

eolf-seq1

SEQUENCE LISTING

<110> GlaxoSmithKline Biologicals s.a
 Glaxo Group Limited
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 Gelinas, Anne-Marie
 Brown, James R
 Murphy, Dennis
 Mettens, Pascal

<120> MODIFIED ANTIGENS

<130> VB64094PCT

<150> US61/298,710

<151> 2010-01-27

<160> 180

<170> PatentIn version 3.5

<210> 1

<211> 392

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<221> MISC_FEATURE

<223> Strain H37RV

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Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
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Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
 35 40 45

Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
 50 55 60

Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
 65 70 75 80

Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
 85 90 95

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

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

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

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Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
145 150 155 160

Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
165 170 175

Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
180 185 190

Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
195 200 205

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

Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
225 230 235 240

Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
245 250 255

Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
260 265 270

Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
275 280 285

Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
290 295 300

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

Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
325 330 335

Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
340 345 350

Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
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Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
370 375 380

Lys Val Leu Val Arg Asn Val Val
385 390

<210> 2
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<213> Mycobacterium tuberculosis

<223> Strain H37Rv

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gatcgtcagc	tcatcagcct	gatccacgac	caggccaacg	cggtccagac	gacctgcgac	300
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<213> Mycobacterium tuberculosis

<223> Strain CDC1551

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 35 40 45
 Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
 50 55 60
 Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
 65 70 75 80
 Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
 85 90 95
 Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
 100 105 110
 Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
 115 120 125
 Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
 130 135 140
 Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
 145 150 155 160
 Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
 165 170 175
 Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile
 180 185 190
 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
 195 200 205
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 210 215 220
 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
 225 230 235 240
 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
 245 250 255
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 260 265 270
 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
 275 280 285
 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
 290 295 300

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

Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
325 330 335

Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
340 345 350

Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
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Lys Val Leu Val Arg Asn Val Val
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<210> 4
<211> 392
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<221> MISC_FEATURE
<223> Strain F11

<400> 4

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Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
35 40 45

Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
50 55 60

Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
65 70 75 80

Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
85 90 95

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

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

eolf-seql

Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
 130 135 140
 Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
 145 150 155 160
 Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
 165 170 175
 Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile
 180 185 190
 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
 195 200 205
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 210 215 220
 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
 225 230 235 240
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 245 250 255
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 260 265 270
 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
 275 280 285
 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
 290 295 300
 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
 305 310 315 320
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
 325 330 335
 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
 340 345 350
 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
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 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
 370 375 380
 Lys Val Leu Val Arg Asn Val Val
 385 390

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 <213> Mycobacterium tuberculosis

<220>
 <221> MISC_FEATURE
 <223> Strain Haarlem A

<400> 5

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Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
 35 40 45

Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
 50 55 60

Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
 65 70 75 80

Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
 85 90 95

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

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

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

Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
 145 150 155 160

~~Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala~~
 165 170 175

Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile
 180 185 190

Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
 195 200 205

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

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Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
225 230 235 240

Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
245 250 255

Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
260 265 270

Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
275 280 285

Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
290 295 300

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

Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
325 330 335

Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
340 345 350

Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
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Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
370 375 380

Lys Val Leu Val Arg Asn Val Val
385 390

<210> 6
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<213> Mycobacterium tuberculosis

<220>
<221> MISC_FEATURE
<223> Strain C

<400> 6

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Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
35 40 45

eof-seq1

Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
50 55 60

Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
65 70 75 80

Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
85 90 95

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

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

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

Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
145 150 155 160

Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
165 170 175

Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile
180 185 190

Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
195 200 205

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

Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
225 230 235 240

Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
245 250 255

Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
260 265 270

Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
275 280 285

Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
290 295 300

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

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Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
325 330 335

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340 345 350

Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
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370 375 380

Lys Val Leu Val Arg Asn Val Val
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<213> Mycobacterium bovis

<220>
<221> MISC_FEATURE
<223> Strain BCG

<400> 7

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Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
35 40 45

Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
50 55 60

Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
65 70 75 80

Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
85 90 95

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

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

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

eof-seq1

Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
145 150 155 160

Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
165 170 175

Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile
180 185 190

Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
195 200 205

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

Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
225 230 235 240

Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
245 250 255

Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
260 265 270

Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
275 280 285

Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
290 295 300

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

Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
325 330 335

Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
340 345 350

Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
355 360 365

Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
370 375 380

Lys Val Leu Val Arg Asn Val Val
385 390

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<212> PRT

<213> Mycobacterium tuberculosis

<220>

<221> mat_peptide

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25 30 35Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Gln Arg
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<211> 97

<212> PRT

<213> Mycobacterium tuberculosis

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35 40 45Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys
50 55 60Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
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eolf-seq1

Phe

<210> 10
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 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 10

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Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val
 35 40 45

Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
 50 55 60

Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
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Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
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 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 11

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Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
 35 40 45

Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
 50 55 60

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

Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
 85 90 95

Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
 100 105 110

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Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
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Gly Pro Pro Ala
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<210> 12
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<212> PRT
<213> Mycobacterium tuberculosis
<400> 12

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Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
35 40 45

Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
50 55 60

Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
65 70 75 80

Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
85 90 95

Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
100 105 110

Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
115 120 125

Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
130 135 140

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

Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
165 170 175

Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
180 185 190

Ala Ala Ser
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eof-seq1

<210> 13
 <211> 391
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 13

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Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp
 20 25 30

Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35 40 45

Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50 55 60

Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65 70 75 80

Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
 85 90 95

Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
 100 105 110

Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
 115 120 125

Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
 130 135 140

Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala
 145 150 155 160

Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr
 165 170 175

Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser
 180 185 190

Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
 195 200 205

Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
 210 215 220

Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
 225 230 235 240

Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
 245 250 255
 Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
 260 265 270
 Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
 275 280 285
 Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
 290 295 300
 Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
 305 310 315 320
 Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
 325 330 335
 Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
 340 345 350
 Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
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 Pro His Ser Pro Ala Ala Gly
 385 390

<210> 14
 <211> 423
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 14

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Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val
 35 40 45

Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala
 50 55 60

Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala
 65 70 75 80

Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala
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															90					95										
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Asn	Arg	Ser	Arg	Leu	Met	Ser	Leu	Val	Ala	Ala	Asn	Ile	Leu	Gly	Gln															
		115					120					125																		
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	130					135					140																			
Ala	Gln	Asp	Ala	Ala	Val	Met	Tyr	Ser	Tyr	Glu	Gly	Ala	Ser	Ala	Ala															
145					150					155					160															
Ala	Ser	Ala	Leu	Pro	Pro	Phe	Thr	Pro	Pro	Val	Gln	Gly	Thr	Gly	Pro															
				165					170					175																
Ala	Gly	Pro	Ala	Ala	Ala	Ala	Ala	Ala	Thr	Gln	Ala	Ala	Gly	Ala	Gly															
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Ala	Val	Ala	Asp	Ala	Gln	Ala	Thr	Leu	Ala	Gln	Leu	Pro	Pro	Gly	Ile															
		195					200					205																		
Leu	Ser	Asp	Ile	Leu	Ser	Ala	Leu	Ala	Ala	Asn	Ala	Asp	Pro	Leu	Thr															
	210					215				220																				
Ser	Gly	Leu	Leu	Gly	Ile	Ala	Ser	Thr	Leu	Asn	Pro	Gln	Val	Gly	Ser															
225					230					235					240															
Ala	Gln	Pro	Ile	Val	Ile	Pro	Thr	Pro	Ile	Gly	Glu	Leu	Asp	Val	Ile															
				245					250					255																
Ala	Leu	Tyr	Ile	Ala	Ser	Ile	Ala	Thr	Gly	Ser	Ile	Ala	Leu	Ala	Ile															
			260					265					270																	
Thr	Asn	Thr	Ala	Arg	Pro	Trp	His	Ile	Gly	Leu	Tyr	Gly	Asn	Ala	Gly															
		275					280					285																		
Gly	Leu	Gly	Pro	Thr	Gln	Gly	His	Pro	Leu	Ser	Ser	Ala	Thr	Asp	Glu															
	290					295					300																			
Pro	Glu	Pro	His	Trp	Gly	Pro	Phe	Gly	Gly	Ala	Ala	Pro	Val	Ser	Ala															
305					310					315					320															
Gly	Val	Gly	His	Ala	Ala	Leu	Val	Gly	Ala	Leu	Ser	Val	Pro	His	Ser															
				325					330					335																
Trp	Thr	Thr	Ala	Ala	Pro	Glu	Ile	Gln	Leu	Ala	Val	Gln	Ala	Thr	Pro															
			340					345					350																	
Thr	Phe	Ser	Ser	Ser	Ala	Gly	Ala	Asp	Pro	Thr	Ala	Leu	Asn	Gly	Met															

eo1f-seq1

<400> 16

Met Gln Leu Val Asp Arg Val Arg Gly Ala Val Thr Gly Met Ser Arg
-40 -35 -30

Arg Leu Val Val Gly Ala Val Gly Ala Ala Leu Val Ser Gly Leu Val
-25 -20 -15

Gly Ala Val Gly Gly Thr Ala Thr Ala Gly Ala Phe Ser Arg Pro Gly
-10 -5 -1 1 5

Leu Pro Val Glu Tyr Leu Gln Val Pro Ser Pro Ser Met Gly Arg Asp
10 15 20

Ile Lys Val Gln Phe Gln Ser Gly Gly Ala Asn Ser Pro Ala Leu Tyr
25 30 35

Leu Leu Asp Gly Leu Arg Ala Gln Asp Asp Phe Ser Gly Trp Asp Ile
40 45 50

Asn Thr Pro Ala Phe Glu Trp Tyr Asp Gln Ser Gly Leu Ser Val Val
55 60 65 70

Met Pro Val Gly Gly Gln Ser Ser Phe Tyr Ser Asp Trp Tyr Gln Pro
75 80 85

Ala Cys Gly Lys Ala Gly Cys Gln Thr Tyr Lys Trp Glu Thr Phe Leu
90 95 100

Thr Ser Glu Leu Pro Gly Trp Leu Gln Ala Asn Arg His Val Lys Pro
105 110 115

Thr Gly Ser Ala Val Val Gly Leu Ser Met Ala Ala Ser Ser Ala Leu
120 125 130

Thr Leu Ala Ile Tyr His Pro Gln Gln Phe Val Tyr Ala Gly Ala Met
135 140 145 150

Ser Gly Leu Leu Asp Pro Ser Gln Ala Met Gly Pro Thr Leu Ile Gly
155 160 165

Leu Ala Met Gly Asp Ala Gly Gly Tyr Lys Ala Ser Asp Met Trp Gly
170 175 180

Pro Lys Glu Asp Pro Ala Trp Gln Arg Asn Asp Pro Leu Leu Asn Val
185 190 195

Gly Lys Leu Ile Ala Asn Asn Thr Arg Val Trp Val Tyr Cys Gly Asn
200 205 210

Gly Lys Pro Ser Asp Leu Gly Gly Asn Asn Leu Pro Ala Lys Phe Leu
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100

90

95

Leu Pro Gln Trp Leu Ser Ala Asn Arg Ala Val Lys Pro Thr Gly Ser
105 110 115 120

Ala Ala Ile Gly Leu Ser Met Ala Gly Ser Ser Ala Met Ile Leu Ala
125 130 135

Ala Tyr His Pro Gln Gln Phe Ile Tyr Ala Gly Ser Leu Ser Ala Leu
140 145 150

Leu Asp Pro Ser Gln Gly Met Gly Pro Ser Leu Ile Gly Leu Ala Met
155 160 165

Gly Asp Ala Gly Gly Tyr Lys Ala Ala Asp Met Trp Gly Pro Ser Ser
170 175 180

Asp Pro Ala Trp Glu Arg Asn Asp Pro Thr Gln Gln Ile Pro Lys Leu
185 190 195 200

Val Ala Asn Asn Thr Arg Leu Trp Val Tyr Cys Gly Asn Gly Thr Pro
205 210 215

Asn Glu Leu Gly Gly Ala Asn Ile Pro Ala Glu Phe Leu Glu Asn Phe
220 225 230

Val Arg Ser Ser Asn Leu Lys Phe Gln Asp Ala Tyr Asn Ala Ala Gly
235 240 245

Gly His Asn Ala Val Phe Asn Phe Pro Pro Asn Gly Thr His Ser Trp
250 255 260

Glu Tyr Trp Gly Ala Gln Leu Asn Ala Met Lys Gly Asp Leu Gln Ser
265 270 275 280

Ser Leu Gly Ala Gly
285

<210> 18
<211> 144
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<221> INIT_MET
<222> (1)..(1)

<220>
<221> mat_peptide
<222> (2)..(144)

