SEQUENCE LISTING - RECTIFICATION

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Rae, Chris
Kehoe, Haixing
Peterson, Bret
Cheung, Chingnam

<120> IMMUNOSTIMULATORY BACTERIA DELIVERY PLATFORMS AND
THEIR USE FOR DELIVERY OF THERAPEUTIC PRODUCTS

<130> 62131-1707PC

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<150> 62/990,404
<151> 2020-03-16

<150> 62/962,162
<151> 2020-01-16

<150> 62/934,503
<151> 2019-11-12

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<223> programmed death-ligand 1 (PD-L1), isoform 1

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<223> CTNNB1 (Beta-catenin), isoform 1

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<220>
<223> Strain LT2 Aspartate-semialdehyde dehydrogenase
(asd)

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<213> Salmonella typhimurium

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<213> Homo sapiens

<220>
<223> programmed cell death protein 2 (PD-2), isoform 1

<400> 51
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gaatccaggg aagataaaat ttttcagaag tttaaaactc agatagccct tgaaccagaa 660
cagattctta gatatggcag aggtattgcc cccatctgga tttctggtga aaatattcct 720
caagaaaagg atattccaga ttgcccctgt ggtgccaaga gaatattgga attccaggtc 780
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tttgtgtgga agcaggatgt aacagataca ccg   933

<210> 52
<211> 819
<212> DNA

<213> Homo sapiens

<220>
<223> programmed death-ligand 2 (PD-L2), isoform 1

<400> 52
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cctgtcacca caacaaagag ggaagtgaac agtgctatc   819

<210> 53
<211> 669
<212> DNA
<213> Homo sapiens

<220>
<223> cytotoxic T-lymphocyte-associated protein 4
      (CTLA-4), isoform 1

<400> 53
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gcatctccag gcaaagccac tgaggtccgg gtgacagtgc ttcggcaggc tgacagccag 240
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ctgggcatag gcaacggaac ccagatttat gtaattgatc cagaaccgtg cccagattct 480
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ctcacagctg tttctttgag caaaatgcta aagaaaagaa gccctcttac aacaggggtc 600
tatgtgaaaa tgcccccaac agagccagaa tgtgaaaagc aatttcagcc ttattttatt 660
cccatcaat   669

<210> 54
<211> 969
<212> DNA
<213> Homo sapiens

<220>

<223> CD47 transcript variant 1

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gaaaatattc ttattgttat tttcccaatt tttgctatac tcctgttctg gggacagttt 480
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gaatattcat taaagaatgc tactggcctt ggtttaattg tgacttctac agggatatta 660
atattacttc actactatgt gtttagtaca gcgattggat taacctcctt cgtcattgcc 720
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aatgatgaa 969

<210> 55
<211> 1209
<212> DNA
<213> Homo sapiens

<220>
<223> indoleamine 2,3-dioxygenase (IDO) 1

<400> 55
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gtgggctttg ctctgccaaa tccacaggaa aatctacctg atttttataa tgactggatg 120
ttcattgcta aacatctgcc tgatctcata gagtctggcc agcttcgaga aagagttgag 180
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cctcctattt tggtttatgc agactgtgtc ttggcaaact ggaagaaaaa ggatcctaat 420
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aaggaaggt 1209

<210> 56
<211> 1260
<212> DNA
<213> Homo sapiens

<220>
<223> indoleamine 2,3-dioxygenase (IDO) 2

<400> 56
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cttcttccag attctctgaa agaacttcca gatcattata ggccttggat ggaaattgcc 180
aacaaacttc ctcaattgat tgatgctcac cagcttcaag ctcatgtgga caagatgccc 240
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<210> 57
<211> 2310
<212> DNA
<213> Homo sapiens

<220>
<223> signal transducer and activator of transcription 3
(STAT3)

<400> 57
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ctgggagaga ttgaccagca gtatagccgc ttcctgcaag agtcgaatgt tctctatcag 240
cacaatctac gaagaatcaa gcagtttctt cagagcaggt atcttgagaa gccaatggag 300
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<210> 58
<211> 1575
<212> DNA
<213> Homo sapiens

<220>
<223> lymphocyte-activation gene 3 (LAG3)

<400> 58
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gagccggagc agctc 1575

<210> 59
<211> 903
<212> DNA
<213> Homo sapiens

<220>
<223> T cell immunoglobulin and mucin-domain
containing-3 (TIM-3)

<400> 59
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tcctcagaag tggaatacag agcggaggtc ggtcagaatg cctatctgcc ctgcttctac 120
accccagccg ccccagggaa cctcgtgccc gtctgctggg gcaaaggagc ctgtcctgtg 180
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gaaaaattta acctgaagtt ggtcatcaaa ccagccaagg tcacccctgc accgactcgg 420
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gaagaaaaca tctataccat tgaagagaac gtatatgaag tggaggagcc caatgagtat 840
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cca 903

<210> 60
<211> 732
<212> DNA

<213> Homo sapiens

<220>
<223> T cell immunoreceptor with Ig and ITIM domains
(TIGIT), isoform 1

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gtccaggcag aagctgcacc tgctgggctc tgtggagagc agcggggaga ggactgtgcc 660
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acagagactg gt 732

<210> 61
<211> 1065
<212> DNA
<213> Homo sapiens

<220>
<223> GALECTIN-9/LGALS9, isoform 1

<400> 61
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<210> 62

<211> 720
<212> DNA
<213> Homo sapiens

<220>
<223> LIGHT/TNSF14

<400> 62
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<210> 63
<211> 849
<212> DNA
<213> Homo sapiens

<220>
<223> HVEM/TNSFR14 (receptor for LIGHT ligand)

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<210> 64
<211> 660
<212> DNA
<213> Homo sapiens

<220>
<223> CD28

<400> 64
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<210> 65
<211> 1578
<212> DNA
<213> Homo sapiens

<220>
<223> carcinoembryonic antigen-related cell adhesion
      molecule 1 (CEACAM1, or CD66a)

<400> 65
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<210> 66
<211> 864
<212> DNA
<213> Homo sapiens

<220>
<223> CD80/B7-1

<400> 66
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gaagtgaaag aagtggcaac gctgtcctgt ggtcacaatg tttctgttga agagctggca 180
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gacttcccta cacctagtat atctgacttt gaaattccaa cttctaatat tagaaggata 480
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agaagggaaa gtgtacgccc tgta 864

<210> 67
<211> 995
<212> DNA
<213> Homo sapiens

<220>
<223> CD86/B7-2

<400> 67
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agacatcttc atgcgacaaa agtgatacat gtttt 995

<210> 68
<211> 1095
<212> DNA
<213> Homo sapiens

<220>
<223> CD244/2B4

<400> 68
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ccaaacagca tacagacgaa ggttgacagc attgcatgga agaagttgct gccctcacaa 180
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<210> 69
<211> 1251
<212> DNA
<213> Homo sapiens

<220>
<223> CD155/PVR

<400> 69
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<210> 70
<211> 1614
<212> DNA
<213> Homo sapiens

<220>
<223> CD122/nectin-2

<400> 70
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<210> 71
<211> 1008
<212> DNA
<213> Homo sapiens

<220>
<223> CD226 antigen

<400> 71
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<210> 72
<211> 545
<212> DNA
<213> Homo sapiens

<220>
<223> CD160 antigen

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<210> 73
<211> 264
<212> DNA
<213> Homo sapiens

<220>
<223> human U6 RNA Pol III promoter

<400> 73
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atcttgtgga aaggacgaaa ctag 264

<210> 74
<211> 99
<212> DNA
<213> Homo sapiens

<220>
<223> human H1 RNA Pol III promoter

<400> 74
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tgggaatctt ataagttctg tatgagacca ctccctagg 99

<210> 75
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> shRNA-encoding sequence targeting muPD-L1

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<210> 76
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> shRNA-encoding sequence targeting muSIRPA

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<210> 77
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> shRNA-encoding sequence targeting muTREX1, clone 1

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<210> 78
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> shRNA-encoding sequence targeting muTREX1, clone 2

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<210> 79
<211> 3966
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector1-human shTREX1-1_shPDL1-1

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<212> DNA
<213> Salmonella typhimurium

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<223> aroC

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<212> DNA
<213> Salmonella typhimurium

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<212> DNA
<213> Salmonella typhimurium

<220>
<223> PhoP

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<212> DNA
<213> Salmonella typhimurium

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<223> PhoQ

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<211> 2731
<212> DNA
<213> Salmonella typhimurium

<220>
<223> Adenylate cyclase (cyaA)

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<210> 87
<211> 826
<212> DNA
<213> Salmonella typhimurium

<220>
<223> cAMP-activated global transcriptional regulator
(crp)

<400> 87
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<210> 88

<211> 1566
<212> DNA
<213> Homo sapiens

<220>
<223> cyclic GMP-AMP (cGAMP) synthase (cGAS), isoform 1

<400> 88
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cccgaggccg ccctgcctaa ggcgggaaag ttcggccccg ccaggaagtc gggatcccgg 180
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gccaaaaagg cccctcagcg cgcccaggac acgcagccgt ctgacgccac cagcgccccc 300
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gaattt 1566

<210> 89
<211> 1137
<212> DNA
<213> Homo sapiens

<220>
<223> Stimulator of Interferon Genes (STING)(H232 Allele)

<400> 89
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gcagccttgg ttctgctgag tgcctgcctg gtgacccttt gggggctagg agagccacca 120
gagcacactc tccggtacct ggtgctccac ctagcctccc tgcagctggg actgctgtta 180
aacggggtct gcagcctggc tgaggagctg cgccacatcc actccaggta ccggggcagc 240
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<210> 90
<211> 972
<212> DNA
<213> Salmonella typhimurium

<220>
<223> lipid A biosynthesis myristoyltransferase (msbB)

<400> 90
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tttgagcagc ttcaggatcc aggtgtactg ttccggatgc gggccgacaa aaatttcgac 120
ctcttcgttc atccgtctgg cgatagtgtg gtcgtcagcc gtgagcagat cgtccattgg 180
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tttggtttcc at 972

<210> 91
<211> 1038
<212> DNA
<213> Salmonella typhimurium

<220>
<223> Phosphoribosylaminoimidazole synthetase (purI)

<400> 91
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aatcaccatg ccgacgccgc agttaaaggt acggtacatt tcatgtcggc tgacattacc 180
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<210> 92
<211> 426
<212> DNA
<213> Homo sapiens

<220>
<223> Survivin (SVN)/BIRC5, isoform 1

<400> 92
atgggtgccc cgacgttgcc ccctgcctgg cagcccttc tcaaggacca ccgcatctct 60
acattcaaga actggccctt cttggagggc tgcgcctgca ccccggagcg gatggccgag 120
gctggcttca tccactgccc cactgagaac gagccagact tggcccagtg tttcttctgc 180
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tcgtccggtt gcgctttcct ttctgtcaag aagcagtttg aagaattaac ccttggtgaa 300
tttttgaaac tggacagaga aagagccaag aacaaaattg caaaggaaac caacaataag 360
aagaaagaat ttgaggaaac tgcggagaaa gtgcgccgtg ccatcgagca gctggctgcc 420
atggat   426

<210> 93
<211> 285
<212> DNA
<213> E. coli

<220>
<223> araBAD promoter (pBAD)

<400> 93
aagaaaccaa ttgtccatat tgcatcagac attgccgtca ctgcgtcttt tactggctct 60
tctcgctaac caaaccggta accccgctta ttaaaagcat tctgtaacaa agcgggacca 120
aagccatgac aaaaacgcgt aacaaaagtg tctataatca cggcagaaaa gtccacattg 180

attatttgca cggcgtcaca ctttgctatg ccatagcatt tttatccata agattagcgg 240
atcttacctg acgcttttta tcgcaactct ctactgtttc tccat 285

<210> 94
<211> 459
<212> DNA
<213> Homo sapiens

<220>
<223> Interleukin 2 (IL-2)

<400> 94
atgtacagga tgcaactcct gtcttgcatt gcactaagtc ttgcacttgt cacaaacagt 60
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tggattacct tttgtcaaag catcatctca acactgact 459

<210> 95
<211> 567
<212> DNA
<213> Homo sapiens

<220>
<223> Interferon (IFN) alpha

<400> 95
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ttggctgtga agaaatactt ccgaagaatc actctctatc tgacagagaa gaaatacagc 480
ccttgtgcct gggaggttgt cagagcagaa atcatgagat ccctctcttt atcaacaaac 540
ttgcaagaaa gattaaggag gaaggaa 567

<210> 96
<211> 729
<212> DNA
<213> Homo sapiens

<220>
<223> CD48, isoform 1

<400> 96

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ctcctggtga ccagcattca aggtcacttg gtacatatga ccgtggtctc cggcagcaac 120
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<210> 97
<211> 1602
<212> DNA
<213> Homo sapiens

<220>
<223> CD276/B7-H3, isoform 1

<400> 97
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<210> 98
<211> 846
<212> DNA
<213> Homo sapiens

<220>
<223> B7-H4/VTCN1

<400> 98
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ctaaaa 846

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<211> 867
<212> DNA
<213> Homo sapiens

<220>
<223> BTLA/CD272, isoform 1

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gaagtttatt ctaatccatg cctggaagaa aacaaaccag gcattgttta tgcttccctg 780
aaccattctg tcattggacc gaactcaaga ctggcaagaa atgtaaaaga agcaccaaca 840
gaatatgcat ccatatgtgt gaggagt 867

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<212> DNA
<213> Homo sapiens

<220>
<223> Chemokine (C-C motif) ligand 4 (CCL4)

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tgggtccagg agtacgtgta tgacctggaa ctgaac 276

<210> 101
<211> 3537
<212> DNA
<213> Homo sapiens

<220>
<223> CD103/ITGAE

<400> 101
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<211> 1671
<212> DNA
<213> Homo sapiens

<220>
<223> CD19, isoform 1

<400> 102
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<210> 103
<211> 579
<212> DNA
<213> Homo sapiens

<220>
<223> Interleukin 18 (IL-18), isoform 1

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cttgaatcta aattatcagt cataagaaat ttgaatgacc aagttctctt cattgaccaa 180
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gaaatgaatc ctcctgataa catcaaggat acaaaaagtg acatcatatt ctttcagaga 420
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<210> 104
<211> 1005
<212> DNA
<213> Homo sapiens

<220>
<223> Fas ligand

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<210> 105
<211> 1023
<212> DNA
<213> Salmonella typhimurium

<220>
<223> firA/SSC

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gac 1023

<210> 106
<211> 918

<212> DNA
<213> E. coli

<220>
<223> htrB

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ggcgttcctt cacgctat   918

<210> 107
<211> 717
<212> DNA
<213> Salmonella typhimurium

<220>
<223> ompR

<400> 107
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<210> 108
<211> 498
<212> DNA
<213> Homo sapiens

<220>
<223> Inteferon (IFN) gamma

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ggtcgaagag catcccag 498

<210> 109
<211> 699
<212> DNA
<213> Homo sapiens

<220>
<223> Tumor necrosis factor (TNF) alpha

<400> 109
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<210> 110
<211> 825
<212> DNA
<213> Homo sapiens

<220>
<223> Atg5 long isoform

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<220>
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<213> Homo sapiens

<220>

<223> Toll-like receptor 2 (TLR2)

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<213> Homo sapiens

<220>

<223> TLR4, isoform 1

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<213> Homo sapiens

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<223> TLR5

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<212> DNA
<213> Homo sapiens

<220>
<223> TLR3, isoform 1

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<212> DNA
<213> Homo sapiens

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<223> TLR8, isoform 1

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<212> DNA
<213> Homo sapiens

<220>
<223> Interleukin 6 (IL-6)

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<212> DNA
<213> Homo sapiens

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<223> MyD88, isoform 1

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<212> DNA
<213> Homo sapiens

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<220>
<223> IPS-1/MAVS, isoform 1

<400> 123
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cgactgcggg ccacctgcac actctcaggg aaccgggaca ccctctggca tctcttcaat 180
acccttcagc ggcggcccgg ctgggtggag tacttcattg cggcactgag gggctgtgag 240
ctagttgatc tcgcggacga agtggcctct gtctaccaga gctaccagcc tcggacctcg 300
gaccgtcccc cagacccact ggagccaccg tcacttcctg ctgagaggcc agggcccccc 360
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cccatgcctg tccaggagac ccaggcgcca gagtccccag gagagaattc agagcaagcc 480
ctgcagacgc tcagccccag agccatccca aggaatccag atggtggccc cctggagtcc 540
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gaactgggca gtacccacac agcaggtgcg acctccagcc tcacaccatc ccgtgggcct 660
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accttgatgc ctgtgaacac agtggccctg aaagtgcctg ccaacccagc atctgtcagc 960
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<210> 124
<211> 2775
<212> DNA
<213> Homo sapiens

<220>
<223> RIG-1/DDX58, isoform 1

<400> 124
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ctgttggagc tccaggagga aggctggttc cgtggctttt tggatgccct agaccatgca 240
ggttattctg gactttatga agccattgaa agttgggatt tcaaaaaaat tgaaaagttg 300
gaggagtata gattactttt aaaacgttta caaccagaat ttaaaaccag aattatccca 360
accgatatca tttctgatct gtctgaatgt ttaattaatc aggaatgtga agaaattcta 420
cagatttgct ctactaaggg gatgatggca ggtgcagaga aattggtgga atgccttctc 480
agatcagaca aggaaaactg gcccaaaact ttgaaacttg ctttggagaa agaaaggaac 540
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gaggataaga tggaaacttc tgacatacag attttctacc aagaagatcc agaatgccag 660
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gctgacgtaa gagtgataga ggaatgccat tacactgtgc ttggagatgc ttttaaggaa 2520
tgctttgtga gtagaccaca tcccaagcca aagcagtttt caagttttga aaaaagagca 2580
aagatattct gtgcccgaca gaactgcagc catgactggg gaatccatgt gaagtacaag 2640
acatttgaga ttccagttat aaaaattgaa agttttgtgg tggaggatat tgcaactgga 2700
gttcagacac tgtactcgaa gtggaaggac tttcattttg agaagatacc atttgatcca 2760
gcagaaatgt ccaaa 2775

<210> 125
<211> 1494
<212> DNA
<213> Homo sapiens

<220>
<223> IRF5, transcript variant 2

<400> 125
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ctggtggccc aggtgaacag ctgccagtac ccagggcttc aatgggtcaa cggggaaaag 120
aaattattct gcatcccctg gaggcatgcc acaaggcatg gtcccagcca ggacggagat 180
aacaccatct tcaaggcctg ggccaaggag acagggaaat acaccgaagg cgtggatgaa 240
gccgatccgg ccaagtggaa ggccaacctg cgctgtgccc ttaacaagag ccgggacttc 300
cgcctcatct acgacgggcc ccgggacatg ccacctcagc cctacaagat ctacgaggtc 360
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ggagaggagg aggaagaaga ggaagagctg cagaggatgt tgccaagcct gagcctcaca 480
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ccgcccactc tgcagccgcc cgtggtgctg ggtccccctg ctccagaccc cagccccctg 600
gctcctcccc ctggcaaccc tgctggcttc agggagcttc tctctgaggt cctggagcct 660
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<210> 126
<211> 1284
<212> DNA
<213> Homo sapiens

<220>
<223> IRF3, isoform 1

<400> 126
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cacggcctac ggcaggatgc acagcaggag gatttcggaa tcttccaggc ctgggccgag 180
gccactggtg catatgttcc cgggagggat aagccagacc tgccaacctg gaagaggaat 240
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ctggatgagt tactgggtaa catggtgttg gccccactcc cagatccggg acccccaagc 480
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ccactctccc tcacctccga ccagtacaag gcctacctgc aggacttggt ggagggcatg 1260
gatttccagg gccctgggga gagc 1284

<210> 127
<211> 1275
<212> DNA
<213> Homo sapiens

<220>
<223> TANK

<400> 127
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atggatagag attctgcagt aaaagaatta cagcaaaaga ctgagaacta tgagcagaga 120
atacgtgaac aacaggaaca gctgtcactt caacagacta ttattgacaa gctaaaatct 180

cagttacttc ttgtgaattc cactcaagat aacaattatg gctgtgttcc tctgcttgaa 240
gacagtgaaa caagaaagaa taatttgact cttgatcagc cacaagataa agtgatttca 300
ggaatagcaa gagaaaaact accaaaggta agaagacaag aggtttcttc tcctagaaaa 360
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gcagttttcc caccatccat tacatccagg ggggatttcc ttcggcatct taattcacac 1260
ttcaatggag agact 1275

<210> 128
<211> 2136
<212> DNA
<213> Homo sapiens

<220>
<223> TRIF/TICAM1

<400> 128
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tcccaggcgc ccgaggacaa gacgcaggag gcagaa 2136

<210> 129
<211> 381
<212> DNA
<213> Homo sapiens

<220>
<223> Batf3

<400> 129
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aaccagccgc agccgcagcc gcagcagcag agccctgagg atgatgacag gaaggtccga 120
aggagagaaa aaaaccgagt tgctgctcag agaagtcgga agaagcagac ccagaaggct 180
gacaagctcc atgaggaata tgagagcctg gagcaagaaa acaccatgct gcggagagag 240
atcgggaagc tgacagagga gctgaagcac ctgacagagg cactgaagga gcacgagaag 300
atgtgcccgc tgctgctctg ccctatgaac tttgtgccag tgcctccccg gccggaccct 360
gtggccggct gcttgccccg a 381

<210> 130
<211> 459
<212> DNA
<213> Homo sapiens

<220>
<223> IL-4, isoform 1

<400> 130
atgggtctca cctcccaact gcttcccccct ctgttcttcc tgctagcatg tgccggcaac 60
tttgtccacg gacacaagtg cgatatcacc ttacaggaga tcatcaaaac tttgaacagc 120
ctcacagagc agaagactct gtgcaccgag ttgaccgtaa cagacatctt tgctgcctcc 180
aagaacacaa ctgagaagga aaccttctgc agggctgcga ctgtgctccg gcagttctac 240
agccaccatg agaaggacac tcgctgcctg ggtgcgactg cacagcagtt ccacaggcac 300
aagcagctga tccgattcct gaaacggctc gacaggaacc tctggggcct ggcgggcttg 360
aattcctgtc ctgtgaagga agccaaccag agtacgttgg aaaacttctt ggaaaggcta 420
aagacgatca tgagagagaa atattcaaag tgttcgagc 459

<210> 131
<211> 534
<212> DNA
<213> Homo sapiens

<220>
<223> IL-10

<400> 131
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caagccttgt ctgagatgat ccagttttac ctggaggagg tgatgcccca agctgagaac 300
caagacccag acatcaaggc gcatgtgaac tccctggggg agaacctgaa gaccctcagg 360
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caggtgaaga atgcctttaa taagctccaa gagaaaggca tctacaaagc catgagtgag 480
tttgacatct tcatcaacta catagaagcc tacatgacaa tgaagatacg aaac   534

<210> 132
<211> 759
<212> DNA
<213> Homo sapiens

<220>
<223> IL-12 alpha

<400> 132
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catccagcgg ctcgccctgt gtccctgcag tgccggctca gcatgtgtcc agcgcgcagc 120
ctcctccttg tggctaccct ggtcctcctg gaccacctca gtttggccag aaacctcccc 180
gtggccactc cagacccagg aatgttccca tgccttcacc actcccaaaa cctgctgagg 240
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aatgggagtt gcctggcctc cagaaagacc tcttttatga tggccctgtg ccttagtagt 480
atttatgaag acttgaagat gtaccaggtg gagttcaaga ccatgaatgc aaagcttctg 540
atggatccta agaggcagat ctttctagat caaaacatgc tggcagttat tgatgagctg 600
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gatttttata aaactaaaat caagctctgc atacttcttc atgctttcag aattcgggca 720
gtgactattg atagagtgat gagctatctg aatgcttcc   759

<210> 133
<211> 986
<212> DNA
<213> Homo sapiens

<220>
<223> IL-12 beta

<400> 133
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gcgaatgggc atctgtgccc tgcagt 986

<210> 134
<211> 276
<212> DNA
<213> Homo sapiens

<220>
<223> MIP-1 alpha/ CCL3

<400> 134
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cagattccac agaatttcat agctgactac tttgagacga gcagccagtg ctccaagccc 180
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gtccagaaat atgtcagcga cctggagctg agtgcc 276

<210> 135
<211> 1530
<212> DNA
<213> Homo sapiens

<220>
<223> CD39/ENTPD1, isoform 1

<400> 135
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aaagcattgc cagaaaacgt taagtatggg attgtgctgg atgcgggttc ttctcacaca 180
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aagccttcat atttctggaa agatatggta 1530

<210> 136
<211> 1722
<212> DNA
<213> Homo sapiens

<220>
<223> CD73/NT5E, isoform 1

<400> 136
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ctggagcaga ccagcgagga ctccagcaag tgcgtcaacg ccagccgctg catgggtggc 180
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tcgggttttg aaatggataa actcatcgct cagaaagtga ggggtgtgga cgtcgtggtg 720
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gcagttgaag gtcggatcaa gttttccaca ggaagtcact gccatggaag cttttcttta 1680
atatttcttt cactttgggc agtgatcttt gttttatacc aa 1722

<210> 137
<211> 297
<212> DNA
<213> Homo sapiens

<220>
<223> IL-8 (CXCL8)

<400> 137
atgacttcca agctggccgt ggctctcttg gcagccttcc tgatttctgc agctctgtgt 60
gaaggtgcag ttttgccaag gagtgctaaa gaacttagat gtcagtgcat aaagacatac 120
tccaaacctt tccaccccaa atttatcaaa gaactgagag tgattgagag tggaccacac 180
tgcgccaaca cagaaattat tgtaaagctt tctgatggaa gagagctctg tctggacccc 240
aaggaaaact gggtgcagag ggttgtggag aagtttttga agagggctga gaattca 297

<210> 138
<211> 1596
<212> DNA
<213> Homo sapiens

<220>
<223> ICAM1

<400> 138
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acccccatga aaccgaacac acaagccacg cctccc 1596

<210> 139
<211> 1488
<212> DNA
<213> Homo sapiens

<220>
<223> angiopoietin 2, isoform 1

<400> 139
atgtggcaga ttgttttctt tactctgagc tgtgatcttg tcttggccgc agcctataac 60
aactttcgga agagcatgga cagcatagga aagaagcaat atcaggtcca gcatgggtcc 120
tgcagctaca ctttcctcct gccagagatg gacaactgcc gctcttcctc cagcccctac 180
gtgtccaatg ctgtgcagag ggacgcgccg ctcgaatacg atgactcggt gcagaggctg 240
caagtgctgg agaacatcat ggaaaacaac actcagtggc taatgaagct tgagaattat 300
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acggctgtga tgatagaaat agggacaaac ctgttgaacc aaacagcgga gcaaacgcgg 420
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ccacagaggc agaacacaaa taagttcaac ggcattaaat ggtactactg gaaaggctca 1440
ggctattcgc tcaaggccac aaccatgatg atccgaccag cagatttc 1488

