SEQUENCE LISTING

<110> KANEKA CORPORATION

<120> PROTEIN LIGAND FOR AFFINITY ISOLATION MATRIX

<130> B120413W001

<140> PCT/JP2013/075656
<141> 2013-09-24

<150> JP2012-208762
<151> 2012-09-21

<160> 26

<170> PatentIn version 3.5

<210> 1
<211> 56
<212> PRT
<213> Staphylococcus aureus

<400> 1

Ala Gln His Asp Glu Ala Gln Gln Asn Ala Phe Tyr Gln Val Leu Asn
1 5 10 15

Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser Leu
20 25 30

Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly Glu Ala Gln Lys
35 40 45

Leu Asn Asp Ser Gln Ala Pro Lys
50 55

<210> 2
<211> 61
<212> PRT
<213> Staphylococcus aureus

<400> 2

Ala Asp Ala Gln Gln Asn Asn Phe Asn Lys Asp Gln Gln Ser Ala Phe
1 5 10 15

Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly
20 25 30

Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Thr Asn Val Leu
35 40 45

Gly Glu Ala Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys
50 55 60

<210> 3
<211> 58
<212> PRT
<213> Staphylococcus aureus

<400> 3

Ala Asp Asn Asn Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile

1 5 10 15

Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln
20 25 30

Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ser Glu Ala
35 40 45

Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys
50 55

<210> 4
<211> 58
<212> PRT
<213> Staphylococcus aureus

<400> 4

Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile
1 5 10 15

Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln
20 25 30

Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala
35 40 45

Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys
50 55

<210> 5
<211> 58
<212> PRT
<213> Staphylococcus aureus

<400> 5

Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile
1 5 10 15

Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln
20 25 30

Ser Leu Lys Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala
35 40 45

Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys
50 55

<210> 6
<211> 58
<212> PRT
<213> Zdomain

<400> 6

Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile
1 5 10 15

Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln
20 25 30

Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala
35 40 45

Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys
50 55

<210> 7
<211> 58
<212> PRT
<213> SpA C domain mutant

<400> 7

Ala Asp Asn Arg Phe Asn Arg Glu Gln Gln Asn Ala Phe Tyr Glu Ile
1 5 10 15

Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Ala Phe Ile Gln
20 25 30

Arg Leu Arg Asp Asp Pro Ser Val Ser Arg Glu Ile Leu Ala Glu Ala
35 40 45

Gln Arg Leu Asn Asp Ala Gln Ala Pro Lys
50 55

<210> 8

<211> 290
<212> PRT
<213> SpA C domain mutant

<400> 8

```
Ala Asp Asn Arg Phe Asn Arg Glu Gln Gln Asn Ala Phe Tyr Glu Ile
1               5                  10                  15

Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Ala Phe Ile Gln
            20                  25                  30

Arg Leu Arg Asp Asp Pro Ser Val Ser Arg Glu Ile Leu Ala Glu Ala
        35                  40                  45

Gln Arg Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn Arg Phe Asn
    50                  55                  60

Arg Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
65                  70                  75                  80

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

Ser Val Ser Arg Glu Ile Leu Ala Glu Ala Gln Arg Leu Asn Asp Ala
            100                 105                 110

Gln Ala Pro Lys Ala Asp Asn Arg Phe Asn Arg Glu Gln Gln Asn Ala
        115                 120                 125
```

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn
130 135 140

Ala Phe Ile Gln Arg Leu Arg Asp Asp Pro Ser Val Ser Arg Glu Ile
145 150 155 160

Leu Ala Glu Ala Gln Arg Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp
165 170 175

Asn Arg Phe Asn Arg Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His
180 185 190

Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Ala Phe Ile Gln Arg Leu
195 200 205

Arg Asp Asp Pro Ser Val Ser Arg Glu Ile Leu Ala Glu Ala Gln Arg
210 215 220

Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn Arg Phe Asn Arg Glu
225 230 235 240

Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Thr Glu
245 250 255

Glu Gln Arg Asn Ala Phe Ile Gln Arg Leu Arg Asp Asp Pro Ser Val
260 265 270

Ser Arg Glu Ile Leu Ala Glu Ala Gln Arg Leu Asn Asp Ala Gln Ala
275 280 285

Pro Lys
290

<210> 9
<211> 232
<212> PRT
<213> SpA C domain mutant

<400> 9

Ala Asp Asn Arg Phe Asn Arg Glu Gln Gln Asn Ala Phe Tyr Glu Ile
1 5 10 15

Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Ala Phe Ile Gln
20 25 30

Arg Leu Arg Asp Asp Pro Ser Val Ser Arg Glu Ile Leu Ala Glu Ala
35 40 45

Gln Arg Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn Arg Phe Asn
50 55 60

Arg Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
65 70 75 80

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

Ser Val Ser Arg Glu Ile Leu Ala Glu Ala Gln Arg Leu Asn Asp Ala
100 105 110

Gln Ala Pro Lys Ala Asp Asn Arg Phe Asn Arg Glu Gln Gln Asn Ala
115 120 125

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn
130 135 140

Ala Phe Ile Gln Arg Leu Arg Asp Asp Pro Ser Val Ser Arg Glu Ile
145 150 155 160

Leu Ala Glu Ala Gln Arg Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp
165 170 175

Asn Arg Phe Asn Arg Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His
180 185 190

Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Ala Phe Ile Gln Arg Leu
195 200 205

Arg Asp Asp Pro Ser Val Ser Arg Glu Ile Leu Ala Glu Ala Gln Arg
210 215 220

Leu Asn Asp Ala Gln Ala Pro Lys
225 230

<210> 10
<211> 232
<212> PRT
<213> SpA C domain mutant

<400> 10

Ala Asp Asn Arg Phe Asn Arg Glu Gln Gln Asn Ala Phe Tyr Glu Ile
1 5 10 15

Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Ala Phe Ile Gln
20 25 30

Arg Leu Arg Asp Asp Pro Ser Val Ser Arg Glu Ile Leu Ala Glu Ala
35 40 45

Gln Arg Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn Arg Phe Asn
50 55 60

Arg Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
65 70 75 80

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

Ser Val Ser Arg Glu Ile Leu Ala Glu Ala Gln Arg Leu Asn Asp Ala
100 105 110

Gln Ala Pro Lys Ala Asp Asn Arg Phe Asn Arg Glu Gln Gln Asn Ala
115 120 125

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn
130 135 140

Ala Phe Ile Gln Arg Leu Arg Asp Asp Pro Ser Val Ser Arg Glu Ile
145 150 155 160

Leu Ala Glu Ala Gln Arg Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp
165 170 175

Asn Arg Phe Asn Arg Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His
180 185 190

Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Ala Phe Ile Gln Arg Leu
195 200 205

