 3 (IGS3) for E. coli Fab expression

<400> 26
aagctttaat agaggagagt gttgaggagg aaaaaaaaat gaagaaa 47

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

<220>
<223> oligonucleotide cassette encoding intergenic sequence 4 (IGS4)

for E. coli Fab expression

<400> 27
aagctttaat agaggagagt gttgacgagg attatataat gaagaaa 47

<210> 28
<211> 810
<212> DNA
<213> Escherichia coli

<400> 28
atgaaatcac tgtttaaagt aacgctgctg gcgaccacaa tggccgttgc cctgcatgca 60

ccaatcactt ttgctgctga agctgcaaaa cctgctacag ctgctgacag caaagcagcg 120

ttcaaaaatg acgatcagaa atcagcttat gcactgggtg cctcgctggg tcgttacatg 180

gaaaactctc taaaagaaca agaaaaactg ggcatcaaac tggataaaga tcagctgatc 240

gctggtgttc aggatgcatt tgctgataag agcaaactct ccgaccaaga gatcgaacag 300

actctacaag cattcgaagc tcgcgtgaag tcttctgctc aggcgaagat ggaaaaagac 360

gcggctgata acgaagcaaa aggtaaagag taccgcgaga aatttgccaa agagaaaggt 420

gtgaaaacct cttcaactgg tctggtttat caggtagtag aagccggtaa aggcgaagca 480

ccgaaagaca gcgatactgt tgtagtgaac tacaaaggta cgctgatcga cggtaaagag 540

ttcgacaact cttacacccg tggtgaaccg ctttctttcc gtctggacgg tgttatcccg 600

ggttggacag aaggtctgaa gaacatcaag aaaggcggta agatcaaact ggttattcca 660

ccagaactgg cttacggcaa agcgggtgtt ccggggatcc caccgaattc taccctggtg 720

tttgacgtag agctgctgga tgtgaaacca gcgccgaagg ctgatgcaaa gccggaagct 780

gatgcgaaag ccgcagattc tgctaaaaaa 810

<210> 29
<211> 270
<212> PRT
<213> Escherichia coli

<400> 29

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

Ala Leu His Ala Pro Ile Thr Phe Ala Ala Glu Ala Ala Lys Pro Ala
20 25 30

Thr Ala Ala Asp Ser Lys Ala Ala Phe Lys Asn Asp Asp Gln Lys Ser
35 40 45

Ala Tyr Ala Leu Gly Ala Ser Leu Gly Arg Tyr Met Glu Asn Ser Leu
50 55 60

Lys Glu Gln Glu Lys Leu Gly Ile Lys Leu Asp Lys Asp Gln Leu Ile
65 70 75 80

```
Ala Gly Val Gln Asp Ala Phe Ala Asp Lys Ser Lys Leu Ser Asp Gln
                85                  90                  95

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

Ala Gln Ala Lys Met Glu Lys Asp Ala Ala Asp Asn Glu Ala Lys Gly
        115                 120                 125

Lys Glu Tyr Arg Glu Lys Phe Ala Lys Glu Lys Gly Val Lys Thr Ser
    130                 135                 140

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

Pro Lys Asp Ser Asp Thr Val Val Val Asn Tyr Lys Gly Thr Leu Ile
                165                 170                 175

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

Phe Arg Leu Asp Gly Val Ile Pro Gly Trp Thr Glu Gly Leu Lys Asn
        195                 200                 205

Ile Lys Lys Gly Gly Lys Ile Lys Leu Val Ile Pro Pro Glu Leu Ala
    210                 215                 220

Tyr Gly Lys Ala Gly Val Pro Gly Ile Pro Pro Asn Ser Thr Leu Val
225                 230                 235                 240

Phe Asp Val Glu Leu Leu Asp Val Lys Pro Ala Pro Lys Ala Asp Ala
                245                 250                 255

Lys Pro Glu Ala Asp Ala Lys Ala Ala Asp Ser Ala Lys Lys
            260                 265                 270
```

<210> 30
<211> 828
<212> DNA
<213> Artificial Sequence

<220>
<223> the FkpA tagged gene

<400> 30

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atgaaatcac tgtttaaagt aacgctgctg gcgaccacaa tggccgttgc cctgcacgca      60

ccaatcactt ttgctgctga agctgcaaaa cctgctactg ctgctgacag caaagcagcg      120

ttcaaaaatg acgatcagaa atcagcttat gcactgggtg cctcgctggg tcgttacatg      180

gaaaactctc taaaagaaca agaaaaactg ggcatcaaac tggataaaga tcaactgatc      240

gctggtgttc aggatgcatt tgctgataag agcaaactct ccgaccaaga gatcgaacag      300

actctacaag catttgaagc tcgcgtgaag tcttctgctc aggcgaagat ggaaaaagac      360
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gcggctgata acgaagcaaa aggtaaagag taccgcgaga aatttgccaa agagaaaggt 420

