SEQUENCE LISTING

<110> University of Basel

<120> Virulence attenuated bacteria based protein delivery

<130> P5239PC00

<160> 131

<170> PatentIn version 3.5

<210> 1
<211> 219
<212> PRT
<213> Yersinia enterocolitica

<400> 1

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                  10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30


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


Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60


Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80


Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95


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


Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125
```

```
Leu Gln Lys Asn His Asp Gln Phe Ala Thr Gly Ser Gly Pro Leu Arg
    130                 135                 140

Gly Ser Ile Thr Gln Cys Gln Gly Leu Met Gln Phe Cys Gly Gly Glu
145                 150                 155                 160

Leu Gln Ala Glu Ala Ser Ala Ile Leu Asn Thr Pro Val Cys Gly Ile
                165                 170                 175

Pro Phe Ser Gln Trp Gly Thr Val Gly Gly Ala Ala Ser Ala Tyr Val
            180                 185                 190

Ala Ser Gly Val Asp Leu Thr Gln Ala Ala Asn Glu Ile Lys Gly Leu
        195                 200                 205

Gly Gln Gln Met Gln Gln Leu Leu Ser Leu Met
    210                 215
```

<210> 2
<211> 138
<212> PRT
<213> Yersinia enterocolitica

<400> 2

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80
```

```
Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95


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


Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125


Leu Gln Lys Asn His Asp Gln Phe Ala Thr
    130                 135


<210>  3
<211>  169
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YopE1-138-MycHis

<400>  3

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30


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


Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60


Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80


Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95
```

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


Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125


Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Phe Glu
    130                 135                 140


Lys Leu Gly Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser
145                 150                 155                 160


Ala Val Asp His His His His His His
                165
```

<210> 4
<211> 20
<212> PRT
<213> Salmonella enterica

<400> 4

```
Met Pro Tyr Thr Ser Val Ser Thr Tyr Ala Arg Ala Leu Ser Gly Asn
1               5                   10                  15


Lys Leu Pro His
            20
```

<210> 5
<211> 210
<212> PRT
<213> Salmonella enterica

<400> 5

```
Met Pro Tyr Thr Ser Val Ser Thr Tyr Ala Arg Ala Leu Ser Gly Asn
1               5                   10                  15


Lys Leu Pro His Val Ala Ala Gly Asp Tyr Glu Asn Lys Leu Ser Thr
            20                  25                  30
```

```
Lys Ile Met Lys Gly Ile Leu Tyr Val Leu Thr Ala Gly Leu Ala Tyr
        35                  40                  45

Gly Phe Thr Arg Val Ile Glu His Tyr Cys Asn Val Thr Pro Lys Val
    50                  55                  60

Ala Glu Phe Cys Ala Asn Ala Gly Asn Ile His Asn His Leu Ala Asp
65                  70                  75                  80

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

Arg Met Leu Thr Phe Glu Gln Leu Ser Leu Ile Ala Glu Gly Lys Pro
            100                 105                 110

Ile Val Arg Ile Ser Asp Gly Glu His Thr Val Glu Val Glu Gly Thr
        115                 120                 125

Phe Glu Glu Ile Cys Met Arg Leu Glu Glu Gly Phe Phe Glu Ala Pro
    130                 135                 140

Ala Tyr Tyr Asp Tyr Asp Ile Asp Glu Lys Tyr Lys Thr Val Arg Glu
145                 150                 155                 160

Arg Met Ala Ala Tyr Asn Ala Leu Pro Gln Ala Leu Gly Ala Ile Pro
                165                 170                 175

Cys Leu Glu Tyr Tyr Ile Ala Arg Ala Ser Asn Met Gln Glu Ala Lys
            180                 185                 190

Ala Gln Trp Ala Ala Asp Ile Lys Ala Arg Tyr His Asn Tyr Leu Asp
        195                 200                 205

Asn Tyr
    210
```

<210> 6
<211> 81
<212> PRT
<213> Salmonella enterica

<400> 6

Val Thr Lys Ile Thr Leu Ser Pro Gln Asn Phe Arg Ile Gln Lys Gln
1   5   10   15

Glu Thr Thr Leu Leu Lys Glu Lys Ser Thr Glu Lys Asn Ser Leu Ala
            20   25   30

Lys Ser Ile Leu Ala Val Lys Asn His Phe Ile Glu Leu Arg Ser Lys
        35   40   45

Leu Ser Glu Arg Phe Ile Ser His Lys Asn Thr Glu Ser Ser Ala Thr
    50   55   60

His Phe His Arg Gly Ser Ala Ser Glu Gly Arg Ala Val Leu Thr Asn
65   70   75   80

Lys

<210> 7
<211> 105
<212> PRT
<213> Salmonella enterica

<400> 7

Val Thr Lys Ile Thr Leu Ser Pro Gln Asn Phe Arg Ile Gln Lys Gln
1   5   10   15

Glu Thr Thr Leu Leu Lys Glu Lys Ser Thr Glu Lys Asn Ser Leu Ala
            20   25   30

Lys Ser Ile Leu Ala Val Lys Asn His Phe Ile Glu Leu Arg Ser Lys
        35   40   45

```
Leu Ser Glu Arg Phe Ile Ser His Lys Asn Thr Glu Ser Ser Ala Thr
    50                  55                  60

His Phe His Arg Gly Ser Ala Ser Glu Gly Arg Ala Val Leu Thr Asn
65                  70                  75                  80

Lys Val Val Lys Asp Phe Met Leu Gln Thr Leu Asn Asp Ile Asp Ile
                85                  90                  95

Arg Gly Ser Ala Ser Lys Asp Pro Ala
            100                 105
```

<210> 8
<211> 310
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Ink4C

<400> 8

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95
```

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Ala
    130                 135                 140

Glu Pro Trp Gly Asn Glu Leu Ala Ser Ala Ala Ala Arg Gly Asp Leu
145                 150                 155                 160

Glu Gln Leu Thr Ser Leu Leu Gln Asn Asn Val Asn Val Asn Ala Gln
                165                 170                 175

Asn Gly Phe Gly Arg Thr Ala Leu Gln Val Met Lys Leu Gly Asn Pro
            180                 185                 190

Glu Ile Ala Arg Arg Leu Leu Leu Arg Gly Ala Asn Pro Asp Leu Lys
        195                 200                 205

Asp Arg Thr Gly Phe Ala Val Ile His Asp Ala Ala Arg Ala Gly Phe
    210                 215                 220

Leu Asp Thr Leu Gln Ala Leu Pro Glu Phe Gln Ala Asp Val Asn Ile
225                 230                 235                 240

Glu Asp Asn Glu Gly Asn Leu Pro Leu His Leu Ala Ala Lys Glu Gly
                245                 250                 255

His Leu Arg Val Val Glu Phe Leu Val Lys His Thr Ala Ser Asn Val
            260                 265                 270

Gly His Arg Asn His Lys Gly Asp Thr Ala Cys Asp Leu Ala Arg Leu
        275                 280                 285

Tyr Gly Arg Asn Glu Val Val Ser Leu Met Gln Ala Asn Gly Ala Gly
    290                 295                 300
```

```
Gly Ala Thr Asn Leu Gln
305                 310


<210>  9
<211>  465
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YopE1-138 - ET1

<400>  9

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30


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


Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60


Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80


Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95


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


Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125


Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Pro
    130                 135                 140
```

```
Arg Pro Lys Leu Lys Ser Asp Asp Glu Val Leu Glu Ala Ala Thr Val
145                 150                 155                 160

Val Leu Lys Arg Cys Gly Pro Ile Glu Phe Thr Leu Ser Gly Val Ala
                165                 170                 175

Lys Glu Val Gly Leu Ser Arg Ala Ala Leu Ile Gln Arg Phe Thr Asn
            180                 185                 190

Arg Asp Thr Leu Leu Val Arg Met Met Glu Arg Gly Val Glu Gln Val
        195                 200                 205

Arg His Tyr Leu Asn Ala Ile Pro Ile Gly Ala Gly Pro Gln Gly Leu
    210                 215                 220

Trp Glu Phe Leu Gln Val Leu Val Arg Ser Met Asn Thr Arg Asn Asp
225                 230                 235                 240

Phe Ser Val Asn Tyr Leu Ile Ser Trp Tyr Glu Leu Gln Val Pro Glu
                245                 250                 255

Leu Arg Thr Leu Ala Ile Gln Arg Asn Arg Ala Val Val Glu Gly Ile
            260                 265                 270

Arg Lys Arg Leu Pro Pro Gly Ala Pro Ala Ala Ala Glu Leu Leu Leu
        275                 280                 285

His Ser Val Ile Ala Gly Ala Thr Met Gln Trp Ala Val Asp Pro Asp
    290                 295                 300

Gly Glu Leu Ala Asp His Val Leu Ala Gln Ile Ala Ala Ile Leu Cys
305                 310                 315                 320

Leu Met Phe Pro Glu His Asp Asp Phe Gln Leu Leu Gln Ala His Ala
                325                 330                 335
```

```
Ser Ala Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile
            340                 345                 350

Glu Gly Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly
        355                 360                 365

Leu Ala Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg
    370                 375                 380

Leu Ser Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His
385                 390                 395                 400

Leu Asp Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp
                405                 410                 415

Phe Asp Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe
            420                 425                 430

Thr Pro His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe
        435                 440                 445

Glu Phe Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly
    450                 455                 460

Gly
465
```

<210> 10
<211> 324
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - 2x TEVsite - INK4C

<400> 10

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15
```

```
Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Glu Asn
    130                 135                 140

Leu Tyr Phe Gln Ser Glu Asn Leu Tyr Phe Gln Ser Met Ala Glu Pro
145                 150                 155                 160

Trp Gly Asn Glu Leu Ala Ser Ala Ala Ala Arg Gly Asp Leu Glu Gln
                165                 170                 175

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

Phe Gly Arg Thr Ala Leu Gln Val Met Lys Leu Gly Asn Pro Glu Ile
        195                 200                 205

Ala Arg Arg Leu Leu Leu Arg Gly Ala Asn Pro Asp Leu Lys Asp Arg
    210                 215                 220
```

```
Thr Gly Phe Ala Val Ile His Asp Ala Ala Arg Ala Gly Phe Leu Asp
225                 230                 235                 240


Thr Leu Gln Ala Leu Pro Glu Phe Gln Ala Asp Val Asn Ile Glu Asp
                245                 250                 255


Asn Glu Gly Asn Leu Pro Leu His Leu Ala Ala Lys Glu Gly His Leu
            260                 265                 270


Arg Val Val Glu Phe Leu Val Lys His Thr Ala Ser Asn Val Gly His
        275                 280                 285


Arg Asn His Lys Gly Asp Thr Ala Cys Asp Leu Ala Arg Leu Tyr Gly
    290                 295                 300


Arg Asn Glu Val Val Ser Leu Met Gln Ala Asn Gly Ala Gly Gly Ala
305                 310                 315                 320


Thr Asn Leu Gln



<210>  11
<211>  479
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YopE1-138 - 2x TEVsite - ET1

<400>  11

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30


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

```
Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Glu Asn
    130                 135                 140

Leu Tyr Phe Gln Ser Glu Asn Leu Tyr Phe Gln Ser Met Pro Arg Pro
145                 150                 155                 160

Lys Leu Lys Ser Asp Asp Glu Val Leu Glu Ala Ala Thr Val Val Leu
                165                 170                 175

Lys Arg Cys Gly Pro Ile Glu Phe Thr Leu Ser Gly Val Ala Lys Glu
            180                 185                 190

Val Gly Leu Ser Arg Ala Ala Leu Ile Gln Arg Phe Thr Asn Arg Asp
        195                 200                 205

Thr Leu Leu Val Arg Met Met Glu Arg Gly Val Glu Gln Val Arg His
    210                 215                 220

Tyr Leu Asn Ala Ile Pro Ile Gly Ala Gly Pro Gln Gly Leu Trp Glu
225                 230                 235                 240
```

```
Phe Leu Gln Val Leu Val Arg Ser Met Asn Thr Arg Asn Asp Phe Ser
                245                 250                 255

Val Asn Tyr Leu Ile Ser Trp Tyr Glu Leu Gln Val Pro Glu Leu Arg
            260                 265                 270

Thr Leu Ala Ile Gln Arg Asn Arg Ala Val Val Glu Gly Ile Arg Lys
        275                 280                 285

Arg Leu Pro Pro Gly Ala Pro Ala Ala Ala Glu Leu Leu Leu His Ser
    290                 295                 300

Val Ile Ala Gly Ala Thr Met Gln Trp Ala Val Asp Pro Asp Gly Glu
305                 310                 315                 320

Leu Ala Asp His Val Leu Ala Gln Ile Ala Ala Ile Leu Cys Leu Met
                325                 330                 335

Phe Pro Glu His Asp Asp Phe Gln Leu Leu Gln Ala His Ala Ser Ala
            340                 345                 350

Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
        355                 360                 365

Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
    370                 375                 380

Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
385                 390                 395                 400

Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
                405                 410                 415

Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
            420                 425                 430

Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
        435                 440                 445
```

```
His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
    450                 455                 460


Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly
465                 470                 475


<210>  12
<211>  380
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YopE1-138 - TEV protease S219V

<400>  12

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30


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


Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60


Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80


Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95


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


Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125
```

```
Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Glu Ser Leu Phe
    130                 135                 140

Lys Gly Pro Arg Asp Tyr Asn Pro Ile Ser Ser Thr Ile Cys His Leu
145                 150                 155                 160

Thr Asn Glu Ser Asp Gly His Thr Thr Ser Leu Tyr Gly Ile Gly Phe
                165                 170                 175

Gly Pro Phe Ile Ile Thr Asn Lys His Leu Phe Arg Arg Asn Asn Gly
            180                 185                 190

Thr Leu Leu Val Gln Ser Leu His Gly Val Phe Lys Val Lys Asn Thr
        195                 200                 205

Thr Thr Leu Gln Gln His Leu Ile Asp Gly Arg Asp Met Ile Ile Ile
    210                 215                 220

Arg Met Pro Lys Asp Phe Pro Pro Phe Pro Gln Lys Leu Lys Phe Arg
225                 230                 235                 240

Glu Pro Gln Arg Glu Glu Arg Ile Cys Leu Val Thr Thr Asn Phe Gln
                245                 250                 255

Thr Lys Ser Met Ser Ser Met Val Ser Asp Thr Ser Cys Thr Phe Pro
            260                 265                 270

Ser Ser Asp Gly Ile Phe Trp Lys His Trp Ile Gln Thr Lys Asp Gly
        275                 280                 285

Gln Cys Gly Ser Pro Leu Val Ser Thr Arg Asp Gly Phe Ile Val Gly
    290                 295                 300

Ile His Ser Ala Ser Asn Phe Thr Asn Thr Asn Asn Tyr Phe Thr Ser
305                 310                 315                 320
```

```
Val Pro Lys Asn Phe Met Glu Leu Leu Thr Asn Gln Glu Ala Gln Gln
                325                 330                 335


Trp Val Ser Gly Trp Arg Leu Asn Ala Asp Ser Val Leu Trp Gly Gly
            340                 345                 350


His Lys Val Phe Met Val Lys Pro Glu Glu Pro Phe Gln Pro Val Lys
        355                 360                 365


Glu Ala Thr Gln Leu Met Asn Arg Arg Arg Arg Arg
    370                 375                 380


<210>  13
<211>  332
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YopE1-138 - 2x TEVsite - Flag - INK4C

<400>  13

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30


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


Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60


Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80


Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95
```

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Glu Asn
    130                 135                 140

Leu Tyr Phe Gln Ser Glu Asn Leu Tyr Phe Gln Ser Asp Tyr Lys Asp
145                 150                 155                 160

Asp Asp Asp Lys Met Ala Glu Pro Trp Gly Asn Glu Leu Ala Ser Ala
                165                 170                 175

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

Val Asn Val Asn Ala Gln Asn Gly Phe Gly Arg Thr Ala Leu Gln Val
        195                 200                 205

Met Lys Leu Gly Asn Pro Glu Ile Ala Arg Arg Leu Leu Leu Arg Gly
    210                 215                 220

Ala Asn Pro Asp Leu Lys Asp Arg Thr Gly Phe Ala Val Ile His Asp
225                 230                 235                 240

Ala Ala Arg Ala Gly Phe Leu Asp Thr Leu Gln Ala Leu Pro Glu Phe
                245                 250                 255

Gln Ala Asp Val Asn Ile Glu Asp Asn Glu Gly Asn Leu Pro Leu His
            260                 265                 270

Leu Ala Ala Lys Glu Gly His Leu Arg Val Val Glu Phe Leu Val Lys
        275                 280                 285

His Thr Ala Ser Asn Val Gly His Arg Asn His Lys Gly Asp Thr Ala
    290                 295                 300
```

Cys Asp Leu Ala Arg Leu Tyr Gly Arg Asn Glu Val Val Ser Leu Met
305 310 315 320

Gln Ala Asn Gly Ala Gly Gly Ala Thr Asn Leu Gln
325 330

<210> 14
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138-Ubiquitin

<400> 14

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

```
Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Met Gln Ile Phe
    130                 135                 140

Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Pro Ser
145                 150                 155                 160

Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile
                165                 170                 175

Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
            180                 185                 190

Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His
        195                 200                 205

Leu Val Leu Arg Leu Arg Gly Gly Phe Glu Ala Ser Lys Leu Gly Pro
    210                 215                 220

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His
225                 230                 235                 240

His His His His His
                245
```

<210> 15
<211> 419
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138-Ubiquitin-Flag-INK4C-MycHis

<400> 15

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30
```

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Met Gln Ile Phe
    130                 135                 140

Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Pro Ser
145                 150                 155                 160

Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile
                165                 170                 175

Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
            180                 185                 190

Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His
        195                 200                 205

Leu Val Leu Arg Leu Arg Gly Gly Phe Glu Asp Tyr Lys Asp Asp Asp
    210                 215                 220
```

```
Asp Lys Met Ala Glu Pro Trp Gly Asn Glu Leu Ala Ser Ala Ala Ala
225                 230                 235                 240


Arg Gly Asp Leu Glu Gln Leu Thr Ser Leu Leu Gln Asn Asn Val Asn
                245                 250                 255


Val Asn Ala Gln Asn Gly Phe Gly Arg Thr Ala Leu Gln Val Met Lys
            260                 265                 270


Leu Gly Asn Pro Glu Ile Ala Arg Arg Leu Leu Leu Arg Gly Ala Asn
        275                 280                 285


Pro Asp Leu Lys Asp Arg Thr Gly Phe Ala Val Ile His Asp Ala Ala
    290                 295                 300


Arg Ala Gly Phe Leu Asp Thr Leu Gln Ala Leu Pro Glu Phe Gln Ala
305                 310                 315                 320


Asp Val Asn Ile Glu Asp Asn Glu Gly Asn Leu Pro Leu His Leu Ala
                325                 330                 335


Ala Lys Glu Gly His Leu Arg Val Val Glu Phe Leu Val Lys His Thr
            340                 345                 350


Ala Ser Asn Val Gly His Arg Asn His Lys Gly Asp Thr Ala Cys Asp
        355                 360                 365


Leu Ala Arg Leu Tyr Gly Arg Asn Glu Val Val Ser Leu Met Gln Ala
    370                 375                 380


Asn Gly Ala Gly Gly Ala Thr Asn Leu Gln Lys Leu Gly Pro Glu Gln
385                 390                 395                 400


Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His
                405                 410                 415


His His His
```

<210> 16
<211> 318
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - z-BIM

<400> 16

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30


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


Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60


Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80


Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95


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


Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125


Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Ser
    130                 135                 140


Asp Thr Ser Arg Glu Gln Thr Leu Ala Asn Gly Pro Ala Ser Gln Gly
145                 150                 155                 160
```

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

Asp Phe Pro Gln Pro Gly Glu Gly Asp Pro Leu Arg Gly Gly Ile Ser
            180                 185                 190

Met Ser Asn Asn Gln Ser Arg Ser Pro Met Asn Arg Thr Phe Ser Arg
        195                 200                 205

Ser Ser Ser Gly Tyr Phe Ser Val Asp Ser Asp Ser Val Pro Gly Ser
    210                 215                 220

Pro Leu Met Pro Asn Ile Ser Glu Ala Gln Asp Gly Gln Asn Asp Glu
225                 230                 235                 240

Val Trp Leu Ser Glu His Ser His Gln His Leu Gln Met Ala Ala Pro
                245                 250                 255

Val Ala Ala Leu Pro Pro Glu Met Val Val Ala Arg Glu Leu Arg Arg
            260                 265                 270

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

Asn Gln Leu Arg Ala Pro Asn Glu His Ala Ile Val Leu Trp Met Asn
    290                 295                 300

Val Ile Ile Gly Arg Leu Val His Phe Phe Leu Arg Arg Arg
305                 310                 315
```

<210> 17
<211> 337
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - human Bid

<400> 17

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Asp
    130                 135                 140

Cys Glu Val Asn Asn Gly Ser Ser Leu Arg Asp Glu Cys Ile Thr Asn
145                 150                 155                 160

Leu Leu Val Phe Gly Phe Leu Gln Ser Cys Ser Asp Asn Ser Phe Arg
                165                 170                 175

Arg Glu Leu Asp Ala Leu Gly His Glu Leu Pro Val Leu Ala Pro Gln
            180                 185                 190
```

```
Trp Glu Gly Tyr Asp Glu Leu Gln Thr Asp Gly Asn Arg Ser Ser His
        195                 200                 205

Ser Arg Leu Gly Arg Ile Glu Ala Asp Ser Glu Ser Gln Glu Asp Ile
    210                 215                 220

Ile Arg Asn Ile Ala Arg His Leu Ala Gln Val Gly Asp Ser Met Asp
225                 230                 235                 240

Arg Ser Ile Pro Pro Gly Leu Val Asn Gly Leu Ala Leu Gln Leu Arg
                245                 250                 255

Asn Thr Ser Arg Ser Glu Glu Asp Arg Asn Arg Asp Leu Ala Thr Ala
            260                 265                 270

Leu Glu Gln Leu Leu Gln Ala Tyr Pro Arg Asp Met Glu Lys Glu Lys
        275                 280                 285

Thr Met Leu Val Leu Ala Leu Leu Leu Ala Lys Lys Val Ala Ser His
    290                 295                 300

Thr Pro Ser Leu Leu Arg Asp Val Phe His Thr Thr Val Asn Phe Ile
305                 310                 315                 320

Asn Gln Asn Leu Arg Thr Tyr Val Arg Ser Leu Ala Arg Asn Gly Met
                325                 330                 335

Asp
```

<210> 18
<211> 277
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - human t-Bid

<400> 18

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Gly Asn
    130                 135                 140

Arg Ser Ser His Ser Arg Leu Gly Arg Ile Glu Ala Asp Ser Glu Ser
145                 150                 155                 160

Gln Glu Asp Ile Ile Arg Asn Ile Ala Arg His Leu Ala Gln Val Gly
                165                 170                 175

Asp Ser Met Asp Arg Ser Ile Pro Pro Gly Leu Val Asn Gly Leu Ala
            180                 185                 190

Leu Gln Leu Arg Asn Thr Ser Arg Ser Glu Glu Asp Arg Asn Arg Asp
        195                 200                 205
```

```
Leu Ala Thr Ala Leu Glu Gln Leu Leu Gln Ala Tyr Pro Arg Asp Met
    210                 215                 220


Glu Lys Glu Lys Thr Met Leu Val Leu Ala Leu Leu Leu Ala Lys Lys
225                 230                 235                 240


Val Ala Ser His Thr Pro Ser Leu Leu Arg Asp Val Phe His Thr Thr
                245                 250                 255


Val Asn Phe Ile Asn Gln Asn Leu Arg Thr Tyr Val Arg Ser Leu Ala
            260                 265                 270


Arg Asn Gly Met Asp
        275


<210>  19
<211>  163
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YopE1-138 - Y. enterocolitica codon optimized murine BID BH3 part

<400>  19

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30


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


Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60


Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80
```

```
Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95


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


Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125


Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Phe Glu
    130                 135                 140


Glu Ile Ile His Asn Ile Ala Arg His Leu Ala Gln Ile Gly Asp Glu
145                 150                 155                 160


Met Asp His
```

<210> 20
<211> 156
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Y. enterocolitica codon optimized murine Bax BH3 part

<400> 20

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30


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


Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60
```

```
Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80


Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95


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


Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125


Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Lys Lys Leu Ser
    130                 135                 140


Glu Cys Leu Arg Arg Ile Gly Asp Glu Leu Asp Ser
145                 150                 155


<210>  21
<211>  276
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YopE1-138-Y. enterocolitica codon optimized murine tBid

<400>  21

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30


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


Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60
```

```
Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Gly Ser Gln Ala
    130                 135                 140

Ser Arg Ser Phe Asn Gln Gly Arg Ile Glu Pro Asp Ser Glu Ser Gln
145                 150                 155                 160

Glu Glu Ile Ile His Asn Ile Ala Arg His Leu Ala Gln Ile Gly Asp
                165                 170                 175

Glu Met Asp His Asn Ile Gln Pro Thr Leu Val Arg Gln Leu Ala Ala
            180                 185                 190

Gln Phe Met Asn Gly Ser Leu Ser Glu Glu Asp Lys Arg Asn Cys Leu
        195                 200                 205

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

Asn Asp Lys Ala Met Leu Ile Met Thr Met Leu Leu Ala Lys Lys Val
225                 230                 235                 240

Ala Ser His Ala Pro Ser Leu Leu Arg Asp Val Phe His Thr Thr Val
                245                 250                 255
```

```
Asn Phe Ile Asn Gln Asn Leu Phe Ser Tyr Val Arg Asn Leu Val Arg
            260                 265                 270