<400> 18

Met Ala Thr Thr Leu Pro Val Gln Arg His Pro Arg Ser Leu Phe Pro
Page 21

eolf-seq1

-1 1 5 10 15

Glu Phe Ser Glu Leu Phe Ala Ala Phe Pro Ser Phe Ala Gly Leu Arg
20 25 30

Pro Thr Phe Asp Thr Arg Leu Met Arg Leu Glu Asp Glu Met Lys Glu
35 40 45

Gly Arg Tyr Glu Val Arg Ala Glu Leu Pro Gly Val Asp Pro Asp Lys
50 55 60

Asp Val Asp Ile Met Val Arg Asp Gly Gln Leu Thr Ile Lys Ala Glu
65 70 75

Arg Thr Glu Gln Lys Asp Phe Asp Gly Arg Ser Glu Phe Ala Tyr Gly
80 85 90 95

Ser Phe Val Arg Thr Val Ser Leu Pro Val Gly Ala Asp Glu Asp Asp
100 105 110

Ile Lys Ala Thr Tyr Asp Lys Gly Ile Leu Thr Val Ser Val Ala Val
115 120 125

Ser Glu Gly Lys Pro Thr Glu Lys His Ile Gln Ile Arg Ser Thr Asn
130 135 140

<210> 19
<211> 228
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<221> mat_peptide
<222> (24)..(228)

<400> 19

Met Arg Ile Lys Ile Phe Met Leu Val Thr Ala Val Val Leu Leu Cys
-20 -15 -10

Cys Ser Gly Val Ala Thr Ala Ala Pro Lys Thr Tyr Cys Glu Glu Leu
-5 -1 1 5

Lys Gly Thr Asp Thr Gly Gln Ala Cys Gln Ile Gln Met Ser Asp Pro
10 15 20 25

Ala Tyr Asn Ile Asn Ile Ser Leu Pro Ser Tyr Tyr Pro Asp Gln Lys
30 35 40

Ser Leu Glu Asn Tyr Ile Ala Gln Thr Arg Asp Lys Phe Leu Ser Ala
45 50 55

Ala Thr Ser Ser Thr Pro Arg Glu Ala Pro Tyr Glu Leu Asn Ile Thr
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35

40

45

Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
50 55 60

Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
65 70 75 80

Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
85 90 95

Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
100 105 110

Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
115 120 125

Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
130 135 140

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

Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
165 170 175

Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
180 185 190

Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
195 200 205

Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
210 215 220

Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
225 230 235 240

Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
245 250 255

Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
260 265 270

Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
275 280 285

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

Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly

305	310	eolf-seq1 315	320
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Pro Pro Ala

<210> 21
 <211> 323
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ser/Ala mutant of mature Mtb32A

<400> 21

Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 1 5 10 15

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

Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 35 40 45

Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 50 55 60

Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 65 70 75 80

Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 85 90 95

Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 100 105 110

Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 115 120 125

Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 130 135 140

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

Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ala
 165 170 175

Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 180 185 190

Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 195 200 205

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Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
210 215 220

Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
225 230 235 240

Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
245 250 255

Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
260 265 270

Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
275 280 285

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

Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
305 310 315 320

Pro Pro Ala

<210> 22
<211> 96
<212> PRT
<213> Mycobacterium tuberculosis

<400> 22

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

<210> 23
<211> 723
<212> PRT
<213> Artificial sequence

eof-seq1

<220>

<223> Mtb72f

<400> 23

Met Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly
1 5 10 15

Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg
20 25 30

Ser Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu
35 40 45

Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg
50 55 60

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

Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met
85 90 95

Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr
100 105 110

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

Glu Gly Pro Pro Ala Glu Phe Met Val Asp Phe Gly Ala Leu Pro Pro
130 135 140

Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser Leu
145 150 155 160

Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe Ser
165 170 175

Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly Ser
180 185 190

Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro Tyr
195 200 205

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

Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
225 230 235 240

Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
245 250 255

eo1f-seq1

Ile Ala Thr Asn₂₆₀ Leu Leu Gly Gln Asn₂₆₅ Thr Pro Ala Ile Ala₂₇₀ Val Asn

Glu Ala Glu₂₇₅ Tyr Gly Glu Met Trp₂₈₀ Ala Gln Asp Ala Ala₂₈₅ Ala Met Phe

Gly Tyr₂₉₀ Ala Ala Ala Thr Ala₂₉₅ Thr Ala Thr Ala Thr₃₀₀ Leu Leu Pro Phe

Glu₃₀₅ Glu Ala Pro Glu₃₁₀ Met Thr Ser Ala Gly Gly₃₁₅ Leu Leu Glu Gln Ala₃₂₀

Ala Ala Val Glu₃₂₅ Glu Ala Ser Asp Thr Ala₃₃₀ Ala Ala Asn Gln Leu₃₃₅ Met

Asn Asn Val₃₄₀ Pro Gln Ala Leu Gln Gln₃₄₅ Leu Ala Gln Pro Thr₃₅₀ Gln Gly

Thr Thr₃₅₅ Pro Ser Ser Lys Leu Gly₃₆₀ Gly Leu Trp Lys Thr₃₆₅ Val Ser Pro

His Arg₃₇₀ Ser Pro Ile Ser Asn₃₇₅ Met Val Ser Met Ala₃₈₀ Asn Asn His Met

Ser Met Thr Asn Ser Gly₃₉₀ Val Ser Met Thr Asn₃₉₅ Thr Leu Ser Ser Met₄₀₀

Leu Lys Gly Phe Ala₄₀₅ Pro Ala Ala Ala Ala₄₁₀ Gln Ala Val Gln Thr Ala₄₁₅

Ala Gln Asn Gly₄₂₀ Val Arg Ala Met Ser₄₂₅ Ser Leu Gly Ser Ser₄₃₀ Leu Gly

Ser Ser Gly₄₃₅ Leu Gly Gly Gly Val₄₄₀ Ala Ala Asn Leu Gly₄₄₅ Arg Ala Ala

Ser Val Gly Ser Leu Ser Val₄₅₅ Pro Gln Ala Trp Ala₄₆₀ Ala Ala Asn Gln

Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu₄₇₅ Thr Ser Leu Thr Ser₄₈₀

Ala Ala Glu Arg Gly₄₈₅ Pro Gly Gln Met Leu₄₉₀ Gly Gly Leu Pro Val₄₉₅ Gly

Gln Met Gly Ala Arg Ala Gly Gly Gly₅₀₅ Leu Ser Gly Val Leu₅₁₀ Arg Val

Pro Pro Arg₅₁₅ Pro Tyr Val Met Pro₅₂₀ His Ser Pro Ala Ala₅₂₅ Gly Asp Ile

eo1f-seq1

Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
530 535 540

Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val Val
545 550 555 560

Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
565 570 575

Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
580 585 590

Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
595 600 605

Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
610 615 620

Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
625 630 635 640

Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
645 650 655

Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
660 665 670

Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
675 680 685

Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
690 695 700

Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
705 710 715 720

Ala Ala Ser

<210> 24
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> M72

<400> 24

Met Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly
1 5 10 15

eolf-seq1

Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg
20 25 30

Ser Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu
35 40 45

Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg
50 55 60

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

Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met
85 90 95

Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr
100 105 110

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

Glu Gly Pro Pro Ala Glu Phe Met Val Asp Phe Gly Ala Leu Pro Pro
130 135 140

Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser Leu
145 150 155 160

Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe Ser
165 170 175

Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly Ser
180 185 190

Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro Tyr
195 200 205

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

Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
225 230 235 240

Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
245 250 255

Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
260 265 270

Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe
275 280 285

eolf-seq1

Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
290 295 300

Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
305 310 315 320

Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met
325 330 335

Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln Gly
340 345 350

Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro
355 360 365

His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met
370 375 380

Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met
385 390 395 400

Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Gln Thr Ala
405 410 415

Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly
420 425 430

Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala
435 440 445

Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn Gln
450 455 460

Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser
465 470 475 480

Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val Gly
485 490 495

Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val Leu Arg Val
500 505 510

Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp Ile
515 520 525

Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
530 535 540

Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val Val
545 550 555 560

eolf-seql

Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
565 570 575

Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
580 585 590

Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
595 600 605

Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
610 615 620

Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
625 630 635 640

Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
645 650 655

Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
660 665 670

Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
675 680 685

Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ala
690 695 700

Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
705 710 715 720

Ala Ala Ser

<210> 25
<211> 702
<212> PRT
<213> Artificial sequence

<220>
<223> Mtb71f

<400> 25

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val
1 5 10 15

Val Ala Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn
20 25 30

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

Pro Pro Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly
50 55 60

eof-seq1

Ala Ala Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn
65 70 75 80

Asn Tyr Glu Leu Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala
85 90 95

His Gly Ala Met Ile Arg Ala Gln Ala Ala Ser Leu Glu Ala Glu His
100 105 110

Gln Ala Ile Val Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly
115 120 125

Ala Gly Ser Val Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn
130 135 140

Phe Gln Val Ile Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln
145 150 155 160

Ala Ala Gly Asn Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser
165 170 175

Trp Ala Thr Ser Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val
180 185 190

Ala Ser Gln Ser Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr
195 200 205

Ile Gly Gln Ala Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln
210 215 220

Gly Glu Ser Ser Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala
225 230 235 240

Ala Ala Ala Lys Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu
245 250 255

Gly Glu Ala Ala Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ala Ser
260 265 270

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

Val Asn Ser Ser Arg Met Tyr Ser Gly Pro Gly Pro Glu Ser Met Leu
290 295 300

Ala Ala Ala Ala Ala Trp Asp Gly Val Ala Ala Glu Leu Thr Ser Ala
305 310 315 320

Ala Val Ser Tyr Gly Ser Val Val Ser Thr Leu Ile Val Glu Pro Trp
325 330 335

colf-seq1

Met Gly Pro Ala Ala Ala Ala Met Ala Ala Ala Ala Thr Pro Tyr Val
340 345 350

Gly Trp Leu Ala Ala Thr Ala Ala Leu Ala Lys Glu Thr Ala Thr Gln
355 360 365

Ala Arg Ala Ala Ala Glu Ala Phe Gly Thr Ala Phe Ala Met Thr Val
370 375 380

Pro Pro Ser Leu Val Ala Ala Asn Arg Ser Arg Leu Met Ser Leu Val
385 390 395 400

Ala Ala Asn Ile Leu Gly Gln Asn Ser Ala Ala Ile Ala Ala Thr Gln
405 410 415

Ala Glu Tyr Ala Glu Met Trp Ala Gln Asp Ala Ala Val Met Tyr Ser
420 425 430

Tyr Glu Gly Ala Ser Ala Ala Ala Ser Ala Leu Pro Pro Phe Thr Pro
435 440 445

Pro Val Gln Gly Thr Gly Pro Ala Gly Pro Ala Ala Ala Ala Ala Ala
450 455 460

Thr Gln Ala Ala Gly Ala Gly Ala Val Ala Asp Ala Gln Ala Thr Leu
465 470 475 480

Ala Gln Leu Pro Pro Gly Ile Leu Ser Asp Ile Leu Ser Ala Leu Ala
485 490 495

Ala Asn Ala Asp Pro Leu Thr Ser Gly Leu Leu Gly Ile Ala Ser Thr
500 505 510

Leu Asn Pro Gln Val Gly Ser Ala Gln Pro Ile Val Ile Pro Thr Pro
515 520 525

Ile Gly Glu Leu Asp Val Ile Ala Leu Tyr Ile Ala Ser Ile Ala Thr
530 535 540

Gly Ser Ile Ala Leu Ala Ile Thr Asn Thr Ala Arg Pro Trp His Ile
545 550 555 560

Gly Leu Tyr Gly Asn Ala Gly Gly Leu Gly Pro Thr Gln Gly His Pro
565 570 575

Leu Ser Ser Ala Thr Asp Glu Pro Glu Pro His Trp Gly Pro Phe Gly
580 585 590

Gly Ala Ala Pro Val Ser Ala Gly Val Gly His Ala Ala Leu Val Gly
595 600 605

eof-seq1

Ala Leu Ser Val Pro His Ser Trp Thr Thr Ala Ala Pro Glu Ile Gln
610 615 620

Leu Ala Val Gln Ala Thr Pro Thr Phe Ser Ser Ser Ala Gly Ala Asp
625 630 635 640

Pro Thr Ala Leu Asn Gly Met Pro Ala Gly Leu Leu Ser Gly Met Ala
645 650 655

Leu Ala Ser Leu Ala Ala Arg Gly Thr Thr Gly Gly Gly Gly Thr Arg
660 665 670

Ser Gly Thr Ser Thr Asp Gly Gln Glu Asp Gly Arg Lys Pro Pro Val
675 680 685

Val Val Ile Arg Glu Gln Pro Pro Pro Gly Asn Pro Pro Arg
690 695 700

<210> 26
<211> 920
<212> PRT
<213> Artificial Sequence

<220>
<223> M72-Mtb9.9-Mtb9.8

<400> 26

Met Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly
1 5 10 15

Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg
20 25 30

Ser Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu
35 40 45

Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg
50 55 60

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

Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met
85 90 95

Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr
100 105 110

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

Glu Gly Pro Pro Ala Glu Phe Met Val ^{eolf-seql} Asp Phe Gly Ala Leu Pro Pro
 130 135 140

Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser Leu
 145 150 155 160

Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe Ser
 165 170 175

Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly Ser
 180 185 190

Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro Tyr
 195 200 205

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

Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
 225 230 235 240

Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
 245 250 255

Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
 260 265 270

Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe
 275 280 285

Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
 290 295 300

Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
 305 310 315 320

Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met
 325 330 335

Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln Gly
 340 345 350

Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro
 355 360 365

His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met
 370 375 380

Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met
 385 390 395 400

eolf-seq1

Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Gln Thr Ala
405 410 415

Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly
420 425 430

ser ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala
435 440 445

ser val Gly Ser Leu Ser val Pro Gln Ala Trp Ala Ala Ala Asn Gln
450 455 460

Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser
465 470 475 480

Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro val Gly
485 490 495

Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly val Leu Arg val
500 505 510

Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp Ile
515 520 525

Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
530 535 540

Pro Leu Asp Pro Ser Ala Met val Ala Gln val Gly Pro Gln val val
545 550 555 560

Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala val Gly Ala Gly Thr
565 570 575

Gly Ile val Ile Asp Pro Asn Gly val val Leu Thr Asn Asn His Val
580 585 590

Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser val Gly Ser Gly Gln
595 600 605

Thr Tyr Gly Val Asp Val val Gly Tyr Asp Arg Thr Gln Asp Val Ala
610 615 620

val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
625 630 635 640

Gly Gly val Ala val Gly Glu Pro val val Ala Met Gly Asn Ser Gly
645 650 655

Gly Gln Gly Gly Thr Pro Arg Ala val Pro Gly Arg val val Ala Leu
660 665 670

Gly Gln Thr val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 675 680 eolf-seq1 685
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ala
 690 695 700
 Gly Gly Pro val val Asn Gly Leu Gly Gln val val Gly Met Asn Thr
 705 710 715 720
 Ala Ala Ser Ser Thr Met Thr Ile Asn Tyr Gln Phe Gly Asp val Asp
 725 730 735
 Ala His Gly Ala Met Ile Arg Ala Gln Ala Ala Ser Leu Glu Ala Glu
 740 745 750
 His Gln Ala Ile val Arg Asp val Leu Ala Ala Gly Asp Phe Trp Gly
 755 760 765
 Gly Ala Gly Ser val Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg
 770 775 780
 Asn Phe Gln val Ile Tyr Glu Gln Ala Asn Ala His Gly Gln Lys val
 785 790 795 800
 Gln Ala Ala Gly Asn Asn Met Ala Gln Thr Asp Ser Ala val Gly Ser
 805 810 815
 Ser Trp Ala Thr Ser Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu
 820 825 830
 val Ala Ser Gln Ser Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His
 835 840 845
 Thr Ile Gly Gln Ala Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His
 850 855 860
 Gln Gly Glu Ser Ser Ala Ala Phe Gln Ala Ala His Ala Arg Phe val
 865 870 875 880
 Ala Ala Ala Ala Lys val Asn Thr Leu Leu Asp val Ala Gln Ala Asn
 885 890 895
 Leu Gly Glu Ala Ala Gly Thr Tyr val Ala Ala Asp Ala Ala Ala Ala
 900 905 910
 Ser Thr Tyr Thr Gly Phe Pro Trp
 915 920

<210> 27
 <211> 1010
 <212> PRT
 <213> Artificial sequence

eolf-seq1

<220>

<223> M103

<400> 27

Met Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly
1 5 10 15

Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg
20 25 30

Ser Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu
35 40 45

Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg
50 55 60

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

Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met
85 90 95

Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr
100 105 110

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

Glu Gly Pro Pro Ala Glu Phe Met Val Asp Phe Gly Ala Leu Pro Pro
130 135 140

Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser Leu
145 150 155 160

Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe Ser
165 170 175

Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly Ser
180 185 190

Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro Tyr
195 200 205

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

Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
225 230 235 240

Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
245 250 255

eo1f-seq1

Ile Ala Thr Asn₂₆₀ Leu Leu Gly Gln Asn₂₆₅ Thr Pro Ala Ile Ala₂₇₀ Val Asn

Glu Ala Glu₂₇₅ Tyr Gly Glu Met Trp₂₈₀ Ala Gln Asp Ala Ala₂₈₅ Ala Met Phe

Gly Tyr₂₉₀ Ala Ala Ala Thr Ala₂₉₅ Thr Ala Thr Ala Thr₃₀₀ Leu Leu Pro Phe

Glu₃₀₅ Glu Ala Pro Glu₃₁₀ Met Thr Ser Ala Gly Gly₃₁₅ Leu Leu Glu Gln Ala₃₂₀

Ala Ala Val Glu₃₂₅ Glu Ala Ser Asp Thr Ala₃₃₀ Ala Ala Asn Gln Leu₃₃₅ Met

Asn Asn Val₃₄₀ Pro Gln Ala Leu Gln Gln₃₄₅ Leu Ala Gln Pro Thr₃₅₀ Gln Gly

Thr Thr₃₅₅ Pro Ser Ser Lys Leu Gly₃₆₀ Gly Leu Trp Lys Thr₃₆₅ Val Ser Pro

His Arg₃₇₀ Ser Pro Ile Ser Asn₃₇₅ Met Val Ser Met Ala₃₈₀ Asn Asn His Met

Ser Met Thr Asn Ser Gly₃₉₀ Val Ser Met Thr Asn₃₉₅ Thr Leu Ser Ser Met₄₀₀

Leu Lys Gly Phe Ala₄₀₅ Pro Ala Ala Ala Ala₄₁₀ Gln Ala Val Gln Thr Ala₄₁₅

Ala Gln Asn Gly₄₂₀ Val Arg Ala Met Ser₄₂₅ Ser Leu Gly Ser₄₃₀ Ser Leu Gly

Ser Ser Gly₄₃₅ Leu Gly Gly Gly Val₄₄₀ Ala Ala Asn Leu Gly₄₄₅ Arg Ala Ala

Ser Val₄₅₀ Gly Ser Leu Ser Val₄₅₅ Pro Gln Ala Trp Ala₄₆₀ Ala Ala Ala Asn Gln

Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu₄₇₅ Thr Ser Leu Thr Ser₄₈₀

Ala Ala Glu Arg Gly₄₈₅ Pro Gly Gln Met Leu₄₉₀ Gly Gly Leu Pro Val₄₉₅ Gly

Gln Met Gly Ala Arg Ala Gly Gly Gly₅₀₅ Leu Ser Gly Val Leu₅₁₀ Arg Val

Pro Pro Arg₅₁₅ Pro Tyr Val Met Pro₅₂₀ His Ser Pro Ala Ala₅₂₅ Gly Asp Ile

eo1f-seq1

Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
530 535 540

Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val Val
545 550 555 560

Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
565 570 575

Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
580 585 590

Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
595 600 605

Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
610 615 620

Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
625 630 635 640

Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
645 650 655

Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
660 665 670

Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
675 680 685

Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ala
690 695 700

Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
705 710 715 720

Ala Ala Ser Ser Gly Phe Ser Arg Pro Gly Leu Pro Val Glu Tyr Leu
725 730 735

Gln Val Pro Ser Pro Ser Met Gly Arg Asp Ile Lys Val Gln Phe Gln
740 745 750

Ser Gly Gly Asn Asn Ser Pro Ala Val Tyr Leu Leu Asp Gly Leu Arg
755 760 765

Ala Gln Asp Asp Tyr Asn Gly Trp Asp Ile Asn Thr Pro Ala Phe Glu
770 775 780

Trp Tyr Tyr Gln Ser Gly Leu Ser Ile Val Met Pro Val Gly Gly Gln
785 790 795 800

eof-seq1

Ser Ser Phe Tyr Ser Asp Trp Tyr Ser Pro Ala Cys Gly Lys Ala Gly
805 810 815

Cys Gln Thr Tyr Lys Trp Glu Thr Phe Leu Thr Ser Glu Leu Pro Gln
820 825 830

Trp Leu Ser Ala Asn Arg Ala Val Lys Pro Thr Gly Ser Ala Ala Ile
835 840 845

Gly Leu Ser Met Ala Gly Ser Ser Ala Met Ile Leu Ala Ala Tyr His
850 855 860

Pro Gln Gln Phe Ile Tyr Ala Gly Ser Leu Ser Ala Leu Leu Asp Pro
865 870 875 880

Ser Gln Gly Met Gly Pro Ser Leu Ile Gly Leu Ala Met Gly Asp Ala
885 890 895

Gly Gly Tyr Lys Ala Ala Asp Met Trp Gly Pro Ser Ser Asp Pro Ala
900 905 910

Trp Glu Arg Asn Asp Pro Thr Gln Gln Ile Pro Lys Leu Val Ala Asn
915 920 925

Asn Thr Arg Leu Trp Val Tyr Cys Gly Asn Gly Thr Pro Asn Glu Leu
930 935 940

Gly Gly Ala Asn Ile Pro Ala Glu Phe Leu Glu Asn Phe Val Arg Ser
945 950 955 960

Ser Asn Leu Lys Phe Gln Asp Ala Tyr Asn Ala Ala Gly Gly His Asn
965 970 975

Ala Val Phe Asn Phe Pro Pro Asn Gly Thr His Ser Trp Glu Tyr Trp
980 985 990

Gly Ala Gln Leu Asn Ala Met Lys Gly Asp Leu Gln Ser Ser Leu Gly
995 1000 1005

Ala Gly
1010

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<211> 1148
<212> PRT
<213> Artificial sequence

<220>
<223> M114

<400> 28

eolf-seq1

Met Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly
1 5 10 15

Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg
20 25 30

Ser Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu
35 40 45

Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg
50 55 60

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

Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met
85 90 95

Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr
100 105 110

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

Glu Gly Pro Pro Ala Glu Phe Met Val Asp Phe Gly Ala Leu Pro Pro
130 135 140

Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser Leu
145 150 155 160

Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe Ser
165 170 175

Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly Ser
180 185 190

Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro Tyr
195 200 205

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

Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
225 230 235 240

Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
245 250 255

Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
260 265 270

eolf-seql

Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe
275 280 285

Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
290 295 300

Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
305 310 315 320

Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met
325 330 335

Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln Gly
340 345 350

Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro
355 360 365

His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met
370 375 380

Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met
385 390 395 400

Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Gln Thr Ala
405 410 415

Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly
420 425 430

Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala
435 440 445

Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn Gln
450 455 460

Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser
465 470 475 480

Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val Gly
485 490 495

Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val Leu Arg Val
500 505 510

Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp Ile
515 520 525

Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
530 535 540

eolf-seq1

Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val Val
545 550 555 560

Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
565 570 575

Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
580 585 590

Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
595 600 605

Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
610 615 620

Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
625 630 635 640

Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
645 650 655

Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
660 665 670

Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
675 680 685

Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ala
690 695 700

Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
705 710 715 720

Ala Ala Ser Ser Thr Met Asp Phe Gly Leu Leu Pro Pro Glu Val Asn
725 730 735

Ser Ser Arg Met Tyr Ser Gly Pro Gly Pro Glu Ser Met Leu Ala Ala
740 745 750

Ala Ala Ala Trp Asp Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val
755 760 765

Ser Tyr Gly Ser Val Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly
770 775 780

Pro Ala Ala Ala Ala Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp
785 790 795 800

Leu Ala Ala Thr Ala Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg
805 810 815

eolf-seq1
 Ala Ala Ala Glu Ala Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro
 820 825 830
 Ser Leu Val Ala Ala Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala
 835 840 845
 Asn Ile Leu Gly Gln Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu
 850 855 860
 Tyr Ala Glu Met Trp Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu
 865 870 875 880
 Gly Ala Ser Ala Ala Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val
 885 890 895
 Gln Gly Thr Gly Pro Ala Gly Pro Ala Ala Ala Ala Ala Thr Gln
 900 905 910
 Ala Ala Gly Ala Gly Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln
 915 920 925
 Leu Pro Pro Gly Ile Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn
 930 935 940
 Ala Asp Pro Leu Thr Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn
 945 950 955 960
 Pro Gln Val Gly Ser Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly
 965 970 975
 Glu Leu Asp Val Ile Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser
 980 985 990
 Ile Ala Leu Ala Ile Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu
 995 1000 1005
 Tyr Gly Asn Ala Gly Gly Leu Gly Pro Thr Gln Gly His Pro Leu
 1010 1015 1020
 Ser Ser Ala Thr Asp Glu Pro Glu Pro His Trp Gly Pro Phe Gly
 1025 1030 1035
 Gly Ala Ala Pro Val Ser Ala Gly Val Gly His Ala Ala Leu Val
 1040 1045 1050
 Gly Ala Leu Ser Val Pro His Ser Trp Thr Thr Ala Ala Pro Glu
 1055 1060 1065
 Ile Gln Leu Ala Val Gln Ala Thr Pro Thr Phe Ser Ser Ser Ala
 1070 1075 1080

eolf-seq1

Gly Ala Asp Pro Thr Ala Leu Asn Gly Met Pro Ala Gly Leu Leu
 1085 1090 1095

Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg Gly Thr Thr Gly
 1100 1105 1110

Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly Gln Glu Asp
 1115 1120 1125

Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro Pro Pro
 1130 1135 1140

Gly Asn Pro Pro Arg
 1145

<210> 29
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 29

Phe Ile Ile Asp Pro Thr Ile Ser Ala
 1 5

<210> 30
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 30

Ile Leu Tyr Ser Ser Leu Glu Tyr Phe
 1 5

<210> 31
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 31

Leu Glu Tyr Phe Glu Lys Ala Leu Glu
 1 5

<210> 32
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 32

Tyr Ala Gly Lys Asn Arg Asn His Val
 1 5

<210> 33
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis

eolf-seq1

<400> 33

Leu Ile His Asp Gln Ala Asn Ala Val
1 5

<210> 34

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 34

Phe Val Arg Pro Val Ala Val Asp Leu
1 5

<210> 35

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 35

Leu Thr Tyr Ile Pro Val Val Gly His
1 5

<210> 36

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 36

Tyr Ile Pro Val Val Gly His Ala Leu
1 5

<210> 37

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 37

Tyr Leu Val Val Lys Thr Leu Ile Asn
1 5

<210> 38

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 38

Leu Val Val Lys Thr Leu Ile Asn Ala
1 5

<210> 39

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 39

eolf-seq1

Val Lys Thr Leu Ile Asn Ala Thr Gln
1 5

<210> 40
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<400> 40

Leu Lys Leu Leu Ala Lys Leu Ala Glu
1 5

<210> 41
<211> 9
<212> PRT
<213> Mycobacterium tuberculosis
<400> 41

Leu Val Ala Ala Ala Ile Ala Asp Ile
1 5

<210> 42
<211> 9
<212> PRT
<213> Mycobacterium tuberculosis
<400> 42

Ile Ile Ser Asp Val Ala Asp Ile Ile
1 5

<210> 43
<211> 9
<212> PRT
<213> Mycobacterium tuberculosis
<400> 43

Trp Glu Phe Ile Thr Asn Ala Leu Asn
1 5

<210> 44
<211> 9
<212> PRT
<213> Mycobacterium tuberculosis
<400> 44

Leu Phe Gly Ala Ala Gly Leu Ser Ala
1 5

<210> 45
<211> 9
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<213> Mycobacterium tuberculosis
<400> 45

Leu Ala His Ala Asp Ser Leu Ala Ser

1

5

<210> 46
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 46

Leu Ala Ser Ser Ala Ser Leu Pro Ala
 1 5

<210> 47
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 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 47

Phe Gly Gly Leu Pro Ser Leu Ala Gln
 1 5

<210> 48
 <211> 9
 <212> PRT
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<400> 48

Phe Ile Ile Asp Pro Thr Ile Ser Ala
 1 5

<210> 49
 <211> 9
 <212> PRT
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<400> 49

Ile Ile Asp Pro Thr Ile Ser Ala Ile
 1 5

<210> 50
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 50

Pro Thr Ile Ser Ala Ile Asp Gly Leu
 1 5

<210> 51
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 <212> PRT
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<400> 51

Thr Ile Ser Ala Ile Asp Gly Leu Tyr
 1 5

eo1f-seq1

<210> 52
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 52
 Ser Ala Ile Asp Gly Leu Tyr Asp Leu
 1 5

<210> 53
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 53

Ala Ile Asp Gly Leu Tyr Asp Leu Leu
 1 5

<210> 54
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 54

Leu Tyr Asp Leu Leu Gly Ile Gly Ile
 1 5

<210> 55
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 55

Ile Pro Asn Gln Gly Gly Ile Leu Tyr
 1 5

<210> 56
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 56

Gly Ile Leu Tyr Ser Ser Leu Glu Tyr
 1 5

<210> 57
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 57

Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
 1 5

<210> 58

eolf-seq1

<211> 9
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 <213> Mycobacterium tuberculosis
 <400> 58
 Ser Leu Glu Tyr Phe Glu Lys Ala Leu
 1 5

<210> 59
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 59
 Tyr Phe Glu Lys Ala Leu Glu Glu Leu
 1 5

<210> 60
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 60
 Phe Glu Lys Ala Leu Glu Glu Leu Ala
 1 5

<210> 61
 <211> 9
 <212> PRT
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 <400> 61
 Asn His Val Asn Phe Phe Gln Glu Leu
 1 5

<210> 62
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 62
 Glu Leu Ala Asp Leu Asp Arg Gln Leu
 1 5

<210> 63
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 63
 Leu Ala Asp Leu Asp Arg Gln Leu Ile
 1 5

<210> 64
 <211> 9
 <212> PRT

<213> Mycobacterium tuberculosis

<400> 64

Asp Leu Asp Arg Gln Leu Ile Ser Leu
1 5

<210> 65

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 65

Leu Asp Arg Gln Leu Ile Ser Leu Ile
1 5

<210> 66

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 66

Ala Val Gln Thr Thr Arg Asp Ile Leu
1 5

<210> 67

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 67

Glu Gly Ala Lys Lys Gly Leu Glu Phe
1 5

<210> 68

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 68

Lys Gly Leu Glu Phe Val Arg Pro Val
1 5

<210> 69

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 69

Gly Leu Glu Phe Val Arg Pro Val Ala
1 5

<210> 70

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

eolf-seq1

<400> 70

Leu Glu Phe Val Arg Pro Val Ala Val
1 5

<210> 71

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 71

Phe Val Arg Pro Val Ala Val Asp Leu
1 5

<210> 72

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 72

Arg Pro Val Ala Val Asp Leu Thr Tyr
1 5

<210> 73

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 73

Ala Val Asp Leu Thr Tyr Ile Pro Val
1 5

<210> 74

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 74

Thr Tyr Ile Pro Val Val Gly His Ala
1 5

<210> 75

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 75

Tyr Ile Pro Val Val Gly His Ala Leu
1 5

<210> 76

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 76

Leu Ser Ala Ala Phe Gln Ala Pro Phe
1 5

<210> 77
<211> 9
<212> PRT
<213> Mycobacterium tuberculosis

<400> 77

Ser Ala Ala Phe Gln Ala Pro Phe Cys
1 5

<210> 78
<211> 9
<212> PRT
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<400> 78

Ala Ala Phe Gln Ala Pro Phe Cys Ala
1 5

<210> 79
<211> 9
<212> PRT
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<400> 79

Phe Gln Ala Pro Phe Cys Ala Gly Ala
1 5

<210> 80
<211> 9
<212> PRT
<213> Mycobacterium tuberculosis

<400> 80

Ala Pro Phe Cys Ala Gly Ala Met Ala
1 5

<210> 81
<211> 9
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<213> Mycobacterium tuberculosis

<400> 81

Pro Phe Cys Ala Gly Ala Met Ala Val
1 5

<210> 82
<211> 9
<212> PRT
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<400> 82

Ala Met Ala Val Val Gly Gly Ala Leu
1 5

<210> 83
 <211> 9
 <212> PRT
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<400> 83

Ala Val Val Gly Gly Ala Leu Ala Tyr
 1 5

<210> 84
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 84

Gly Ala Leu Ala Tyr Leu Val Val Lys
 1 5

<210> 85
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 85

Leu Ala Tyr Leu Val Val Lys Thr Leu
 1 5

<210> 86
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 86

Ala Tyr Leu Val Val Lys Thr Leu Ile
 1 5

<210> 87
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 87

Lys Thr Leu Ile Asn Ala Thr Gln Leu
 1 5

<210> 88
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 88

Thr Leu Ile Asn Ala Thr Gln Leu Leu
 1 5

eolf-seq1

<210> 89
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 89
 Ile Asn Ala Thr Gln Leu Leu Lys Leu
 1 5

<210> 90
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 90
 Asn Ala Thr Gln Leu Leu Lys Leu Leu
 1 5

<210> 91
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 91
 Gln Leu Leu Lys Leu Leu Ala Lys Leu
 1 5

<210> 92
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 92
 Lys Leu Leu Ala Lys Leu Ala Glu Leu
 1 5

<210> 93
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 Leu Leu Ala Lys Leu Ala Glu Leu Val
 1 5

<210> 94
 <211> 9
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 Lys Leu Ala Glu Leu Val Ala Ala Ala
 1 5

<210> 95
 <211> 9

<212> PRT
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 <400> 95

Leu Ala Glu Leu Val Ala Ala Ala Ile
 1 5

<210> 96
 <211> 9
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Leu Val Ala Ala Ala Ile Ala Asp Ile
 1 5

<210> 97
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 97

Ala Ile Ala Asp Ile Ile Ser Asp Val
 1 5

<210> 98
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis
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Ile Ala Asp Ile Ile Ser Asp Val Ala
 1 5

<210> 99
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 99

Ile Ser Asp Val Ala Asp Ile Ile Lys
 1 5

<210> 100
 <211> 9
 <212> PRT
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Thr Leu Gly Glu Val Trp Glu Phe Ile
 1 5

<210> 101
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 <213> Mycobacterium tuberculosis

<400> 101

Phe Ile Thr Asn Ala Leu Asn Gly Leu
 1 5

<210> 102

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 102

Asn Ala Leu Asn Gly Leu Lys Glu Leu
 1 5

<210> 103

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 103

Lys Leu Thr Gly Trp Val Thr Gly Leu
 1 5

<210> 104

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 104

Leu Thr Gly Trp Val Thr Gly Leu Phe
 1 5

<210> 105

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 105

Gly Trp Ser Asn Leu Glu Ser Phe Phe
 1 5

<210> 106

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 106

Asn Leu Glu Ser Phe Phe Ala Gly Val
 1 5

<210> 107

<211> 9

<212> PRT

<213> Mycobacterium tuberculosis

<400> 107

eof-seq1

Ser Phe Phe Ala Gly Val Pro Gly Leu
1 5

<210> 108
<211> 9
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<400> 108

Gly Leu Thr Gly Ala Thr Ser Gly Leu
1 5

<210> 109
<211> 9
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Leu Ser Gln Val Thr Gly Leu Phe Gly
1 5

<210> 110
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Ser Gln Val Thr Gly Leu Phe Gly Ala
1 5

<210> 111
<211> 9
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Leu Ser Ala Ser Ser Gly Leu Ala His
1 5

<210> 112
<211> 9
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<400> 112

Ala Ser Ser Gly Leu Ala His Ala Asp
1 5

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<213> Mycobacterium tuberculosis
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Ser Gly Leu Ala His Ala Asp Ser Leu

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 <212> PRT
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<400> 114

Gly Leu Ala His Ala Asp Ser Leu Ala
 1 5

<210> 115
 <211> 9
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<400> 115

Ser Leu Ala Ser Ser Ala Ser Leu Pro
 1 5

<210> 116
 <211> 9
 <212> PRT
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<400> 116

Ala Ser Ser Ala Ser Leu Pro Ala Leu
 1 5

<210> 117
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 117

Ser Gly Phe Gly Gly Leu Pro Ser Leu
 1 5

<210> 118
 <211> 9
 <212> PRT
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<400> 118

Leu Pro Ser Leu Ala Gln Val His Ala
 1 5

<210> 119
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 119

His Ala Ala Ser Thr Arg Gln Ala Leu
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eolf-seq1

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 <213> Mycobacterium tuberculosis

<400> 120

Ser Thr Arg Gln Ala Leu Arg Pro Arg
 1 5

<210> 121
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 121

Arg Pro Arg Ala Asp Gly Pro Val Gly
 1 5

<210> 122
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 122

Glu Gln Val Gly Gly Gln Ser Gln Leu
 1 5

<210> 123
 <211> 9
 <212> PRT
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<400> 123

Gly Ala Ser Lys Gly Thr Thr Thr Lys
 1 5

<210> 124
 <211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 124

Ala Ser Lys Gly Thr Thr Thr Lys Lys
 1 5

<210> 125
 <211> 9
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<400> 125

Lys Gly Thr Thr Thr Lys Lys Tyr Ser
 1 5

<210> 126

eof-seq1

<211> 9
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 126

Thr Glu Asp Ala Glu Arg Ala Pro Val
 1 5

<210> 127
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 127

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
 1 5 10 15

Leu Tyr Asp Leu
 20

<210> 128
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 128

Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly
 1 5 10 15

Gly Ile Leu Tyr
 20

<210> 129
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 129

Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala
 1 5 10 15

Leu Glu Glu Leu
 20

<210> 130
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 130

Glu Lys Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp
 1 5 10 15

Leu Gly Ser Ala
 20

eolf-seq1

<210> 131
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 131

Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg
 1 5 10 15

Asn His Val Asn
 20

<210> 132
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 132

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

Arg Gln Leu Ile
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<210> 133
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 133

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

Val Gln Thr Thr
 20

<210> 134
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 134

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

Gly Leu Glu Phe
 20

<210> 135
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 135

eo1f-seq1

Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr
1 5 10 15

Tyr Ile Pro Val
20

<210> 136
<211> 27
<212> PRT
<213> Mycobacterium tuberculosis

<400> 136

Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly
1 5 10 15

His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe
20 25

<210> 137
<211> 20
<212> PRT
<213> Mycobacterium tuberculosis

<400> 137

Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val Val Gly
1 5 10 15

Gly Ala Leu Ala
20

<210> 138
<211> 20
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<213> Mycobacterium tuberculosis

<400> 138

Val Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn
1 5 10 15

Ala Thr Gln Leu
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<210> 139
<211> 20
<212> PRT
<213> Mycobacterium tuberculosis

<400> 139

Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu
1 5 10 15

Leu Val Ala Ala
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eolf-seq1

<210> 140
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 140

Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val
 1 5 10 15

Ala Asp Ile Ile
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<210> 141
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 141

