SEQUENCE LISTING

<110> Transgene SA

<120> Fusion of heterooligomeric mycobacterial antigens

<130> B366981 D34574

<150> EP 14305030.0
<151> 2014-01-09

<160> 33

<170> PatentIn version 3.5

<210> 1
<211> 208
<212> PRT
<213> artificial sequence

<220>
<223> fusion between CFP10 and its partner ESAT-6

<400> 1

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Met Ala Glu Met Lys Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly
1               5                  10                  15

Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val
            20                  25                  30

Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly
        35                  40                  45

Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys
    50                  55                  60

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

Val Gln Tyr Ser Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser
                85                  90                  95

Gln Met Gly Phe Gly Pro Lys Gln Gly Glu Asp Asp Gly Ser Thr Gly
            100                 105                 110

Gly Pro Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala
        115                 120                 125

Ser Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu
    130                 135                 140

Gly Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly
145                 150                 155                 160

Ser Glu Ala Tyr Gln Gly Val Gln Gln Lys Trp Asp Ala Thr Ala Thr
                165                 170                 175
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Glu Leu Asn Asn Ala Leu Gln Asn Leu Ala Arg Thr Ile Ser Glu Ala
            180                 185                 190

Gly Gln Ala Met Ala Ser Thr Glu Gly Asn Val Thr Gly Met Phe Ala
        195                 200                 205
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<210> 2
<211> 205
<212> PRT
<213> artificial sequence

<220>
<223> fusion between TB10.4 and its parner TB9.8 (Rv0287)

<400> 2

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Met Ser Gln Ile Met Tyr Asn Tyr Pro Ala Met Leu Gly His Ala Gly
1               5                   10                  15

Asp Met Ala Gly Tyr Ala Gly Thr Leu Gln Ser Leu Gly Ala Glu Ile
            20                  25                  30

Ala Val Glu Gln Ala Ala Leu Gln Ser Ala Trp Gln Gly Asp Thr Gly
        35                  40                  45

Ile Thr Tyr Gln Ala Trp Gln Ala Gln Trp Asn Gln Ala Met Glu Asp
    50                  55                  60

Leu Val Arg Ala Tyr His Ala Met Ser Ser Thr His Glu Ala Asn Thr
65                  70                  75                  80

Met Ala Met Met Ala Arg Asp Thr Ala Glu Ala Ala Lys Trp Gly Gly
                85                  90                  95

Gly Pro Lys Gln Gly Glu Asp Asp Gly Ser Thr Gly Gly Ser Leu Leu
            100                 105                 110

Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
        115                 120                 125

Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala
    130                 135                 140

Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln
145                 150                 155                 160

Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys Val Asn Thr Leu
                165                 170                 175

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

Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly Phe
```

195 200 205

<210> 3
<211> 113
<212> PRT
<213> artificial sequence

<220>
<223> mutant of Rv1813 antigen

<400> 3

Asp Ala His Leu Ala Asn Gly Ser Met Ser Glu Val Met Met Ser Glu
1 5 10 15

Ile Ala Gly Leu Pro Ile Pro Pro Ile Ile His Tyr Gly Ala Ile Ala
20 25 30

Tyr Ala Pro Ser Gly Ala Ser Gly Lys Ala Trp His Gln Arg Thr Pro
35 40 45

Ala Arg Ala Glu Gln Val Ala Leu Glu Lys Cys Gly Asp Lys Thr Cys
50 55 60

Lys Val Val Ser Arg Phe Thr Arg Cys Gly Ala Val Ala Tyr Asn Gly
65 70 75 80

Ser Lys Tyr Gln Gly Gly Thr Gly Leu Thr Arg Arg Ala Ala Glu Asp
85 90 95

Asp Ala Val Asn Arg Leu Glu Gly Gly Arg Ile Val Asn Trp Ala Cys
100 105 110

Asn

<210> 4
<211> 293
<212> PRT
<213> artificial sequence

<220>
<223> mutant of Ag85B antigen

<400> 4

Gly Gly Ala Ala Thr Ala Gly Ala Phe Ser Arg Pro Gly Leu Pro Val
1 5 10 15

Glu Tyr Leu Gln Val Pro Ser Pro Ser Met Gly Arg Asp Ile Lys Val
20 25 30

Gln Phe Gln Ser Gly Gly Asn Asn Ser Pro Ala Val Tyr Leu Leu Asp
35 40 45

Gly Leu Arg Ala Gln Asp Asp Tyr Asn Gly Trp Asp Ile Asn Thr Pro

50 55 60

Ala Phe Glu Trp Tyr Tyr Gln Ser Gly Leu Ser Ile Val Met Pro Val
65 70 75 80

Gly Gly Gln Ser Ser Phe Tyr Ser Asp Trp Tyr Ser Pro Ala Cys Gly
85 90 95

Lys Ala Gly Cys Gln Thr Tyr Lys Trp Glu Thr Phe Leu Thr Ser Glu
100 105 110

Leu Pro Gln Trp Leu Ser Ala Asn Arg Ala Val Lys Pro Thr Gly Ser
115 120 125

Ala Ala Ile Gly Leu Ser Met Ala Gly Ser Ser Ala Met Ile Leu Ala
130 135 140

Ala Tyr His Pro Gln Gln Phe Ile Tyr Ala Gly Ser Leu Ser Ala Leu
145 150 155 160

Leu Asp Pro Ser Gln Gly Met Gly Pro Ser Leu Ile Gly Leu Ala Met
165 170 175

Gly Asp Ala Gly Gly Tyr Lys Ala Ala Asp Met Trp Gly Pro Ser Ser
180 185 190

Asp Pro Ala Trp Glu Arg Asn Asp Pro Thr Gln Gln Ile Pro Lys Leu
195 200 205

Val Ala Asn Asn Thr Arg Leu Trp Val Tyr Cys Gly Asn Gly Thr Pro
210 215 220

Asn Glu Leu Gly Gly Ala Asn Ile Pro Ala Glu Phe Leu Glu Asn Phe
225 230 235 240

Val Arg Ser Ser Asn Leu Lys Phe Gln Asp Ala Tyr Asn Ala Ala Gly
245 250 255

Gly His Asn Ala Val Phe Asn Phe Pro Pro Asn Gly Thr His Ser Trp
260 265 270

Glu Tyr Trp Gly Ala Gln Leu Asn Ala Met Lys Gly Asp Leu Gln Ser
275 280 285

Ser Leu Gly Ala Gly
290

<210> 5
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> isolated cleavage site F2A of the foot and mouth disease virus

<400> 5

Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
1 5 10 15

Glu Ser Asn Pro Gly Pro
20

<210> 6
<211> 18
<212> PRT
<213> artificial sequence

<220>
<223> isolated cleavage site 2A peptide of the Thosea asigna virus

<400> 6

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
1 5 10 15

Gly Pro

<210> 7
<211> 20
<212> PRT
<213> artificial sequence

<220>
<223> isolated cleavge site 2A peptide of Equine rhinitis A virus

<400> 7

Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp Val Glu Ser
1 5 10 15

Asn Pro Gly Pro
20

<210> 8
<211> 357
<212> PRT
<213> artificial sequence

<220>
<223> fusion of modified RpfB and RpfD resuscitation Mtb antigens

<400> 8

Met Thr Val Asp Gly Thr Ala Met Arg Val Thr Thr Met Lys Ser Arg
1 5 10 15

Val Ile Asp Ile Val Glu Glu Asn Gly Phe Ser Val Asp Asp Arg Asp
20 25 30

Asp Leu Tyr Pro Ala Ala Gly Val Gln Val His Asp Ala Asp Thr Ile