<210> 140
<211> 2766
<212> DNA

<213> Homo sapiens

<220>
<223> NLRP3, isoform 2

<400> 140
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gacttgaaga aatttaagat gcacttagag gactatcctc cccagaaggg ctgcatcccc 120
ctcccgaggg gtcagacaga gaaggcagac catgtggatc tagccacgct aatgatcgac 180
ttcaatgggg aggagaaggc gtgggccatg gccgtgtgga tcttcgctgc gatcaacagg 240
agagaccttt atgagaaagc aaaaagagat gagccgaagt ggggttcaga taatgcacgt 300
gtttcgaatc ccactgtgat atgccaggaa gacagcattg aagaggagtg gatgggttta 360
ctggagtacc tttcgagaat ctctatttgt aaaatgaaga aagattaccg taagaagtac 420
agaaagtacg tgagaagcag attccagtgc attgaagaca ggaatgcccg tctgggtgag 480
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cagcagagct gcctcctgca gaacctgggg ttgtctgaaa tgtatttcaa ttatgagaca 2700
aaaagtgcgt tagaaacact tcaagaagaa aagcctgagc tgaccgtcgt ctttgagcct 2760
tcttgg 2766

<210> 141
<211> 831
<212> DNA
<213> Homo sapiens

<220>
<223> CD40, isoform 1

<400> 141
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gaaccaccca ctgcatgcag agaaaaacag tacctaataa acagtcagtg ctgttctttg 120
tgccagccag gacagaaact ggtgagtgac tgcacagagt tcactgaaac ggaatgcctt 180
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gtcacccagg aggatggcaa agagagtcgc atctcagtgc aggagagaca g 831

<210> 142
<211> 783
<212> DNA
<213> Homo sapiens

<220>
<223> CD40 ligand (CD40L)

<400> 142
atgatcgaaa catacaacca aacttctccc cgatctgcgg ccactggact gcccatcagc 60
atgaaaattt ttatgtattt acttactgtt tttcttatca cccagatgat tgggtcagca 120
ctttttgctg tgtatcttca tagaaggttg gacaagatag aagatgaaag gaatcttcat 180
gaagattttg tattcatgaa aacgatacag agatgcaaca caggagaaag atccttatcc 240
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aacaaagagg agacgaagaa agaaaacagc tttgaaatgc aaaaaggtga tcagaatcct 360
caaattgcgg cacatgtcat aagtgaggcc agcagtaaaa caacatctgt gttacagtgg 420
gctgaaaaag gatactacac catgagcaac aacttggtaa ccctggaaaa tgggaaacag 480
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cgggaagctt cgagtcaagc tccatttata gccagcctct gcctaaagtc ccccggtaga 600
ttcgagagaa tcttactcag agctgcaaat acccacagtt ccgccaaacc ttgcgggcaa 660
caatccattc acttgggagg agtatttgaa ttgcaaccag gtgcttcggt gtttgtcaat 720
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ctc 783

<210> 143
<211> 579
<212> DNA
<213> Homo sapiens

<220>
<223> CD-70 antigen, isoform 1

<400> 143
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actgatgaga ccttctttgg agtgcagtgg gtgcgcccc 579

<210> 144
<211> 765
<212> DNA
<213> Homo sapiens

<220>
<223> CD137 (4-1BB, TNFRSF9)

<400> 144
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acaagatcat tgcaggatcc ttgtagtaac tgcccagctg gtacattctg tgataataac 120
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acctgtgaca tatgcaggca gtgtaaaggt gttttcagga ccaggaagga gtgttcctcc 240
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tgtagctgcc gatttccaga agaagaagaa ggaggatgtg aactg 765

<210> 145
<211> 807
<212> DNA
<213> Homo sapiens

<220>
<223> CD200, isoform 1

<400> 145
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gagcagctgt acacacctgc ttccttaaaa tgctctctgc aaaatgccca ggaagccctc 180
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aaccatgggg tggtgatcca gcctgcctat aaggacaaga taaacattac ccagctggga 300
ctccaaaact caaccatcac cttctggaat atcaccctgg aggatgaagg gtgttacatg 360
tgtctcttca ataccttttgg ttttgggaag atctcaggaa cggcctgcct caccgtctat 420
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aatagtacag tgactctgtc tcacccaaat gggaccacgt ctgttaccag catcctccat 600
atcaaagacc ctaagaatca ggtggggaag gaggtgatct gccaggtgct gcacctgggg 660
actgtgaccg actttaagca aaccgtcaac aaaggctatt ggttttcagt tccgctattg 720
ctaagcattg tttccctggt aattcttctc gtcctaatct caatcttact gtactggaaa 780
cgtcaccgga atcaggaccg agagccc 807

<210> 146
<211> 1236
<212> DNA
<213> Homo sapiens

<220>
<223> A2aR (ADORA2A)

<400> 146
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accaactact ttgtggtgtc actggcggcg gccgacatcg cagtgggtgt gctcgccatc 180
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ccagacgtgg agctccttag ccatgagctc aagggagtgt gcccagagcc ccctggccta 1200
gatgaccccc tggcccagga tggagcagga gtgtcc 1236

<210> 147
<211> 723
<212> DNA
<213> Homo sapiens

<220>
<223> GITR/TNFRSF18, isoform 1

<400> 147
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gcgctcagcc tgggtcagcg ccccaccggg ggtcccgggt gcggccctgg gcgcctcctg 120
cttgggacgg gaacggacgc gcgctgctgc cgggttcaca cgacgcgctg ctgccgcgat 180
tacccgggcg aggagtgctg ttccgagtgg gactgcatgt gtgtccagcc tgaattccac 240
tgcggagacc cttgctgcac gacctgccgg caccaccctt gtcccccagg ccaggggtga 300
cagtcccagg ggaaattcag ttttggcttc cagtgtatcg actgtgcctc ggggaccttc 360
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gagacccagc tgctgctgga ggtgccgccg tcgaccgaag acgccagaag ctgccagttc 660
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gtg   723

<210> 148
<211> 1362
<212> DNA
<213> Homo sapiens

<220>
<223> B7-H6 (NCR3LG1)

<400> 148
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aatgacaatg tcaccatatt ctgcaatatc ttttattccc aacccctcaa catcacgtct 180
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ttttttggag atcaccaaga ggcattccga cctggagcca ttgtgtctcc atggaggctg 300
aagagtgggg acgcctcact gcggctgcct ggaatccagc tggaggaagc aggagagtac 360
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gcttccccag ccagcagatt gttgctggat caagtgggca tgaaagagaa tgaagacaaa 480
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gttctatcct cccaaccccc aactttactg ttacccctac ag 1362

<210> 149
<211> 597
<212> DNA
<213> Homo sapiens

<220>
<223> ICOS, isoform 1

<400> 149
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ttatgcaaat atcctgacat tgtccagcaa tttaaaatgc agttgctgaa agggggggcaa 180
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cattctcatg ccaactatta cttctgcaac ctatcaattt ttgatcctcc tccttttaaa 360
gtaactctta caggaggata tttgcatatt tatgaatcac aactttgttg ccagctgaag 420
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atttgttggc ttacaaaaaa gaagtattca tccagtgtgc acgaccctaa cggtgaatac 540
atgttcatga gagcagtgaa cacagccaaa aaatctagac tcacagatgt gacccta 597

<210> 150
<211> 906
<212> DNA
<213> Homo sapiens

<220>
<223> ICOS ligand, isoform 1

<400> 150
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caggagaagg aagtcagagc gatggtaggc agcgacgtgg agctcagctg cgcttgccct 120
gaaggaagcc gttttgattt aaatgatgtt tacgtatatt ggcaaaccag tgagtcgaaa 180
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cacgtt 906

<210> 151
<211> 1344
<212> DNA
<213> Homo sapiens

<220>
<223> gp49B/LILRB4, isoform 1

<400> 151
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atgcaggcag ggcccctccc caaacccacc ctctgggctg agccaggctc tgtgatcagc 120
tgggggaact ctgtgaccat ctggtgtcag gggaccctgg aggctcggga gtaccgtctg 180
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cgcagccctg taggctggtc acagcccagt gacccctgg agctggtgat gacaggagcc 360
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gcccatcccc tactgcatct gagatcagag cacggagctc agcagcacca ggctgaattc 540
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<210> 152
<211> 1896
<212> DNA
<213> Homo sapiens

<220>
<223> PIR-B/LILRB3, isoform 1

<400> 152
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tacagctctg caggctggtc agagcccagc gacccctgg agctggtgat gacaggattc 360

tacaacaaac ccaccctctc agccctgccc agccctgtgg tggcctcagg ggggaatatg 420
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gctgagccca gcatctacgc cactctggcc atccac 1896

<210> 153
<211> 1014
<212> DNA
<213> Homo sapiens

<220>
<223> HLA-G alpha chain

<400> 153
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tcttccctgc ccaccatccc catcatgggt atcgttgctg gcctggttgt ccttgcagct 960
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<210> 154
<211> 1092
<212> DNA
<213> Homo sapiens

<220>
<223> TIM1/HAVCR1

<400> 154
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gctgtcacat ccatgtgctg gaatagaggc tcatgttctc tattcacatg ccaaaatggc 180
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tatgccacgg ac 1092

<210> 155
<211> 1134
<212> DNA
<213> Homo sapiens

<220>
<223> TIM4/TIMD4, isoform 1

<400> 155
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<210> 156
<211> 831
<212> DNA
<213> Homo sapiens

<220>
<223> OX-40/CD134/TNFRSF4

<400> 156
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<213> Homo sapiens

<220>
<223> OX-40L/CD252/TNFSF4, isoform 1

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gcctctctga cttacaaaga caaagtctac ttgaatgtga ccactgacaa tacctccctg 480
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tgtgtcctt 549

<210> 158
<211> 1950
<212> DNA
<213> Homo sapiens

<220>
<223> ILT-2/LILRB1, isoform 1

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<210> 159

<211> 1794
<212> DNA
<213> Homo sapiens

<220>
<223> ILT-4/LILRB2, isoform 1

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<211> 717
<212> DNA
<213> Homo sapiens

<220>
<223> BCL-2 isoform alpha

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<210> 161
<211> 4050
<212> DNA
<213> Homo sapiens

<220>
<223> MDR1/ABCB1, isoform 1

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<210> 162
<211> 990
<212> DNA
<213> Homo sapiens

<220>
<223> Arginase1, isoform 1

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<210> 163
<211> 3459
<212> DNA
<213> Homo sapiens

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<223> nitric oxide synthase, inducible (iNOS/NOS2),
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<211> 567
<212> DNA
<213> Homo sapiens

<220>
<223> KRAS

<400> 165
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<211> 1809
<212> DNA
<213> Homo sapiens

<220>
<223> PLK1

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<210> 167
<211> 876
<212> DNA
<213> Salmonella typhimurium

<220>
<223> dapA, strain LT2

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<210> 168
<211> 819
<212> DNA
<213> Salmonella typhimurium

<220>
<223> dapB, strain LT2

<400> 168
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<210> 169
<211> 876
<212> DNA
<213> E. coli

<220>
<223> dapA

<400> 169
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<210> 170
<211> 819
<212> DNA
<213> E. coli

<220>
<223> dapB

<400> 170
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<211> 1218
<212> DNA
<213> E. coli

<220>
<223> dapC

<400> 171
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<211> 822
<212> DNA
<213> E. coli

<220>
<223> dapD

<400> 172
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<212> DNA
<213> E. coli

<220>
<223> dapE

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<212> DNA
<213> Homo sapiens

<220>
<223> MCC

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<210> 183
<211> 2253

<212> DNA
<213> Homo sapiens

<220>
<223> EZH2, isoform 1

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<210> 184
<211> 1053
<212> DNA

<213> Homo sapiens

<220>
<223> NIPP1/PPP1R8, isoform alpha

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<210> 185
<211> 990
<212> DNA
<213> Homo sapiens

<220>
<223> PPP1CA, isoform 1

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<211> 1818
<212> DNA
<213> Homo sapiens

<220>
<223> TAK1/MAP3K7, isoform 1B

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<211> 204
<212> DNA
<213> Unknown

<220>
<223> CMV promoter

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tttccaaaat gtcgtaacaa ctccgcccca ttgacgcaaa tgggcggtag gcgtgtacgg 180
tgggaggtct atataagcag agct 204

<210> 188
<211> 1212
<212> DNA
<213> Homo sapiens

<220>
<223> Caspase-1, isoform alpha

<400> 188
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<211> 885
<212> DNA
<213> Homo sapiens

<220>
<223> cyclin-D1/CCND1

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<210> 190
<211> 996
<212> DNA
<213> Homo sapiens

<220>
<223> A2b receptor (ADORA2B)

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<210> 191
<211> 1242
<212> DNA

<213> Homo sapiens

<220>
<223> HHLA2, isoform 1

<400> 191
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<220>
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<223> Human TGF-beta isoform1 shRNA target 8

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<223> flic-2 primer

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<223> flic-3 primer

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<223> flic-4 primer

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<220>
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<223> ASD gene orf + 85 bp upstream

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<212> DNA
<213> Artificial Sequence

<220>
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<213> Artificial Sequence

<220>
<223> miR-16-2

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<210> 249
<211> 165
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (55)...(75)
<223> n may be any nucleotide

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<222> (97)...(117)
<223> n may be any nucleotide

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<400> 249
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ggtaacgcgg aattcgcaac tattttatca atttttgcg tcgac 165

<210> 250
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<212> DNA
<213> Salmonella typhimurium

<220>
<223> endA

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<210> 251
<211> 235
<212> PRT
<213> Salmonella typhimurium

<220>
<223> endonuclease I (encoded by endA)

<400> 251
Met Tyr Arg Asn Phe Ser Phe Ala Ala Ala Leu Leu Ala Ala Ala Phe
 1   5   10   15
Ser Gly Gln Ala Leu Ala Asp Gly Ile Asn Asn Phe Ser Gln Ala Lys
            20   25   30
Ala Ala Ser Val Lys Val Asn Ala Asp Ala Pro Gly Ser Phe Tyr Cys
        35   40   45
Gly Cys Gln Ile Arg Trp Gln Gly Lys Lys Gly Val Val Asp Leu Glu
    50   55   60
Ser Cys Gly Tyr Lys Val Arg Lys Asn Glu Asn Arg Ala Arg Arg Ile
65   70   75   80
Glu Trp Glu His Val Val Pro Ala Trp Gln Phe Gly His Gln Arg Gln
                85   90   95
Cys Trp Gln Asp Gly Gly Arg Lys Asn Cys Ala Lys Asp Pro Val Tyr
            100   105   110
Arg Lys Met Glu Ser Asp Met His Asn Leu Gln Pro Ala Ile Gly Glu

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        115                 120                 125
Val Asn Gly Asp Arg Gly Asn Phe Met Tyr Ser Gln Trp Asn Gly Gly
    130                 135                 140
Glu Gly Gln Tyr Gly Gln Cys Ala Met Lys Val Asp Phe Lys Ala Lys
145                 150                 155                 160
Ile Ala Glu Pro Pro Ala Arg Ala Arg Gly Ala Ile Ala Arg Ile Tyr
                165                 170                 175
Phe Tyr Met Arg Asp Gln Tyr Gln Leu Lys Leu Ser Arg Gln Gln Thr
            180                 185                 190
Gln Leu Phe Asn Val Trp Asp Lys Gln Tyr Pro Val Thr Ala Trp Glu
        195                 200                 205
Cys Glu Arg Asp Ala Arg Ile Ala Lys Val Gln Gly Asn His Asn Pro
    210                 215                 220
Tyr Val Gln Arg Ala Cys Gln Ala Arg Lys Ser
225                 230                 235
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<210> 252
<211> 78
<212> DNA
<213> Homo sapiens

<220>
<223> microRNA-103a1 (miR-103a1)

<400> 252
tactgccctc ggcttcttta cagtgctgcc ttgttgcata tggatcaagc agcattgtac 60
agggctatga aggcattg 78

<210> 253
<211> 71
<212> DNA
<213> Homo sapiens

<220>
<223> microRNA-30a (miR-30a)

<400> 253
gcgactgtaa acatcctcga ctggaagctg tgaagccaca gatgggcttt cagtcggatg 60
tttgcagctg c 71

<210> 254
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> pMB1 origin of replication

<400> 254
aaaggatctt cttgagatcc ttttttctg cgcgtaatct gctgcttgca aacaaaaaaa 60
ccaccgctac cagcggtggt ttgtttgccg gatcaagagc taccaactct ttttccgaag 120
gtaactggct tcagcagagc gcagatacca aatactgttc ttctagtgta gccgtagtta 180
ggccaccact tcaagaactc tgtagcaccg cctacatacc tcgctctgct aatcctgtta 240
ccagtggctg ctgccagtgg cgataagtcg tgtcttaccg ggttggactc aagacgatag 300
ttaccggata aggcgcagcg gtcgggctga cgggggggtt cgtgcacaca gcccagcttg 360
gagcgaacga cctacaccga actgagatac ctacagcgtg agctatgaga aagcgccacg 420
cttcccgaag ggagaaaggc ggacaggtat ccggtaagcg gcagggtcgg aacaggagag 480
cgcacgaggg agcttccagg gggaaacgcc tggtatcttt atagtcctgt cgggtttcgc 540
cacctctgac ttgagcgtcg atttttgtga tgctcgtcag gggggcggag cctatggaaa 600
aacgccagca acgcg 615

<210> 255
<211> 913
<212> DNA
<213> Artificial Sequence

<220>
<223> p15A origin of replication

<400> 255
gcgctagcgg agtgtatact ggcttactat gttggcactg atgagggtgt cagtgaagtg 60
cttcatgtgg caggagaaaa aaggctgcac cggtgcgtca gcagaatatg tgatacagga 120
tatattccgc ttcctcgctc actgactcgc tacgctcggt cgttcgactg cggcgagcgg 180
aaatggctta cgaacggggc ggagatttcc tggaagatgc caggaagata cttaacaggg 240
aagtgagagg gccgcggcaa agccgttttt ccataggctc cgccccctg acaagcatca 300
cgaaatctga cgctcaaatc agtggtggcg aaacccgaca ggactataaa gataccaggc 360
gtttcccccct ggcggctccc tcgtgcgctc tcctgttcct gcctttcggt ttaccggtgt 420
cattccgctg ttatggccgc gtttgtctca ttccacgcct gacactcagt tccgggtagg 480
cagttcgctc caagctggac tgtatgcacg aacccccgt tcagtccgac cgctgcgcct 540
tatccggtaa ctatcgtctt gagtccaacc cggaaagaca tgcaaaagca ccactggcag 600
cagccactgg taattgattt agaggagtta gtcttgaagt catgcgccgg ttaaggctaa 660
actgaaagga caagttttgg tgactgcgct cctccaagcc agttacctcg gttcaaagag 720
ttggtagctc agagaacctt cgaaaaaccg ccctgcaagg cggtttttc gttttcagag 780
caagagatta cgcgcagacc aaaacgatct caagaagatc atcttattaa tcagataaaa 840
tatttctaga tttcagtgca atttatctct tcaaatgtag cacctgaagt cagccccata 900
cgatataagt tgt 913

<210> 256
<211> 223
<212> DNA
<213> Artificial Sequence

<220>
<223> pSC101 origin of replication

<400> 256
gagttataca cagggctggg atctattctt tttatctttt tttattcttt ctttattcta 60
taaattataa ccacttgaat ataaacaaaa aaaacacaca aaggtctagc ggaatttaca 120
gagggtctag cagaatttac aagttttcca gcaaaggtct agcagaattt acagataccc 180
acaactcaaa ggaaaaggac tagtaattat cattgactag ccc 223

<210> 257
<211> 602
<212> DNA
<213> E. coli

<220>
<223> ColE1 origin of replication

<400> 257
aggatcttct tgagatcctt tttttctgcg cgtaatctgc tgcttgcaaa caaaaaaacc 60
accgctacca acggtggttt gtttgccgga tcaagagcta ccaactcttt ttccgaaggt 120
aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc cgtagtcggg 180
ccactacttc aagaactctg tagcaccgtt tgtgccatca tcgctctgct aatccggtta 240
ccagtggctg ctgccagtgg cgttaaggcg tgccttaccg ggttggactc aagacgatag 300
ttaccggata aggcgcagcg gtcgggctga acgggggggtt cgtgcacaca gcccagcttg 360
gagcgaacga cctacaccga actgagatac caacagcgtg agctatgaga aagcgccacg 420
cttcccgaag ggagaaaggc ggacaggtat ccggtaagcg gcagggtcgg aacaggagag 480
cgcacgaggg agcttccagg gggaaacgcc tggtatcttt atagtcctgt cgggtttcgc 540
cacctctgac ttgagcgtct atttttgtga tgctcgtcag gggggcggag cctatggaaa 600
aa 602

<210> 258
<211> 201
<212> DNA
<213> Pseudomonas syringae

<220>
<223> pPS10 origin of replication

<400> 258
acctgaccgg cgcggaagcg ctcttgatct ttttttcttg tttttacttg ttgttccttg 60
ttttcgtaat tttaactata tgatttataa gaaaaaaaag ggtttaaagg ggacagattc 120
agggtttaaa ggggacagat tcagggttta aaggggacag attcagggtt taaaggggac 180
agattcaggc tgatatccac a 201

<210> 259
<211> 617
<212> DNA
<213> E. coli

<220>

<223> RK2 origin of replication

<400> 259
ccgggctggt tgccctcgcc gctgggctgg cggccgtcta tggccctgca aacgcgccag 60
aaacgccgtc gaagccgtgt gcgagacacc gcggccgccg gcgttgtgga taccacgcgg 120
aaaacttggc cctcactgac agatgagggg cggacgttga cacttgaggg gccgactcac 180
ccggcgcggc gttgacagat gaggggcagg ctcgatttcg gccggcgacg tggagctggc 240
cagcctcgca aatcggcgaa aacgcctgat tttacgcgag tttcccacag atgatgtgga 300
caagcctggg gataagtgcc ctgcggtatt gacacttgag gggcgcgact actgacagat 360
gaggggcgcg atccttgaca cttgaggggc agagtgatga cagatgaggg gcgcacctat 420
tgacatttga ggggctgtcc acaggcagaa aatccagcat ttgcaagggt ttccgcccgt 480
ttttcggcca ccgctaacct gtcttttaac ctgcttttaa accaatattt ataaaccttg 540
tttttaacca gggctgcgcc ctggcgcgtg accgcgcacg ccgaaggggg gtgccccccc 600
ttctcgaacc ctcccgg   617

<210> 260
<211> 639
<212> DNA
<213> E. coli

<220>
<223> R6K alpha origin of replication

<400> 260
tcttacttct ttgcgtagct gttaaataca gcgttgtttt gataaaatca tcattatcat 60
cgataatgct ttcttcaatt tttttatcct tactctttaa taaagcactt gctaataact 120
tcataccttt tgcaactgtc aaatttggtt catcagggta aatgctttta aggcatacta 180
acaaataatc atggtcttca tcttcaactc taaactgaat ttttttcatc ataactccca 240
acaagaaccg actgtaggtc accgggcaaa cgctgaaaaa taacgtcgaa tgacgtcatt 300
ttgcggcgtt tgccctatcc tgcatcgcag tagaaaatgc cacaactgaa attgtgcttc 360
agtatgtaca gaaatgcaaa atctgaggga tttcgtagct gaaagatcgc cagtcttcga 420
ccgtaaggat aggagttgct gtaagacctg tgcggggcgt tcgcttcgcg aacgggtctg 480
gcaggggca caagcgctgt gctgtgatat atgcaaaaga agccacccac gaacgggagg 540
gcttcggcga atcgactata gtgatctatt tacccggctg attgtcgcct tctagccctc 600
gcgggcatca tgcaaccagt gcctgaattt agttatatg   639

<210> 261
<211> 1027
<212> DNA
<213> E. coli

<220>
<223> R6K beta origin of replication

<400> 261
tgaagctttt tttatgaatt tatctgaagc tgatgcagct tttctcaagg tatttgatga 60
aaccgtacct cccaaaaaag ctaaggggtg atatatggct aaaatttacg atttccctca 120
aggagccgaa cgccgcagga tgcaccgcaa aatccagtgg aacaacgctg taaaattatc 180

taaaaatggc tggagtaagc cagaggttaa acgctggtct tttttagcat tcatctcaac 240
tggctggtat tactttcgcc tttcggtagc agtcattttc catatcatta ctatttgtgg 300
tttagctgtg ctcgcggcgt taagcaatac gatattctgg attggtggcg cgatatgtct 360
tgtaacctgg tatacaaatg accatcaaat ttggagtact aacaatctta ctatccctat 420
tgttttcgga ctttgggtgt taagtttagt agctgcacca ctcatagatt ttttcagtca 480
aaaattgccc ttttatcgtc ttcttgtgcc tgatgcgaag cgtgaggaag tgggcgaaga 540
tgattcttaa agccctgccc tgtacggctt taacgccttc tcgcggtaga tctatggatg 600
ttgagaatgt agtatggtta tactgcgatg caggataggg caaacgccgt aaaatgacgt 660
ctttgacgtt atttttcagc gcttgcccgg tgacctacag tcggtgcttg ttgggagatt 720
ttatgaagtt tactagtaaa ggattttatc agtgataaat atgcaaaggc tattaacatt 780
ttaaatgata accttaaaga aaactactat gtttttttatg gtgtaaggtt aagtgaaatt 840
ctttttcctg caagtgatta tggtacagat gatttttta aggagtttga ggaaataaac 900
aacgttacct tgcctttagt tgtttttgaa ataaatgaac gtgaacctgt gattgtaatt 960
ggttttgatg aaataaatcc tgcgattctt atagagaaat ccggtataaa ggttttagta 1020
atcggac 1027

<210> 262
<211> 442
<212> DNA
<213> E. coli

<220>
<223> R6K gamma origin of replication

<400> 262
gatcgctagt ttgttttgac tccatccatt agggcttcta aaacgccttc taaggccatg 60
tcagccgtta agtgttcctg tgtcactgaa aattgctttg agaggctcta agggcttctc 120
agtgcgttac atccctggct tgttgtccac aaccgttaaa ccttaaaagc tttaaaagcc 180
ttatatattc ttttttttct tataaaactt aaaaccttag aggctattta agttgctgat 240
ttatattaat tttattgttc aaacatgaga gcttagtacg tgaaacatga gagcttagta 300
cgttagccat gagagcttag tacgttagcc atgagggttt agttcgttaa acatgagagc 360
ttagtacgtt aaacatgaga gcttagtacg tgaaacatga gagcttagta cgtactatca 420
acaggttgaa ctgctgatct tc 442

<210> 263
<211> 242
<212> DNA
<213> Enterobacteria phage P1

<220>
<223> P1 origin of plasmid replication oriR

<400> 263
tttcccgtca acacacatcc tatatcccgc cagcacacat tagcaacccg tcagcacaca 60
tttttatccc tccagcacac atcgttttcc ctccagcaca catcgcgata cacttctaag 120
ccagacgtgg cgcggcctgc aacgatcagg gatctatatg gatctaattg ggatctgtat 180
ggacctgatt attggatcta tccagtggat aatgtggata agtgaaaaac cggccaacgt 240
ag 242