Ser Asp Val Ala Asp Ile Ile Lys Gly Thr Leu Gly Glu Val Trp Glu
 1 5 10 15

Phe Ile Thr Asn
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<210> 142
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 142

Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp
 1 5 10 15

Asp Lys Leu Thr
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<210> 143
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 143

Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 1 5 10 15

Gly Trp Ser Asn
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<210> 144
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 144

eolf-seq1

Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro
 1 5 10 15

Gly Leu Thr Gly
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<210> 145
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 145

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

Gly Leu Phe Gly
 20

<210> 146
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 146

Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly
 1 5 10 15

Leu Ala His Ala
 20

<210> 147
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 147

Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu
 1 5 10 15

Pro Ala Leu Ala
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<210> 148
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 148

Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly
 1 5 10 15

Gly Leu Pro Ser
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eo1f-seq1

<210> 149
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 149

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

Arg Gln Ala Leu
 20

<210> 150
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 150

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

Ala Ala Ala Glu
 20

<210> 151
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 151

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

Ser Ala Gln Gly
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<210> 152
 <211> 19
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 152

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

Met Gly Gly

<210> 153
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 153

Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly

1	5	10	15
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eof-seq1
 Thr Thr Thr Lys
 20

<210> 154
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 154

Ser	Lys	Gly	Thr	Thr	Thr	Lys	Lys	Tyr	Ser	Glu	Gly	Ala	Ala	Ala	Gly
1				5					10						15

Thr Glu Asp Ala
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<210> 155
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 155

Ala	Ala	Gly	Thr	Glu	Asp	Ala	Glu	Arg	Ala	Pro	Val	Glu	Ala	Asp	Ala
1				5					10						15

Gly Gly Gly Gln
 20

<210> 156
 <211> 20
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 156

Arg	Ala	Pro	Val	Glu	Ala	Asp	Ala	Gly	Gly	Gly	Gln	Lys	Val	Leu	Val
1				5					10						15

Arg Asn Val Val
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<210> 157
 <211> 1053
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 157

Met	Asn	Phe	Ser	Val	Leu	Pro	Pro	Glu	Ile	Asn	Ser	Ala	Leu	Ile	Phe
1				5					10						15

Ala	Gly	Ala	Gly	Pro	Glu	Pro	Met	Ala	Ala	Ala	Ala	Thr	Ala	Trp	Asp
			20					25					30		

Gly	Leu	Ala	Met	Glu	Leu	Ala	Ser	Ala	Ala	Ala	Ser	Phe	Gly	Ser	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

co1f-seq1

35

40

45

Thr Ser Gly Leu Val Gly Gly Ala Trp Gln Gly Ala Ser Ser Ser Ala
50 55 60

Met Ala Ala Ala Ala Ala Pro Tyr Ala Ala Trp Leu Ala Ala Ala Ala
65 70 75 80

Val Gln Ala Glu Gln Thr Ala Ala Gln Ala Ala Ala Met Ile Ala Glu
85 90 95

Phe Glu Ala Val Lys Thr Ala Val Val Gln Pro Met Leu Val Ala Ala
100 105 110

Asn Arg Ala Asp Leu Val Ser Leu Val Met Ser Asn Leu Phe Gly Gln
115 120 125

Asn Ala Pro Ala Ile Ala Ala Ile Glu Ala Thr Tyr Glu Gln Met Trp
130 135 140

Ala Ala Asp Val Ser Ala Met Ser Ala Tyr His Ala Gly Ala Ser Ala
145 150 155 160

Ile Ala Ser Ala Leu Ser Pro Phe Ser Lys Pro Leu Gln Asn Leu Ala
165 170 175

Gly Leu Pro Ala Trp Leu Ala Ser Gly Ala Pro Ala Ala Ala Met Thr
180 185 190

Ala Ala Ala Gly Ile Pro Ala Leu Ala Gly Gly Pro Thr Ala Ile Asn
195 200 205

Leu Gly Ile Ala Asn Val Gly Gly Gly Asn Val Gly Asn Ala Asn Asn
210 215 220

Gly Leu Ala Asn Ile Gly Asn Ala Asn Leu Gly Asn Tyr Asn Phe Gly
225 230 235 240

Ser Gly Asn Phe Gly Asn Ser Asn Ile Gly Ser Ala Ser Leu Gly Asn
245 250 255

Asn Asn Ile Gly Phe Gly Asn Leu Gly Ser Asn Asn Val Gly Val Gly
260 265 270

Asn Leu Gly Asn Leu Asn Thr Gly Phe Ala Asn Thr Gly Leu Gly Asn
275 280 285

Phe Gly Phe Gly Asn Thr Gly Asn Asn Asn Ile Gly Ile Gly Leu Thr
290 295 300

Gly Asn Asn Gln Ile Gly Ile Gly Gly Leu Asn Ser Gly Thr Gly Asn

305	310	eolf-seq1		320
		315		
Phe Gly Leu Phe	Asn Ser Gly Ser Gly	Asn Val Gly Phe Phe	Asn Ser	
	325	330	335	
Gly Asn Gly	Asn Phe Gly Ile Gly	Asn Ser Gly Asn Phe	Asn Thr Gly	
	340	345	350	
Gly Trp	Asn Ser Gly His Gly	Asn Thr Gly Phe Phe	Asn Ala Gly Ser	
	355	360	365	
Phe	Asn Thr Gly Met Leu	Asp Val Gly Asn Ala	Asn Thr Gly Ser Leu	
	370	375	380	
Asn Thr Gly Ser Tyr	Asn Met Gly Asp Phe	Asn Pro Gly Ser Ser	Asn	
385	390	395	400	
Thr Gly Thr Phe	Asn Thr Gly Asn Ala	Asn Thr Gly Phe Leu	Asn Ala	
	405	410	415	
Gly Asn Ile	Asn Thr Gly Val Phe	Asn Ile Gly His Met	Asn Asn Gly	
	420	425	430	
Leu Phe	Asn Thr Gly Asp Met	Asn Asn Gly Val Phe	Tyr Arg Gly Val	
	435	440	445	
Gly Gln Gly Ser Leu Gln	Phe Ser Ile Thr Thr	Pro Asp Leu Thr Leu		
	450	455	460	
Pro Pro Leu Gln Ile	Pro Gly Ile Ser Val	Pro Ala Phe Ser Leu Pro		
465	470	475	480	
Ala Ile Thr Leu	Pro Ser Leu Asn Ile	Pro Ala Ala Thr Thr	Pro Ala	
	485	490	495	
Asn Ile Thr	Val Gly Ala Phe Ser	Leu Pro Gly Leu Thr	Leu Pro Ser	
	500	505	510	
Leu Asn Ile	Pro Ala Ala Thr Thr	Pro Ala Asn Ile Thr	Val Gly Ala	
	515	520	525	
Phe Ser Leu Pro Gly Leu	Thr Leu Pro Ser Leu	Asn Ile Pro Ala Ala		
	530	535	540	
Thr Thr Pro Ala Asn	Ile Thr Val Gly Ala	Phe Ser Leu Pro Gly	Leu	
545	550	555	560	
Thr Leu Pro Ser	Leu Asn Ile Pro Ala	Ala Thr Thr Pro Ala	Asn Ile	
	565	570	575	
Thr Val Gly Ala Phe Ser Leu Pro Gly	Leu Thr Leu Pro Ser Leu Asn			

eo1f-seq1

580

585

590

Ile Pro Ala Ala Thr Thr Pro Ala Asn Ile Thr Val Gly Ala Phe Ser
595 600 605

Leu Pro Gly Leu Thr Leu Pro Ser Leu Asn Ile Pro Ala Ala Thr Thr
610 615 620

Pro Ala Asn Ile Thr Val Ser Gly Phe Gln Leu Pro Pro Leu Ser Ile
625 630 635 640

Pro Ser Val Ala Ile Pro Pro Val Thr Val Pro Pro Ile Thr Val Gly
645 650 655

Ala Phe Asn Leu Pro Pro Leu Gln Ile Pro Glu Val Thr Ile Pro Gln
660 665 670

Leu Thr Ile Pro Ala Gly Ile Thr Ile Gly Gly Phe Ser Leu Pro Ala
675 680 685

Ile His Thr Gln Pro Ile Thr Val Gly Gln Ile Gly Val Gly Gln Phe
690 695 700

Gly Leu Pro Ser Ile Gly Trp Asp Val Phe Leu Ser Thr Pro Arg Ile
705 710 715 720

Thr Val Pro Ala Phe Gly Ile Pro Phe Thr Leu Gln Phe Gln Thr Asn
725 730 735

Val Pro Ala Leu Gln Pro Pro Gly Gly Gly Leu Ser Thr Phe Thr Asn
740 745 750

Gly Ala Leu Ile Phe Gly Glu Phe Asp Leu Pro Gln Leu Val Val His
755 760 765

Pro Tyr Thr Leu Thr Gly Pro Ile Val Ile Gly Ser Phe Phe Leu Pro
770 775 780

Ala Phe Asn Ile Pro Gly Ile Asp Val Pro Ala Ile Asn Val Asp Gly
785 790 795 800

Phe Thr Leu Pro Gln Ile Thr Thr Pro Ala Ile Thr Thr Pro Glu Phe
805 810 815

Ala Ile Pro Pro Ile Gly Val Gly Gly Phe Thr Leu Pro Gln Ile Thr
820 825 830

Thr Gln Glu Ile Ile Thr Pro Glu Leu Thr Ile Asn Ser Ile Gly Val
835 840 845

Gly Gly Phe Thr Leu Pro Gln Ile Thr Thr Pro Pro Ile Thr Thr Pro

eolf-seql 860

850

855

Pro Leu Thr Ile Asp Pro Ile Asn Leu Thr Gly Phe Thr Leu Pro Gln
865 870 875 880

Ile Thr Thr Pro Pro Ile Thr Thr Pro Pro Leu Thr Ile Asp Pro Ile
885 890 895

Asn Leu Thr Gly Phe Thr Leu Pro Gln Ile Thr Thr Pro Pro Ile Thr
900 905 910

Thr Pro Pro Leu Thr Ile Glu Pro Ile Gly Val Gly Gly Phe Thr Thr
915 920 925

Pro Pro Leu Thr Val Pro Gly Ile His Leu Pro Ser Thr Thr Ile Gly
930 935 940

Ala Phe Ala Ile Pro Gly Gly Pro Gly Tyr Phe Asn Ser Ser Thr Ala
945 950 955 960

Pro Ser Ser Gly Phe Phe Asn Ser Gly Ala Gly Gly Asn Ser Gly Phe
965 970 975

Gly Asn Asn Gly Ser Gly Leu Ser Gly Trp Phe Asn Thr Asn Pro Ala
980 985 990

Gly Leu Leu Gly Gly Ser Gly Tyr Gln Asn Phe Gly Gly Leu Ser Ser
995 1000 1005

Gly Phe Ser Asn Leu Gly Ser Gly Val Ser Gly Phe Ala Asn Arg
1010 1015 1020

Gly Ile Leu Pro Phe Ser Val Ala Ser Val Val Ser Gly Phe Ala
1025 1030 1035

Asn Ile Gly Thr Asn Leu Ala Gly Phe Phe Gln Gly Thr Thr Ser
1040 1045 1050

<210> 158

<211> 450

<212> PRT

<213> Mycobacterium tuberculosis

<400> 158

Met Ser Glu Leu Ser Val Ala Thr Gly Ala Val Ser Thr Ala Ser Ser
1 5 10 15

Ser Ile Pro Met Pro Ala Gly Val Asn Pro Ala Asp Leu Ala Ala Glu
20 25 30

Leu Ala Ala Val Val Thr Glu Ser Val Asp Glu Asp Tyr Leu Leu Tyr
35 40 45

eo1f-seq1

Glu Cys Asp Gly Gln Trp Val Leu Ala Ala Gly Val Gln Ala Met Val
 50 55 60
 Glu Leu Asp Ser Asp Glu Leu Arg Val Ile Arg Asp Gly Val Thr Arg
 65 70 75 80
 Arg Gln Gln Trp Ser Gly Arg Pro Gly Ala Ala Leu Gly Glu Ala Val
 85 90 95
 Asp Arg Leu Leu Leu Glu Thr Asp Gln Ala Phe Gly Trp Val Ala Phe
 100 105 110
 Glu Phe Gly Val His Arg Tyr Gly Leu Gln Gln Arg Leu Ala Pro His
 115 120 125
 Thr Pro Leu Ala Arg Val Phe Ser Pro Arg Thr Arg Ile Met Val Ser
 130 135 140
 Glu Lys Glu Ile Arg Leu Phe Asp Ala Gly Ile Arg His Arg Glu Ala
 145 150 155 160
 Ile Asp Arg Leu Leu Ala Thr Gly Val Arg Glu Val Pro Gln Ser Arg
 165 170 175
 Ser Val Asp Val Ser Asp Asp Pro Ser Gly Phe Arg Arg Arg Val Ala
 180 185 190
 Val Ala Val Asp Glu Ile Ala Ala Gly Arg Tyr His Lys Val Ile Leu
 195 200 205
 Ser Arg Cys Val Glu Val Pro Phe Ala Ile Asp Phe Pro Leu Thr Tyr
 210 215 220
 Arg Leu Gly Arg Arg His Asn Thr Pro Val Arg Ser Phe Leu Leu Gln
 225 230 235 240
 Leu Gly Gly Ile Arg Ala Leu Gly Tyr Ser Pro Glu Leu Val Thr Ala
 245 250 255
 Val Arg Ala Asp Gly Val Val Ile Thr Glu Pro Leu Ala Gly Thr Arg
 260 265 270
 Ala Leu Gly Arg Gly Pro Ala Ile Asp Arg Leu Ala Arg Asp Asp Leu
 275 280 285
 Glu Ser Asn Ser Lys Glu Ile Val Glu His Ala Ile Ser Val Arg Ser
 290 295 300
 Ser Leu Glu Glu Ile Thr Asp Ile Ala Glu Pro Gly Ser Ala Ala Val
 305 310 315 320

