

SEQUENCE LISTING

<110> INTREXON ACTOBIOTICS N.V.

<120> MUCOADHESIVE MICROORGANISM

<130> 205350-0031-00-WO

<140>

<141>

<150> 62/394,024

<151> 2016-09-13

<160> 25

<170> PatentIn version 3.5

<210> 1

<211> 838

<212> PRT

<213> Lactobacillus reuteri

<220>

<221> MISC_FEATURE

<222> (1)..(50)

<223> Signal sequence

<220>

<221> MISC_FEATURE

<222> (51)..(838)

<223> Mature protein

<400> 1

Met	Leu	Ser	Arg	Lys	Asn	Tyr	Lys	Glu	Thr	Ile	Arg	Lys	Gln	Thr	Pro
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Thr	Lys	Gln	Tyr	Tyr	Thr	Ile	Lys	Lys	Leu	Thr	Val	Gly	Val	Thr	Ser
			20					25					30		

Val	Leu	Ile	Gly	Leu	Ser	Phe	Met	Gly	Glu	Leu	Glu	Gly	Asp	Ser	Val
		35					40					45			

His	Ala	Asp	Thr	Met	Thr	Ala	Ser	Ser	Glu	Ser	Thr	Ser	Val	Thr	Ser
	50					55					60				

Thr Thr Ala Gln Asp Gly Leu Lys Lys Ser Pro Gln Leu Tyr Leu Gln
65 70 75 80

Val Thr Asp Thr Asn Asn Pro Ser Thr Pro Leu Ser Ala Ser Ser Thr
85 90 95

Gly Thr Ser Lys Asn Val Thr Ser Ser Ala Ala Val Gln Val Lys Ser
100 105 110

Ala Ser Asp Glu Glu Asp Ser Asp Ser Thr Leu Ala Lys Gly Glu Asn
115 120 125

Lys Phe Ala Arg Ser Ala Val Lys Asp Ser Val Thr Asp Gly Lys Thr
130 135 140

Ser Thr Ala Glu Ile Asn Pro Ala Lys Leu Ser Ser Pro Ala Leu Ile
145 150 155 160

Thr Gln Leu Asn Gln Ser Leu Ala Lys Ser Ser Thr Ser Asp Ala Ala
165 170 175

Lys Ala Asn Asp Glu Leu Glu Ile Lys Ala Thr Asp Pro Thr Asn Tyr
180 185 190

Pro Asn Cys Gly Asp Val Tyr Gly Pro Leu Phe Glu Leu Asp Ala Ser
195 200 205

Gly Gln Leu Val Asn Lys Asp Glu Val Ile Ser Leu Lys Asp Met Tyr
210 215 220

Ile Phe Gln Ile Leu Lys Leu Val Asn Thr Lys Asp Ser Asp Phe Gln
225 230 235 240

Tyr Val Ile Leu Thr Met Asn Arg Lys Asp Thr Ala Asp Arg Ser Val
245 250 255

Tyr Leu Phe Val Thr Gly Ser Asn Tyr Ser Asn Ala Val Val Val Lys

260

265

270

Val Lys Pro Asn Asp Thr Tyr Glu Leu Ser Lys Thr Gly Tyr Ser Val
 275 280 285

Thr Tyr Thr Glu Pro Thr Thr Ile Asn Gly His Tyr Val Asp Gly Thr
 290 295 300

Phe Tyr Val Thr Gly Ser Thr Tyr Asp Asp Gly Phe Ile Met Pro Asp
 305 310 315 320

Trp Gln Leu Gln His Leu Gln Ile Ile Tyr Ser Leu Gly Asn Tyr Asp
 325 330 335

Pro Ser Asn Thr Asp Ala Thr Ser Val Cys Glu Ile Met Pro Ser Tyr
 340 345 350

Glu Lys Val Pro Val Ile Lys Tyr Ser Gly Val Pro Ser Asn Ile Ser
 355 360 365

Gln Pro Lys Val Tyr Ile Thr Gly Phe Thr Gly Gln Glu Phe Asn Val
 370 375 380

Thr Asp Ile Ile Asn Asn Tyr Lys Lys Val Phe Lys Gly Tyr Tyr Leu
 385 390 395 400

Gln Asn Pro Asn Val Ala Ser Met Gly Thr Leu Ser Gln Phe Glu Asn
 405 410 415

Gly Gly Tyr Tyr Leu Lys Thr Tyr Tyr Asp Asn Asp Gly Asn Val Asp
 420 425 430

Phe Lys Gly Leu Tyr His Gln Ile Asp Asp Gln Gly Thr Met Ser Val
 435 440 445

Ser Val Leu Asn Ala Asp Asn Lys Thr Ile Val Gly Pro Glu Asn Ile
 450 455 460

Leu Ala Gly Lys Ser His Asn Phe Asn Phe Asn Gly His Asn Trp Ile
465 470 475 480

Ala Arg Asn Pro Tyr Val Thr Ser Ser Ala His Glu Val Ile Leu Lys
485 490 495

Tyr Ala Lys Leu Gly Ser Val Ile Pro Val Asp Glu Asn Gly Asn Lys
500 505 510

Ile Asn Asp Gly Trp Gln Tyr Val Asn Asp Pro Asp Asp Ala Ser Lys
515 520 525

Ala Thr Ser Pro Tyr Glu Lys Ala Pro Val Ile Asp Gly Tyr Val Ala
530 535 540

Val Asn Pro Asp Glu Thr Ile Val Leu Pro His Asn Leu Ser Ser Asp
545 550 555 560

Thr Lys Ile Tyr Tyr Arg Lys Arg Ile Lys Val Thr Tyr Ser Gly Ser
565 570 575

Asp Ser Lys Thr Tyr Asp Gly Asn Pro Ala Asn Phe Glu Pro Thr Thr
580 585 590

Val Gln Trp Ser Gly Leu Lys Gly Leu Asn Thr Ser Thr Leu Thr Ser
595 600 605

Ala Asp Phe Thr Trp Asn Thr Ala Asp Lys Lys Ala Pro Thr Asp Ala
610 615 620

Gly Lys Tyr Thr Leu Ser Leu Asn Thr Thr Gly Glu Ala Ala Leu Arg
625 630 635 640

Lys Ala Asn Pro Asn Tyr Asp Leu Lys Thr Ile Ser Gly Ser Tyr Thr
645 650 655

Tyr Thr Ile Asn Pro Leu Gly Ile Val Thr Val Asn Tyr Lys Gly Tyr

660

665

670

Asp Lys Lys Val Tyr Asp Gly Gln Pro Gly Thr Ile Asn Pro Gly Lys
 675 680 685

Leu Thr Trp Ser Lys Leu Pro Asp Gly Thr Ser Leu Lys Met Pro Thr
 690 695 700

Trp Ser Ile Asp Asp Phe Ala Trp Glu Thr Ala Asp Gly Leu Ala Pro
 705 710 715 720

Thr Ala Val Gly Thr Tyr Arg Ile Ile Leu Thr Asp Ala Gly Lys Ala
 725 730 735

Ala Leu Lys Lys Ile Asn Pro Asn Tyr Asp Leu Ser Ser Ile Thr Gly
 740 745 750

Val Phe Thr Tyr Glu Ile Lys Pro Ala Gln Thr Pro Glu Ile Leu Gly
 755 760 765

Gln Thr Pro Glu Gln Gln Pro Gly Gln Asn Thr Asn Gln Ser Gly Ala
 770 775 780

Glu Asn Gly Phe Gly Ser Ser Thr Arg Pro Asn Ala Ser Thr Asn Ser
 785 790 795 800

Asn Leu Asn Gln Leu Pro Gln Thr Gly Asn Glu His Ser Asn Thr Ala
 805 810 815

Leu Ala Gly Leu Ala Leu Ala Phe Leu Thr Ala Met Leu Gly Leu Gly
 820 825 830

Lys Lys Arg Lys His Asp
 835

<210> 2

<211> 2517

<212> DNA

<213> Lactobacillus reuteri

<220>

<221> misc_feature

<222> (1)..(150)

<223> Signal sequence

<220>

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<222> (151)..(2514)

<223> Mature protein

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<221> misc_feature

<222> (2515)..(2517)