Asn Glu Met Asp
        275


<210>  22
<211>  167
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YopE1-138- codon optimized murine tBid BH3 extended part

<400>  22

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30


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


Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60


Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80


Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95


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


Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125
```

```
Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Phe Glu
    130                 135                 140

Glu Ile Ile His Asn Ile Ala Arg His Leu Ala Gln Ile Gly Asp Glu
145                 150                 155                 160

Met Asp His Asn Ile Gln Pro
                165
```

<210> 23
<211> 168
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138-10 Aa linker - Y. enterocolitica codon optimized murine tBid BH3 part

<400> 23

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115   120   125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Phe Glu
    130   135   140

Ala Gly Gly Ala Glu Glu Ile Ile His Asn Ile Ala Arg His Leu Ala
145   150   155   160

Gln Ile Gly Asp Glu Met Asp His
                165

<210> 24
<211> 186
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138-Y. enterocolitica codon optimized murine Bax BH3 part-
       Y. enterocolitica codon optimized murine tBid BH3 part

<400> 24

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1   5   10   15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20   25   30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50   55   60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65   70   75   80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85   90   95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Gly Ala Ile Asp
    130                 135                 140

Ala Lys Lys Leu Ser Glu Cys Leu Arg Arg Ile Gly Asp Glu Leu Asp
145                 150                 155                 160

Ser Gly Ala Phe Asp Ala Glu Glu Ile Ile His Asn Ile Ala Arg His
                165                 170                 175

Leu Ala Gln Ile Gly Asp Glu Met Asp His
            180                 185


<210>  25
<211>  165
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YopE1-138 - Y. enterocolitica codon optimized murine BID BH3 part
       (ready for insertion of further domains)

<400>  25

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
```

```
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Gly Ala Ile Asp
    130                 135                 140

Ala Glu Glu Ile Ile His Asn Ile Ala Arg His Leu Ala Gln Ile Gly
145                 150                 155                 160

Asp Glu Met Asp His
                165
```

<210> 26
<211> 161
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Y. enterocolitica codon optimized murine Bax BH3 part (ready for insertion of further domains)

<400> 26

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30
```

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Gly Ala Ile Asp
    130                 135                 140

Ala Lys Lys Leu Ser Glu Cys Leu Arg Arg Ile Gly Asp Glu Leu Asp
145                 150                 155                 160

Ser
```

<210> 27
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - (Y. enterocolitica codon optimized murine BID BH3 part)2

<400> 27

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15
```

```
Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Gly Ala Ile Asp
    130                 135                 140

Ala Glu Glu Ile Ile His Asn Ile Ala Arg His Leu Ala Gln Ile Gly
145                 150                 155                 160

Asp Glu Met Asp His Gly Ala Phe Asp Ala Glu Glu Ile Ile His Asn
                165                 170                 175

Ile Ala Arg His Leu Ala Gln Ile Gly Asp Glu Met Asp His
            180                 185                 190
```

<210> 28
<211> 186
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - (Y. enterocolitica codon optimized murine BID BH3 part)(Y. enterocolitica codon optimized murine Bax BH3 part)

<400> 28

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                  10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30


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


Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60


Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80


Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95


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


Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125


Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Gly Ala Ile Asp
    130                 135                 140


Ala Glu Glu Ile Ile His Asn Ile Ala Arg His Leu Ala Gln Ile Gly
145                 150                 155                 160


Asp Glu Met Asp His Gly Ala Phe Asp Ala Lys Lys Leu Ser Glu Cys
                165                 170                 175
```

```
Leu Arg Arg Ile Gly Asp Glu Leu Asp Ser
            180                 185


<210>  29
<211>  20
<212>  PRT
<213>  Mus musculus

<400>  29

Glu Glu Ile Ile His Asn Ile Ala Arg His Leu Ala Gln Ile Gly Asp
1               5                   10                  15


Glu Met Asp His
            20


<210>  30
<211>  14
<212>  PRT
<213>  Mus musculus

<400>  30

Ile Ala Arg His Leu Ala Gln Ile Gly Asp Glu Met Asp His
1               5                   10


<210>  31
<211>  20
<212>  PRT
<213>  Homo sapiens

<400>  31

Glu Asp Ile Ile Arg Asn Ile Ala Arg His Leu Ala Gln Val Gly Asp
1               5                   10                  15


Ser Met Asp Arg
            20


<210>  32
<211>  15
<212>  PRT
<213>  Homo sapiens
```

<400> 32

Ile Ala Arg His Leu Ala Gln Val Gly Asp Ser Met Asp Arg Ser
1 5 10 15

<210> 33
<211> 17
<212> PRT
<213> Mus musculus

<400> 33

Lys Lys Leu Ser Glu Cys Leu Arg Arg Ile Gly Asp Glu Leu Asp Ser
1 5 10 15

Asn

<210> 34
<211> 14
<212> PRT
<213> Mus musculus

<400> 34

Leu Ser Glu Cys Leu Arg Arg Ile Gly Asp Glu Leu Asp Ser
1 5 10

<210> 35
<211> 17
<212> PRT
<213> Homo sapiens

<400> 35

Lys Lys Leu Ser Glu Cys Leu Lys Arg Ile Gly Asp Glu Leu Asp Ser
1 5 10 15

Asn

<210> 36
<211> 14
<212> PRT

<213> Homo sapiens

<400> 36

Leu Ser Glu Cys Leu Lys Arg Ile Gly Asp Glu Leu Asp Ser
1 5 10

<210> 37
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Y. enterocolitica codon optimized human RIG-1 two CARD domains (Aa. 1-245)

<400> 37

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

```
Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Thr
    130                 135                 140

Thr Glu Gln Arg Arg Ser Leu Gln Ala Phe Gln Asp Tyr Ile Arg Lys
145                 150                 155                 160

Thr Leu Asp Pro Thr Tyr Ile Leu Ser Tyr Met Ala Pro Trp Phe Arg
                165                 170                 175

Glu Glu Glu Val Gln Tyr Ile Gln Ala Glu Lys Asn Asn Lys Gly Pro
            180                 185                 190

Met Glu Ala Ala Thr Leu Phe Leu Lys Phe Leu Leu Glu Leu Gln Glu
        195                 200                 205

Glu Gly Trp Phe Arg Gly Phe Leu Asp Ala Leu Asp His Ala Gly Tyr
    210                 215                 220

Ser Gly Leu Tyr Glu Ala Ile Glu Ser Trp Asp Phe Lys Lys Ile Glu
225                 230                 235                 240

Lys Leu Glu Glu Tyr Arg Leu Leu Leu Lys Arg Leu Gln Pro Glu Phe
                245                 250                 255

Lys Thr Arg Ile Ile Pro Thr Asp Ile Ile Ser Asp Leu Ser Glu Cys
            260                 265                 270

Leu Ile Asn Gln Glu Cys Glu Glu Ile Leu Gln Ile Cys Ser Thr Lys
        275                 280                 285

Gly Met Met Ala Gly Ala Glu Lys Leu Val Glu Cys Leu Leu Arg Ser
    290                 295                 300

Asp Lys Glu Asn Trp Pro Lys Thr Leu Lys Leu Ala Leu Glu Lys Glu
305                 310                 315                 320

Arg Asn Lys Phe Ser Glu Leu Trp Ile Val Glu Lys Gly Ile Lys Asp
```

```
                325                 330                 335

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

Ile Phe Tyr Gln Glu Asp Pro Glu Cys Gln Asn Leu Ser Glu Asn Ser
        355                 360                 365

Cys Pro Pro Ser Glu Val Ser Asp Thr Asn Leu Tyr Ser Pro Phe Lys
    370                 375                 380

Pro Arg Asn
385
```

<210> 38
<211> 388
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Y. enterocolitica codon optimized murine RIG-1 two CARD domains (Aa. 1-246)

<400> 38

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80
```

```
Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Thr
    130                 135                 140

Ala Glu Gln Arg Gln Asn Leu Gln Ala Phe Arg Asp Tyr Ile Lys Lys
145                 150                 155                 160

Ile Leu Asp Pro Thr Tyr Ile Leu Ser Tyr Met Ser Ser Trp Leu Glu
                165                 170                 175

Asp Glu Glu Val Gln Tyr Ile Gln Ala Glu Lys Asn Asn Lys Gly Pro
            180                 185                 190

Met Glu Ala Ala Ser Leu Phe Leu Gln Tyr Leu Leu Lys Leu Gln Ser
        195                 200                 205

Glu Gly Trp Phe Gln Ala Phe Leu Asp Ala Leu Tyr His Ala Gly Tyr
    210                 215                 220

Cys Gly Leu Cys Glu Ala Ile Glu Ser Trp Asp Phe Gln Lys Ile Glu
225                 230                 235                 240

Lys Leu Glu Glu His Arg Leu Leu Leu Arg Arg Leu Glu Pro Glu Phe
                245                 250                 255

Lys Ala Thr Val Asp Pro Asn Asp Ile Leu Ser Glu Leu Ser Glu Cys
            260                 265                 270

Leu Ile Asn Gln Glu Cys Glu Glu Ile Arg Gln Ile Arg Asp Thr Lys
        275                 280                 285
```

```
Gly Arg Met Ala Gly Ala Glu Lys Met Ala Glu Cys Leu Ile Arg Ser
    290                 295                 300


Asp Lys Glu Asn Trp Pro Lys Val Leu Gln Leu Ala Leu Glu Lys Asp
305                 310                 315                 320


Asn Ser Lys Phe Ser Glu Leu Trp Ile Val Asp Lys Gly Phe Lys Arg
                325                 330                 335


Ala Glu Ser Lys Ala Asp Glu Asp Asp Gly Ala Glu Ala Ser Ser Ile
            340                 345                 350


Gln Ile Phe Ile Gln Glu Glu Pro Glu Cys Gln Asn Leu Ser Gln Asn
        355                 360                 365


Pro Gly Pro Pro Ser Glu Ala Ser Ser Asn Asn Leu His Ser Pro Leu
    370                 375                 380


Lys Pro Arg Asn
385
```

<210> 39
<211> 348
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Y. enterocolitica codon optimized S. cerevisiae GCN4 (Aa. 249-278) - Y. enterocolitica codon optimized P. aeruginosa WspR (Aa. 172-347)

<400> 39

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30
```

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Arg Met
    130                 135                 140

Lys Gln Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His
145                 150                 155                 160

Leu Glu Asn Glu Val Ala Arg Leu Lys Lys Leu Val Asn Ser Asp Gly
                165                 170                 175

Leu Thr Gly Leu Ser Asn Arg Arg His Phe Asp Glu Tyr Leu Glu Met
            180                 185                 190

Glu Trp Arg Arg Ser Leu Arg Glu Gln Ser Gln Leu Ser Leu Leu Met
        195                 200                 205

Ile Asp Val Asp Tyr Phe Lys Ser Tyr Asn Asp Thr Phe Gly His Val
    210                 215                 220

Ala Gly Asp Glu Ala Leu Arg Gln Val Ala Gly Ala Ile Arg Glu Gly
225                 230                 235                 240
```

```
Cys Ser Arg Ser Ser Asp Leu Ala Ala Arg Tyr Gly Gly Glu Glu Phe
                245                 250                 255


Ala Met Val Leu Pro Gly Thr Ser Pro Gly Gly Ala Arg Leu Leu Ala
            260                 265                 270


Glu Lys Val Arg Arg Thr Val Glu Ser Leu Gln Ile Ser His Asp Gln
        275                 280                 285


Pro Arg Pro Gly Ser His Leu Thr Val Ser Ile Gly Val Ser Thr Leu
    290                 295                 300


Val Pro Gly Gly Gly Gly Gln Thr Phe Arg Val Leu Ile Glu Met Ala
305                 310                 315                 320


Asp Gln Ala Leu Tyr Gln Ala Lys Asn Asn Gly Arg Asn Gln Val Gly
                325                 330                 335


Leu Met Glu Gln Pro Val Pro Pro Ala Pro Ala Gly
            340                 345


<210>  40
<211>  561
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YopE1-138 - Y. enterocolitica codon optimized murine IRF3 S397D