<210> 264
<211> 792
<212> DNA
<213> Artificial Sequence

<220>
<223> R1 origin of replication

<400> 264
ttatccacat ttaactgcaa gggacttccc cataaggtta caaccgttca tgtcataaag 60
cgccagccgc cagtcttaca gggtgcaatg tatcttttaa acacctgttt atatctcctt 120
taaactactt aattacattc atttaaaaag aaaacctatt cactgcctgt cctgtggaca 180
gacagatatg cacctcccac cgcaagcggc gggccccgac cggagccact ttagttacaa 240
cacacaaaaa caacctccag aaaaaccccg gtccagcgca gaaccgaaac cacaaagccc 300
ctccctcata actgaaaagc ggccccgccc cggcccaaag ggccggaaca gagtcgcttt 360
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gtacacgctc gtaagcggcc ctcacggccc gctaacgcgg agatacgccc cgacttcggg 480
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ccgggcttcg gcggttttac tcctgtatca tatgaaacaa cagagtgccg ccttccatgc 660
cgctgatgcg gcatatcctg gtaacgatat ctgaattgtt atacatgtgt atatacgtgg 720
taatgacaaa aataggacaa gttaaaaatt tacaggcgat gcaatgattc aaacacgtaa 780
tcaatatctg ca   792

<210> 265
<211> 2920
<212> DNA
<213> Artificial Sequence

<220>
<223> pWSK origin of replication

<400> 265
ccgatgccct tgagagcctt caacccagtc agctccttcc ggtgggcgcg gggcatgact 60
atcgtcgccg cacttatgac tgtcttcttt atcatgcaac tcgtaggaca gggtgccggc 120
agcgctctgg gtcattttcg gcgaggaccg ctttcgctgg agcgcgacga tgatcggcct 180
gtcgcttgcg gtattcggaa tcttgcacgc cctcgctcaa gccttcgtca ctggtcccgc 240
caccaaacgt ttcggcgaga agcaggccat tatcgccggc atggcggccg acgcgctggg 300
ctacgtcttg ctggcgttcg cgacgcgagg ctggatggcc ttccccatta tgattcttct 360
cgcttccggc ggcatcggga tgcccgcgtt gcaggccatg ctgtccaggc aggtagatga 420
cgaccatcag ggacagcttc aaggatcgct cgcggctctt accagcctaa cttcgatcat 480
tggaccgctg atcgtcacgg cgatttatgc cgcctcggcg agcacatgga acgggttggc 540
atggattgta ggcgccgccc tataccttgt ctgcctcccc gcgttgcgtc gcggtgcatg 600
gagccgggcc acctcgacct gaatggaagc cggcggcacc tcgctaacgg attcaccact 660
ccgcagaccc gccataaaac gccctgagaa gcccgtgacg ggcttttctt gtattatggg 720
tagtttcctt gcatgaatcc ataaaaggcg cctgtagtgc catttacccc cattcactgc 780
cagagccgtg agcgcagcga actgaatgtc acgaaaaaga cagcgactca ggtgcctgat 840

ggtcggagac aaaaggaata ttcagcgatt tgcccgagct tgcgagggtg ctacttaagc 900
ctttagggtt ttaaggtctg ttttgtagag gagcaaacag cgtttgcgac atccttttgt 960
aatactgcgg aactgactaa agtagtgagt tatacacagg gctgggatct attcttttta 1020
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cacacaaagg tctagcggaa tttacagagg gtctagcaga atttacaagt tttccagcaa 1140
aggtctagca gaatttacag atacccacaa ctcaaaggaa aaggactagt aattatcatt 1200
gactagccca tctcaattgg tatagtgatt aaaatcacct agaccaattg agatgtatgt 1260
ctgaattagt tgttttcaaa gcaaatgaac tagcgattag tcgctatgac ttaacggagc 1320
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caaggaaaga acggacggta tcgttcactt ataaccaata cgctcagatg atgaacatca 1440
gtagggaaaa tgcttatggt gtattagcta aagcaaccag agagctgatg acgagaactg 1500
tggaaatcag gaatcctttg gttaaaggct ttgagatttt ccagtggaca aactatgcca 1560
agttctcaag cgaaaaatta gaattagttt ttagtgaaga gatattgcct tatcttttcc 1620
agttaaaaaa attcataaaa tataatctgg aacatgttaa gtcttttgaa aacaaatact 1680
ctatgaggat ttatgagtgg ttattaaaag aactaacaca aaagaaaact cacaaggcaa 1740
atatagagat tagccttgat gaatttaagt tcatgttaat gcttgaaaat aactaccatg 1800
agtttaaaag gcttaaccaa tgggttttga aaccaataag taaagattta aacacttaca 1860
gcaatatgaa attggtggtt gataagcgag gccgcccgac tgatacgttg attttccaag 1920
ttgaactaga tagacaaatg gatctcgtaa ccgaacttga gaacaaccag ataaaaatga 1980
atggtgacaa aataccaaca accattacat cagattccta cctacataac ggactaagaa 2040
aaacactaca cgatgcttta actgcaaaaa ttcagctcac cagttttgag gcaaaatttt 2100
tgagtgacat gcaaagtaag tatgatctca atggttcgtt ctcatggctc acgcaaaaac 2160
aacgaaccac actagagaac atactggcta aatacggaag gatctgaggt tcttatggct 2220
cttgtatcta tcagtgaagc atcaagacta acaaacaaaa gtagaacaac tgttcaccgt 2280
tacatatcaa agggaaaact gtccatatgc acagatgaaa acggtgtaaa aaagatagat 2340
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aatgtaacag atgaacagca tgtaacacct aatagaacag gtgaaaccag taaaacaaag 2460
caactagaac atgaaattga acacctgaga caacttgtta cagctcaaca gtcacacata 2520
gacagcctga aacaggcgat gctgcttatc gaatcaaagc tgccgacaac acgggagcca 2580
gtgacgcctc ccgtggggaa aaaatcatgg caattctgga agaaatagcg ctttcagccg 2640
gcaaaccggc tgaagccgga tctgcgattc tgataacaaa ctagcaacac cagaacagcc 2700
cgtttgcggg cagcaaaacc cgtacttttg gacgttccgg cggttttttg tggcgagtgg 2760
tgttcgggcg gtgcgcgcaa gatccattat gttaaacggg cgagtttaca tctcaaaacc 2820
gcccgcttaa caccatcaga aatcctcagc gcgattttaa gcaccaaccc ccccccgtaa 2880
cacccaaatc catactgaaa gtggctttgt tgaataaatc 2920

<210> 266
<211> 37
<212> DNA
<213> E. coli

<220>
<223> ColE2 origin of replication

<400> 266
aaaatgagac cagataagcc ttatcagata acagcgc 37

<210> 267

<211> 668
<212> DNA
<213> Artificial Sequence

<220>
<223> pUC origin of replication

<400> 267
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cataggctcc gccccctga cgagcatcac aaaaatcgac gctcaagtca gaggtggcga 120
aacccgacag gactataaag ataccaggcg tttccccctg gaagctccct cgtgcgctct 180
cctgttccga ccctgccgct taccggatac ctgtccgcct ttctcccttc gggaagcgtg 240
gcgctttctc atagctcacg ctgtaggtat ctcagttcgg tgtaggtcgt tcgctccaag 300
ctgggctgtg tgcacgaacc ccccgttcag cccgaccgct gcgccttatc cggtaactat 360
cgtcttgagt ccaacccggt aagacacgac ttatcgccac tggcagcagc cactggtaac 420
aggattagca gagcgaggta tgtaggcggt gctacagagt tcttgaagtg gtggcctaac 480
tacggctaca ctagaagaac agtatttggt atctgcgctc tgctgaagcc agttaccttc 540
ggaaaaagag ttggtagctc ttgatccggc aaacaaacca ccgctggtag cggtggtttt 600
tttgtttgca agcagcagat tacgcgcaga aaaaaaggat ctcaagaaga tcctttgatc 660
ttttctac 668

<210> 268
<211> 457
<212> DNA
<213> Bacteriophage F1

<220>
<223> F1 origin of replication

<400> 268
gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg cagcgtgacc 60
gctacacttg ccagcgccct agcgcccgct cctttcgctt tcttcccttc ctttctcgcc 120
acgttcgccg gctttccccg tcaagctcta aatcgggggc tccctttagg gttccgattt 180
agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc acgtagtggg 240
ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt ctttaatagt 300
ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc ttttgattta 360
taagggattt tgccgatttc ggcctattgg ttaaaaaatg agctgattta acaaaaattt 420
aacgcgaatt ttaacaaaat attaacgctt acaattt 457

<210> 269
<211> 534
<212> DNA
<213> Homo sapiens

<220>
<223> IL-7

<400> 269
atgttccatg tttcttttag gtatatcttt ggacttcctc ccctgatcct tgttctgttg 60

ccagtagcat catctgattg tgatattgaa ggtaaagatg gcaaacaata tgagagtgtt 120
ctaatggtca gcatcgatca attattggac agcatgaaag aaattggtag caattgcctg 180
aataatgaat ttaacttttt taaaagacat atctgtgatg ctaataagga aggtatgttt 240
ttattccgtg ctgctcgcaa gttgaggcaa tttcttaaaa tgaatagcac tggtgatttt 300
gatctccact tattaaaagt ttcagaaggc acaacaatac tgttgaactg cactggccag 360
gttaaaggaa gaaaaccagc tgccctgggt gaagcccaac caacaaagag tttggaagaa 420
aataaatctt taaaggaaca gaaaaaactg aatgacttgt gtttcctaaa gagactatta 480
caagagataa aaacttgttg gaataaaatt ttgatgggca ctaaagaaca ctga 534

<210> 270
<211> 987
<212> DNA
<213> Homo sapiens

<220>
<223> IL12B

<400> 270
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gtggccatat gggaactgaa gaaagatgtt tatgtcgtag aattggattg gtatccggat 120
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<213> Homo sapiens

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<212> DNA
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<212> DNA
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<212> DNA
<213> Homo sapiens

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<212> DNA
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<220>
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<400> 296
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<212> DNA
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<220>
<223> TNFRSF17

<400> 297
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tgtaatgcaa gtgtgaccaa ttcagtgaaa ggaacgaatg cgattctctg gacctgtttg 180
ggactgagct taataatttc tttggcagtt ttcgtgctaa tgtttttgct aaggaagata 240
aactctgaac cattaaagga cgagtttaaa aacacaggat caggtctcct gggcatggct 300
aacattgacc tggaaaagag caggactggt gatgaaatta ttcttccgag aggcctcgag 360
tacacggtgg aagaatgcac ctgtgaagac tgcatcaaga gcaaaccgaa ggtcgactct 420
gaccattgct ttccactccc agctatggag gaaggcgcaa ccattcttgt caccacgaaa 480
acgaatgact attgcaagag cctgccagct gctttgagtg ctacggagat agagaaatca 540
atttctgcta ggtaa 555

<210> 298
<211> 1254
<212> DNA
<213> Homo sapiens

<220>
<223> TNFRSF19

<400> 298
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gatcggtctg gaaactgtgt tccctgcaac cagtgtgggc caggcatgga gttgtctaag 180
gaatgtggct tcggctatgg ggaggatgca cagtgtgtga cgtgccggct gcacaggttc 240

aaggaggact ggggcttcca gaaatgcaag ccctgtctgg actgcgcagt ggtgaaccgc 300
tttcagaagg caaattgttc agccaccagt gatgccatct gcggggactg cttgccagga 360
ttttatagga agacgaaact tgtcggcttt caagacatgg agtgtgtgcc ttgtggagac 420
cctcctcctc cttacgaacc gcactgtgcc agcaaggtca acctcgtgaa gatcgcgtcc 480
acggcctcca gcccacggga cacggcgctg gctgccgtta tctgcagcgc tctggccacc 540
gtcctgctgg ccctgctcat cctctgtgtc atctattgta agagacagtt tatggagaag 600
aaacccagct ggtctctgcg gtcacaggac attcagtaca acggctctga gctgtcgtgt 660
tttgacagac ctcagctcca cgaatatgcc cacagagcct gctgccagtg ccgccgtgac 720
tcagtgcaga cctgcgggcc ggtgcgcttg ctcccatcca tgtgctgtga ggaggcctgc 780
agccccaacc cggcgactct tggttgtggg gtgcattctg cagccagtct tcaggcaaga 840
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tgtggcgagt tttcagatgc ctggcctctg atgcagaatc ccatgggtgg tgacaacatc 960
tctttttgtg actcttatcc tgaactcact ggagaagaca ttcattctct caatccagaa 1020
cttgaaagct caacgtcttt ggattcaaat agcagtcaag atttggttgg tggggctgtt 1080
ccagtccagt ctcattctga aaactttaca gcagctactg atttatctag atataacaac 1140
acactggtag aatcagcatc aactcaggat gcactaacta tgagaagcca gctagatcag 1200
gagagtggtg ctgtcatcca cccagccact cagacgtccc tccaggaagc ttaa 1254

<210> 299
<211> 1293
<212> DNA
<213> Homo sapiens

<220>
<223> RELT

<400> 299
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ctcgccaccc tgacatcaac aacccttttgg cagtgcccac ctggggagga gcccgacctg 120
gacccagggc agggcacatt atgcaggccc tgccccccag gcaccttctc agctgcatgg 180
ggctccagcc catgccagcc ccatgcccgt tgcagccttt ggaggaggct ggaggcccag 240
gtgggcatgg caactcgaga tacactctgt ggagactgct ggcctgggtg gtttgggcct 300
tgggggggttc cccgcgttcc atgtcaacca tgttcctggg cacctctggg tactcatggc 360
tgtgatgagt gggggcggcg ggcccgacgt ggcgtggagg tggcagcagg ggccagcagc 420
ggtggtgaga cacggcagcc tgggaacggc acccgggcag gtggcccaga ggagacagcc 480
gcccagtacg cggtcatcgc catcgtccct gtcttctgcc tcatggggct gttgggcatc 540
ctggtgtgca acctcctcaa gcggaagggc taccactgca cggcgcacaa ggaggtcggg 600
cccggccctg gaggtggagg cagtggaatc aaccctgcct accggactga ggatgccaat 660
gaggacacca ttggggtcct ggtgcgcttg atcacagaga agaaagagaa tgctgcggcc 720
ctggaggagc tgctgaaaga gtaccacagc aaacagctgg tgcagacgag ccacaggcct 780
gtgtccaagc tgccgccagc gcccccgaac gtgccacaca tctgcccgca ccgccaccat 840
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aagaagtggc ccgaggtgct gctgtcccct gaggctgtag ccgccactac tcctgttccc 960
agccttctgc ctaacccgac cagggttccc aaggccgggg ccaaggcagg gcgtcagggc 1020
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cctgactccc cacagcctgg cctcccccct gagcagcagg ccctgctagg aagtggcgga 1200
agccgtacaa agtggctgaa gcccccagca gagaacaagg ccgaggagaa ccgctatgtg 1260
gtccggctaa gtgagagcaa cctggtcatc tga 1293

<210> 300
<211> 1968
<212> DNA
<213> Homo sapiens

<220>
<223> TNFRSF21

<400> 300
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gctcagccag aacagaaggc ctcgaatctc attggcacat accgccatgt tgaccgtgcc 180
accggccagg tgctaacctg tgacaagtgt ccagcaggaa cctatgtctc tgagcattgt 240
accaacacaa gcctgcgcgt ctgcagcagt tgccctgtgg ggacctttac caggcatgag 300
aatggcatag agaaatgcca tgactgtagt cagccatgcc catggccaat gattgagaaa 360
ttaccttgtg ctgccttgac tgaccgagaa tgcacttgcc cacctggcat gttccagtct 420
aacgctacct gtgcccccca tacggtgtgt cctgtgggtt ggggtgtgcg gaagaaaggg 480
acagagactg aggatgtgcg gtgtaagcag tgtgctcggg gtaccttctc agatgtgcct 540
tctagtgtga tgaaatgcaa agcatacaca gactgtctga gtcagaacct ggtggtgatc 600
aagccgggga ccaaggagac agacaacgtc tgtggcacac tcccgtcctt ctccagctcc 660
acctcacctt cccctggcac agccatcttt ccacgccctg agcacatgga aacccatgaa 720
gtcccttcct ccacttatgt tcccaaaggc atgaactcaa cagaatccaa ctcttctgcc 780
tctgttagac caaaggtact gagtagcatc caggaaggga cagtccctga caacacaagc 840
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cagcaaggcc cccaccacag acacatcctg aagctgctgc cgtccatgga ggccactggg 960
ggcgagaagt ccagcacgcc catcaagggc cccaagaggg gacatcctag acagaaccta 1020
cacaagcatt ttgacatcaa tgagcatttg ccctggatga ttgtgctttt cctgctgctg 1080
gtgcttgtgg tgattgtggt gtgcagtatc cggaaaagct cgaggactct gaaaaagggg 1140
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acccagaacc gggagaaatg gatctactac tgcaatggcc atggtatcga tatcctgaag 1260
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gcagctctgc agcactggac catccggggc cccgaggcca gcctcgccca gctaattagc 1440
gccctgcgcc agcaccggag aaacgatgtt gtggagaaga ttcgtgggct gatggaagac 1500
accacccagc tggaaactga caaactagct ctcccgatga gccccagccc gcttagcccg 1560
agccccatcc ccagccccaa cgcgaaactt gagaattccg ctctcctgac ggtggagcct 1620
tccccacagg acaagaacaa gggcttcttc gtggatgagt cggagcccct tctccgctgt 1680
gactctacat ccagcggctc ctccgcgctg agcaggaacg gttcctttat taccaaagaa 1740
aagaaggaca cagtgttgcg gcaggtacgc ctggacccct gtgacttgca gcctatcttt 1800
gatgacatgc tccactttct aaatcctgag gagctgcggg tgattgaaga gattccccag 1860
gctgaggaca aactagaccg gctattcgaa attattggag tcaagagcca ggaagccagc 1920
cagaccctcc tggactctgt ttatagccat cttcctgacc tgctgtag 1968

<210> 301
<211> 1254
<212> DNA
<213> Homo sapiens

<220>
<223> TNFRSF25

<400> 301
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aagaagattg gtctgttttg ttgcagaggc tgcccagcgg ggcactacct gaaggcccct 180
tgcacggagc cctgcggcaa ctccacctgc cttgtgtgtc cccaagacac cttcttggcc 240
tgggagaacc accataattc tgaatgtgcc cgctgccagg cctgtgatga gcaggcctcc 300
caggtggcgc tggagaactg ttcagcagtg gccgacaccc gctgtggctg taagccaggc 360
tggtttgtgg agtgccaggt cagccaatgt gtcagcagtt cacccttcta ctgccaacca 420
tgcctagact gcggggccct gcaccgccac acacggctac tctgttcccg cagagatact 480
gactgtggga cctgcctgcc tggcttctat gaacatggcg atggctgcgt gtcctgcccc 540
acgagcaccc tggggagctg tccagagcgc tgtgccgctg tctgtggctg gaggcagatg 600
ttctgggtcc aggtgctcct ggctggcctt gtggtccccc tcctgcttgg ggccaccctg 660
acctacacat accgccactg ctggcctcac aagcccctgg ttactgcaga tgaagctggg 720
atggaggctc tgaccccacc accggccacc catctgtcac ccttggacag cgcccacacc 780
cttctagcac ctcctgacag cagtgagaag atctgcaccg tccagttggt gggtaacagc 840
tggacccctg gctaccccga gacccaggag gcgctctgcc cgcaggtgac atggtcctgg 900
gaccagttgc ccagcagagc tcttggcccc gctgctgcgc ccacactctc gccagagtcc 960
ccagccggct cgccagccat gatgctgcag ccgggcccgc agctctacga cgtgatggac 1020
gcggtcccag cgcggcgctg gaaggagttc gtgcgcacgc tggggctgcg cgaggcagag 1080
atcgaagccg tggaggtgga gatcggccgc ttccgagacc agcagtacga gatgctcaag 1140
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gggctggacg gctgcgtgga agacttgcgc agccgcctgc agcgcggccc gtga 1254

<210> 302
<211> 1347
<212> DNA
<213> Homo sapiens

<220>
<223> EDAR

<400> 302
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acggggctgt gccaggagtg ccccccgtgt gggccgggag aggagcccta cctgtcctgt 180
ggctacggca ccaaagacga ggactacggc tgcgtcccct gcccggcgga gaagttttcc 240
aaaggaggct accagatatg caggcgtcac aaagactgtg agggcttctt ccgggccacc 300
gtgctgacac caggggacat ggagaatgac gctgagtgtg gcccttgcct ccctggctac 360
tacatgctgg agaacagacc gaggaacatc tatggcatgg tctgctactc ctgcctcctg 420
gcaccccccа acaccaagga atgtgtggga gccacttcag gagcttctgc caacttccct 480
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gccatcgtcc tcatcatcat gttctacatc ctgaagacaa agccctctgc cccagcctgt 660
tgcaccagcc acccggggaa gagcgtggag gcccaagtga gcaaggacga ggagaagaaa 720
gaggccccag acaacgtggt gatgttctcc gagaaggatg aatttgagaa gctgacagca 780
actccagcaa agcccaccaa gagcgagaac gatgcctcat ccgagaatga gcagctgctg 840
agccggagcg tcgacagtga tgaggagccc gcccctgaca agcagggctc cccggagctg 900
tgcctgctgt cgctggttca cctggccagg gagaagtctg ccaccagcaa caagtcagcc 960
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gaaggtctta gccccacgga gctgccattt gattgcctcg agaagactag ccgaatgctc 1080
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<210> 303
<211> 894
<212> DNA
<213> Homo sapiens

<220>
<223> EDA2R

<400> 303
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tgcacagcct gccctcctcg caggtacaaa agcagctggg gccaccacag atgtcagagt 180
tgcatcacct gtgctgtcat caatcgtgtt cagaaggtca actgcacagc tacctctaat 240
gctgtctgtg gggactgttt gcccaggttc taccgaaaga cacgcattgg aggcctgcag 300
gaccaagagt gcatcccgtg cacgaagcag acccccacct ctgaggttca atgtgccttc 360
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gcactggtga gcagcctgct agtggtgttt accctggcct tcctggggct cttcttcctc 480
tactgcaagc agttcttcaa cagacattgc cagcgtggag gtttgctgca gtttgaggct 540
gataaaacag caaaggagga atctctcttc cccgtgccac ccagcaagga gaccagtgct 600
gagtcccaag tgagtgagaa catctttcag acccagccac ttaaccctat cctcgaggac 660
gactgcagct cgactagtgg cttccccaca caggagtcct ttaccatggc ctcctgcacc 720
tcagagagcc actcccactg ggtccacagc cccatcgaat gcacagagct ggacctgcaa 780
aagttttcca gctctgcctc ctatactgga gctgagacct tgggggggaaa cacagtcgaa 840
agcactggag acaggctgga gctcaatgtg ccctttgaag ttcccagccc ttaa 894

<210> 304
<211> 1137
<212> DNA
<213> Artificial Sequence

<220>
<223> STING (R232 Allele)

<220>
<221> allele
<222> (694)...(696)
<223> nnn = CGT, CGC, CGA, CGG, AGA or AGG

<400> 304
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gcagccttgg ttctgctgag tgcctgcctg gtgacccttt gggggctagg agagccacca 120
gagcacactc tccggtacct ggtgctccac ctagcctccc tgcagctggg actgctgtta 180

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aacggggtct gcagcctggc tgaggagctg cgccacatcc actccaggta ccggggcagc 240
tactggagga ctgtgcgggc ctgcctgggc tgccccctcc gccgtggggc cctgttgctg 300
ctgtccatct atttctacta ctccctccca aatgcggtcg gcccgccctt cacttggatg 360
cttgccctcc tgggcctctc gcaggcactg aacatcctcc tgggcctcaa gggcctggcc 420
ccagctgaga tctctgcagt gtgtgaaaaa gggaatttca acgtggccca tgggctggca 480
tggtcatatt acatcggata tctgcggctg atcctgccag agctccaggc ccggattcga 540
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ctcctcccat tggactgtgg ggtgcctgat aacctgagta tggctgaccc caacattcgc 660
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gttactgtgg gcagcttgaa gacctcagcg gtgcccagta cctccacgat gtcccaagag 1080
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<210> 305
<211> 379
<212> PRT
<213> Homo sapiens

<220>
<223> Human STING (R232 Allele)

<400> 305
Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 1               5                  10                  15
Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
            20                  25                  30
Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
        35                  40                  45
Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
    50                  55                  60
Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65                  70                  75                  80
Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
                85                  90                  95
Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
            100                 105                 110
Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
        115                 120                 125
Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
    130                 135                 140
Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala
145                 150                 155                 160
Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
                165                 170                 175
Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
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            180                 185                 190
Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
        195                 200                 205
Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
    210                 215                 220
Leu Pro Gln Gln Thr Gly Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr
225                 230                 235                 240
Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
                245                 250                 255
Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
            260                 265                 270
Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
        275                 280                 285
Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
    290                 295                 300
Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305                 310                 315                 320
Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
                325                 330                 335
Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
            340                 345                 350
Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
        355                 360                 365
Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
    370                 375


<210> 306
<211> 379
<212> PRT
<213> Homo sapiens

<220>
<223> Human STING (H232 Allele)

<400> 306
Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 1               5                  10                  15
Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
            20                  25                  30
Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
        35                  40                  45
Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
    50                  55                  60
Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65                  70                  75                  80
Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
                85                  90                  95
Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
            100                 105                 110
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Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
        115                 120                 125
Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
    130                 135                 140
Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala
145                 150                 155                 160
Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
                165                 170                 175
Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
            180                 185                 190
Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
        195                 200                 205
Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
    210                 215                 220
Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
225                 230                 235                 240
Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
                245                 250                 255
Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
            260                 265                 270
Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
        275                 280                 285
Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
    290                 295                 300
Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305                 310                 315                 320
Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
                325                 330                 335
Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
            340                 345                 350
Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
        355                 360                 365
Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
    370                 375


<210> 307
<211> 379
<212> PRT
<213> Homo sapiens

<220>
<223> Human STING (Q293 Allele)

<400> 307
Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 1               5                  10                  15
Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
            20                  25                  30
Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
```

```
        35                  40                  45
Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
    50                  55                  60
Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65                  70                  75                  80
Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
                85                  90                  95
Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
            100                 105                 110
Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
        115                 120                 125
Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
    130                 135                 140
Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala
145                 150                 155                 160
Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
                165                 170                 175
Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
            180                 185                 190
Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
        195                 200                 205
Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
    210                 215                 220
Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg Val Tyr
225                 230                 235                 240
Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
                245                 250                 255
Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
            260                 265                 270
Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
        275                 280                 285
Lys Leu Phe Cys Gln Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
    290                 295                 300
Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305                 310                 315                 320
Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
                325                 330                 335
Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
            340                 345                 350
Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
        355                 360                 365
Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
    370                 375


