

eolf-seq1
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
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

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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
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Pro His Ser Pro Ala Ala Gly
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<211> 1173
<212> DNA
<213> Mycobacterium tuberculosis H37Rv

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 <211> 391
 <212> PRT
 <213> Mycobacterium tuberculosis F11
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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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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
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
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
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
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370

375

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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 gtcggtgggtc tgggggtctga cgggtggggtc gtggataggt      180
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gcggggcagg ccgagctgac cgccgcccag gtccggggtt ctgcggcggc ctacgagacg      300
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tacggcgaga tgtggggcca agacgccgcc gcgatgtttg gctacgccgc ggcgacggcg      480
acggcgacgg cgacgttgct gccgttcgag gaggcgccgg agatgaccag cgcggtggg      540
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<210> 5
<211> 723
<212> PRT
<213> Artificial Sequence<220>
<223> M72 fusion protein

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 Ser Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu
 Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg
 Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp
 Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met
 Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr
 Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala
 Glu Gly Pro Pro Ala Glu Phe Met Val Asp Phe Gly Ala Leu Pro Pro
 Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser Leu
 Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe Ser
 Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly Ser
 Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro Tyr
 Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala
 Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
 Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
 Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
 Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe

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

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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
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Ala Ala Ser

<210> 6
<211> 2172
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence for M72 fusion

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cgagtccaac gcgtggtcgg gagcgtccg gcggcaagtc tcggcatctc caccggcgac	240
gtgatcaccg cggtcgacgg cgctccgatc aactcggcca ccgcgatggc ggacgcgctt	300
aacgggcatc atcccggta cgtcatctcg gtgacctggc aaaccaagtc gggcggcacg	360
cgtacagggg acgtgacatt ggccgagggg cccccggccg aattcatggt ggatttcggg	420
gcgttaccac cggagatcaa ctccgcgagg atgtacgccg gcccgggttc ggcctcgctg	480

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600	tttcagtcgg tggctcgggg tctgacggtg gggtcgtgga taggttcgtc ggccgggtctg
660	atgttgccgg cggcttcggc gtatgttgccg tgatgtagcg tcaccgcggg gcaggccgag
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840	ctcttgggc aaaaacaccc ggcatcgcg gtcaacagag ccgaatacgg cgaagatgtg
900	gcccaagag ccgcgcgat gtttgctac gccgcgcga cggcgacggc gacggcgag
960	ttgttcggt tcgaaggagc gccgagatg accagcgcg gtgggtctct cgaagcaggc
1020	gccgcgtcg aggaaggctc cgaacacggc gggcgaacc agtgatgaa caatgtgccc
1080	caggcgtgc aacagctggc ccagcccaag caggcacaac cgccttctc caagctgggt
1140	ggccttgga agacgtctc gccgatcgg tcgcgatca gcaacatgtt gtcgatggcc
1200	aacaacaca tgtcgatgac caactcgggt gttgcgatga ccaacacctt gagctcgatg
1260	ttgaaggct ttgctcggc ggccggccgc caggccgtgc aaaccgcggc gcaaaacggg
1320	gtccggcgga tgaactcgt ggacagctcg ctgggtctt cgggtctggg cgggtgggtg
1380	gccgccaat tgggtcgggc ggctcgtc gttcgttgt cgtgcggca ggccctgggc
1440	gggcccaac aggcagtac ccgcgcgcg cggcgctgc cgtgaaccag cctgaaccagc
1500	gccgcggaag gaggccgg gcagatgctg ggccggctgc cgttgggca gatgggcgc
1560	aggccgggt gtgggtctag tgtgtgctg cgtgttcgc cgcgacctt tgtgatggcg
1620	catctccgg caggccgga tatcgcccg ccggccttgt cgcaggaagg gttcggccgac
1680	ttcccgcg tcgccctga ccgtcgcg atgttcggcc aagtggggc acaggtgtc
1740	aacatcaaca ccaactggg ctacaacaac gccgtggcg ccgggacgg catcgtcatc
1800	gattcccaag gtgtcgtgtt gaccacaac cagtgatcg cggcgccac cgacatcaat
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1920	caggatgtcg cgtgctgca gctgcgggt gccggtggcc tgcggtcggc ggcgatcgtt
1980	ggcggcgtcg cgtttgtga gccgtcgtc gcgatgggca acagcgttgg gcagggcgga
2040	acgccccgt cgtgtcctgg cagggtgtc gccgtcggcc aaaccgtgca ggcgtcggat
2100	tcgctgacgg gtgcccgaag gacatgaaac gggttgatcc agttcgatgc cgcgatccag
2160	cccggtgatg cgggcgggcc cgtctcaac ggcctagac aggtgtcgg tatgaacacg
2172	ggcggtctt ag