<400>  40

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30


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

```
Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Glu
    130                 135                 140

Thr Pro Lys Pro Arg Ile Leu Pro Trp Leu Val Ser Gln Leu Asp Leu
145                 150                 155                 160

Gly Gln Leu Glu Gly Val Ala Trp Leu Asp Glu Ser Arg Thr Arg Phe
                165                 170                 175

Arg Ile Pro Trp Lys His Gly Leu Arg Gln Asp Ala Gln Met Ala Asp
            180                 185                 190

Phe Gly Ile Phe Gln Ala Trp Ala Glu Ala Ser Gly Ala Tyr Thr Pro
        195                 200                 205

Gly Lys Asp Lys Pro Asp Val Ser Thr Trp Lys Arg Asn Phe Arg Ser
    210                 215                 220

Ala Leu Asn Arg Lys Glu Val Leu Arg Leu Ala Ala Asp Asn Ser Lys
225                 230                 235                 240
```

```
Asp Pro Tyr Asp Pro His Lys Val Tyr Glu Phe Val Thr Pro Gly Ala
                245                 250                 255

Arg Asp Phe Val His Leu Gly Ala Ser Pro Asp Thr Asn Gly Lys Ser
            260                 265                 270

Ser Leu Pro His Ser Gln Glu Asn Leu Pro Lys Leu Phe Asp Gly Leu
        275                 280                 285

Ile Leu Gly Pro Leu Lys Asp Glu Gly Ser Ser Asp Leu Ala Ile Val
    290                 295                 300

Ser Asp Pro Ser Gln Gln Leu Pro Ser Pro Asn Val Asn Asn Phe Leu
305                 310                 315                 320

Asn Pro Ala Pro Gln Glu Asn Pro Leu Lys Gln Leu Leu Ala Glu Glu
                325                 330                 335

Gln Trp Glu Phe Glu Val Thr Ala Phe Tyr Arg Gly Arg Gln Val Phe
            340                 345                 350

Gln Gln Thr Leu Phe Cys Pro Gly Gly Leu Arg Leu Val Gly Ser Thr
        355                 360                 365

Ala Asp Met Thr Leu Pro Trp Gln Pro Val Thr Leu Pro Asp Pro Glu
    370                 375                 380

Gly Phe Leu Thr Asp Lys Leu Val Lys Glu Tyr Val Gly Gln Val Leu
385                 390                 395                 400

Lys Gly Leu Gly Asn Gly Leu Ala Leu Trp Gln Ala Gly Gln Cys Leu
                405                 410                 415

Trp Ala Gln Arg Leu Gly His Ser His Ala Phe Trp Ala Leu Gly Glu
            420                 425                 430

Glu Leu Leu Pro Asp Ser Gly Arg Gly Pro Asp Gly Glu Val His Lys
        435                 440                 445
```

```
Asp Lys Asp Gly Ala Val Phe Asp Leu Arg Pro Phe Val Ala Asp Leu
    450                 455                 460


Ile Ala Phe Met Glu Gly Ser Gly His Ser Pro Arg Tyr Thr Leu Trp
465                 470                 475                 480


Phe Cys Met Gly Glu Met Trp Pro Gln Asp Gln Pro Trp Val Lys Arg
                485                 490                 495


Leu Val Met Val Lys Val Val Pro Thr Cys Leu Lys Glu Leu Leu Glu
            500                 505                 510


Met Ala Arg Glu Gly Gly Ala Ser Ser Leu Lys Thr Val Asp Leu His
        515                 520                 525


Ile Asp Asn Ser Gln Pro Ile Ser Leu Thr Ser Asp Gln Tyr Lys Ala
    530                 535                 540


Tyr Leu Gln Asp Leu Val Glu Asp Met Asp Phe Gln Ala Thr Gly Asn
545                 550                 555                 560


Ile
```

<210> 41
<211> 553
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Y. enterocolitica codon optimized V. Cholerae DncV (M3toL413)

<400> 41

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
```

```
            20                  25                  30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Thr
    130                 135                 140

Trp Asn Phe His Gln Tyr Tyr Thr Asn Arg Asn Asp Gly Leu Met Gly
145                 150                 155                 160

Lys Leu Val Leu Thr Asp Glu Glu Lys Asn Asn Leu Lys Ala Leu Arg
                165                 170                 175

Lys Ile Ile Arg Leu Arg Thr Arg Asp Val Phe Glu Glu Ala Lys Gly
            180                 185                 190

Ile Ala Lys Ala Val Lys Lys Ser Ala Leu Thr Phe Glu Ile Ile Gln
        195                 200                 205

Glu Lys Val Ser Thr Thr Gln Ile Lys His Leu Ser Asp Ser Glu Gln
    210                 215                 220
```

```
Arg Glu Val Ala Lys Leu Ile Tyr Glu Met Asp Asp Asp Ala Arg Asp
225                 230                 235                 240

Glu Phe Leu Gly Leu Thr Pro Arg Phe Trp Thr Gln Gly Ser Phe Gln
                245                 250                 255

Tyr Asp Thr Leu Asn Arg Pro Phe Gln Pro Gly Gln Glu Met Asp Ile
            260                 265                 270

Asp Asp Gly Thr Tyr Met Pro Met Pro Ile Phe Glu Ser Glu Pro Lys
        275                 280                 285

Ile Gly His Ser Leu Leu Ile Leu Leu Val Asp Ala Ser Leu Lys Ser
    290                 295                 300

Leu Val Ala Glu Asn His Gly Trp Lys Phe Glu Ala Lys Gln Thr Cys
305                 310                 315                 320

Gly Arg Ile Lys Ile Glu Ala Glu Lys Thr His Ile Asp Val Pro Met
                325                 330                 335

Tyr Ala Ile Pro Lys Asp Glu Phe Gln Lys Lys Gln Ile Ala Leu Glu
            340                 345                 350

Ala Asn Arg Ser Phe Val Lys Gly Ala Ile Phe Glu Ser Tyr Val Ala
        355                 360                 365

Asp Ser Ile Thr Asp Asp Ser Glu Thr Tyr Glu Leu Asp Ser Glu Asn
    370                 375                 380

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

Pro Lys Ile Val Glu Asp Trp Phe Asn Asp Ser Cys Ile Arg Ile Gly
                405                 410                 415

Lys His Leu Arg Lys Val Cys Arg Phe Met Lys Ala Trp Arg Asp Ala
```

```
            420                 425                 430

Gln Trp Asp Val Gly Gly Pro Ser Ser Ile Ser Leu Met Ala Ala Thr
        435                 440                 445

Val Asn Ile Leu Asp Ser Val Ala His Asp Ala Ser Asp Leu Gly Glu
    450                 455                 460

Thr Met Lys Ile Ile Ala Lys His Leu Pro Ser Glu Phe Ala Arg Gly
465                 470                 475                 480

Val Glu Ser Pro Asp Ser Thr Asp Glu Lys Pro Leu Phe Pro Pro Ser
                485                 490                 495

Tyr Lys His Gly Pro Arg Glu Met Asp Ile Met Ser Lys Leu Glu Arg
            500                 505                 510

Leu Pro Glu Ile Leu Ser Ser Ala Glu Ser Ala Asp Ser Lys Ser Glu
        515                 520                 525

Ala Leu Lys Lys Ile Asn Met Ala Phe Gly Asn Arg Val Thr Asn Ser
    530                 535                 540

Glu Leu Ile Val Leu Ala Lys Ala Leu
545                 550


<210>  42
<211>  272
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YopE1-138 - Y. enterocolitica codon optimized B. cereus_DisA-like
       (PDB: 2FB5; Aa. 76-205)

<400>  42

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15
```

```
Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Ser Ser
    130                 135                 140

Ser Phe Ile Thr Thr Ala Ile Gln His Leu Ser Ala Arg Lys His Gly
145                 150                 155                 160

Ala Leu Ile Val Val Glu Arg Asn Glu Thr Leu Glu Ala Leu Ile Gln
                165                 170                 175

Thr Gly Thr Thr Leu Asn Ala His Leu Thr Ala Pro Leu Leu Glu Ser
            180                 185                 190

Ile Phe Tyr Pro Gly Asn Pro Leu His Asp Gly Ala Val Leu Val Lys
        195                 200                 205

Asn Asn His Ile Val Ser Ala Ala Asn Ile Leu Pro Leu Thr Lys Ser
    210                 215                 220
```

```
Thr Glu Val Asp Pro Glu Leu Gly Thr Arg His Arg Ala Ala Ile Gly
225                 230                 235                 240


Leu Ser Glu Lys Ser Asp Ala Leu Ile Leu Val Val Ser Glu Glu Thr
                245                 250                 255


Gly Arg Thr Ser Phe Ala Leu Asn Gly Ile Leu Tyr Thr Ile Ser Leu
            260                 265                 270


<210>  43
<211>  564
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YopE1-138 - Y. enterocolitica codon optimized Anemonae (N.
       vectensis) cGAS (Ensembl: A7SFB5.1)

<400>  43

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30


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


Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60


Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80


Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95


Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
```

```
            100                 105                 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Ala
    130                 135                 140

Thr Leu Glu Arg Leu Leu Asp Leu Leu Arg Glu Tyr His Leu Asp Asp
145                 150                 155                 160

Val Leu Phe His Asn Ser Thr Pro Glu Leu Gly Ile Gln His Arg Ser
                165                 170                 175

Arg Pro Lys Gln Lys Arg Ile Ile Arg Gly Lys Lys Gln Gln Lys Ser
            180                 185                 190

Lys Lys Leu Lys Arg Asn Glu Gln Gln Gln Pro Phe Pro Lys Gly Asp
        195                 200                 205

Leu Glu Thr Leu Arg Arg Phe Ser Val Thr Asp Val Lys Ile Ser Lys
    210                 215                 220

Gln Ser Thr Lys Trp Ala Lys Lys Met Ala Asp Lys His Leu Glu Ile
225                 230                 235                 240

Ile Arg Lys His Cys Lys Thr Asn Ser Ile Lys Leu Phe Asn His Phe
                245                 250                 255

Glu Tyr Thr Gly Ser Phe Tyr Glu His Leu Lys Thr Ile Asp Ala Asp
            260                 265                 270

Glu Leu Asp Ile Met Val Ala Leu Ser Ile Lys Met Asp Glu Leu Glu
        275                 280                 285

Val Glu Gln Val Thr Pro Gly Tyr Ala Gly Leu Lys Leu Arg Asp Thr
    290                 295                 300
```

```
Pro Ser Asn Arg Asn Lys Tyr Asn Asp Leu Thr Ile Ala Asp Asn Tyr
305                 310                 315                 320

Gly Arg Tyr Leu Ser Pro Glu Lys Val Ser Arg Trp Phe Phe Ser Leu
                325                 330                 335

Val Gln Lys Ala Val Asn Thr Tyr Lys Asp Glu Ile Pro Gln Thr Glu
            340                 345                 350

Val Lys Leu Thr Asp Asn Gly Pro Ala Thr Thr Leu Val Ile Thr Tyr
        355                 360                 365

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

Leu Val Pro Ala Leu Leu Phe Lys Asp Lys Thr Lys Pro Ala Gly Asp
385                 390                 395                 400

Asp Leu Arg Ala Trp His Tyr Val Ala Lys Thr Ile Pro Lys Gly Ala
                405                 410                 415

Arg Leu Lys Glu Pro Leu Pro Phe Arg Ser Glu Leu Leu Trp Arg Gln
            420                 425                 430

Ser Phe Ser Leu Lys Glu Lys His Leu Met Asp Lys Leu Asp Lys Asp
        435                 440                 445

Asp Asn Gly Cys Arg Arg Glu Met Val Arg Ile Val Lys Thr Ile Val
    450                 455                 460

Lys Lys Asp Pro Thr Leu Ala Gln Leu Ser Ser Tyr His Ile Lys Thr
465                 470                 475                 480

Ala Phe Leu Gln Tyr Asn Phe Ser Asp Val Lys Leu Asp Trp Glu Gly
                485                 490                 495

Lys Lys Leu Ala Glu Arg Phe Leu His Phe Leu Glu Phe Leu Arg Asp
```

```
            500                 505                 510

Arg Val Lys Asp Lys Thr Leu Asn Asn Tyr Phe Ile Thr Asp Leu Asn
        515                 520                 525

Leu Leu Asp Asp Leu Asn Asp Ser Asn Ile Asp Asn Ile Ala Asn Arg
    530                 535                 540

Leu Asp Lys Ile Ile Gln Asn Glu Thr Glu Arg Ala Lys Ile Phe Thr
545                 550                 555                 560

Thr Gln Arg Gln
```

<210> 44
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Y. enterocolitica codon optimized murine MDA5 two CARD domains (minimal: Aa 1-190)

<400> 44

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80
```

```
Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Ser
    130                 135                 140

Ile Val Cys Ser Ala Glu Asp Ser Phe Arg Asn Leu Ile Leu Phe Phe
145                 150                 155                 160

Arg Pro Arg Leu Lys Met Tyr Ile Gln Val Glu Pro Val Leu Asp His
                165                 170                 175

Leu Ile Phe Leu Ser Ala Glu Thr Lys Glu Gln Ile Leu Lys Lys Ile
            180                 185                 190

Asn Thr Cys Gly Asn Thr Ser Ala Ala Glu Leu Leu Leu Ser Thr Leu
        195                 200                 205

Glu Gln Gly Gln Trp Pro Leu Gly Trp Thr Gln Met Phe Val Glu Ala
    210                 215                 220

Leu Glu His Ser Gly Asn Pro Leu Ala Ala Arg Tyr Val Lys Pro Thr
225                 230                 235                 240

Leu Thr Asp Leu Pro Ser Pro Ser Ser Glu Thr Ala His Asp Glu Cys
                245                 250                 255

Leu His Leu Leu Thr Leu Leu Gln Pro Thr Leu Val Asp Lys Leu Leu
            260                 265                 270

Ile Asn Asp Val Leu Asp Thr Cys Phe Glu Lys Gly Leu Leu Thr Val
        275                 280                 285
```

```
Glu Asp Arg Asn Arg Ile Ser Ala Ala Gly Asn Ser Gly Asn Glu Ser
    290                 295                 300

Gly Val Arg Glu Leu Leu Arg Arg Ile Val Gln Lys Glu Asn Trp Phe
305                 310                 315                 320

Ser Thr Phe Leu Asp Val Leu Arg Gln Thr Gly Asn
                325                 330
```

