

eolf-seql
SEQUENCE LISTING

<110> GlaxoSmithKline Biologicals sa
Godart, Stephane
Laanan, Amina
Lemoine, Dominique

<120> Novel compositions

<130> VB64442A

<150> US61/422723

<151> 2010-12-14

<160> 17

<170> PatentIn version 3.5

<210> 1

<211> 391

<212> PRT

<213> Mycobacterium tuberculosis H37Rv

<400> 1

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Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp
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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

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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
355 360 365

Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
370 375 380

Pro His Ser Pro Ala Ala Gly
385 390

<210> 2
<211> 1173
<212> DNA
<213> Mycobacterium tuberculosis H37Rv

<400> 2
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<210> 3
 <211> 391
 <212> PRT
 <213> Mycobacterium tuberculosis F11

<400> 3

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Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
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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

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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
 355 360 365

Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met

370

375

eolf-seql
380Pro His Ser Pro Ala Ala Gly
385 390

<210> 4
 <211> 1173
 <212> DNA
 <213> Mycobacterium tuberculosis F11

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 tcggccgcgt cggcgtttca gtcgggtggc tgggggtctga cgggtggggtc gtggataggt 180
 tcgtcggcgg gtctgatggg ggcggcggcc tcgccgtatg tggcgtggat gagcgtcacc 240
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 ccctatgtga tgccgcattc tccggcggcc ggc 1173

<210> 5
 <211> 723
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M72 fusion protein

<400> 5

Met Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly
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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

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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

eo1f-seq1

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> 6

<211> 2172

<212> DNA

<213> Artificial Sequence

<220>

<223> Coding sequence for M72 fusion

<400> 6

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catatcgggc ctaccgcctt cctcggcttg ggtgttgtcg acaacaacgg caacggcgca 180

cgagtccaac gcgtggtcgg gagcgctccg gcggcaagtc tcggcatctc caccggcgac 240

gtgatcaccg cggtcgacgg cgctccgatc aactcggcca ccgcgatggc ggacgcgctt 300

aacgggcatc atcccgggtga cgtcatctcg gtgacctggc aaaccaagtc gggcggcacg 360

cgtacaggga acgtgacatt ggccgaggga ccccggccg aattcatggt ggatttcggg 420

gcgttaccac cggagatcaa ctccgcgagg atgtacgccg gcccggggttc ggcctcgctg 480

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atggtggcgg cggcctcgcc gtatgtggcg tggatgagcg tcaccgcggg gcaggccgag      660
ctgaccgccg cccaggtccg ggttgctgcg gcggcctacg agacggcgta tgggctgacg      720
gtgccccgcg cggtgatcgc cgagaaccgt gctgaactga tgattctgat agcgaccaac      780
ctcttggggc aaaacacccc ggcgatcgcg gtcaacgagg ccgaatacgg cgagatgtgg      840
gccaagacg ccgccgcgat gtttggttac gccgcggcga cggcgacggc gacggcgacg      900
ttgctgccgt tcgaggaggc gccggagatg accagcgcgg gtgggctcct cgagcaggcc      960
gccgcggtcg aggaggcctc cgacaccgcc gcggcgaacc agttgatgaa caatgtgccc     1020
caggcgctgc aacagctggc ccagcccacg cagggcacca cgccttcttc caagctgggt     1080
ggcctgtgga agacggtctc gccgcatcgg tcgccgatca gcaacatggt gtcgatggcc     1140
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<210> 7
 <211> 725
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M72 fusion with 2 additional his residues

colf-seql

<400> 7

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

Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala
35 40 45

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala
275 280 285

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

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

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

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

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

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

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

Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Gln
405 410 415

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

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

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

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

Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro
485 490 495

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

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

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

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

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

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

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

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

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

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

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

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

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

Asp Ala Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met
705 710 715 720

Asn Thr Ala Ala Ser
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<210> 8
<211> 2178
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence for M72 fusion with 2 additonal his residues

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ggcgacagag tccaacgcgt ggtcgggagc gtcggcgcg caagtctcgg catctccacc 240
ggcgacgtga tcaccgcggt cgacggcgct ccatcaact cggccaccgc gatggcggac 300