<223> Stop codon

<400> 2

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tatactatta agaaattaac tgttgggggtt acttcggtat taattgggtct atcctttatg 120

ggagaactag aaggggatag cgttcatgcg gacacgatga cagcaagcag tgagtcaaca 180

agtgttacgt cgacgactgc tcaggatggg ttaaaaaaat ctccacaact ctatttgcaa 240

gttactgata caaataaccc aagtacacca ttaagtgtt catccacagg gactagtaag 300

aatgttacct catcagctgc ggtacaagtg aagtccgcta gtgatgaaga agatagtgat 360

tctacactag ctaagggaga aaataaat tctcggtcag cagtaaaaga ttcagtcact 420

gatgggaaaa caagtacagc agaaattaat cgggcaaat taagcagtcc tgctttaata 480

acgcaactca accaatcctt agctaagagc agtacgagtg atgcagcaaa agctaattgat 540

gagttagaaa ttaaagcaac agatccgact aattatccaa actgtggcga tgtgtatggg 600

ccattatttg aattggatgc tagcggacag cttgttaata aagatgaagt tatatctctt 660

aaagatatgt atattttcca aatattgaaa ttagtaaata caaaagatag tgactttcaa 720

tatgtaatat taacaatgaa tcgtaaagat actgcagata ggtctgtata tctttttgta 780

actggaagca attatagtaa tgctgttggt gttaaagtaa agccaaatga tacttatgaa 840

ttaagtaaaa ctggatatag tgttacttat acagaaccaa caactataaa tggacattat 900

gttgatggaa ctttttatgt tacaggaagt acttacgatg atggttttat aatgccagat 960

tggcaactgc agcaccttca gattatatat agtttaggaa attatgatcc aagcaatact	1020
gacgcaacat cagtttgtga aataatgcca agttatgaaa aggtaccggt aattaaatat	1080
agtggagtac cttcaaatat tagccaacct aaggtttaca ttaccgggtt tacgggtcaa	1140
gagtttaacg ttacagatat tattaacaat tataagaaag tttttaaggg ctactatctt	1200
caaaatccta atgtggcgtc catgggaact ctttccaat ttgagaatgg tggttattac	1260
ttaaagacat attatgataa tgatggtaat gttgacttta agggcttgta tcatcaaatt	1320
gatgatcagg gaacaatgag tgtgagtgtt cttaatgcag ataataaaac aattgttgga	1380
cctgaaaata ttcttgctgg taaatcgcat aactttaact ttaatgggtca taactggatt	1440
gcgcggaatc cttatgtcac tagttcagct cacgaagtca tattaagta tgctaagta	1500
ggttcagtta ttcctgttga tgaaaacgga aataaaataa acgatggatg gcaatatgtt	1560
aatgatccag atgatgcttc caaagccact agcccatatg aaaaagcgcc agttatcgat	1620
ggttatgtag ctgtaaattcc agatgaaacg atcgttcttc ctcataactt aagtagtgac	1680
acaaagattt attaccgaaa gaggattaaa gttacctata gtggtagtga cagcaagacc	1740
tacgatggta acccagctaa cttcgagcca acgacagttc agtggagtgg cttgaaagga	1800
ctgaacactt caaccttaac gtccgctgac ttcacgtgga atactgcgga taagaaggca	1860
ccaacggatg ccggttaagta cacacttagt ttgaatacga ccggagaagc agccttacgt	1920
aaggctaacc cgaactatga tctcaagaca attagcggta gttacaccta cacgattaat	1980
ccactaggga ttgtgactgt aaattacaag ggctatgata agaaagtcta tgatgggtcaa	2040
cctggaacga ttaatccggg taaattaacg tggagtaagt tgccagatgg tacttcattg	2100
aagatgccaa catggagtat agatgatttc gcttgggaaa cagctgatgg cttagcacca	2160
acggcagtag gaacttatcg gattatcttg acggatgctg gtaaggctgc actaaagaag	2220
attaatccaa attatgactt aagcagtatt actggtgtct ttacttatga aattaagcca	2280
gcacagacac cagaaatctt aggccaaaca cctgagcaac aaccaggcca aaataactaat	2340
caatcaggag ctgaaaacgg ctttggttct tctacaaggc ctaatgcatc aactaactcc	2400
aatcttaatc aacttcaca gactggtaat gagcattcta atactgcact tgctggtcta	2460

gcattggctt tcttgactgc tatgcttggt ttgggcaaga agcgtaaaca tgattaa 2517

<210> 3
<211> 59
<212> PRT
<213> Homo sapiens

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Glu Glu Tyr Val Gly Leu Ser Ala Asn Gln Cys Ala Val Pro Ala Lys
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Asp Arg Val Asp Cys Gly Tyr Pro His Val Thr Pro Lys Glu Cys Asn
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Asn Arg Gly Cys Cys Phe Asp Ser Arg Ile Pro Gly Val Pro Trp Cys
35 40 45

Phe Lys Pro Leu Gln Glu Ala Glu Cys Thr Phe
50 55

<210> 4
<211> 180
<212> DNA
<213> Homo sapiens

<400> 4
gaagaatacg ttggtctttc agctaaccaa tgtgctgttc cagctaaaga tcgtgttgat 60
tgtggttacc cacacgttac tccaaaagaa tgtaacaacc gtggttggtg ttttgattca 120
cgtatcccag gtgttccatg gtgttttaaa ccacttcaag aagctgaatg tactttttta 180

<210> 5
<211> 27
<212> PRT
<213> Lactococcus lactis

<400> 5
Met Lys Lys Lys Ile Ile Ser Ala Ile Leu Met Ser Thr Val Ile Leu
1 5 10 15

Ser Ala Ala Ala Pro Leu Ser Gly Val Tyr Ala

<210> 6
 <211> 81
 <212> DNA
 <213> Lactococcus lactis

<400> 6
 atgaaaaaaa agattatctc agctatTTTA atgtctacag tgatactttc tgctgcagcc 60
 ccgttgtcag gtgtttacgc c 81

<210> 7
 <211> 81
 <212> DNA
 <213> Lactococcus lactis

<400> 7
 atgaagaaga aaatcattag tgccatctta atgtctacag tgattctttc agctgcagct 60
 cctttatcag gcgtttatgc a 81

<210> 8
 <211> 86
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

<220>
 <221> MISC_FEATURE
 <222> (1)..(27)
 <223> SSusp45

<220>
 <221> MISC_FEATURE
 <222> (28)..(86)
 <223> hTFF3

<400> 8
 Met Lys Lys Lys Ile Ile Ser Ala Ile Leu Met Ser Thr Val Ile Leu
 1 5 10 15

Ser Ala Ala Ala Pro Leu Ser Gly Val Tyr Ala Glu Glu Tyr Val Gly
20 25 30

Leu Ser Ala Asn Gln Cys Ala Val Pro Ala Lys Asp Arg Val Asp Cys
35 40 45

Gly Tyr Pro His Val Thr Pro Lys Glu Cys Asn Asn Arg Gly Cys Cys
50 55 60

Phe Asp Ser Arg Ile Pro Gly Val Pro Trp Cys Phe Lys Pro Leu Gln
65 70 75 80

Glu Ala Glu Cys Thr Phe
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<210> 9
<211> 261
<212> DNA
<213> Artificial Sequence

<220>
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polynucleotide

<220>
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<222> (1)..(258)

<220>
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<222> (1)..(81)
<223> SSusp45

<220>
<221> misc_feature
<222> (82)..(258)
<223> hTFF3

<220>
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<222> (259)..(261)
<223> Stop codon

<400> 9

atg aaa aaa aag att atc tca gct att tta atg tct aca gtg ata ctt	48
Met Lys Lys Lys Ile Ile Ser Ala Ile Leu Met Ser Thr Val Ile Leu	
1 5 10 15	
tct gct gca gcc ccg ttg tca ggt gtt tac gcc gaa gaa tac gtt ggt	96
Ser Ala Ala Ala Pro Leu Ser Gly Val Tyr Ala Glu Glu Tyr Val Gly	
20 25 30	
ctt tca gct aac caa tgt gct gtt cca gct aaa gat cgt gtt gat tgt	144
Leu Ser Ala Asn Gln Cys Ala Val Pro Ala Lys Asp Arg Val Asp Cys	
35 40 45	
ggt tac cca cac gtt act cca aaa gaa tgt aac aac cgt ggt tgt tgt	192
Gly Tyr Pro His Val Thr Pro Lys Glu Cys Asn Asn Arg Gly Cys Cys	
50 55 60	
ttt gat tca cgt atc cca ggt gtt cca tgg tgt ttt aaa cca ctt caa	240
Phe Asp Ser Arg Ile Pro Gly Val Pro Trp Cys Phe Lys Pro Leu Gln	
65 70 75 80	
gaa gct gaa tgt act ttt taa	261
Glu Ala Glu Cys Thr Phe	
85	