<210> 45
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Y. enterocolitica codon optimized murine MDA5 two CARD domains (extended: Aa 1-315)

<400> 45

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
```

```
            100                 105                 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Ser
    130                 135                 140

Ile Val Cys Ser Ala Glu Asp Ser Phe Arg Asn Leu Ile Leu Phe Phe
145                 150                 155                 160

Arg Pro Arg Leu Lys Met Tyr Ile Gln Val Glu Pro Val Leu Asp His
                165                 170                 175

Leu Ile Phe Leu Ser Ala Glu Thr Lys Glu Gln Ile Leu Lys Lys Ile
            180                 185                 190

Asn Thr Cys Gly Asn Thr Ser Ala Ala Glu Leu Leu Leu Ser Thr Leu
        195                 200                 205

Glu Gln Gly Gln Trp Pro Leu Gly Trp Thr Gln Met Phe Val Glu Ala
    210                 215                 220

Leu Glu His Ser Gly Asn Pro Leu Ala Ala Arg Tyr Val Lys Pro Thr
225                 230                 235                 240

Leu Thr Asp Leu Pro Ser Pro Ser Ser Glu Thr Ala His Asp Glu Cys
                245                 250                 255

Leu His Leu Leu Thr Leu Leu Gln Pro Thr Leu Val Asp Lys Leu Leu
            260                 265                 270

Ile Asn Asp Val Leu Asp Thr Cys Phe Glu Lys Gly Leu Leu Thr Val
        275                 280                 285

Glu Asp Arg Asn Arg Ile Ser Ala Ala Gly Asn Ser Gly Asn Glu Ser
    290                 295                 300
```

```
Gly Val Arg Glu Leu Leu Arg Arg Ile Val Gln Lys Glu Asn Trp Phe
305                 310                 315                 320


Ser Thr Phe Leu Asp Val Leu Arg Gln Thr Gly Asn Asp Ala Leu Phe
                325                 330                 335


Gln Glu Leu Thr Gly Gly Gly Cys Pro Glu Asp Asn Thr Asp Leu Ala
            340                 345                 350


Asn Ser Ser His Arg Asp Gly Pro Ala Ala Asn Glu Cys Leu Leu Pro
        355                 360                 365


Ala Val Asp Glu Ser Ser Leu Glu Thr Glu Ala Trp Asn Val Asp Asp
    370                 375                 380


Ile Leu Pro Glu Ala Ser Cys Thr Asp Ser Ser Val Thr Thr Glu Ser
385                 390                 395                 400


Asp Thr Ser Leu Ala Glu Gly Ser Val Ser Cys Phe Asp Glu Ser Leu
                405                 410                 415


Gly His Asn Ser Asn Met Gly Arg Asp Ser Gly Thr Met Gly Ser Asp
            420                 425                 430


Ser Asp Glu Ser Val Ile Gln Thr Lys Arg Val Ser Pro Glu Pro Glu
        435                 440                 445


Leu Gln Leu Arg Pro Tyr Gln Met Glu
    450                 455


<210>  46
<211>  332
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YopE1-138 - Y. enterocolitica codon optimized human MDA5 two CARD
       domains (minimal: Aa 1-190)
```

<400> 46

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Ser
    130                 135                 140

Asn Gly Tyr Ser Thr Asp Glu Asn Phe Arg Tyr Leu Ile Ser Cys Phe
145                 150                 155                 160

Arg Ala Arg Val Lys Met Tyr Ile Gln Val Glu Pro Val Leu Asp Tyr
                165                 170                 175

Leu Thr Phe Leu Pro Ala Glu Val Lys Glu Gln Ile Gln Arg Thr Val
            180                 185                 190
```

```
Ala Thr Ser Gly Asn Met Gln Ala Val Glu Leu Leu Leu Ser Thr Leu
        195                 200                 205

Glu Lys Gly Val Trp His Leu Gly Trp Thr Arg Glu Phe Val Glu Ala
    210                 215                 220

Leu Arg Arg Thr Gly Ser Pro Leu Ala Ala Arg Tyr Met Asn Pro Glu
225                 230                 235                 240

Leu Thr Asp Leu Pro Ser Pro Ser Phe Glu Asn Ala His Asp Glu Tyr
                245                 250                 255

Leu Gln Leu Leu Asn Leu Leu Gln Pro Thr Leu Val Asp Lys Leu Leu
            260                 265                 270

Val Arg Asp Val Leu Asp Lys Cys Met Glu Glu Glu Leu Leu Thr Ile
        275                 280                 285

Glu Asp Arg Asn Arg Ile Ala Ala Ala Glu Asn Asn Gly Asn Glu Ser
    290                 295                 300

Gly Val Arg Glu Leu Leu Lys Arg Ile Val Gln Lys Glu Asn Trp Phe
305                 310                 315                 320

Ser Ala Phe Leu Asn Val Leu Arg Gln Thr Gly Asn
                325                 330
```

<210> 47
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Y. enterocolitica codon optimized human MDA5 two CARD domains (extended: Aa 1-314)

<400> 47

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15
```

```
Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Ser
    130                 135                 140

Asn Gly Tyr Ser Thr Asp Glu Asn Phe Arg Tyr Leu Ile Ser Cys Phe
145                 150                 155                 160

Arg Ala Arg Val Lys Met Tyr Ile Gln Val Glu Pro Val Leu Asp Tyr
                165                 170                 175

Leu Thr Phe Leu Pro Ala Glu Val Lys Glu Gln Ile Gln Arg Thr Val
            180                 185                 190

Ala Thr Ser Gly Asn Met Gln Ala Val Glu Leu Leu Leu Ser Thr Leu
        195                 200                 205

Glu Lys Gly Val Trp His Leu Gly Trp Thr Arg Glu Phe Val Glu Ala
```

```
    210                 215                 220

Leu Arg Arg Thr Gly Ser Pro Leu Ala Ala Arg Tyr Met Asn Pro Glu
225                 230                 235                 240

Leu Thr Asp Leu Pro Ser Pro Ser Phe Glu Asn Ala His Asp Glu Tyr
                245                 250                 255

Leu Gln Leu Leu Asn Leu Leu Gln Pro Thr Leu Val Asp Lys Leu Leu
            260                 265                 270

Val Arg Asp Val Leu Asp Lys Cys Met Glu Glu Glu Leu Leu Thr Ile
        275                 280                 285

Glu Asp Arg Asn Arg Ile Ala Ala Ala Glu Asn Asn Gly Asn Glu Ser
    290                 295                 300

Gly Val Arg Glu Leu Leu Lys Arg Ile Val Gln Lys Glu Asn Trp Phe
305                 310                 315                 320

Ser Ala Phe Leu Asn Val Leu Arg Gln Thr Gly Asn Asn Glu Leu Val
                325                 330                 335

Gln Glu Leu Thr Gly Ser Asp Cys Ser Glu Ser Asn Ala Glu Ile Glu
            340                 345                 350

Asn Leu Ser Gln Val Asp Gly Pro Gln Val Glu Glu Gln Leu Leu Ser
        355                 360                 365

Thr Thr Val Gln Pro Asn Leu Glu Lys Glu Val Trp Gly Met Glu Asn
    370                 375                 380

Asn Ser Ser Glu Ser Ser Phe Ala Asp Ser Ser Val Val Ser Glu Ser
385                 390                 395                 400

Asp Thr Ser Leu Ala Glu Gly Ser Val Ser Cys Leu Asp Glu Ser Leu
                405                 410                 415
```

```
Gly His Asn Ser Asn Met Gly Ser Asp Ser Gly Thr Met Gly Ser Asp
            420                 425                 430


Ser Asp Glu Glu Asn Val Ala Ala Arg Ala Ser Pro Glu Pro Glu Leu
        435                 440                 445


Gln Leu Arg Pro Tyr Gln Met Glu
    450                 455


<210>  48
<211>  219
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YopE1-138 - Y. enterocolitica codon optimized human MAVS CARD
       domain (minimal: Aa 1-77)

<400>  48

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30


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


Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60


Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80


Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95


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

```
Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125


Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Pro
    130                 135                 140


Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe Ser Asn
145                 150                 155                 160


Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro Cys Leu
                165                 170                 175


Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu Ser Gly
            180                 185                 190


Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg Arg Pro
        195                 200                 205


Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg
    210                 215


<210>  49
<211>  142
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YopE1-138 - Y. enterocolitica codon optimized murine MAVS CARD
       domain (minimal: Aa 1-77)

<400>  49

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30


Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
```

```
        35                  40                  45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg
    130                 135                 140
```

<210> 50
<211> 1675
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutator sequence for generation of YopE1-138 - Y. enterocolitica codon optimized murine RIG-1 two CARD domains (Aa. 1-246) integrated on the pYV plasmid

<400> 50

```
gaatagacag cgaaagttgt tgaaataatt gagtgatagc ttgttcaaat gaatacattt       60

gatctcctaa tagttagata aaatatcaac ttaaccaaag cactctcggc agaccatcaa      120

ttttagccta taatttttag tttttatttt gtctaatata acaacaaaaa cagcagcggt      180

tttttatata accaccggct attttcccac taagataacc ttgttttaat agccaaggga      240

ataaatagtc atgaaaatat catcatttat ttctacatca ctgcccctgc cggcatcagt      300

gtcaggatct agcagcgtag gagaaatgtc tgggcgctca gtctcacagc aaaaaagtga      360
```