```
        35                  40                  45

Val Leu Arg Arg Ser Arg Pro Leu Gln Ile Ser Leu Asp Gly His Asp
    50                  55                  60

Ala Lys Gln Val Trp Thr Thr Ala Ser Thr Val Asp Glu Ala Leu Ala
65                  70                  75                  80

Gln Leu Ala Met Thr Asp Thr Ala Pro Ala Ala Ala Ser Arg Ala Ser
                85                  90                  95

Arg Val Pro Leu Ser Gly Met Ala Leu Pro Val Val Ser Ala Lys Thr
            100                 105                 110

Val Gln Leu Asn Asp Gly Gly Leu Val Arg Thr Val His Leu Pro Ala
        115                 120                 125

Pro Asn Val Ala Gly Leu Leu Ser Ala Ala Gly Val Pro Leu Leu Gln
    130                 135                 140

Ser Asp His Val Val Pro Ala Ala Thr Ala Pro Ile Val Glu Gly Met
145                 150                 155                 160

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

Pro Leu Pro Pro Asn Ala Arg Arg Val Glu Asp Pro Glu Met Asn Met
            180                 185                 190

Ser Arg Glu Val Val Glu Asp Pro Gly Val Pro Gly Thr Gln Asp Val
        195                 200                 205

Thr Phe Ala Val Ala Glu Val Asn Gly Val Glu Thr Gly Arg Leu Pro
    210                 215                 220

Val Ala Asn Val Val Val Thr Pro Ala His Glu Ala Val Val Arg Val
225                 230                 235                 240

Gly Thr Lys Pro Gly Thr Glu Val Pro Pro Val Ile Asp Gly Ser Ile
                245                 250                 255

Trp Asp Ala Ile Ala Gln Cys Lys Ser Gly Gly Asn Trp Ala Ala Asn
            260                 265                 270

Thr Gly Asn Gly Leu Tyr Gly Gly Leu Gln Ile Ser Gln Ala Ala Trp
        275                 280                 285

Asp Ser Asn Gly Gly Val Gly Ser Pro Ala Ala Ala Ser Pro Gln Gln
    290                 295                 300

Gln Ile Glu Val Ala Asp Asn Ile Met Lys Thr Ala Gly Pro Gly Ala
```

eolf-seql

305 310 315 320

Trp Pro Lys Cys Ser Ser Cys Ser Gln Gly Asp Ala Pro Leu Gly Ser
325 330 335

Leu Thr His Ile Leu Thr Phe Leu Ala Ala Glu Thr Gly Gly Cys Ser
340 345 350

Gly Ser Arg Asp Asp
355

<210> 9
<211> 457
<212> PRT
<213> artificial sequence

<220>
<223> fusion of Rv2626 with Ag85B** Mtb antigens with F2A cleavage site in between

<400> 9

Met Thr Thr Ala Arg Asp Ile Met Asn Ala Gly Val Thr Cys Val Gly
1 5 10 15

Glu His Glu Thr Leu Thr Ala Ala Ala Gln Tyr Met Arg Glu His Asp
20 25 30

Ile Gly Ala Leu Pro Ile Cys Gly Asp Asp Asp Arg Leu His Gly Met
35 40 45

Leu Thr Asp Arg Asp Ile Val Ile Lys Gly Leu Ala Ala Gly Leu Asp
50 55 60

Pro Asn Thr Ala Thr Ala Gly Glu Leu Ala Arg Asp Ser Ile Tyr Tyr
65 70 75 80

Val Asp Ala Asn Ala Ser Ile Gln Glu Met Leu Asn Val Met Glu Glu
85 90 95

His Gln Val Arg Arg Val Pro Val Ile Ser Glu His Arg Leu Val Gly
100 105 110

Ile Val Thr Glu Ala Asp Ile Ala Arg His Leu Pro Glu His Ala Ile
115 120 125

Val Gln Phe Val Lys Ala Ile Cys Ser Pro Met Ala Leu Ala Ser Gly
130 135 140

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

Asn Pro Gly Pro Gly Gly Ala Ala Thr Ala Gly Ala Phe Ser Arg Pro
165 170 175