<210> 10
 <211> 874
 <212> PRT
 <213> Artificial Sequence

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 <222> (28)..(86)
 <223> hTFF3

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 <222> (87)..(874)
 <223> CmbA

<400> 10

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

Ser Ala Ala Ala Pro Leu Ser Gly Val Tyr Ala Glu Glu Tyr Val Gly
20 25 30

Leu Ser Ala Asn Gln Cys Ala Val Pro Ala Lys Asp Arg Val Asp Cys
35 40 45

Gly Tyr Pro His Val Thr Pro Lys Glu Cys Asn Asn Arg Gly Cys Cys
50 55 60

Phe Asp Ser Arg Ile Pro Gly Val Pro Trp Cys Phe Lys Pro Leu Gln
65 70 75 80

Glu Ala Glu Cys Thr Phe Asp Thr Met Thr Ala Ser Ser Glu Ser Thr
85 90 95

Ser Val Thr Ser Thr Thr Ala Gln Asp Gly Leu Lys Lys Ser Pro Gln
100 105 110

Leu Tyr Leu Gln Val Thr Asp Thr Asn Asn Pro Ser Thr Pro Leu Ser
115 120 125

Ala Ser Ser Thr Gly Thr Ser Lys Asn Val Thr Ser Ser Ala Ala Val
130 135 140

Gln Val Lys Ser Ala Ser Asp Glu Glu Asp Ser Asp Ser Thr Leu Ala
145 150 155 160

Lys Gly Glu Asn Lys Phe Ala Arg Ser Ala Val Lys Asp Ser Val Thr
165 170 175

Asp Gly Lys Thr Ser Thr Ala Glu Ile Asn Pro Ala Lys Leu Ser Ser
180 185 190

Pro Ala Leu Ile Thr Gln Leu Asn Gln Ser Leu Ala Lys Ser Ser Thr

195

200

205

Ser Asp Ala Ala Lys Ala Asn Asp Glu Leu Glu Ile Lys Ala Thr Asp
 210 215 220

Pro Thr Asn Tyr Pro Asn Cys Gly Asp Val Tyr Gly Pro Leu Phe Glu
 225 230 235 240

Leu Asp Ala Ser Gly Gln Leu Val Asn Lys Asp Glu Val Ile Ser Leu
 245 250 255

Lys Asp Met Tyr Ile Phe Gln Ile Leu Lys Leu Val Asn Thr Lys Asp
 260 265 270

Ser Asp Phe Gln Tyr Val Ile Leu Thr Met Asn Arg Lys Asp Thr Ala
 275 280 285

Asp Arg Ser Val Tyr Leu Phe Val Thr Gly Ser Asn Tyr Ser Asn Ala
 290 295 300

Val Val Val Lys Val Lys Pro Asn Asp Thr Tyr Glu Leu Ser Lys Thr
 305 310 315 320

Gly Tyr Ser Val Thr Tyr Thr Glu Pro Thr Thr Ile Asn Gly His Tyr
 325 330 335

Val Asp Gly Thr Phe Tyr Val Thr Gly Ser Thr Tyr Asp Asp Gly Phe
 340 345 350

Ile Met Pro Asp Trp Gln Leu Gln His Leu Gln Ile Ile Tyr Ser Leu
 355 360 365

Gly Asn Tyr Asp Pro Ser Asn Thr Asp Ala Thr Ser Val Cys Glu Ile
 370 375 380

Met Pro Ser Tyr Glu Lys Val Pro Val Ile Lys Tyr Ser Gly Val Pro
 385 390 395 400

Ser Asn Ile Ser Gln Pro Lys Val Tyr Ile Thr Gly Phe Thr Gly Gln
405 410 415

Glu Phe Asn Val Thr Asp Ile Ile Asn Asn Tyr Lys Lys Val Phe Lys
420 425 430

Gly Tyr Tyr Leu Gln Asn Pro Asn Val Ala Ser Met Gly Thr Leu Ser
435 440 445

Gln Phe Glu Asn Gly Gly Tyr Tyr Leu Lys Thr Tyr Tyr Asp Asn Asp
450 455 460

Gly Asn Val Asp Phe Lys Gly Leu Tyr His Gln Ile Asp Asp Gln Gly
465 470 475 480

Thr Met Ser Val Ser Val Leu Asn Ala Asp Asn Lys Thr Ile Val Gly
485 490 495

Pro Glu Asn Ile Leu Ala Gly Lys Ser His Asn Phe Asn Phe Asn Gly
500 505 510

His Asn Trp Ile Ala Arg Asn Pro Tyr Val Thr Ser Ser Ala His Glu
515 520 525

Val Ile Leu Lys Tyr Ala Lys Leu Gly Ser Val Ile Pro Val Asp Glu
530 535 540

Asn Gly Asn Lys Ile Asn Asp Gly Trp Gln Tyr Val Asn Asp Pro Asp
545 550 555 560

Asp Ala Ser Lys Ala Thr Ser Pro Tyr Glu Lys Ala Pro Val Ile Asp
565 570 575

Gly Tyr Val Ala Val Asn Pro Asp Glu Thr Ile Val Leu Pro His Asn
580 585 590

Leu Ser Ser Asp Thr Lys Ile Tyr Tyr Arg Lys Arg Ile Lys Val Thr

595

600

605

Tyr Ser Gly Ser Asp Ser Lys Thr Tyr Asp Gly Asn Pro Ala Asn Phe
 610 615 620

Glu Pro Thr Thr Val Gln Trp Ser Gly Leu Lys Gly Leu Asn Thr Ser
 625 630 635 640

Thr Leu Thr Ser Ala Asp Phe Thr Trp Asn Thr Ala Asp Lys Lys Ala
 645 650 655

Pro Thr Asp Ala Gly Lys Tyr Thr Leu Ser Leu Asn Thr Thr Gly Glu
 660 665 670

Ala Ala Leu Arg Lys Ala Asn Pro Asn Tyr Asp Leu Lys Thr Ile Ser
 675 680 685

Gly Ser Tyr Thr Tyr Thr Ile Asn Pro Leu Gly Ile Val Thr Val Asn
 690 695 700

Tyr Lys Gly Tyr Asp Lys Lys Val Tyr Asp Gly Gln Pro Gly Thr Ile
 705 710 715 720

Asn Pro Gly Lys Leu Thr Trp Ser Lys Leu Pro Asp Gly Thr Ser Leu
 725 730 735

Lys Met Pro Thr Trp Ser Ile Asp Asp Phe Ala Trp Glu Thr Ala Asp
 740 745 750

Gly Leu Ala Pro Thr Ala Val Gly Thr Tyr Arg Ile Ile Leu Thr Asp
 755 760 765

Ala Gly Lys Ala Ala Leu Lys Lys Ile Asn Pro Asn Tyr Asp Leu Ser
 770 775 780

Ser Ile Thr Gly Val Phe Thr Tyr Glu Ile Lys Pro Ala Gln Thr Pro
 785 790 795 800

Glu Ile Leu Gly Gln Thr Pro Glu Gln Gln Pro Gly Gln Asn Thr Asn
805 810 815

Gln Ser Gly Ala Glu Asn Gly Phe Gly Ser Ser Thr Arg Pro Asn Ala
820 825 830

Ser Thr Asn Ser Asn Leu Asn Gln Leu Pro Gln Thr Gly Asn Glu His
835 840 845

Ser Asn Thr Ala Leu Ala Gly Leu Ala Leu Ala Phe Leu Thr Ala Met
850 855 860

Leu Gly Leu Gly Lys Lys Arg Lys His Asp
865 870

<210> 11
<211> 2625
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
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<220>
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<222> (1)..(81)
<223> SSusp45

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<223> hTFF3

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<222> (259)..(2622)
<223> CmbA