eof-seq1

Ile Asp Phe Met Thr Val Arg Glu Arg Gly Ser Val Gln His Leu Gly
325 330 335

Ser Thr Ile Arg Ala Arg Leu Asp Pro Ser Ser Asp Arg Met Ala Ala
340 345 350

Leu Glu Ala Leu Phe Pro Ala Val Thr Ala Ser Gly Ile Pro Lys Ala
355 360 365

Ala Gly Val Glu Ala Ile Phe Arg Leu Asp Glu Cys Pro Arg Gly Leu
370 375 380

Tyr Ser Gly Ala Val Val Met Leu Ser Ala Asp Gly Gly Leu Asp Ala
385 390 395 400

Ala Leu Thr Leu Arg Ala Ala Tyr Gln Val Gly Gly Arg Thr Trp Leu
405 410 415

Arg Ala Gly Ala Gly Ile Ile Glu Glu Ser Glu Pro Glu Arg Glu Phe
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Glu Glu Thr Cys Glu Lys Leu Ser Thr Leu Thr Pro Tyr Leu Val Ala
435 440 445

Arg Gln
450

<210> 159
<211> 324
<212> PRT
<213> Mycobacterium tuberculosis

<400> 159

Met Ser Asp Gln Val Pro Lys Pro His Arg His His Ile Trp Arg Ile
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Thr Arg Arg Thr Leu Ser Lys Ser Trp Asp Asp Ser Ile Phe Ser Glu
20 25 30

~~Ser Ala Gln Ala Ala Phe Trp Ser Ala Leu Ser Leu Pro Pro Leu Leu~~
35 40 45

Leu Gly Met Leu Gly Ser Leu Ala Tyr Val Ala Pro Leu Phe Gly Pro
50 55 60

Asp Thr Leu Pro Ala Ile Glu Lys Ser Ala Leu Ser Thr Ala His Ser
65 70 75 80

Phe Phe Ser Pro Ser Val Val Asn Glu Ile Ile Glu Pro Thr Ile Gly
85 90 95

eolf-seq1

Asp Ile Thr Asn₁₀₀ Asn Ala Arg Gly Glu₁₀₅ Val Ala Ser Leu Gly₁₁₀ Phe Leu

Ile Ser Leu₁₁₅ Trp Ala Gly Ser Ser₁₂₀ Ala Ile Ser Ala Phe₁₂₅ Val Asp Ala

Val Val₁₃₀ Glu Ala His Asp Gln₁₃₅ Thr Pro Leu Arg His₁₄₀ Pro Val Arg Gln

Arg Phe Phe Ala Leu Phe₁₅₀ Leu Tyr Val Val₁₅₅ Met Leu Val Phe Leu Val₁₆₀

Ala Thr Ala Pro Val₁₆₅ Met Val Val Gly Pro₁₇₀ Arg Lys Val Ser Glu₁₇₅ His

Ile Pro Glu Ser₁₈₀ Leu Ala Asn Leu Leu₁₈₅ Arg Tyr Gly Tyr Tyr₁₉₀ Pro Ala

Leu Ile Leu₁₉₅ Gly Leu Thr Val Gly₂₀₀ Val Ile Leu Leu Tyr₂₀₅ Arg Val Ala

Leu Pro Val₂₁₀ Pro Leu Pro Thr₂₁₅ His Arg Leu Val Leu₂₂₀ Gly Ala Val Leu

Ala Ile Ala Val Phe Leu₂₃₀ Ile Ala Thr Leu Gly₂₃₅ Leu Arg Val Tyr Leu₂₄₀

Ala Trp Ile Thr Arg₂₄₅ Thr Gly Tyr Thr Tyr₂₅₀ Gly Ala Leu Ala Thr Pro₂₅₅

Ile Ala Phe Leu₂₆₀ Leu Phe Ala Phe Phe₂₆₅ Gly Gly Phe Ala Ile₂₇₀ Met Leu

Gly Ala Glu₂₇₅ Leu Asn Ala Ala Val₂₈₀ Gln Glu Glu Trp Pro₂₈₅ Ala Pro Ala

Thr His Ala His Arg Leu Gly₂₉₅ Asn Trp Leu Lys Ala₃₀₀ Arg Ile Gly Val

Gly Thr Thr Thr Tyr Ser Ser Thr Ala Gln His Ser Ala Val Ala Ala

Glu Pro Pro Ser

<210> 160
<211> 1176
<212> DNA
<213> Artificial Sequence

<220>
<223> E.coli codon optimised H37Rv R3616c polynucleotide

eof-seq1

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ctgggtattg gtattccgaa tcagggtggg attctgtata gcagcctgga atattttgaa      120
aaagccctgg aagaactggc agcagcattt ccgggtgatg gttggctggg tagcgagca      180
gataaatatg ccggtaaaaa tcgcaatcat gtgaattttt ttcagggaact ggccgatctg      240
gatcgtcagc tgattagcct gattcatgac caggcaaatg cagttcagac caccgtgat      300
attctggaag gtgccaaaaa aggtctggaa tttgttcgtc cgggtggcagt tgatctgacc      360
tatattccgg ttgttgggtca tgcactgagc gcagcatttc aggcaccgtt ttgtgccggt      420
gcaatggcag ttgtgggtgg tgctctggca tatctggttg tgaaaaccct gattaatgca      480
accagctgc tgaaactgct ggcaaaactg gcagaactgg ttgcagcagc aattgcagat      540
attatttccg atgtggccga tattattaaa ggcaccctgg gcgaagtttg ggaatttatt      600
accaatgccc tgaatggctc gaaagaactg tgggataaac tgaccggttg gggtaccggt      660
ctgttttagc gtggttggag caatctggaa tctttttttg ccggtgttcc ggttctgacc      720
ggtgcaacca gcggtctgag ccaggtgaca ggtctgtttg gagcagctgg tctgagtgt      780
agtagcggtc tggctcatgc agatagcctg gcaagcagcg catctctgcc tgcactggca      840
ggcattggtg gtggatccgg ttttggtggt ctgccgagcc tggcacaggt tcatgcagca      900
agcaccctgc aggcactgcg tccgcgtgca gatggaccgg ttggagcagc agcagaacag      960
gttggtggtc agagccagct ggtagcgca cagggtagcc aggggtatggg tgggtccggtg     1020
ggcatgggtg gtatgcatcc gagcagcggg gcaagcaaag gcaccaccac caaaaaatat     1080
agcgaaggag cagctgctgg caccgaagat gcagaacgtg caccggttga agcagatgcc     1140
ggtggaggtc agaaagttct ggttcgcaat gtggtg      1176

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<210> 161
<211> 344
<212> PRT
<213> Artificial Sequence

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<220>
<223> H37RV RV3616c with deleted residues 136-183

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```

<400> 161

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Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
1           5           10          15
Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
20          25          30
Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
35          40          45
Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
50          55          60

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eolf-seq1

Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
65 70 75 80

Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
85 90 95

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

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

Leu Ser Ala Ala Phe Gln Ala Asp Val Ala Asp Ile Ile Lys Gly Thr
130 135 140

Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
145 150 155 160

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

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

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

Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
210 215 220

ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
225 230 235 240

Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
245 250 255

Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
260 265 270

Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
275 280 285

Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
290 295 300

Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
305 310 315 320

Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
325 330 335

eof-seq1

Lys Val Leu Val Arg Asn Val Val
340

<210> 162
<211> 381
<212> PRT
<213> Artificial Sequence

<220>
<223> H37Rv RV3616c with deleted residues 150-160

<400> 162

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
1 5 10 15

Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
20 25 30

Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
35 40 45

Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
50 55 60

Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
65 70 75 80

Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
85 90 95

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

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

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

Val Gly Gly Ala Leu Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala
145 150 155 160

Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp
165 170 175

Ile Ile Lys Gly Thr Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala
180 185 190

Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr
195 200 205

Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly
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eof-seq1 220

210

215

Val Pro Gly Leu Thr Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly
225 230 235 240

Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala
245 250 255

Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly
260 265 270

Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala
275 280 285

Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly
290 295 300

Ala Ala Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln
305 310 315 320

Gly Ser Gln Gly Met Gly Gly Pro Val Gly Met Gly Gly Met His Pro
325 330 335

Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly
340 345 350

Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp
355 360 365

Ala Gly Gly Gly Gln Lys Val Leu Val Arg Asn Val Val
370 375 380

<210> 163

<211> 373

<212> PRT

<213> Artificial sequence

<220>

<223> H37Rv Rv3616c with deleted residues 136-154

<400> 163

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
1 5 10 15

Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
20 25 30

Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
35 40 45

Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
50 55 60

eolf-seql

Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
65 70 75 80

Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
85 90 95

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

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

Leu Ser Ala Ala Phe Gln Ala Lys Thr Leu Ile Asn Ala Thr Gln Leu
130 135 140

Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala
145 150 155 160

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

Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp
180 185 190

Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser
195 200 205

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

Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser
225 230 235 240

Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser
245 250 255

Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu
260 265 270

Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg
275 280 285

Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly
290 295 300

Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro
305 310 315 320

Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr
325 330 335

eo1f-seq1

Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala
340 345 350

Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu
355 360 365

Val Arg Asn Val Val
370

<210> 164

<211> 375

<212> PRT

<213> Artificial Sequence

<220>

<223> H37Rv RV3616c with deleted residues 166-182

<400> 164

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
1 5 10 15

Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
20 25 30

Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
35 40 45

Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
50 55 60

Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
65 70 75 80

Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
85 90 95

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

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

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

Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
145 150 155 160

Thr Gln Leu Leu Lys Ser Asp Val Ala Asp Ile Ile Lys Gly Thr Leu
165 170 175

Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys Glu

eolf-seq1

180 185 190

Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly
195 200 205

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

Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly
225 230 235 240

Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser
245 250 255

Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly
260 265 270

Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala
275 280 285

Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val
290 295 300

Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly
305 310 315 320

Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys
325 330 335

Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu
340 345 350

Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys
355 360 365

Val Leu Val Arg Asn Val Val
370 375

<210> 165

<211> 387

<212> PRT

<213> Artificial Sequence

<220>

<223> H37RV RV3616c with deleted residues 135-139

<400> 165

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
1 5 10 15

Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
20 25 30

eolf-seql

Tyr Ser Ser₃₅ Leu Glu Tyr Phe Glu₄₀ Lys Ala Leu Glu₄₅ Glu Leu Ala Ala
 Ala Phe Pro Gly Asp Gly Trp₅₅ Leu Gly Ser Ala Ala₆₀ Asp Lys Tyr Ala
 Gly Lys Asn Arg Asn His₇₀ Val Asn Phe Phe₇₅ Gln Glu Leu Ala Asp Leu₈₀
 Asp Arg Gln Leu Ile₈₅ Ser Leu Ile His Asp₉₀ Gln Ala Asn Ala Val₉₅ Gln
 Thr Thr Arg Asp₁₀₀ Ile Leu Glu Gly Ala₁₀₅ Lys Lys Gly Leu Glu₁₁₀ Phe Val
 Arg Pro Val₁₁₅ Ala Val Asp Leu Thr₁₂₀ Tyr Ile Pro Val Val₁₂₅ Gly His Ala
 Leu Ser₁₃₀ Ala Ala Phe Gln Gly₁₃₅ Ala Met Ala Val Val₁₄₀ Gly Gly Ala Leu
 Ala Tyr Leu Val Val Lys₁₅₀ Thr Leu Ile Asn Ala₁₅₅ Thr Gln Leu Leu Lys₁₆₀
 Leu Leu Ala Lys Leu₁₆₅ Ala Glu Leu Val Ala₁₇₀ Ala Ala Ala Ile Ala Asp Ile₁₇₅
 Ile Ser Asp Val₁₈₀ Ala Asp Ile Ile Lys₁₈₅ Gly Thr Leu Gly Glu₁₉₀ Val Trp
 Glu Phe Ile₁₉₅ Thr Asn Ala Leu Asn₂₀₀ Gly Leu Lys Glu Leu₂₀₅ Trp Asp Lys
 Leu Thr Gly Trp Val Thr Gly₂₁₅ Leu Phe Ser Arg Gly₂₂₀ Trp Ser Asn Leu
 Glu Ser Phe Phe Ala Gly₂₃₀ Val Pro Gly Leu Thr₂₃₅ Gly Ala Thr Ser Gly₂₄₀
 Leu Ser Gln Val Thr₂₄₅ Gly Leu Phe Gly Ala₂₅₀ Ala Gly Leu Ser Ala₂₅₅ Ser
 Ser Gly Leu Ala₂₆₀ His Ala Asp Ser Leu₂₆₅ Ala Ser Ser Ala Ser Leu Pro
 Ala Leu Ala Gly Ile Gly Gly Gly₂₈₀ Ser Gly Phe Gly Gly₂₈₅ Leu Pro Ser
 Leu Ala Gln Val His Ala Ala₂₉₅ Ser Thr Arg Gln Ala₃₀₀ Leu Arg Pro Arg

eolf-seq1

Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser
305 310 315 320

Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly
325 330 335

Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr
340 345 350

Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg
355 360 365

Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg
370 375 380

Asn Val Val
385

<210> 166
<211> 388
<212> PRT
<213> Artificial Sequence

<220>
<223> H37RV RV3616c with deleted residues 142-145

<400> 166

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
1 5 10 15

Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
20 25 30

Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
35 40 45

Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
50 55 60

Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
65 70 75 80

Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
85 90 95

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

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

Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Gly Gly Ala
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eolf-seql