gtgaaaacct cttcaactgg tctggtttat caggtagtag aagccggtaa aggcgaagca 480

ccgaaagaca gcgatactgt tgtagtgaac tacaaaggta cgctgatcga cggtaaagag 540

ttcgacaact cttacacccg tggtgaaccg ctttctttcc gtctggacgg tgttatcccg 600

ggttggacag aaggtctgaa gaacatcaag aaaggcggta agataaaact ggttattcca 660

ccagaactgg cttacggcaa agcgggtgtt ccggggattc caccaaattc taccctggtg 720

tttgacgtag agctgctgga tgtgaaacca gcgccgaagg ctgatgcaaa gccggaagct 780

gatgcgaaag ccgcagattc tgctaaaaaa caccatcacc atcaccac 828

<210> 31
<211> 276
<212> PRT
<213> Artificial Sequence

<220>
<223> FkpA his tagged gene

<400> 31

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

Ala Leu His Ala Pro Ile Thr Phe Ala Ala Glu Ala Ala Lys Pro Ala
20 25 30

Thr Ala Ala Asp Ser Lys Ala Ala Phe Lys Asn Asp Asp Gln Lys Ser
35 40 45

Ala Tyr Ala Leu Gly Ala Ser Leu Gly Arg Tyr Met Glu Asn Ser Leu
50 55 60

Lys Glu Gln Glu Lys Leu Gly Ile Lys Leu Asp Lys Asp Gln Leu Ile
65 70 75 80

Ala Gly Val Gln Asp Ala Phe Ala Asp Lys Ser Lys Leu Ser Asp Gln
85 90 95

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

Ala Gln Ala Lys Met Glu Lys Asp Ala Ala Asp Asn Glu Ala Lys Gly
115 120 125

Lys Glu Tyr Arg Glu Lys Phe Ala Lys Glu Lys Gly Val Lys Thr Ser
130 135 140

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

eolf-seql

Pro Lys Asp Ser Asp Thr Val Val Val Asn Tyr Lys Gly Thr Leu Ile
165 170 175

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

Phe Arg Leu Asp Gly Val Ile Pro Gly Trp Thr Glu Gly Leu Lys Asn
195 200 205

Ile Lys Lys Gly Gly Lys Ile Lys Leu Val Ile Pro Pro Glu Leu Ala
210 215 220

Tyr Gly Lys Ala Gly Val Pro Gly Ile Pro Pro Asn Ser Thr Leu Val
225 230 235 240

Phe Asp Val Glu Leu Leu Asp Val Lys Pro Ala Pro Lys Ala Asp Ala
245 250 255

Lys Pro Glu Ala Asp Ala Lys Ala Ala Asp Ser Ala Lys Lys His His
260 265 270

His His His His
275

<210> 32
<211> 486
<212> DNA
<213> Escherichia coli

<400> 32
gtgaaaaagt ggttattagc tgcaggtctc ggtttagcac tggcaacttc tgctcaggcg 60

gctgacaaaa ttgcaatcgt caacatgggc agcctgttcc agcaggtagc gcagaaaacc 120

ggtgtttcta acacgctgga aaatgagttc aaaggccgtg ccagcgaact gcagcgtatg 180

gaaaccgatc tgcaggctaa aatgaaaaag ctgcagtcca tgaaagcggg cagcgatcgc 240

actaagctgg aaaaagacgt gatggctcag cgccagactt ttgctcagaa agcgcaggct 300

tttgagcagg atcgcgcacg tcgttccaac gaagaacgcg gcaaactggt tactcgtatc 360

cagactgctg tgaaatccgt tgccaacagc caggatatcg atctggttgt tgatgcaaac 420

gccgttgctt acaacagcag cgatgtaaaa gacatcactg ccgacgtact gaaacaggtt 480

aaataa 486

<210> 33
<211> 161
<212> PRT
<213> Escherichia coli

<400> 33

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

eolf-seql

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

Phe Gln Gln Val Ala Gln Lys Thr Gly Val Ser Asn Thr Leu Glu Asn
35 40 45

Glu Phe Lys Gly Arg Ala Ser Glu Leu Gln Arg Met Glu Thr Asp Leu
50 55 60

Gln Ala Lys Met Lys Lys Leu Gln Ser Met Lys Ala Gly Ser Asp Arg
65 70 75 80

Thr Lys Leu Glu Lys Asp Val Met Ala Gln Arg Gln Thr Phe Ala Gln
85 90 95

Lys Ala Gln Ala Phe Glu Gln Asp Arg Ala Arg Arg Ser Asn Glu Glu
100 105 110

Arg Gly Lys Leu Val Thr Arg Ile Gln Thr Ala Val Lys Ser Val Ala
115 120 125

Asn Ser Gln Asp Ile Asp Leu Val Val Asp Ala Asn Ala Val Ala Tyr
130 135 140

Asn Ser Ser Asp Val Lys Asp Ile Thr Ala Asp Val Leu Lys Gln Val
145 150 155 160

Lys

<210> 34
<211> 501
<212> DNA
<213> Artificial Sequence

<220>
<223> skp his tagged gene

<400> 34
atgaaaaagt ggttattagc cgcaggtctc ggtttagcac tggcaacttc tgctcaggcg 60

gctgacaaaa ttgcaatcgt caacatgggc agcctgttcc agcaggtagc gcagaaaacc 120

ggtgtttcta acacgctgga aaatgagttc aaaggccgtg ccagcgaact ccagcgtatg 180

gaaaccgatc tccaggctaa aatgaaaaag ctgcaatcca tgaaagcggg cagcgatcgc 240

actaagctgg aaaaagacgt gatggctcag cgccagactt ttgctcagaa agcgcaggct 300

tttgagcagg atcgcgcacg tcgttccaac gaagaacgcg gcaaactggt tactcgtatc 360

cagactgctg tgaaatccgt tgccaacagc caggaaatcg atctggttgt tgatgcaaac 420

gccgttgctt acaacagcag cgatgtaaaa gacatcactg ccgacgtact gaaacaggtt 480

aaacaccatc accatcacca c 501

<210> 35
<211> 167
<212> PRT
<213> Artificial Sequence

<220>
<223> skp his tagged gene

<400> 35

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

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

Phe Gln Gln Val Ala Gln Lys Thr Gly Val Ser Asn Thr Leu Glu Asn
        35                  40                  45