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<222> (2623)..(2625)

<223> Stop codon

<400> 11

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

tct	gct	gca	gcc	ccg	ttg	tca	ggg	gtt	tac	gcc	gaa	gaa	tac	gtt	ggg	96
Ser	Ala	Ala	Ala	Pro	Leu	Ser	Gly	Val	Tyr	Ala	Glu	Glu	Tyr	Val	Gly	
			20					25					30			

ctt	tca	gct	aac	caa	tgt	gct	gtt	cca	gct	aaa	gat	cgt	gtt	gat	tgt	144
Leu	Ser	Ala	Asn	Gln	Cys	Ala	Val	Pro	Ala	Lys	Asp	Arg	Val	Asp	Cys	
		35					40					45				

ggg	tac	cca	cac	gtt	act	cca	aaa	gaa	tgt	aac	aac	cgt	ggg	tgt	tgt	192
Gly	Tyr	Pro	His	Val	Thr	Pro	Lys	Glu	Cys	Asn	Asn	Arg	Gly	Cys	Cys	
	50					55					60					

ttt	gat	tca	cgt	atc	cca	ggg	gtt	cca	tgg	tgt	ttt	aaa	cca	ctt	caa	240
Phe	Asp	Ser	Arg	Ile	Pro	Gly	Val	Pro	Trp	Cys	Phe	Lys	Pro	Leu	Gln	
65					70				75					80		

gaa	gct	gaa	tgt	act	ttt	gac	acg	atg	aca	gca	agc	agt	gag	tca	aca	288
Glu	Ala	Glu	Cys	Thr	Phe	Asp	Thr	Met	Thr	Ala	Ser	Ser	Glu	Ser	Thr	
				85					90					95		

agt	gtt	acg	tcg	acg	act	gct	cag	gat	ggg	tta	aaa	aaa	tct	cca	caa	336
Ser	Val	Thr	Ser	Thr	Thr	Ala	Gln	Asp	Gly	Leu	Lys	Lys	Ser	Pro	Gln	
			100					105						110		

ctc	tat	ttg	caa	gtt	act	gat	aca	aat	aac	cca	agt	aca	cca	tta	agt	384
Leu	Tyr	Leu	Gln	Val	Thr	Asp	Thr	Asn	Asn	Pro	Ser	Thr	Pro	Leu	Ser	
		115					120					125				

gct	tca	tcc	aca	ggg	act	agt	aag	aat	gtt	acc	tca	tca	gct	gcg	gta	432
Ala	Ser	Ser	Thr	Gly	Thr	Ser	Lys	Asn	Val	Thr	Ser	Ser	Ala	Ala	Val	
		130					135				140					

caa	gtg	aag	tcc	gct	agt	gat	gaa	gaa	gat	agt	gat	tct	aca	cta	gct	480
Gln	Val	Lys	Ser	Ala	Ser	Asp	Glu	Glu	Asp	Ser	Asp	Ser	Thr	Leu	Ala	
145					150				155					160		

aag	gga	gaa	aat	aaa	ttt	gct	cgg	tca	gca	gta	aaa	gat	tca	gtc	act	528
Lys	Gly	Glu	Asn	Lys	Phe	Ala	Arg	Ser	Ala	Val	Lys	Asp	Ser	Val	Thr	
				165					170					175		

gat ggg aaa aca agt aca gca gaa att aat ccg gca aaa tta agc agt Asp Gly Lys Thr Ser Thr Ala Glu Ile Asn Pro Ala Lys Leu Ser Ser	576
180 185 190	
cct gct tta ata acg caa ctc aac caa tcc tta gct aag agc agt acg Pro Ala Leu Ile Thr Gln Leu Asn Gln Ser Leu Ala Lys Ser Ser Thr	624
195 200 205	
agt gat gca gca aaa gct aat gat gag tta gaa att aaa gca aca gat Ser Asp Ala Ala Lys Ala Asn Asp Glu Leu Glu Ile Lys Ala Thr Asp	672
210 215 220	
ccg act aat tat cca aac tgt ggc gat gtg tat ggg cca tta ttt gaa Pro Thr Asn Tyr Pro Asn Cys Gly Asp Val Tyr Gly Pro Leu Phe Glu	720
225 230 235 240	
ttg gat gct agc gga cag ctt gtt aat aaa gat gaa gtt ata tct ctt Leu Asp Ala Ser Gly Gln Leu Val Asn Lys Asp Glu Val Ile Ser Leu	768
245 250 255	
aaa gat atg tat att ttc caa ata ttg aaa tta gta aat aca aaa gat Lys Asp Met Tyr Ile Phe Gln Ile Leu Lys Leu Val Asn Thr Lys Asp	816
260 265 270	
agt gac ttt caa tat gta ata tta aca atg aat cgt aaa gat act gca Ser Asp Phe Gln Tyr Val Ile Leu Thr Met Asn Arg Lys Asp Thr Ala	864
275 280 285	
gat agg tct gta tat ctt ttt gta act gga agc aat tat agt aat gct Asp Arg Ser Val Tyr Leu Phe Val Thr Gly Ser Asn Tyr Ser Asn Ala	912
290 295 300	
gtt gtt gtt aaa gta aag cca aat gat act tat gaa tta agt aaa act Val Val Val Lys Val Lys Pro Asn Asp Thr Tyr Glu Leu Ser Lys Thr	960
305 310 315 320	
gga tat agt gtt act tat aca gaa cca aca act ata aat gga cat tat Gly Tyr Ser Val Thr Tyr Thr Glu Pro Thr Thr Ile Asn Gly His Tyr	1008
325 330 335	
gtt gat gga act ttt tat gtt aca gga agt act tac gat gat ggt ttt Val Asp Gly Thr Phe Tyr Val Thr Gly Ser Thr Tyr Asp Asp Gly Phe	1056
340 345 350	
ata atg cca gat tgg caa ctg cag cac ctt cag att ata tat agt tta Ile Met Pro Asp Trp Gln Leu Gln His Leu Gln Ile Ile Tyr Ser Leu	1104
355 360 365	
gga aat tat gat cca agc aat act gac gca aca tca gtt tgt gaa ata Gly Asn Tyr Asp Pro Ser Asn Thr Asp Ala Thr Ser Val Cys Glu Ile	1152

370	375	380	
atg cca agt tat gaa aag gta ccg gta att aaa tat agt gga gta cct			1200
Met Pro Ser Tyr Glu Lys Val Pro Val Ile Lys Tyr Ser Gly Val Pro			
385	390	395	400
tca aat att agc caa cct aag gtt tac att acc ggg ttt acg ggt caa			1248
Ser Asn Ile Ser Gln Pro Lys Val Tyr Ile Thr Gly Phe Thr Gly Gln			
	405	410	415
gag ttt aac gtt aca gat att att aac aat tat aag aaa gtt ttt aag			1296
Glu Phe Asn Val Thr Asp Ile Ile Asn Asn Tyr Lys Lys Val Phe Lys			
	420	425	430
ggc tac tat ctt caa aat cct aat gtg gcg tcc atg gga act ctt tcc			1344
Gly Tyr Tyr Leu Gln Asn Pro Asn Val Ala Ser Met Gly Thr Leu Ser			
	435	440	445
caa ttt gag aat ggt ggt tat tac tta aag aca tat tat gat aat gat			1392
Gln Phe Glu Asn Gly Gly Tyr Tyr Leu Lys Thr Tyr Tyr Asp Asn Asp			
	450	455	460
ggt aat gtt gac ttt aag ggc ttg tat cat caa att gat gat cag gga			1440
Gly Asn Val Asp Phe Lys Gly Leu Tyr His Gln Ile Asp Asp Gln Gly			
465	470	475	480
aca atg agt gtg agt gtt ctt aat gca gat aat aaa aca att gtt gga			1488
Thr Met Ser Val Ser Val Leu Asn Ala Asp Asn Lys Thr Ile Val Gly			
	485	490	495
cct gaa aat att ctt gct ggt aaa tcg cat aac ttt aac ttt aat ggt			1536
Pro Glu Asn Ile Leu Ala Gly Lys Ser His Asn Phe Asn Phe Asn Gly			
	500	505	510
cat aac tgg att gcg cgg aat cct tat gtc act agt tca gct cac gaa			1584
His Asn Trp Ile Ala Arg Asn Pro Tyr Val Thr Ser Ser Ala His Glu			
	515	520	525
gtc ata tta aag tat gct aag tta ggt tca gtt att cct gtt gat gaa			1632
Val Ile Leu Lys Tyr Ala Lys Leu Gly Ser Val Ile Pro Val Asp Glu			
	530	535	540
aac gga aat aaa ata aac gat gga tgg caa tat gtt aat gat cca gat			1680
Asn Gly Asn Lys Ile Asn Asp Gly Trp Gln Tyr Val Asn Asp Pro Asp			
545	550	555	560
gat gct tcc aaa gcc act agc cca tat gaa aaa gcg cca gtt atc gat			1728
Asp Ala Ser Lys Ala Thr Ser Pro Tyr Glu Lys Ala Pro Val Ile Asp			
	565	570	575

