SEQUENCE LISTING

<110> Wyeth LLC
Flannery, Carl R
Corcoran, Christopher J
Freeman, Bethany A
Racie, Lisa A

<120> RECOMBINANT LUBRICIN MOLECULES AND USES THEREOF

<130> 50657-01404WOPT

<160> 29

<170> PatentIn version 3.3

<210> 1
<211> 155
<212> DNA
<213> Artificial

<220>
<223> Nucleotide sequence of synthetic cDNA cassette-1.

<400> 1
cgcgcccaca actccaaaag agcccgcacc taccacgaca aagtcagctc ctactacgcc 60

caaagagcca gcgccgacga ctactaaaga accggcaccc accacgccta aggagccagc 120

tcctactaca acgaaaccgg caccaaccac tccgg 155

<210> 2
<211> 51
<212> PRT
<213> Artificial

<220>
<223> Translation of SEQ ID NO: 1.

<400> 2

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
1 5 10 15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
20 25 30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Pro Ala Pro
35 40 45

Thr Thr Pro
50

<210> 3
<211> 125
<212> DNA
<213> Artificial

<220>
<223> Nucleotide sequence of synthetic cDNA cassette-2.

<400> 3
taaagaacca gcccctacta cgacaaagga gcctgcaccc acaaccacga agagcgcacc 60

cacaacacca aaggagccgg cccctacgac tcctaaggaa cccaaaccgg caccaaccac 120

tccgg 125

<210> 4
<211> 41
<212> PRT
<213> Artificial

<220>
<223> Translation of SEQ ID NO: 3.

<400> 4

Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr Thr Thr
1 5 10 15

Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Pro Lys
20 25 30

Glu Pro Lys Pro Ala Pro Thr Thr Pro
35 40

<210> 5
<211> 8049
<212> DNA
<213> Artificial

<220>
<223> pTmed2 vector containing recombinant PRG4-Lub:1 cDNA construct.