tcaatatgca aacaatctgg ccgggcgcac tgaaagccct cagggttcca gcttagccag 420

ccgtatcatt gagaggttat catcaatggc ccactctgtg attggattta tccaacgcat 480

gttctcggag gggagccata aaccggtggt gacaccagca ctcacgcctg cacaaatgcc 540

aagccctacg tctttcagtg atagtatcaa gcaacttgct gctgagacgc tgccaaaata 600

catgcagcag ttgagtagct tggatgcaga gacgctgcag aaaaatcatg accagttcgc 660

cacgctcgag tctagaatga ccgccgaaca acgccaaaat ctgcaagcct ttcgcgatta 720

tattaaaaaa attctggatc cgacctatat tctgagctat atgagcagct ggctggaaga 780

tgaagaagtg caatatattc aagccgaaaa aaataataaa ggtccgatgg aagccgccag 840

cctgtttctg caatatctgc tgaaactgca aagcgaaggt tggtttcaag cctttctgga 900

tgccctgtat catgccggtt attgtggtct gtgtgaagcc attgaaagct gggattttca 960

aaaaattgaa aaactggaag aacatcgcct gctgctgcgc cgcctggaac cggaatttaa 1020

agccaccgtg gatccgaatg atattctgag cgaactgagc gaatgtctga ttaatcaaga 1080

atgtgaagaa attcgccaaa ttcgcgatac caaaggtcgc atggccggtg ccgaaaaaat 1140

ggccgaatgt ctgattcgca gcgataaaga aaattggccg aaagtgctgc aactggccct 1200

ggaaaaagat aatagcaaat ttagcgaact gtggattgtg gataaaggtt ttaaacgcgc 1260

cgaaagcaaa gccgatgaag atgatggtgc cgaagccagc agcattcaaa tttttattca 1320

agaagaaccg gaatgtcaaa atctgagcca aaatccgggt ccgccgagcg aagccagcag 1380

caataatctg catagcccgc tgaaaccgcg caattaatat ggataaaaac aaggggggtag 1440

tgtttccccc tttttctatc aatattgcga atatcttcgt ccctgatctt tcaggggcga 1500

atcgtttttt agcatgctca ttgttagaat ttctgactta tctctcttct gtattactac 1560

tcatactctg gaaaatcctg agcatttata tctatggatt gatgcagcac tcgagaaatc 1620

aaaatatcat tgctaagcgt tatatagtat ataccgtgct ttttatactg aaaac 1675

<210> 51
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_285

<400> 51
cataccatgg gagtgagcaa gggcgag 27

<210> 52
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_286

<400> 52
ggaagatctt tacttgtaca gctcgtccat 30

<210> 53
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_287

<400> 53
cggggtacct caactaaatg accgtggtg 29

<210> 54
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_288

<400> 54
gttaaagctt ttcgaatcta gactcgagcg tggcgaactg gtc 43

<210> 55
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_387

<400> 55
cgtatctaga atggactgtg aggtcaacaa 30

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_391

<400> 56
cgtatctaga ggcaaccgca gca 23

<210> 57
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_389

<400> 57
gttaaagctt tcagtccatc ccatttctg 29

<210> 58
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_436

<400> 58
cgtatctaga atgccccgcc cc 22

<210> 59
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_437

<400> 59

gttaaagctt ctacccaccg tactcgtcaa t 31

<210> 60
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_438

<400> 60
cgtatctaga atgtctgaca cgtccagaga g 31

<210> 61
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_439

<400> 61
gttaaagctt tcatcttctt cgcaggaaaa ag 32

<210> 62
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_463

<400> 62
cagtctcgag gaaagcttgt ttaaggggc 29

<210> 63
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_464

<400> 63
cagtttcgaa ttagcgacgg cgacg 25

<210> 64
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_476

<400> 64
gttaaagctt ttacttgtac agctcgtcca t 31

<210> 65
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_494

<400> 65
cgtatctaga atggccgagc cttg 24

<210> 66
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_495

<400> 66
gttaaagctt ttattgaaga tttgtggctc c 31

<210> 67
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_504

<400> 67
cgtatctaga gaaaatctgt attttcaaag tgaaaatctg tattttcaaa gtatgccccg 60

cccc 64

<210> 68
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_505

<400> 68
gttaaagctt cccaccgtac tcgtcaattc 30

<210> 69
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_508

<400> 69
cgtatctaga gaaaatctgt attttcaaag tgaaaatctg tattttcaaa gtatggccga 60

gccttg 66

<210> 70
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_509

<400> 70
gttaaagctt ttgaagattt gtggctccc 29

<210> 71
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_511

<400> 71
cgtatctaga gaaaatctgt attttcaaag tgaaaatctg tattttcaaa gtgtgagcaa 60

gggcgag 67

<210> 72
<211> 91
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_512

<400> 72
cgtatctaga gaaaatctgt attttcaaag tgaaaatctg tattttcaaa gtccgccgaa 60

aaaaaaacgt aaagttgtga gcaagggcga g 91

<210> 73
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_513

<400> 73
gttaaagctt ttaaacttta cgttttttt tcggcggctt gtacagctcg tccat 55

<210> 74
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_515

<400> 74
cgtatctaga gaaaatctgt attttcaaag tgaaaatctg tattttcaaa gtgattataa 60

agatgatgat gataaaatgg ccgagccttg 90

<210> 75
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_677

<400> 75
ttactattcg aagaaattat tcataatatt gcccgccatc tggcccaaat tggtgatgaa 60

atggatcatt aagcttggag ta 82

<210> 76
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_678

<400> 76
tactccaagc ttaatgatcc atttcatcac caatttgggc cagatggcgg gcaatattat 60

gaataatttc ttcgaatagt aa 82

<210> 77
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_682

<400> 77
ttactactcg agaaaaaact gagcgaatgt ctgcgccgca ttggtgatga actggatagc 60

taagcttgga gta 73

<210> 78
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_683

<400> 78
tactccaagc ttagctatcc agttcatcac caatgcggcg cagacattcg ctcagttttt 60

tctcgagtag taa 73

<210> 79

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

<220>
<223> Primer No. : Si_580

<400> 79
catgccatgg atttatggtc atagatatga cctc 34

<210> 80
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_612

<400> 80
cggggtacca tgaggtagct tatttcctga taaag 35

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

<220>
<223> Primer No. : Si_613

<400> 81
cggggtacca taattgtcca aatagttatg gtagc 35

<210> 82
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_614

<400> 82
catgccatgg cggcaaggct cctc 24

<210> 83
<211> 29
<212> DNA

<213> Artificial Sequence

<220>
<223> Primer No. : Si_615

<400> 83
cggggtacct ttatttgtca acactgccc 29

<210> 84
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_616

<400> 84
cggggtacct gcggggtctt tactcg 26

<210> 85
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_585

<400> 85
cagtctcgag atgcagatct tcgtcaagac 30

<210> 86
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_586

<400> 86
gttaaagctt gctagcttcg aaaccaccac gtagacgtaa gac 43

<210> 87
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_588

<400> 87
cagtttcgaa gattataaag atgatgatga taaaatggcc gagccttg 48

<210> 88
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 733

<400> 88
ttactactcg agggtgccat cgatgccgaa gaaattattc ataatattgc ccg 53

<210> 89
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 735

<400> 89
tactccttcg aattaatgat ccatttcatc accaatttg 39

<210> 90
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 736

<400> 90
ttactactcg agggtgccat cgatgccaaa aaactgagcg aatgtctgcg 50

<210> 91
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 738

<400> 91
tactccttcg aattagctat ccagttcatc accaatg 37

<210> 92
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 734

<400> 92
tactccttcg aaggcaccat gatccatttc atcaccaatt tgg 43

<210> 93
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 725

<400> 93
ttactattcg aagaaattat tcataatatt gcc 33

<210> 94
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 726

<400> 94
tactccaagc ttacggttga atattatgat ccatttcatc accaatttgg 50

<210> 95
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 727

<400> 95

ttactattcg aagccggtgg tgccgaagaa attattcata atattgccc 49

<210> 96
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 728

<400> 96
tactccaagc ttaatgatcc atttcatca 29

<210> 97
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 737

<400> 97
tactccttcg aaggcaccgc tatccagttc atcaccaatg 40

<210> 98
<211> 394
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 2xTEVsite - EGFP

<400> 98

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser

```
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Glu Asn
    130                 135                 140

Leu Tyr Phe Gln Ser Glu Asn Leu Tyr Phe Gln Ser Val Ser Lys Gly
145                 150                 155                 160

Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly
                165                 170                 175

Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
            180                 185                 190

Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
        195                 200                 205

Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val
    210                 215                 220

Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe
225                 230                 235                 240

Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
                245                 250                 255
```

```
Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly
            260                 265                 270

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
        275                 280                 285

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
    290                 295                 300

Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
305                 310                 315                 320

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
                325                 330                 335

His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
            340                 345                 350

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
        355                 360                 365

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
    370                 375                 380

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
385                 390


<210>  99
<211>  401
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YopE1-138 - 2xTEVsite - NLS - EGFP

<400>  99

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15
```

```
Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Glu Asn
    130                 135                 140

Leu Tyr Phe Gln Ser Val Ser Lys Gly Gln Ser Pro Pro Lys Lys Lys
145                 150                 155                 160

Arg Lys Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
                165                 170                 175

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
            180                 185                 190

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

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
```

```
    210                 215                 220

Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
225                 230                 235                 240

Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
                245                 250                 255

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
            260                 265                 270

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
        275                 280                 285

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
    290                 295                 300

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
305                 310                 315                 320

Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                325                 330                 335

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
            340                 345                 350

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
        355                 360                 365

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
    370                 375                 380

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
385                 390                 395                 400

Lys
```

<210> 100
<211> 402
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - 2xTEVsite - EGFP - NLS

<400> 100

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30


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


Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60


Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80


Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95


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


Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125


Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Glu Asn
    130                 135                 140


Leu Tyr Phe Gln Ser Glu Asn Leu Tyr Phe Gln Ser Val Ser Lys Gly
145                 150                 155                 160
```

```
Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly
                165                 170                 175

Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
            180                 185                 190

Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
        195                 200                 205

Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val
    210                 215                 220

Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe
225                 230                 235                 240

Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
                245                 250                 255

Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly
            260                 265                 270

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
        275                 280                 285

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
    290                 295                 300

Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
305                 310                 315                 320

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
                325                 330                 335

His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
            340                 345                 350

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
```

355 360 365

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
370 375 380

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Pro Pro Lys Lys Lys Arg
385 390 395 400

Lys Val

<210> 101
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 869

<400> 101
gatcgtcgac ttaagttcaa tggagcgttt aatatc 36

<210> 102
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 870

<400> 102
ctttgactgg cgagaaacgc tcttaacatg aggctgagct c 41

<210> 103
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 871

<400> 103
gagctcagcc tcatgttaag agcgtttctc gccagtcaaa g 41

<210> 104
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 872

<400> 104
gatagccccc gagcctgtgc actttgtcat taacctcagc 40

<210> 105
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 873

<400> 105
gctgaggtta atgacaaagt gcacaggctc gggggctatc 40

<210> 106
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 874

<400> 106
catgtctaga ccctcagcat aataacgact c 31

<210> 107
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 600

<400> 107
catgacatgt tggcgtttct cgcc 24

<210> 108

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

<220>
<223> primer No. 601

<400> 108
catgacatgt attaacctca gccctgacta taag 34

<210> 109
<211> 138
<212> DNA
<213> Artificial Sequence

<220>
<223> Multiple cloning site of pBad_Si_1 and pBad_Si_2

<400> 109
gttcgccacg ctcgagtcta gattcgaaaa gcttgggccc gaacaaaaac tcatctcaga 60

agaggatctg aatagcgccg tcgaccatca tcatcatcat cattgagttt aaacggtctc 120

cagcttggct gttttggc 138

<210> 110
<211> 371
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Y. enterocolitica codon optimized murine RIG1 CARD domains (Aa. 1-229)

<400> 110

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

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

```
Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Thr
    130                 135                 140

Ala Glu Gln Arg Gln Asn Leu Gln Ala Phe Arg Asp Tyr Ile Lys Lys
145                 150                 155                 160

Ile Leu Asp Pro Thr Tyr Ile Leu Ser Tyr Met Ser Ser Trp Leu Glu
                165                 170                 175

Asp Glu Glu Val Gln Tyr Ile Gln Ala Glu Lys Asn Asn Lys Gly Pro
            180                 185                 190

Met Glu Ala Ala Ser Leu Phe Leu Gln Tyr Leu Leu Lys Leu Gln Ser
        195                 200                 205

Glu Gly Trp Phe Gln Ala Phe Leu Asp Ala Leu Tyr His Ala Gly Tyr
    210                 215                 220

Cys Gly Leu Cys Glu Ala Ile Glu Ser Trp Asp Phe Gln Lys Ile Glu
225                 230                 235                 240

Lys Leu Glu Glu His Arg Leu Leu Leu Arg Arg Leu Glu Pro Glu Phe
                245                 250                 255
```

```
Lys Ala Thr Val Asp Pro Asn Asp Ile Leu Ser Glu Leu Ser Glu Cys
            260                 265                 270


Leu Ile Asn Gln Glu Cys Glu Glu Ile Arg Gln Ile Arg Asp Thr Lys
        275                 280                 285


Gly Arg Met Ala Gly Ala Glu Lys Met Ala Glu Cys Leu Ile Arg Ser
    290                 295                 300


Asp Lys Glu Asn Trp Pro Lys Val Leu Gln Leu Ala Leu Glu Lys Asp
305                 310                 315                 320


Asn Ser Lys Phe Ser Glu Leu Trp Ile Val Asp Lys Gly Phe Lys Arg
                325                 330                 335


Ala Glu Ser Lys Ala Asp Glu Asp Asp Gly Ala Glu Ala Ser Ser Ile
            340                 345                 350


Gln Ile Phe Ile Gln Glu Glu Pro Glu Cys Gln Asn Leu Ser Gln Asn
        355                 360                 365


Pro Gly Pro
    370
```

<210> 111
<211> 360
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Y. enterocolitica codon optimized murine RIG1 CARD domains (Aa. 1-218)

<400> 111

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
```

```
            20                  25                  30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Thr
    130                 135                 140

Ala Glu Gln Arg Gln Asn Leu Gln Ala Phe Arg Asp Tyr Ile Lys Lys
145                 150                 155                 160

Ile Leu Asp Pro Thr Tyr Ile Leu Ser Tyr Met Ser Ser Trp Leu Glu
                165                 170                 175

Asp Glu Glu Val Gln Tyr Ile Gln Ala Glu Lys Asn Asn Lys Gly Pro
            180                 185                 190

Met Glu Ala Ala Ser Leu Phe Leu Gln Tyr Leu Leu Lys Leu Gln Ser
        195                 200                 205

Glu Gly Trp Phe Gln Ala Phe Leu Asp Ala Leu Tyr His Ala Gly Tyr
    210                 215                 220
```

```
Cys Gly Leu Cys Glu Ala Ile Glu Ser Trp Asp Phe Gln Lys Ile Glu
225                 230                 235                 240


Lys Leu Glu Glu His Arg Leu Leu Leu Arg Arg Leu Glu Pro Glu Phe
                245                 250                 255


Lys Ala Thr Val Asp Pro Asn Asp Ile Leu Ser Glu Leu Ser Glu Cys
            260                 265                 270


Leu Ile Asn Gln Glu Cys Glu Glu Ile Arg Gln Ile Arg Asp Thr Lys
        275                 280                 285


Gly Arg Met Ala Gly Ala Glu Lys Met Ala Glu Cys Leu Ile Arg Ser
    290                 295                 300


Asp Lys Glu Asn Trp Pro Lys Val Leu Gln Leu Ala Leu Glu Lys Asp
305                 310                 315                 320


Asn Ser Lys Phe Ser Glu Leu Trp Ile Val Asp Lys Gly Phe Lys Arg
                325                 330                 335


Ala Glu Ser Lys Ala Asp Glu Asp Asp Gly Ala Glu Ala Ser Ser Ile
            340                 345                 350


Gln Ile Phe Ile Gln Glu Glu Pro
        355                 360
```