```
Gly Leu Pro Val Glu Tyr Leu Gln Val Pro Ser Pro Ser Met Gly Arg
            180                 185                 190

Asp Ile Lys Val Gln Phe Gln Ser Gly Gly Asn Asn Ser Pro Ala Val
        195                 200                 205

Tyr Leu Leu Asp Gly Leu Arg Ala Gln Asp Asp Tyr Asn Gly Trp Asp
    210                 215                 220

Ile Asn Thr Pro Ala Phe Glu Trp Tyr Tyr Gln Ser Gly Leu Ser Ile
225                 230                 235                 240

Val Met Pro Val Gly Gly Gln Ser Ser Phe Tyr Ser Asp Trp Tyr Ser
                245                 250                 255

Pro Ala Cys Gly Lys Ala Gly Cys Gln Thr Tyr Lys Trp Glu Thr Phe
            260                 265                 270

Leu Thr Ser Glu Leu Pro Gln Trp Leu Ser Ala Asn Arg Ala Val Lys
        275                 280                 285

Pro Thr Gly Ser Ala Ala Ile Gly Leu Ser Met Ala Gly Ser Ser Ala
    290                 295                 300

Met Ile Leu Ala Ala Tyr His Pro Gln Gln Phe Ile Tyr Ala Gly Ser
305                 310                 315                 320

Leu Ser Ala Leu Leu Asp Pro Ser Gln Gly Met Gly Pro Ser Leu Ile
                325                 330                 335

Gly Leu Ala Met Gly Asp Ala Gly Gly Tyr Lys Ala Ala Asp Met Trp
            340                 345                 350

Gly Pro Ser Ser Asp Pro Ala Trp Glu Arg Asn Asp Pro Thr Gln Gln
        355                 360                 365

Ile Pro Lys Leu Val Ala Asn Asn Thr Arg Leu Trp Val Tyr Cys Gly
    370                 375                 380

Asn Gly Thr Pro Asn Glu Leu Gly Gly Ala Asn Ile Pro Ala Glu Phe
385                 390                 395                 400

Leu Glu Asn Phe Val Arg Ser Ser Asn Leu Lys Phe Gln Asp Ala Tyr
                405                 410                 415

Asn Ala Ala Gly Gly His Asn Ala Val Phe Asn Phe Pro Pro Asn Gly
            420                 425                 430

Thr His Ser Trp Glu Tyr Trp Gly Ala Gln Leu Asn Ala Met Lys Gly
        435                 440                 445
```

Asp Leu Gln Ser Ser Leu Gly Ala Gly
    450   455

<210> 10
<211> 436
<212> PRT
<213> artificial sequence

<220>
<223> fusion of Rv2626 and Ag85B** Mtb antigens

<400> 10

Met Thr Thr Ala Arg Asp Ile Met Asn Ala Gly Val Thr Cys Val Gly
1   5   10   15

Glu His Glu Thr Leu Thr Ala Ala Ala Gln Tyr Met Arg Glu His Asp
            20   25   30

Ile Gly Ala Leu Pro Ile Cys Gly Asp Asp Asp Arg Leu His Gly Met
        35   40   45

Leu Thr Asp Arg Asp Ile Val Ile Lys Gly Leu Ala Ala Gly Leu Asp
    50   55   60

Pro Asn Thr Ala Thr Ala Gly Glu Leu Ala Arg Asp Ser Ile Tyr Tyr
65   70   75   80

Val Asp Ala Asn Ala Ser Ile Gln Glu Met Leu Asn Val Met Glu Glu
                85   90   95

His Gln Val Arg Arg Val Pro Val Ile Ser Glu His Arg Leu Val Gly
            100   105   110

Ile Val Thr Glu Ala Asp Ile Ala Arg His Leu Pro Glu His Ala Ile
        115   120   125

Val Gln Phe Val Lys Ala Ile Cys Ser Pro Met Ala Leu Ala Ser Gly
    130   135   140

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

Tyr Leu Gln Val Pro Ser Pro Ser Met Gly Arg Asp Ile Lys Val Gln
                165   170   175

Phe Gln Ser Gly Gly Asn Asn Ser Pro Ala Val Tyr Leu Leu Asp Gly
            180   185   190

Leu Arg Ala Gln Asp Asp Tyr Asn Gly Trp Asp Ile Asn Thr Pro Ala
        195   200   205

Phe Glu Trp Tyr Tyr Gln Ser Gly Leu Ser Ile Val Met Pro Val Gly
210 215 220

Gly Gln Ser Ser Phe Tyr Ser Asp Trp Tyr Ser Pro Ala Cys Gly Lys
225 230 235 240

Ala Gly Cys Gln Thr Tyr Lys Trp Glu Thr Phe Leu Thr Ser Glu Leu
245 250 255

Pro Gln Trp Leu Ser Ala Asn Arg Ala Val Lys Pro Thr Gly Ser Ala
260 265 270

Ala Ile Gly Leu Ser Met Ala Gly Ser Ser Ala Met Ile Leu Ala Ala
275 280 285

Tyr His Pro Gln Gln Phe Ile Tyr Ala Gly Ser Leu Ser Ala Leu Leu
290 295 300

Asp Pro Ser Gln Gly Met Gly Pro Ser Leu Ile Gly Leu Ala Met Gly
305 310 315 320

Asp Ala Gly Gly Tyr Lys Ala Ala Asp Met Trp Gly Pro Ser Ser Asp
325 330 335

Pro Ala Trp Glu Arg Asn Asp Pro Thr Gln Gln Ile Pro Lys Leu Val
340 345 350

Ala Asn Asn Thr Arg Leu Trp Val Tyr Cys Gly Asn Gly Thr Pro Asn
355 360 365

Glu Leu Gly Gly Ala Asn Ile Pro Ala Glu Phe Leu Glu Asn Phe Val
370 375 380

Arg Ser Ser Asn Leu Lys Phe Gln Asp Ala Tyr Asn Ala Ala Gly Gly
385 390 395 400

His Asn Ala Val Phe Asn Phe Pro Pro Asn Gly Thr His Ser Trp Glu
405 410 415

Tyr Trp Gly Ala Gln Leu Asn Ala Met Lys Gly Asp Leu Gln Ser Ser
420 425 430

Leu Gly Ala Gly
435

<210> 11
<211> 235
<212> PRT
<213> artificial sequence

<220>
<223> fusion of Rv3407 and Rv1813** Mtb antigens with E2A cleavage site in between

<400> 11