<210> 308
<211> 379
<212> PRT
<213> Homo sapiens
```

<220>
<223> Human STING (HAQ allele; R71H/G230A/R293Q)

<400> 308
Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 1   5   10   15
Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
            20   25   30
Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
        35   40   45
Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
    50   55   60
Ser Leu Ala Glu Glu Leu His His Ile His Ser Arg Tyr Arg Gly Ser
65   70   75   80
Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
                85   90   95
Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
            100   105   110
Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
        115   120   125
Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
    130   135   140
Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala
145   150   155   160
Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
                165   170   175
Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
            180   185   190
Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
        195   200   205
Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
    210   215   220
Leu Pro Gln Gln Thr Ala Asp His Ala Gly Ile Lys Asp Arg Val Tyr
225   230   235   240
Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
                245   250   255
Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
            260   265   270
Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
        275   280   285
Lys Leu Phe Cys Gln Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
    290   295   300
Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305   310   315   320
Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
                325   330   335
Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
            340   345   350
Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
        355   360   365

```
Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
    370                 375


<210> 309
<211> 379
<212> PRT
<213> Homo sapiens

<220>
<223> Human STING (AQ allele; G230A/R293Q)

<400> 309
Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 1               5                  10                  15
Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
            20                  25                  30
Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
        35                  40                  45
Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
    50                  55                  60
Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65                  70                  75                  80
Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
                85                  90                  95
Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
            100                 105                 110
Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
        115                 120                 125
Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
    130                 135                 140
Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala
145                 150                 155                 160
Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
                165                 170                 175
Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
            180                 185                 190
Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
        195                 200                 205
Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
    210                 215                 220
Leu Pro Gln Gln Thr Ala Asp His Ala Gly Ile Lys Asp Arg Val Tyr
225                 230                 235                 240
Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
                245                 250                 255
Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
            260                 265                 270
Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
        275                 280                 285
Lys Leu Phe Cys Gln Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
```

```
    290                 295                 300
Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305                 310                 315                 320
Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
                325                 330                 335
Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
            340                 345                 350
Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
        355                 360                 365
Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
    370                 375


<210> 310
<211> 1025
<212> PRT
<213> Homo sapiens

<220>
<223> MDA5/IFIH1

<400> 310
Met Ser Asn Gly Tyr Ser Thr Asp Glu Asn Phe Arg Tyr Leu Ile Ser
 1               5                  10                  15
Cys Phe Arg Ala Arg Val Lys Met Tyr Ile Gln Val Glu Pro Val Leu
            20                  25                  30
Asp Tyr Leu Thr Phe Leu Pro Ala Glu Val Lys Glu Gln Ile Gln Arg
        35                  40                  45
Thr Val Ala Thr Ser Gly Asn Met Gln Ala Val Glu Leu Leu Leu Ser
    50                  55                  60
Thr Leu Glu Lys Gly Val Trp His Leu Gly Trp Thr Arg Glu Phe Val
65                  70                  75                  80
Glu Ala Leu Arg Arg Thr Gly Ser Pro Leu Ala Ala Arg Tyr Met Asn
                85                  90                  95
Pro Glu Leu Thr Asp Leu Pro Ser Pro Ser Phe Glu Asn Ala His Asp
            100                 105                 110
Glu Tyr Leu Gln Leu Leu Asn Leu Leu Gln Pro Thr Leu Val Asp Lys
        115                 120                 125
Leu Leu Val Arg Asp Val Leu Asp Lys Cys Met Glu Glu Glu Leu Leu
    130                 135                 140
Thr Ile Glu Asp Arg Asn Arg Ile Ala Ala Ala Glu Asn Asn Gly Asn
145                 150                 155                 160
Glu Ser Gly Val Arg Glu Leu Leu Lys Arg Ile Val Gln Lys Glu Asn
                165                 170                 175
Trp Phe Ser Ala Phe Leu Asn Val Leu Arg Gln Thr Gly Asn Asn Glu
            180                 185                 190
Leu Val Gln Glu Leu Thr Gly Ser Asp Cys Ser Glu Ser Asn Ala Glu
        195                 200                 205
Ile Glu Asn Leu Ser Gln Val Asp Gly Pro Gln Val Glu Glu Gln Leu
    210                 215                 220
```

```
Leu Ser Thr Thr Val Gln Pro Asn Leu Glu Lys Glu Val Trp Gly Met
225                 230                 235                 240
Glu Asn Asn Ser Ser Glu Ser Ser Phe Ala Asp Ser Ser Val Val Ser
                245                 250                 255
Glu Ser Asp Thr Ser Leu Ala Glu Gly Ser Val Ser Cys Leu Asp Glu
            260                 265                 270
Ser Leu Gly His Asn Ser Asn Met Gly Ser Asp Ser Gly Thr Met Gly
        275                 280                 285
Ser Asp Ser Asp Glu Glu Asn Val Ala Ala Arg Ala Ser Pro Glu Pro
    290                 295                 300
Glu Leu Gln Leu Arg Pro Tyr Gln Met Glu Val Ala Gln Pro Ala Leu
305                 310                 315                 320
Glu Gly Lys Asn Ile Ile Ile Cys Leu Pro Thr Gly Ser Gly Lys Thr
                325                 330                 335
Arg Val Ala Val Tyr Ile Ala Lys Asp His Leu Asp Lys Lys Lys Lys
            340                 345                 350
Ala Ser Glu Pro Gly Lys Val Ile Val Leu Val Asn Lys Val Leu Leu
        355                 360                 365
Val Glu Gln Leu Phe Arg Lys Glu Phe Gln Pro Phe Leu Lys Lys Trp
    370                 375                 380
Tyr Arg Val Ile Gly Leu Ser Gly Asp Thr Gln Leu Lys Ile Ser Phe
385                 390                 395                 400
Pro Glu Val Val Lys Ser Cys Asp Ile Ile Ile Ser Thr Ala Gln Ile
                405                 410                 415
Leu Glu Asn Ser Leu Leu Asn Leu Glu Asn Gly Glu Asp Ala Gly Val
            420                 425                 430
Gln Leu Ser Asp Phe Ser Leu Ile Ile Ile Asp Glu Cys His His Thr
        435                 440                 445
Asn Lys Glu Ala Val Tyr Asn Asn Ile Met Arg His Tyr Leu Met Gln
    450                 455                 460
Lys Leu Lys Asn Asn Arg Leu Lys Lys Glu Asn Lys Pro Val Ile Pro
465                 470                 475                 480
Leu Pro Gln Ile Leu Gly Leu Thr Ala Ser Pro Gly Val Gly Gly Ala
                485                 490                 495
Thr Lys Gln Ala Lys Ala Glu Glu His Ile Leu Lys Leu Cys Ala Asn
            500                 505                 510
Leu Asp Ala Phe Thr Ile Lys Thr Val Lys Glu Asn Leu Asp Gln Leu
        515                 520                 525
Lys Asn Gln Ile Gln Glu Pro Cys Lys Lys Phe Ala Ile Ala Asp Ala
    530                 535                 540
Thr Arg Glu Asp Pro Phe Lys Glu Lys Leu Leu Glu Ile Met Thr Arg
545                 550                 555                 560
Ile Gln Thr Tyr Cys Gln Met Ser Pro Met Ser Asp Phe Gly Thr Gln
                565                 570                 575
Pro Tyr Glu Gln Trp Ala Ile Gln Met Glu Lys Lys Ala Ala Lys Lys
            580                 585                 590
Gly Asn Arg Lys Glu Arg Val Cys Ala Glu His Leu Arg Lys Tyr Asn
        595                 600                 605
Glu Ala Leu Gln Ile Asn Asp Thr Ile Arg Met Ile Asp Ala Tyr Thr
    610                 615                 620
```

```
His Leu Glu Thr Phe Tyr Asn Glu Glu Lys Asp Lys Lys Phe Ala Val
625                 630                 635                 640
Ile Glu Asp Asp Ser Asp Glu Gly Gly Asp Asp Glu Tyr Cys Asp Gly
                645                 650                 655
Asp Glu Asp Glu Asp Asp Leu Lys Lys Pro Leu Lys Leu Asp Glu Thr
            660                 665                 670
Asp Arg Phe Leu Met Thr Leu Phe Phe Glu Asn Asn Lys Met Leu Lys
        675                 680                 685
Arg Leu Ala Glu Asn Pro Glu Tyr Glu Asn Glu Lys Leu Thr Lys Leu
    690                 695                 700
Arg Asn Thr Ile Met Glu Gln Tyr Thr Arg Thr Glu Glu Ser Ala Arg
705                 710                 715                 720
Gly Ile Ile Phe Thr Lys Thr Arg Gln Ser Ala Tyr Ala Leu Ser Gln
                725                 730                 735
Trp Ile Thr Glu Asn Glu Lys Phe Ala Glu Val Gly Val Lys Ala His
            740                 745                 750
His Leu Ile Gly Ala Gly His Ser Ser Glu Phe Lys Pro Met Thr Gln
        755                 760                 765
Asn Glu Gln Lys Glu Val Ile Ser Lys Phe Arg Thr Gly Lys Ile Asn
    770                 775                 780
Leu Leu Ile Ala Thr Thr Val Ala Glu Glu Gly Leu Asp Ile Lys Glu
785                 790                 795                 800
Cys Asn Ile Val Ile Arg Tyr Gly Leu Val Thr Asn Glu Ile Ala Met
                805                 810                 815
Val Gln Ala Arg Gly Arg Ala Arg Ala Asp Glu Ser Thr Tyr Val Leu
            820                 825                 830
Val Ala His Ser Gly Ser Gly Val Ile Glu His Glu Thr Val Asn Asp
        835                 840                 845
Phe Arg Glu Lys Met Met Tyr Lys Ala Ile His Cys Val Gln Asn Met
    850                 855                 860
Lys Pro Glu Glu Tyr Ala His Lys Ile Leu Glu Leu Gln Met Gln Ser
865                 870                 875                 880
Ile Met Glu Lys Lys Met Lys Thr Lys Arg Asn Ile Ala Lys His Tyr
                885                 890                 895
Lys Asn Asn Pro Ser Leu Ile Thr Phe Leu Cys Lys Asn Cys Ser Val
            900                 905                 910
Leu Ala Cys Ser Gly Glu Asp Ile His Val Ile Glu Lys Met His His
        915                 920                 925
Val Asn Met Thr Pro Glu Phe Lys Glu Leu Tyr Ile Val Arg Glu Asn
    930                 935                 940
Lys Ala Leu Gln Lys Lys Cys Ala Asp Tyr Gln Ile Asn Gly Glu Ile
945                 950                 955                 960
Ile Cys Lys Cys Gly Gln Ala Trp Gly Thr Met Met Val His Lys Gly
                965                 970                 975
Leu Asp Leu Pro Cys Leu Lys Ile Arg Asn Phe Val Val Val Phe Lys
            980                 985                 990
Asn Asn Ser Thr Lys Lys Gln Tyr Lys Lys Trp Val Glu Leu Pro Ile
        995                 1000                1005
Thr Phe Pro Asn Leu Asp Tyr Ser Glu Cys Cys Leu Phe Ser Asp Glu
    1010                1015                1020
```

Asp
1025

<210> 311
<211> 925
<212> PRT
<213> Homo sapiens

<220>
<223> RIG-I/DDX58

<400> 311
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Met Thr Thr Glu Gln Arg Arg Ser Leu Gln Ala Phe Gln Asp Tyr Ile
 1               5                  10                  15
Arg Lys Thr Leu Asp Pro Thr Tyr Ile Leu Ser Tyr Met Ala Pro Trp
            20                  25                  30
Phe Arg Glu Glu Glu Val Gln Tyr Ile Gln Ala Glu Lys Asn Asn Lys
        35                  40                  45
Gly Pro Met Glu Ala Ala Thr Leu Phe Leu Lys Phe Leu Leu Glu Leu
    50                  55                  60
Gln Glu Glu Gly Trp Phe Arg Gly Phe Leu Asp Ala Leu Asp His Ala
65                  70                  75                  80
Gly Tyr Ser Gly Leu Tyr Glu Ala Ile Glu Ser Trp Asp Phe Lys Lys
                85                  90                  95
Ile Glu Lys Leu Glu Glu Tyr Arg Leu Leu Leu Lys Arg Leu Gln Pro
            100                 105                 110
Glu Phe Lys Thr Arg Ile Ile Pro Thr Asp Ile Ile Ser Asp Leu Ser
        115                 120                 125
Glu Cys Leu Ile Asn Gln Glu Cys Glu Glu Ile Leu Gln Ile Cys Ser
    130                 135                 140
Thr Lys Gly Met Met Ala Gly Ala Glu Lys Leu Val Glu Cys Leu Leu
145                 150                 155                 160
Arg Ser Asp Lys Glu Asn Trp Pro Lys Thr Leu Lys Leu Ala Leu Glu
                165                 170                 175
Lys Glu Arg Asn Lys Phe Ser Glu Leu Trp Ile Val Glu Lys Gly Ile
            180                 185                 190
Lys Asp Val Glu Thr Glu Asp Leu Glu Asp Lys Met Glu Thr Ser Asp
        195                 200                 205
Ile Gln Ile Phe Tyr Gln Glu Asp Pro Glu Cys Gln Asn Leu Ser Glu
    210                 215                 220
Asn Ser Cys Pro Pro Ser Glu Val Ser Asp Thr Asn Leu Tyr Ser Pro
225                 230                 235                 240
Phe Lys Pro Arg Asn Tyr Gln Leu Glu Leu Ala Leu Pro Ala Met Lys
                245                 250                 255
Gly Lys Asn Thr Ile Ile Cys Ala Pro Thr Gly Cys Gly Lys Thr Phe
            260                 265                 270
Val Ser Leu Leu Ile Cys Glu His His Leu Lys Lys Phe Pro Gln Gly
        275                 280                 285
Gln Lys Gly Lys Val Val Phe Phe Ala Asn Gln Ile Pro Val Tyr Glu
```

```
    290                 295                 300
Gln Gln Lys Ser Val Phe Ser Lys Tyr Phe Glu Arg His Gly Tyr Arg
305                 310                 315                 320
Val Thr Gly Ile Ser Gly Ala Thr Ala Glu Asn Val Pro Val Glu Gln
                325                 330                 335
Ile Val Glu Asn Asn Asp Ile Ile Ile Leu Thr Pro Gln Ile Leu Val
            340                 345                 350
Asn Asn Leu Lys Lys Gly Thr Ile Pro Ser Leu Ser Ile Phe Thr Leu
        355                 360                 365
Met Ile Phe Asp Glu Cys His Asn Thr Ser Lys Gln His Pro Tyr Asn
    370                 375                 380
Met Ile Met Phe Asn Tyr Leu Asp Gln Lys Leu Gly Gly Ser Ser Gly
385                 390                 395                 400
Pro Leu Pro Gln Val Ile Gly Leu Thr Ala Ser Val Gly Val Gly Asp
                405                 410                 415
Ala Lys Asn Thr Asp Glu Ala Leu Asp Tyr Ile Cys Lys Leu Cys Ala
            420                 425                 430
Ser Leu Asp Ala Ser Val Ile Ala Thr Val Lys His Asn Leu Glu Glu
        435                 440                 445
Leu Glu Gln Val Val Tyr Lys Pro Gln Lys Phe Phe Arg Lys Val Glu
    450                 455                 460
Ser Arg Ile Ser Asp Lys Phe Lys Tyr Ile Ile Ala Gln Leu Met Arg
465                 470                 475                 480
Asp Thr Glu Ser Leu Ala Lys Arg Ile Cys Lys Asp Leu Glu Asn Leu
                485                 490                 495
Ser Gln Ile Gln Asn Arg Glu Phe Gly Thr Gln Lys Tyr Glu Gln Trp
            500                 505                 510
Ile Val Thr Val Gln Lys Ala Cys Met Val Phe Gln Met Pro Asp Lys
        515                 520                 525
Asp Glu Glu Ser Arg Ile Cys Lys Ala Leu Phe Leu Tyr Thr Ser His
    530                 535                 540
Leu Arg Lys Tyr Asn Asp Ala Leu Ile Ile Ser Glu His Ala Arg Met
545                 550                 555                 560
Lys Asp Ala Leu Asp Tyr Leu Lys Asp Phe Phe Ser Asn Val Arg Ala
                565                 570                 575
Ala Gly Phe Asp Glu Ile Glu Gln Asp Leu Thr Gln Arg Phe Glu Glu
            580                 585                 590
Lys Leu Gln Glu Leu Glu Ser Val Ser Arg Asp Pro Ser Asn Glu Asn
        595                 600                 605
Pro Lys Leu Glu Asp Leu Cys Phe Ile Leu Gln Glu Glu Tyr His Leu
    610                 615                 620
Asn Pro Glu Thr Ile Thr Ile Leu Phe Val Lys Thr Arg Ala Leu Val
625                 630                 635                 640
Asp Ala Leu Lys Asn Trp Ile Glu Gly Asn Pro Lys Leu Ser Phe Leu
                645                 650                 655
Lys Pro Gly Ile Leu Thr Gly Arg Gly Lys Thr Asn Gln Asn Thr Gly
            660                 665                 670
Met Thr Leu Pro Ala Gln Lys Cys Ile Leu Asp Ala Phe Lys Ala Ser
        675                 680                 685
Gly Asp His Asn Ile Leu Ile Ala Thr Ser Val Ala Asp Glu Gly Ile
```

```
    690                 695                 700
Asp Ile Ala Gln Cys Asn Leu Val Ile Leu Tyr Glu Tyr Val Gly Asn
705                 710                 715                 720
Val Ile Lys Met Ile Gln Thr Arg Gly Arg Gly Arg Ala Arg Gly Ser
                725                 730                 735
Lys Cys Phe Leu Leu Thr Ser Asn Ala Gly Val Ile Glu Lys Glu Gln
            740                 745                 750
Ile Asn Met Tyr Lys Glu Lys Met Met Asn Asp Ser Ile Leu Arg Leu
        755                 760                 765
Gln Thr Trp Asp Glu Ala Val Phe Arg Glu Lys Ile Leu His Ile Gln
    770                 775                 780
Thr His Glu Lys Phe Ile Arg Asp Ser Gln Glu Lys Pro Lys Pro Val
785                 790                 795                 800
Pro Asp Lys Glu Asn Lys Lys Leu Leu Cys Arg Lys Cys Lys Ala Leu
                805                 810                 815
Ala Cys Tyr Thr Ala Asp Val Arg Val Ile Glu Glu Cys His Tyr Thr
            820                 825                 830
Val Leu Gly Asp Ala Phe Lys Glu Cys Phe Val Ser Arg Pro His Pro
        835                 840                 845
Lys Pro Lys Gln Phe Ser Ser Phe Glu Lys Arg Ala Lys Ile Phe Cys
    850                 855                 860
Ala Arg Gln Asn Cys Ser His Asp Trp Gly Ile His Val Lys Tyr Lys
865                 870                 875                 880
Thr Phe Glu Ile Pro Val Ile Lys Ile Glu Ser Phe Val Val Glu Asp
                885                 890                 895
Ile Ala Thr Gly Val Gln Thr Leu Tyr Ser Lys Trp Lys Asp Phe His
            900                 905                 910
Phe Glu Lys Ile Pro Phe Asp Pro Ala Glu Met Ser Lys
        915                 920                 925
```

<210> 312
<211> 427
<212> PRT
<213> Homo sapiens

<220>
<223> IRF-3, isofom 1

```
<400> 312
Met Gly Thr Pro Lys Pro Arg Ile Leu Pro Trp Leu Val Ser Gln Leu
 1               5                  10                  15
Asp Leu Gly Gln Leu Glu Gly Val Ala Trp Val Asn Lys Ser Arg Thr
            20                  25                  30
Arg Phe Arg Ile Pro Trp Lys His Gly Leu Arg Gln Asp Ala Gln Gln
        35                  40                  45
Glu Asp Phe Gly Ile Phe Gln Ala Trp Ala Glu Ala Thr Gly Ala Tyr
    50                  55                  60
Val Pro Gly Arg Asp Lys Pro Asp Leu Pro Thr Trp Lys Arg Asn Phe
65                  70                  75                  80
Arg Ser Ala Leu Asn Arg Lys Glu Gly Leu Arg Leu Ala Glu Asp Arg
```

```
                85                  90                  95
Ser Lys Asp Pro His Asp Pro His Lys Ile Tyr Glu Phe Val Asn Ser
            100                 105                 110
Gly Val Gly Asp Phe Ser Gln Pro Asp Thr Ser Pro Asp Thr Asn Gly
        115                 120                 125
Gly Gly Ser Thr Ser Asp Thr Gln Glu Asp Ile Leu Asp Glu Leu Leu
    130                 135                 140
Gly Asn Met Val Leu Ala Pro Leu Pro Asp Pro Gly Pro Pro Ser Leu
145                 150                 155                 160
Ala Val Ala Pro Glu Pro Cys Pro Gln Pro Leu Arg Ser Pro Ser Leu
                165                 170                 175
Asp Asn Pro Thr Pro Phe Pro Asn Leu Gly Pro Ser Glu Asn Pro Leu
            180                 185                 190
Lys Arg Leu Leu Val Pro Gly Glu Glu Trp Glu Phe Glu Val Thr Ala
        195                 200                 205
Phe Tyr Arg Gly Arg Gln Val Phe Gln Gln Thr Ile Ser Cys Pro Glu
    210                 215                 220
Gly Leu Arg Leu Val Gly Ser Glu Val Gly Asp Arg Thr Leu Pro Gly
225                 230                 235                 240
Trp Pro Val Thr Leu Pro Asp Pro Gly Met Ser Leu Thr Asp Arg Gly
                245                 250                 255
Val Met Ser Tyr Val Arg His Val Leu Ser Cys Leu Gly Gly Gly Leu
            260                 265                 270
Ala Leu Trp Arg Ala Gly Gln Trp Leu Trp Ala Gln Arg Leu Gly His
        275                 280                 285
Cys His Thr Tyr Trp Ala Val Ser Glu Glu Leu Leu Pro Asn Ser Gly
    290                 295                 300
His Gly Pro Asp Gly Glu Val Pro Lys Asp Lys Glu Gly Gly Val Phe
305                 310                 315                 320
Asp Leu Gly Pro Phe Ile Val Asp Leu Ile Thr Phe Thr Glu Gly Ser
                325                 330                 335
Gly Arg Ser Pro Arg Tyr Ala Leu Trp Phe Cys Val Gly Glu Ser Trp
            340                 345                 350
Pro Gln Asp Gln Pro Trp Thr Lys Arg Leu Val Met Val Lys Val Val
        355                 360                 365
Pro Thr Cys Leu Arg Ala Leu Val Glu Met Ala Arg Val Gly Gly Ala
    370                 375                 380
Ser Ser Leu Glu Asn Thr Val Asp Leu His Ile Ser Asn Ser His Pro
385                 390                 395                 400
Leu Ser Leu Thr Ser Asp Gln Tyr Lys Ala Tyr Leu Gln Asp Leu Val
                405                 410                 415
Glu Gly Met Asp Phe Gln Gly Pro Gly Glu Ser
            420                 425


<210> 313
<211> 503
<212> PRT
<213> Homo sapiens
```

<220>
<223> IRF-7, isoform A

<400> 313
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Met Ala Leu Ala Pro Glu Arg Ala Ala Pro Arg Val Leu Phe Gly Glu
 1               5                  10                  15
Trp Leu Leu Gly Glu Ile Ser Ser Gly Cys Tyr Glu Gly Leu Gln Trp
            20                  25                  30
Leu Asp Glu Ala Arg Thr Cys Phe Arg Val Pro Trp Lys His Phe Ala
        35                  40                  45
Arg Lys Asp Leu Ser Glu Ala Asp Ala Arg Ile Phe Lys Ala Trp Ala
    50                  55                  60
Val Ala Arg Gly Arg Trp Pro Pro Ser Ser Arg Gly Gly Gly Pro Pro
65                  70                  75                  80
Pro Glu Ala Glu Thr Ala Glu Arg Ala Gly Trp Lys Thr Asn Phe Arg
                85                  90                  95
Cys Ala Leu Arg Ser Thr Arg Arg Phe Val Met Leu Arg Asp Asn Ser
            100                 105                 110
Gly Asp Pro Ala Asp Pro His Lys Val Tyr Ala Leu Ser Arg Glu Leu
        115                 120                 125
Cys Trp Arg Glu Gly Pro Gly Thr Asp Gln Thr Glu Ala Glu Ala Pro
    130                 135                 140
Ala Ala Val Pro Pro Pro Gln Gly Gly Pro Pro Gly Pro Phe Leu Ala
145                 150                 155                 160
His Thr His Ala Gly Leu Gln Ala Pro Gly Pro Leu Pro Ala Pro Ala
                165                 170                 175
Gly Asp Lys Gly Asp Leu Leu Leu Gln Ala Val Gln Gln Ser Cys Leu
            180                 185                 190
Ala Asp His Leu Leu Thr Ala Ser Trp Gly Ala Asp Pro Val Pro Thr
        195                 200                 205
Lys Ala Pro Gly Glu Gly Gln Glu Gly Leu Pro Leu Thr Gly Ala Cys
    210                 215                 220
Ala Gly Gly Pro Gly Leu Pro Ala Gly Glu Leu Tyr Gly Trp Ala Val
225                 230                 235                 240
Glu Thr Thr Pro Ser Pro Gly Pro Gln Pro Ala Ala Leu Thr Thr Gly
                245                 250                 255
Glu Ala Ala Ala Pro Glu Ser Pro His Gln Ala Glu Pro Tyr Leu Ser
            260                 265                 270
Pro Ser Pro Ser Ala Cys Thr Ala Val Gln Glu Pro Ser Pro Gly Ala
        275                 280                 285
Leu Asp Val Thr Ile Met Tyr Lys Gly Arg Thr Val Leu Gln Lys Val
    290                 295                 300
Val Gly His Pro Ser Cys Thr Phe Leu Tyr Gly Pro Pro Asp Pro Ala
305                 310                 315                 320
Val Arg Ala Thr Asp Pro Gln Gln Val Ala Phe Pro Ser Pro Ala Glu
                325                 330                 335
Leu Pro Asp Gln Lys Gln Leu Arg Tyr Thr Glu Glu Leu Leu Arg His
            340                 345                 350
Val Ala Pro Gly Leu His Leu Glu Leu Arg Gly Pro Gln Leu Trp Ala
        355                 360                 365
```