Glu Phe Lys Gly Arg Ala Ser Glu Leu Gln Arg Met Glu Thr Asp Leu
    50                  55                  60

Gln Ala Lys Met Lys Lys Leu Gln Ser Met Lys Ala Gly Ser Asp Arg
65                  70                  75                  80

Thr Lys Leu Glu Lys Asp Val Met Ala Gln Arg Gln Thr Phe Ala Gln
                85                  90                  95

Lys Ala Gln Ala Phe Glu Gln Asp Arg Ala Arg Arg Ser Asn Glu Glu
            100                 105                 110

Arg Gly Lys Leu Val Thr Arg Ile Gln Thr Ala Val Lys Ser Val Ala
        115                 120                 125

Asn Ser Gln Glu Ile Asp Leu Val Val Asp Ala Asn Ala Val Ala Tyr
    130                 135                 140

Asn Ser Ser Asp Val Lys Asp Ile Thr Ala Asp Val Leu Lys Gln Val
145                 150                 155                 160

Lys His His His His His His
                165
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<210> 36
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CA170 1519 Ab CDRH1

<400> 36

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Gly Phe Thr Phe Ser Asn Tyr Gly Met Val
1               5                  10
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<210> 37
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CA170_1519 Ab CDRH2

<400> 37

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

Gly

<210> 38
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> CA170_1519 Ab CDRH3

<400> 38

Gly Ile Val Arg Pro Phe Leu Tyr
1 5

<210> 39
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CA170_1519 Ab CDRL1

<400> 39

Lys Ser Ser Gln Ser Leu Val Gly Ala Ser Gly Lys Thr Tyr Leu Tyr
1 5 10 15

<210> 40
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CA170_1519 Ab CDRL2

<400> 40

Leu Val Ser Thr Leu Asp Ser
1 5

<210> 41
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CA170_1519 Ab CDRL3

<400> 41

Leu Gln Gly Thr His Phe Pro His Thr
1 5

<210> 42
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Rat Ab 1519 VL region

<400> 42

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Val Gly Ala
20 25 30

Ser Gly Lys Thr Tyr Leu Tyr Trp Leu Phe Gln Arg Ser Gly Gln Ser
35 40 45

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

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

Arg Arg Val Glu Ala Asp Asp Leu Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Thr His Phe Pro His Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 43
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Rat Ab 1519 VL region

<400> 43
gatgttgtga tgacccagac tccactgtct ttgtcggttg cccttggaca accagcctcc 60

atctcttgca agtcaagtca gagcctcgta ggtgctagtg gaaagacata tttgtattgg 120

ttatttcaga ggtccggcca gtctccaaag cgactaatct atctggtgtc cacactggac 180

tctggaattc ctgataggtt cagtggcagt ggagcagaga cagattttac tcttaaaatc 240

cgcagagtgg aagccgatga tttgggagtt tattactgct tgcaaggtac acattttcct 300

cacacgtttg gagctgggac caagctggaa ttgaaa 336

<210> 44
<211> 132

<212> PRT
<213> Artificial Sequence

<220>
<223> Rat Ab 1519 VL region

<400> 44

Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Met Leu Trp Ile Gln
1 5 10 15

Gly Thr Ser Gly Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Ser
20 25 30

Val Ala Leu Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
35 40 45

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

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

Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ala Glu Thr Asp Phe
85 90 95

Thr Leu Lys Ile Arg Arg Val Glu Ala Asp Asp Leu Gly Val Tyr Tyr
100 105 110

Cys Leu Gln Gly Thr His Phe Pro His Thr Phe Gly Ala Gly Thr Lys
115 120 125

Leu Glu Leu Lys
130

<210> 45
<211> 396
<212> DNA
<213> Artificial Sequence

<220>
<223> Rat Ab 1519 VL region

<400> 45
atgatgagtc ctgcccagtt cctgtttctg ctgatgctct ggattcaggg aaccagtggt 60

gatgttgtga tgacccagac tccactgtct ttgtcggttg cccttggaca accagcctcc 120

atctcttgca agtcaagtca gagcctcgta ggtgctagtg gaaagacata tttgtattgg 180

ttatttcaga ggtccggcca gtctccaaag cgactaatct atctggtgtc cacactggac 240

tctggaattc ctgataggtt cagtggcagt ggagcagaga cagattttac tcttaaaatc 300

cgcagagtgg aagccgatga tttgggagtt tattactgct tgcaaggtac acattttcct 360

cacacgtttg gagctgggac caagctggaa ttgaaa 396

<210> 46
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Rat Ab 1519 VH region

<400> 46

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

Ser Met Lys Leu Ser Cys Val Val Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

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

Ala Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr Tyr Arg Asp Ser Val
50 55 60

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

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

Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser
115

<210> 47
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Rat Ab 1519 VH region

<400> 47
gaggtgccgc tggtggagtc tgggggcggc tcagtgcagc ctgggaggtc catgaaactc 60

tcctgtgtag tctcaggatt cactttcagt aattatggca tggtctgggt ccgccaggct 120

ccaaagaagg gtctggagtg ggtcgcatat attgattctg atggtgataa tacttactac 180

cgagattccg tgaagggccg attcactatc tccagaaata atgcaaaaag caccctatat 240

ttgcaaatgg acagtctgag gtctgaggac acggccactt attactgtac aacagggatt 300

gtccggccct ttctctattg gggccaagga accacggtca ccgtctcg 348

<210> 48
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Rat Ab 1519 VH region