130 135 140

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

Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp
165 170 175

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

Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp
195 200 205

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

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

Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala
245 250 255

Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu
260 265 270

Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro
275 280 285

Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro
290 295 300

Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln
305 310 315 320

Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val
325 330 335

Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr
340 345 350

Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu
355 360 365

Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val
370 375 380

Arg Asn Val Val
385

<210> 167

eof-seq1

<211> 384
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H37Rv RV3616c with deleted residues 138-145

<400> 167

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
 1 5 10 15

Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
 20 25 30

Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
 35 40 45

Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
 50 55 60

Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
 65 70 75 80

Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
 85 90 95

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

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

Leu Ser Ala Ala Phe Gln Ala Pro Phe Gly Gly Ala Leu Ala Tyr Leu
 130 135 140

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

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

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

Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly
 195 200 205

Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe
 210 215 220

Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly Leu Ser Gln
 225 230 235 240

eo1f-seq1

Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly Leu
245 250 255

Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro Ala Leu Ala
260 265 270

Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser Leu Ala Gln
275 280 285

Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg Ala Asp Gly
290 295 300

Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val
305 310 315 320

Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly Met Gly Gly
325 330 335

Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr Lys Lys Tyr
340 345 350

Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val
355 360 365

Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg Asn Val Val
370 375 380

<210> 168

<211> 384

<212> PRT

<213> Artificial Sequence

<220>

<223> H37Rv Rv3616c with deleted residues 145-152

<400> 168

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
1 5 10 15

Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
20 25 30

Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
35 40 45

Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
50 55 60

Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
65 70 75 80

Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
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90

95

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

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

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

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

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

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

Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly
195 200 205

Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe
210 215 220

Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly Leu Ser Gln
225 230 235 240

Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly Leu
245 250 255

Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro Ala Leu Ala
260 265 270

Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser Leu Ala Gln
275 280 285

Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg Ala Asp Gly
290 295 300

Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val
305 310 315 320

Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly Met Gly Gly
325 330 335

Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr Lys Lys Tyr
340 345 350

Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val
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355

360

365

Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg Asn Val Val
 370 375 380

<210> 169

<211> 386

<212> PRT

<213> Artificial sequence

<220>

<223> H37Rv RV3616c with deleted residues 149-154

<400> 169

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
 1 5 10 15

Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
 20 25 30

Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
 35 40 45

Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
 50 55 60

Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
 65 70 75 80

Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
 85 90 95

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

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

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

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

Leu Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile
 165 170 175

Ser Asp Val Ala Asp Ile Ile Lys Gly Thr Leu Gly Glu Val Trp Glu
 180 185 190

Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu
 195 200 205

eof-seq1

Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu
 210 215 220

Ser Phe Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly Leu
 225 230 235 240

Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser
 245 250 255

Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro Ala
 260 265 270

Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser Leu
 275 280 285

Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg Ala
 290 295 300

Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser Gln
 305 310 315 320

Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly Met
 325 330 335

Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr Lys
 340 345 350

Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala
 355 360 365

Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg Asn
 370 375 380

Val Val
 385

<210> 170
 <211> 1032
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> H37RV RV3616c with deleted codons for residues 136-183

<400> 170	
atgagccgtg cctttattat tgatccgacc attagcgcaa ttgatggtct gtatgatctg	60
ctgggtattg gtattccgaa tcagggtggt attctgtata gcagcctgga atattttgaa	120
aaagccctgg aagaactggc agcagcattt ccgggtgatg gttggctggg tagcgcagca	180
gataaatatg ccggtaaaaa tcgcaatcat gtgaattttt ttcaggaact ggccgatctg	240
gatcgtcagc tgattagcct gattcatgac caggcaaattg cagttcagac caccctgat	300

960 ggaccggcttg gaggcagcagc agaacaggtt ggtggtcaga gccagcttgt tagcgcacag
 900 ccgaagcccttg cacaggttca tgcagcaagc acccgtcagg cactgcgtcc gcgtgcagat
 840 agcagcgcat ctctgccttg actgagcagg attggttggt gatccggtt tgggtgcttg
 780 ctgtttggag cagctgtgtc gagtgtcagt agcgtcttg ctcatgcaga tagccctggca
 720 ttttttttccg gtgttccggg tctgaccggt gcaaccaggc gtcctgagcca ggtgacaggt
 660 gataaacaga ccggttgggt taacggtctg tttaagcgtg gttgagcaca tctggaatct
 600 accctgggcg aagtttggga atttatacc aatgcccctga atgtcttgaa agaactgttg
 540 gaactgtgtg cagcagcaat tgcagatat atttcgagt tggccgatat tatataaggc
 480 gcaatggcag ttgttgggtg tgccttgacc cagctgtctga aactgcctggc aaaaactggca
 420 tatattccgg ttgttgttca tgcactgagc gacgcatctc aggcaccgtt ttgtgcctgg
 360 attcttggaag gtcgcaaaaa agtcttgga ttgttctgc cgttgagagt tgatctgacc
 300 gatcgtcagc tgattagcct gattcatgac caggcaaatg cagttcagac caccgctgat
 240 gataaatatg ccgtaaaaaa tcgcaatcat gtgaatttt ttcaaggaaat ggcgatctg
 180 aaagcccttg aagaactgag agcagcatct ccggttgatg gttgctggg tagcgacaga
 120 ctggttatg gtatccgaa tcagggtgtg attctgtata gcagccctga atattttgaa
 60 atgagcgtg ccttatat tgatccgacc atagcgcaa ttgatgtct gtatgatctg

<220> H37RV RV3616c with deleted codons for residues 150-160

<210> 171
 <211> 1143
 <212> DNA
 <213> Artificial Sequence

1032 cgcattgtg tg
 1020 gaagatgcag aacgtgcacc gttgaaagca gatgccgtg gagttcagaa agttcttgtt
 960 agcgttgcaa gcaaaagcac caccaccaaa aatatagcg aaggagcagc tgcctggcacc
 900 aggcacagg gtagccaggg tatggttgtt ccggtgggca tgggtggtat gcatccgagc
 840 cgtgcagatg gaccggttg agcagcagca gaacaggtg gttgtcagag ccagctgtgt
 780 ggtgtctgc cgaagccctgc acaggttcat gcagcaagca ccgctcagc actgcgtccg
 720 agcctggcaa gcagcgcatc tctgcctgca ctggcaggca ttggtggtg atccggttt
 660 gtgacaggtc tgtttggagc agctgtctg agtgcctagt gcgtctggc tcatgcagat
 600 ctggaatctt tttttccgg tgttccggt ctgaccggt caaccagcg tctgaagccag
 540 gaactgtggg ataactgac cgtttgggt accggtctgt ttagccgtgg ttgagcaat
 480 attaagca cccctggcga agtttgga ttatatca atgcccctga ttgtctgaaa
 420 tatattccgg ttgttgttca tgcactgagc gcagcatctc aggcagatgt ggcgatat
 360 attctggaag gtcgcaaaaa agtcttgaa ttgttctgc cgttgagagt tgatctgacc

eolf-seq1

ggtagccagg gtatgggtgg tccggtgggc atgggtggta tgcacccgag cagcgggtgca	1020
agcaaaggca ccaccaccaa aaaatatagc gaaggagcag ctgctggcac cgaagatgca	1080
gaacgtgcac cggttgaagc agatgccggt ggaggtcaga aagttctggt tgcgaatgtg	1140
gtg	1143

<210> 172
 <211> 1119
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> H37Rv Rv3616c with deleted codons for residues 136-154

<400> 172	
atgagccgtg cttttattat tgatccgacc attagcgcaa ttgatggctct gtatgatctg	60
ctgggtattg gtattccgaa tcagggtggt attctgtata gcagcctgga atattttgaa	120
aaagccctgg aagaactggc agcagcattt ccgggtgatg gttggctggg tagcgcagca	180
gataaatatg ccggtaaaaa tcgcaatcat gtgaatTTTT ttcaggaact ggccgatctg	240
gatcgtcagc tgattagcct gattcatgac caggcaaatg cagttcagac caccctgat	300
attctggaag gtgccaaaaa aggtctggaa ttgttctgct cggtaggcagt tgatctgacc	360
tatattccgg ttgttgggtca tgcactgagc gcagcatttc aggcaaaaac cctgattaat	420
gcaaccagc tgctgaaact gctggcaaaa ctggcagaac tggttgagc agcaattgca	480
gatattattt ccgatgtggc cgatattatt aaaggcacc tgggcgaagt ttgggaattt	540
attaccaatg ccctgaatgg tctgaaagaa ctgtgggata aactgaccgg ttgggttacc	600
ggtctgttta gccgtgggtg gagcaatctg gaatctTTTT ttgccgggtgt tccgggtctg	660
accggtgcaa ccagcggctc gagccagggt acaggctctgt ttggagcagc tggctgagt	720
gctagtagcg gtctgggtca tgcagatagc ctggcaagca gcgcatctct gcctgcaactg	780
gcaggcattg gtggtggatc cggttttggt ggtctgccga gcctggcaca ggttcatgca	840
gcaagcacc gtcaggcact gcgtccgct gcagatggac cggttggagc agcagcagaa	900
caggttggtg gtcagagcca gctggttagc gcacagggtg gccagggtat ggggtgtccg	960
gtgggcatgg gtggtatgca tccgagcagc ggtgcaagca aaggcaccac caccaaaaaa	1020
tatagcgaag gagcagctgc tggcaccgaa gatgcagaac gtgcaccggt tgaagcagat	1080
gccggtggag gtcagaaaagt tctggttcgc aatgtggtg	1119

<210> 173
 <211> 1125
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> H37Rv Rv3616c with deleted codons for residues 166-182

<400> 173	
atgagccgtg cttttattat tgatccgacc attagcgcaa ttgatggctct gtatgatctg	60

660 ggtctgaaag aactgtggga taaactgacc ggttgggta ccggtctgt tagccgtgt
 600 gccgatat ttaagggcac cctggcgaa gtttgggaat ttattacca tgccttgat
 540 ctgtcgcaa aactggcaga actgttgca gacgcaatg cagatatat ttccgattg
 480 ggtgtgttc tggcatatct ggttgtgaaa accctgatta atgcaacca gctgtgaaa
 420 tatattccg tgttgtgca tgcactgagc gacgcatctc aggttgcaat ggcagtgtg
 360 attctggaag gtgcacaaaa aggtctgaa ttgttctgc cgttgagat tgatctgacc
 300 gatctcagc tgattagcct gattcatgac cagcacaatg cagttcagac caccctgat
 240 gataaatat ccgtaaaaa tcgcaatcat gtgaatttt ttcaagaaat gccgattg
 180 aagccctgg aagaactggc agcagcatct ccggtgatg gttgctggg tagcgagca
 120 ctgggtatg gtattccgaa tcagggtgt attctgtata gcagcctga atatttgaa
 60 atgagccgt ccttatat tgatccgacc attagcgcaa ttgatgtct gtatgattg

<210> 174
 <211> 1161
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> H37RV RV3616c with deleted codons for residues 135-139