<400> 5
catatgcggt gtgaaatacc gcacagatgc gtaaggagaa aataccgcat caggcgtact 60

gagtcattag ggactttcca atgggttttg cccagtacat aaggtcaata ggggtgaatc 120

aacaggaaag tcccattgga gccaagtaca ctgagtcaat agggactttc cattgggttt 180

tgcccagtac aaaaggtcaa tagggggtga gtcaatgggt ttttcccatt attggcacgt 240

acataaggtc aatagggggtg agtcattggg tttttccagc caatttaatt aaaacgccat 300

gtactttccc accattgacg tcaatgggct attgaaacta atgcaacgtg acctttaaac 360

ggtactttcc catagctgat taatgggaaa gtaccgttct cgagccaata cacgtcaatg 420

ggaagtgaaa gggcagccaa aacgtaacac cgccccggtt ttcccctgga aattccatat 480

tggcacgcat tctattggct gagctgcgtt ctacgtgggt ataagaggcg cgaccagcgt 540

cggtaccgtc gcagtcttcg gtctgaccac cgtagaacgc agagctcctc gctgcagccc 600

aagctctgtt gggctcgcgg ttgaggacaa actcttcgcg gtctttccag tactcttgga 660

tcggaaaccc gtcggcctcc gaacggtact ccgccaccga gggacctgag cgagtccgca 720

tcgaccggat cggaaaacct ctcgactgtt ggggtgagta ctccctctca aaagcgggca 780

tgacttctgc gctaagattg tcagtttcca aaaacgagga ggatttgata ttcacctggc 840

ccgcggtgat gcctttgagg gtggccgcgt ccatctggtc agaaaagaca atcttttgt 900

tgtcaagctt gaggtgtggc aggcttgaga tctggccata cacttgagtg acaatgacat 960

ccactttgcc tttctctcca caggtgtcca ctcccaggtc caactgcaga cttcgaattc 1020

tactgagtcg acccaccatg gcatggaaaa cacttcccat ttacctgttg ttgctgctgt 1080

ctgttttcgt gattcagcaa gtttcatctc aagatttatc aagctgtgca gggagatgtg 1140

gggaagggta ttctagagat gccacctgca actgtgatta taactgtcaa cactacatgg 1200

agtgctgccc tgatttcaag agagtctgca ctgcggagct ttcctgtaaa ggccgctgct 1260

ttgagtcctt cgagagaggg agggagtgtg actgcgacgc ccaatgtaag aagtatgaca 1320

agtgctgtcc cgattatgag agtttctgtg cagaagtgca taatcccaca tcaccaccat 1380

cttcaaagaa agcacctcca ccttcaggag catctcaaac catcaaatca acaaccaaac 1440

gttcacccaa accaccaaac aagaagaaga ctaagaaagt tatagaatca gaggaaataa 1500

cagaagaaca ttctgtttct gaaaatcaag agtcctcctc cagtagcagt tcaagtagtt 1560

cgtcgtcgac aatttggaaa atcaagtctt ccaaaaattc agctgctaat agagaattac 1620

agaagaaact caaagtaaaa gataacaaga agaacagaac taaaaagaaa cctaccccca 1680

aaccaccagt tgtagatgaa gctggaagtg gattggacaa tggtgacttc aaggtcacaa 1740

ctcctgacac gtctaccacc caacacaata aagtcagcac atctcccaag atcacaacag 1800

caaaaccaat aaatcccaga cccagtcttc cacctaattc tgatacatct aaagagacgt 1860

ctttgacagt gaataaagag acaacagttg aaactaaaga aactactaca acaaataaac 1920

agacttcaac tgatggaaaa gagaagacta cttccgctaa agagacacaa agtatagaga 1980

aaacatctgc taaagattta gcacccacat ctaaagtgct ggctaaacct acacccaaag 2040

ctgaaactac aaccaaaggc cctgctctca ccactcccaa ggagcccacg cccaccactc 2100

ccaaggagcc tgcatctacc acacccaaag agcccacacc taccaccatc aagagcgcgc 2160

ccacaactcc aaaagagccc gcacctacca cgacaaagtc agctcctact acgcccaaag 2220

agccagcgcc gacgactact aaagaaccgg cacccaccac gcctaaggag ccagctccta 2280

ctacaacgaa accggcacca accactccgg aaacacctcc tccaaccact tcagaggtct 2340

ctactccaac taccaccaag gagcctacca ctatccacaa aagccctgat gaatcaactc 2400

ctgagctttc tgcagaaccc acaccaaaag ctcttgaaaa cagtcccaag gaacctggtg 2460

tacctacaac taagacgccg gcggcgacta aacctgaaat gactacaaca gctaaagaca 2520

agacaacaga aagagactta cgtactacac ctgaaactac aactgctgca cctaagatga 2580

caaaagagac agcaactaca acagaaaaaa ctaccgaatc caaaataaca gctacaacca 2640

cacaagtaac atctaccaca actcaagata ccacaccatt caaaattact actcttaaaa 2700

caactactct tgcacccaaa gtaactacaa caaaaaagac aattactacc actgagatta 2760

tgaacaaacc tgaagaaaca gctaaaccaa aagacagagc tactaattct aaagcgacaa 2820

ctcctaaacc tcaaaagcca accaaagcac ccaaaaaacc cacttctacc aaaaagccaa 2880

aaacaatgcc tagagtgaga aaaccaaaga cgacaccaac tccccgcaag atgacatcaa 2940

caatgccaga attgaaccct acctcaagaa tagcagaagc catgctccaa accaccacca 3000

gacctaacca aactccaaac tccaaactag ttgaagtaaa tccaaagagt gaagatgcag 3060

gtggtgctga aggagaaaca cctcatatgc ttctcaggcc ccatgtgttc atgcctgaag 3120

ttactcccga catggattac ttaccgagag tacccaatca aggcattatc atcaatccca 3180

tgctttccga tgagaccaat atatgcaatg gtaagccagt agatggactg actactttgc 3240

gcaatgggac attagttgca ttccgaggtc attatttctg gatgctaagt ccattcagtc 3300

caccatctcc agctcgcaga attactgaag tttggggtat tccttccccc attgatactg 3360

tttttactag gtgcaactgt gaaggaaaaa ctttcttctt taaggattct cagtactggc 3420

gttttaccaa tgatataaaa gatgcagggt accccaaacc aattttcaaa ggatttggag 3480

gactaactgg acaaatagtg gcagcgcttt caacagctaa atataagaac tggcctgaat 3540

ctgtgtattt tttcaagaga ggtggcagca ttcagcagta tatttataaa caggaacctg 3600

tacagaagtg ccctggaaga aggcctgctc taaattatcc agtgtatgga gaaatgacac 3660

aggttaggag acgtcgcttt gaacgtgcta taggaccttc tcaaacacac accatcagaa 3720

ttcaatattc acctgccaga ctggcttatc aagacaaagg tgtccttcat aatgaagtta 3780

aagtgagtat actgtggaga ggacttccaa atgtggttac ctcagctata tcactgccca 3840

acatcagaaa acctgacggc tatgattact atgccttttc taaagatcaa tactataaca 3900

ttgatgtgcc tagtagaaca gcaagagcaa ttactactcg ttctgggcag accttatcca 3960

aagtctggta caactgtcct taagcggccg ccgcaaattc taacgttact ggccgaagcc 4020

gcttggaata aggccggtgt gcgtttgtct atatgttatt ttccaccata ttgccgtctt 4080

ttggcaatgt gagggcccgg aaacctggcc ctgtcttctt gacgagcatt cctaggggtc 4140

tttcccctct cgccaaagga atgcaaggtc tgttgaatgt cgtgaaggaa gcagttcctc 4200

tggaagcttc ttgaagacaa acaacgtctg tagcgaccct ttgcaggcag cggaacccc 4260

cacctggcga caggtgcctc tgcggccaaa agccacgtgt ataagataca cctgcaaagg 4320

cggcacaacc ccagtgccac gttgtgagtt ggatagttgt ggaaagagtc aaatggctct 4380

cctcaagcgt attcaacaag gggctgaagg atgcccagaa ggtaccccat tgtatgggat 4440

ctgatctggg gcctcggtgc acatgcttta catgtgttta gtcgaggtta aaaaacgtct 4500

aggcccccg aaccacgggg acgtggtttt cctttgaaaa acacgattgc tcgagccatc 4560

atggttcgac cattgaactg catcgtcgcc gtgtcccaaa atatggggat tggcaagaac 4620

ggagacctac cctggcctcc gctcaggaac gagttcaagt acttccaaag aatgaccaca 4680

acctcttcag tggaaggtaa acagaatctg gtgattatgg gtaggaaaac ctggttctcc 4740

attcctgaga agaatcgacc tttaaaggac agaattaata tagttctcag tagagaactc 4800

aaagaaccac cacgaggagc tcattttctt gccaaaagtt tggatgatgc cttaagactt 4860

attgaacaac cggaattggc aagtaaagta gacatggttt ggatagtcgg aggcagttct 4920

gtttaccagg aagccatgaa tcaaccaggc cacctcagac tctttgtgac aaggatcatg 4980

caggaatttg aaagtgacac gtttttccca gaaattgatt tggggaaata taaacttctc 5040

ccagaatacc caggcgtcct ctctgaggtc caggaggaaa aaggcatcaa gtataagttt 5100

gaagtctacg agaagaaaga ctaacaggaa gatgctttca agttctctgc tcccctccta 5160

aagctatgca ttttttataa gaccatggga cttttgctgg ctttagatca taatcagcca 5220

taccacattt gtagaggttt tacttgcttt aaaaaacctc ccacacctcc ccctgaacct 5280

gaaacataaa atgaatgcaa ttgttgttgt taacttgttt attgcagctt ataatggtta 5340

caaataaagc aatagcatca caaatttcac aaataaagca ttttttttcac tgcattctag 5400

ttgtggtttg tccaaactca tcaatgtatc ttatcatgtc tggatccccg gccaacggtc 5460

tggtgacccg gctgcgagag ctcggtgtac ctgagacgcg agtaagccct tgagtcaaag 5520

acgtagtcgt tgcaagtccg caccaggtac tgatcatcga tgctagaccg tgcaaaagga 5580

gagcctgtaa gcgggcactc ttccgtggtc tggtggataa attcgcaagg gtatcatggc 5640

ggacgaccgg ggttcgaacc ccggatccgg ccgtccgccg tgatccatcc ggttaccgcc 5700

cgcgtgtcga acccaggtgt gcgacgtcag acaacggggg agcgctcctt ttggcttcct 5760

tccaggcgcg gcggctgctg cgctagcttt tttggcgagc tcgaattaat tctgcattaa 5820

tgaatcggcc aacgcgcggg gagaggcggt ttgcgtattg ggcgctcttc cgcttcctcg 5880

ctcactgact cgctgcgctc ggtcgttcgg ctgcggcgag cggtatcagc tcactcaaag 5940

gcggtaatac ggttatccac agaatcaggg gataacgcag gaaagaacat gtgagcaaaa 6000

ggccagcaaa aggccaggaa ccgtaaaaag gccgcgttgc tggcgttttt ccataggctc 6060

cgccccccctg acgagcatca caaaaatcga cgctcaagtc agaggtggcg aaacccgaca 6120

ggactataaa gataccaggc gtttcccccct ggaagctccc tcgtgcgctc tcctgttccg 6180

accctgccgc ttaccggata cctgtccgcc tttctccctt cgggaagcgt ggcgctttct 6240

caatgctcac gctgtaggta tctcagttcg gtgtaggtcg ttcgctccaa gctgggctgt 6300

gtgcacgaac cccccgttca gcccgaccgc tgcgccttat ccggtaacta tcgtcttgag 6360

tccaacccgg taagacacga cttatcgcca ctggcagcag ccactggtaa caggattagc 6420

agagcgaggt atgtaggcgg tgctacagag ttcttgaagt ggtggcctaa ctacggctac 6480

actagaagga cagtatttgg tatctgcgct ctgctgaagc cagttacctt cggaaaaaga 6540

gttggtagct cttgatccgg caaacaaacc accgctggta gcggtggttt ttttgtttgc 6600

aagcagcaga ttacgcgcag aaaaaaagga tctcaagaag atccttttgat cttttctacg 6660

gggtctgacg ctcagtggaa cgaaaactca cgttaaggga ttttggtcat gagattatca 6720

aaaaggatct tcacctagat ccttttaaat taaaaatgaa gttttaaatc aatctaaagt 6780

atatatgagt aaacttggtc tgacagttac caatgcttaa tcagtgaggc acctatctca 6840

gcgatctgtc tatttcgttc atccatagtt gcctgactcc ccgtcgtgta gataactacg 6900

atacgggagg gcttaccatc tggccccagt gctgcaatga taccgcgaga cccacgctca 6960

ccggctccag atttatcagc aataaaccag ccagccggaa gggccgagcg cagaagtggt 7020

cctgcaactt tatccgcctc catccagtct attaattgtt gccgggaagc tagagtaagt 7080

agttcgccag ttaatagttt gcgcaacgtt gttgccattg ctacaggcat cgtggtgtca 7140

cgctcgtcgt ttggtatggc ttcattcagc tccggttccc aacgatcaag gcgagttaca 7200

tgatccccca tgttgtgcaa aaaagcggtt agctccttcg gtcctccgat cgttgtcaga 7260

agtaagttgg ccgcagtgtt atcactcatg gttatggcag cactgcataa ttctcttact 7320

gtcatgccat ccgtaagatg cttttctgtg actggtgagt actcaaccaa gtcattctga 7380

gaatagtgta tgcggcgacc gagttgctct tgcccggcgt caatacggga taataccgcg 7440

ccacatagca gaactttaaa agtgctcatc attggaaaac gttcttcggg gcgaaaactc 7500

tcaaggatct taccgctgtt gagatccagt tcgatgtaac ccactcgtgc acccaactga 7560

tcttcagcat cttttacttt caccagcgtt tctgggtgag caaaaacagg aaggcaaaat 7620

gccgcaaaaa agggaataag ggcgacacgg aaatgttgaa tactcatact cttccttttt 7680

caatattatt gaagcattta tcagggttat tgtctcatga gcggatacat atttgaatgt 7740

atttagaaaa ataaacaaat aggggttccg cgcacatttc cccgaaaagt gccacctgac 7800

gtctaagaaa ccattattat catgacatta acctataaaa ataggcgtat cacgaggccc 7860

tttcgtctcg cgcgtttcgg tgatgacggt gaaaacctct gacacatgca gctcccggag 7920

acggtcacag cttgtctgta agcggatgcc gggagcagac aagcccgtca gggcgcgtca 7980

gcgggtgttg gcgggtgtcg gggctggctt aactatgcgg catcagagca gattgtactg 8040

agagtgcac 8049

<210> 6
<211> 2946
<212> DNA
<213> Artificial

<220>
<223> Recombinant PRG4-Lub:1 cDNA construct.