ggt tat gta gct gta aat cca gat gaa acg atc gtt ctt cct cat aac	1776
Gly Tyr Val Ala Val Asn Pro Asp Glu Thr Ile Val Leu Pro His Asn	
580 585 590	
tta agt agt gac aca aag att tat tac cga aag agg att aaa gtt acc	1824
Leu Ser Ser Asp Thr Lys Ile Tyr Tyr Arg Lys Arg Ile Lys Val Thr	
595 600 605	
tat agt ggt agt gac agc aag acc tac gat ggt aac cca gct aac ttc	1872
Tyr Ser Gly Ser Asp Ser Lys Thr Tyr Asp Gly Asn Pro Ala Asn Phe	
610 615 620	
gag cca acg aca gtt cag tgg agt ggc ttg aaa gga ctg aac act tca	1920
Glu Pro Thr Thr Val Gln Trp Ser Gly Leu Lys Gly Leu Asn Thr Ser	
625 630 635 640	
acc tta acg tcc gct gac ttc acg tgg aat act gcg gat aag aag gca	1968
Thr Leu Thr Ser Ala Asp Phe Thr Trp Asn Thr Ala Asp Lys Lys Ala	
645 650 655	
cca acg gat gcc ggt aag tac aca ctt agt ttg aat acg acc gga gaa	2016
Pro Thr Asp Ala Gly Lys Tyr Thr Leu Ser Leu Asn Thr Thr Gly Glu	
660 665 670	
gca gcc tta cgt aag gct aac ccg aac tat gat ctc aag aca att agc	2064
Ala Ala Leu Arg Lys Ala Asn Pro Asn Tyr Asp Leu Lys Thr Ile Ser	
675 680 685	
ggt agt tac acc tac acg att aat cca cta ggg att gtg act gta aat	2112
Gly Ser Tyr Thr Tyr Thr Ile Asn Pro Leu Gly Ile Val Thr Val Asn	
690 695 700	
tac aag ggc tat gat aag aaa gtc tat gat ggt caa cct gga acg att	2160
Tyr Lys Gly Tyr Asp Lys Lys Val Tyr Asp Gly Gln Pro Gly Thr Ile	
705 710 715 720	
aat ccg ggt aaa tta acg tgg agt aag ttg cca gat ggt act tca ttg	2208
Asn Pro Gly Lys Leu Thr Trp Ser Lys Leu Pro Asp Gly Thr Ser Leu	
725 730 735	
aag atg cca aca tgg agt ata gat gat ttc gct tgg gaa aca gct gat	2256
Lys Met Pro Thr Trp Ser Ile Asp Asp Phe Ala Trp Glu Thr Ala Asp	
740 745 750	
ggc tta gca cca acg gca gta gga act tat cgg att atc ttg acg gat	2304
Gly Leu Ala Pro Thr Ala Val Gly Thr Tyr Arg Ile Ile Leu Thr Asp	
755 760 765	
gct ggt aag gct gca cta aag aag att aat cca aat tat gac tta agc	2352
Ala Gly Lys Ala Ala Leu Lys Lys Ile Asn Pro Asn Tyr Asp Leu Ser	

770	775	780	
agt att act ggt gtc ttt act tat gaa att aag cca gca cag aca cca			2400
Ser Ile Thr Gly Val Phe Thr Tyr Glu Ile Lys Pro Ala Gln Thr Pro			
785	790	795	800
gaa atc tta ggc caa aca cct gag caa caa cca ggc caa aat act aat			2448
Glu Ile Leu Gly Gln Thr Pro Glu Gln Gln Pro Gly Gln Asn Thr Asn			
	805	810	815
caa tca gga gct gaa aac ggc ttt ggt tct tct aca agg cct aat gca			2496
Gln Ser Gly Ala Glu Asn Gly Phe Gly Ser Ser Thr Arg Pro Asn Ala			
	820	825	830
tca act aac tcc aat ctt aat caa ctt cca cag act ggt aat gag cat			2544
Ser Thr Asn Ser Asn Leu Asn Gln Leu Pro Gln Thr Gly Asn Glu His			
	835	840	845
tct aat act gca ctt gct ggt cta gca ttg gct ttc ttg act gct atg			2592
Ser Asn Thr Ala Leu Ala Gly Leu Ala Leu Ala Phe Leu Thr Ala Met			
	850	855	860
ctt ggt ttg ggc aag aag cgt aaa cat gat taa			2625
Leu Gly Leu Gly Lys Lys Arg Lys His Asp			
865	870		

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 <211> 16
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown:
 rpmD sequence

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taaggaggaa aaaatg	16

<210> 13
 <211> 10
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown:
 rpmD sequence

<400> 13

ggaggaaaaa

10

<210> 14

<211> 985

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 14

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Val His Ala Asp Thr Pro Ser Asn Asp Lys Pro Val Val Val Thr Thr
35 40 45