1125 gcagatgccg gttggaggtca gaaagtctg gttcgcaatg tgtgt
 1080 aaaaaatata gcgaaggagc agctgctggc accgaagatg cagaacgtgc accggttgaa
 1020 ggtccgtgtg gcatgggttg tatgcattccg agcagcgttg caagcaagg caccacaccc
 960 gcagaacagg tgttgtgtca gaggcagctg gttagcgcac aggttagcca ggtatgtgt
 900 catgcagcaa gccaccgtca ggcactgctc ccgctgtcag atgaccggt tgagcagca
 840 gcactggcag gcatgtgttg tgcattcgtt ttgtgtgtc tgcgagcct ggcacaggt
 780 ctgaagtcta gttagcgtct ggtcatgca gatagccttg caagcagcgc atctctgct
 720 ggtctgaccg gtgcacaacag cgtcttgagc caggttgacag gtctgttttg agcagctgt
 660 gttaaccgtc tgttagccg tgttggagc aatctggaat cttttttgc cgtgttccg
 600 gaattatata ccaatgccct gaattgtctg aaagaactgt gggataaact gaccggttg
 540 acccagctgc tgaatccga tgtggcggat attattaag gcaaccctgg cgaagtgtg
 480 gcaatggcag ttgttgggtg tgccttgca tatctgttg tgaaaaacct gattaatgca
 420 tatattccg tgttgtgtca tgcactgagc gacgcatctc aggcacggt ttgtgcggt
 360 attctggaag gtgcacaaaa aggtctgaa ttgttctgc cgttgagat tgatctgacc
 300 gatctcagc tgattagcct gattcatgac cagcacaatg cagttcagac caccctgat
 240 gataaatat ccgtaaaaa tcgcaatcat gtgaatttt ttcaagaaat gccgattg
 180 aagccctgg aagaactggc agcagcatct ccggtgatg gttgctggg tagcgagca
 120 ctgggtatg gtattccgaa tcagggtgt attctgtata gcagcctga atatttgaa

1164 aagattcttg ttccgaattg ggtg
1140 gctgctggca ccgaagatgc agaacgtgca ccggttgaag cagatgccgg tggaggtcag
1080 atgcatccga gcaagcggtc aagcaaggc acccaacca aaaaataag cgaagagagca
1020 agccagctgg ttacgcaca ggttagccag ggtatgggtg gtcgggtgg catgggtggt
960 gcaatgctgc cggctgcaga tggaccggtt ggaagcagca cagaacaagt tgggtggtcag
900 ggaaccggtt ttggtgtctt gccgagcctg gcaagaattc atgcagcaag caccggtcag
840 gctcatgcaag atagccctgc aagcagcga tctctgctg cactggcagg catgtgtgtg
780 ggtctgagcc aggtgacag tctgtttgga gcaagctgtc tgaagtgtag tagcgggtctg
720 ggttgagca atctggaatc tttttttgcc ggtgttccgg gtcctgaaccg tgcacaaccag
660 aatggtctga aagaactgtg gataaaactg accggttggg ttaccggtct gtttagccgt
600 gtggccgata ttataaagg caccctgggc gaagtltggg aatttatcac caatgccctg
540 aaacctgctg caaaactgca agaactgtt gcaagcagca atgcagatat tattccgat
480 gcaaggtgtg ctctgcatat tctgttgtg aaaaacctga ttaatgcaac ccagctgctg
420 tatattccgg ttgttgttca tgcaactgagc gcaagcattc aggcacctt ttgtgcccgt
360 attctggaag gtgccaaaaa aggtcttgaa ttgttctgc cgttggtcag ttgatttgacc
300 gatcgtcagc tgattagcct gattcatgac caggcaaatg cagttcagac caccggtgat
240 gataaatatg ccgtaaaaaa tcgcaatcat gtgaatttt ttcaaggaaat ggcgcatctg
180 aaagccctgg aagaactgca agcagcattt ccgggtgatg gttggctggg tagcgcagca
120 ctgggtatg gtattccgaa tcagggtgtt attctgtata gcagcctgga atatttgaa
60 atgagccgtg ccttatatat tgatccgacc attagcgcaa ttgattgtct gtatgatctg

<210> 175
<211> 1164
<212> DNA
<213> Artificial Sequence
<220>
<223> H37RV RV3616c with deleted codons for residues 142-145

1161 gttctgttc gcaatgtgt g
1140 gctggcaccg aagatgcaga acgtgccacc gttgaagcag atgccggtgg aggtcagaaa
1080 catccgagca gcggtgcagc caaagcacc acccaaaaa aatatagcga aggagcagct
1020 cagctgttta gcgcacagg tagccagggt atgggtgttc cgttggtgat ggtgtgtatg
960 ctgctccgc gtgcagatgg accggttga gcaagcagca aacaggttgg tgttcagagc
900 tccggtttg gtgtctgcc gagcctgca cagttcatg cagcaagcac ccgtcagagca
840 catgcagata gccctgcagc cagcgcattc ctgcctgac tggcaggcat tgtgtgtga
780 ctgagccagg tgacaggtct gtttgagca gctgtctga gtgctagtac cgtcttgct
720 tggagcaatc tggaatctt ttgtccggt gttccgggtc tgaccggtg aaccagcgtg

eof-seq1

<210>	176	
<211>	1152	
<212>	DNA	
<213>	Artificial Sequence	
<220>		H37RV RV3616c with deleted codons for residues 138-145
<223>		
<400>	176	atgaagccgtg cctttattat tgatccgacc attagcgcaa ttgatgtct gtatgatctg
		60
		120 ctgggtatg gtattccgaa tcagggtgtg attctgtata gcaagccctgga atatttgaa
		180 aagagccctgg aagaactggc agcagcatct ccgggtgatg gttgctggg tagcgcaagca
		240 gataaatatg ccggtaaaaa tcgcaatcat gtgaatttt ttcaagaaact ggcgatctg
		300 gatcgtcagc tgattagcct gattcatgac caggcaaatg cagttcagac caccggtgat
		360 attctgggaag gtgcacaaaa aggtcttgaa ttgttctgc cgttggcagt tgatctgacc
		420 tatattccgg ttgttgttca tgcaactgagc gcagcatctc aggcaccgtt ttgttgtct
		480 ctggcatatc ttgttgtgaa aaccttgatc aatgcaacc agctgtgaa actgttgca
		540 aaacctggcag aactgttgc agcagcaatt gcagatatc ttccgatgt ggcgatatt
		600 attaaagca cccctggcga agtttgga ttattacca atgcccctgaa ttgtctgaaa
		660 gaaactgtgg ataaactgac cgtttgggt accgtctgt ttagccgtgg ttggaagcaat
		720 ctggaatctt ttttgcgg ttgtccgggt ctgaccgtg caaccagcgg tctgaagccag
		780 gtgacagctc tgtttggagc agctgtcttg agtgcctagc gcgtcttgc tcatgcagat
		840 agcctggcaa gcagcgcatc tctgcctgca ctggcaggca ttgttgttg atccggttt
		900 gttgtcttgc cgaagccctgc acaggttcat gcagcaagca cccgtcaggc actgcgtccg
		960 cgtgcagatg gaacggttgg agcagcagca gaacaggttg gtgtcagag ccagctgtt
		1020 agcgcacagg gttagccagg ttatgggtgt ccggtgggca ttgggtgtat gcatccgagc
		1080 agcgttgcaa gcaaaaggcac caccaccaa aaatatagcg aaggaagcgc tgcctggcacc
		1140 gaagatgcag aacgtgcacc gttgaaagca gatgccggtg gaggtcagaa agttctgtt
		1152 cgcaatgtg tg

780 agccaagtga caggtctgtt tggagcagct ggtctgagtg ctagtagcgg tctggtcat
 720 agcaatcttg aatcttttt tgcgggtgtt ccgggtctga ccggtgcaac cagcggcttg
 660 ctgaagaac tgtgggataa actgaccggt tgggtaccg gtcgtttaa ccgtggttg
 600 gatatataa aagccacct gggcgaagt tgggaattta ttaaccaatgc cctgaatgt
 540 ctggcaaaaac tggcagaact ggttcagca gcaattgca atattattc cgtgtggcc
 480 gcaatggcag tgtgtggttg tgcataaac ctgattaatg caaccagct gctgaactg
 420 tatattccgg tgtgtgtca tgcactgagc gcaagcattc aggcaccgtt ttgtgccgt
 360 attcttggaag gtgcacaaaag aggtctgga ttgttctgtc cgttgagcgt tgatctgacc
 300 gatctcagc tgatagcct gattcatgac caggcaaatg cagttcagac caccggtgat
 240 gataaatatg ccgtataaaa tcgcaatcat gtgaatttt ttcaaggact ggcgcatcg
 180 aaagcccttg aagaacttgc agcagcattt ccgggtgag gtggctggg tagcgacga
 120 ctgggtatg gtatccgaa tcagggtgtg attctgtata gcagccctga atatttgaa
 60 atgagccgtg ccttatat tgatccgacc atagcgcaa ttgatgtct gtatgatctg

<400> 178
 <220> H37Rv RV3616c with deleted codons for residues 149-154
 <223>

<210> 178
 <211> 1158
 <212> DNA
 <213> Artificial Sequence

1152 cgaatgttg tg
 1140 gaagatgcaag aacgtgcacc gttgaagca gatgccggtg gagtcagaa agttctgtt
 1080 agcgttgcaa gcaaaagcac caccacaaa aatatagcg aaggagcagc tgcctggcacc
 1020 agcgcaagg gtagccaggg tatgggtgtt ccgttgga tgggtgttat gcatccgagc
 960 cgtgcagatg gaacggttg agcagcagca gaacaggttg gtgtcagag ccagctgtt
 900 ggtgtctgc cgaagcctgc acagttcat gcagcaagca ccgtcagc actgcgtccg
 840 agcctggcaa gcagcgcatc tctgcctga ctggcaggca ttgtgtgtg atccggttt
 780 gtgacagtc tgtttgagc agctgtctg agtgcata gctgtcggc tcatgagat
 720 ctggaattt tttttccgg tgttccggt ctgaccggt caaccagcg tctgagccag
 660 gaactgtgg ataaactgac cgttgtgtt accgtctgt ttagccgttg ttgagcaat
 600 ataaagca cccgtggcga agttggga ttatatca atgcccgtga tgtctgaaa
 540 aaactggcag aactgttgc agcagcaat gcagatat tttccgatt ggcgatatt
 480 gcaatggcag ttgttgtga aacctgat aatgcaacc agctctgaa actgctgca
 420 tatattccgg tgttgttca tgcactgagc gcagcattc aggcaccgt ttgtgccgt
 360 attcttggaag gtgcacaaa aggtctgga ttgttctgtc cgttgagcgt tgatctgacc
 300 gatctcagc tgatagcct gattcatgac caggcaaatg cagttcagac caccggtgat

eof-seq1

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gcagatagcc tggcaagcag cgcattctctg cctgcactgg caggcattgg tgggtggatcc      840
ggttttgggtg gtctgccgag cctggcacag gttcatgcag caagcaccgg tcaggcactg      900
cgtccgcgtg cagatggacc ggttggagca gcagcagaac aggttggtgg tcagagccag      960
ctgggttagcg cacagggttag ccagggtatg ggtggtccgg tgggcatggg tggtatgcat    1020
ccgagcagcg gtgcaagcaa aggcaccacc accaaaaaat atagcgaagg agcagctgct    1080
ggcaccgaag atgcagaacg tgcaccggtt gaagcagatg ccggtggagg tcagaaagtt    1140
ctggttcgca atgtggtg                                     1158
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<210> 179
 <211> 391
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Rearrangement around the residues 137-139 from M. tuberculosis H37Rv strain, including deletion of Cys138

<400> 179

Met Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val
 1 5 10 15

Val Lys Thr Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys
 20 25 30

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

Ala Asp Ile Ile Lys Gly Thr Leu Gly Glu Val Trp Glu Phe Ile Thr
 50 55 60

Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp
 65 70 75 80

Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe
 85 90 95

Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly Leu Ser Gln Val
 100 105 110

Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly Leu Ala
 115 120 125

His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro Ala Leu Ala Gly
 130 135 140

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

His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro
 165 170 175

eof-seq1

Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val Ser
180 185 190

Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly Met Gly Gly Met
195 200 205

His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser
210 215 220

Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val Glu
225 230 235 240

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

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

Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu Tyr Ser
275 280 285

Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala Ala Phe
290 295 300

Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala Gly Lys
305 310 315 320

Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu Asp Arg
325 330 335

Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln Thr Thr
340 345 350

Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val Arg Pro
355 360 365

Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala Leu Ser
370 375 380

Ala Ala Phe Gln Ala Pro Phe
385 390

<210> 180
<211> 392
<212> PRT
<213> Artificial sequence

<220>
<223> Rearrangement around the residues 152-153 from M. tuberculosis
H37Rv strain

<400> 180

eo1f-seq1

Met Val Val Lys Thr Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu
1 5 10 15

Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser
20 25 30

Asp Val Ala Asp Ile Ile Lys Gly Thr Leu Gly Glu Val Trp Glu Phe
35 40 45

Ile Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr
50 55 60

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

Phe Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly Leu Ser
85 90 95

Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly
100 105 110

Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro Ala Leu
115 120 125

Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser Leu Ala
130 135 140

Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg Ala Asp
145 150 155 160

Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser Gln Leu
165 170 175

Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly Met Gly
180 185 190

Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr Lys Lys
195 200 205

Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro
210 215 220

Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg Asn Val
225 230 235 240

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

Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
260 265 270

eolf-seq1

Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
 275 285
 Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
 290 300
 Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
 305 310 315 320
 Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
 325 330 335
 Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
 340 345 350
 Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
 355 360 365
 Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
 370 375 380
 Val Gly Gly Ala Leu Ala Tyr Leu
 385 390