<400> 6
atggcatgga aaacacttcc catttacctg ttgttgctgc tgtctgtttt cgtgattcag 60

caagtttcat ctcaagattt atcaagctgt gcagggagat gtggggaagg gtattctaga 120

gatgccacct gcaactgtga ttataactgt caacactaca tggagtgctg ccctgatttc 180

aagagagtct gcactgcgga gctttcctgt aaaggccgct gctttgagtc cttcgagaga 240

gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgctg tcccgattat 300

gagagtttct gtgcagaagt gcataatccc acatcaccac catcttcaaa gaaagcacct 360

ccaccttcag gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca 420

aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt 480

tctgaaaatc aagagtcctc ctccagtagc agttcaagta gttcgtcgtc gacaatttgg 540

aaaatcaagt cttccaaaaa ttcagctgct aatagagaat tacagaagaa actcaaagta 600

aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgtagat 660

gaagctggaa gtggattgga caatggtgac ttcaaggtca caactcctga cacgtctacc 720

acccaacaca ataaagtcag cacatctccc aagatcacaa cagcaaaacc aataaatccc 780

agacccagtc ttccacctaa ttctgataca tctaaagaga cgtctttgac agtgaataaa 840

gagacaacag ttgaaactaa agaaactact acaacaaata aacagacttc aactgatgga 900

aaagagaaga ctacttccgc taaagagaca caaagtatag agaaaacatc tgctaaagat 960

ttagcaccca catctaaagt gctggctaaa cctacaccca aagctgaaac tacaaccaaa 1020

ggccctgctc tcaccactcc caaggagccc acgcccacca ctcccaagga gcctgcatct 1080

accacaccca aagagcccac acctaccacc atcaagagcg cgcccacaac tccaaaagag 1140

cccgcaccta ccacgacaaa gtcagctcct actacgccca aagagccagc gccgacgact 1200

actaaagaac cggcacccac cacgcctaag gagccagctc ctactacaac gaaaccggca 1260

ccaaccactc cggaaacacc tcctccaacc acttcagagg tctctactcc aactaccacc 1320

aaggagccta ccactatcca caaaagccct gatgaatcaa ctcctgagct ttctgcagaa 1380

cccacaccaa aagctcttga aaacagtccc aaggaacctg gtgtacctac aactaagacg 1440

ccggcggcga ctaaacctga aatgactaca acagctaaag acaagacaac agaaagagac 1500

ttacgtacta cacctgaaac tacaactgct gcacctaaga tgacaaaaga gacagcaact 1560

acaacagaaa aaactaccga atccaaaata acagctacaa ccacacaagt aacatctacc 1620

acaactcaag ataccacacc attcaaaatt actactctta aaacaactac tcttgcaccc 1680

aaagtaacta caacaaaaaa gacaattact accactgaga ttatgaacaa acctgaagaa 1740

acagctaaac caaaagacag agctactaat tctaaagcga caactcctaa acctcaaaag 1800

ccaaccaaag cacccaaaaa acccacttct accaaaaagc caaaaacaat gcctagagtg 1860

agaaaaccaa agacgacacc aactccccgc aagatgacat caacaatgcc agaattgaac 1920

cctacctcaa gaatagcaga agccatgctc caaaccacca ccagacctaa ccaaactcca 1980

aactccaaac tagttgaagt aaatccaaag agtgaagatg caggtggtgc tgaaggagaa 2040

acacctcata tgcttctcag gccccatgtg ttcatgcctg aagttactcc cgacatggat 2100

tacttaccga gagtacccaa tcaaggcatt atcatcaatc ccatgctttc cgatgagacc 2160

aatatatgca atggtaagcc agtagatgga ctgactactt tgcgcaatgg gacattagtt 2220

gcattccgag gtcattattt ctggatgcta agtccattca gtccaccatc tccagctcgc 2280

agaattactg aagtttgggg tattccttcc cccattgata ctgtttttac taggtgcaac 2340

tgtgaaggaa aaactttctt ctttaaggat tctcagtact ggcgttttac caatgatata 2400

aaagatgcag ggtaccccaa accaattttc aaaggatttg gaggactaac tggacaaata 2460

gtggcagcgc tttcaacagc taaatataag aactggcctg aatctgtgta ttttttcaag 2520

agaggtggca gcattcagca gtatatttat aaacaggaac ctgtacagaa gtgccctgga 2580

agaaggcctg ctctaaatta tccagtgtat ggagaaatga cacaggttag gagacgtcgc 2640

tttgaacgtg ctataggacc ttctcaaaca cacaccatca gaattcaata ttcacctgcc 2700

agactggctt atcaagacaa aggtgtcctt cataatgaag ttaaagtgag tatactgtgg 2760

agaggacttc caaatgtggt tacctcagct atatcactgc ccaacatcag aaaacctgac 2820

ggctatgatt actatgcctt ttctaaagat caatactata acattgatgt gcctagtaga 2880

acagcaagag caattactac tcgttctggg cagaccttat ccaaagtctg gtacaactgt 2940

ccttaa 2946

<210> 7
<211> 981
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of entire PRG4-LUB:1 protein.

<400> 7

Met Ala Trp Lys Thr Leu Pro Ile Tyr Leu Leu Leu Leu Ser Val
1 5 10 15

Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly
20 25 30

Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr
35 40 45

Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys
50 55 60

Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg
65 70 75 80

Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys
85 90 95

Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser
100 105 110

Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr
115 120 125

Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys
130 135 140

Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val
145 150 155 160

Ser Glu Asn Gln Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
165 170 175

Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg
180 185 190

Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr
195 200 205

Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser

```
    210                 215                 220

Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr
225                 230                 235                 240

Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys
                245                 250                 255

Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys
            260                 265                 270

Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu
        275                 280                 285

Thr Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr
    290                 295                 300

Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp
305                 310                 315                 320

Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu
                325                 330                 335

Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro
            340                 345                 350

Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro
        355                 360                 365

Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
    370                 375                 380

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
385                 390                 395                 400

Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
                405                 410                 415

Thr Lys Pro Ala Pro Thr Thr Pro Glu Thr Pro Pro Pro Thr Thr Ser
            420                 425                 430

Glu Val Ser Thr Pro Thr Thr Thr Lys Glu Pro Thr Thr Ile His Lys
        435                 440                 445

Ser Pro Asp Glu Ser Thr Pro Glu Leu Ser Ala Glu Pro Thr Pro Lys
    450                 455                 460

Ala Leu Glu Asn Ser Pro Lys Glu Pro Gly Val Pro Thr Thr Lys Thr
465                 470                 475                 480

Pro Ala Ala Thr Lys Pro Glu Met Thr Thr Thr Ala Lys Asp Lys Thr
                485                 490                 495

Thr Glu Arg Asp Leu Arg Thr Thr Pro Glu Thr Thr Thr Ala Ala Pro
            500                 505                 510

Lys Met Thr Lys Glu Thr Ala Thr Thr Thr Glu Lys Thr Thr Glu Ser
        515                 520                 525
```

```
Lys Ile Thr Ala Thr Thr Thr Gln Val Thr Ser Thr Thr Thr Gln Asp
    530                 535                 540

Thr Thr Pro Phe Lys Ile Thr Thr Leu Lys Thr Thr Thr Leu Ala Pro
545                 550                 555                 560

Lys Val Thr Thr Thr Lys Lys Thr Ile Thr Thr Thr Glu Ile Met Asn
                565                 570                 575

Lys Pro Glu Glu Thr Ala Lys Pro Lys Asp Arg Ala Thr Asn Ser Lys
            580                 585                 590

Ala Thr Thr Pro Lys Pro Gln Lys Pro Thr Lys Ala Pro Lys Lys Pro
        595                 600                 605

Thr Ser Thr Lys Lys Pro Lys Thr Met Pro Arg Val Arg Lys Pro Lys
    610                 615                 620

Thr Thr Pro Thr Pro Arg Lys Met Thr Ser Thr Met Pro Glu Leu Asn
625                 630                 635                 640

Pro Thr Ser Arg Ile Ala Glu Ala Met Leu Gln Thr Thr Thr Arg Pro
                645                 650                 655

Asn Gln Thr Pro Asn Ser Lys Leu Val Glu Val Asn Pro Lys Ser Glu
            660                 665                 670

Asp Ala Gly Gly Ala Glu Gly Glu Thr Pro His Met Leu Leu Arg Pro
        675                 680                 685

His Val Phe Met Pro Glu Val Thr Pro Asp Met Asp Tyr Leu Pro Arg
    690                 695                 700

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

Asn Ile Cys Asn Gly Lys Pro Val Asp Gly Leu Thr Thr Leu Arg Asn
                725                 730                 735

Gly Thr Leu Val Ala Phe Arg Gly His Tyr Phe Trp Met Leu Ser Pro
            740                 745                 750

Phe Ser Pro Pro Ser Pro Ala Arg Arg Ile Thr Glu Val Trp Gly Ile
        755                 760                 765

Pro Ser Pro Ile Asp Thr Val Phe Thr Arg Cys Asn Cys Glu Gly Lys
    770                 775                 780

Thr Phe Phe Phe Lys Asp Ser Gln Tyr Trp Arg Phe Thr Asn Asp Ile
785                 790                 795                 800

Lys Asp Ala Gly Tyr Pro Lys Pro Ile Phe Lys Gly Phe Gly Gly Leu
                805                 810                 815

Thr Gly Gln Ile Val Ala Ala Leu Ser Thr Ala Lys Tyr Lys Asn Trp
            820                 825                 830

Pro Glu Ser Val Tyr Phe Phe Lys Arg Gly Gly Ser Ile Gln Gln Tyr
        835                 840                 845
```

```
Ile Tyr Lys Gln Glu Pro Val Gln Lys Cys Pro Gly Arg Arg Pro Ala
    850                 855                 860

Leu Asn Tyr Pro Val Tyr Gly Glu Met Thr Gln Val Arg Arg Arg Arg
865                 870                 875                 880

Phe Glu Arg Ala Ile Gly Pro Ser Gln Thr His Thr Ile Arg Ile Gln
                885                 890                 895

Tyr Ser Pro Ala Arg Leu Ala Tyr Gln Asp Lys Gly Val Leu His Asn
            900                 905                 910

Glu Val Lys Val Ser Ile Leu Trp Arg Gly Leu Pro Asn Val Val Thr
        915                 920                 925

Ser Ala Ile Ser Leu Pro Asn Ile Arg Lys Pro Asp Gly Tyr Asp Tyr
    930                 935                 940

Tyr Ala Phe Ser Lys Asp Gln Tyr Tyr Asn Ile Asp Val Pro Ser Arg
945                 950                 955                 960

Thr Ala Arg Ala Ile Thr Thr Arg Ser Gly Gln Thr Leu Ser Lys Val
                965                 970                 975

Trp Tyr Asn Cys Pro
            980
```

<210> 8
<211> 157
<212> DNA
<213> Artificial

<220>
<223> Lub:1 DNA insert from synthetic cDNA cassette-1.