<400> 48

Met Asp Ile Ser Leu Ser Leu Ala Phe Leu Val Leu Phe Ile Lys Gly
1 5 10 15

Val Arg Cys Glu Val Pro Leu Val Glu Ser Gly Gly Gly Ser Val Gln
20 25 30

Pro Gly Arg Ser Met Lys Leu Ser Cys Val Val Ser Gly Phe Thr Phe
35 40 45

Ser Asn Tyr Gly Met Val Trp Val Arg Gln Ala Pro Lys Lys Gly Leu
50 55 60

Glu Trp Val Ala Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr Tyr Arg
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asn Asn Ala Lys Ser
85 90 95

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

Tyr Tyr Cys Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln
115 120 125

Gly Thr Thr Val Thr Val Ser
130 135

<210> 49
<211> 405
<212> DNA
<213> Artificial Sequence

<220>
<223> Rat Ab 1519 VH region

<400> 49
atggacatca gtctcagctt ggctttcctt gtccttttca taaaaggtgt ccggtgtgag 60

gtgccgctgg tggagtctgg gggcggctca gtgcagcctg ggaggtccat gaaactctcc 120

tgtgtagtct caggattcac tttcagtaat tatggcatgg tctgggtccg ccaggctcca 180

aagaagggtc tggagtgggt cgcatatatt gattctgatg gtgataatac ttactaccga 240

gattccgtga agggccgatt cactatctcc agaaataatg caaaaagcac cctatatttg 300

caaatggaca gtctgaggtc tgaggacacg gccacttatt actgtacaac agggattgtc 360

cggccctttc tctattgggg ccaaggaacc acggtcaccg tctcg 405

<210> 50
<211> 112

<212> PRT
<213> Artificial Sequence

<220>
<223> 1519 gL20 V-region

<400> 50

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 Ser Ser Gln Ser Leu Val Gly Ala
20 25 30

Ser Gly Lys Thr Tyr Leu Tyr Trp Leu Phe Gln Lys Pro Gly Lys Ala
35 40 45

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

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
65 70 75 80

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Gly
85 90 95

Thr His Phe Pro His Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 51
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> 1519 gL20 V-region

<400> 51
gatatccaga tgacccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact 60

attacctgta aaagctccca gtccctggtg ggtgcaagcg gcaaaaccta cctgtactgg 120

ctcttccaga aaccgggcaa agctccgaaa cgcctgatct atctggtgtc taccctggat 180

agcggtattc cgtctcgttt ctccggtagc ggtagcggta ccgaattcac gctgaccatt 240

agctccctcc agccggagga ctttgctacc tattactgcc tccagggcac tcattttccg 300

cacactttcg gccagggtac caaactggaa atcaaa 336

<210> 52
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> 1519 gL20 V-region

<400> 52

eolf-seql

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1 5 10 15

Thr Val Ala Gln Ala Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
20 25 30

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

Ser Leu Val Gly Ala Ser Gly Lys Thr Tyr Leu Tyr Trp Leu Phe Gln
50 55 60

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

Asp Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu
85 90 95

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

Tyr Cys Leu Gln Gly Thr His Phe Pro His Thr Phe Gly Gln Gly Thr
115 120 125

Lys Leu Glu Ile Lys
130

<210> 53
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> 1519 gL20 V-region

<400> 53
atgaaaaaga cagctatcgc aattgcagtg gccttggctg gtttcgctac cgtagcgcaa 60

gctgatatcc agatgaccca gagtccaagc agtctctccg ccagcgtagg cgatcgtgtg 120

actattacct gtaaaagctc ccagtccctg gtgggtgcaa gcggcaaaac ctacctgtac 180

tggctcttcc agaaaccggg caaagctccg aaacgcctga tctatctggt gtctaccctg 240

gatagcggta ttccgtctcg tttctccggt agcggtagcg gtaccgaatt cacgctgacc 300

attagctccc tccagccgga ggactttgct acctattact gcctccaggg cactcatttt 360

ccgcacactt tcggccaggg taccaaactg gaaatcaaa 399

<210> 54
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> 1519 gL20 light chain (V + constant)

<400> 54

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 Ser Ser Gln Ser Leu Val Gly Ala
20 25 30

Ser Gly Lys Thr Tyr Leu Tyr Trp Leu Phe Gln Lys Pro Gly Lys Ala
35 40 45

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

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
65 70 75 80

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Gly
85 90 95

Thr His Phe Pro His Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

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

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

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

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 55
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> 1519 gL20 light chain (V + constant)

<400> 55
gatatccaga tgacccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact 60

attacctgta aaagctccca gtccctggtg ggtgcaagcg gcaaaaccta cctgtactgg 120

ctcttccaga aaccgggcaa agctccgaaa cgcctgatct atctggtgtc taccctggat 180

agcggtattc cgtctcgttt ctccggtagc ggtagcggta ccgaattcac gctgaccatt 240

agctccctcc agccggagga ctttgctacc tattactgcc tccagggcac tcattttccg 300

cacactttcg gccagggtac caaactggaa atcaaacgta cggtagcggc cccatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcaccagta acaaaaagtt ttaatagagg ggagtgt 657

<210> 56
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> 1519 gL20 light chain

<400> 56

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1 5 10 15

Thr Val Ala Gln Ala Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
20 25 30