Arg Asp Asp Pro Ser Val Ser Arg Glu Ile Leu Ala Glu Ala Gln Arg
210 215 220

Leu Asn Asp Ala Gln Ala Pro Arg
225 230

<210> 11
<211> 896
<212> DNA
<213> Code DNA

<400> 11
ccatggcttt cgctgcagat aaccgtttta accgtgaaca acaaaacgct ttctacgaaa 60

tcctgcactt gccaaacctt actgaagaac aacgtaatgc tttcatccaa cgtctgcgcg 120

atgatccatc tgtatcccgt gaaattttgg cagaggctca acgacttaac gacgctcagg 180

cgcctaaggc tgataaccgc ttcaaccgag aacaacaaaa cgcttttttat gaaatccttc 240

acctgccaaa tcttacagaa gaacaacgca acgcattcat tcaacgcttg cgtgatgacc 300

cttccgttag ccgagagatc ctggctgaag cacaacgttt gaatgatgcg caagcaccaa 360

aagctgataa tcgattcaac cgtgaacaac aaaatgcatt ctacgaaatc ttgcaccttc 420

ctaacctgac tgaagagcag cgtaacgctt ttatccagcg tttgagagac gatccatctg 480

tctcccgtga aattctcgca gaagcgcaac gcctgaacga tgctcaagct ccgaaagcag 540

acaaccgttt caatcgcgaa cagcaaaacg cgttttatga aattctgcat cttccaaact 600

tgacagagga acaacgcaat gctttcatcc aacgactgcg tgatgatccg agcgtttctc 660

gagaaatctt ggctgaagca caacgtctga acgacgctca agctccaaaa gcggataaca 720

gatttaaccg tgaacaacaa aatgctttct acgagatctt gcaccttccg aacctgactg 780

aagaacaacg taacgcattt attcagagat tgcgcgatga cccatccgta agccgtgaga 840

tcctggcaga agctcaacgt ttgaatgatg cacaagctcc aaaataatct agaaaa 896

<210> 12
<211> 29
<212> DNA
<213> synthetic oligonucleotide

<400> 12
ctcccatggc tttcgctgca gataaccgc 29

<210> 13
<211> 34
<212> DNA
<213> synthetic oligonucleotide

<400> 13
ttttctagat tattttggag cttgtgcatc attc 34

<210> 14
<211> 725
<212> DNA
<213> Code DNA

<400> 14
ctcccatggc tttcgctgca gataaccgct tcaaccgaga acaacaaaac gctttttatg 60

aaatccttca cctgccaaat cttacagaag aacaacgcaa cgcattcatt caacgcttgc 120

gtgatgaccc ttccgttagc cgagagatcc tggctgaagc acaacgtttg aatgatgcgc 180

aagcaccaaa agctgataat cgattcaacc gtgaacaaca aaatgcattc tacgaaatct 240

tgcaccttcc taacctgact gaagagcagc gtaacgcttt tatccagcgt ttgagagacg 300

atccatctgt ctcccgtgaa attctcgcag aagcgcaacg cctgaacgat gctcaagctc 360

cgaaagcaga caaccgtttc aatcgcgaac agcaaaacgc gttttatgaa attctgcatc 420

ttccaaactt gacagaggaa caacgcaatg ctttcatcca acgactgcgt gatgatccga 480

gcgtttctcg agaaatcttg gctgaagcac aacgtctgaa cgacgctcaa gctccaaaag 540

cggataacag atttaaccgt gaacaacaaa atgctttcta cgagatcttg caccttccga 600

acctgactga agaacaacgt aacgcattta ttcagagatt gcgcgatgac ccatccgtaa 660

gccgtgagat cctggcagaa gctcaacgtt tgaatgatgc acaagctcca aaataatcta 720

gaaaa 725

<210> 15
<211> 34
<212> DNA
<213> synthetic oligonucleotide

<400> 15
ttttctagat taacgtggag cttgtgcatc attc 34

<210> 16
<211> 725
<212> DNA
<213> Code DNA

<400> 16
ctcccatggc tttcgctgca gataaccgct tcaaccgaga acaacaaaac gctttttatg 60

aaatccttca cctgccaaat cttacagaag aacaacgcaa cgcattcatt caacgcttgc 120

gtgatgaccc ttccgttagc cgagagatcc tggctgaagc acaacgtttg aatgatgcgc 180

aagcaccaaa agctgataat cgattcaacc gtgaacaaca aaatgcattc tacgaaatct 240

tgcaccttcc taacctgact gaagagcagc gtaacgcttt tatccagcgt ttgagagacg 300

atccatctgt ctcccgtgaa attctcgcag aagcgcaacg cctgaacgat gctcaagctc 360

cgaaagcaga caaccgtttc aatcgcgaac agcaaaacgc gttttatgaa attctgcatc 420

ttccaaactt gacagaggaa caacgcaatg ctttcatcca acgactgcgt gatgatccga 480

gcgtttctcg agaaatcttg gctgaagcac aacgtctgaa cgacgctcaa gctccaaaag 540

cggataacag atttaaccgt gaacaacaaa atgctttcta cgagatcttg caccttccga 600

acctgactga agaacaacgt aacgcattta ttcagagatt gcgcgatgac ccatccgtaa 660

gccgtgagat cctggcagaa gctcaacgtt tgaatgatgc acaagctcca cgttaatcta 720

gaaaa 725

<210> 17
<211> 58
<212> PRT
<213> SpA C domain mutant

<400> 17

Ala Asp Asn Arg Phe Asn Arg Glu Gln Gln Asn Ala Phe Tyr Glu Ile
1 5 10 15

Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Ala Phe Ile Gln
20 25 30

```
Leu Leu Arg Asp Asp Pro Ser Val Ser Arg Glu Ile Leu Ala Glu Ala
        35                  40                  45

Arg Arg Leu Asn Asp Ala Gln Ala Pro Lys
    50                  55
```

