

eolf-seq1
SEQUENCE LISTING

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

<120> Novel compositions

<130> VB64442

<150> US61/422723

<151> 2010-12-14

<160> 13

<170> PatentIn version 3.5

<210> 1

<211> 723

<212> PRT

<213> Artificial Sequence

<220>

<223> M72 fusion protein

<400> 1

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

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 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
 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

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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
675 680 685

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

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

Ala Ala Ser

<210> 2
<211> DNA
<212>
<213> Artificial Sequence
<220>
<223> coding sequence for M72 fusion
<400> 2

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180 catatcgggc ctaccggcct cctcggcttg ggtgttgtcg acaacaacgg caacggcgca
240 cgaattccaac gcgttgttcg gacgctccg gcggcaagtc tcggcatctc caccggcgac
300 gtgatcaccc cgttcgacgg cgtccgatac aactcggcca cggcagatgg ggaacgcgtt
360 aacgggcatc atcccggtga cgtcatctcg gtgaacctgg aaacccaagt gggcggcgacg
420 cgtacaggga acgtgacatt ggccgaggga ccccgccg aattcatgtt ggatttcggg
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540 gtggccggcg ctacgatttg ggaacggctg gcgaagtgaac tgtttcggc cgcgttcggc
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660 atgttgtcgg cggcctccgc gtatgttggc ttgataggcg tcaccggcgg ggacggcgag
720 ctgaaccggc ccaagttccg ggttgttcg gcggcctacg agaacggcgta tgggtctgacg
780 gtgccccccc cgttgatcgc cgaagaacct gctgaactga tgattctgat agcgaccaca
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1140 ggcttgtgga agacggcttc gccgcatcgg tcgcccgatca gcaacatgtt gtcgatatgccc
1200 aacaacaaca tgtcgaatgac caactcgggt gtgtcgaatga ccaacacctt gtagctcga
1260 ttgaagggtc ttgtccggc ggccggccgc caggccgtgc aaacccggcg gcaaaaaagg
1320 gtcggggcga tgaactcgtt ggacagctcg ctgggttctt cgggtcctgg cggttgggggtg
1380 gccgcccaac ttgggtcggc ggctcgttc ggttcgttgt cgttcgacga ggctctgggc
1440 gccgcccaac aggcagtcac ccggcggcgg cgggcgtcgc cgttgaccaa cctgaaccag
1500 gccgcggaaa gagggcccg gacgaatcgt ggccggcgtc cggttggggca gatggggcgcc
1560 agggccggtg gtgggtccag ttgttgtcgt cgtgttccgc cggacacctt tgtgatgcgcg

eof-seq1

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 aacatcaaca ccaaactggg ctacaacaac gccgtgggcg ccgggaccgg catcgatc 1740
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 gcgttcagcg tcgggtccgg ccaaacttac ggcgtcgatg tggtcgggta tgaccgcacc 1860
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 acgccccgtg cgggtgcctgg cagggtgggtc gcgctcggcc aaaccgtgca ggcgtcggat 2040
 tcgctgaccg gtgccgaaga gacattgaac gggttgatcc agttcgatgc cgcgatccag 2100
 cccggtgatg cgggcggggc cgctcgtcaac ggcctaggac aggtgggtcgg tatgaacacg 2160
 gccgcgtcct ag 2172

<210> 3
 <211> 725
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M72 fusion with 2 additional his residues
 <400> 3

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

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

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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

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

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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

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

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Gln 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 725

<210> 4
<211> 2178
<212> DNA
<213> Artificial Sequence
<220>
<223> coding sequence for M72 fusion with 2 additional his residues

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attccgatacg ggcaggcgat ggcgatcgcg ggcagatcc gatcgggttg ggggttcaccc 120
accgttcata tcggccctac cgcttccctc ggccttgggt ttgtcgcgaac caacggcaac 180
ggcgacagag tccaacgcgt gttcgggagc gttccggcgg caagtctcgg catctccaccc 240
ggcgacgtga tcaaccgcgt cgaaggcgtc ccgatcaact cggccacccg gatggcggag 300
ggcgttaacg ggcatacccg cgttgacgtc atctcggtga cctggcaaac caagtccggg 360
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ttcgggcgt taccaaccga gatcaatcc ggcagatgt acgcccggcc gggttcggcc 480
tcgctgttgg ccgcgcgtca gatgtgggac agcgttggcg gtgaacctgt ttccggccgcg 540
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ggtctgatgg ttggcggcgc ctgcggatat gttgcgttga ttgagcgtcac cgcggggcag 660
gscgagctga ccgcggccca gttccgggtt gctcggcggc cctacgagac ggcgtatagg 720
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tcgatgttga aggccttgc tcggcggcg gccggccag cgttcgcaaac cgcggcgcaa 1260
aacggggtcc gggcgatgag ctgcctgggc agctcgcgtg gttcttcggg tctggggcgt 1320
gggttgcccg ccaacttggg tcgggcggcc ccaacttggg tcgggcggcc 1380

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accagcgccg cggaagagg gcccgggcag atgctgggcg ggctgccggt ggggcagatg	1500
ggcgccaggg ccggtggtgg gctcagtggg gtgctgcgtg ttccgccgag accctatgtg	1560
atgccgcatt ctccggcagc cggcgatata gccccgccgg ccttgctgca ggaccggttc	1620
gccgacttcc ccgcgctgcc cctcgacccg tccgcgatgg tcgcccagt ggggccacag	1680
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gtcatcgatc ccaacggtgt cgtgctgacc aacaaccacg tgatcgggg cgccaccgac	1800
atcaatgcgt tcagcgctcg ctcgggcaa acctacggcg tcgatgtggg cgggtatgac	1860
cgcaccagg atgtcgcggt gctgcagctg cgcggtgccg gtggcctgcc gtcggcgggc	1920
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ggcggaacgc cccgtgcggt gcctggcagg gtggctcgcg tcggccaaac cgtgcaggcg	2040
tcggattcgc tgaccggtgc cgaagagaca ttgaacgggt tgatccagtt cgatgccgag	2100
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aacacggccg cgtcctag	2178