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

Ser Leu Val Gly Ala Ser Gly Lys Thr Tyr Leu Tyr Trp Leu Phe Gln
50 55 60

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

Asp Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu
85 90 95

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

Tyr Cys Leu Gln Gly Thr His Phe Pro His Thr Phe Gly Gln Gly Thr
115 120 125

Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
130 135 140

eolf-seql

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

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

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
180 185 190

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

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
210 215 220

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235 240

<210> 57
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<223> 1519 gL20 light chain

<400> 57
atgaaaaaga cagctatcgc aattgcagtg gccttggctg gtttcgctac cgtagcgcaa 60

gctgatatcc agatgaccca gagtccaagc agtctctccg ccagcgtagg cgatcgtgtg 120

actattacct gtaaaagctc ccagtccctg gtgggtgcaa gcggcaaaac ctacctgtac 180

tggctcttcc agaaaccggg caaagctccg aaacgcctga tctatctggt gtctaccctg 240

gatagcggta ttccgtctcg tttctccggt agcggtagcg gtaccgaatt cacgctgacc 300

attagctccc tccagccgga ggactttgct acctattact gcctccaggg cactcatttt 360

ccgcacactt tcggccaggg taccaaactg gaaatcaaac gtacggtagc ggccccatct 420

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 480

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 540

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 600

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 660

gaagtcaccc atcagggcct gagctcacca gtaacaaaaa gttttaatag aggggagtgt 720

<210> 58
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> 1519 gH20 V-region

<400> 58

eolf-seql

Glu Val Pro 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 Thr Phe Ser Asn Tyr
20 25 30

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

Ala Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr Tyr Arg Asp Ser Val
50 55 60

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

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

Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser
115

<210> 59
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> 1519 gH20 V-region

<400> 59
gaggttccgc tggtcgagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc 60

tcttgtgcag tatctggctt cacgttctcc aactacggta tggtgtgggt tcgtcaggct 120

ccaggtaaag gtctggaatg ggtggcgtat attgactccg acggcgacaa cacctactat 180

cgcgactctg tgaaaggtcg cttcaccatt tcccgcgata acgccaaatc cagcctgtac 240

ctgcagatga acagcctgcg tgctgaagat actgcggtgt actattgcac cactggcatc 300

gtgcgtccgt ttctgtattg gggtcagggt accctcgtta ctgtctcg 348

<210> 60
<211> 137
<212> PRT
<213> Artificial Sequence

<220>
<223> 1519 gH20 V-region

<400> 60

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1 5 10 15

Thr Val Ala Gln Ala Glu Val Pro Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

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

Thr Phe Ser Asn Tyr Gly Met Val Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ala Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr
65 70 75 80

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

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

Ala Val Tyr Tyr Cys Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp
115 120 125

Gly Gln Gly Thr Leu Val Thr Val Ser
130 135

<210> 61
<211> 411
<212> DNA
<213> Artificial Sequence

<220>
<223> 1519 gH20 V-region

<400> 61
atgaagaaga ctgctatagc aattgcagtg gcgctagctg gtttcgccac cgtggcgcaa 60

gctgaggttc cgctggtcga gtctggaggc gggcttgtcc agcctggagg gagcctgcgt 120

ctctcttgtg cagtatctgg cttcacgttc tccaactacg gtatggtgtg ggttcgtcag 180

gctccaggta aaggtctgga atgggtggcg tatattgact ccgacggcga caacacctac 240

tatcgcgact ctgtgaaagg tcgcttcacc atttcccgcg ataacgccaa atccagcctg 300

tacctgcaga tgaacagcct gcgtgctgaa gatactgcgg tgtactattg caccactggc 360

atcgtgcgtc cgtttctgta ttggggtcag ggtaccctcg ttactgtctc g 411

<210> 62
<211> 228
<212> PRT
<213> Artificial Sequence

<220>
<223> 1519gH20 Fab' heavy chain (V + human gamma-1 CH1 + hinge)

<400> 62

Glu Val Pro 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 Thr Phe Ser Asn Tyr
20 25 30

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

Ala Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr Tyr Arg Asp Ser Val
50 55 60

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

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

Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln Gly Thr Leu
100 105 110

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

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

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

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

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

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

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

Thr Cys Ala Ala
225

<210> 63
<211> 684
<212> DNA
<213> Artificial Sequence

<220>
<223> 1519gH20 Fab' heavy chain (V + human gamma-1 CH1 + hinge)

<400> 63
gaggttccgc tggtcgagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc 60

tcttgtgcag tatctggctt cacgttctcc aactacggta tggtgtgggt tcgtcaggct 120

ccaggtaaag gtctggaatg ggtggcgtat attgactccg acggcgacaa cacctactat 180

cgcgactctg tgaaaggtcg cttcaccatt tcccgcgata acgccaaatc cagcctgtac 240

ctgcagatga acagcctgcg tgctgaagat actgcggtgt actattgcac cactggcatc 300

gtgcgtccgt ttctgtattg gggtcagggt accctcgtta ctgtctcgag cgcttctaca 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtcgacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgcgc cgcg 684

<210> 64
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> 1519 gH20 Fab' heavy chain

<400> 64

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1 5 10 15

Thr Val Ala Gln Ala Glu Val Pro Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

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

Thr Phe Ser Asn Tyr Gly Met Val Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ala Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr
65 70 75 80

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

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

Ala Val Tyr Tyr Cys Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp
115 120 125