```
Met Arg Ala Thr Val Gly Leu Val Glu Ala Ile Gly Ile Arg Glu Leu
1               5                  10                  15

Arg Gln His Ala Ser Arg Tyr Leu Ala Arg Val Glu Ala Gly Glu Glu
            20                  25                  30

Leu Gly Val Thr Asn Lys Gly Arg Leu Val Ala Arg Leu Ile Pro Val
        35                  40                  45

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

Ile Pro Ala Arg Arg Pro Gln Asn Leu Leu Asp Val Thr Ala Glu Pro
65                  70                  75                  80

Ala Arg Gly Arg Lys Arg Thr Leu Ser Asp Val Leu Asn Glu Met Arg
                85                  90                  95

Asp Glu Gln Gly Ser Gly Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu
            100                 105                 110

Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Asp Ala His Leu Ala Asn
        115                 120                 125

Gly Ser Met Ser Glu Val Met Met Ser Glu Ile Ala Gly Leu Pro Ile
    130                 135                 140

Pro Pro Ile Ile His Tyr Gly Ala Ile Ala Tyr Ala Pro Ser Gly Ala
145                 150                 155                 160

Ser Gly Lys Ala Trp His Gln Arg Thr Pro Ala Arg Ala Glu Gln Val
                165                 170                 175

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

Thr Arg Cys Gly Ala Val Ala Tyr Asn Gly Ser Lys Tyr Gln Gly Gly
        195                 200                 205

Thr Gly Leu Thr Arg Arg Ala Ala Glu Asp Asp Ala Val Asn Arg Leu
    210                 215                 220