<400> 8

```
gcgcgcccac aactccaaaa gagcccgcac ctaccacgac aaagtcagct cctactacgc     60

ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaggagccag    120

ctcctactac aacgaaaccg gcaccaacca ctccgga                             157
```

<210> 9
<211> 51
<212> PRT
<213> Artificial

<220>
<223> 51 amino acids encoded by Lub:1 DNA insert (4 KEPAPTT sequences between S373 to E425 in SEQ ID NO: 7).

<400> 9

```
Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
1               5                  10                  15
```

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
20 25 30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Pro Ala Pro
35 40 45

Thr Thr Pro
50

<210> 10
<211> 3024
<212> DNA
<213> Artificial

<220>
<223> Recombinant PRG4-Lub:2 cDNA construct.

<400> 10
atggcatgga aaacacttcc catttacctg ttgttgctgc tgtctgtttt cgtgattcag 60

caagtttcat ctcaagattt atcaagctgt gcagggagat gtggggaagg gtattctaga 120

gatgccacct gcaactgtga ttataactgt caacactaca tggagtgctg ccctgatttc 180

aagagagtct gcactgcgga gctttcctgt aaaggccgct gctttgagtc cttcgagaga 240

gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgctg tcccgattat 300

gagagtttct gtgcagaagt gcataatccc acatcaccac catcttcaaa gaaagcacct 360

ccaccttcag gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca 420

aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt 480

tctgaaaatc aagagtcctc ctccagtagc agttcaagta gttcgtcgtc gacaatttgg 540

aaaatcaagt cttccaaaaa ttcagctgct aatagagaat tacagaagaa actcaaagta 600

aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgtagat 660

gaagctggaa gtggattgga caatggtgac ttcaaggtca caactcctga cacgtctacc 720

acccaacaca ataaagtcag cacatctccc aagatcacaa cagcaaaacc aataaatccc 780

agacccagtc ttccacctaa ttctgataca tctaaagaga cgtctttgac agtgaataaa 840

gagacaacag ttgaaactaa agaaactact acaacaaata aacagacttc aactgatgga 900

aaagagaaga ctacttccgc taaagagaca caaagtatag agaaaacatc tgctaaagat 960

ttagcaccca catctaaagt gctggctaaa cctacaccca aagctgaaac tacaaccaaa 1020

ggccctgctc tcaccactcc caaggagccc acgcccacca ctcccaagga gcctgcatct 1080

accacaccca aagagcccac acctaccacc atcaagagcg cgcccacaac tccaaaagag 1140

cccgcaccta ccacgacaaa gtcagctcct actacgccca aagagccagc gccgacgact 1200

actaaagaac cggcacccac cacgcctaaa gaaccagccc ctactacgac aaaggagcct 1260

gcacccacaa ccacgaagag cgcacccaca acaccaaagg agccggcccc tacgactcct 1320

aaggaaccca aaccggcacc aaccactccg gaaacacctc ctccaaccac ttcagaggtc 1380

tctactccaa ctaccaccaa ggagcctacc actatccaca aaagccctga tgaatcaact 1440

cctgagcttt ctgcagaacc cacaccaaaa gctcttgaaa acagtcccaa ggaacctggt 1500

gtacctacaa ctaagacgcc ggcggcgact aaacctgaaa tgactacaac agctaaagac 1560

aagacaacag aaagagactt acgtactaca cctgaaacta caactgctgc acctaagatg 1620

acaaaagaga cagcaactac aacagaaaaa actaccgaat ccaaaataac agctacaacc 1680

acacaagtaa catctaccac aactcaagat accacaccat tcaaaattac tactcttaaa 1740

acaactactc ttgcacccaa agtaactaca acaaaaaaga caattactac cactgagatt 1800

atgaacaaac ctgaagaaac agctaaacca aaagacagag ctactaattc taaagcgaca 1860

actcctaaac ctcaaaagcc aaccaaagca cccaaaaaac ccacttctac caaaaagcca 1920

aaaacaatgc ctagagtgag aaaaccaaag acgacaccaa ctccccgcaa gatgacatca 1980

acaatgccag aattgaaccc tacctcaaga atagcagaag ccatgctcca aaccaccacc 2040

agacctaacc aaactccaaa ctccaaacta gttgaagtaa atccaaagag tgaagatgca 2100

ggtggtgctg aaggagaaac acctcatatg cttctcaggc cccatgtgtt catgcctgaa 2160

gttactcccg acatggatta cttaccgaga gtacccaatc aaggcattat catcaatccc 2220

atgctttccg atgagaccaa tatatgcaat ggtaagccag tagatggact gactactttg 2280

cgcaatggga cattagttgc attccgaggt cattatttct ggatgctaag tccattcagt 2340

ccaccatctc cagctcgcag aattactgaa gtttggggta ttccttcccc cattgatact 2400

gtttttacta ggtgcaactg tgaaggaaaa actttcttct ttaaggattc tcagtactgg 2460

cgttttacca atgatataaa agatgcaggg taccccaaac caattttcaa aggatttgga 2520

ggactaactg gacaaatagt ggcagcgctt tcaacagcta aatataagaa ctggcctgaa 2580

tctgtgtatt ttttcaagag aggtggcagc attcagcagt atatttataa acaggaacct 2640

gtacagaagt gccctggaag aaggcctgct ctaaattatc cagtgtatgg agaaatgaca 2700

caggttagga gacgtcgctt tgaacgtgct ataggacctt ctcaaacaca caccatcaga 2760

attcaatatt cacctgccag actggcttat caagacaaag gtgtccttca taatgaagtt 2820

aaagtgagta tactgtggag aggacttcca aatgtggtta cctcagctat atcactgccc 2880

aacatcagaa aacctgacgg ctatgattac tatgcctttt ctaaagatca atactataac 2940

attgatgtgc ctagtagaac agcaagagca attactactc gttctgggca gaccttatcc 3000

aaagtctggt acaactgtcc ttaa 3024

<210> 11
<211> 1007
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of entire PRG4-LUB:2 protein.