```
Arg Arg Met Gly Lys Cys Lys Val Tyr Trp Glu Val Gly Gly Pro Pro
    370                 375                 380
Gly Ser Ala Ser Pro Ser Thr Pro Ala Cys Leu Leu Pro Arg Asn Cys
385                 390                 395                 400
Asp Thr Pro Ile Phe Asp Phe Arg Val Phe Phe Gln Glu Leu Val Glu
                405                 410                 415
Phe Arg Ala Arg Gln Arg Arg Gly Ser Pro Arg Tyr Thr Ile Tyr Leu
            420                 425                 430
Gly Phe Gly Gln Asp Leu Ser Ala Gly Arg Pro Lys Glu Lys Ser Leu
        435                 440                 445
Val Leu Val Lys Leu Glu Pro Trp Leu Cys Arg Val His Leu Glu Gly
    450                 455                 460
Thr Gln Arg Glu Gly Val Ser Ser Leu Asp Ser Ser Ser Leu Ser Leu
465                 470                 475                 480
Cys Leu Ser Ser Ala Asn Ser Leu Tyr Asp Asp Ile Glu Cys Phe Leu
                485                 490                 495
Met Glu Leu Glu Gln Pro Ala
            500
```

<210> 314
<211> 1184
<212> DNA
<213> Artificial Sequence

<220>
<223> Elongation factor 1 (EF1) alpha promoter

<400> 314
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cgtgaggctc cggtgcccgt cagtgggcag agcgcacatc gcccacagtc cccgagaagt 60
tgggggggagg ggtcggcaat tgaaccggtg cctagagaag gtggcgcggg gtaaactggg 120
aaagtgatgt cgtgtactgg ctccgccttt ttcccgaggg tgggggagaa ccgtatataa 180
gtgcagtagt cgccgtgaac gttcttttтc gcaacgggtt tgccgccaga acacaggtaa 240
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<211> 664
<212> DNA
<213> Salmonella typhimurium

<220>
<223> csgD

<400> 335
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cagttacctg attacgcact caggaaatta ccgctacaac agcaccgagt ccgcattact 480
cactcatcgc gaaaaagaga tcctcaataa gttacgtatt ggtgcctcta ataatgaaat 540
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gtaa 664

<210> 336
<211> 558
<212> DNA
<213> Salmonella typhimurium

<220>
<223> rck (resistance to complement killing)

<400> 336
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<210> 337
<211> 4369
<212> DNA
<213> Salmonella typhimurium

<220>
<223> pagP

<400> 337
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<210> 338
<211> 1500
<212> DNA
<213> Salmonella typhimurium

<220>
<223> fliC

<400> 338

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<210> 339
<211> 1528
<212> DNA
<213> Salmonella typhimurium

<220>
<223> fljB

<400> 339
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<210> 340
<211> 537
<212> DNA
<213> Yersinia enterocolitica

<220>
<223> ail (attachment invasion locus)

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<210> 341
<211> 1286
<212> DNA
<213> Salmonella typhimurium

<220>
<223> pgtE (outer membrane serine protease)

<400> 341
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<210> 342
<211> 254
<212> PRT
<213> Homo sapiens

<220>
<223> 4-1BBL

<400> 342
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            20                  25                  30
Ala Gly Leu Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe
        35                  40                  45
Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser
    50                  55                  60
Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp
65                  70                  75                  80
Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val
                85                  90                  95
Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp
            100                 105                 110
Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu
        115                 120                 125
Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe
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Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser
145                 150                 155                 160
Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala
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Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala
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Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala
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Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His
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225                 230                 235                 240
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<210> 343
<211> 4899
<212> DNA
<213> Homo sapiens

<220>
<223> 4-1BBL

<400> 343

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<210> 344
<211> 309
<212> PRT
<213> Mus musculus

<220>
<223> 4-1BBL

<400> 344
Met Asp Gln His Thr Leu Asp Val Glu Asp Thr Ala Asp Ala Arg His
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Pro Ala Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr
            20   25   30
Gly Leu Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr
        35   40   45
Asn Ala Ala Leu Pro Thr Asp Ala Ala Tyr Pro Ala Val Asn Val Arg
    50   55   60
Asp Arg Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His
65   70   75   80
Pro Lys Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Leu Ile Ala
                85   90   95
Ala Cys Val Pro Ile Phe Thr Arg Thr Glu Pro Arg Pro Ala Leu Thr
            100   105   110
Ile Thr Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn Asn Ala Asp Gln
        115   120   125
Val Thr Pro Val Ser His Ile Gly Cys Pro Asn Thr Thr Gln Gln Gly
    130   135   140
Ser Pro Val Phe Ala Lys Leu Leu Ala Lys Asn Gln Ala Ser Leu Cys
145   150   155   160
Asn Thr Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser Tyr
                165   170   175
Leu Ser Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys Glu Leu Val Val
            180   185   190
Asp Ser Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro
        195   200   205
Thr Phe Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val
    210   215   220
Leu Gln Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr
225   230   235   240
Val Glu Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser
                245   250   255
Trp Ser Gln Leu Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly
            260   265   270
Leu Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu
        275   280   285
Leu Ser Tyr Pro Asn Thr Thr Ser Phe Gly Leu Phe Leu Val Lys Pro
    290   295   300

Asp Asn Pro Trp Glu
305

<210> 345
<211> 2472
<212> DNA
<213> Mus musculus

<220>
<223> 4-1BBL

<400> 345
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ggatgccaga catccagcag gtacttcgtg cccctcggat gcggcgctcc tcagagatac 240
cgggctcctc gcggacgctg cgctcctctc agatactgtg cgccccacaa atgccgcgct 300
ccccacggat gctgcctacc ctgcggttaa tgttcgggat cgcgaggccg cgtggccgcc 360
tgcactgaac ttctgttccc gccacccaaa gctctatggc ctagtcgctt tggttttgct 420
gcttctgatc gccgcctgtg ttcctatctt cacccgcacc gagcctcggc cagcgctcac 480
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aatgtgtttg ta 2472

<210> 346
<211> 589
<212> DNA
<213> Artificial Sequence

<220>
<223> Woodchuck Hepatitis Virus Posttranscriptional
Regulatory Element (WPRE)

<400> 346
aatcaacctc tggattacaa aatttgtgaa agattgactg gtattcttaa ctatgttgct 60
ccttttacgc tatgtggata cgctgcttta atgcctttgt atcatgctat tgcttcccgt 120
atggctttca ttttctcctc cttgtataaa tcctggttgc tgtctcttta tgaggagttg 180
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gcctgtgttg ccacctggat tctgcgcggg acgtccttct gctacgtccc ttcggccctc 480
aatccagcgg accttccttc ccgcggcctg ctgccggctc tgcggcctct tccgcgtctt 540
cgccttcgcc ctcagacgag tcggatctcc ctttgggccg cctccccgc 589

<210> 347
<211> 534
<212> DNA
<213> Artificial Sequence

<220>
<223> Hepatitis B Virus Posttranscriptional Regulatory
Element (HPRE)

<400> 347
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gcttggccat aggccatcag cgcatgcgtg gaacctttgt ggctcctctg ccgatccata 120
ctgcggaact cctagccgct tgttttgctc gcagccggtc tggggcaaag ctcatcggaa 180
ctgacaattc tgtcgtcctc tcgcggaaat atacatcgtt tccatggctg ctaggttgta 240
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cggtccgtgt gcacttcgct tcacctctgc acgttgcatg gagaccaccg tgaacgccca 480
tcagatcctg cccaaggtct tacataagag gactcttgga ctcccagcaa tgtc 534

<210> 348
<211> 398
<212> PRT
<213> Danio rerio

<220>
<223> WT Zebrafish STING (zfSTING)

<400> 348
Met Ser Val Met Gly Glu Asp Ala Leu Val Pro Arg Ala Arg Ser Arg
 1   5   10   15
Leu Pro Val Met Cys Ala Ala Gly Leu Gly Phe Leu Thr Leu Ala Val
            20   25   30
Ala Trp Leu Leu Asp Ser Asp Lys Phe Ser Glu Arg Ala Gly Ile Ile
        35   40   45
Ala Phe Gly Leu Met Leu Glu Arg Phe Ile Tyr Cys Ile Cys Leu Leu
    50   55   60
Ala Glu Glu Leu Leu Phe His Ser Arg Gln Arg Tyr His Gly Arg Met
65   70   75   80
Ser Glu Ile Phe Arg Ala Cys Phe Arg Gly Ser Gly Ile Leu Gly Met
                85   90   95
Cys Ala Ile Phe Leu Met Leu Met Leu Gly Gly Val Ser Phe Ser Val
            100   105   110
Lys Gln Trp Ser His Phe Asn Leu Met Cys Ala Gly Tyr Met Leu Leu
        115   120   125
Asn Ser Leu Gly Val Leu Gly Pro Ala Pro Val Glu Ile Ser Glu Ile
    130   135   140
Cys Glu Ala Lys Lys Met Asn Val Ala His Gly Leu Ala Trp Ser Phe
145   150   155   160
Tyr Ile Gly Tyr Leu Lys Phe Leu Leu Pro Ala Leu Glu Val Asn Val
                165   170   175
Arg Glu Tyr Ser Arg Arg Glu Arg Leu Ser Ser Pro Arg Leu His Ile
            180   185   190
Leu Leu Pro Leu Asn Ala Arg Val Pro Ser Lys Pro Glu Glu Glu Asp
        195   200   205
Thr Asn Val Val Phe His Glu Asn Leu Pro Asp Leu Lys Leu Asp Arg
    210   215   220
Ala Gly Val Arg Lys Arg Ser Tyr Thr Asn Ser Val Tyr Lys Ile Thr
225   230   235   240
His Asn Asn Glu Thr Phe Ser Cys Ile Leu Glu Tyr Ala Thr Pro Leu
                245   250   255
Leu Thr Leu Tyr Gln Met Ser Gln Glu Ser Ser Ala Gly Phe Gly Glu
            260   265   270
Arg Glu Arg Lys Gln Gln Val Leu Leu Phe Tyr Arg Thr Leu Ser Gln
        275   280   285
Ile Leu Asp Asn Ser Leu Glu Cys Arg Asn Arg Tyr Arg Leu Ile Leu
    290   295   300
Leu Asn Asp Glu His Thr Gly Asp Pro His Tyr Leu Ser Arg Glu Leu
305   310   315   320
Phe Gln Asn Leu Lys Gln Gln Asp Gly Glu Ile Phe Met Asp Pro Thr

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                325                 330                 335
Asn Glu Val His Pro Val Pro Glu Glu Gly Pro Val Gly Asn Cys Asn
            340                 345                 350
Gly Ala Leu Gln Ala Thr Phe His Glu Glu Pro Met Ser Asp Glu Pro
        355                 360                 365
Thr Leu Met Phe Ser Arg Pro Gln Ser Leu Arg Ser Glu Pro Val Glu
    370                 375                 380
Thr Thr Asp Tyr Phe Asn Pro Ser Ser Ala Met Lys Gln Asn
385                 390                 395


<210> 349
<211> 381
<212> PRT
<213> Sarcophilus harrisii

<220>
<223> WT Tasmanian devil STING (tazSTING)

<400> 349
Met Pro Arg Ser His Leu His Pro Ser Ile Pro Gln Pro Arg Gly Trp
 1               5                  10                  15
Gly Ala Gln Lys Ala Ala Cys Val Leu Leu Ser Leu Cys Met Ala Ala
            20                  25                  30
Val Tyr Ile Leu Gly Glu Ser Ala Ala Phe Thr Leu Gln Trp Leu Leu
        35                  40                  45
Phe Tyr Phe Thr Thr Val Gln Val Gly Leu Leu Leu Lys Gly Ala Tyr
    50                  55                  60
Cys Leu Ala Glu Glu Leu Tyr His Ile Gln Ser Arg His Gln Gly Ser
65                  70                  75                  80
Tyr Trp Gln Ala Ile Gln Ala Cys Ile His Tyr Pro Phe Gln Arg Ile
                85                  90                  95
Ser Leu Leu Leu Leu Ser Gly Tyr Phe Tyr Val Thr Leu Ser Asn Lys
            100                 105                 110
Pro Asn Pro Ser Leu Thr Trp Thr Phe Ala Leu Leu Gly Leu Ser His
        115                 120                 125
Ala Leu Ser Phe Ile Leu Gly Leu Gln Asn Leu Thr Ser Ala Glu Ile
    130                 135                 140
Ser Glu Val Cys Glu Lys Arg His Leu Asn Val Ala His Gly Leu Ala
145                 150                 155                 160
Trp Ser Tyr Tyr Ile Gly Tyr Leu Lys Leu Ile Leu Pro Gly Leu Gln
                165                 170                 175
Thr Arg Ile Gln Ile Tyr Asn Gln Phe Asn Lys Asp Val Leu Arg Ser
            180                 185                 190
Pro Glu Gly His Arg Leu His Ile Leu Ile Pro Leu Asp Cys Ser Val
        195                 200                 205
Pro Asp Asn Leu Ser Gln Ala Asp Pro Asn Ile Gln Phe Leu Gln Glu
    210                 215                 220
Leu Pro Gln His Lys Leu Asp Arg Ala Gly Ile Lys Gly Arg Ile Tyr
225                 230                 235                 240
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Thr Asn Ser Ile Tyr Lys Ile Ser Glu Asp Gly Gln Pro Ala Glu Val
                245                 250                 255
Cys Val Leu Glu Phe Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
            260                 265                 270
Gln Asp Ala Arg Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
        275                 280                 285
Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Glu Asp Ala Pro Glu
    290                 295                 300
Ala Arg Asp Cys Cys Arg Leu Val Val Tyr Gln Glu Pro Glu Asp Lys
305                 310                 315                 320
Ala Val Ser Asn Phe Ser Leu Ser Lys Glu Ile Leu Arg His Leu Arg
                325                 330                 335
Gln Glu Arg Gln Glu Glu Phe Ala Ile Gly Pro Lys Arg Ala Met Thr
            340                 345                 350
Val Thr Thr Ser Ser Thr Leu Ser Gln Glu Pro Gln Leu Leu Ile Ser
        355                 360                 365
Gly Met Glu Gln Pro Leu Ser Leu Arg Thr Asp Gly Phe
    370                 375                 380


<210> 350
<211> 381
<212> PRT
<213> Artificial Sequence

<220>
<223> Tasmanian devil STING (tazSTING) C206Y

<400> 350
Met Pro Arg Ser His Leu His Pro Ser Ile Pro Gln Pro Arg Gly Trp
 1               5                  10                  15
Gly Ala Gln Lys Ala Ala Cys Val Leu Leu Ser Leu Cys Met Ala Ala
            20                  25                  30
Val Tyr Ile Leu Gly Glu Ser Ala Ala Phe Thr Leu Gln Trp Leu Leu
        35                  40                  45
Phe Tyr Phe Thr Thr Val Gln Val Gly Leu Leu Leu Lys Gly Ala Tyr
    50                  55                  60
Cys Leu Ala Glu Glu Leu Tyr His Ile Gln Ser Arg His Gln Gly Ser
65                  70                  75                  80
Tyr Trp Gln Ala Ile Gln Ala Cys Ile His Tyr Pro Phe Gln Arg Ile
                85                  90                  95
Ser Leu Leu Leu Leu Ser Gly Tyr Phe Tyr Val Thr Leu Ser Asn Lys
            100                 105                 110
Pro Asn Pro Ser Leu Thr Trp Thr Phe Ala Leu Leu Gly Leu Ser His
        115                 120                 125
Ala Leu Ser Phe Ile Leu Gly Leu Gln Asn Leu Thr Ser Ala Glu Ile
    130                 135                 140
Ser Glu Val Cys Glu Lys Arg His Leu Asn Val Ala His Gly Leu Ala
145                 150                 155                 160
Trp Ser Tyr Tyr Ile Gly Tyr Leu Lys Leu Ile Leu Pro Gly Leu Gln
```

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                165                 170                 175
Thr Arg Ile Gln Ile Tyr Asn Gln Phe Asn Lys Asp Val Leu Arg Ser
            180                 185                 190
Pro Glu Gly His Arg Leu His Ile Leu Ile Pro Leu Asp Tyr Ser Val
        195                 200                 205
Pro Asp Asn Leu Ser Gln Ala Asp Pro Asn Ile Gln Phe Leu Gln Glu
    210                 215                 220
Leu Pro Gln His Lys Leu Asp Arg Ala Gly Ile Lys Gly Arg Ile Tyr
225                 230                 235                 240
Thr Asn Ser Ile Tyr Lys Ile Ser Glu Asp Gly Gln Pro Ala Glu Val
                245                 250                 255
Cys Val Leu Glu Phe Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
            260                 265                 270
Gln Asp Ala Arg Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
        275                 280                 285
Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Glu Asp Ala Pro Glu
    290                 295                 300
Ala Arg Asp Cys Cys Arg Leu Val Val Tyr Gln Glu Pro Glu Asp Lys
305                 310                 315                 320
Ala Val Ser Asn Phe Ser Leu Ser Lys Glu Ile Leu Arg His Leu Arg
                325                 330                 335
Gln Glu Arg Gln Glu Glu Phe Ala Ile Gly Pro Lys Arg Ala Met Thr
            340                 345                 350
Val Thr Thr Ser Ser Thr Leu Ser Gln Glu Pro Gln Leu Leu Ile Ser
        355                 360                 365
Gly Met Glu Gln Pro Leu Ser Leu Arg Thr Asp Gly Phe
    370                 375                 380
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<210> 351
<211> 381
<212> PRT
<213> Artificial Sequence

<220>
<223> Tasmanian devil STING (tazSTING) R284G

<400> 351

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Met Pro Arg Ser His Leu His Pro Ser Ile Pro Gln Pro Arg Gly Trp
 1               5                  10                  15
Gly Ala Gln Lys Ala Ala Cys Val Leu Leu Ser Leu Cys Met Ala Ala
            20                  25                  30
Val Tyr Ile Leu Gly Glu Ser Ala Ala Phe Thr Leu Gln Trp Leu Leu
        35                  40                  45
Phe Tyr Phe Thr Thr Val Gln Val Gly Leu Leu Leu Lys Gly Ala Tyr
    50                  55                  60
Cys Leu Ala Glu Glu Leu Tyr His Ile Gln Ser Arg His Gln Gly Ser
65                  70                  75                  80
Tyr Trp Gln Ala Ile Gln Ala Cys Ile His Tyr Pro Phe Gln Arg Ile
                85                  90                  95
Ser Leu Leu Leu Leu Ser Gly Tyr Phe Tyr Val Thr Leu Ser Asn Lys
```

```
            100                 105                 110
Pro Asn Pro Ser Leu Thr Trp Thr Phe Ala Leu Leu Gly Leu Ser His
        115                 120                 125
Ala Leu Ser Phe Ile Leu Gly Leu Gln Asn Leu Thr Ser Ala Glu Ile
    130                 135                 140
Ser Glu Val Cys Glu Lys Arg His Leu Asn Val Ala His Gly Leu Ala
145                 150                 155                 160
Trp Ser Tyr Tyr Ile Gly Tyr Leu Lys Leu Ile Leu Pro Gly Leu Gln
                165                 170                 175
Thr Arg Ile Gln Ile Tyr Asn Gln Phe Asn Lys Asp Val Leu Arg Ser
            180                 185                 190
Pro Glu Gly His Arg Leu His Ile Leu Ile Pro Leu Asp Cys Ser Val
        195                 200                 205
Pro Asp Asn Leu Ser Gln Ala Asp Pro Asn Ile Gln Phe Leu Gln Glu
    210                 215                 220
Leu Pro Gln His Lys Leu Asp Arg Ala Gly Ile Lys Gly Arg Ile Tyr
225                 230                 235                 240
Thr Asn Ser Ile Tyr Lys Ile Ser Glu Asp Gly Gln Pro Ala Glu Val
                245                 250                 255
Cys Val Leu Glu Phe Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
            260                 265                 270
Gln Asp Ala Arg Ala Gly Phe Ser Arg Glu Asp Gly Leu Glu Gln Ala
        275                 280                 285
Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Glu Asp Ala Pro Glu
    290                 295                 300
Ala Arg Asp Cys Cys Arg Leu Val Val Tyr Gln Glu Pro Glu Asp Lys
305                 310                 315                 320
Ala Val Ser Asn Phe Ser Leu Ser Lys Glu Ile Leu Arg His Leu Arg
                325                 330                 335
Gln Glu Arg Gln Glu Glu Phe Ala Ile Gly Pro Lys Arg Ala Met Thr
            340                 345                 350
Val Thr Thr Ser Ser Thr Leu Ser Gln Glu Pro Gln Leu Leu Ile Ser
        355                 360                 365
Gly Met Glu Gln Pro Leu Ser Leu Arg Thr Asp Gly Phe
    370                 375                 380


<210> 352
<211> 379
<212> PRT
<213> Artificial Sequence

<220>
<223> WT human STING-tasmanian devil CTT

<400> 352
Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 1               5                  10                  15
Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
            20                  25                  30
```

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Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
        35                  40                  45
Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
    50                  55                  60
Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65                  70                  75                  80
Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
                85                  90                  95
Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
            100                 105                 110
Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
        115                 120                 125
Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
    130                 135                 140
Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala
145                 150                 155                 160
Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
                165                 170                 175
Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
            180                 185                 190
Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
        195                 200                 205
Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
    210                 215                 220
Leu Pro Gln Gln Thr Gly Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr
225                 230                 235                 240
Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
                245                 250                 255
Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
            260                 265                 270
Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
        275                 280                 285
Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
    290                 295                 300
Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305                 310                 315                 320
Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
                325                 330                 335
Arg Gln Glu Glu Phe Ala Ile Gly Pro Lys Arg Ala Met Thr Val Thr
            340                 345                 350
Thr Ser Ser Thr Leu Ser Gln Glu Pro Gln Leu Leu Ile Ser Gly Met
        355                 360                 365
Glu Gln Pro Leu Ser Leu Arg Thr Asp Gly Phe
    370                 375
```

<210> 353
<211> 379
<212> PRT
<213> Artificial Sequence

<220>
<223> human STING C206Y-tasmanian devil CTT

<400> 353
Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 1   5   10   15
Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
            20   25   30
Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
        35   40   45
Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
    50   55   60
Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65   70   75   80
Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
                85   90   95
Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
            100   105   110
Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
        115   120   125
Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
    130   135   140
Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala
145   150   155   160
Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
                165   170   175
Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
            180   185   190
Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Tyr Gly Val
        195   200   205
Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
    210   215   220
Leu Pro Gln Gln Thr Gly Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr
225   230   235   240
Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
                245   250   255
Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
            260   265   270
Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
        275   280   285
Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
    290   295   300
Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305   310   315   320
Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
                325   330   335
Arg Gln Glu Glu Phe Ala Ile Gly Pro Lys Arg Ala Met Thr Val Thr
            340   345   350
Thr Ser Ser Thr Leu Ser Gln Glu Pro Gln Leu Leu Ile Ser Gly Met

```
        355                 360                 365
Glu Gln Pro Leu Ser Leu Arg Thr Asp Gly Phe
    370                 375


<210> 354
<211> 379
<212> PRT
<213> Artificial Sequence

<220>
<223> human STING R284G-tasmanian devil CTT

<400> 354
Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 1               5                  10                  15
Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
            20                  25                  30
Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
        35                  40                  45
Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
    50                  55                  60
Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65                  70                  75                  80
Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
                85                  90                  95
Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
            100                 105                 110
Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
        115                 120                 125
Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
    130                 135                 140
Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala
145                 150                 155                 160
Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
                165                 170                 175
Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
            180                 185                 190
Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
        195                 200                 205
Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
    210                 215                 220
Leu Pro Gln Gln Thr Gly Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr
225                 230                 235                 240
Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
                245                 250                 255
Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
            260                 265                 270
Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Gly Leu Glu Gln Ala
        275                 280                 285
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Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
    290                 295                 300
Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305                 310                 315                 320
Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
                325                 330                 335
Arg Gln Glu Glu Phe Ala Ile Gly Pro Lys Arg Ala Met Thr Val Thr
            340                 345                 350
Thr Ser Ser Thr Leu Ser Gln Glu Pro Gln Leu Leu Ile Ser Gly Met
        355                 360                 365
Glu Gln Pro Leu Ser Leu Arg Thr Asp Gly Phe
    370                 375


<210> 355
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> WT human STING delTRAF6 binding motif
     (Asp-Phe-Ser at C-terminal removed)

<400> 355
Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 1               5                  10                  15
Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
            20                  25                  30
Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
        35                  40                  45
Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
    50                  55                  60
Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65                  70                  75                  80
Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
                85                  90                  95
Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
            100                 105                 110
Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
        115                 120                 125
Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
    130                 135                 140
Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala
145                 150                 155                 160
Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
                165                 170                 175
Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
            180                 185                 190
Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
        195                 200                 205
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Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
    210                 215                 220
Leu Pro Gln Gln Thr Gly Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr
225                 230                 235                 240
Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
                245                 250                 255
Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
            260                 265                 270
Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
        275                 280                 285
Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
    290                 295                 300
Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305                 310                 315                 320
Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
                325                 330                 335
Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
            340                 345                 350
Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
        355                 360                 365
Glu Lys Pro Leu Pro Leu Arg Thr
    370                 375


<210> 356
<211> 377
<212> PRT
<213> Felis catus

<220>
<223> WT cat STING (catSTING)

<400> 356
Met Pro Arg Thr Gly Leu His Pro Ser Ile Pro Arg Pro Arg Gly Met
 1               5                  10                  15
Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ala Val Cys Leu Ala Ala
            20                  25                  30
Leu Trp Arg Leu Gly Glu Ser Pro Asp His Thr Leu Arg Trp Leu Val
        35                  40                  45
Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Phe Thr Gly Val Cys
    50                  55                  60
His Leu Thr Glu Glu Leu Cys His Leu His Ser Arg Tyr Gln Gly Ser
65                  70                  75                  80
Tyr Trp Arg Ala Met Lys Ala Cys Leu Gly Ser Pro Val Arg Ser Gly
                85                  90                  95
Ala Leu Leu Leu Leu Ser Cys Tyr Phe Tyr Ser Thr Leu Pro Ser Thr
            100                 105                 110
Asp Leu Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln Ala
        115                 120                 125
Leu Asn Ile Leu Leu Asp Leu Gln Gly Leu Ala Pro Ala Glu Val Ser
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```
    130                 135                 140
Ala Val Cys Glu Lys Lys Asn Phe Asn Val Ala His Gly Leu Ala Trp
145                 150                 155                 160
Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Gly Leu Pro Ala
                165                 170                 175
Arg Val Leu Thr Cys Asn Gln Leu His Asn Asn Ile Leu Arg Gly Thr
            180                 185                 190
Gly Ser His Arg Leu His Ile Leu Phe Pro Leu Asp Cys Gly Val Pro
        195                 200                 205
Asp Asp Met Ser Val Ala Asp Pro Asn Ile Arg Phe Leu Tyr Glu Leu
    210                 215                 220
Pro Gln Gln Ser Ala Asp Arg Ala Gly Ile Lys Gly Arg Val Tyr Thr
225                 230                 235                 240
Asn Ser Val Tyr Ala Leu Leu Glu Asn Gly Gln Gln Ala Gly Ile Cys
                245                 250                 255
Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser Gln
            260                 265                 270
Asp Gly Arg Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala Lys
        275                 280                 285
Leu Phe Cys Arg Ile Leu Glu Asp Ile Leu Ala Asp Thr Pro Glu Cys
    290                 295                 300
Gln Asn Asn Cys Arg Leu Ile Val Tyr Gln Glu Pro Glu Glu Gly Ser
305                 310                 315                 320
Asn Phe Ser Leu Ser Gln Glu Ile Leu Arg His Leu Arg Gln Glu Glu
                325                 330                 335
Arg Glu Val Thr Val Gly Ser Val Gly Thr Ser Met Val Arg Asn Pro
            340                 345                 350
Ser Val Leu Ser Gln Glu Pro Asn Leu Leu Ile Ser Gly Met Glu Gln
        355                 360                 365
Pro Leu Pro Leu Arg Thr Asp Val Phe
    370                 375


<210> 357
<211> 377
<212> PRT
<213> Artificial Sequence

<220>
<223> cat STING C205Y

<400> 357
Met Pro Arg Thr Gly Leu His Pro Ser Ile Pro Arg Pro Arg Gly Met
 1               5                  10                  15
Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ala Val Cys Leu Ala Ala
            20                  25                  30
Leu Trp Arg Leu Gly Glu Ser Pro Asp His Thr Leu Arg Trp Leu Val
        35                  40                  45
Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Phe Thr Gly Val Cys
    50                  55                  60
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His Leu Thr Glu Glu Leu Cys His Leu His Ser Arg Tyr Gln Gly Ser
65                  70                  75                  80
Tyr Trp Arg Ala Met Lys Ala Cys Leu Gly Ser Pro Val Arg Ser Gly
                85                  90                  95
Ala Leu Leu Leu Leu Ser Cys Tyr Phe Tyr Ser Thr Leu Pro Ser Thr
            100                 105                 110
Asp Leu Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln Ala
        115                 120                 125
Leu Asn Ile Leu Leu Asp Leu Gln Gly Leu Ala Pro Ala Glu Val Ser
    130                 135                 140
Ala Val Cys Glu Lys Lys Asn Phe Asn Val Ala His Gly Leu Ala Trp
145                 150                 155                 160
Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Gly Leu Pro Ala
                165                 170                 175
Arg Val Leu Thr Cys Asn Gln Leu His Asn Asn Ile Leu Arg Gly Thr
            180                 185                 190
Gly Ser His Arg Leu His Ile Leu Phe Pro Leu Asp Tyr Gly Val Pro
        195                 200                 205
Asp Asp Met Ser Val Ala Asp Pro Asn Ile Arg Phe Leu Tyr Glu Leu
    210                 215                 220
Pro Gln Gln Ser Ala Asp Arg Ala Gly Ile Lys Gly Arg Val Tyr Thr
225                 230                 235                 240
Asn Ser Val Tyr Ala Leu Leu Glu Asn Gly Gln Gln Ala Gly Ile Cys
                245                 250                 255
Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser Gln
            260                 265                 270
Asp Gly Arg Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala Lys
        275                 280                 285
Leu Phe Cys Arg Ile Leu Glu Asp Ile Leu Ala Asp Thr Pro Glu Cys
    290                 295                 300
Gln Asn Asn Cys Arg Leu Ile Val Tyr Gln Glu Pro Glu Glu Gly Ser
305                 310                 315                 320
Asn Phe Ser Leu Ser Gln Glu Ile Leu Arg His Leu Arg Gln Glu Glu
                325                 330                 335
Arg Glu Val Thr Val Gly Ser Val Gly Thr Ser Met Val Arg Asn Pro
            340                 345                 350
Ser Val Leu Ser Gln Glu Pro Asn Leu Leu Ile Ser Gly Met Glu Gln
        355                 360                 365
Pro Leu Pro Leu Arg Thr Asp Val Phe
    370                 375
```