Ile Ala Ser Asn Ser Ser Ala Val Glu Ala Glu Thr Ala Ser Ser Ser
50 55 60

Ser Ser Ser Ala Val Lys Ala Glu Thr Thr Ser Ala Ser Ser Ser Ser
65 70 75 80

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

Ala Glu Thr Thr Ser Ala Ser Ser Ser Ser Ala Val Lys Ala Glu Thr
100 105 110

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

Ser Ser Ser Ser Ala Val Lys Ala Glu Thr Thr Ser Ala Ser Ser Ser
130 135 140

Ser Ala Val Lys Ala Glu Thr Ala Ser Ser Ser Ser Ser Ser Ala Val

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

Ser Gly Thr Tyr Leu Phe Pro Thr Gln Ile Gly Tyr Gly Glu Asn Ala
355 360 365

Thr Val Asn Asp Tyr Met Leu Thr Pro Gly Asn Asp Phe Ile Ile Pro
370 375 380

Thr Arg Phe Asn Thr Ile Arg Asn Asp Val Tyr Leu Thr Met Arg Ser
385 390 395 400

Arg Ala Tyr Phe Gly Ala Gly Leu Gln Gly Ala Gln Ala Ser Leu Thr
405 410 415

Ala Thr Ser Asn Gly Lys Pro Val Val Gly Ser Ser Glu Asn Ser Lys
420 425 430

Phe Tyr Ile Asp Thr Asp Ser Asn Val Tyr Leu Thr Lys Gln Gly Phe
435 440 445

Asp Gln Leu Gly Asn Phe Gly Lys Ile Met Ala Pro Phe Val Tyr Thr
450 455 460

Ser Ala Ser Asn Asp Leu Lys Lys Val Gly Ile Asp Lys Phe Ser Ala
465 470 475 480

Met Met Asn Gln Gly Leu Ser Ser Ile Gln Ser Lys Ser Gly Ala Asn
485 490 495

Thr Ile Val Ser Gly Asn Gly Gly Gln Ile Gln Leu Ser Gly Phe Asn
500 505 510

Arg Glu Thr Asp Leu Asp Gly Ala Phe Ser Ser Ser Ile Ser Asp Arg
515 520 525

Glu Asn Asp Ala Leu Lys Asn Thr Asp Val Asn Phe Tyr Met Tyr Thr
530 535 540

Lys Gly Asn Thr Glu Thr Asn Val Thr Thr Pro Leu Ala Pro Asn Gly

545		550		555		560									
Tyr	His	Leu	Tyr	Ser	Pro	Asn	Val	Ser	Glu	Phe	Lys	Ile	Gln	Thr	Thr
				565					570					575	
Arg	Pro	Tyr	Phe	Ser	Trp	Thr	Gly	Asp	Ile	Ser	Asn	Ala	Ile	Lys	Ile
			580					585					590		
Ser	Glu	Ala	Asn	Ala	Asp	Phe	Asp	Asp	Leu	Leu	Gly	Ser	Asn	Ser	Leu
		595					600					605			
Gln	Val	Thr	Asp	Asn	Gly	Val	Asp	Ser	Asp	Gly	Thr	Pro	Ile	Ser	Val
	610					615					620				
Asp	Leu	Asn	Arg	Val	Arg	Ile	Arg	Ile	Ser	Glu	Asp	Gly	Gly	Ser	Thr
625					630					635					640
Tyr	Ser	Asn	Asp	Ser	Tyr	Thr	Leu	Asn	Asp	Leu	Lys	Ala	Leu	Leu	Thr
				645					650						655
Ser	Gly	Asn	Ile	Thr	Val	Pro	Lys	Ile	Val	Ile	Ala	Tyr	Thr	Tyr	Ser
			660					665					670		
Ala	Thr	Asp	Ser	Lys	Thr	Asp	Asn	Ile	Gly	Lys	Leu	Pro	Ser	Glu	Ile
		675					680					685			
Asp	Asp	Asn	Thr	Gly	Ala	Tyr	Ala	Val	Pro	Phe	Thr	Arg	Thr	Leu	Thr
	690					695					700				
Asn	Asp	Ile	Pro	Asp	Lys	Lys	Ser	Asn	Ile	Thr	Val	Lys	Tyr	Ile	Asp
705					710					715					720
Ile	Ser	Gly	Asn	Thr	Ile	Ser	Asp	Asn	Ile	Val	Lys	Ala	Gly	Asn	Val
			725						730					735	
Gly	Asp	Ser	Tyr	Thr	Thr	Glu	Gln	Lys	Ala	Ile	Pro	Gly	Tyr	Thr	Phe
			740					745					750		

Lys Ala Val Gln Gly Asn Pro Thr Gly Gln Phe Thr Ser Asp Ala Gln
755 760 765

Thr Val Thr Tyr Val Tyr Thr Lys Asp Pro Val Ala Gly Gly Ser Val
770 775 780

Thr Ala Lys Tyr Val Asp Thr Ser Gly Asn Ala Ile Ser Asp Asn Val
785 790 795 800

Val Lys Thr Gly Asn Ile Gly Asp Thr Tyr Ser Thr Lys Gln Lys Thr
805 810 815

Ile Pro Gly Tyr Thr Phe Lys Glu Val Gln Gly Ser Val Ser Gly Gln
820 825 830

Phe Thr Asn Gln Glu Gln Thr Val Thr Tyr Val Tyr Thr Lys Asp Pro
835 840 845

Val Ala Gly Ala His Ile Ile Ala Lys Tyr Val Asp Glu Asn Gly Asn
850 855 860

Thr Ile Ser Asp Asn Val Val Lys Ser Gly Asn Ile Gly Asp Ser Tyr
865 870 875 880

Thr Thr Glu Gln Lys Ala Ile Pro Gly Tyr Thr Phe Lys Ala Val Gln
885 890 895

Gly Asn Pro Thr Gly Gln Phe Thr Ser Asp Ala Gln Thr Val Thr Tyr
900 905 910

Ile Tyr Thr Lys Val Lys Thr Ser Gly Gly Ser Glu Thr Pro Thr Pro
915 920 925

Ser Lys Thr Ile Ala Thr Lys Ser Ser Thr Asn Thr Ile Ser Ser Ser
930 935 940

Thr Leu Pro Lys Thr Gly Asp Ser Gln Val Ser Thr Leu Phe Gly Met

945 950 955 960

Val Val Gly Phe Phe Ile Phe Gly Ala Gly Thr Leu Ser Leu Phe Phe
 965 970 975

Asn Ser Lys Arg Lys Arg Lys Ser Lys
 980 985

<210> 15
 <211> 3180
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
 <221> CDS
 <222> (208)..(3162)

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 tctgagaggt tattttggga aatactattg aaccatatcg aggtgggtgtg gtataatgaa 180
 gggaattaaa aaagatagga aaatttc atg aaa aaa aag att atc tca gct att 234
 Met Lys Lys Lys Ile Ile Ser Ala Ile
 1 5
 tta atg tct aca gtg ata ctt tct gct gca gcc ccg ttg tca ggt gtt 282
 Leu Met Ser Thr Val Ile Leu Ser Ala Ala Ala Pro Leu Ser Gly Val
 10 15 20 25
 tac gct ttc aat gga gcg gtc gtg cac gcg gat aca ccg agc aat gac 330
 Tyr Ala Phe Asn Gly Ala Val Val His Ala Asp Thr Pro Ser Asn Asp
 30 35 40
 aaa cct gtg gtt gta aca acc att gcg tca aac tca tct gcc gtt gaa 378
 Lys Pro Val Val Val Thr Thr Ile Ala Ser Asn Ser Ser Ala Val Glu
 45 50 55
 gct gag act gcc agc agt tct tca tca agt gcc gta aaa gcg gaa acg 426
 Ala Glu Thr Ala Ser Ser Ser Ser Ser Ser Ala Val Lys Ala Glu Thr

60	65	70	
acc agc gcc tct tct tca agt gct gta aaa gct gag aca gcc tct agc Thr Ser Ala Ser Ser Ser Ser Ala Val Lys Ala Glu Thr Ala Ser Ser	474		
75	80	85	
agt tca agc tca gcc gta aag gca gaa act acg agt gca tca tct tca Ser Ser Ser Ser Ala Val Lys Ala Glu Thr Thr Ser Ala Ser Ser Ser	522		
90	95	100	105
tca gcg gta aag gcg gag acc gct agc tct tct tct agt agt gct gtg Ser Ala Val Lys Ala Glu Thr Ala Ser Ser Ser Ser Ser Ser Ala Val	570		
110	115	120	
aaa gcc gag acg acg agc gca tct tca tct tct gct gtt aag gcg gaa Lys Ala Glu Thr Thr Ser Ala Ser Ser Ser Ser Ala Val Lys Ala Glu	618		
125	130	135	
aca aca agc gct tct agc tca agc gcc gtc aaa gca gaa aca gcg agt Thr Thr Ser Ala Ser Ser Ser Ser Ala Val Lys Ala Glu Thr Ala Ser	666		
140	145	150	
tca tct tct agt agt gca gtt aaa gcc gaa act acc tct gcc agc tca Ser Ser Ser Ser Ser Ala Val Lys Ala Glu Thr Thr Ser Ala Ser Ser	714		
155	160	165	
tct tca gca gca aag gcg gat acc acc agc gca gct agt tca tct gcg Ser Ser Ala Ala Lys Ala Asp Thr Thr Ser Ala Ala Ser Ser Ser Ala	762		
170	175	180	185
gca aag agc gac agt tca ctt gtg aaa ggg cgt gtt tat gcc tct acg Ala Lys Ser Asp Ser Ser Leu Val Lys Gly Arg Val Tyr Ala Ser Thr	810		
190	195	200	
tat tta gag tca aac aag aac tat tat acc gat ccg gct atc agt cgt Tyr Leu Glu Ser Asn Lys Asn Tyr Tyr Thr Asp Pro Ala Ile Ser Arg	858		
205	210	215	
ggc ttt tta gac agt ccg ata tct aaa gag tta ctt ggt gat caa aat Gly Phe Leu Asp Ser Pro Ile Ser Lys Glu Leu Leu Gly Asp Gln Asn	906		
220	225	230	
tgg aat atg ttt caa gtt gct gtc agc aag aac ctt gtc tca tat aat Trp Asn Met Phe Gln Val Ala Val Ser Lys Asn Leu Val Ser Tyr Asn	954		
235	240	245	
cca gga atg acg ttt aac caa tat tac ttg gcg aat aat atc tca cca Pro Gly Met Thr Phe Asn Gln Tyr Tyr Leu Ala Asn Asn Ile Ser Pro	1002		
250	255	260	265