Glu Gly Gly Arg Ile Val Asn Trp Ala Cys Asn
225                 230                 235
```

<210> 12
<211> 212
<212> PRT
<213> artificial sequence

<220>
<223> fusion of Rv3407 and Rv1813* Mtb antigens

<400> 12

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Met Arg Ala Thr Val Gly Leu Val Glu Ala Ile Gly Ile Arg Glu Leu
1               5                  10                  15

Arg Gln His Ala Ser Arg Tyr Leu Ala Arg Val Glu Ala Gly Glu Glu
            20                  25                  30

Leu Gly Val Thr Asn Lys Gly Arg Leu Val Ala Arg Leu Ile Pro Val
        35                  40                  45

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

Ile Pro Ala Arg Arg Pro Gln Asn Leu Leu Asp Val Thr Ala Glu Pro
65                  70                  75                  80

Ala Arg Gly Arg Lys Arg Thr Leu Ser Asp Val Leu Asn Glu Met Arg
                85                  90                  95

Asp Glu Gln Asp Ala His Leu Ala Asn Gly Ser Met Ser Glu Val Met
            100                 105                 110

Met Ser Glu Ile Ala Gly Leu Pro Ile Pro Pro Ile Ile His Tyr Gly
        115                 120                 125

Ala Ile Ala Tyr Ala Pro Ser Gly Ala Ser Gly Lys Ala Trp His Gln
    130                 135                 140

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

Lys Thr Cys Lys Val Val Ser Arg Phe Thr Arg Cys Gly Ala Val Ala
                165                 170                 175

Tyr Asn Gly Ser Lys Tyr Gln Gly Gly Thr Gly Leu Thr Arg Arg Ala
            180                 185                 190

Ala Glu Asp Asp Ala Val Asn Arg Leu Glu Gly Gly Arg Ile Val Asn
        195                 200                 205

Trp Ala Cys Asn
    210
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<210> 13
<211> 637
<212> DNA
<213> artificial sequence

<220>
<223> nt sequence encoding the fusion of CFP10 with its partner ESAT6

<400> 13
accatggccg agatgaagac cgatgccgcc accctggctc aggaagccgg caacttcgag 60

agaatcagcg gcgacctgaa aacccagatc gaccaggtgg aaagcaccgc cggatctctg 120

cagggacagt ggcggggagc tgctggaaca gctgctcagg ctgctgtcgt gcggtttcag 180

gaagctgcca acaagcagaa gcaggaactg gacgagatca gcaccaacat ccggcaggcc 240

ggcgtgcagt acagcagagc cgatgaggaa cagcagcagg ccctgtccag ccagatgggc 300

tttggaccta agcagggcga ggatgatggc tctacaggcg gccctaccga gcagcagtgg 360

aacttcgccg gaattgaggc cgctgccagc gccatccagg gcaacgtgac atccatccac 420

agcctgctgg acgagggcaa gcagagcctg acaaaactgg ctgctgcctg gggcggctct 480

ggctctgaag cttatcaggg cgtgcagcag aagtgggacg ccaccgccac cgagctgaac 540

aacgccctgc agaacctggc ccggacaatc tctgaagccg gacaggccat ggccagcacc 600

gagggcaatg tgaccggcat gtttgcctaa tttttgt 637

<210> 14
<211> 628
<212> DNA
<213> artificial sequence

<220>
<223> nt sequence coding for the fusion of TB10.4 Mtb antigen with its partner TB9.8 (Rv0287)

<400> 14
accatgagcc agatcatgta caactacccc gccatgctgg gccacgccgg cgatatggct 60

ggatatgccg gcacactgca gagcctgggt gccgagattg ccgtggaaca ggctgccctc 120

cagtctgcct ggcagggcga taccggcatc acataccagg cttggcaggc ccagtggaac 180

caggccatgg aagatctcgt gcgggcctac cacgccatga gcagcacaca cgaggccaac 240

accatggcca tgatggcccg ggatacagcc gaggccgcta agtggggagg aggccccaaa 300

caaggagaag atgacggcag caccggagga agtctgctcg acgcccacat ccctcagctc 360

gtggctagcc agtctgcctt tgccgccaaa gccggcctga tgagacacac cattggccag 420

gccgaacagg ccgccatgtc tgcccaggct tttcaccagg gcgaaagcag cgccgccttt 480

caggccgccc atgccagatt tgtggccgct gccgctaaag tgaacaccct cctggacgtg 540

gcccaggcca atctgggaga agccgccgga acttacgtgg ccgcagatgc cgctgctgcc 600

agcacctaca caggcttcta gtttttct 628

<210> 15
<211> 1084
<212> DNA
<213> artificial sequence

<220>
<223> nt sequence coding for the fusion of mutant RpfB and RpfD Mtb antigens

<400> 15

accatgaccg tggacggcac cgccatgaga gtgaccacca tgaagtccag agtgatcgac 60

atcgtggaag agaacggctt cagcgtggac gaccgggacg acctgtatcc tgctgctgga 120

gtgcaggtcc acgacgccga tacaatcgtg ctgcggagaa gcagacccct gcagatcagc 180

ctggatggcc acgacgccaa gcaggtctgg accacagcca gcacagtgga tgaagccctg 240

gcccagctgg ccatgaccga tacagctcca gccgccgcta gcagagctag cagagtgcct 300

ctgtctggca tggccctgcc tgtggtgtct gccaagaccg tgcagctgaa cgatggcggc 360

ctcgtgcgga cagtgcatct gcctgctcct aatgtggccg gcctgctgtc tgcagcaggc 420

gtgccactgc tgcagagcga tcatgtggtg cctgccgcca cagcccctat cgtggaaggc 480