<400> 11

Met Ala Trp Lys Thr Leu Pro Ile Tyr Leu Leu Leu Leu Leu Ser Val
1 5 10 15

Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly
20 25 30

Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr
35 40 45

Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys
50 55 60

Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg
65 70 75 80

Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys
85 90 95

Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser
100 105 110

Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr
115 120 125

Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys
130 135 140

Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val
145 150 155 160

Ser Glu Asn Gln Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
165 170 175

Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg
180 185 190

Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr
195 200 205

Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser
210 215 220

Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr
225 230 235 240

```
Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys
                245                 250                 255

Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys
            260                 265                 270

Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu
        275                 280                 285

Thr Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr
    290                 295                 300

Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp
305                 310                 315                 320

Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu
                325                 330                 335

Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro
            340                 345                 350

Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro
        355                 360                 365

Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
    370                 375                 380

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
385                 390                 395                 400

Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
                405                 410                 415

Thr Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro
            420                 425                 430

Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr
        435                 440                 445

Thr Pro Glu Thr Pro Pro Pro Thr Thr Ser Glu Val Ser Thr Pro Thr
    450                 455                 460

Thr Thr Lys Glu Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr
465                 470                 475                 480

Pro Glu Leu Ser Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro
                485                 490                 495

Lys Glu Pro Gly Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro
            500                 505                 510

Glu Met Thr Thr Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg
        515                 520                 525

Thr Thr Pro Glu Thr Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr
    530                 535                 540

Ala Thr Thr Thr Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr
545                 550                 555                 560
```

```
Thr Gln Val Thr Ser Thr Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile
                565                 570                 575

Thr Thr Leu Lys Thr Thr Thr Leu Ala Pro Lys Val Thr Thr Thr Lys
            580                 585                 590

Lys Thr Ile Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala
        595                 600                 605

Lys Pro Lys Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro
    610                 615                 620

Gln Lys Pro Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro
625                 630                 635                 640

Lys Thr Met Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg
                645                 650                 655

Lys Met Thr Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala
            660                 665                 670

Glu Ala Met Leu Gln Thr Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser
        675                 680                 685

Lys Leu Val Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu
    690                 695                 700

Gly Glu Thr Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu
705                 710                 715                 720

Val Thr Pro Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile
                725                 730                 735

Ile Ile Asn Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys
            740                 745                 750

Pro Val Asp Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe
        755                 760                 765

Arg Gly His Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro
    770                 775                 780

Ala Arg Arg Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr
785                 790                 795                 800

Val Phe Thr Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp
                805                 810                 815

Ser Gln Tyr Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro
            820                 825                 830

Lys Pro Ile Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala
        835                 840                 845

Ala Leu Ser Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe
    850                 855                 860

Phe Lys Arg Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro
```

```
865                 870                 875                 880

Val Gln Lys Cys Pro Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr
                885                 890                 895

Gly Glu Met Thr Gln Val Arg Arg Arg Phe Glu Arg Ala Ile Gly
            900                 905                 910

Pro Ser Gln Thr His Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu
        915                 920                 925

Ala Tyr Gln Asp Lys Gly Val Leu His Asn Glu Val Lys Val Ser Ile
    930                 935                 940

Leu Trp Arg Gly Leu Pro Asn Val Val Thr Ser Ala Ile Ser Leu Pro
945                 950                 955                 960

Asn Ile Arg Lys Pro Asp Gly Tyr Asp Tyr Tyr Ala Phe Ser Lys Asp
                965                 970                 975

Gln Tyr Tyr Asn Ile Asp Val Pro Ser Arg Thr Ala Arg Ala Ile Thr
            980                 985                 990

Thr Arg Ser Gly Gln Thr Leu Ser  Lys Val Trp Tyr Asn  Cys Pro
        995                 1000                1005
```

<210> 12
<211> 235
<212> DNA
<213> Artificial

<220>
<223> Lub:2 DNA insert from synthetic cDNA cassette-1 and one synthetic cDNA cassette-2 sequence.

<400> 12

```
gcgcgcccac aactccaaaa gagcccgcac ctaccacgac aaagtcagct cctactacgc     60

ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaagaaccag    120

cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc acaacaccaa    180

aggagccggc ccctacgact cctaaggaac ccaaaccggc accaaccact ccgga         235
```

<210> 13
<211> 77
<212> PRT
<213> Artificial

<220>
<223> 77 amino acids encoded by Lub:2 DNA insert (6 KEPAPTT sequences between S373 and E451 in SEQ ID NO: 11).

<400> 13

```
Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
1               5                   10                  15
```

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
20 25 30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
35 40 45

Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro
50 55 60

Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
65 70 75

<210> 14
<211> 3117
<212> DNA
<213> Artificial

<220>
<223> Recombinant PRG4-Lub:3 cDNA construct.