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ttcggggcgt	taccaccgga	gatcaactcc	gcgaggatgt	acgccggccc	gggttcggcc	480
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ctgggtggcc	tgtggaagac	ggtctcgccg	catcggtcgc	cgatcagcaa	catggtgtcg	1140
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tcgatgttga	agggttttgc	tccggcgggc	gccgcccagg	ccgtgcaaac	cgcggcgcaa	1260
aacgggggtcc	gggcgatgag	ctcgtctggc	agctcgttgg	gttcttcggg	tctgggcggt	1320
ggggtggccg	ccaacttggg	tcgggcggcc	tcggtcgggt	cgttgctcgg	gccgcaggcc	1380
tgggcccgcg	ccaaccaggc	agtcacccc	gcggcgcggg	cgctgccgct	gaccagcctg	1440
accagcgccg	cggaaagagg	gcccgggcag	atgctggggc	ggctgccggt	ggggcagatg	1500
ggcgccaggg	ccggtggtgg	gctcagtgg	gtgctgcgtg	ttccgccgcg	accctatgtg	1560
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gccgacttcc	ccgcgctgcc	cctcgacccg	tccgcgatgg	tcgccaagt	ggggccacag	1680
gtggtcaaca	tcaacaccaa	actgggctac	aacaacgccg	tgggcgccgg	gaccggcatc	1740
gtcatcgatc	ccaacggtgt	cgtgctgacc	aacaaccacg	tgatcgcggg	cgccaccgac	1800
atcaatgcgt	tcagcgtcgg	ctccggccaa	acctacggcg	tcgatgtggt	cgggtatgac	1860
cgcacccagg	atgtcgcggt	gctgcagctg	cgcggtgccg	gtggcctgcc	gtcggcgggc	1920
atcgggtggc	gcgtcgcggt	tggtagagccc	gtcgtcgcga	tgggcaacag	cgggtgggcag	1980
ggcggaacgc	cccgtgcggt	gcctggcagg	gtggtcgcgc	tcggccaaac	cgtgcaggcg	2040
tcggattcgc	tgaccggtgc	cgaagagaca	ttgaacgggt	tgatccagtt	cgatgccgcg	2100
atccagcccc	gtgatgcggg	cgggcccgtc	gtcaacggcc	taggacaggt	ggtcggtatg	2160
aacacggccg	cgtcctag					2178

<210> 9

<211> 723

eolf-seql

<212> PRT
<213> Artificial Sequence

<220>
<223> Mtb72f fusion

<400> 9

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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 Tyr Glu Thr Ala Tyr Gly Leu Thr
225     230     235     240

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eolf-seql

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
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		