<210> 358
<211> 377
<212> PRT
<213> Artificial Sequence

<220>
<223> cat STING R283G

<400> 358
Met Pro Arg Thr Gly Leu His Pro Ser Ile Pro Arg Pro Arg Gly Met
 1   5   10   15
Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ala Val Cys Leu Ala Ala
            20   25   30
Leu Trp Arg Leu Gly Glu Ser Pro Asp His Thr Leu Arg Trp Leu Val
        35   40   45
Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Phe Thr Gly Val Cys
    50   55   60
His Leu Thr Glu Glu Leu Cys His Leu His Ser Arg Tyr Gln Gly Ser
65   70   75   80
Tyr Trp Arg Ala Met Lys Ala Cys Leu Gly Ser Pro Val Arg Ser Gly
                85   90   95
Ala Leu Leu Leu Leu Ser Cys Tyr Phe Tyr Ser Thr Leu Pro Ser Thr
            100   105   110
Asp Leu Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln Ala
        115   120   125
Leu Asn Ile Leu Leu Asp Leu Gln Gly Leu Ala Pro Ala Glu Val Ser
    130   135   140
Ala Val Cys Glu Lys Lys Asn Phe Asn Val Ala His Gly Leu Ala Trp
145   150   155   160
Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Gly Leu Pro Ala
                165   170   175
Arg Val Leu Thr Cys Asn Gln Leu His Asn Asn Ile Leu Arg Gly Thr
            180   185   190
Gly Ser His Arg Leu His Ile Leu Phe Pro Leu Asp Cys Gly Val Pro
        195   200   205
Asp Asp Met Ser Val Ala Asp Pro Asn Ile Arg Phe Leu Tyr Glu Leu
    210   215   220
Pro Gln Gln Ser Ala Asp Arg Ala Gly Ile Lys Gly Arg Val Tyr Thr
225   230   235   240
Asn Ser Val Tyr Ala Leu Leu Glu Asn Gly Gln Gln Ala Gly Ile Cys
                245   250   255
Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser Gln
            260   265   270
Asp Gly Arg Ala Gly Phe Ser Arg Glu Asp Gly Leu Glu Gln Ala Lys
        275   280   285
Leu Phe Cys Arg Ile Leu Glu Asp Ile Leu Ala Asp Thr Pro Glu Cys
    290   295   300
Gln Asn Asn Cys Arg Leu Ile Val Tyr Gln Glu Pro Glu Glu Gly Ser
305   310   315   320
Asn Phe Ser Leu Ser Gln Glu Ile Leu Arg His Leu Arg Gln Glu Glu
                325   330   335
Arg Glu Val Thr Val Gly Ser Val Gly Thr Ser Met Val Arg Asn Pro
            340   345   350
Ser Val Leu Ser Gln Glu Pro Asn Leu Leu Ile Ser Gly Met Glu Gln
        355   360   365
Pro Leu Pro Leu Arg Thr Asp Val Phe
    370   375

<210> 359
<211> 377
<212> PRT
<213> Callithrix jacchus

<220>
<223> WT Marmoset STING

<400> 359
Met Pro His Ser Ser Leu His Pro Ser Ile Pro His Pro Arg Gly His
 1   5   10   15
Gly Ala Gln Glu Ala Ala Leu Val Leu Leu Ser Val Cys Leu Val Thr
            20   25   30
Leu Trp Trp Leu Arg Glu Ala Pro Glu Asp Ile Leu Arg Phe Leu Val
        35   40   45
Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Arg Leu Cys
    50   55   60
Ser Leu Ala Glu Glu Leu Arg His Val His Thr Arg Tyr Gln Gly Ser
65   70   75   80
Tyr Trp Arg Ala Val Arg Ala Cys Leu Gly Cys Pro Ile Arg Leu Gly
                85   90   95
Ala Gln Leu Leu Leu Ser Ile Tyr Phe Tyr Cys Phe Leu Pro Asn Gly
            100   105   110
Arg Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Phe Ser Gln Ala Leu
        115   120   125
Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala
    130   135   140
Val Cys Glu Lys Arg Asn Phe Asn Val Ala His Gly Leu Ala Trp Ser
145   150   155   160
Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Gly Phe Gln Ala Arg
                165   170   175
Ile Arg Thr Tyr Asn Gln His Asn Asn Asn Val Leu Arg Gly Pro Ala
            180   185   190
Ser Gln Arg Leu Tyr Ile Leu Phe Pro Leu Asp Cys Gly Val Pro Asp
        195   200   205
Asn Leu Ser Thr Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys Leu Pro
    210   215   220
Gln Glu Thr Ile Asp Arg Ala Gly Ile Lys Gly Arg Val Tyr Thr Asn
225   230   235   240
Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Ala Cys Val
                245   250   255
Leu Glu Tyr Ala Ser Pro Leu Gln Thr Leu Phe Ala Met Ser Gln Tyr
            260   265   270
Gly Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala Lys Leu
        275   280   285
Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu Ser Gln
    290   295   300
Asn Asn Cys Arg Leu Ile Val Tyr Glu Glu Pro Ala Asp Gly Ser Ser
305   310   315   320

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Phe Leu Leu Ser Gln Glu Val Leu Gln His Leu Arg Gln Glu Glu Glu
                325                 330                 335
Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Glu Val Pro Ser Thr
            340                 345                 350
Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met Glu Lys
        355                 360                 365
Pro Leu Pro Leu Arg Ser Asp Leu Phe
    370                 375


<210> 360
<211> 378
<212> PRT
<213> Bos taurus

<220>
<223> WT Cattle/Bovine STING

<400> 360
Met Pro His Ser Ser Leu His Pro Ser Ile Pro Gln Pro Arg Gly Leu
 1               5                  10                  15
Arg Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Ala
            20                  25                  30
Leu Trp Gly Leu Gly Glu Pro Pro Asp Tyr Thr Leu Lys Trp Leu Val
        35                  40                  45
Leu His Leu Ala Ser Gln Gln Met Gly Leu Leu Ile Lys Gly Ile Cys
    50                  55                  60
Ser Leu Ala Glu Glu Leu Cys His Val His Ser Arg Tyr His Gly Ser
65                  70                  75                  80
Tyr Trp Arg Ala Val Arg Ala Cys Leu Cys Ser Ser Met Arg Cys Gly
                85                  90                  95
Ala Leu Leu Leu Leu Ser Cys Tyr Phe Tyr Cys Ser Leu Pro Asn Met
            100                 105                 110
Ala Asp Leu Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
        115                 120                 125
Ala Leu Asn Ile Leu Leu Gly Leu Gln Gly Leu Ala Pro Ala Glu Val
    130                 135                 140
Ser Ala Ile Cys Glu Lys Arg Asn Phe Asn Val Ala His Gly Leu Ala
145                 150                 155                 160
Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Gly Leu Pro
                165                 170                 175
Ala Arg Ile Gln Ile Tyr Asn Gln Phe His Asn Asn Thr Leu Gln Gly
            180                 185                 190
Ala Gly Ser His Arg Leu His Ile Leu Phe Pro Leu Asp Cys Gly Val
        195                 200                 205
Pro Asp Asp Leu Asn Val Ala Asp Pro Asn Ile Arg Phe Leu His Glu
    210                 215                 220
Leu Pro Gln Gln Ser Ala Asp Arg Ala Gly Ile Lys Gly Arg Val Tyr
225                 230                 235                 240
Thr Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Val
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```
                245                 250                 255
Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
            260                 265                 270
Gln Asp Gly Arg Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
        275                 280                 285
Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asn Ala Pro Glu
    290                 295                 300
Ser Gln Asn Asn Cys Arg Leu Ile Val Tyr Gln Glu Pro Ala Glu Gly
305                 310                 315                 320
Ser Ser Phe Ser Leu Ser Gln Glu Ile Leu Gln His Leu Arg Gln Glu
                325                 330                 335
Glu Arg Glu Val Thr Met Gly Ser Thr Glu Thr Ser Val Met Pro Gly
            340                 345                 350
Ser Ser Val Leu Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Leu Glu
        355                 360                 365
Lys Pro Leu Pro Leu Arg Ser Asp Val Phe
    370                 375


<210> 361
<211> 375
<212> PRT
<213> Struthio camelus australis

<220>
<223> WT Ostrich STING

<400> 361
Met Ala His Glu Ser Gly Thr Pro Ser Asn Pro Ala Thr Pro Leu Ile
 1               5                  10                  15
Pro Lys Ala Arg Glu Gly Arg Ala Gln His Ala Ala Tyr Val Leu Leu
            20                  25                  30
Ala Leu Cys Ala Ala Ala Leu Tyr Leu Ala Gly Glu Pro Val Val His
        35                  40                  45
Ile Ala Arg Ser Phe Thr Ser His Phe Val Ala Leu Gln Ile Gly Ala
    50                  55                  60
Leu Leu Lys Gly Ile Cys Tyr Leu Val Glu Glu Ile Phe His Leu Glu
65                  70                  75                  80
Thr Arg His Arg Gly Ser Phe Arg Arg Ala Leu Ser Ala Cys Leu His
                85                  90                  95
Leu Arg Trp His Val Thr Leu Leu Leu Val Cys Gly Ser Ala Tyr Val
            100                 105                 110
Ala Leu Leu Asp Gly Asp Glu Gln Pro Leu Gly Leu His Leu Gly Leu
        115                 120                 125
Ala Cys Leu Cys Gln Leu Leu Ile Leu Ala Leu Gly Leu His Lys Pro
    130                 135                 140
Ser Ala Val Glu Ile Ser Glu Met Ser Glu Arg Ser Lys Gln Asn Val
145                 150                 155                 160
Ala His Gly Leu Ala Trp Ser Tyr Tyr Val Gly Tyr Leu Lys Ile Val
                165                 170                 175
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Leu Pro Arg Leu Lys Glu Ser Met Glu Asn Ile Gly Arg Thr Asn Pro
            180                 185                 190
Asn Met Leu Ala His Lys Glu Thr Trp Lys Leu His Ile Leu Val Pro
        195                 200                 205
Leu Ser Cys Asn Ile Cys Asp Asp Leu Glu Lys Ala Asp Ser Asn Ile
    210                 215                 220
Gln Tyr Ala Met Asp Leu Pro Glu Thr Thr Leu Thr Arg Ala Gly Thr
225                 230                 235                 240
Lys Lys Arg Val Tyr Arg Asn Thr Leu Tyr Lys Ile Lys Asp Glu Asp
                245                 250                 255
Lys Phe Arg Phe Cys Val Val Glu Tyr Ala Thr Pro Leu Gln Ser Leu
            260                 265                 270
Tyr Ala Met Ser Gln Asp Glu Cys Ala Ala Phe Ser Arg Glu Asp Arg
        275                 280                 285
Ile Glu Gln Ala Lys Leu Phe Tyr Arg Thr Leu Glu Glu Ile Leu Gln
    290                 295                 300
Ser Ala Lys Glu Cys Ala Gly Thr Tyr Arg Leu Ile Val Tyr Glu Glu
305                 310                 315                 320
Ser Gly Glu Ala Glu Thr His Phe Leu Ser Arg Glu Ile Leu Arg His
                325                 330                 335
Leu Gln Gln Gln Arg Gln Glu Glu Tyr Thr Val Cys Asp Gly Thr Leu
            340                 345                 350
Cys Ser Thr Asp Leu Ser Leu Gln Ile Ser Glu Ser Asp Leu Pro Gln
        355                 360                 365
Pro Leu Arg Ser Asp Cys Leu
    370                 375


<210> 362
<211> 382
<212> PRT
<213> Nipponia nippon

<220>
<223> WT Crested ibis STING

<400> 362
Met Ser Gln Glu Pro Gln Trp Leu Ser His Pro Thr Ala Leu Leu Ile
 1               5                  10                  15
Pro Lys Ala Arg Gly Gly Arg Ala Gln His Ala Val Tyr Leu Leu Leu
            20                  25                  30
Ala Leu Cys Ala Ala Val Leu Tyr Leu Ala Gly Glu Pro Leu Val Pro
        35                  40                  45
Ser Ala Arg Ser Leu Ile Ser His Phe Met Ala Leu Gln Ile Gly Val
    50                  55                  60
Leu Leu Lys Gly Thr Cys Tyr Leu Ala Glu Glu Ile Phe His Leu Gln
65                  70                  75                  80
Ser Arg His His Gly Ser Phe Trp Arg Ala Leu Ser Ala Cys Phe Pro
                85                  90                  95
Leu Arg Trp His Gly Leu Met Leu Leu Val Cys Gly Ser Ala Tyr Val
```

```
            100                 105                 110
Ala Leu Leu Glu Asp Gly Gln Pro Leu Gly Leu His Leu Gly Leu Ala
        115                 120                 125
Ser Leu Cys Gln Leu Leu Ile Leu Ala Leu Gly Leu His Lys Pro Ser
    130                 135                 140
Ala Val Glu Met Ser Glu Met Ser Glu Arg Ser Lys Gln Asn Val Ala
145                 150                 155                 160
His Gly Leu Ala Trp Ser Tyr Tyr Val Gly Tyr Leu Lys Ile Val Leu
                165                 170                 175
Pro Arg Val Lys Lys Ser Met Glu Glu Phe Ser Arg Ala Asn Pro Asn
            180                 185                 190
Val Leu Ala Arg Arg Glu Thr Trp Lys Leu His Ile Leu Val Pro Leu
        195                 200                 205
Ser Cys Asp Val Tyr Asp Asp Leu Glu Lys Ala Asp Ser Asn Ile Gln
    210                 215                 220
Tyr Leu Met Asp Leu Pro Glu Thr Thr Leu Thr Arg Ala Gly Thr Lys
225                 230                 235                 240
Lys Arg Val Tyr Lys His Ser Leu Tyr Thr Ile Arg Asp Glu Gly Asn
                245                 250                 255
Lys Leu Trp His Cys Ala Val Glu Tyr Ala Thr Pro Leu Gln Ser Leu
            260                 265                 270
Tyr Ala Met Ser Gln Asp Glu Tyr Ala Ala Phe Ser Arg Glu Asp Arg
        275                 280                 285
Leu Glu Gln Ala Lys Leu Phe Tyr Arg Thr Leu Glu Glu Ile Leu Lys
    290                 295                 300
Gly Ser Lys Glu Cys Ala Gly Thr Tyr Arg Leu Ile Val Tyr Glu Glu
305                 310                 315                 320
Ser Gly Glu Ala Glu Thr His Ser Leu Ser Arg Asp Ile Leu Trp His
                325                 330                 335
Leu Arg Gln Gln Cys His Glu Glu Tyr Thr Val Tyr Glu Gly Asn Gln
            340                 345                 350
Pro His Asn Pro Ser Thr Thr Leu His Ser Thr Glu Leu Asn Leu Gln
        355                 360                 365
Ile Ser Glu Ser Asp Leu Pro Gln Pro Leu Arg Ser Asp Cys
    370                 375                 380


<210> 363
<211> 380
<212> PRT
<213> Latimeria chalumnae

<220>
<223> WT Coelacanth STING
      (UniProtKB entry H3A3G4)

<400> 363
Phe Gly Leu Gln Asn Met Ser Ala Ile Ile Pro Gln Pro Arg Gly Asn
 1               5                  10                  15
Arg Ala Asn Gln Met Ala Tyr Phe Ile Ile Thr Val Ile Leu Met Leu
```

```
            20                  25                  30
Leu Trp Ile Phe Arg Asn Ile Met Asp Asn Val Leu Glu Val Ile Ala
        35                  40                  45
Leu His Ile Leu Leu Leu Gln Gly Ala Ala Ile Met Lys Gly Ile Cys
    50                  55                  60
Asn Phe Ala Glu Glu Val Asn His Val Gln Pro Arg Tyr Gly Gly Ser
65                  70                  75                  80
Tyr Trp Lys Ala Leu Glu Ala Cys Leu Asn Leu Ser Lys Tyr Asp Val
                85                  90                  95
Met Lys Ile Val Phe Ala Gly Val Leu Trp Trp His Phe Ser Ser Ser
            100                 105                 110
Leu Phe Val Val Trp Phe Leu His Leu Leu Val Ser Cys Leu Cys His
        115                 120                 125
Leu Leu Asn Asn Val Leu Gly Val Leu Lys Pro Ser Pro Val Glu Val
    130                 135                 140
Ser Glu Ile Tyr Glu Arg Asn Arg Ile Gly Val Ala His Gly Leu Ala
145                 150                 155                 160
Trp Ser Tyr Tyr Leu Gly Tyr Leu Lys Leu Val Leu Pro Glu Leu Glu
                165                 170                 175
Asp Arg Ile Lys Ser Tyr Asn Val Ser His Gly Asn Leu Leu Lys His
            180                 185                 190
Lys Glu Thr Trp Arg Leu His Ile Leu Leu Pro Leu Ser Cys Ser Ile
        195                 200                 205
Phe Asp Asn Leu Ala Asp Val Asp Ser Asn Ile Glu Phe Leu Asp Asn
    210                 215                 220
Leu Ser Glu Leu Gln Ile Asn Arg Ala Gly Ile Lys Gly Arg Ser Tyr
225                 230                 235                 240
Lys His Ser Leu Tyr Gln Val Leu Asp Glu Asp Lys Arg Pro His Tyr
                245                 250                 255
Cys Ile Leu Glu Tyr Ala Thr Pro Leu Lys Ser Leu Leu Glu Met Ser
            260                 265                 270
Lys Glu Ala Ser Ala Glu Phe Thr Lys Glu Asp Arg Leu Glu Gln Thr
        275                 280                 285
Lys Leu Phe Tyr Arg Thr Leu Lys Asp Ile Leu Asp Asn Ser Gln Glu
    290                 295                 300
Cys Arg Gly Arg Phe Arg Leu Val Ile Tyr Asp Gly Arg Glu Asp Ser
305                 310                 315                 320
Gly Lys Ser His Phe Leu Ser Lys Glu Leu Leu Arg His Leu Asn Gln
                325                 330                 335
Gln Gln Lys Glu Glu Tyr Phe Met Ser Glu Gln Thr Gln Pro Asn Ser
            340                 345                 350
Ser Ser Thr Ser Cys Leu Ser Thr Glu Pro Gln Leu Met Ile Ser Asp
        355                 360                 365
Thr Asp Ala Pro His Thr Leu Lys Arg Gln Val Cys
    370                 375                 380


<210> 364
<211> 405
<212> PRT
```

<213> Latimeria chalumnae

<220>
<223> WT Coelecanth STING
(Isoform X1; NCBI Accession No. XP_005989369.1)

<400> 364
Met Cys Phe Ile Gln Val Leu Asp Ile Thr Ile Ile Thr Gln Met Leu
 1   5   10   15
Gln Gly Glu Tyr Phe Gly Leu Gln Asn Met Ser Ala Ile Ile Pro Gln
            20   25   30
Pro Arg Gly Asn Arg Ala Asn Gln Met Ala Tyr Phe Ile Ile Thr Val
        35   40   45
Ile Leu Met Leu Leu Trp Ile Phe Arg Asn Ile Met Asp Asn Val Leu
    50   55   60
Glu Val Ile Ala Leu His Ile Leu Leu Leu Gln Gly Ala Ala Ile Met
65   70   75   80
Lys Gly Ile Cys Asn Phe Ala Glu Glu Val Asn His Val Gln Pro Arg
                85   90   95
Tyr Gly Gly Ser Tyr Trp Lys Ala Leu Glu Ala Cys Leu Asn Leu Ser
            100   105   110
Lys Tyr Asp Val Met Lys Ile Val Phe Ala Gly Val Leu Trp Trp His
        115   120   125
Phe Ser Ser Ser Leu Phe Val Val Trp Phe Leu His Leu Leu Val Ser
    130   135   140
Cys Leu Cys His Leu Leu Asn Asn Val Leu Gly Val Leu Lys Pro Ser
145   150   155   160
Pro Val Glu Val Ser Glu Ile Tyr Glu Arg Asn Arg Ile Gly Val Ala
                165   170   175
His Gly Leu Ala Trp Ser Tyr Tyr Leu Gly Tyr Leu Lys Leu Val Leu
            180   185   190
Pro Glu Leu Glu Asp Arg Ile Lys Ser Tyr Asn Val Ser His Gly Asn
        195   200   205
Leu Leu Lys His Lys Glu Thr Trp Arg Leu His Ile Leu Leu Pro Leu
    210   215   220
Ser Cys Ser Ile Phe Asp Asn Leu Ala Asp Val Asp Ser Asn Ile Glu
225   230   235   240
Phe Leu Asp Asn Leu Ser Glu Leu Gln Ile Asn Arg Ala Gly Ile Lys
                245   250   255
Gly Arg Ser Tyr Lys His Ser Leu Tyr Gln Val Leu Asp Glu Asp Lys
            260   265   270
Arg Pro His Tyr Cys Ile Leu Glu Tyr Ala Thr Pro Leu Lys Ser Leu
        275   280   285
Leu Glu Met Ser Lys Glu Ala Ser Ala Glu Phe Thr Lys Glu Asp Arg
    290   295   300
Leu Glu Gln Thr Lys Leu Phe Tyr Arg Thr Leu Lys Asp Ile Leu Asp
305   310   315   320
Asn Ser Gln Glu Cys Arg Gly Arg Phe Arg Leu Val Ile Tyr Asp Asp
                325   330   335
Cys Gln Asp Val Leu Asp Gly Glu Asp Ser Gly Lys Ser His Phe Leu

```
            340                 345                 350
Ser Lys Glu Leu Leu Arg His Leu Asn Gln Gln Gln Lys Glu Glu Tyr
        355                 360                 365
Phe Met Ser Glu Gln Thr Gln Pro Asn Ser Ser Ser Thr Ser Cys Leu
    370                 375                 380
Ser Thr Glu Pro Gln Leu Met Ile Ser Asp Thr Asp Ala Pro His Thr
385                 390                 395                 400
Leu Lys Ser Gly Phe
                405


<210> 365
<211> 378
<212> PRT
<213> Sus scrofa

<220>
<223> WT Boar STING

<400> 365
Met Pro Tyr Ser Ser Leu His Pro Ser Ile Pro Gln Pro Arg Gly Leu
 1               5                  10                  15
Arg Ala Gln Val Ala Ala Leu Val Leu Leu Gly Ala Cys Leu Val Ala
            20                  25                  30
Leu Trp Gly Leu Gly Glu Leu Pro Glu Tyr Thr Leu Arg Trp Leu Val
        35                  40                  45
Leu His Leu Ala Ser Gln Gln Ile Gly Leu Leu Val Lys Gly Leu Cys
    50                  55                  60
Ser Leu Ala Glu Glu Leu Cys His Val His Ser Arg Tyr Gln Ser Ser
65                  70                  75                  80
Tyr Trp Arg Ala Ala Arg Ala Cys Leu Gly Cys Pro Ile Arg Cys Gly
                85                  90                  95
Ala Leu Leu Leu Leu Ser Cys Tyr Phe Tyr Phe Ser Ile Arg Asp Lys
            100                 105                 110
Ala Gly Leu Pro Leu Pro Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
        115                 120                 125
Ala Leu Asn Ile Leu Leu Gly Leu Gln His Leu Ala Pro Ala Glu Val
    130                 135                 140
Ser Ala Ile Cys Glu Lys Arg Asn Phe Asn Val Ala His Gly Leu Ala
145                 150                 155                 160
Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Gly Leu Arg
                165                 170                 175
Ala Arg Ile Gln Ala Tyr Asn Gln Arg His Lys Asn Val Leu Gly Gly
            180                 185                 190
Ile Gly Asn His Arg Leu His Ile Leu Phe Pro Leu Asp Cys Gly Val
        195                 200                 205
Pro Asp Asp Leu Ser Val Ala Asp Pro Asn Ile Arg Phe Leu His Glu
    210                 215                 220
Leu Pro Gln Gln Ser Ala Asp Arg Ala Gly Ile Lys Gly Arg Val Tyr
225                 230                 235                 240
```