<400> 14
atggcatgga aaacacttcc catttacctg ttgttgctgc tgtctgtttt cgtgattcag 60

caagtttcat ctcaagattt atcaagctgt gcagggagat gtggggaagg gtattctaga 120

gatgccacct gcaactgtga ttataactgt caacactaca tggagtgctg ccctgatttc 180

aagagagtct gcactgcgga gctttcctgt aaaggccgct gctttgagtc cttcgagaga 240

gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgctg tcccgattat 300

gagagtttct gtgcagaagt gcataatccc acatcaccac catcttcaaa gaaagcacct 360

ccaccttcag gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca 420

aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt 480

tctgaaaatc aagagtcctc ctccagtagc agttcaagta gttcgtcgtc gacaatttgg 540

aaaatcaagt cttccaaaaa ttcagctgct aatagagaat tacagaagaa actcaaagta 600

aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgtagat 660

gaagctggaa gtggattgga caatggtgac ttcaaggtca caactcctga cacgtctacc 720

acccaacaca ataaagtcag cacatctccc aagatcacaa cagcaaaacc aataaatccc 780

agacccagtc ttccacctaa ttctgataca tctaaagaga cgtctttgac agtgaataaa 840

gagacaacag ttgaaactaa agaaactact acaacaaata aacagacttc aactgatgga 900

aaagagaaga ctacttccgc taaagagaca caaagtatag agaaaacatc tgctaaagat 960

ttagcaccca catctaaagt gctggctaaa cctacaccca aagctgaaac tacaaccaaa 1020

ggccctgctc tcaccactcc caaggagccc acgcccacca ctcccaagga gcctgcatct 1080

accacaccca aagagcccac acctaccacc atcaagagcg cgcccacaac tccaaaagag 1140

cccgcaccta ccacgacaaa gtcagctcct actacgccca aagagccagc gccgacgact 1200

actaaagaac cggcacccac cacgcctaaa gaaccagccc ctactacgac aaaggagcct 1260

gcacccacaa ccacgaagag cgcacccaca acaccaaagg agccggcccc tacgactcct 1320

aaagaaccag cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc 1380

acaacaccaa aggagccggc ccctacgact cctaaggaac ccaaaccggc accaaccact 1440

ccggaaacac ctcctccaac cacttcagag gtctctactc caactaccac caaggagcct 1500

accactatcc acaaaagccc tgatgaatca actcctgagc tttctgcaga acccacacca 1560

aaagctcttg aaaacagtcc caaggaacct ggtgtaccta caactaagac gccggcggcg 1620

actaaacctg aaatgactac aacagctaaa gacaagacaa cagaaagaga cttacgtact 1680

acacctgaaa ctacaactgc tgcacctaag atgacaaaag agacagcaac tacaacagaa 1740

aaaactaccg aatccaaaat aacagctaca accacacaag taacatctac cacaactcaa 1800

gataccacac cattcaaaat tactactctt aaaacaacta ctcttgcacc caaagtaact 1860

acaacaaaaa agacaattac taccactgag attatgaaca aacctgaaga aacagctaaa 1920

ccaaaagaca gagctactaa ttctaaagcg acaactccta aacctcaaaa gccaaccaaa 1980

gcacccaaaa aacccacttc taccaaaaag ccaaaaacaa tgcctagagt gagaaaacca 2040

aagacgacac caactccccg caagatgaca tcaacaatgc cagaattgaa ccctacctca 2100

agaatagcag aagccatgct ccaaaccacc accagaccta accaaactcc aaactccaaa 2160

ctagttgaag taaatccaaa gagtgaagat gcaggtggtg ctgaaggaga aacacctcat 2220

atgcttctca ggccccatgt gttcatgcct gaagttactc ccgacatgga ttacttaccg 2280

agagtaccca atcaaggcat tatcatcaat cccatgcttt ccgatgagac caatatatgc 2340

aatggtaagc cagtagatgg actgactact ttgcgcaatg ggacattagt tgcattccga 2400

ggtcattatt tctggatgct aagtccattc agtccaccat ctccagctcg cagaattact 2460

gaagtttggg gtattccttc ccccattgat actgttttta ctaggtgcaa ctgtgaagga 2520

aaaactttct tctttaagga ttctcagtac tggcgtttta ccaatgatat aaaagatgca 2580

gggtacccca aaccaatttt caaaggattt ggaggactaa ctggacaaat agtggcagcg 2640

ctttcaacag ctaaatataa gaactggcct gaatctgtgt atttttttcaa gagaggtggc 2700

agcattcagc agtatattta taaacaggaa cctgtacaga agtgccctgg aagaaggcct 2760

gctctaaatt atccagtgta tggagaaatg acacaggtta ggagacgtcg ctttgaacgt 2820

gctataggac cttctcaaac acacaccatc agaattcaat attcacctgc cagactggct 2880

tatcaagaca aaggtgtcct tcataatgaa gttaaagtga gtatactgtg gagaggactt 2940

ccaaatgtgg ttacctcagc tatatcactg cccaacatca gaaaacctga cggctatgat 3000

tactatgcct tttctaaaga tcaatactat aacattgatg tgcctagtag aacagcaaga 3060

gcaattacta ctcgttctgg gcagacctta tccaaagtct ggtacaactg tccttaa 3117

<210> 15
<211> 1038
<212> PRT
<213> Artificial

<220>
<223> amino acid sequence of entire PRG4-LUB:3 protein

<400> 15

Met Ala Trp Lys Thr Leu Pro Ile Tyr Leu Leu Leu Leu Leu Ser Val
1 5 10 15

Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly
20 25 30

Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr
35 40 45

Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys
50 55 60

Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg
65 70 75 80

Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys
85 90 95

Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser
100 105 110

Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr
115 120 125

Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys
130 135 140

Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val
145 150 155 160

Ser Glu Asn Gln Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
165 170 175

Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg
180 185 190

Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr
195 200 205

```
Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser
    210                 215                 220

Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr
225                 230                 235                 240

Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys
                245                 250                 255

Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys
            260                 265                 270

Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu
        275                 280                 285

Thr Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr
    290                 295                 300

Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp
305                 310                 315                 320

Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu
                325                 330                 335

Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro
            340                 345                 350

Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro
        355                 360                 365

Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
    370                 375                 380

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
385                 390                 395                 400

Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
                405                 410                 415

Thr Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro
            420                 425                 430

Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr
        435                 440                 445

Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys
    450                 455                 460

Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr
465                 470                 475                 480

Pro Glu Thr Pro Pro Pro Thr Thr Ser Glu Val Ser Thr Pro Thr Thr
                485                 490                 495

Thr Lys Glu Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr Pro
            500                 505                 510

Glu Leu Ser Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro Lys
        515                 520                 525
```

```
Glu Pro Gly Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro Glu
    530                 535                 540

Met Thr Thr Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg Thr
545                 550                 555                 560

Thr Pro Glu Thr Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr Ala
                565                 570                 575

Thr Thr Thr Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr Thr
            580                 585                 590

Gln Val Thr Ser Thr Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile Thr
        595                 600                 605

Thr Leu Lys Thr Thr Thr Leu Ala Pro Lys Val Thr Thr Thr Lys Lys
    610                 615                 620

Thr Ile Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala Lys
625                 630                 635                 640

Pro Lys Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro Gln
                645                 650                 655

Lys Pro Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro Lys
            660                 665                 670

Thr Met Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg Lys
        675                 680                 685

Met Thr Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala Glu
    690                 695                 700

Ala Met Leu Gln Thr Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser Lys
705                 710                 715                 720

Leu Val Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu Gly
                725                 730                 735

Glu Thr Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu Val
            740                 745                 750

Thr Pro Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile Ile
        755                 760                 765

Ile Asn Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro
    770                 775                 780

Val Asp Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe Arg
785                 790                 795                 800

Gly His Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro Ala
                805                 810                 815

Arg Arg Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr Val
            820                 825                 830

Phe Thr Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp Ser
```

```
        835                 840                 845

Gln Tyr Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro Lys
    850                 855                 860

Pro Ile Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala Ala
865                 870                 875                 880

Leu Ser Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe Phe
                885                 890                 895

Lys Arg Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro Val
            900                 905                 910

Gln Lys Cys Pro Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr Gly
        915                 920                 925

Glu Met Thr Gln Val Arg Arg Arg Arg Phe Glu Arg Ala Ile Gly Pro
    930                 935                 940

Ser Gln Thr His Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu Ala
945                 950                 955                 960

Tyr Gln Asp Lys Gly Val Leu His Asn Glu Val Lys Val Ser Ile Leu
                965                 970                 975

Trp Arg Gly Leu Pro Asn Val Val Thr Ser Ala Ile Ser Leu Pro Asn
            980                 985                 990

Ile Arg Lys Pro Asp Gly Tyr Asp  Tyr Tyr Ala Phe Ser  Lys Asp Gln
        995                 1000                1005

Tyr Tyr  Asn Ile Asp Val Pro  Ser Arg Thr Ala Arg  Ala Ile Thr
    1010                1015                1020

Thr Arg  Ser Gly Gln Thr Leu  Ser Lys Val Trp Tyr  Asn Cys Pro
    1025                1030                1035
```

<210> 16
<211> 328
<212> DNA
<213> Artificial

<220>
<223> Lub:3 DNA insert from synthetic cDNA cassette-1 and two synthetic cDNA cassette-2 sequences.

<400> 16

```
gcgcgcccac aactccaaaa gagcccgcac ctaccacgac aaagtcagct cctactacgc     60

ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaagaaccag    120

cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc acaacaccaa    180

aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag gagcctgcac    240

ccacaaccac gaagagcgca cccacaacac caaaggagcc ggcccctacg actcctaagg    300
```

aacccaaacc ggcaccaacc actccgga 328

<210> 17
<211> 108
<212> PRT
<213> Artificial

<220>
<223> 108 amino acids encoded by Lub:3 DNA insert (9 KEPAPTT sequences between S373 and E482 in SEQ ID NO: 15)

<400> 17

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
1 5 10 15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
20 25 30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
35 40 45

Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro
50 55 60

Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro
65 70 75 80

Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
85 90 95

Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
100 105

<210> 18
<211> 3210
<212> DNA
<213> Artificial

<220>
<223> recombinant PRG4-Lub:4 cDNA construct.

<400> 18
atggcatgga aaacacttcc catttacctg ttgttgctgc tgtctgtttt cgtgattcag 60

caagtttcat ctcaagattt atcaagctgt gcagggagat gtggggaagg gtattctaga 120

gatgccacct gcaactgtga ttataactgt caacactaca tggagtgctg ccctgatttc 180

aagagagtct gcactgcgga gctttcctgt aaaggccgct gctttgagtc cttcgagaga 240

gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgctg tcccgattat 300

gagagtttct gtgcagaagt gcataatccc acatcaccac catcttcaaa gaaagcacct 360

ccaccttcag gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca 420

aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt 480

tctgaaaatc aagagtcctc ctccagtagc agttcaagta gttcgtcgtc gacaatttgg 540

aaaatcaagt cttccaaaaa ttcagctgct aatagagaat tacagaagaa actcaaagta 600

aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgtagat 660

gaagctggaa gtggattgga caatggtgac ttcaaggtca caactcctga cacgtctacc 720

acccaacaca ataaagtcag cacatctccc aagatcacaa cagcaaaacc aataaatccc 780

agacccagtc ttccacctaa ttctgataca tctaaagaga cgtctttgac agtgaataaa 840

gagacaacag ttgaaactaa agaaactact acaacaaata aacagacttc aactgatgga 900

aaagagaaga ctacttccgc taaagagaca caaagtatag agaaaacatc tgctaaagat 960

ttagcaccca catctaaagt gctggctaaa cctacaccca aagctgaaac tacaaccaaa 1020

ggccctgctc tcaccactcc caaggagccc acgcccacca ctcccaagga gcctgcatct 1080

accacaccca aagagcccac acctaccacc atcaagagcg cgcccacaac tccaaaagag 1140

cccgcaccta ccacgacaaa gtcagctcct actacgccca aagagccagc gccgacgact 1200

actaaagaac cggcacccac cacgcctaaa gaaccagccc ctactacgac aaaggagcct 1260

gcacccacaa ccacgaagag cgcacccaca acaccaaagg agccggcccc tacgactcct 1320

aaagaaccag cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc 1380

acaacaccaa aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag 1440

gagcctgcac ccacaaccac gaagagcgca cccacaacac caaaggagcc ggcccctacg 1500

actcctaagg aacccaaacc ggcaccaacc actccggaaa cacctcctcc aaccacttca 1560

gaggtctcta ctccaactac caccaaggag cctaccacta tccacaaaag ccctgatgaa 1620

tcaactcctg agctttctgc agaacccaca ccaaaagctc ttgaaaacag tcccaaggaa 1680

cctggtgtac ctacaactaa gacgccggcg gcgactaaac ctgaaatgac tacaacagct 1740

aaagacaaga caacagaaag agacttacgt actacacctg aaactacaac tgctgcacct 1800

aagatgacaa aagagacagc aactacaaca gaaaaaacta ccgaatccaa aataacagct 1860

acaaccacac aagtaacatc taccacaact caagatacca caccattcaa aattactact 1920

cttaaaacaa ctactcttgc acccaaagta actacaacaa aaaagacaat tactaccact 1980

gagattatga acaaacctga agaaacagct aaaccaaaag acagagctac taattctaaa 2040

gcgacaactc ctaaacctca aaagccaacc aaagcaccca aaaaacccac ttctaccaaa 2100

aagccaaaaa caatgcctag agtgagaaaa ccaaagacga caccaactcc ccgcaagatg 2160

acatcaacaa tgccagaatt gaaccctacc tcaagaatag cagaagccat gctccaaacc 2220

accaccagac ctaaccaaac tccaaactcc aaactagttg aagtaaatcc aaagagtgaa 2280

gatgcaggtg gtgctgaagg agaaacacct catatgcttc tcaggcccca tgtgttcatg 2340

cctgaagtta ctcccgacat ggattactta ccgagagtac ccaatcaagg cattatcatc 2400

aatcccatgc tttccgatga gaccaatata tgcaatggta agccagtaga tggactgact 2460

actttgcgca atgggacatt agttgcattc cgaggtcatt atttctggat gctaagtcca 2520

ttcagtccac catctccagc tcgcagaatt actgaagttt ggggtattcc ttccccccatt 2580

gatactgttt ttactaggtg caactgtgaa ggaaaaactt tcttctttaa ggattctcag 2640

tactggcgtt ttaccaatga tataaaagat gcagggtacc ccaaaccaat tttcaaagga 2700

tttggaggac taactggaca aatagtggca gcgctttcaa cagctaaata taagaactgg 2760

cctgaatctg tgtatttttt caagagaggt ggcagcattc agcagtatat ttataaacag 2820

gaacctgtac agaagtgccc tggaagaagg cctgctctaa attatccagt gtatggagaa 2880

atgacacagg ttaggagacg tcgctttgaa cgtgctatag gaccttctca aacacacacc 2940

atcagaattc aatattcacc tgccagactg gcttatcaag acaaaggtgt ccttcataat 3000

gaagttaaag tgagtatact gtggagagga cttccaaatg tggttacctc agctatatca 3060

ctgcccaaca tcagaaaacc tgacggctat gattactatg ccttttctaa agatcaatac 3120

tataacattg atgtgcctag tagaacagca agagcaatta ctactcgttc tgggcagacc 3180

ttatccaaag tctggtacaa ctgtccttaa 3210

<210> 19
<211> 1069
<212> PRT
<213> Artificial

<220>
<223> amino acid sequence of entire PRG4-LUB:4 protein.