<210> 18
<211> 174
<212> PRT
<213> SpA C domain mutant

<400> 18

```
Ala Asp Asn Arg Phe Asn Arg Glu Gln Gln Asn Ala Phe Tyr Glu Ile
1               5                   10                  15

Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Ala Phe Ile Gln
            20                  25                  30

Leu Leu Arg Asp Asp Pro Ser Val Ser Arg Glu Ile Leu Ala Glu Ala
        35                  40                  45

Arg Arg Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn Arg Phe Asn
    50                  55                  60

Arg Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
65                  70                  75                  80
```

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

Ser Val Ser Arg Glu Ile Leu Ala Glu Ala Arg Arg Leu Asn Asp Ala
100 105 110

Gln Ala Pro Lys Ala Asp Asn Arg Phe Asn Arg Glu Gln Gln Asn Ala
115 120 125

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn
130 135 140

Ala Phe Ile Gln Leu Leu Arg Asp Asp Pro Ser Val Ser Arg Glu Ile
145 150 155 160

Leu Ala Glu Ala Arg Arg Leu Asn Asp Ala Gln Ala Pro Lys
165 170

<210> 19
<211> 551
<212> DNA
<213> Code DNA

<400> 19
ctcccatggc tttcgctgca gacaaccgtt tcaatcgcga acagcaaaac gcgttttatg 60

aaattctgca tcttccaaac ttgacagagg aacaacgcaa tgctttcatc caactgctgc 120

gtgatgatcc gagcgtttct cgtgaaatct tggctgaagc acgtcgcctg aacgacgctc 180

aagctccaaa agcggataac cgttttaacc gtgaacaaca aaatgctttc tacgagatct 240

tgcaccttcc gaacctgact gaagaacaac gtaacgcatt tattcagttg ttgcgtgatg 300

acccatccgt aagccgcgag atcctggcag aagctcgccg cttgaatgat gcacaagctc 360

caaaagcaga caaccgcttt aaccgcgaac aacaaaatgc attctacgaa atcttgcacc 420

ttcctaacct gactgaggag caacgcaatg ctttcatcca attgcttcgc gatgatccaa 480

gcgtaagccg tgaaattttg gctgaagctc gtcgtctgaa cgatgcacaa gctccaaaat 540

aatctagaaa a 551

<210> 20
<211> 290
<212> PRT
<213> SpA C domain mutant

<400> 20

Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile
1 5 10 15

Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Ala Phe Ile Gln
20 25 30

Glu Leu Lys Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala
35 40 45

Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn Lys Phe Asn
50 55 60

Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
65 70 75 80

Thr Glu Glu Gln Arg Asn Ala Phe Ile Gln Glu Leu Lys Asp Asp Pro
85 90 95

Ser Val Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala
100 105 110

Gln Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala
115 120 125

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn
130 135 140

Ala Phe Ile Gln Glu Leu Lys Asp Asp Pro Ser Val Ser Lys Glu Ile
145 150 155 160

Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp
165 170 175

Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His
180 185 190

Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Ala Phe Ile Gln Glu Leu
195 200 205