self-seq1

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
675 680 685

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> 10

<211> 2172

<212> DNA

<213> Artificial Sequence

<220>

<223> Coding sequence for Mtb72f fusion

<400> 10

atgacggccg cgtccgataa cttccagctg tcccaggggtg ggcaggggatt cgccattccg 60

atcgggacagg cgatggcgat cgcggggccag atccgatcgg gtgggggggtc acccaccgtt 120

eolf-seql

catatcgggc	ctaccgcctt	cctcggcttg	ggtgttgtcg	acaacaacgg	caacggcgca	180
cgagtccaac	gcgtggtcgg	gagcgctccg	gcggcaagtc	tcggcatctc	caccggcgac	240
gtgatcaccg	cggtcgacgg	cgctccgatc	aactcggcca	ccgcgatggc	ggacgcgctt	300
aacgggcatc	atcccgggtga	cgtcatctcg	gtgacctggc	aaaccaagtc	gggcggcacg	360
cgtacagggga	acgtgacatt	ggccgagggga	ccccgggccg	aattcatggt	ggatttcggg	420
gcgttaccac	cggagatcaa	ctccgcgagg	atgtacgccg	gcccgggttc	ggcctcgctg	480
gtggccgcgg	ctcagatgtg	ggacagcgtg	gcgagtgacc	tgttttcggc	cgcgtcggcg	540
tttcagtcgg	tggctctggg	tctgacggtg	gggtcgtgga	taggttcgtc	ggcgggtctg	600
atggtggcgg	cggcctcgcc	gtatgtggcg	tggatgagcg	tcaccgcggg	gcaggccgag	660
ctgaccgccg	cccagggtccg	ggttgctgcg	gcggcctacg	agacggcgta	tgggctgacg	720
gtgccccgc	cggtgatcgc	cgagaaccgt	gctgaactga	tgattctgat	agcgaccaac	780
ctcttggggc	aaaacacccc	ggcgatcgcg	gtcaacgagg	ccgaatacgg	cgagatgtgg	840
gccaagacg	ccgccgcgat	gtttggctac	gccgcggcga	cggcgacggc	gacggcgacg	900
ttgctgccgt	tcgaggaggc	gccggagatg	accagcgcg	gtgggctcct	cgagcaggcc	960
gccgcggctg	aggaggcctc	cgacaccgcc	gcggcgaacc	agttgatgaa	caatgtgccc	1020
caggcgctgc	aacagctggc	ccagcccacg	cagggcacca	cgccttcttc	caagctgggt	1080
ggcctgtgga	agacggctctc	gccgcacg	tcgccgatca	gcaacatggt	gtcgatggcc	1140
aacaaccaca	tgtcgatgac	caactcgggt	gtgtcgatga	ccaacacctt	gagctcgatg	1200
ttgaagggt	ttgctccggc	ggcggccgcc	caggccgtgc	aaaccgcggc	gcaaaacggg	1260
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gccgcggaaa	gagggcccg	gcagatgctg	ggcgggctgc	cgggtggggca	gatgggcgcc	1500
agggccggtg	gtgggctcag	tgggtgtgctg	cgtgttccgc	cgcgacccta	tgtgatgccg	1560
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aacatcaaca	ccaaactggg	ctacaacaac	gccgtggggc	ccgggaccgg	catcgtcac	1740
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caggatgtcg	cgggtgctga	gctgcgcggt	gccggtggcc	tgccgtcggc	ggcgatcgg	1920
ggcggcgctg	cggttgggtga	gcccgtcgtc	gcgatgggca	acagcgggtg	gcagggcgga	1980
acgccccgtg	cgggtgcctg	caggggtggc	gcgctcggcc	aaaccgtgca	ggcgctcgat	2040
tcgctgaccg	gtgccgaaga	gacattgaac	gggttgatcc	agttcgatgc	cgcgatccag	2100
cccgggtgatt	cgggcggggc	cgtcgtcaac	ggcctaggac	aggtgggtcg	tatgaacacg	2160

eolf-seql

gccgctcct ag

2172

<210> 11
 <211> 729
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mtb72f fusion with 6 additional his residues