<400> 19

Met Ala Trp Lys Thr Leu Pro Ile Tyr Leu Leu Leu Leu Leu Ser Val
1 5 10 15

Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly
20 25 30

Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr
35 40 45

Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys
50 55 60

Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg

65 70 75 80

Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys
85 90 95

Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser
100 105 110

Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr
115 120 125

Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys
130 135 140

Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val
145 150 155 160

Ser Glu Asn Gln Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
165 170 175

Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg
180 185 190

Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr
195 200 205

Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser
210 215 220

Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr
225 230 235 240

Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys
245 250 255

Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys
260 265 270

Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu
275 280 285

Thr Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr
290 295 300

Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp
305 310 315 320

Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu
325 330 335

Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro
340 345 350

Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro
355 360 365

Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
370 375 380

```
Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
385                 390                 395                 400

Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
                405                 410                 415

Thr Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro
            420                 425                 430

Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr
        435                 440                 445

Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys
    450                 455                 460

Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys
465                 470                 475                 480

Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu
                485                 490                 495

Pro Ala Pro Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
            500                 505                 510

Glu Thr Pro Pro Pro Thr Thr Ser Glu Val Ser Thr Pro Thr Thr Thr
        515                 520                 525

Lys Glu Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr Pro Glu
    530                 535                 540

Leu Ser Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro Lys Glu
545                 550                 555                 560

Pro Gly Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro Glu Met
                565                 570                 575

Thr Thr Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg Thr Thr
            580                 585                 590

Pro Glu Thr Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr Ala Thr
        595                 600                 605

Thr Thr Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr Thr Gln
    610                 615                 620

Val Thr Ser Thr Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile Thr Thr
625                 630                 635                 640

Leu Lys Thr Thr Thr Leu Ala Pro Lys Val Thr Thr Thr Lys Lys Thr
                645                 650                 655

Ile Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala Lys Pro
            660                 665                 670

Lys Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro Gln Lys
        675                 680                 685

Pro Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro Lys Thr
    690                 695                 700
```

```
Met Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg Lys Met
705                 710                 715                 720

Thr Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala Glu Ala
                725                 730                 735

Met Leu Gln Thr Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser Lys Leu
            740                 745                 750

Val Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu Gly Glu
        755                 760                 765

Thr Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu Val Thr
    770                 775                 780

Pro Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile Ile Ile
785                 790                 795                 800

Asn Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro Val
                805                 810                 815

Asp Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe Arg Gly
            820                 825                 830

His Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro Ala Arg
        835                 840                 845

Arg Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr Val Phe
    850                 855                 860

Thr Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp Ser Gln
865                 870                 875                 880

Tyr Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro Lys Pro
                885                 890                 895

Ile Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala Ala Leu
            900                 905                 910

Ser Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe Phe Lys
        915                 920                 925

Arg Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro Val Gln
    930                 935                 940

Lys Cys Pro Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr Gly Glu
945                 950                 955                 960

Met Thr Gln Val Arg Arg Arg Arg Phe Glu Arg Ala Ile Gly Pro Ser
                965                 970                 975

Gln Thr His Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu Ala Tyr
            980                 985                 990

Gln Asp Lys Gly Val Leu His Asn  Glu Val Lys Val Ser  Ile Leu Trp
        995                 1000                1005

Arg Gly  Leu Pro Asn Val Val  Thr Ser Ala Ile Ser  Leu Pro Asn
```

```
    1010                1015                1020

Ile Arg  Lys Pro Asp Gly Tyr  Asp Tyr Tyr Ala Phe  Ser Lys Asp
    1025                1030                1035

Gln Tyr  Tyr Asn Ile Asp Val  Pro Ser Arg Thr Ala  Arg Ala Ile
    1040                1045                1050

Thr Thr  Arg Ser Gly Gln Thr  Leu Ser Lys Val Trp  Tyr Asn Cys
    1055                1060                1065

Pro
```

<210> 20
<211> 421
<212> DNA
<213> Artificial

<220>
<223> Lub:4 DNA insert from cDNA cassette-1 and three synthetic cDNA cassette-2 sequences.

<400> 20

```
gcgcgcccac aactccaaaa gagcccgcac ctaccacgac aaagtcagct cctactacgc     60

ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaagaaccag    120

cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc acaacaccaa    180

aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag gagcctgcac    240

ccacaaccac gaagagcgca cccacaacac caaaggagcc ggcccctacg actcctaaag    300

aaccagcccc tactacgaca aaggagcctg cacccacaac cacgaagagc gcacccacaa    360

caccaaagga gccggccccct acgactccta aggaacccaa accggcacca accactccgg    420

a                                                                    421
```

<210> 21
<211> 139
<212> PRT
<213> Artificial

<220>
<223> 139 amino acids encoded by Lub:4 DNA insert (12 KEPAPTT sequences between S373 and E513 in SEQ ID NO: 19)

<400> 21

```
Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
1               5                  10                  15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
            20                  25                  30
```

```
Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
        35                  40                  45

Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro
    50                  55                  60

Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro
65                  70                  75                  80

Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
                85                  90                  95

Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr
            100                 105                 110

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
        115                 120                 125

Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
    130                 135
```

<210> 22
<211> 3303
<212> DNA
<213> Artificial

<220>
<223> Recombinant PRG4-Lub:5 cDNA construct

<400> 22

```
atggcatgga aaacacttcc catttacctg ttgttgctgc tgtctgtttt cgtgattcag     60

caagtttcat ctcaagattt atcaagctgt gcagggagat gtggggaagg gtattctaga    120

gatgccacct gcaactgtga ttataactgt caacactaca tggagtgctg ccctgatttc    180

aagagagtct gcactgcgga gctttcctgt aaaggccgct gctttgagtc cttcgagaga    240

gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgctg tcccgattat    300

gagagtttct gtgcagaagt gcataatccc acatcaccac catcttcaaa gaaagcacct    360

ccaccttcag gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca    420

aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt    480

tctgaaaatc aagagtcctc ctccagtagc agttcaagta gttcgtcgtc gacaatttgg    540

aaaatcaagt cttccaaaaa ttcagctgct aatagagaat tacagaagaa actcaaagta    600

aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgtagat    660

gaagctggaa gtggattgga caatggtgac ttcaaggtca caactcctga cacgtctacc    720

acccaacaca ataaagtcag cacatctccc aagatcacaa cagcaaaacc aataaatccc    780

agacccagtc ttccacctaa ttctgataca tctaaagaga cgtctttgac agtgaataaa    840
```