atgcagatcc aggtcacacg gaaccggatc aagaaagtga ccgagcggct gcccctgcct 540

cccaacgcta gaagagtgga agatcccgag atgaacatga gcagagaggt ggtcgaggac 600

cctggcgtgc caggcacaca ggatgtgaca ttcgccgtgg ccgaagtgaa cggcgtggaa 660

accggcagac tgcccgtggc caatgtggtg gtcacaccag cccatgaggc cgtcgtcaga 720

gtgggcacaa agcctggcac agaggtgcca cccgtgatcg acggcagcat ctgggatgcc 780

attgcccagt gcaagagcgg cggaaactgg gccgccaata ccggcaatgg cctctatggc 840

ggcctgcaga tctctcaggc cgcctgggat tctaatggcg gcgtgggatc tcctgccgct 900

gcctctccac agcagcagat cgaggtggcc gacaacatca tgaagacagc cggacctggc 960

gcctggccca agtgtagcag ttgttctcag ggcgacgccc ctctgggcag cctgacacac 1020

atcctgacat ttctggccgc cgagacaggc ggatgtagcg gctctagaga tgactagttt 1080

ttct 1084

<210> 16
<211> 1384
<212> DNA
<213> artificial sequence

<220>
<223> nt sequence coding for the fusion of Rv2626 with Ag85B** Mtb antigens with peptide 2A cleavage site in between

<400> 16
accatgacaa ccgccagaga catcatgaac gccggcgtga cctgtgtggg cgagcacgag 60

acactgacag ccgccgctca gtacatgaga gagcacgaca tcggcgccct gcccatctgc 120

ggcgacgatg atagactgca cggcatgctg accgaccggg acatcgtgat caagggcctg 180

gctgctggcc tggaccccaa tactgctaca gctggcgagc tggcaagaga cagcatctac 240

tacgtggacg ccaacgccag catccaggaa atgctgaacg tgatggaaga acaccaggtc 300

cgacgggtgc ccgtgatcag cgaacacaga ctcgtgggca tcgtgaccga ggccgatatc 360

gccagacatc tgcccgagca cgccatcgtg cagttcgtga aggccatctg cagccccatg 420

gccctggcct ctggcagcgg agagggcaga ggcagcctgc tgacatgtgg tgacgtagag 480

gagaatccag gacctggcgg agctgctaca gccggcgcct tctctagacc tggcctgccc 540

gtggaatacc tgcaggtccc aagccccagc atgggccggg atatcaaggt gcagtttcag 600

agcggcggca acaacagccc tgccgtgtat ctgctggatg gcctgagagc ccaggacgac 660

tacaacggct gggacatcaa cacccctgcc ttcgagtggt actaccagag cggcctgtcc 720

atcgtgatgc ctgtgggcgg ccagagcagc ttctacagcg actggtacag ccccgcctgt 780

ggcaaagccg gctgccagac ctacaagtgg gagacattcc tgacctccga gctgccccag 840

tggctgagcg ccaatagagc cgtgaagcct acaggctctg ccgccatcgg actgagcatg 900

gccggaagct ctgccatgat cctggccgcc tatcaccctc agcagttcat ctacgccggc 960

agcctgtctg ccctgctgga cccttctcag ggcatgggcc cttctctgat cggactggct 1020

atgggcgacg ctggcggata caaggccgcc gatatgtggg gccctagcag cgatcctgcc 1080

tgggagagaa acgaccccac ccagcagatc cccaagctgg tggccaacaa cacccggctg 1140

tgggtgtact gcggcaacgg cacccctaat gaactgggcg gagccaatat ccccgccgag 1200

ttcctggaaa acttcgtgcg gagcagcaac ctgaagttcc aggatgccta caacgccgct 1260

ggcggccaca acgccgtgtt caacttccct cccaatggca cccacagctg ggagtactgg 1320

ggagcccagc tgaacgccat gaagggcgat ctgcagtcct ctctgggagc cggctaattt 1380

ttct 1384

<210> 17
<211> 1321
<212> DNA
<213> artificial sequence

<220>
<223> nt sequence coding for the fusion of Rv2626 with Ag85B** Mtb antigens

<400> 17
accatgacaa ccgccagaga catcatgaac gccggcgtga cctgtgtggg cgagcacgag 60

acactgacag ccgccgctca gtacatgaga gagcacgaca tcggcgccct gcccatctgc 120

ggcgacgatg atagactgca cggcatgctg accgaccggg acatcgtgat caagggcctg 180

gctgctggcc tggaccccaa tactgctaca gctggcgagc tggcaagaga cagcatctac 240

tacgtggacg ccaacgccag catccaggaa atgctgaacg tgatggaaga acaccaggtc 300

cgacgggtgc ccgtgatcag cgaacacaga ctcgtgggca tcgtgaccga ggccgatatc 360

gccagacatc tgcccgagca cgccatcgtg cagttcgtga aggccatctg cagccccatg 420

gccctggcct ctggcggagc tgctacagcc ggcgccttct ctagacctgg cctgcccgtg 480

gaatacctgc aggtcccaag ccccagcatg ggccgggata tcaaggtgca gtttcagagc 540

ggcggcaaca acagccctgc cgtgtatctg ctggatggcc tgagagccca ggacgactac 600

aacggctggg acatcaacac ccctgccttc gagtggtact accagagcgg cctgtccatc 660

gtgatgcctg tgggcggcca gagcagcttc tacagcgact ggtacagccc cgcctgtggc 720

aaagccggct gccagaccta caagtgggag acattcctga cctccgagct gccccagtgg 780

ctgagcgcca atagagccgt gaagcctaca ggctctgccg ccatcggact gagcatggcc 840

ggaagctctg ccatgatcct ggccgcctat caccctcagc agttcatcta cgccggcagc 900

ctgtctgccc tgctggaccc ttctcagggc atgggccctt ctctgatcgg actggctatg 960

ggcgacgctg gcggatacaa ggccgccgat atgtggggcc ctagcagcga tcctgcctgg 1020

gagagaaacg accccaccca gcagatcccc aagctggtgg ccaacaacac ccggctgtgg 1080

gtgtactgcg gcaacggcac ccctaatgaa ctgggcggag ccaatatccc cgccgagttc 1140

ctggaaaact tcgtgcggag cagcaacctg aagttccagg atgcctacaa cgccgctggc 1200

ggccacaacg ccgtgttcaa cttccctccc aatggcaccc acagctggga gtactgggga 1260

gcccagctga acgccatgaa gggcgatctg cagtcctctc tgggagccgg ctaatttttc 1320

t 1321

<210> 18
<211> 718
<212> DNA