gaa gat aat ttc atc gtt tat cct cgt tta acc aat caa ata gta aga	1050
Glu Asp Asn Phe Ile Val Tyr Pro Arg Leu Thr Asn Gln Ile Val Arg	
270 275 280	
tta aag agt gga gcc tat ttg aac gcg aac cct aac cct aag ggg gcg	1098
Leu Lys Ser Gly Ala Tyr Leu Asn Ala Asn Pro Asn Pro Lys Gly Ala	
285 290 295	
aaa gac gat agt ggc aac ata gtc gac tac ata act tat gtt ggc cct	1146
Lys Asp Asp Ser Gly Asn Ile Val Asp Tyr Ile Thr Tyr Val Gly Pro	
300 305 310	
acg gac gat cgt ggt gcg tac tgg ggg gac aaa gag ctt gaa gat ccg	1194
Thr Asp Asp Arg Gly Ala Tyr Trp Gly Asp Lys Glu Leu Glu Asp Pro	
315 320 325	
gtg ctt ttc tct cga ctt act gtg ggt gag ttg ccg agt gct tct gag	1242
Val Leu Phe Ser Arg Leu Thr Val Gly Glu Leu Pro Ser Ala Ser Glu	
330 335 340 345	
ggc acg ctt ggc ttg ttt aac agt gga aca tat ctt ttc cct aca caa	1290
Gly Thr Leu Gly Leu Phe Asn Ser Gly Thr Tyr Leu Phe Pro Thr Gln	
350 355 360	
ata ggc tac ggt gaa aac gcc aca gtt aac gat tac atg ctt acc cct	1338
Ile Gly Tyr Gly Glu Asn Ala Thr Val Asn Asp Tyr Met Leu Thr Pro	
365 370 375	
ggt aat gac ttc atc ata cca act cga ttt aat acg atc cgt aat gac	1386
Gly Asn Asp Phe Ile Ile Pro Thr Arg Phe Asn Thr Ile Arg Asn Asp	
380 385 390	
gtg tac tta acg atg cga tct cgt gca tac ttc ggg gct gga tta caa	1434
Val Tyr Leu Thr Met Arg Ser Arg Ala Tyr Phe Gly Ala Gly Leu Gln	
395 400 405	
ggg gca cag gca agt tta acc gca acc tct aat gga aaa ccg gta gtg	1482
Gly Ala Gln Ala Ser Leu Thr Ala Thr Ser Asn Gly Lys Pro Val Val	
410 415 420 425	
ggg tca tca gag aac agc aaa ttt tac ata gac aca gac agt aat gtc	1530
Gly Ser Ser Glu Asn Ser Lys Phe Tyr Ile Asp Thr Asp Ser Asn Val	
430 435 440	
tat ctt aca aaa cag ggg ttt gat caa ctt ggt aac ttt ggt aaa ata	1578
Tyr Leu Thr Lys Gln Gly Phe Asp Gln Leu Gly Asn Phe Gly Lys Ile	
445 450 455	
atg gct cca ttc gtt tat acg agc gct tca aac gat ttg aag aag gtc	1626
Met Ala Pro Phe Val Tyr Thr Ser Ala Ser Asn Asp Leu Lys Lys Val	

460	465	470	
gga ata gac aaa ttc tca gcc atg atg aac caa ggg ttg agt agc ata Gly Ile Asp Lys Phe Ser Ala Met Met Asn Gln Gly Leu Ser Ser Ile 475 480 485			1674
caa agc aag tct ggg gca aac acc atc gta tca ggg aac ggc ggc cag Gln Ser Lys Ser Gly Ala Asn Thr Ile Val Ser Gly Asn Gly Gly Gln 490 495 500 505			1722
att caa ttg agc ggt ttc aat aga gaa aca gac ttg gat gga gca ttc Ile Gln Leu Ser Gly Phe Asn Arg Glu Thr Asp Leu Asp Gly Ala Phe 510 515 520			1770
tca tct tca ata agc gat cgt gag aac gat gca tta aag aat aca gat Ser Ser Ser Ile Ser Asp Arg Glu Asn Asp Ala Leu Lys Asn Thr Asp 525 530 535			1818
gtc aac ttc tat atg tat acg aaa ggc aac aca gaa act aat gtg acg Val Asn Phe Tyr Met Tyr Thr Lys Gly Asn Thr Glu Thr Asn Val Thr 540 545 550			1866
acg ccg ttg gcc ccg aat ggg tac cac ctt tac tca cca aac gta tct Thr Pro Leu Ala Pro Asn Gly Tyr His Leu Tyr Ser Pro Asn Val Ser 555 560 565			1914
gaa ttc aag ata cag act acc aga cct tac ttc tca tgg acg gga gac Glu Phe Lys Ile Gln Thr Thr Arg Pro Tyr Phe Ser Trp Thr Gly Asp 570 575 580 585			1962
ata agt aat gct ata aaa att tct gaa gcc aat gcg gat ttc gat gat Ile Ser Asn Ala Ile Lys Ile Ser Glu Ala Asn Ala Asp Phe Asp Asp 590 595 600			2010
tta ctt ggt agt aac tca tta cag gtt act gat aat ggg gtg gac agc Leu Leu Gly Ser Asn Ser Leu Gln Val Thr Asp Asn Gly Val Asp Ser 605 610 615			2058
gac ggt acc cct ata tct gtc gac ctt aat cgt gtc aga ata aga ata Asp Gly Thr Pro Ile Ser Val Asp Leu Asn Arg Val Arg Ile Arg Ile 620 625 630			2106
tct gag gac gga ggg agt aca tat tct aac gat tct tat acg ctt aat Ser Glu Asp Gly Gly Ser Thr Tyr Ser Asn Asp Ser Tyr Thr Leu Asn 635 640 645			2154
gac tta aaa gcc tta ttg acc agc gga aac atc act gtc cct aag ata Asp Leu Lys Ala Leu Leu Thr Ser Gly Asn Ile Thr Val Pro Lys Ile 650 655 660 665			2202

gtt atc gct tat acc tac tct gcg act gat tca aaa act gat aac atc Val Ile Ala Tyr Thr Tyr Ser Ala Thr Asp Ser Lys Thr Asp Asn Ile 670 675 680	2250
ggc aag tta ccg tct gaa att gac gac aac aca ggc gcg tac gcc gtt Gly Lys Leu Pro Ser Glu Ile Asp Asp Asn Thr Gly Ala Tyr Ala Val 685 690 695	2298
ccg ttc aca cgt acg ttg acg aat gac att cca gat aaa aaa agt aac Pro Phe Thr Arg Thr Leu Thr Asn Asp Ile Pro Asp Lys Lys Ser Asn 700 705 710	2346
att acg gtc aag tat atc gat atc tct ggt aat acc ata tct gat aac Ile Thr Val Lys Tyr Ile Asp Ile Ser Gly Asn Thr Ile Ser Asp Asn 715 720 725	2394
ata gtt aaa gcc ggt aat gtt ggc gat tca tat aca aca gaa caa aaa Ile Val Lys Ala Gly Asn Val Gly Asp Ser Tyr Thr Thr Glu Gln Lys 730 735 740 745	2442
gca ata ccg gga tac acc ttc aaa gcc gta caa ggt aat cca acc ggt Ala Ile Pro Gly Tyr Thr Phe Lys Ala Val Gln Gly Asn Pro Thr Gly 750 755 760	2490
caa ttc acg tct gat gct caa aca gtg acg tac gtt tac acg aag gat Gln Phe Thr Ser Asp Ala Gln Thr Val Thr Tyr Val Tyr Thr Lys Asp 765 770 775	2538
cca gtg gca ggc ggc agc gtc acc gct aag tat gtc gat acc agt ggg Pro Val Ala Gly Gly Ser Val Thr Ala Lys Tyr Val Asp Thr Ser Gly 780 785 790	2586
aac gcc atc tct gat aac gtt gtt aaa acc ggt aac atc ggc gat acc Asn Ala Ile Ser Asp Asn Val Val Lys Thr Gly Asn Ile Gly Asp Thr 795 800 805	2634
tac agt act aag cag aag acc ata ccg gga tat act ttc aaa gag gtt Tyr Ser Thr Lys Gln Lys Thr Ile Pro Gly Tyr Thr Phe Lys Glu Val 810 815 820 825	2682
caa gga tct gtt agc gga caa ttt acc aat cag gaa caa acg gtc act Gln Gly Ser Val Ser Gly Gln Phe Thr Asn Gln Glu Gln Thr Val Thr 830 835 840	2730
tat gta tac act aaa gat ccg gtc gct ggt gcc cat atc ata gca aaa Tyr Val Tyr Thr Lys Asp Pro Val Ala Gly Ala His Ile Ile Ala Lys 845 850 855	2778
tac gta gac gag aat ggt aac acg ata tca gac aac gtt gtg aag tca Tyr Val Asp Glu Asn Gly Asn Thr Ile Ser Asp Asn Val Val Lys Ser 860 865 870 875	2826