<210> 7
 <211> 725
 <212> PRT
 <213> Artificial Sequence

<220> M72 fusion with 2 additional his residues

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 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
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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 additional his residues

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360	gpcctaaacg ggcatacacc cgttgacgtc atctcgttga ccttgcaaac caagtccggc
420	ggcacgcgtta cagggaacgt gacattggcc gagggaacccc cggccgaatt catgttgat
480	ttcggggcgt taccacccgga gatacaatcc gcagagatgt accgcccggccc gggttcggcc
540	tcgtctgttg cccgcccctca gatgtgggac agcgtggcga gtgaacctgt ttccggcccg
600	tcggcgttc agtcggttgt ctgggtcttg accgttgggt cgttgatagg ttctgtccggc
660	ggtctgatgg ttggcgccgc ctgcgccgtat gtggcgttga tgagcgtcac cggggggcag
720	ggcgaagctga cccgcccga ggtccgggtt gctggcggg cctaagagac ggcgtatggg
780	ctgaacgttg ccccgccgtt gatcgccgag aacgttgctg aactgatgat tctgatagcg
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900	atgttggccc aagaagccgc cgcgatgttt ggtacggccg cggcgagccg gacggcgacg
960	gcgaacgttg tgccttcga ggaagcgccg gagatgaaca gcgcgggttg gctccctcga
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1200	atggccaaca accacatgtc gatgaaccaac tcgggttgtt cgatgaacca cacccttgagc
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1320	aaagggttcc gggcgatgag ctgcctggg agctcgcttg gttcttccgg ttctgggcgt
1380	gggttggccc ccaacttgg ttggcgccg tccgttcgtt cgttgttcgt gccgcaggcc
1440	ttggcccgcc ccaaccagg agtcaacccc ggggcgccgg cgttcgccgt gaccagccctg
1500	accagcgccg cggaaagagg gcccgggcag atgtctggcg ggttcgggt ggggcagatg
1560	ggcgccaagg cggttgttg gctcagttgt gtgcctgcgt ttccggccg accctatgtg
1620	atgcgccatt ctccggcagc cggcgatatc gcccgccgg ccttgtcga ggaacggttc
1680	gccgaattcc ccgcgttcgc cctcgacccc tcgcgatgg tcgcccgaat gggggccaag
1740	gtgttcaaca tcaaaccaaa actyggctac aaacaagccg ttggcgccgg gaccggcatc
1800	gtcatcgtac ccaacgttgt cgtctgacccc aaacaaccaa tgatcggcg gccaaccgac
1860	atcaatgtct tcagcgttcg ctccggccaa acctaacggc tcgatgttgt cgggtatgac
1920	cgaacccagg atgtccgggt gctgcagctg cgcgttgccg gtggccctgc gtcggcgccg
1980	atcgttggcg gcttcgggt ttgttgaagccc gtctgtcgcga ttgggcaacag cgttgggca
2040	ggcggaacgc cccgttcgggt gcctggcagg gtgtgtcgcgc tcggccaacac cgtgcaggcg
2100	tcgatctgc tgaccggctc cgaagagaca ttgaacgggt tgatccaatt cgaagcccg
2160	atccagcccg gtatcgggg cgggcccttc gtcaaacgggt taggacaggt ggtcggtatg
2178	aaacagcccg cgtccta

eo1f-seq1

<212> PRT
<213> Artificial Sequence

<220>
<223> Mtb72f fusion

<400> 9

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
 Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp 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

eolf-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 ggcagggatt cgccattccg 60
atcgggcagg cgatggcgat cgcgggccag atccgatcgg gtgggggggtc acccaccgtt 120