<210> 112
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Y. enterocolitica codon optimized murine MDA5 (Aa. 1-294)

<400> 112

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15
```

```
Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Ser
    130                 135                 140

Ile Val Cys Ser Ala Glu Asp Ser Phe Arg Asn Leu Ile Leu Phe Phe
145                 150                 155                 160

Arg Pro Arg Leu Lys Met Tyr Ile Gln Val Glu Pro Val Leu Asp His
                165                 170                 175

Leu Ile Phe Leu Ser Ala Glu Thr Lys Glu Gln Ile Leu Lys Lys Ile
            180                 185                 190

Asn Thr Cys Gly Asn Thr Ser Ala Ala Glu Leu Leu Leu Ser Thr Leu
        195                 200                 205
```

```
Glu Gln Gly Gln Trp Pro Leu Gly Trp Thr Gln Met Phe Val Glu Ala
    210                 215                 220

Leu Glu His Ser Gly Asn Pro Leu Ala Ala Arg Tyr Val Lys Pro Thr
225                 230                 235                 240

Leu Thr Asp Leu Pro Ser Pro Ser Ser Glu Thr Ala His Asp Glu Cys
                245                 250                 255

Leu His Leu Leu Thr Leu Leu Gln Pro Thr Leu Val Asp Lys Leu Leu
            260                 265                 270

Ile Asn Asp Val Leu Asp Thr Cys Phe Glu Lys Gly Leu Leu Thr Val
        275                 280                 285

Glu Asp Arg Asn Arg Ile Ser Ala Ala Gly Asn Ser Gly Asn Glu Ser
    290                 295                 300

Gly Val Arg Glu Leu Leu Arg Arg Ile Val Gln Lys Glu Asn Trp Phe
305                 310                 315                 320

Ser Thr Phe Leu Asp Val Leu Arg Gln Thr Gly Asn Asp Ala Leu Phe
                325                 330                 335

Gln Glu Leu Thr Gly Gly Gly Cys Pro Glu Asp Asn Thr Asp Leu Ala
            340                 345                 350

Asn Ser Ser His Arg Asp Gly Pro Ala Ala Asn Glu Cys Leu Leu Pro
        355                 360                 365

Ala Val Asp Glu Ser Ser Leu Glu Thr Glu Ala Trp Asn Val Asp Asp
    370                 375                 380

Ile Leu Pro Glu Ala Ser Cys Thr Asp Ser Ser Val Thr Thr Glu Ser
385                 390                 395                 400

Asp Thr Ser Leu Ala Glu Gly Ser Val Ser Cys Phe Asp Glu Ser Leu
                405                 410                 415
```

Gly His Asn Ser Asn Met Gly Arg Asp Ser Gly Thr Met Gly Ser Asp
420 425 430

Ser Asp Glu Ser
435

<210> 113
<211> 373
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Y. enterocolitica codon optimized murine MDA5 (Aa. 1-231)

<400> 113

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr

```
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Ser
    130                 135                 140

Ile Val Cys Ser Ala Glu Asp Ser Phe Arg Asn Leu Ile Leu Phe Phe
145                 150                 155                 160

Arg Pro Arg Leu Lys Met Tyr Ile Gln Val Glu Pro Val Leu Asp His
                165                 170                 175

Leu Ile Phe Leu Ser Ala Glu Thr Lys Glu Gln Ile Leu Lys Lys Ile
            180                 185                 190

Asn Thr Cys Gly Asn Thr Ser Ala Ala Glu Leu Leu Leu Ser Thr Leu
        195                 200                 205

Glu Gln Gly Gln Trp Pro Leu Gly Trp Thr Gln Met Phe Val Glu Ala
    210                 215                 220

Leu Glu His Ser Gly Asn Pro Leu Ala Ala Arg Tyr Val Lys Pro Thr
225                 230                 235                 240

Leu Thr Asp Leu Pro Ser Pro Ser Ser Glu Thr Ala His Asp Glu Cys
                245                 250                 255

Leu His Leu Leu Thr Leu Leu Gln Pro Thr Leu Val Asp Lys Leu Leu
            260                 265                 270

Ile Asn Asp Val Leu Asp Thr Cys Phe Glu Lys Gly Leu Leu Thr Val
        275                 280                 285

Glu Asp Arg Asn Arg Ile Ser Ala Ala Gly Asn Ser Gly Asn Glu Ser
    290                 295                 300

Gly Val Arg Glu Leu Leu Arg Arg Ile Val Gln Lys Glu Asn Trp Phe
305                 310                 315                 320
```

Ser Thr Phe Leu Asp Val Leu Arg Gln Thr Gly Asn Asp Ala Leu Phe
325 330 335

Gln Glu Leu Thr Gly Gly Gly Cys Pro Glu Asp Asn Thr Asp Leu Ala
340 345 350

Asn Ser Ser His Arg Asp Gly Pro Ala Ala Asn Glu Cys Leu Leu Pro
355 360 365

Ala Val Asp Glu Ser
370

<210> 114
<211> 349
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138- Y. enterocolitica codon optimized B. subtilis CdaS L44F constitutive active version

<400> 114

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Lys
    130                 135                 140

Ala Met Arg Tyr Glu Gln Ile Ser Glu Asn Ala Phe Lys Gly Lys Ile
145                 150                 155                 160

Gln Val Tyr Leu Glu Gln Ile Leu Gly Asp Ala Ser Leu Ile Leu Lys
                165                 170                 175

Thr Leu His Glu Lys Asp Gln Cys Leu Phe Cys Glu Leu Asp Asp Leu
            180                 185                 190

Gly His Val Phe Gln Asp Met Gln Gly Ile Ala Ser Ser Phe Tyr Leu
        195                 200                 205

Gln Ser Tyr Ile Glu Glu Phe Thr Pro Ala Phe Ile Glu Leu Ala Lys
    210                 215                 220

Ala Ile Lys Ala Leu Ser Glu His Lys His Gly Ala Leu Ile Val Ile
225                 230                 235                 240

Glu Arg Ala Asp Pro Val Glu Arg Phe Ile Gln Lys Gly Thr Ser Leu
                245                 250                 255

His Ala Glu Ile Ser Ser Ser Leu Ile Glu Ser Ile Phe Phe Pro Gly
            260                 265                 270

Asn Pro Leu His Asp Gly Ala Leu Leu Val Arg Glu Asn Lys Leu Val
        275                 280                 285
```

Ser Ala Ala Asn Val Leu Pro Leu Thr Thr Lys Glu Val Asp Ile His
290 295 300

Leu Gly Thr Arg His Arg Ala Ala Leu Gly Met Ser Gly Tyr Thr Asp
305 310 315 320

Ala Leu Val Leu Val Val Ser Glu Glu Thr Gly Lys Met Ser Phe Ala
325 330 335

Lys Asp Gly Val Leu Tyr Pro Leu Ile Ser Pro Arg Thr
340 345

<210> 115
<211> 504
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138- Y. enterocolitica codon optimized human cGAS (Aa. 161-522)

<400> 115

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Gly Ala
    130                 135                 140

Ser Lys Leu Arg Ala Val Leu Glu Lys Leu Lys Leu Ser Arg Asp Asp
145                 150                 155                 160

Ile Ser Thr Ala Ala Gly Met Val Lys Gly Val Val Asp His Leu Leu
                165                 170                 175

Leu Arg Leu Lys Cys Asp Ser Ala Phe Arg Gly Val Gly Leu Leu Asn
            180                 185                 190

Thr Gly Ser Tyr Tyr Glu His Val Lys Ile Ser Ala Pro Asn Glu Phe
        195                 200                 205

Asp Val Met Phe Lys Leu Glu Val Pro Arg Ile Gln Leu Glu Glu Tyr
    210                 215                 220

Ser Asn Thr Arg Ala Tyr Tyr Phe Val Lys Phe Lys Arg Asn Pro Lys
225                 230                 235                 240

Glu Asn Pro Leu Ser Gln Phe Leu Glu Gly Glu Ile Leu Ser Ala Ser
                245                 250                 255

Lys Met Leu Ser Lys Phe Arg Lys Ile Ile Lys Glu Glu Ile Asn Asp
            260                 265                 270

Ile Lys Asp Thr Asp Val Ile Met Lys Arg Lys Arg Gly Gly Ser Pro
        275                 280                 285

Ala Val Thr Leu Leu Ile Ser Glu Lys Ile Ser Val Asp Ile Thr Leu
```

```
    290                 295                 300

Ala Leu Glu Ser Lys Ser Ser Trp Pro Ala Ser Thr Gln Glu Gly Leu
305                 310                 315                 320

Arg Ile Gln Asn Trp Leu Ser Ala Lys Val Arg Lys Gln Leu Arg Leu
                325                 330                 335

Lys Pro Phe Tyr Leu Val Pro Lys His Ala Lys Glu Gly Asn Gly Phe
            340                 345                 350

Gln Glu Glu Thr Trp Arg Leu Ser Phe Ser His Ile Glu Lys Glu Ile
        355                 360                 365

Leu Asn Asn His Gly Lys Ser Lys Thr Cys Cys Glu Asn Lys Glu Glu
    370                 375                 380

Lys Cys Cys Arg Lys Asp Cys Leu Lys Leu Met Lys Tyr Leu Leu Glu
385                 390                 395                 400

Gln Leu Lys Glu Arg Phe Lys Asp Lys Lys His Leu Asp Lys Phe Ser
                405                 410                 415

Ser Tyr His Val Lys Thr Ala Phe Phe His Val Cys Thr Gln Asn Pro
            420                 425                 430

Gln Asp Ser Gln Trp Asp Arg Lys Asp Leu Gly Leu Cys Phe Asp Asn
        435                 440                 445

Cys Val Thr Tyr Phe Leu Gln Cys Leu Arg Thr Glu Lys Leu Glu Asn
    450                 455                 460

Tyr Phe Ile Pro Glu Phe Asn Leu Phe Ser Ser Asn Leu Ile Asp Lys
465                 470                 475                 480

Arg Ser Lys Glu Phe Leu Thr Lys Gln Ile Glu Tyr Glu Arg Asn Asn
                485                 490                 495
```

Glu Phe Pro Val Phe Asp Glu Phe
            500

<210> 116
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138- Y. enterocolitica codon optimized human MAVS CARD (Aa.
       1-100)

<400> 116

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1   5   10   15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20   25   30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50   55   60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65   70   75   80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85   90   95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115   120   125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Pro
    130   135   140

```
Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe Ser Asn
145                 150                 155                 160


Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro Cys Leu
                165                 170                 175


Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu Ser Gly
            180                 185                 190


Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg Arg Pro
        195                 200                 205


Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu Leu Val
    210                 215                 220


Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Glu Ser Tyr Gln Pro Arg
225                 230                 235                 240


Thr Ser
```

<210> 117
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138- Y. enterocolitica codon optimized Anemonae (N. vectensis) cGAS (Aa. 60-422) (Ensembl: A7SFB5.1)

<400> 117

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30


Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
```

```
        35                  40                  45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Gln Pro
    130                 135                 140

Phe Pro Lys Gly Asp Leu Glu Thr Leu Arg Arg Phe Ser Val Thr Asp
145                 150                 155                 160

Val Lys Ile Ser Lys Gln Ser Thr Lys Trp Ala Lys Lys Met Ala Asp
                165                 170                 175

Lys His Leu Glu Ile Ile Arg Lys His Cys Lys Thr Asn Ser Ile Lys
            180                 185                 190

Leu Phe Asn His Phe Glu Tyr Thr Gly Ser Phe Tyr Glu His Leu Lys
        195                 200                 205

Thr Ile Asp Ala Asp Glu Leu Asp Ile Met Val Ala Leu Ser Ile Lys
    210                 215                 220

Met Asp Glu Leu Glu Val Glu Gln Val Thr Pro Gly Tyr Ala Gly Leu
225                 230                 235                 240
```

```
Lys Leu Arg Asp Thr Pro Ser Asn Arg Asn Lys Tyr Asn Asp Leu Thr
                245                 250                 255

Ile Ala Asp Asn Tyr Gly Arg Tyr Leu Ser Pro Glu Lys Val Ser Arg
            260                 265                 270

Trp Phe Phe Ser Leu Val Gln Lys Ala Val Asn Thr Tyr Lys Asp Glu
        275                 280                 285

Ile Pro Gln Thr Glu Val Lys Leu Thr Asp Asn Gly Pro Ala Thr Thr
    290                 295                 300

Leu Val Ile Thr Tyr Arg Glu Gly Asp Lys Pro Gln Glu Lys Asn Arg
305                 310                 315                 320

Arg Leu Ser Ile Asp Leu Val Pro Ala Leu Leu Phe Lys Asp Lys Thr
                325                 330                 335

Lys Pro Ala Gly Asp Asp Leu Arg Ala Trp His Tyr Val Ala Lys Thr
            340                 345                 350

Ile Pro Lys Gly Ala Arg Leu Lys Glu Pro Leu Pro Phe Arg Ser Glu
        355                 360                 365

Leu Leu Trp Arg Gln Ser Phe Ser Leu Lys Glu Lys His Leu Met Asp
    370                 375                 380

Lys Leu Asp Lys Asp Asp Asn Gly Cys Arg Arg Glu Met Val Arg Ile
385                 390                 395                 400

Val Lys Thr Ile Val Lys Lys Asp Pro Thr Leu Ala Gln Leu Ser Ser
                405                 410                 415

Tyr His Ile Lys Thr Ala Phe Leu Gln Tyr Asn Phe Ser Asp Val Lys
            420                 425                 430

Leu Asp Trp Glu Gly Lys Lys Leu Ala Glu Arg Phe Leu His Phe Leu
```

```
        435                 440                 445

Glu Phe Leu Arg Asp Arg Val Lys Asp Lys Thr Leu Asn Asn Tyr Phe
    450                 455                 460

Ile Thr Asp Leu Asn Leu Leu Asp Asp Leu Asn Asp Ser Asn Ile Asp
465                 470                 475                 480

Asn Ile Ala Asn Arg Leu Asp Lys Ile Ile Gln Asn Glu Thr Glu Arg
                485                 490                 495

Ala Lys Ile Phe Thr Thr Gln Arg Gln
            500                 505
```