```
Thr Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Pro Ala Gly Val
                245                 250                 255
Cys Val Leu Gly Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
            260                 265                 270
Gln Asp Gly Arg Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
        275                 280                 285
Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
    290                 295                 300
Ala Gln Asn Asn Cys Arg Leu Ile Val Tyr Gln Glu Pro Thr Glu Gly
305                 310                 315                 320
Gly Ser Phe Ser Leu Ser Gln Glu Ile Leu Arg His Leu Arg Gln Glu
                325                 330                 335
Glu Arg Glu Val Thr Met Gly Ser Ala Glu Thr Ser Val Val Pro Thr
            340                 345                 350
Ser Ser Thr Leu Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met Glu
        355                 360                 365
Gln Pro Leu Pro Leu Arg Ser Asp Ile Phe
    370                 375


<210> 366
<211> 380
<212> PRT
<213> Rousettus aegyptiacus

<220>
<223> WT Bat STING

<400> 366
Met Ser His Ser Ser Leu His Pro Ser Val Pro Arg Pro Arg Gly Arg
 1               5                  10                  15
Arg Ala Arg Asn Ile Ala Ala Phe Val Leu Leu Ile Val Cys Leu Ala
            20                  25                  30
Ala Leu Trp Leu Ser Gly Lys Pro Ser Glu Tyr Thr Leu Arg Cys Leu
        35                  40                  45
Val Leu His Leu Ala Ser Gln Gln Leu Gly Leu Leu Ser Asn Arg Val
    50                  55                  60
Cys Tyr Leu Ala Glu Glu Leu Ser His Ile His Ser Arg Tyr Gln Gly
65                  70                  75                  80
Asn Tyr Trp Arg Ala Val Arg Ala Cys Leu Ser Cys Pro Ile Arg Phe
                85                  90                  95
Gly Val Val Leu Leu Val Ser Phe Phe Phe Tyr Thr Ser Leu Pro Asn
            100                 105                 110
Ile Asp Asp Leu Pro Leu Thr Trp Met Leu Ala His Leu Gly Leu Ser
        115                 120                 125
Glu Ala Leu Asn Ile Leu Leu Gly Leu Arg Gly Leu Thr Pro Ala Glu
    130                 135                 140
Val Ser Thr Val Cys Glu Gln Arg His Phe Asn Val Ala His Gly Leu
145                 150                 155                 160
Ala Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Gly Leu
```

```
                165                 170                 175
Arg Ala Arg Ile His Thr Tyr Asn Gln Leu His Gly Asn Thr Leu Gln
            180                 185                 190
Gly Val Gly Ser His Arg Leu Tyr Ile Leu Phe Pro Leu Asp Cys Gly
        195                 200                 205
Val Leu Asp Asp Leu Ser Ala Ala Asp Pro Asn Ile Arg Phe Leu Arg
    210                 215                 220
Glu Leu Pro Arg Gln Ser Ser Asp Arg Ala Gly Ile Lys Asn Arg Val
225                 230                 235                 240
Tyr Thr Asn Ser Val Tyr Glu Leu Leu Glu Lys Gly Lys Pro Val Gly
                245                 250                 255
Thr Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met
            260                 265                 270
Ser Gln Asp Ala Arg Ala Gly Phe Ser Gln Glu Asp Arg Leu Glu Gln
        275                 280                 285
Ala Lys Leu Phe Cys Arg Thr Leu Ala Asp Ile Leu Ala Asp Asp Pro
    290                 295                 300
Glu Ser Gln Lys Ser Cys Arg Leu Ile Val Tyr Gln Glu Pro Thr Glu
305                 310                 315                 320
Glu Ser Asp Phe Ser Leu Ser Gln Ala Ile Leu Lys His Leu Arg Gln
                325                 330                 335
Glu Glu Lys Glu Glu Val Thr Val Gly Thr Val Gly Thr Tyr Glu Ala
            340                 345                 350
Pro Gly Ser Ser Thr Leu His Gln Glu Pro Glu Leu Leu Ile Ser Gly
        355                 360                 365
Met Asp Gln Pro Leu Pro Leu Arg Thr Asp Ile Phe
    370                 375                 380


<210> 367
<211> 387
<212> PRT
<213> Trichechus manatus latirostris

<220>
<223> WT Manatee STING

<400> 367
Met Val Glu Met Pro His Ser Ser Leu His Pro Ser Ile Pro Arg His
 1               5                  10                  15
Arg Gly His Gly Ile Gln Lys Ala Ala Phe Val Leu Leu Val Ala Cys
            20                  25                  30
Leu Val Ala Leu Trp Glu Leu Gly Glu Pro Pro Gly His Thr Leu Gln
        35                  40                  45
Trp Leu Val Cys Gln Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Lys
    50                  55                  60
Val Ile Cys Ser Leu Ala Glu Glu Leu Cys His Val His Ser Arg Tyr
65                  70                  75                  80
Gln Ser Ser Tyr Trp Arg Ala Val Arg Ala Cys Met Gly Cys Pro Ile
                85                  90                  95
```

```
Arg Arg Gly Ala Leu Leu Leu Leu Ser Cys Tyr Phe Tyr Phe Cys Phe
            100                 105                 110
Pro Asn Met Ala Asp Leu Pro Leu Thr Trp Thr Leu Ala Leu Leu Gly
        115                 120                 125
Leu Leu Gln Ala Met Asn Ile Leu Leu Ser Leu Gln Gly Leu Thr Pro
    130                 135                 140
Ala Glu Ile Ser Ala Ile Cys Glu Lys Arg Asn Leu Asn Val Ala His
145                 150                 155                 160
Gly Leu Ala Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro
                165                 170                 175
Gly Leu Gln Asp Arg Ile Arg Ile Tyr Asn Leu Gln His Asn Asn Met
            180                 185                 190
Leu Arg Gly Thr Gly Ser Gln Arg Leu His Ile Leu Phe Pro Leu Asp
        195                 200                 205
Cys Gly Val Pro Asn Asp Leu Ser Val Ala Asp Ala Asn Ile Arg Phe
    210                 215                 220
Leu Gln Lys Leu Pro Gln Gln Ser Ala Asp Cys Ala Gly Ile Lys Gly
225                 230                 235                 240
Arg Val Tyr Thr Asn Ser Val Tyr Gln Leu Leu Glu His Gly Gln Pro
                245                 250                 255
Ala Gly Ile Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe
            260                 265                 270
Ala Met Ser Gln Asp Gly Arg Ala Gly Phe Ser Arg Glu Asp Arg Leu
        275                 280                 285
Glu Gln Ala Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp
    290                 295                 300
Ala Pro Glu Tyr Gln Asn Asn Cys Arg Leu Ile Val Tyr Gln Glu Ser
305                 310                 315                 320
Ala Glu Gly Ser Ser Phe Ser Leu Ser Gln Glu Ile Leu Arg His Leu
                325                 330                 335
Arg Gln Glu Glu Arg Glu Glu Val Thr Val Gly Ser Val Gly Thr Ser
            340                 345                 350
Val Val Pro Ser Pro Ser Ser Pro Ser Thr Ser Ser Leu Ser Gln Glu
        355                 360                 365
Pro Lys Leu Leu Ile Ser Gly Met Glu Gln Pro Leu Pro Leu Arg Thr
    370                 375                 380
Asp Val Phe
385
```

<210> 368
<211> 378
<212> PRT
<213> Callorhinchus milii

<220>
<223> WT Ghost shark STING

<400> 368
Met Ser Asp Ser Ile Pro Arg Pro Arg Gly Lys Val Ala Thr Tyr Val

```
 1               5                  10                  15
Gly Leu Ile Leu Met Ser Gly Leu Ala Cys Leu Tyr Phe Met Leu Thr
            20                  25                  30
Pro Asp Tyr His Ile Lys Phe Ile Val Gln Gln Val Ala Gln Gln Leu
        35                  40                  45
Ile Val Ser Phe Phe Ala Leu Cys Leu Leu Arg Leu Cys Glu Phe Val
    50                  55                  60
Glu Glu Leu Gly His Lys Gln Thr Arg Tyr Gln Asn Ser Trp Val Arg
65                  70                  75                  80
Ala Leu Asn Ala Ser Leu Asp Trp Lys Lys Tyr Gly Phe Cys Leu Leu
                85                  90                  95
Ile Ser Leu Leu Phe Asn Trp Val Leu Pro Tyr Glu Lys His Met Ser
            100                 105                 110
Tyr Ala Val Pro Thr Val Gly Gln Thr Ile Ser Leu Thr Cys Phe Cys
        115                 120                 125
Val Leu Phe Leu Lys Val Phe Gln Leu Asp Val Leu Ser Pro Ala Gln
    130                 135                 140
Ile Ser Glu Ile Ser Glu Thr Asn Lys Cys Asn Val Ala His Gly Leu
145                 150                 155                 160
Ala Trp Ser Tyr Tyr Leu Gly Tyr Leu Lys Ile Val Leu Pro Lys Leu
                165                 170                 175
Glu Glu Lys Ile Asn Gln Tyr His Arg Glu Tyr Gly Asn Val Leu Gln
            180                 185                 190
Gln Lys Gly Lys Lys Leu Tyr Ile Leu Ile Pro Phe Ser Cys Lys Val
        195                 200                 205
Leu Asp Lys Leu Glu Lys Val Asp Thr Asn Ile Val Phe Tyr Gln Asn
    210                 215                 220
Leu Pro Glu Leu Leu Val Asp Arg Ala Gly Ile Lys Ser Arg Ser Tyr
225                 230                 235                 240
Lys His Ser Ile Tyr Leu Ile Tyr Asp Gln Lys Lys Gln Gln Pro His
                245                 250                 255
His Cys Ile Leu Glu Tyr Ala Thr Pro Leu Arg Ser Leu Phe Glu Met
            260                 265                 270
Thr Asn Asp Ser Ala Ala Ala Phe Ser Lys Glu Gln Arg Leu Asp Gln
        275                 280                 285
Ala Lys Leu Phe Tyr Arg Thr Leu Lys Ser Ile Leu Asn Asn Val Pro
    290                 295                 300
Glu Val Thr Gly Ser Tyr Arg Leu Ile Pro Tyr Asp Asp Asp Leu Glu
305                 310                 315                 320
Gly Ala Glu Leu Gly Pro His Phe Val Ser Glu Glu Ile Leu Lys His
                325                 330                 335
Met Arg Gln Glu Leu Thr Glu Tyr Pro Val Ala Glu Pro Ser Asn Ala
            340                 345                 350
Asn Glu Thr Asp Cys Met Ser Ser Glu Pro His Leu Met Ile Ser Asp
        355                 360                 365
Asp Pro Lys Pro Leu Arg Ser Tyr Cys Pro
    370                 375
```

<210> 369

<211> 378
<212> PRT
<213> Mus musculus

<220>
<223> WT Mouse STING

<400> 369
Met Pro Tyr Ser Asn Leu His Pro Ala Ile Pro Arg Pro Arg Gly His
 1   5   10   15
Arg Ser Lys Tyr Val Ala Leu Ile Phe Leu Val Ala Ser Leu Met Ile
            20   25   30
Leu Trp Val Ala Lys Asp Pro Pro Asn His Thr Leu Lys Tyr Leu Ala
        35   40   45
Leu His Leu Ala Ser His Glu Leu Gly Leu Leu Leu Lys Asn Leu Cys
    50   55   60
Cys Leu Ala Glu Glu Leu Cys His Val Gln Ser Arg Tyr Gln Gly Ser
65   70   75   80
Tyr Trp Lys Ala Val Arg Ala Cys Leu Gly Cys Pro Ile His Cys Met
                85   90   95
Ala Met Ile Leu Leu Ser Ser Tyr Phe Tyr Phe Leu Gln Asn Thr Ala
            100   105   110
Asp Ile Tyr Leu Ser Trp Met Phe Gly Leu Leu Val Leu Tyr Lys Ser
        115   120   125
Leu Ser Met Leu Leu Gly Leu Gln Ser Leu Thr Pro Ala Glu Val Ser
    130   135   140
Ala Val Cys Glu Glu Lys Lys Leu Asn Val Ala His Gly Leu Ala Trp
145   150   155   160
Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Gly Leu Gln Ala
                165   170   175
Arg Ile Arg Met Phe Asn Gln Leu His Asn Asn Met Leu Ser Gly Ala
            180   185   190
Gly Ser Arg Arg Leu Tyr Ile Leu Phe Pro Leu Asp Cys Gly Val Pro
        195   200   205
Asp Asn Leu Ser Val Val Asp Pro Asn Ile Arg Phe Arg Asp Met Leu
    210   215   220
Pro Gln Gln Asn Ile Asp Arg Ala Gly Ile Lys Asn Arg Val Tyr Ser
225   230   235   240
Asn Ser Val Tyr Glu Ile Leu Glu Asn Gly Gln Pro Ala Gly Val Cys
                245   250   255
Ile Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser Gln
            260   265   270
Asp Ala Lys Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala Lys
        275   280   285
Leu Phe Cys Arg Thr Leu Glu Glu Ile Leu Glu Asp Val Pro Glu Ser
    290   295   300
Arg Asn Asn Cys Arg Leu Ile Val Tyr Gln Glu Pro Thr Asp Gly Asn
305   310   315   320
Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Ile Arg Gln Glu Glu
                325   330   335

```
Lys Glu Glu Val Thr Met Asn Ala Pro Met Thr Ser Val Ala Pro Pro
            340                 345                 350
Pro Ser Val Leu Ser Gln Glu Pro Arg Leu Leu Ile Ser Gly Met Asp
        355                 360                 365
Gln Pro Leu Pro Leu Arg Thr Asp Leu Ile
    370                 375
```

<210> 370
<211> 43
<212> PRT
<213> Homo sapiens

<220>
<223> Human STING C-terminal tail (CTT)

<400> 370
```
Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
 1               5                  10                  15
Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
            20                  25                  30
Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
        35                  40
```

<210> 371
<211> 43
<212> PRT
<213> Sarcophilus harrisii

<220>
<223> Tasmanian devil STING C-terminal tail (CTT)

<400> 371
```
Arg Gln Glu Glu Phe Ala Ile Gly Pro Lys Arg Ala Met Thr Val Thr
 1               5                  10                  15
Thr Ser Ser Thr Leu Ser Gln Glu Pro Gln Leu Leu Ile Ser Gly Met
            20                  25                  30
Glu Gln Pro Leu Ser Leu Arg Thr Asp Gly Phe
        35                  40
```

<210> 372
<211> 43
<212> PRT
<213> Callithrix jacchus

<220>
<223> Marmoset STING C-terminal tail (CTT)

<400> 372
Glu Glu Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Glu Val Pro
 1   5   10   15
Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
            20   25   30
Glu Lys Pro Leu Pro Leu Arg Ser Asp Leu Phe
        35   40

<210> 373
<211> 42
<212> PRT
<213> Bos taurus

<220>
<223> Cattle/Bovine STING C-terminal tail (CTT)

<400> 373
Glu Arg Glu Val Thr Met Gly Ser Thr Glu Thr Ser Val Met Pro Gly
 1   5   10   15
Ser Ser Val Leu Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Leu Glu
            20   25   30
Lys Pro Leu Pro Leu Arg Ser Asp Val Phe
        35   40

<210> 374
<211> 42
<212> PRT
<213> Felis catus

<220>
<223> Cat STING C-terminal tail (CTT)

<400> 374
Glu Arg Glu Val Thr Val Gly Ser Val Gly Thr Ser Met Val Arg Asn
 1   5   10   15
Pro Ser Val Leu Ser Gln Glu Pro Asn Leu Leu Ile Ser Gly Met Glu
            20   25   30
Gln Pro Leu Pro Leu Arg Thr Asp Val Phe
        35   40

<210> 375
<211> 35
<212> PRT
<213> Struthio camelus australis

<220>
<223> Ostrich STING C-terminal tail (CTT)

<400> 375
Arg Gln Glu Glu Tyr Thr Val Cys Asp Gly Thr Leu Cys Ser Thr Asp
 1   5   10   15
Leu Ser Leu Gln Ile Ser Glu Ser Asp Leu Pro Gln Pro Leu Arg Ser
            20   25   30
Asp Cys Leu
        35

<210> 376
<211> 42
<212> PRT
<213> Sus scrofa

<220>
<223> Boar STING C-terminal tail (CTT)

<400> 376
Glu Arg Glu Val Thr Met Gly Ser Ala Glu Thr Ser Val Val Pro Thr
 1   5   10   15
Ser Ser Thr Leu Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met Glu
            20   25   30
Gln Pro Leu Pro Leu Arg Ser Asp Ile Phe
        35   40

<210> 377
<211> 43
<212> PRT
<213> Rousettus aegyptiacus

<220>
<223> Bat STING C-terminal tail (CTT)

<400> 377
Glu Lys Glu Glu Val Thr Val Gly Thr Val Gly Thr Tyr Glu Ala Pro
 1   5   10   15
Gly Ser Ser Thr Leu His Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
            20   25   30
Asp Gln Pro Leu Pro Leu Arg Thr Asp Ile Phe
        35   40

<210> 378
<211> 48
<212> PRT
<213> Trichechus manatus latirostris

<220>

<223> Manatee STING C-terminal tail (CTT)

<400> 378
Glu Arg Glu Glu Val Thr Val Gly Ser Val Gly Thr Ser Val Val Pro
 1   5   10   15
Ser Pro Ser Ser Pro Ser Thr Ser Ser Leu Ser Gln Glu Pro Lys Leu
            20   25   30
Leu Ile Ser Gly Met Glu Gln Pro Leu Pro Leu Arg Thr Asp Val Phe
        35   40   45

<210> 379
<211> 43
<212> PRT
<213> Nipponia nippon

<220>
<223> Crested ibis STING C-terminal tail (CTT)

<400> 379
Cys His Glu Glu Tyr Thr Val Tyr Glu Gly Asn Gln Pro His Asn Pro
 1   5   10   15
Ser Thr Thr Leu His Ser Thr Glu Leu Asn Leu Gln Ile Ser Glu Ser
            20   25   30
Asp Leu Pro Gln Pro Leu Arg Ser Asp Cys Phe
        35   40

<210> 380
<211> 43
<212> PRT
<213> Latimeria chalumnae

<220>
<223> Coelacanth STING (SEQ ID NO:363) C-terminal tail
      (CTT)

<400> 380
Gln Lys Glu Glu Tyr Phe Met Ser Glu Gln Thr Gln Pro Asn Ser Ser
 1   5   10   15
Ser Thr Ser Cys Leu Ser Thr Glu Pro Gln Leu Met Ile Ser Asp Thr
            20   25   30
Asp Ala Pro His Thr Leu Lys Arg Gln Val Cys
        35   40

<210> 381
<211> 42
<212> PRT
<213> Latimeria chalumnae

<220>
<223> Coelacanth STING (SEQ ID NO:364) C-terminal tail
(CTT)

<400> 381
Gln Lys Glu Glu Tyr Phe Met Ser Glu Gln Thr Gln Pro Asn Ser Ser
 1   5   10   15
Ser Thr Ser Cys Leu Ser Thr Glu Pro Gln Leu Met Ile Ser Asp Thr
            20   25   30
Asp Ala Pro His Thr Leu Lys Ser Gly Phe
        35   40

<210> 382
<211> 71
<212> PRT
<213> Danio rerio

<220>
<223> Zebrafish STING C-terminal tail (CTT)

<400> 382
Asp Gly Glu Ile Phe Met Asp Pro Thr Asn Glu Val His Pro Val Pro
 1   5   10   15
Glu Glu Gly Pro Val Gly Asn Cys Asn Gly Ala Leu Gln Ala Thr Phe
            20   25   30
His Glu Glu Pro Met Ser Asp Glu Pro Thr Leu Met Phe Ser Arg Pro
        35   40   45
Gln Ser Leu Arg Ser Glu Pro Val Glu Thr Thr Asp Tyr Phe Asn Pro
    50   55   60
Ser Ser Ala Met Lys Gln Asn
65   70

<210> 383
<211> 38
<212> PRT
<213> Callorhinchus milii

<220>
<223> Ghost shark STING C-terminal tail (CTT)

<400> 383
Leu Thr Glu Tyr Pro Val Ala Glu Pro Ser Asn Ala Asn Glu Thr Asp
 1   5   10   15
Cys Met Ser Ser Glu Pro His Leu Met Ile Ser Asp Asp Pro Lys Pro
            20   25   30
Leu Arg Ser Tyr Cys Pro
        35

<210> 384
<211> 43
<212> PRT
<213> Mus musculus

<220>
<223> Mouse STING C-terminal tail (CTT)

<400> 384
Glu Lys Glu Glu Val Thr Met Asn Ala Pro Met Thr Ser Val Ala Pro
 1   5   10   15
Pro Pro Ser Val Leu Ser Gln Glu Pro Arg Leu Leu Ile Ser Gly Met
            20   25   30
Asp Gln Pro Leu Pro Leu Arg Thr Asp Leu Ile
        35   40

<210> 385
<211> 78
<212> PRT
<213> Salmonella typhimurium

<220>
<223> LppA (strain LT2/ ATCC 700720)

<400> 385
Met Asn Arg Thr Lys Leu Val Leu Gly Ala Val Ile Leu Gly Ser Thr
 1   5   10   15
Leu Leu Ala Gly Cys Ser Ser Asn Ala Lys Ile Asp Gln Leu Ser Ser
            20   25   30
Asp Val Gln Thr Leu Asn Ala Lys Val Asp Gln Leu Ser Asn Asp Val
        35   40   45
Asn Ala Met Arg Ser Asp Val Gln Ala Ala Lys Asp Asp Ala Ala Arg
    50   55   60
Ala Asn Gln Arg Leu Asp Asn Gln Ala Thr Lys Tyr Arg Lys
65   70   75

<210> 386
<211> 79
<212> PRT
<213> Salmonella typhimurium

<220>
<223> LppB (strain LT2/ ATCC 700720)

<400> 386
Met Asn Arg Thr Asn Gln Leu Ile Leu Gly Ala Val Val Leu Gly Ser

```
 1               5                  10                  15
Thr Leu Leu Ala Gly Cys Ser Ser Asn Ala Lys Ile Asp Gln Leu Ser
            20                  25                  30
Ser Asp Val Gln Thr Leu Ser Ala Lys Val Glu Gln Leu Ser Asn Asp
        35                  40                  45
Val Asn Ala Met Arg Ser Asp Val Gln Ala Ala Lys Asp Asp Ala Ala
    50                  55                  60
Arg Ala Asn Gln Arg Leu Asp Asn Lys Val Phe Arg Ile Cys Lys
65                  70                  75
```

<210> 387
<211> 237
<212> DNA
<213> Salmonella typhimurium

<220>
<223> lppA

<400> 387
ttacttacgg tatttagtag cctggttgtc cagacgctgg ttagcgcgag ctgcgtcgtc 60
tttagcagcc tgaacgtcgg aacgcattgc gttcacgtcg ttgctcagct ggtcaacttt 120
agcgttcaga gtctgaacgt cagaagacag ctgatcgatt ttagcgttgc tggagcaacc 180
agccagcaga gtagaaccca ggattaccgc gcccagtacc agtttagtac gattcat 237

<210> 388
<211> 240
<212> DNA
<213> Salmonella typhimurium

<220>
<223> lppB

<400> 388
ttatttacag atgcggaata ctttgttgtc cagacgttgg ttcgcgcgag cagcatcgtc 60
tttagcagcc tgaacgtcgg aacgcattgc atttacgtca ttactcagtt gctcaacttt 120
agcgctcagc gtctgtacat cggaagacaa ctgatcgatt ttagcgttgc ttgaacaacc 180
tgccagtaac gtggaaccca gaactactgc acctaagatc agctggttag tacggttcat 240

<210> 389
<211> 254
<212> PRT
<213> Homo sapiens

<220>
<223> Human 4-1BBL, full-length

<220>
<221> DOMAIN
<222> (1)...(28)
<223> Cytoplasmic domain

<220>
<221> DOMAIN
<222> (29)...(49)
<223> Transmembrane domain

<220>
<221> DOMAIN
<222> (50)...(254)
<223> Extracellular domain

<400> 389
```
Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro
 1               5                  10                  15
Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val
            20                  25                  30
Ala Gly Leu Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe
        35                  40                  45
Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser
    50                  55                  60
Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp
65                  70                  75                  80
Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val
                85                  90                  95
Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp
            100                 105                 110
Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu
        115                 120                 125
Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe
    130                 135                 140
Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser
145                 150                 155                 160
Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala
                165                 170                 175
Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala
            180                 185                 190
Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala
        195                 200                 205
Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His
    210                 215                 220
Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val
225                 230                 235                 240
Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
                245                 250
```

<210> 390
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Human 4-1BBL with deleted cytoplasmic domain

<400> 390
Met Trp Ala Leu Val Ala Gly Leu Leu Leu Leu Leu Leu Ala Ala
 1   5   10   15
Ala Cys Ala Val Phe Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg
            20   25   30
Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu
        35   40   45
Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met
    50   55   60
Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu
65   70   75   80
Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly
                85   90   95
Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly
            100   105   110
Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly
        115   120   125
Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg
    130   135   140
Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro
145   150   155   160
Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu
                165   170   175
Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu
            180   185   190
Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu
        195   200   205
Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro
    210   215   220
Arg Ser Glu
225

<210> 391
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> Human 4-1BBL with truncated cytoplasmic domain

<400> 391

```
Met Arg Val Leu Pro Trp Ala Leu Val Ala Gly Leu Leu Leu Leu Leu
 1               5                  10                  15
Leu Leu Ala Ala Ala Cys Ala Val Phe Leu Ala Cys Pro Trp Ala Val
            20                  25                  30
Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg
        35                  40                  45
Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu
    50                  55                  60
Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile
65                  70                  75                  80
Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser
                85                  90                  95
Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val
            100                 105                 110
Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg
        115                 120                 125
Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu
    130                 135                 140
Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val
145                 150                 155                 160
Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe
                165                 170                 175
Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His
            180                 185                 190
Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly
        195                 200                 205
Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly
    210                 215                 220
Leu Pro Ser Pro Arg Ser Glu
225                 230


<210> 392
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> Human 4-1BBL with truncated cytoplasmic domain and
      Myc tag