Lys Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys
210 215 220

Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu
225 230 235 240

Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Thr Glu
245 250 255

Glu Gln Arg Asn Ala Phe Ile Gln Glu Leu Lys Asp Asp Pro Ser Val
260 265 270

Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala
275 280 285

Pro Lys
290

<210> 21
<211> 870
<212> DNA
<213> Code DNA

<400> 21
gcagataaca aatttaacaa agaacaacaa aacgctttct acgaaatcct gcacttgcca 60

aaccttactg aagaacaacg taatgctttc atccaagagc tgaaagatga tccatctgta 120

tccaaagaaa ttttggcaga ggctaaaaaa cttaacgacg ctcaggcgcc taaggctgat 180

aacaaattca acaaagaaca acaaaacgct ttttatgaaa tccttcacct gccaaatctt 240

acagaagaac aacgcaacgc attcattcaa gagttgaagg atgacccttc cgttagcaaa 300

gagatcctgg ctgaagcaaa aaagttgaat gatgcgcaag caccaaaagc tgataataaa 360

ttcaacaaag aacaacaaaa tgcattctac gaaatcttgc accttcctaa cctgactgaa 420

gagcagcgta acgcttttat ccaggaattg aaagacgatc catctgtctc caaagaaatt 480

ctcgcagaag cgaagaaact gaacgatgct caagctccga aagcagacaa caaattcaat 540

aaggaacagc aaaacgcgtt ttatgaaatt ctgcatcttc caaacttgac agaggaacaa 600

cgcaatgctt tcatccaaga gctgaaagat gatccgagcg tttctaagga aatcttggct 660

gaagcaaaaa aactgaacga cgctcaagct ccaaaagcgg ataacaagtt taacaaagaa 720

caacaaaatg ctttctacga gatcttgcac cttccgaacc tgactgaaga acaacgtaac 780

gcatttattc aggagttgaa ggatgaccca tccgtaagca aagagatcct ggcagaagct 840

aaaaaattga atgatgcaca agctccaaaa 870

<210> 22
<211> 174
<212> PRT
<213> SpA C domain mutant

<400> 22

Ala Asp Asn Arg Phe Asn Arg Glu Gln Gln Asn Ala Phe Tyr Glu Ile
1 5 10 15

Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Ala Phe Ile Gln
20 25 30

Leu Leu Arg Asp Asp Pro Ser Val Ser Arg Glu Ile Leu Ala Glu Ala
35 40 45

Arg Arg Leu Asn Asp Ala Gln Ala Pro Arg Ala Asp Asn Arg Phe Asn
50 55 60

Arg Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
65 70 75 80

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

Ser Val Ser Arg Glu Ile Leu Ala Glu Ala Arg Arg Leu Asn Asp Ala
100 105 110

Gln Ala Pro Arg Ala Asp Asn Arg Phe Asn Arg Glu Gln Gln Asn Ala
115 120 125

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn
130 135 140

Ala Phe Ile Gln Leu Leu Arg Asp Asp Pro Ser Val Ser Arg Glu Ile
145 150 155 160

Leu Ala Glu Ala Arg Arg Leu Asn Asp Ala Gln Ala Pro Lys
165 170

<210> 23
<211> 522
<212> DNA
<213> Code DNA

<400> 23
gcagacaacc gtttcaatcg cgaacagcaa aacgcgtttt atgaaattct gcatcttcca 60

aacttgacag aggaacaacg caatgctttc atccaactgc tgcgtgatga tccgagcgtt 120

tctcgtgaaa tcttggctga agcacgtcgc ctgaacgacg ctcaagctcc acgcgcggat 180

aaccgtttta accgtgaaca acaaaatgct ttctacgaga tcttgcacct tccgaacctg 240

actgaagaac aacgtaacgc atttattcag ttgttgcgtg atgacccatc cgtaagccgc 300

gagatcctgg cagaagctcg ccgcttgaat gatgcacaag ctccacgcgc agacaaccgc 360

tttaaccgcg aacaacaaaa tgcattctac gaaatcttgc accttcctaa cctgactgag 420

gagcaacgca atgctttcat ccaattgctt cgcgatgatc caagcgtaag ccgtgaaatt 480

ttggctgaag ctcgtcgtct gaacgatgca caagctccaa aa 522

<210> 24
<211> 58
<212> PRT
<213> SpA C domain mutant

<400> 24

```
Ala Asp Asn Arg Phe Asn Arg Glu Gln Gln Asn Ala Phe Tyr Glu Ile
1               5                  10                  15

Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Ala Phe Ile Gln
            20                  25                  30

Arg Leu Arg Asp Asp Pro Ser Val Ser Arg Glu Ile Leu Ala Glu Ala
        35                  40                  45

Gln Arg Leu Asn Asp Ala Gln Ala Pro Arg
    50                  55
```