gagacaacag ttgaaactaa agaaactact acaacaaata aacagacttc aactgatgga 900

aaagagaaga ctacttccgc taaagagaca caaagtatag agaaaacatc tgctaaagat 960

ttagcaccca catctaaagt gctggctaaa cctacaccca aagctgaaac tacaaccaaa 1020

ggccctgctc tcaccactcc caaggagccc acgcccacca ctcccaagga gcctgcatct 1080

accacaccca aagagcccac acctaccacc atcaagagcg cgcccacaac tccaaaagag 1140

cccgcaccta ccacgacaaa gtcagctcct actacgccca aagagccagc gccgacgact 1200

actaaagaac cggcacccac cacgcctaaa gaaccagccc ctactacgac aaaggagcct 1260

gcacccacaa ccacgaagag cgcacccaca acaccaaagg agccggcccc tacgactcct 1320

aaagaaccag cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc 1380

acaacaccaa aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag 1440

gagcctgcac ccacaaccac gaagagcgca cccacaacac caaaggagcc ggcccctacg 1500

actcctaaag aaccagcccc tactacgaca aaggagcctg cacccacaac cacgaagagc 1560

gcacccacaa caccaaagga gccggcccct acgactccta aggaacccaa accggcacca 1620

accactccgg aaacacctcc tccaaccact tcagaggtct ctactccaac taccaccaag 1680

gagcctacca ctatccacaa aagccctgat gaatcaactc ctgagctttc tgcagaaccc 1740

acaccaaaag ctcttgaaaa cagtcccaag gaacctggtg tacctacaac taagacgccg 1800

gcggcgacta aacctgaaat gactacaaca gctaaagaca agacaacaga aagagactta 1860

cgtactacac ctgaaactac aactgctgca cctaagatga caaaagagac agcaactaca 1920

acagaaaaaa ctaccgaatc caaaataaca gctacaacca cacaagtaac atctaccaca 1980

actcaagata ccacaccatt caaaattact actcttaaaa caactactct tgcacccaaa 2040

gtaactacaa caaaaaagac aattactacc actgagatta tgaacaaacc tgaagaaaca 2100

gctaaaccaa aagacagagc tactaattct aaagcgacaa ctcctaaacc tcaaaagcca 2160

accaaagcac ccaaaaaacc cacttctacc aaaaagccaa aaacaatgcc tagagtgaga 2220

aaaccaaaga cgacaccaac tccccgcaag atgacatcaa caatgccaga attgaaccct 2280

acctcaagaa tagcagaagc catgctccaa accaccacca gacctaacca aactccaaac 2340

tccaaactag ttgaagtaaa tccaaagagt gaagatgcag gtggtgctga aggagaaaca 2400

cctcatatgc ttctcaggcc ccatgtgttc atgcctgaag ttactcccga catggattac 2460

ttaccgagag tacccaatca aggcattatc atcaatccca tgctttccga tgagaccaat 2520

atatgcaatg gtaagccagt agatggactg actactttgc gcaatgggac attagttgca 2580

ttccgaggtc attatttctg gatgctaagt ccattcagtc caccatctcc agctcgcaga 2640

attactgaag tttggggtat tccttccccc attgatactg tttttactag gtgcaactgt 2700

gaaggaaaaa ctttcttctt taaggattct cagtactggc gttttaccaa tgatataaaa 2760

gatgcagggt accccaaacc aattttcaaa ggatttggag gactaactgg acaaatagtg 2820

gcagcgcttt caacagctaa atataagaac tggcctgaat ctgtgtattt tttcaagaga 2880

ggtggcagca ttcagcagta tatttataaa caggaacctg tacagaagtg ccctggaaga 2940

aggcctgctc taaattatcc agtgtatgga gaaatgacac aggttaggag acgtcgcttt 3000

gaacgtgcta taggaccttc tcaaacacac accatcagaa ttcaatattc acctgccaga 3060

ctggcttatc aagacaaagg tgtccttcat aatgaagtta aagtgagtat actgtggaga 3120

ggacttccaa atgtggttac ctcagctata tcactgccca acatcagaaa acctgacggc 3180

tatgattact atgccttttc taaagatcaa tactataaca ttgatgtgcc tagtagaaca 3240

gcaagagcaa ttactactcg ttctgggcag accttatcca aagtctggta caactgtcct 3300

taa 3303

<210> 23
<211> 1100
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of entire PRG4-LUB:5 protein.

<400> 23

Met Ala Trp Lys Thr Leu Pro Ile Tyr Leu Leu Leu Leu Leu Ser Val
1 5 10 15

Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly
20 25 30

Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr
35 40 45

Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys
50 55 60

Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg
65 70 75 80

Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys
85 90 95

Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser
100 105 110

Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr
115 120 125

```
Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys
    130                 135                 140

Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val
145                 150                 155                 160

Ser Glu Asn Gln Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
                165                 170                 175

Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg
            180                 185                 190

Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr
        195                 200                 205

Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser
    210                 215                 220

Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr
225                 230                 235                 240

Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys
                245                 250                 255

Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys
            260                 265                 270

Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu
        275                 280                 285

Thr Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr
    290                 295                 300

Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp
305                 310                 315                 320

Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu
                325                 330                 335

Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro
            340                 345                 350

Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro
        355                 360                 365

Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
    370                 375                 380

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
385                 390                 395                 400

Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
                405                 410                 415

Thr Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro
            420                 425                 430

Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr
```

```
        435                 440                 445

Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys
    450                 455                 460

Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys
465                 470                 475                 480

Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu
                485                 490                 495

Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu
            500                 505                 510

Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro
        515                 520                 525

Ala Pro Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro Glu
    530                 535                 540

Thr Pro Pro Pro Thr Thr Ser Glu Val Ser Thr Pro Thr Thr Thr Lys
545                 550                 555                 560

Glu Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr Pro Glu Leu
                565                 570                 575

Ser Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro Lys Glu Pro
            580                 585                 590

Gly Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro Glu Met Thr
        595                 600                 605

Thr Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg Thr Thr Pro
    610                 615                 620

Glu Thr Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr Ala Thr Thr
625                 630                 635                 640

Thr Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr Thr Gln Val
                645                 650                 655

Thr Ser Thr Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile Thr Thr Leu
            660                 665                 670

Lys Thr Thr Thr Leu Ala Pro Lys Val Thr Thr Thr Lys Lys Thr Ile
        675                 680                 685

Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala Lys Pro Lys
    690                 695                 700

Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro Gln Lys Pro
705                 710                 715                 720

Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro Lys Thr Met
                725                 730                 735

Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg Lys Met Thr
            740                 745                 750
```

```
Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala Glu Ala Met
        755                 760                 765

Leu Gln Thr Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser Lys Leu Val
    770                 775                 780

Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu Gly Glu Thr
785                 790                 795                 800

Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu Val Thr Pro
                805                 810                 815

Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile Ile Ile Asn
            820                 825                 830

Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro Val Asp
        835                 840                 845

Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe Arg Gly His
    850                 855                 860

Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro Ala Arg Arg
865                 870                 875                 880

Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr Val Phe Thr
                885                 890                 895

Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp Ser Gln Tyr
            900                 905                 910

Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro Lys Pro Ile
        915                 920                 925

Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala Ala Leu Ser
    930                 935                 940

Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe Phe Lys Arg
945                 950                 955                 960

Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro Val Gln Lys
                965                 970                 975

Cys Pro Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr Gly Glu Met
            980                 985                 990

Thr Gln Val Arg Arg Arg Arg Phe  Glu Arg Ala Ile Gly  Pro Ser Gln
        995                 1000                1005

Thr His  Thr Ile Arg Ile Gln  Tyr Ser Pro Ala Arg  Leu Ala Tyr
    1010                1015                1020

Gln Asp  Lys Gly Val Leu His  Asn Glu Val Lys Val  Ser Ile Leu
    1025                1030                1035

Trp Arg  Gly Leu Pro Asn Val  Val Thr Ser Ala Ile  Ser Leu Pro
    1040                1045                1050

Asn Ile  Arg Lys Pro Asp Gly  Tyr Asp Tyr Tyr Ala  Phe Ser Lys
    1055                1060                1065
```

```
Asp Gln  Tyr Tyr Asn Ile Asp  Val Pro Ser Arg Thr  Ala Arg Ala
    1070                1075                1080

Ile Thr  Thr Arg Ser Gly Gln  Thr Leu Ser Lys Val  Trp Tyr Asn
    1085                1090                1095

Cys Pro
    1100
```

<210> 24
<211> 514
<212> DNA
<213> Artificial

<220>
<223> Lub:5 DNA insert from cDNA cassette-1 and four synthetic cDNA cassette-2 sequences

<400> 24

```
gcgcgcccac aactccaaaa gagcccgcac ctaccacgac aaagtcagct cctactacgc     60

ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaagaaccag    120

cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc acaacaccaa    180

aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag gagcctgcac    240

ccacaaccac gaagagcgca cccacaacac caaaggagcc ggcccctacg actcctaaag    300

aaccagcccc tactacgaca aaggagcctg cacccacaac cacgaagagc gcacccacaa    360

caccaaagga gccggccccc acgactccta aagaaccagc ccctactacg acaaaggagc    420

ctgcacccac aaccacgaag agcgcaccca caacaccaaa ggagccggcc cctacgactc    480

ctaaggaacc caaaccggca ccaaccactc cgga                                514
```

<210> 25
<211> 170
<212> PRT
<213> Artificial

<220>
<223> 170 amino acids encoded by Lub:5 DNA insert (15 KEPAPTT sequences between S373 and E544 in SEQ ID NO: 23)

<400> 25

```
Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
1               5                  10                  15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
            20                  25                  30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
        35                  40                  45
```

```
Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro
    50                  55                  60

Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro
65                  70                  75                  80

Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
                85                  90                  95

Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr
            100                 105                 110

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
        115                 120                 125

Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr Thr
    130                 135                 140

Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Pro
145                 150                 155                 160

Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
                165                 170
```

<210> 26
<211> 45
<212> PRT
<213> Artificial

<220>
<223> amino acid sequence "APTTPKEPAPTTTKSAPTTPKEPAPTTT KEPAPTTPKEPAPTTTK" (45 amino acids) in preferred PRG4-LUB:N protein

<400> 26

```
Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
1               5                   10                  15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
            20                  25                  30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys
        35                  40                  45
```

<210> 27
<211> 31
<212> PRT
<213> Artificial

<220>
<223> amino acid sequence "KEPAPTTTKEPAPTTTKSAPTTPKEPAPTTP" (31 amino acids) repeated N-1 times in preferred PRG4-LUB:N protein

<400> 27

```
Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr Thr Thr
1               5                   10                  15

Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Pro
            20                  25                  30
```

<210> 28
<211> 22
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence "EPAPTTTKSAPTTPKEPAPTTP" (22 amino acids) joining SEQ ID NO: 26 to (N-2) repeats of SEQ ID NO: 27 in preferred PRG4-LUB:N protein where N = 3 or more.

<400> 28

```
Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu
1               5                   10                  15

Pro Ala Pro Thr Thr Pro
            20
```

<210> 29
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence "KEPKPAPTTP" (10 amino acids) in preferred PRG4-LUB:N protein where N = 2 or more.

<400> 29

```
Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
1               5                   10
```