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

<220>
 <223> Mtb72f fusion
 <400> 5

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	

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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

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

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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

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

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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> 6
<211> 2172
<212> DNA
<213> Artificial sequence

<220>
<223> Coding sequence for Mtb72f fusion

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eolf-seq1

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caggatgtcg cgggtgctga gctgcgcggt gccggtggcc tgccgtcggc ggcgatcgg	1920
ggcggcgtcg cggttggtga gcccgtcgtc gcgatgggca acagcgggtg gcagggcgga	1980
acgccccgtg cgggtgcctg cagggtggtc gcgctcggcc aaaccgtgca ggcgtcggat	2040
tcgctgaccg gtgccgaaga gacattgaac gggttgatcc agttcgatgc cgcgatccag	2100
cccgggtgatt cgggcggggc cgtcgtcaac ggcctaggac aggtgggtcgg tatgaacacg	2160
gccgcgtcct ag	2172

<210> 7

<211> 729

<212> PRT

<213> Artificial Sequence

<220>

<223> Mtb72f fusion with 6 additional his residues

<400> 7

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

eo1f-seq1

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

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

eolf-seq1

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

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

eolf-seq1

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> 8
<211> 2190
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence for M72 fusion with 6 additional his residues

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gggggggtcac ccaccgttca tatcgggcct accgccttcc tcggcttggg tggtgtcgac 180
aacaacggca acggcgcacg agtccaacgc gtggtcggga gcgctccggc ggcaagtctc 240
ggcatctcca ccggcgacgt gatcaccgcg gtcgacggcg ctccgatcaa ctcggccacc 300
gcgatggcgg acgcgcttaa cgggcatcat cccggtgacg tcatctcggg gacctggcaa 360
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ttcatggtgg atttcggggc gttaccaccg gagatcaact ccgcgaggat gtacgccggc 480
ccgggttcgg cctcgctggg ggccgcggct cagatgtggg acagcgtggc gagtgacctg 540
ttttcggccg cgtcggcggt tcagtcgggt gtctgggggtc tgacggtggg gtcgtggata 600
ggttcgtcgg cgggtctgat ggtggcggcg gcctcgccgt atgtggcgtg gatgagcgtc 660
accgcggggc aggccgagct gaccgccgcc cagggtccggg ttgctgcggc ggcctacgag 720
acggcgtatg ggctgacggg 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 cgcggctgag gaggcctccg acaccgccgc ggcgaaccag 1020

1080	ttgatgaaca atgtgccccca ggcgtctgcaaa cagtgtgccc agccccacgca gggcacccacg
1140	ccttcctcca agctgggtgg cctgtggaag acggtctcgc cgcatcgttc gccgatcagc
1200	aaacatgtgtgt cgatggccaa caaccacatg tcgatgacca actcgggtgt gtcgatgacc
1260	aaacacctga gctcgaattt gaaggcttt gctccggcgg cggccggccca gggcgtgcaaa
1320	accgcgcgcc aaaaagggtt ccgggcgatg agctcggctgg gcaggtctgct ggggtcttcg
1380	gggtctggcg gtgggggtgg ccgcaacttg ggtcggggcg cctcggtcgg ttcgtttcgc
1440	gtgcgcgcag cctgggcgc gcccaaccag gcagtcaacc cgggcggcgg ggcgctgcgc
1500	ctgaccagcc tgaaccagcg ccggaagaag gggcccgggc agatgctggg ccggctgcgc
1560	gtggggcaga tgggcgcag ggcgggtgtt gggctcagt ggtgtcgcgc gtttcgcgcgc
1620	cgaacctatg tgatgccga ttctccgca gccggcgata tcggcccgcc ggcctttcgc
1680	caggaccggt tcgccgaatt cccgcgcctg cccctcgacc cgtccgcgat ggtcggccaa
1740	gtggggccac aggttgtcaaa catcaacacc aaactgggtt acaacaacgc cgtggggcgc
1800	gggaaccgca tctgcatcga tcccaacggt gtcgtctga ccaacaacca cgtgatcgcg
1860	ggcgccaccg acatcaatgc gttcagcgtc ggtcccgcc aaacctacgg cgtcgaatgtg
1920	gtcgggtatg accgacacca ggatgtcgcg gtcgtcgaac tgcgcgggtgc cggtyggcctg
1980	ccgttcggcg cgatcgttgg cgcgctcgcg gttgttgagc ccgtcgtcgc gatgggcaac
2040	agggttgggc agggcggaac gccccgtgcg gtcgctggca gggtygtcgc gctcggccaa
2100	accgtgcagg cgtcggattc gctgaaccgt gccgaagaga cattgaacgg gttgatccag
2160	ttcgaatgcc cgatccagcc cgtgtattcg ggcgggcccg tcgtcaacgg cctaggacag
2190	gtgttcggtg tgaacacggc cgcgtccctag
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20	<220> <223> Cpg oligo 1 - Cpg 1826
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18	<210> 10 <211> 18 <212> DNA <213> Artificial Sequence
18	<220> <223> Cpg oligo 2 - Cpg 1758
18	<400> 10 tctccagcg tgcgccat

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<223>	CpG oligo 5 - CpG 1686	
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