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

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145 150 155 160

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

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

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

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
210 215 220

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225 230 235 240

Cys Asp Lys Thr His Thr Cys Ala Ala
245

<210> 65
<211> 747
<212> DNA
<213> Artificial Sequence

<220>
<223> 1519 gH20 Fab' heavy chain

<400> 65
atgaagaaga ctgctatagc aattgcagtg gcgctagctg gtttcgccac cgtggcgcaa 60

gctgaggttc cgctggtcga gtctggaggc gggcttgtcc agcctggagg gagcctgcgt 120

ctctcttgtg cagtatctgg cttcacgttc tccaactacg gtatggtgtg ggttcgtcag 180

gctccaggta aaggtctgga atgggtggcg tatattgact ccgacggcga caacacctac 240

tatcgcgact ctgtgaaagg tcgcttcacc atttcccgcg ataacgccaa atccagcctg 300

tacctgcaga tgaacagcct gcgtgctgaa gatactgcgg tgtactattg caccactggc 360

atcgtgcgtc cgtttctgta ttggggtcag ggtaccctcg ttactgtctc gagcgcttct 420

acaaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 480

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 540

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 600

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 660

tgcaacgtga atcacaagcc cagcaacacc aaggtcgaca agaaagttga gcccaaatct 720

tgtgacaaaa ctcacacatg cgccgcg 747

<210> 66
<211> 444

<212> PRT
<213> Artificial Sequence

<220>
<223> 1519gH20 IgG4 heavy chain (V + human gamma-4P constant)

<400> 66

```
Glu Val Pro 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 Thr Phe Ser Asn Tyr
            20                  25                  30

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

Ala Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr Tyr Arg Asp Ser Val
    50                  55                  60

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

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

Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

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

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

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

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

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240
```

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
245 250 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
260 265 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
275 280 285

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
290 295 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305 310 315 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
340 345 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385 390 395 400

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440

<210> 67
<211> 1939
<212> DNA
<213> Artificial Sequence

<220>
<223> 1519gH20 IgG4 heavy chain (V + human gamma-4P constant, exons)

<400> 67
gaggtaccac ttgtggaaag cggaggaggt cttgtgcagc ctggaggaag tttacgtctc 60

tcttgtgctg tgtctggctt caccttctcc aattacggaa tggtctgggt cagacaagca 120

cctggaaagg gtcttgaatg ggtggcctat attgactctg acggggacaa cacctactat 180

cgggattccg tgaaaggacg cttcacaatc tcccgagata acgccaagag ctcactgtac 240

ctgcagatga atagcctgag agccgaggat actgccgtgt actattgcac aacgggaatc 300

gttaggcctt ttctgtactg gggacagggc accttggtta ctgtctcgag cgcttctaca 360

aagggcccat ccgtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc 600

aacgtagatc acaagcccag caacaccaag gtggacaaga gagttggtga gaggccagca 660

cagggaggga gggtgtctgc tggaagccag gctcagccct cctgcctgga cgcaccccgg 720

ctgtgcagcc ccagcccagg gcagcaaggc atgccccatc tgtctcctca cccggaggcc 780

tctgaccacc ccactcatgc ccagggagag ggtcttctgg atttttccac caggctccgg 840

gcagccacag gctggatgcc cctaccccag gccctgcgca tacaggggca ggtgctgcgc 900

tcagacctgc caagagccat atccgggagg accctgcccc tgacctaagc ccaccccaaa 960

ggccaaactc tccactccct cagctcagac accttctctc ctcccagatc tgagtaactc 1020

ccaatcttct ctctgcagag tccaaatatg gtcccccatg cccaccatgc ccaggtaagc 1080

caacccaggc ctcgccctcc agctcaaggc gggacaggtg ccctagagta gcctgcatcc 1140

agggacaggc cccagccggg tgctgacgca tccacctcca tctcttcctc agcacctgag 1200

ttcctggggg gaccatcagt cttcctgttc cccccaaaac ccaaggacac tctcatgatc 1260

tcccggaccc ctgaggtcac gtgcgtggtg gtggacgtga gccaggaaga ccccgaggtc 1320

cagttcaact ggtacgtgga tggcgtggag gtgcataatg ccaagacaaa gccgcgggag 1380

gagcagttca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1440

ctgaacggca aggagtacaa gtgcaaggtc tccaacaaag gcctcccgtc ctccatcgag 1500

aaaaccatct ccaaagccaa aggtgggacc cacggggtgc gagggccaca tggacagagg 1560

tcagctcggc ccaccctctg ccctgggagt gaccgctgtg ccaacctctg tccctacagg 1620

gcagccccga gagccacagg tgtacaccct gccccatcc caggaggaga tgaccaagaa 1680

ccaggtcagc ctgacctgcc tggtcaaagg cttctacccc agcgacatcg ccgtggagtg 1740

ggagagcaat gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga 1800

cggctccttc ttcctctaca gcaggctaac cgtggacaag agcaggtggc aggaggggaa 1860

tgtcttctca tgctccgtga tgcatgaggc tctgcacaac cactacacac agaagagcct 1920

ctccctgtct ctgggtaaa 1939

<210> 68
<211> 347
<212> PRT
<213> Artificial Sequence

<220>
<223> 1519gL20 FabFv light chain

<400> 68

```
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 Ser Ser Gln Ser Leu Val Gly Ala
            20                  25                  30

Ser Gly Lys Thr Tyr Leu Tyr Trp Leu Phe Gln Lys Pro Gly Lys Ala
        35                  40                  45

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

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
65                  70                  75                  80

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Gly
                85                  90                  95

Thr His Phe Pro His Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110

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

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140

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

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Ser Gly Gly Gly Gly
    210                 215                 220

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
225                 230                 235                 240

Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile
                245                 250                 255

Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn Phe Leu Ser Trp Tyr
            260                 265                 270
```

```
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Glu Ala Ser
        275                 280                 285

Lys Leu Thr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
    290                 295                 300

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

Thr Tyr Tyr Cys Gly Gly Gly Tyr Ser Ser Ile Ser Asp Thr Thr Phe
                325                 330                 335

Gly Cys Gly Thr Lys Val Glu Ile Lys Arg Thr
            340                 345
```