<213> artificial sequence

<220>
<223> nt sequence coding for the fusion of Rv3407 and Rv1813** Mtb antigens with peptide 2A in between

<400> 18
accatgagag ccaccgtggg actggtggaa gccatcggca tcagagagct gagacagcac 60

gccagcagat acctggccag agtggaagcc ggcgaggaac tgggcgtgac caacaagggc 120

agactggtgg ccagactgat ccctgtgcag gccgccgaga gaagcagaga ggccctgatt 180

gagagcggcg tgctgatccc tgccagacgg cctcagaacc tgctggatgt gacagccgag 240

cccgccagag gccggaagag aaccctgagc gacgtgctga acgagatgcg ggatgaacag 300

gggtcaggac agtgcaccaa ctacgctctc ctgaaactgg ccggcgatgt ggaaagcaac 360

cctggccctg atgcccatct ggccaacggc agcatgagcg aagtgatgat gagcgagatc 420

gccggcctgc ccatccctcc catcatccac tatggcgcca ttgcctacgc ccctagcggc 480

gcctctggaa aagcttggca tcagagaaca cccgccagag ccgaacaggt ggccctggaa 540

aagtgcggcg acaagacctg caaggtggtg tcccggttca ccagatgtgg cgccgtggcc 600

tacaacggct ccaagtatca gggcggcacc ggcctgacaa gaagggccgc tgaggacgac 660

gccgtgaaca ggctggaggg aggcagaatc gtgaactggg cctgcaacta atttttct 718

<210> 19
<211> 649
<212> DNA
<213> artificial sequence

<220>
<223> nt sequence coding fro the fusion of Rv3407 and Rv1813* Mtb antigens

<400> 19
accatgagag ccaccgtggg actggtggaa gccatcggca tcagagagct gagacagcac 60

gccagcagat acctggccag agtggaagcc ggcgaggaac tgggcgtgac caacaagggc 120

agactggtgg ccagactgat ccctgtgcag gccgccgaga gaagcagaga ggccctgatt 180

gagagcggcg tgctgatccc tgccagacgg cctcagaacc tgctggatgt gacagccgag 240

cccgccagag gccggaagag aaccctgagc gacgtgctga acgagatgcg ggatgaacag 300

gatgcccatc tggccaacgg cagcatgagc gaagtgatga tgagcgagat cgccggcctg 360

cccatccctc ccatcatcca ctatggcgcc attgcctacg cccctagcgg cgcctctgga 420

aaagcttggc atcagagaac acccgccaga gccgaacagg tggccctgga aaagtgcggc 480

gacaagacct gcaaggtggt gtcccggttc accagatgtg gcgccgtggc ctacaacggc 540

tccaagtatc agggcggcac cggcctgaca agaagggccg ctgaggacga cgccgtgaac 600

aggctggagg gaggcagaat cgtgaactgg gcctgcaact aatttttct 649

<210> 20
<211> 100
<212> DNA
<213> Vaccinia virus

<400> 20
tatattatta agtgtggtgt ttggtcgatg taaaattttt gtcgataaaa attaaaaaat 60

aacttaattt attattgatc tcgtgtgtac aaccgaaatc 100

<210> 21
<211> 114
<212> DNA
<213> Vaccinia virus

<400> 21
tttattctat acttaaaaaa tgaaaataaa tacaaaggtt cttgagggtt gtgttaaatt 60

gaaagcgaga aataatcata aattatttca ttatcgcgat atccgttaag tttg 114

<210> 22
<211> 40
<212> DNA
<213> artificial sequence

<220>
<223> early late promoter of vaccinia virus

<400> 22
aaaaattgaa attttatttt ttttttttgg aatataaata 40

<210> 23
<211> 124
<212> DNA
<213> Vaccinia virus

<400> 23
ccacccactt tttatagtaa gtttttcacc cataaataat aaatacaata attaatttct 60

cgtaaaagta gaaaatatat tctaatttat tgcacggtaa ggaagtagaa tcataaagaa 120

cagt 124

<210> 24
<211> 50

<212> DNA
<213> Vaccinia virus

<400> 24
caagtgacaa caaaaaatga attaataata agtcgttaac gtacgccgcc 50

<210> 25
<211> 298
<212> DNA
<213> Mycobacterium tuberculosis

<400> 25
accatgaccg agcagcagtg gaacttcgcc ggaattgagg ccgctgccag cgccatccag 60

ggcaacgtga catccatcca cagcctgctg gacgagggca agcagagcct gacaaaactg 120

gctgctgcct ggggcggctc tggctctgaa gcttatcagg gcgtgcagca gaagtgggac 180

gccaccgcca ccgagctgaa caacgccctg cagaacctgg cccggacaat ctctgaagcc 240

ggacaggcca tggccagcac cgagggcaat gtgaccggca tgtttgcctg atttttct 298

<210> 26
<211> 313
<212> DNA
<213> Mycobacterium tuberculosis

<400> 26
accatggccg agatgaagac cgatgccgcc accctggctc aggaagccgg caacttcgag 60

agaatcagcg gcgacctgaa aacccagatc gaccaggtgg aaagcaccgc cggatctctg 120

cagggacagt ggcggggagc tgctggaaca gctgctcagg ctgctgtcgt gcggtttcag 180

gaagctgcca acaagcagaa gcaggaactg gacgagatca gcaccaacat ccggcaggcc 240

ggcgtgcagt acagcagagc cgatgaggaa cagcagcagg ccctgtccag ccagatgggc 300

ttttgatttt tgt 313

<210> 27
<211> 442
<212> DNA
<213> Mycobacterium tuberculosis

<400> 27
accatgacaa ccgccagaga catcatgaac gccggcgtga cctgtgtggg cgagcacgag 60

acactgacag ccgccgctca gtacatgaga gagcacgaca tcggcgccct gcccatctgc 120

ggcgacgatg atagactgca cggcatgctg accgaccggg acatcgtgat caagggcctg 180

gctgctggcc tggaccccaa tactgctaca gctggcgagc tggcaagaga cagcatctac 240

tacgtggacg ccaacgccag catccaggaa atgctgaacg tgatggaaga acaccaggtc 300

cgacgggtgc ccgtgatcag cgaacacaga ctcgtgggca tcgtgaccga ggccgatatc 360

gccagacatc tgcccgagca cgccatcgtg cagttcgtga aggccatctg cagccccatg 420

gccctggcct cttgattttt ct 442

<210> 28
<211> 874

<212> DNA
<213> artificial sequence

<220>