<400> 11

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

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

Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
 35 40 45

Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
 50 55 60

Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
 65 70 75 80

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

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

Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
 115 120 125

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

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

Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val
 165 170 175

Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp
 180 185 190

Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val
 195 200 205

Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln
 210 215 220

eolf-seql

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

Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg
245 250 255

Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr
260 265 270

Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln
275 280 285

Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr
290 295 300

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

Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala
325 330 335

Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu
340 345 350

Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu
355 360 365

Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser
370 375 380

Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr
385 390 395 400

Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala
405 410 415

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

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

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

Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro
465 470 475 480

Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu
485 490 495

eolf-seql

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

Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser
515 520 525

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

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

Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn
565 570 575

Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val
580 585 590

Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe
595 600 605

Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp
610 615 620

Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu
625 630 635 640

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

Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro
660 665 670

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

Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
690 695 700

Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln
705 710 715 720

Val Val Gly Met Asn Thr Ala Ala Ser
725

<210> 12
<211> 2190
<212> DNA
<213> Artificial Sequence

<220>

eolf-seq1

<223> Coding sequence for M72 fusion with 6 additional his residues

<400> 12

atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccaggggtggg	60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat ccgatcgggt	120
gggggggtcac ccaccgttca tatcgggcct accgccttcc tcggcttggg tgttgtcgac	180
aacaacggca acggcgcacg agtccaacgc gtggtcggga gcgctccggc ggcaagtctc	240
ggcatctcca ccggcgacgt gatcaccgcg gtcgacggcg ctccgatcaa ctcggccacc	300
gcgatggcgg acgcgcttaa cgggcatcat cccggtgacg tcattctcggg gacctggcaa	360
accaagtccg gcggcacgcg tacagggaac gtgacattgg ccgagggacc cccggccgaa	420
ttcatggtgg atttcggggc gttaccaccg gagatcaact ccgcgaggat gtacgccggc	480
ccgggttcgg cctcgtcgtt ggccgcggct cagatgtggg acagcgtggc gagtgcctg	540
ttttcggccg cgtcggcggt tcagtcggtg gtctggggtc tgacgggtggg gtcgtggata	600
ggttcgtcgg cgggtctgat ggtggcggcg gcctcgccgt atgtggcggt gatgagcgtc	660
accgcggggc aggccgagct gaccgccgcc caggtccggg ttgctgcggc ggcctacgag	720
acggcgtatg ggctgacggt gccccgcgg gtgatcgccg agaaccgtgc tgaactgatg	780
attctgatag cgaccaacct cttggggcaa aacaccccg cgatcgcggt caacgaggcc	840
gaatacggcg agatgtgggc ccaagacgcc gccgcgatgt ttggctacgc cgcggcgacg	900
gcgacggcga cggcgacgtt gctgccgttc gaggaggcgc cggagatgac cagcgcgggt	960
gggctcctcg agcaggccgc cgcggtcgag gaggcctccg acaccgccgc ggcgaaccag	1020
ttgatgaaca atgtgcccc aagcgtgcaa cagctggccc agcccacgca gggcaccacg	1080
ccttcttcca agctgggtgg cctgtggaag acggtctcgc cgcattcggt gccgatcagc	1140
aacatggtgt cgatggccaa caaccacatg tcgatgacca actcgggtgt gtcgatgacc	1200
aacaccttga gtcgatgtt gaagggcttt gtcgggcgg cggccgcca ggccgtgcaa	1260
accgcggcgc aaaacggggt cggggcgatg agctcgttgg gcagctcgtt gggttcttcg	1320
ggtctgggcg gtgggggtgg cggcaacttg ggtcgggcgg cctcggtcgg ttcgttgtcg	1380
gtgccgcagg cctggggcgc ggccaaccag gcagtcaccc cggcggcgcg ggcgtgccg	1440
ctgaccagcc tgaccagcgc cgcggaaaga gggcccgggc agatgctggg cgggctgccg	1500
gtggggcaga tgggcgccag ggccggtggt gggctcagtg gtgtgctgcg tgttcgccg	1560
cgaccctatg tgatgccgca ttctccggca gccggcgata tcgccccgcc ggccttgtcg	1620
caggaccggt tcgccgactt ccccgcgctg cccctcgacc cgtcccgcat ggtcgcccaa	1680
gtggggccac aggtggtcaa catcaacacc aaactgggct acaacaacgc cgtgggcgcc	1740
gggaccggca tcgtcatcga tcccaacggt gtcgtgctga ccaacaacca cgtgatcgcg	1800
ggcgccaccg acatcaatgc gttcagcgtc ggctccggcc aaacctacgg cgtcgatgtg	1860
gtcgggtatg accgcacca ggatgtcgcg gtgctgcagc tcgcgggtgc cggtggcctg	1920
ccgtcggcgg cgatcgggtg cggcgctcgc gttggtgagc ccgtcgtcgc gatgggcaac	1980

eolf-seql

agcgggtgggc agggcggaac gccccgtgcg gtgcctggca ggggtggtcgc gctcggccaa	2040
accgtgcagg cgtcggattc gctgaccggt gccgaagaga cattgaacgg gttgatccag	2100
ttcgatgccg cgatccagcc cgggtgattcg ggcggggcccg tcgtcaacgg cctaggacag	2160
gtggtcggta tgaacacggc cgcgtcctag	2190

<210> 13
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Cpg Oligo 1 - CpG 1826

<400> 13 tccatgacgt tcctgacgtt	20
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<210> 14
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CpG Oligo 2 - CpG 1758

<400> 14 tctcccagcg tgcgcat	18
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<210> 15
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CpG Oligo 3

<400> 15 accgatgacg tcgccggtga cggcaccacg	30
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<210> 16
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CpG Oligo 4 - CpG 2006

<400> 16 tcgtcgtttt gtcgttttgt cgtt	24
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<210> 17
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CpG Oligo 5 - CpG 1686

<400> 17 tccatgacgt tcctgatgct	20
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eolf-seql