<220>
<221> misc_feature
<222> (2)...(11)
<223> Myc tag

<220>
<221> misc_feature
<222> (12)...(15)
<223> Truncated cytoplasmic domain
```

<220>
<221> DOMAIN
<222> (16)...(36)
<223> Transmembrane domain

<220>
<221> DOMAIN
<222> (37)...(241)
<223> Extracellular domain

<400> 392
Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Arg Val Leu Pro Trp
 1   5   10   15
Ala Leu Val Ala Gly Leu Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys
            20   25   30
Ala Val Phe Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser
        35   40   45
Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser
    50   55   60
Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala
65   70   75   80
Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp
                85   90   95
Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser
            100   105   110
Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr
        115   120   125
Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly
    130   135   140
Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala
145   150   155   160
Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser
                165   170   175
Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His
            180   185   190
Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg
        195   200   205
Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu
    210   215   220
Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser
225   230   235   240
Glu

<210> 393
<211> 309
<212> PRT
<213> Mus musculus

<220>
<223> Mouse 4-1BBL, full-length

<220>
<221> DOMAIN
<222> (1)...(82)
<223> Cytoplasmic domain

<220>
<221> DOMAIN
<222> (83)...(103)
<223> transmembrane domain

<220>
<221> DOMAIN
<222> (104)...(309)
<223> extracellular domain

<400> 393
```
Met Asp Gln His Thr Leu Asp Val Glu Asp Thr Ala Asp Ala Arg His
 1               5                  10                  15
Pro Ala Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr
            20                  25                  30
Gly Leu Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr
        35                  40                  45
Asn Ala Ala Leu Pro Thr Asp Ala Ala Tyr Pro Ala Val Asn Val Arg
    50                  55                  60
Asp Arg Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His
65                  70                  75                  80
Pro Lys Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Leu Ile Ala
                85                  90                  95
Ala Cys Val Pro Ile Phe Thr Arg Thr Glu Pro Arg Pro Ala Leu Thr
            100                 105                 110
Ile Thr Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn Asn Ala Asp Gln
        115                 120                 125
Val Thr Pro Val Ser His Ile Gly Cys Pro Asn Thr Thr Gln Gln Gly
    130                 135                 140
Ser Pro Val Phe Ala Lys Leu Leu Ala Lys Asn Gln Ala Ser Leu Cys
145                 150                 155                 160
Asn Thr Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser Tyr
                165                 170                 175
Leu Ser Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys Glu Leu Val Val
            180                 185                 190
Asp Ser Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro
        195                 200                 205
Thr Phe Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val
    210                 215                 220
Leu Gln Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr
225                 230                 235                 240
```

```
Val Glu Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser
                245                 250                 255
Trp Ser Gln Leu Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly
            260                 265                 270
Leu Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu
        275                 280                 285
Leu Ser Tyr Pro Asn Thr Thr Ser Phe Gly Leu Phe Leu Val Lys Pro
    290                 295                 300
Asp Asn Pro Trp Glu
305


<210> 394
<211> 228
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse 4-1BBL with deleted cytoplasmic domain

<400> 394
Met Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Leu Ile Ala Ala
 1               5                  10                  15
Cys Val Pro Ile Phe Thr Arg Thr Glu Pro Arg Pro Ala Leu Thr Ile
            20                  25                  30
Thr Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn Asn Ala Asp Gln Val
        35                  40                  45
Thr Pro Val Ser His Ile Gly Cys Pro Asn Thr Thr Gln Gln Gly Ser
    50                  55                  60
Pro Val Phe Ala Lys Leu Leu Ala Lys Asn Gln Ala Ser Leu Cys Asn
65                  70                  75                  80
Thr Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser Tyr Leu
                85                  90                  95
Ser Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys Glu Leu Val Val Asp
            100                 105                 110
Ser Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro Thr
        115                 120                 125
Phe Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val Leu
    130                 135                 140
Gln Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr Val
145                 150                 155                 160
Glu Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser Trp
                165                 170                 175
Ser Gln Leu Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly Leu
            180                 185                 190
Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu Leu
        195                 200                 205
Ser Tyr Pro Asn Thr Thr Ser Phe Gly Leu Phe Leu Val Lys Pro Asp
    210                 215                 220
Asn Pro Trp Glu
```

225

<210> 395
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse 4-1BBL with truncated cytoplasmic domain

<400> 395
Met Ser Arg His Pro Lys Leu Tyr Gly Leu Val Ala Leu Val Leu Leu
 1   5   10   15
Leu Leu Ile Ala Ala Cys Val Pro Ile Phe Thr Arg Thr Glu Pro Arg
            20   25   30
Pro Ala Leu Thr Ile Thr Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn
        35   40   45
Asn Ala Asp Gln Val Thr Pro Val Ser His Ile Gly Cys Pro Asn Thr
    50   55   60
Thr Gln Gln Gly Ser Pro Val Phe Ala Lys Leu Leu Ala Lys Asn Gln
65   70   75   80
Ala Ser Leu Cys Asn Thr Thr Leu Asn Trp His Ser Gln Asp Gly Ala
                85   90   95
Gly Ser Ser Tyr Leu Ser Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys
            100   105   110
Glu Leu Val Val Asp Ser Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu
        115   120   125
Lys Leu Ser Pro Thr Phe Thr Asn Thr Gly His Lys Val Gln Gly Trp
    130   135   140
Val Ser Leu Val Leu Gln Ala Lys Pro Gln Val Asp Asp Phe Asp Asn
145   150   155   160
Leu Ala Leu Thr Val Glu Leu Phe Pro Cys Ser Met Glu Asn Lys Leu
                165   170   175
Val Asp Arg Ser Trp Ser Gln Leu Leu Leu Leu Lys Ala Gly His Arg
            180   185   190
Leu Ser Val Gly Leu Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr
        195   200   205
Arg Asp Trp Glu Leu Ser Tyr Pro Asn Thr Thr Ser Phe Gly Leu Phe
    210   215   220
Leu Val Lys Pro Asp Asn Pro Trp Glu
225   230

<210> 396
<211> 243
<212> PRT
<213> Artificial Sequence

<220>

<223> Mouse 4-1BBL with truncated cytoplasmic domain and
Myc tag

<220>
<221> misc_feature
<222> (2)...(11)
<223> Myc tag

<220>
<221> misc_feature
<222> (12)...(16)
<223> Truncated cytoplasmic domain

<220>
<221> DOMAIN
<222> (17)...(37)
<223> Transmembrane domain

<220>
<221> DOMAIN
<222> (38)...(243)
<223> Extracellular domain

<400> 396

```
Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Ser Arg His Pro Lys
 1               5                  10                  15
Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Leu Ile Ala Ala Cys
            20                  25                  30
Val Pro Ile Phe Thr Arg Thr Glu Pro Arg Pro Ala Leu Thr Ile Thr
        35                  40                  45
Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn Asn Ala Asp Gln Val Thr
    50                  55                  60
Pro Val Ser His Ile Gly Cys Pro Asn Thr Thr Gln Gln Gly Ser Pro
65                  70                  75                  80
Val Phe Ala Lys Leu Leu Ala Lys Asn Gln Ala Ser Leu Cys Asn Thr
                85                  90                  95
Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser Tyr Leu Ser
            100                 105                 110
Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys Glu Leu Val Val Asp Ser
        115                 120                 125
Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro Thr Phe
    130                 135                 140
Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val Leu Gln
145                 150                 155                 160
Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr Val Glu
                165                 170                 175
Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser Trp Ser
            180                 185                 190
Gln Leu Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly Leu Arg
        195                 200                 205
```

```
Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu Leu Ser
    210                 215                 220
Tyr Pro Asn Thr Thr Ser Phe Gly Leu Phe Leu Val Lys Pro Asp Asn
225                 230                 235                 240
Pro Trp Glu


<210> 397
<211> 379
<212> PRT
<213> Artificial Sequence

<220>
<223> huSTING N154S/R284G tazCTT

<220>
<221> misc_feature
<222> (1)...(336)
<223> huSTING (R232 allelle) with N154S/R284G
      modifications, and without human STING CTT

<220>
<221> misc_feature
<222> (337)...(379)
<223> Tasmanian devil STING CTT

<400> 397
Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 1               5                  10                  15
Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
            20                  25                  30
Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
        35                  40                  45
Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
    50                  55                  60
Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65                  70                  75                  80
Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
                85                  90                  95
Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
            100                 105                 110
Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
        115                 120                 125
Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
    130                 135                 140
Ser Ala Val Cys Glu Lys Gly Asn Phe Ser Val Ala His Gly Leu Ala
145                 150                 155                 160
Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
                165                 170                 175
Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
```

```
            180                 185                 190
Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
        195                 200                 205
Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
    210                 215                 220
Leu Pro Gln Gln Thr Gly Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr
225                 230                 235                 240
Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
                245                 250                 255
Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
            260                 265                 270
Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Gly Leu Glu Gln Ala
        275                 280                 285
Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
    290                 295                 300
Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305                 310                 315                 320
Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
                325                 330                 335
Arg Gln Glu Glu Phe Ala Ile Gly Pro Lys Arg Ala Met Thr Val Thr
            340                 345                 350
Thr Ser Ser Thr Leu Ser Gln Glu Pro Gln Leu Leu Ile Ser Gly Met
        355                 360                 365
Glu Gln Pro Leu Ser Leu Arg Thr Asp Gly Phe
    370                 375


<210> 398
<211> 379
<212> PRT
<213> Artificial Sequence

<220>
<223> huSTING N154S/R284G

<400> 398
Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 1               5                  10                  15
Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
            20                  25                  30
Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
        35                  40                  45
Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
    50                  55                  60
Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65                  70                  75                  80
Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
                85                  90                  95
Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
            100                 105                 110
```

```
Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
        115                 120                 125
Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
    130                 135                 140
Ser Ala Val Cys Glu Lys Gly Asn Phe Ser Val Ala His Gly Leu Ala
145                 150                 155                 160
Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
                165                 170                 175
Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
            180                 185                 190
Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
        195                 200                 205
Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
    210                 215                 220
Leu Pro Gln Gln Thr Gly Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr
225                 230                 235                 240
Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
                245                 250                 255
Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
            260                 265                 270
Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Gly Leu Glu Gln Ala
        275                 280                 285
Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
    290                 295                 300
Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
305                 310                 315                 320
Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
                325                 330                 335
Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
            340                 345                 350
Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met
        355                 360                 365
Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
    370                 375


<210> 399
<211> 378
<212> PRT
<213> Artificial Sequence

<220>
<223> muSTING C205Y

<400> 399
Met Pro Tyr Ser Asn Leu His Pro Ala Ile Pro Arg Pro Arg Gly His
 1               5                  10                  15
Arg Ser Lys Tyr Val Ala Leu Ile Phe Leu Val Ala Ser Leu Met Ile
            20                  25                  30
Leu Trp Val Ala Lys Asp Pro Pro Asn His Thr Leu Lys Tyr Leu Ala
```

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        35                  40                  45
Leu His Leu Ala Ser His Glu Leu Gly Leu Leu Leu Lys Asn Leu Cys
    50                  55                  60
Cys Leu Ala Glu Glu Leu Cys His Val Gln Ser Arg Tyr Gln Gly Ser
65                  70                  75                  80
Tyr Trp Lys Ala Val Arg Ala Cys Leu Gly Cys Pro Ile His Cys Met
                85                  90                  95
Ala Met Ile Leu Leu Ser Ser Tyr Phe Tyr Phe Leu Gln Asn Thr Ala
            100                 105                 110
Asp Ile Tyr Leu Ser Trp Met Phe Gly Leu Leu Val Leu Tyr Lys Ser
        115                 120                 125
Leu Ser Met Leu Leu Gly Leu Gln Ser Leu Thr Pro Ala Glu Val Ser
    130                 135                 140
Ala Val Cys Glu Glu Lys Lys Leu Asn Val Ala His Gly Leu Ala Trp
145                 150                 155                 160
Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Gly Leu Gln Ala
                165                 170                 175
Arg Ile Arg Met Phe Asn Gln Leu His Asn Asn Met Leu Ser Gly Ala
            180                 185                 190
Gly Ser Arg Arg Leu Tyr Ile Leu Phe Pro Leu Asp Tyr Gly Val Pro
        195                 200                 205
Asp Asn Leu Ser Val Val Asp Pro Asn Ile Arg Phe Arg Asp Met Leu
    210                 215                 220
Pro Gln Gln Asn Ile Asp Arg Ala Gly Ile Lys Asn Arg Val Tyr Ser
225                 230                 235                 240
Asn Ser Val Tyr Glu Ile Leu Glu Asn Gly Gln Pro Ala Gly Val Cys
                245                 250                 255
Ile Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser Gln
            260                 265                 270
Asp Ala Lys Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala Lys
        275                 280                 285
Leu Phe Cys Arg Thr Leu Glu Glu Ile Leu Glu Asp Val Pro Glu Ser
    290                 295                 300
Arg Asn Asn Cys Arg Leu Ile Val Tyr Gln Glu Pro Thr Asp Gly Asn
305                 310                 315                 320
Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Ile Arg Gln Glu Glu
                325                 330                 335
Lys Glu Glu Val Thr Met Asn Ala Pro Met Thr Ser Val Ala Pro Pro
            340                 345                 350
Pro Ser Val Leu Ser Gln Glu Pro Arg Leu Leu Ile Ser Gly Met Asp
        355                 360                 365
Gln Pro Leu Pro Leu Arg Thr Asp Leu Ile
    370                 375


<210> 400
<211> 378
<212> PRT
<213> Artificial Sequence
```

<220>
<223> muSTING R283G

<400> 400
Met Pro Tyr Ser Asn Leu His Pro Ala Ile Pro Arg Pro Arg Gly His
 1   5   10   15
Arg Ser Lys Tyr Val Ala Leu Ile Phe Leu Val Ala Ser Leu Met Ile
            20   25   30
Leu Trp Val Ala Lys Asp Pro Pro Asn His Thr Leu Lys Tyr Leu Ala
        35   40   45
Leu His Leu Ala Ser His Glu Leu Gly Leu Leu Leu Lys Asn Leu Cys
    50   55   60
Cys Leu Ala Glu Glu Leu Cys His Val Gln Ser Arg Tyr Gln Gly Ser
65   70   75   80
Tyr Trp Lys Ala Val Arg Ala Cys Leu Gly Cys Pro Ile His Cys Met
                85   90   95
Ala Met Ile Leu Leu Ser Ser Tyr Phe Tyr Phe Leu Gln Asn Thr Ala
            100   105   110
Asp Ile Tyr Leu Ser Trp Met Phe Gly Leu Leu Val Leu Tyr Lys Ser
        115   120   125
Leu Ser Met Leu Leu Gly Leu Gln Ser Leu Thr Pro Ala Glu Val Ser
    130   135   140
Ala Val Cys Glu Glu Lys Lys Leu Asn Val Ala His Gly Leu Ala Trp
145   150   155   160
Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Gly Leu Gln Ala
                165   170   175
Arg Ile Arg Met Phe Asn Gln Leu His Asn Asn Met Leu Ser Gly Ala
            180   185   190
Gly Ser Arg Arg Leu Tyr Ile Leu Phe Pro Leu Asp Cys Gly Val Pro
        195   200   205
Asp Asn Leu Ser Val Val Asp Pro Asn Ile Arg Phe Arg Asp Met Leu
    210   215   220
Pro Gln Gln Asn Ile Asp Arg Ala Gly Ile Lys Asn Arg Val Tyr Ser
225   230   235   240
Asn Ser Val Tyr Glu Ile Leu Glu Asn Gly Gln Pro Ala Gly Val Cys
                245   250   255
Ile Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser Gln
            260   265   270
Asp Ala Lys Ala Gly Phe Ser Arg Glu Asp Gly Leu Glu Gln Ala Lys
        275   280   285
Leu Phe Cys Arg Thr Leu Glu Glu Ile Leu Glu Asp Val Pro Glu Ser
    290   295   300
Arg Asn Asn Cys Arg Leu Ile Val Tyr Gln Glu Pro Thr Asp Gly Asn
305   310   315   320
Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Ile Arg Gln Glu Glu
                325   330   335
Lys Glu Glu Val Thr Met Asn Ala Pro Met Thr Ser Val Ala Pro Pro
            340   345   350
Pro Ser Val Leu Ser Gln Glu Pro Arg Leu Leu Ile Ser Gly Met Asp
        355   360   365

Gln Pro Leu Pro Leu Arg Thr Asp Leu Ile
370 375

<210> 401
<211> 1500
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-human CTLA-4 scFv-Fc

<400> 401
atggagacac ctgcccagct gctgttcctg ctgctgctgt ggctgcccga caccaccggc 60
gagatcgtgc tgacccagtc tcctggcacc ctgagcctga gccccggcga gagagccaca 120
ctgagctgca gagcttctca gagcgtcgga tcttcttatc tggcctggta tcagcaaaag 180
cccggacaag ctcctcggct gctgatctac ggcgccttca gccgggctac aggcatccct 240
gatagattca gcggcagcgg ctctggcact gatttcaccc tgaccattag cagactggaa 300
cctgaggact tcgccgtgta ctactgccag cagtacggga gcagcccttg gacctttgga 360
caaggcacca aggtggaaat caagcgtgga ggaggcggct caggcggcgg aggaagcggc 420
ggcggcggct ccggcggcgg aggcagccag gttcagctgg ttgaaagcgg aggcggcgtg 480
gtccagcctg gtagaagcct gcggctgtct tgcgccgcca gcggctttac atttagcagc 540
tacaccatgc actgggtgcg gcaggcccct ggcaagggcc tggaatgggt caccttcatc 600
agctacgacg gcaacaacaa gtactacgcc gacagcgtga aaggcagatt caccatcagc 660
agagataatt ctaaaaacac cctgtacctg caaatgaaca gcctcagagc cgaggatacc 720
gctatctact actgtgccag aacaggctgg ctgggccgct tcgactactg gggccagggc 780
acactggtga ccgtgtctag cgagcctaag tcttccgata agacacacac ctgccctccg 840
tgccccgccc ctgaactgct cggcggacct agcgtgttcc tgttccctcc aaagcctaag 900
gacaccctga tgatctctcg aacacctgag gtgacctgcg tggtggtgga cgtgtcccac 960
gaggaccccg aggtgaagtt caactggtac gtggacggcg tggaagtgca caacgccaag 1020
acaaaaccta gagaggagca gtacaacagc acctacagag tggtgtccgt gctgaccgtg 1080
ctgcaccagg actggctgaa cggcaaggaa tacaagtgca aggtgtccaa caaggccctg 1140
cctgccccta tcgagaagac catcagcaag gctaaaggcc agcccagaga gccccaggtg 1200
tacacactgc ctccaagcag ggacgagctg accaagaacc aggtcagcct gacatgtctg 1260
gtgaagggct tctacccttc tgacatcgcc gtggaatggg agagcaacgg ccagcccgag 1320
aacaactaca agacgacccc tcctgtgctg gacagcgacg gatccttctt cctgtacagc 1380
aagctgacag ttgataagtc ccggtggcag cagggcaatg tgtttagctg tagcgtgatg 1440
cacgaggccc tgcataatca ctacacccag aaaagcctta gcctgtcccc aggcaaatga 1500

<210> 402
<211> 499
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-human CTLA-4 scFv-Fc

<220>
<221> misc_feature

<222> (1)...(20)
<223> IGKV3-20 leader sequence

<220>
<221> misc_feature
<222> (21)...(129)
<223> Ipilimumab VL domain

<220>
<221> misc_feature
<222> (130)...(149)
<223> Gly-Ser linker

<220>
<221> misc_feature
<222> (150)...(267)
<223> Ipilimumab VH domain

<220>
<221> misc_feature
<222> (268)...(499)
<223> human IgG1 FC w/ C5S mutation in hinge region

<400> 402
Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1   5   10   15
Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
            20   25   30
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
        35   40   45
Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50   55   60
Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro
65   70   75   80
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85   90   95
Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
            100   105   110
Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115   120   125
Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130   135   140
Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val
145   150   155   160
Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                165   170   175
Thr Phe Ser Ser Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Lys
            180   185   190
Gly Leu Glu Trp Val Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr

```
        195                 200                 205
Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
    210                 215                 220
Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
225                 230                 235                 240
Ala Ile Tyr Tyr Cys Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr
                245                 250                 255
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Glu Pro Lys Ser Ser
            260                 265                 270
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
        275                 280                 285
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
    290                 295                 300
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
305                 310                 315                 320
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
                325                 330                 335
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
            340                 345                 350
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
        355                 360                 365
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
    370                 375                 380
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
385                 390                 395                 400
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
                405                 410                 415
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
            420                 425                 430
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
        435                 440                 445
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
    450                 455                 460
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
465                 470                 475                 480
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
                485                 490                 495
Pro Gly Lys
```

<210> 403
<211> 267
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-human CTLA-4 scFv

<220>
<221> misc_feature

<222> (1)...(20)
<223> IGKV3-20 leader sequence

<220>
<221> misc_feature
<222> (21)...(129)
<223> Ipilimumab VL domain

<220>
<221> misc_feature
<222> (130)...(149)
<223> Gly-ser linker

<220>
<221> misc_feature
<222> (150)...(267)
<223> Ipilimumab VH domain

<400> 403
Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1   5   10   15
Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
            20   25   30
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
        35   40   45
Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50   55   60
Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro
65   70   75   80
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85   90   95
Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
            100   105   110
Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115   120   125
Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130   135   140
Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val
145   150   155   160
Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                165   170   175
Thr Phe Ser Ser Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Lys
            180   185   190
Gly Leu Glu Trp Val Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr
        195   200   205
Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
    210   215   220
Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
225   230   235   240
Ala Ile Tyr Tyr Cys Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr

```
                245                 250                 255
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
            260                 265


<210> 404
<211> 264
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-Mouse CTLA-4 scFv

<220>
<221> misc_feature
<222> (1)...(20)
<223> IgK mouse leader sequence

<220>
<221> misc_feature
<222> (21)...(132)
<223> VL of clone 9D9

<220>
<221> misc_feature
<222> (133)...(147)
<223> Gly-Ser linker

<220>
<221> misc_feature
<222> (148)...(264)
<223> VH of clone 9D9

<400> 404
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1               5                  10                  15
Gly Ser Thr Gly Asp Ile Val Met Thr Gln Thr Thr Leu Ser Leu Pro
            20                  25                  30
Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
        35                  40                  45
Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys
    50                  55                  60
Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
65                  70                  75                  80
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
                85                  90                  95
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr
            100                 105                 110
Cys Phe Gln Gly Ser His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys
        115                 120                 125
```

```
Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    130                 135                 140
Gly Gly Ser Glu Ala Lys Leu Gln Glu Ser Gly Pro Val Leu Val Lys
145                 150                 155                 160
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
                165                 170                 175
Thr Asp Tyr Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu
            180                 185                 190
Glu Trp Ile Gly Val Ile Asn Pro Tyr Asn Gly Asp Thr Ser Tyr Asn
        195                 200                 205
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
    210                 215                 220
Thr Ala Tyr Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val
225                 230                 235                 240
Tyr Tyr Cys Ala Arg Tyr Tyr Gly Ser Trp Phe Ala Tyr Trp Gly Gln
                245                 250                 255
Gly Thr Leu Val Thr Val Ser Ser
            260
```

<210> 405
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-Mouse CTLA-4 scFv-Fc

<220>
<221> misc_feature
<222> (1)...(20)
<223> IgK mouse leader sequence

<220>
<221> misc_feature
<222> (21)...(132)
<223> VL of clone 9D9

<220>
<221> misc_feature
<222> (133)...(147)
<223> Gly-Ser linker

<220>
<221> misc_feature
<222> (148)...(264)
<223> VH of clone 9D9

<220>

<221> misc_feature
<222> (265)...(497)
<223> mouse IgG2a Fc

<400> 405
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1   5   10   15
Gly Ser Thr Gly Asp Ile Val Met Thr Gln Thr Thr Leu Ser Leu Pro
            20   25   30
Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
        35   40   45
Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys
    50   55   60
Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
65   70   75   80
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
                85   90   95
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr
            100   105   110
Cys Phe Gln Gly Ser His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys
        115   120   125
Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    130   135   140
Gly Gly Ser Glu Ala Lys Leu Gln Glu Ser Gly Pro Val Leu Val Lys
145   150   155   160
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
                165   170   175
Thr Asp Tyr Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu
            180   185   190
Glu Trp Ile Gly Val Ile Asn Pro Tyr Asn Gly Asp Thr Ser Tyr Asn
        195   200   205
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
    210   215   220
Thr Ala Tyr Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val
225   230   235   240
Tyr Tyr Cys Ala Arg Tyr Tyr Gly Ser Trp Phe Ala Tyr Trp Gly Gln
                245   250   255
Gly Thr Leu Val Thr Val Ser Ser Glu Pro Arg Gly Pro Thr Ile Lys
            260   265   270
Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro
        275   280   285
Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser
    290   295   300
Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp
305   310   315   320
Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr
                325   330   335
Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val
            340   345   350
Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu

```
        355                 360                 365
Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg
    370                 375                 380
Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val
385                 390                 395                 400
Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr
                405                 410                 415
Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr
            420                 425                 430
Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu
        435                 440                 445
Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys
    450                 455                 460
Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu
465                 470                 475                 480
Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly
                485                 490                 495
Lys
```

<210> 406
<211> 417
<212> PRT
<213> Artificial Sequence

<220>
<223> murine soluble TGF-beta Receptor II-Fc Fusion (mu sTGFbRII-Fc)

<220>
<221> misc_feature
<222> (1)...(184)
<223> mouse soluble TGFbeta Receptor II

<220>
<221> misc_feature
<222> (185)...(417)
<223> mouse IgG2a Fc

<400> 406

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

```
65                  70                  75                  80
Val Arg Leu Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys
                85                  90                  95
Ser Ile Thr Ala Ile Cys Glu Lys Pro His Glu Val Cys Val Ala Val
            100                 105                 110
Trp Arg Lys Asn Asp Lys Asn Ile Thr Leu Glu Thr Val Cys His Asp
        115                 120                 125
Pro Lys Leu Thr Tyr His Gly Phe Thr Leu Glu Asp Ala Ala Ser Pro
    130                 135                 140
Lys Cys Val Met Lys Glu Lys Lys Arg Ala Gly Glu Thr Phe Phe Met
145                 150                 155                 160
Cys Ala Cys Asn Met Glu Glu Cys Asn Asp Tyr Ile Ile Phe Ser Glu
                165                 170                 175
Glu Tyr Thr Thr Ser Ser Pro Asp Glu Pro Arg Gly Pro Thr Ile Lys
            180                 185                 190
Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro
        195                 200                 205
Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser
    210                 215                 220
Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp
225                 230                 235                 240
Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr
                245                 250                 255
Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val
            260                 265                 270
Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu
        275                 280                 285
Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg
    290                 295                 300
Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val
305                 310                 315                 320
Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr
                325                 330                 335
Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr
            340                 345                 350
Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu
        355                 360                 365
Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys
    370                 375                 380
Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu
385                 390                 395                 400
Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly
                405                 410                 415
Lys
```

<210> 407
<211> 391
<212> PRT

<213> Artificial Sequence

<220>
<223> Human soluble TGF-beta Receptor II-Fc Fusion (hu
sTGFbRII-Fc)

<220>
<221> misc_feature
<222> (1)...(159)
<223> Human soluble TGF-beta Receptor II

<220>
<221> misc_feature
<222> (160)...(391)
<223> human IgG1 Fc

<400> 407
```
Met Gly Arg Gly Leu Leu Arg Gly Leu Trp Pro Leu His Ile Val Leu
 1               5                  10                  15
Trp Thr Arg Ile Ala Ser Thr Ile Pro Pro His Val Gln Lys Ser Val
            20                  25                  30
Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
        35                  40                  45
Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
    50                  55                  60
Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
65                  70                  75                  80
Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
                85                  90                  95
Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
            100                 105                 110
Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
        115                 120                 125
Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
    130                 135                 140
Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Glu
145                 150                 155                 160
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                165                 170                 175
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            180                 185                 190
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        195                 200                 205
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    210                 215                 220
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
225                 230                 235                 240
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                245                 250                 255
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
```

```
            260                 265                 270
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        275                 280                 285
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
    290                 295                 300
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
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Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
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Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            340                 345                 350
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
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<210> 421
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<223> msbB-4 primer

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