<210> 25
<211> 290
<212> PRT
<213> SpA C domain mutant

<400> 25

```
Ala Asp Asn Arg Phe Asn Arg Glu Gln Gln Asn Ala Phe Tyr Glu Ile
1               5                  10                  15

Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Ala Phe Ile Gln
            20                  25                  30

Arg Leu Arg Asp Asp Pro Ser Val Ser Arg Glu Ile Leu Ala Glu Ala
        35                  40                  45
```

Gln Arg Leu Asn Asp Ala Gln Ala Pro Arg Ala Asp Asn Arg Phe Asn
50 55 60

Arg Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
65 70 75 80

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

Ser Val Ser Arg Glu Ile Leu Ala Glu Ala Gln Arg Leu Asn Asp Ala
100 105 110

Gln Ala Pro Arg Ala Asp Asn Arg Phe Asn Arg Glu Gln Gln Asn Ala
115 120 125

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn
130 135 140

Ala Phe Ile Gln Arg Leu Arg Asp Asp Pro Ser Val Ser Arg Glu Ile
145 150 155 160

Leu Ala Glu Ala Gln Arg Leu Asn Asp Ala Gln Ala Pro Arg Ala Asp
165 170 175

Asn Arg Phe Asn Arg Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His
180 185 190

Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Ala Phe Ile Gln Arg Leu
195 200 205

Arg Asp Asp Pro Ser Val Ser Arg Glu Ile Leu Ala Glu Ala Gln Arg
210 215 220

Leu Asn Asp Ala Gln Ala Pro Arg Ala Asp Asn Arg Phe Asn Arg Glu
225 230 235 240

Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Thr Glu
245 250 255

Glu Gln Arg Asn Ala Phe Ile Gln Arg Leu Arg Asp Asp Pro Ser Val
260 265 270

Ser Arg Glu Ile Leu Ala Glu Ala Gln Arg Leu Asn Asp Ala Gln Ala
275 280 285

Pro Lys
290

<210> 26
<211> 893
<212> DNA
<213> Code DNA

<400> 26
ccatggcttt cgctgcagat aaccgtttta accgtgaaca acaaaacgct ttctacgaaa 60

tcctgcactt gccaaacctt actgaagaac aacgtaatgc tttcatccaa cgtctgcgcg 120

atgatccatc tgtatcccgt gaaattttgg cagaggctca acgacttaac gacgctcagg 180

cgcctcgcgc tgataaccgc ttcaaccgag aacaacaaaa cgcttttttat gaaatccttc 240

acctgccaaa tcttacagaa gaacaacgca acgcattcat tcaacgcttg cgtgatgacc 300

cttccgttag ccgagagatc ctggctgaag cacaacgttt gaatgatgcg caagcaccac 360

gtgctgataa tcgattcaac cgtgaacaac aaaatgcatt ctacgaaatc ttgcaccttc 420

ctaacctgac tgaagagcag cgtaacgctt ttatccagcg tttgagagac gatccatctg 480

tctcccgtga aattctcgca gaagcgcaac gcctgaacga tgctcaagct ccgcgtgcag 540

acaaccgttt caatcgcgaa cagcaaaacg cgttttatga aattctgcat cttccaaact 600

tgacagagga acaacgcaat gctttcatcc aacgactgcg tgatgatccg agcgtttctc 660

gagaaatctt ggctgaagca caacgtctga acgacgctca agctccacga gcggataaca 720

gatttaaccg tgaacaacaa aatgctttct acgagatctt gcaccttccg aacctgactg 780

aagaacaacg taacgcattt attcagagat tgcgcgatga cccatccgta agccgtgaga 840

tcctggcaga agctcaacgt ttgaatgatg cacaagctcc aaaataatct aga 893