<210> 69
<211> 1041
<212> DNA
<213> Artificial Sequence

<220>
<223> 1519gL20 FabFv light chain

<400> 69

```
gatatccaga tgacccagag cccatctagc ttatccgctt ccgttggtga tcgcgtgaca       60

attacgtgta agagctccca atctctcgtg ggtgcaagtg gcaagaccta tctgtactgg      120

ctctttcaga agcctggcaa ggcaccaaaa cggctgatct atctggtgtc taccttgac       180

tctgggatac cgtcacgatt ttccggatct gggagcggaa ctgagttcac actcacgatt      240

tcatcgctgc aacccgagga ctttgctacc tactactgcc tgcaaggcac tcatttccct      300

cacactttcg gccaggggac aaaactcgaa atcaaacgta cggtagcggc cccatctgtc      360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg      420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa      480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctg      540

agcagcaccc tgacgctgtc taaagcagac tacgagaaac acaaagtgta cgcctgcgaa      600

gtcacccatc agggcctgag ctcaccagta acaaaaagtt ttaatagagg ggagtgtagc      660

ggtggcggtg gcagtggtgg gggaggctcc ggaggtggcg gttcagacat acaaatgacc      720

cagagtcctt catcggtatc cgcgtccgtt ggcgataggg tgactattac atgtcaaagc      780

tctcctagcg tctggagcaa ttttctatcc tggtatcaac agaaaccggg gaaggctcca      840

aaacttctga tttatgaagc ctcgaaactc accagtggag ttccgtcaag attcagtggc      900

tctggatcag ggacagactt cacgttgaca atcagttcgc tgcaaccaga ggactttgcg      960

acctactatt gtggtggagg ttacagtagc ataagtgata cgacatttgg gtgcggtact     1020

aaggtggaaa tcaaacgtac c                                               1041
```

<210> 70
<211> 367
<212> PRT
<213> Artificial Sequence

<220>
<223> 1519gL20 FabFv light chain

<400> 70

```
Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
1               5                  10                  15

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

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

Leu Val Gly Ala Ser Gly Lys Thr Tyr Leu Tyr Trp Leu Phe Gln Lys
    50                  55                  60

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

Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
                85                  90                  95

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

Cys Leu Gln Gly Thr His Phe Pro His Thr Phe Gly Gln Gly Thr Lys
        115                 120                 125

Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    130                 135                 140

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

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

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            180                 185                 190

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

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    210                 215                 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Ser
225                 230                 235                 240
```

```
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
                245                 250                 255

Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp
            260                 265                 270

Arg Val Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn Phe
        275                 280                 285

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
    290                 295                 300

Tyr Glu Ala Ser Lys Leu Thr Ser Gly Val Pro Ser Arg Phe Ser Gly
305                 310                 315                 320

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
                325                 330                 335

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gly Gly Tyr Ser Ser Ile Ser
            340                 345                 350

Asp Thr Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Arg Thr
        355                 360                 365
```

<210> 71
<211> 1101
<212> DNA
<213> Artificial Sequence

<220>
<223> 1519gL20 FabFv light chain

<400> 71

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atgtctgtcc ccacccaagt cctcggactc ctgctactct ggcttacaga tgccagatgc        60