<210> 118
<211> 315
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138- Y. enterocolitica codon optimized Listeria CdaA (Aa. 101-273)

<400> 118

```
Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80
```

```
Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Tyr Gly
    130                 135                 140

Ser Arg Ile Glu Arg Glu Gln His His Leu Ile Glu Ser Ile Glu Lys
145                 150                 155                 160

Ser Thr Gln Tyr Met Ala Lys Arg Arg Ile Gly Ala Leu Ile Ser Val
                165                 170                 175

Ala Arg Asp Thr Gly Met Asp Asp Tyr Ile Glu Thr Gly Ile Pro Leu
            180                 185                 190

Asn Ala Lys Ile Ser Ser Gln Leu Leu Ile Asn Ile Phe Ile Pro Asn
        195                 200                 205

Thr Pro Leu His Asp Gly Ala Val Ile Ile Lys Gly Asn Glu Ile Ala
    210                 215                 220

Ser Ala Ala Ser Tyr Leu Pro Leu Ser Asp Ser Pro Phe Leu Ser Lys
225                 230                 235                 240

Glu Leu Gly Thr Arg His Arg Ala Ala Leu Gly Ile Ser Glu Val Thr
                245                 250                 255

Asp Ser Ile Thr Ile Val Val Ser Glu Glu Thr Gly Gly Ile Ser Leu
            260                 265                 270

Thr Lys Gly Gly Glu Leu Phe Arg Asp Val Ser Glu Glu Glu Leu His
        275                 280                 285
```

Lys Ile Leu Leu Lys Glu Leu Val Thr Val Thr Ala Lys Lys Pro Ser
290 295 300

Ile Phe Ser Lys Trp Lys Gly Gly Lys Ser Glu
305 310 315

<210> 119
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 1010

<400> 119
cacatgtcta gacaaccgtt tccgaaaggt gatctg 36

<210> 120
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 1012

<400> 120
atcccaagct tattggcgtt gggtggtaaa aattttg 37

<210> 121
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 1021

<400> 121
cacatgtcta gaatgaccgc cgaacaacgc 30

<210> 122
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 1022

<400> 122
catgaagctt acggacccgg attttggctc 30

<210> 123
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 1023

<400> 123
catgaagctt acggttcttc ttgaataaaa atttgaatg 39

<210> 124
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 1024

<400> 124
catgaagctt attgcagcac tttcggccaa ttt 33

<210> 125
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 1025

<400> 125
cacatgtcta gaatgagcat tgtgtgtagc gc 32

<210> 126
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> primer No. 1026

<400> 126
catgaagctt agctttcatc cacggccgg 29

<210> 127
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 1027

<400> 127
catgaagctt aattaccggt ttggcgcagc 30

<210> 128
<211> 370
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Y. enterocolitica codon optimized human RIG1 CARD domains (Aa. 1-228)

<400> 128

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met

```
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Thr
    130                 135                 140

Thr Glu Gln Arg Arg Ser Leu Gln Ala Phe Gln Asp Tyr Ile Arg Lys
145                 150                 155                 160

Thr Leu Asp Pro Thr Tyr Ile Leu Ser Tyr Met Ala Pro Trp Phe Arg
                165                 170                 175

Glu Glu Glu Val Gln Tyr Ile Gln Ala Glu Lys Asn Asn Lys Gly Pro
            180                 185                 190

Met Glu Ala Ala Thr Leu Phe Leu Lys Phe Leu Leu Glu Leu Gln Glu
        195                 200                 205

Glu Gly Trp Phe Arg Gly Phe Leu Asp Ala Leu Asp His Ala Gly Tyr
    210                 215                 220

Ser Gly Leu Tyr Glu Ala Ile Glu Ser Trp Asp Phe Lys Lys Ile Glu
225                 230                 235                 240

Lys Leu Glu Glu Tyr Arg Leu Leu Leu Lys Arg Leu Gln Pro Glu Phe
                245                 250                 255

Lys Thr Arg Ile Ile Pro Thr Asp Ile Ile Ser Asp Leu Ser Glu Cys
            260                 265                 270

Leu Ile Asn Gln Glu Cys Glu Glu Ile Leu Gln Ile Cys Ser Thr Lys
        275                 280                 285
```

```
Gly Met Met Ala Gly Ala Glu Lys Leu Val Glu Cys Leu Leu Arg Ser
    290                 295                 300

Asp Lys Glu Asn Trp Pro Lys Thr Leu Lys Leu Ala Leu Glu Lys Glu
305                 310                 315                 320

Arg Asn Lys Phe Ser Glu Leu Trp Ile Val Glu Lys Gly Ile Lys Asp
                325                 330                 335

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

Ile Phe Tyr Gln Glu Asp Pro Glu Cys Gln Asn Leu Ser Glu Asn Ser
        355                 360                 365

Cys Pro
    370
```

<210> 129
<211> 358
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Y. enterocolitica codon optimized human RIG1 CARD domains (Aa. 1-217)

<400> 129

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

Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser Gln
            20                  25                  30

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

Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser Ser
    50                  55                  60
```

```
Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu Gly
65                  70                  75                  80

Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met Pro
                85                  90                  95

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

Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr Leu
        115                 120                 125

Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Thr Thr
    130                 135                 140

Glu Gln Arg Arg Ser Leu Gln Ala Phe Gln Asp Tyr Ile Arg Lys Thr
145                 150                 155                 160

Leu Asp Pro Thr Tyr Ile Leu Ser Tyr Met Ala Pro Trp Phe Arg Glu
                165                 170                 175

Glu Glu Val Gln Tyr Ile Gln Ala Glu Lys Asn Asn Lys Gly Pro Met
            180                 185                 190

Glu Ala Ala Thr Leu Phe Leu Lys Phe Leu Leu Glu Leu Gln Glu Glu
        195                 200                 205

Gly Trp Phe Arg Gly Phe Leu Asp Ala Leu Asp His Ala Gly Tyr Ser
    210                 215                 220

Gly Leu Tyr Glu Ala Ile Glu Ser Trp Asp Phe Lys Lys Ile Glu Lys
225                 230                 235                 240

Leu Glu Glu Tyr Arg Leu Leu Leu Lys Arg Leu Gln Pro Glu Phe Lys
                245                 250                 255
```

```
Thr Arg Ile Ile Pro Thr Asp Ile Ile Ser Asp Leu Ser Glu Cys Leu
            260                 265                 270


Ile Asn Gln Glu Cys Glu Glu Ile Leu Gln Ile Cys Ser Thr Lys Gly
        275                 280                 285


Met Met Ala Gly Ala Glu Lys Leu Val Glu Cys Leu Leu Arg Ser Asp
    290                 295                 300


Lys Glu Asn Trp Pro Lys Thr Leu Lys Leu Ala Leu Glu Lys Glu Arg
305                 310                 315                 320


Asn Lys Phe Ser Glu Leu Trp Ile Val Glu Lys Gly Ile Lys Asp Val
                325                 330                 335


Glu Thr Glu Asp Leu Glu Asp Lys Met Glu Thr Ser Asp Ile Gln Ile
            340                 345                 350


Phe Tyr Gln Glu Asp Pro
        355


<210>  130
<211>  243
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YopE1-138 - Y. enterocolitica codon optimized murine MAVS CARD
       domain (Aa. 1-101)

<400>  130

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1               5                   10                  15


Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
            20                  25                  30


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

```
Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
    50                  55                  60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65                  70                  75                  80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
                85                  90                  95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
        115                 120                 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Thr
    130                 135                 140

Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Arg Asp Asn His Ser Lys
145                 150                 155                 160

Phe Cys Cys Val Asp Val Leu Glu Ile Leu Pro Tyr Leu Ser Cys Leu
                165                 170                 175

Thr Ala Ser Asp Gln Asp Arg Leu Arg Ala Ser Tyr Arg Gln Ile Gly
            180                 185                 190

Asn Arg Asp Thr Leu Trp Gly Leu Phe Asn Asn Leu Gln Arg Arg Pro
        195                 200                 205

Gly Trp Val Glu Val Phe Ile Arg Ala Leu Gln Ile Cys Glu Leu Pro
    210                 215                 220

Gly Leu Ala Asp Gln Val Thr Arg Val Tyr Gln Ser Tyr Leu Pro Pro
225                 230                 235                 240

Gly Thr Ser
```

<210> 131
<211> 504
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138- Y. enterocolitica codon optimized murine cGAS (Aa. 146-507)

<400> 131

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

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

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

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

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Glu Pro
130 135 140

```
Asp Lys Leu Lys Lys Val Leu Asp Lys Leu Arg Leu Lys Arg Lys Asp
145                 150                 155                 160

Ile Ser Glu Ala Ala Glu Thr Val Asn Lys Val Val Glu Arg Leu Leu
                165                 170                 175

Arg Arg Met Gln Lys Arg Glu Ser Glu Phe Lys Gly Val Glu Gln Leu
            180                 185                 190

Asn Thr Gly Ser Tyr Tyr Glu His Val Lys Ile Ser Ala Pro Asn Glu
        195                 200                 205

Phe Asp Val Met Phe Lys Leu Glu Val Pro Arg Ile Glu Leu Gln Glu
    210                 215                 220

Tyr Tyr Glu Thr Gly Ala Phe Tyr Leu Val Lys Phe Lys Arg Ile Pro
225                 230                 235                 240

Arg Gly Asn Pro Leu Ser His Phe Leu Glu Gly Glu Val Leu Ser Ala
                245                 250                 255

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

Glu Ile Lys Asp Ile Asp Val Ser Val Glu Lys Glu Lys Pro Gly Ser
        275                 280                 285

Pro Ala Val Thr Leu Leu Ile Arg Asn Pro Glu Glu Ile Ser Val Asp
    290                 295                 300

Ile Ile Leu Ala Leu Glu Ser Lys Gly Ser Trp Pro Ile Ser Thr Lys
305                 310                 315                 320

Glu Gly Leu Pro Ile Gln Gly Trp Leu Gly Thr Lys Val Arg Thr Asn
                325                 330                 335

Leu Arg Arg Glu Pro Phe Tyr Leu Val Pro Lys Asn Ala Lys Asp Gly
            340                 345                 350
```

```
Asn Ser Phe Gln Gly Glu Thr Trp Arg Leu Ser Phe Ser His Thr Glu
        355                 360                 365

Lys Tyr Ile Leu Asn Asn His Gly Ile Glu Lys Thr Cys Cys Glu Ser
    370                 375                 380

Ser Gly Ala Lys Cys Cys Arg Lys Glu Cys Leu Lys Leu Met Lys Tyr
385                 390                 395                 400

Leu Leu Glu Gln Leu Lys Lys Glu Phe Gln Glu Leu Asp Ala Phe Cys
                405                 410                 415

Ser Tyr His Val Lys Thr Ala Ile Phe His Met Trp Thr Gln Asp Pro
            420                 425                 430

Gln Asp Ser Gln Trp Asp Pro Arg Asn Leu Ser Ser Cys Phe Asp Lys
        435                 440                 445

Leu Leu Ala Phe Phe Leu Glu Cys Leu Arg Thr Glu Lys Leu Asp His
    450                 455                 460

Tyr Phe Ile Pro Lys Phe Asn Leu Phe Ser Gln Glu Leu Ile Asp Arg
465                 470                 475                 480

Lys Ser Lys Glu Phe Leu Ser Lys Lys Ile Glu Tyr Glu Arg Asn Asn
                485                 490                 495

Gly Phe Pro Ile Phe Asp Lys Leu
            500
```