180	catatcgggc ctaaccgcctt cctcggcttg ggtgtttgtc acaacaacgg caacggcgca
240	cgaagtccaac gctgtgttcgg gagcgctccg gcggcaagtc tcggcatctc caccggcgac
300	gtgatataccg cgttcgacgg cgtccgatic aactcgacca ccgcatggc ggacgcgcctt
360	aacgggcatic atcccggtga cgtcatctcg gtgaacctgg aaaaaccaagtc gggcggcacg
420	cgtacaggga acgtgacatt ggccgaggga ccccgccgg aattcatggt ggatttcggg
480	gcgttaccaa cggagataca ctcggcgagg atgtacggcg gcccggttc ggccctcgctg
540	gttggccggcg ctacgattgt ggaagcgctg gcgagtgaac tgttttcggc cgcgtcgggc
600	tttcagtctg tgtctctggg tctgaacggt gggttcgtga taggttcgtc ggcgggtctg
660	atgtgtggcg cggctctcgcc gtatgttggc tggatgagcg tcaacggcggg gcaggccggag
720	ctgaacggcg ccaggctccg gttgtcttcg gcggcctacg agacggcgta tgggcctgacg
780	gtgccccccg cgtgtgatic cgaagaacct gctgaacctga tgattctgat agcgaccaac
840	ctcttggggc aaaaacacccc ggcatctcgc gtcaacgagg ccgaatacgg cgaagtgtgg
900	gcccaaggacg ccgcgcgcgat gtttggctac gccgcggcga cgggcagcgc gacggcgacg
960	ttgtctcgct tcgaaggagg gccggagatg aaccagcgcg gttgggtctctt cgaagcaggc
1020	gccgcgtctg aggaaggctct cgaacacccg gcggcgaaac agttgatga caatgtgccc
1080	caggcgctgc aacagctggc ccagcccaag caggcgacca cgccttcttc caagctgggt
1140	ggccttgtga agaacggtct gccgcgatic tcgcgcatca gcaacatggt gtcgatggcc
1200	aaacaacaca tgtcgaatgac caactcgggt gttgtcgatga ccaacacctt gagtctgatg
1260	ttgaagggtt ttgtctccgg gccgcgcgc caggccgctg caagccgctg aaacccggcg
1320	gtccccggcg tgaagctcgt ggacagctcg ctgggtctctt cgggtctggg cgggtgggtg
1380	gccgcccaact tgggtcgggc ggctctcgct ggttcgttgt cgtgtccgca ggccttggcc
1440	gccgcccaacc aggcagctac ccggcgcgcg cgggcgctgc cgtgaacca gctgaacca
1500	gccgcggaaa gaaggcccg gcaagatgctg ggcgggctgc cgttggggca gatgggcggc
1560	agggccgggtg gttgggtcag tgggttcgct cgtgttcggc cgcgacccca ttgtatcgccg
1620	catctctccg cagcccgcg tatcggcccg cggccctgtt cgcaggacgg gttcgcggac
1680	ttcccccgcg tgcctcccg gccgtcccg atgttcgccc aagtggggcc acaagttgtc
1740	aaacataaca ccaaacctgg ctaacaacaa gccgttggcg ccgggacgg catcgtcatc
1800	gatcccaacg gttctgtct gtacaaacaa cagtgaticg cgggcggcca cgaacataat
1860	gcgttcagcg tcggtccgg ccaaacctac gggttcgatic tggtcgggta tgaccggcacc
1920	caggatgtcgg cggtcgtcga gctgcgggt gcccggtggc tgccgtcggc ggcgatcgggt
1980	ggcggcgtcgg cgttggta gcccgctctg cgcgatggca aacagcgttg gcaggcgga
2040	acggcccgctg cgtgtcccg cagggtgtc gccgttcggc aaaccgtgca ggcgtcggat
2100	tcgctgacgg gtgcggaa gaacatgaac gggttgatcc agttcgatgc cgcgatacca
2160	ccccgtgatc cggcgggcc cgtctcaac gccctaggac aggtgtcgg tatgaacaacg

gccgcgtcct ag

<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

eo1f-seq1

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

eol-f-seq1

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

```

agcgggtgggc agggcggaac gccccgtgcg gtgcctggca gggtggtcgc gctcggccaa      2040
accgtgcagg cgtcggattc gctgaccggt gccgaagaga cattgaacgg gttgatccag      2100
ttcgatgccg cgatccagcc cggtgattcg ggcggggccc 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

```

```

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

```

```

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

```

```

<400> 14
tctcccagcg tgcgccat      18

```

```

<210> 15
<211> 30
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> CpG Oligo 3

```

```

<400> 15
accgatgacg tcgccggtga cggcaccacg      30

```

```

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

```

```

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

```

```

<400> 16
tcgtcgtttt gtcgttttgt cgtt      24

```

```

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

```

```

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

```

```

<400> 17
tccatgacgt tcctgatgct      20

```

eolf-seq1