gatatccaga tgacccagag cccatctagc ttatccgctt ccgttggtga tcgcgtgaca       120

attacgtgta agagctccca atctctcgtg ggtgcaagtg gcaagaccta tctgtactgg       180

ctctttcaga agcctggcaa ggcaccaaaa cggctgatct atctggtgtc taccttgac        240

tctgggatac cgtcacgatt ttccggatct gggagcggaa ctgagttcac actcacgatt       300

tcatcgctgc aacccgagga ctttgctacc tactactgcc tgcaaggcac tcatttccct       360

cacactttcg gccaggggac aaaactcgaa atcaaacgta cggtagcggc cccatctgtc       420

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg       480

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa       540

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctg       600

agcagcaccc tgacgctgtc taaagcagac tacgagaaac acaaagtgta cgcctgcgaa       660

gtcacccatc agggcctgag ctcaccagta acaaaaagtt ttaatagagg ggagtgtagc       720

ggtggcggtg gcagtggtgg gggaggctcc ggaggtggcg gttcagacat acaaatgacc       780
```

cagagtcctt catcggtatc cgcgtccgtt ggcgataggg tgactattac atgtcaaagc 840

tctcctagcg tctggagcaa ttttctatcc tggtatcaac agaaaccggg gaaggctcca 900

aaacttctga tttatgaagc ctcgaaactc accagtggag ttccgtcaag attcagtggc 960

tctggatcag ggacagactt cacgttgaca atcagttcgc tgcaaccaga ggactttgcg 1020

acctactatt gtggtggagg ttacagtagc ataagtgata cgacatttgg gtgcggtact 1080

aaggtggaaa tcaaacgtac c 1101

<210> 72
<211> 357
<212> PRT
<213> Artificial Sequence

<220>
<223> 1519gH20 FabFv heavy chain

<400> 72

Glu Val Pro 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 Thr Phe Ser Asn Tyr
20 25 30

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

Ala Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr Tyr Arg Asp Ser Val
50 55 60

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

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

Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln Gly Thr Leu
100 105 110

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

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

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

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

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

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

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

Gly Ser Gly Gly Gly Gly Thr Gly Gly Gly Gly Ser Glu Val Gln Leu
225 230 235 240

Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
245 250 255

Ser Cys Ala Val Ser Gly Ile Asp Leu Ser Asn Tyr Ala Ile Asn Trp
260 265 270

Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Ile Gly Ile Ile Trp
275 280 285

Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys Gly Arg Phe Thr
290 295 300

Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser
305 310 315 320

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Thr Val Pro
325 330 335

Gly Tyr Ser Thr Ala Pro Tyr Phe Asp Leu Trp Gly Gln Gly Thr Leu
340 345 350

Val Thr Val Ser Ser
355

<210> 73
<211> 1071
<212> DNA
<213> Artificial Sequence

<220>
<223> 1519gH20 FabFv heavy chain

<400> 73
gaggtaccac ttgtggaaag cggaggaggt cttgtgcagc ctggaggaag tttacgtctc 60

tcttgtgctg tgtctggctt caccttctcc aattacggaa tggtctgggt cagacaagca 120

cctggaaagg gtcttgaatg ggtggcctat attgactctg acggggacaa cacctactat 180

cgggattccg tgaaaggacg cttcacaatc tcccgagata acgccaagag ctcactgtac 240

ctgcagatga atagcctgag agccgaggat actgccgtgt actattgcac aacgggaatc 300

gttaggcctt ttctgtactg gggacagggc accttggtta ctgtctcgag cgcgtccaca 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccag tgacggtgtc gtggaactca 480

ggtgccctga ccagcggcgt tcacaccttc ccggctgtcc tacagtcttc aggactctac 540

tccctgagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtcgataaga aagttgagcc caaatcttgt 660

agtggaggtg ggggctcagg tggaggcggg accggtggag gtggcagcga ggttcaactg 720

cttgagtctg gaggaggcct agtccagcct ggagggagcc tgcgtctctc ttgtgcagta 780

agcggcatcg acctgagcaa ttacgccatc aactgggtga gacaagctcc ggggaagtgt 840

ttagaatgga tcggtataat atgggccagt gggacgacct tttatgctac atgggcgaaa 900

ggaaggttta caattagccg ggacaatagc aaaaacaccg tgtatctcca aatgaactcc 960

ttgcgagcag aggacacggc ggtgtactat tgtgctcgca ctgtcccagg ttatagcact 1020

gcaccctact tcgatctgtg gggacaaggg accctggtga ctgtttcaag t 1071

<210> 74
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> 1519gH20 FabFv heavy chain

<400> 74

Met Glu Trp Ser Trp Val Phe Leu Phe Phe Leu Ser Val Thr Thr Gly
1 5 10 15

Val His Ser Glu Val Pro 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 Thr Phe
35 40 45

Ser Asn Tyr Gly Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ala Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr Tyr Arg
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser
85 90 95

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

Tyr Tyr Cys Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln
115 120 125

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

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
145                 150                 155                 160

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

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

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

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
    210                 215                 220

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Ser
225                 230                 235                 240

Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Gly Gly Gly Ser Glu
                245                 250                 255

Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
            260                 265                 270

Leu Arg Leu Ser Cys Ala Val Ser Gly Ile Asp Leu Ser Asn Tyr Ala
        275                 280                 285

Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Ile Gly
    290                 295                 300

Ile Ile Trp Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys Gly
305                 310                 315                 320

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln
                325                 330                 335

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
            340                 345                 350

Thr Val Pro Gly Tyr Ser Thr Ala Pro Tyr Phe Asp Leu Trp Gly Gln
        355                 360                 365

Gly Thr Leu Val Thr Val Ser Ser
    370                 375
```

<210> 75
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Wild type Tsp 5'

<400> 75

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
20

<210> 76
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Wild type Tsp 5'

<400> 76
atgaacatgt tttttaggct taccgcgtta gctggcctgc ttgcaatagc aggccagacc 60

ttcgct 66

<210> 77
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutated Tsp 5' fragment

<400> 77

Met Asn Ser Phe Leu Gly Leu Pro Arg Leu Ala Cys Leu Gln Gln Ala
1 5 10 15

Arg His Leu

<210> 78
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutated Tsp 5' fragment

<400> 78
atgaattcgt ttttaggctt accgcgttag ctggcctgct tgcaatagca ggccagacat 60

taattg 66

<210> 79
<211> 20
<212> PRT
<213> Artificial

<220>
<223> Mutated delta ptr (protease III) 5'

<400> 79

Ile Pro Arg Ser Thr Trp Phe Lys Ala Leu Leu Leu Leu Val Ala Leu
1 5 10 15

Trp Ala His Cys
20

<210> 80
<211> 66
<212> DNA
<213> Artificial

<220>
<223> Mutated delta ptr (protease III) 5'

<400> 80
tgaattcccc gcagcacctg gttcaaagca ttattgttgt tagttgccct ttgggcacat 60

taatgt 66

<210> 81
<211> 21
<212> PRT
<213> Artificial

<220>
<223> Wild-type ptr (protease III) 5'

<400> 81

Met Pro Arg Ser Thr Trp Phe Lys Ala Leu Leu Leu Leu Val Ala Leu
1 5 10 15

Trp Ala Pro Leu Ser
20

<210> 82
<211> 66
<212> DNA
<213> Artificial

<220>
<223> Wild-type ptr (protease III) 5'

<400> 82
tgaatgcccc gcagcacctg gttcaaagca ttattgttgt tagttgccct ttgggcaccc 60

ttaagt 66