<223> nt sequence coding for mutant Ag85B* Mtb antigen

<400> 28
accatggcct tctctagacc tggcctgccc gtggaatacc tgcaggtccc aagccccagc 60

atgggccggg atatcaaggt gcagtttcag agcggcggca acaacagccc tgccgtgtat 120

ctgctggatg gcctgagagc ccaggacgac tacaacggct gggacatcaa cacccctgcc 180

ttcgagtggt actaccagag cggcctgtcc atcgtgatgc ctgtgggcgg ccagagcagc 240

ttctacagcg actggtacag ccccgcctgt ggcaaagccg gctgccagac ctacaagtgg 300

gagacattcc tgacctccga gctgccccag tggctgagcg ccaatagagc cgtgaagcct 360

acaggctctg ccgccatcgg actgagcatg gccggaagct ctgccatgat cctggccgcc 420

tatcaccctc agcagttcat ctacgccggc agcctgtctg ccctgctgga cccttctcag 480

ggcatgggcc cttctctgat cggactggct atgggcgacg ctggcggata caaggccgcc 540

gatatgtggg gccctagcag cgatcctgcc tgggagagaa acgaccccac ccagcagatc 600

cccaagctgg tggccaacaa cacccggctg tgggtgtact gcggcaacgg cacccctaat 660

gaactgggcg gagccaatat ccccgccgag ttcctggaaa acttcgtgcg gagcagcaac 720

ctgaagttcc aggatgccta caacgccgct ggcggccaca acgccgtgtt caacttccct 780

cccaatggca cccacagctg ggagtactgg ggagcccagc tgaacgccat gaagggcgat 840

ctgcagtcct ctctgggagc cggctgattt ttgt 874

<210> 29
<211> 304
<212> DNA
<213> Mycobacterium tuberculosis

<400> 29
accatgagcc tgctggacgc ccacatccct cagctggtgg ccagccagtc tgcctttgcc 60

gccaaagccg gcctgatgag acacaccatt ggccaggccg aacaggccgc catgtctgcc 120

caggcttttc accagggcga aagcagcgcc gcctttcagg ccgcccatgc cagatttgtg 180

gccgctgccg ctaaagtgaa caccctgctg gatgtggccc aggccaatct gggagaagcc 240

gccggaactt acgtggccgc agatgccgct gctgccagca cctacacagg cttctgattt 300

ttct 304

<210> 30
<211> 301
<212> DNA
<213> Mycobacterium tuberculosis

<400> 30
accatgagcc agatcatgta caactacccc gccatgctgg gccacgccgg cgatatggct 60

ggatatgccg gcacactgca gagcctgggt gccgagattg ccgtggaaca ggctgccctc 120

cagtctgcct ggcagggcga taccggcatc acataccagg cttggcaggc ccagtggaac 180

caggccatgg aagatctcgt gcgggcctac cacgccatga gcagcacaca cgaggccaac 240

accatggcca tgatggcccg ggatacagcc gaggccgcta agtggggagg ataatttttc 300

t 301

<210> 31
<211> 310
<212> DNA
<213> Mycobacterium tuberculosis

<400> 31
accatgagag ccaccgtggg actggtggaa gccatcggca tcagagagct gagacagcac 60

gccagcagat acctggccag agtggaagcc ggcgaggaac tgggcgtgac caacaagggc 120

agactggtgg ccagactgat ccctgtgcag gccgccgaga gaagcagaga ggccctgatt 180

gagagcggcg tgctgatccc tgccagacgg cctcagaacc tgctggatgt gacagccgag 240

cccgccagag gccggaagag aaccctgagc gacgtgctga acgagatgcg ggatgaacag 300

taatttttct 310

<210> 32
<211> 1192
<212> DNA
<213> Mycobacterium tuberculosis

<400> 32
accatggtgg acttcggcgc cctgcctccc gagattaata gcgccaggat gtacgccggc 60

cctggcagcg cttctctggt ggccgctgcc aagatgtggg atagcgtggc cagcgacctg 120

ttctctgccg ccagcgcatt tcagagcgtc gtgtggggac tcactgtggg ctcttggatc 180

ggatcttctg ccggtctgat ggccgctgct gcctctcctt atgtggcctg gatgagcgtg 240

accgccggac aggcacagct gacagctgca caggtccgag tggctgccgc cgcttacgag 300

acagcctaca gactgacagt gcctccaccc gtgatcgccg agaatcggac cgagctcatg 360

accctgaccg ccaccaatct gctcggccag aacacccctg ccatcgaggc caatcaggcc 420

gcctactctc aaatgtgggg ccaagatgcc gaggctatgt acggctatgc agccacagcc 480

gccactgcta cagaagccct gctgcccttc gaagatgccc ctctgatcac aaaccctggc 540

ggcctgctgg aacaggccgt ggctgtggaa gaggccatcg ataccgctgc cgccaaccaa 600

ctcatgaaca acgtgccaca ggccctccag cagctggctc agcctgctca gggcgtggtg 660

ccttctagca agctcggcgg actgtggacc gccgtgtctc ctcatctgag ccctctgagc 720

aacgtgtcct ctatcgccaa caaccacatg agcatgatgg gcaccggcgt gtccatgacc 780

aacaccctgc acagcatgct gaagggactg gcccctgctg ctgcccaggc tgtggaaaca 840

gccgccgaaa atggcgtgtg ggccatgagc agcctgggct ctcagctggg aagctccctc 900

ggttcttctg gactgggagc tggcgtggcc gccaatctgg gaagagctgc ttctgtcggc 960

agcctgtctg tgcctcctgc ttgggccgct gctaaccagg ctgtgacacc agctgctaga 1020

gccctgcctc tgaccagcct gacatctgcc gctcagacag cccctggcca catgctggga 1080

ggactgcctc tgggccactc tgtgaatgcc ggcagcggca tcaacaacgc cctgagagtg 1140

cctgccagag cctacgccat ccccagaact ccagccgctg gctaattttt gt 1192

<210> 33
<211> 307
<212> DNA
<213> Mycobacterium tuberculosis

<400> 33
accatgagct tcaccgccca gcctgaaatg ctggccgctg ctgctggcga gctgagatct 60

ctgggagcca cactgaaggc cagcaatgcc gctgccgccg tgcctacaac aggcgtggtg 120

cctcctgccg ccgatgaagt gtctctgctg ctggccaccc agttcagaac ccacgccgcc 180

acataccaga ccgcctctgc caaagccgcc gtgatccacg agcagttcgt gaccacactg 240

gccaccagcg ccagctccta cgccgataca gaggccgcca atgccgtcgt gacaggctga 300

tttttct 307