860	865	870	
ggt aac att ggg gat tct tac act act gag caa aag gca att cct gga			2874
Gly Asn Ile Gly Asp Ser Tyr Thr Thr Glu Gln Lys Ala Ile Pro Gly			
875	880	885	
tac act ttt aaa gct gtt cag gga aac cca acg gga caa ttc acc agt			2922
Tyr Thr Phe Lys Ala Val Gln Gly Asn Pro Thr Gly Gln Phe Thr Ser			
890	895	900	905
gac gcc cag acg gtg acc tac ata tac act aaa gtg aaa aca tct ggt			2970
Asp Ala Gln Thr Val Thr Tyr Ile Tyr Thr Lys Val Lys Thr Ser Gly			
	910	915	920
ggg agc gaa acc cca acg ccg tca aaa acg att gca acc aag tca agt			3018
Gly Ser Glu Thr Pro Thr Pro Ser Lys Thr Ile Ala Thr Lys Ser Ser			
	925	930	935
aca aac aca atc tct agt tct aca ctt ccg aag acg ggc gat agt caa			3066
Thr Asn Thr Ile Ser Ser Ser Thr Leu Pro Lys Thr Gly Asp Ser Gln			
	940	945	950
gtg tct act tta ttc ggc atg gtg gtg ggg ttc ttc ata ttt ggg gcg			3114
Val Ser Thr Leu Phe Gly Met Val Val Gly Phe Phe Ile Phe Gly Ala			
	955	960	965
gga acc ttg agc tta ttt ttt aac agt aag cga aaa aga aag tca aag			3162
Gly Thr Leu Ser Leu Phe Phe Asn Ser Lys Arg Lys Arg Lys Ser Lys			
970	975	980	985
taaattaatc tataagtt			3180

<210> 16

<211> 998

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 16

Met	Val	Ser	Lys	Asn	Asn	Val	Gln	Phe	Tyr	Asp	Lys	Lys	Asn	Asp	Asn
1				5					10					15	

Gln	Gln	Arg	Trp	Gly	Leu	Arg	Lys	Thr	Ser	Phe	Gly	Leu	Ala	Ser	Leu
		20					25					30			

Leu Leu Gly Thr Ser Phe Val Leu Phe Asn Gly Ala Val Val His Ala
35 40 45

Asp Thr Pro Ser Asn Asp Lys Pro Val Val Val Thr Thr Ile Ala Ser
50 55 60

Asn Ser Ser Ala Val Glu Ala Glu Thr Ala Ser Ser Ser Ser Ser
65 70 75 80

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

Ala Glu Thr Ala Ser Ser Ser Ser Ser Ser Ala Val Lys Ala Glu Thr
100 105 110

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

Ser Ser Ser Ser Ala Val Lys Ala Glu Thr Thr Ser Ala Ser Ser Ser
130 135 140

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

Lys Ala Glu Thr Ala Ser Ser Ser Ser Ser Ser Ala Val Lys Ala Glu
165 170 175

Thr Thr Ser Ala Ser Ser Ser Ser Ala Ala Lys Ala Asp Thr Thr Ser
180 185 190

Ala Ala Ser Ser Ser Ala Ala Lys Ser Asp Ser Ser Leu Val Lys Gly
195 200 205

Arg Val Tyr Ala Ser Thr Tyr Leu Glu Ser Asn Lys Asn Tyr Tyr Thr
210 215 220

Asp Pro Ala Ile Ser Arg Gly Phe Leu Asp Ser Pro Ile Ser Lys Glu

225		230		235		240									
Leu	Leu	Gly	Asp	Gln	Asn	Trp	Asn	Met	Phe	Gln	Val	Ala	Val	Ser	Lys
				245					250					255	
Asn	Leu	Val	Ser	Tyr	Asn	Pro	Gly	Met	Thr	Phe	Asn	Gln	Tyr	Tyr	Leu
			260					265					270		
Ala	Asn	Asn	Ile	Ser	Pro	Glu	Asp	Asn	Phe	Ile	Val	Tyr	Pro	Arg	Leu
			275				280					285			
Thr	Asn	Gln	Ile	Val	Arg	Leu	Lys	Ser	Gly	Ala	Tyr	Leu	Asn	Ala	Asn
			290				295					300			
Pro	Asn	Pro	Lys	Gly	Ala	Lys	Asp	Asp	Ser	Gly	Asn	Ile	Val	Asp	Tyr
305					310					315					320
Ile	Thr	Tyr	Val	Gly	Pro	Thr	Asp	Asp	Arg	Gly	Ala	Tyr	Trp	Gly	Asp
				325					330					335	
Lys	Glu	Leu	Glu	Asp	Pro	Val	Leu	Phe	Ser	Arg	Leu	Thr	Val	Gly	Glu
			340					345					350		
Leu	Pro	Ser	Ala	Ser	Glu	Gly	Thr	Leu	Gly	Leu	Phe	Asn	Ser	Gly	Thr
			355				360					365			
Tyr	Leu	Phe	Pro	Thr	Gln	Ile	Gly	Tyr	Gly	Glu	Asn	Ala	Thr	Val	Asn
			370			375					380				
Asp	Tyr	Met	Leu	Thr	Pro	Gly	Asn	Asp	Phe	Ile	Ile	Pro	Thr	Arg	Phe
385					390					395					400
Asn	Thr	Ile	Arg	Asn	Asp	Val	Tyr	Leu	Thr	Met	Arg	Ser	Arg	Ala	Tyr
			405					410						415	
Phe	Gly	Ala	Gly	Leu	Gln	Gly	Ala	Gln	Ala	Ser	Leu	Thr	Ala	Thr	Ser
			420					425					430		

Asn Gly Lys Pro Val Val Gly Ser Ser Glu Asn Ser Lys Phe Tyr Ile
435 440 445

Asp Thr Asp Ser Asn Val Tyr Leu Thr Lys Gln Gly Phe Asp Gln Leu
450 455 460

Gly Asn Phe Gly Lys Ile Met Ala Pro Phe Val Tyr Thr Ser Ala Ser
465 470 475 480

Asn Asp Leu Lys Lys Val Gly Ile Asp Lys Phe Ser Ala Met Met Asn
485 490 495

Gln Gly Leu Ser Ser Ile Gln Ser Lys Ser Gly Ala Asn Thr Ile Val
500 505 510

Ser Gly Asn Gly Gly Gln Ile Gln Leu Ser Gly Phe Asn Arg Glu Thr
515 520 525

Asp Leu Asp Gly Ala Phe Ser Ser Ser Ile Ser Asp Arg Glu Asn Asp
530 535 540

Ala Leu Lys Asn Thr Asp Val Asn Phe Tyr Met Tyr Thr Lys Gly Asn
545 550 555 560

Thr Glu Thr Asn Val Thr Thr Pro Leu Ala Pro Asn Gly Tyr His Leu
565 570 575

Tyr Ser Pro Asn Val Ser Glu Phe Lys Ile Gln Thr Thr Arg Pro Tyr
580 585 590

Phe Ser Trp Thr Gly Asp Ile Ser Asn Ala Ile Lys Ile Ser Glu Ala
595 600 605

Asn Ala Asp Phe Asp Asp Leu Leu Gly Ser Asn Ser Leu Gln Val Thr
610 615 620

Asp Asn Gly Val Asp Ser Asp Gly Thr Pro Ile Ser Val Asp Leu Asn

625		630		635		640
Arg Val Arg Ile	Arg Ile Ser Glu Asp	Gly Gly Ser Thr Tyr	Ser Asn			
	645	650	655			
Asp Ser Tyr Thr	Leu Asn Asp Leu	Lys Ala Leu Leu Thr	Ser Gly Asn			
	660	665	670			
Ile Thr Val Pro	Lys Ile Val Ile	Ala Tyr Thr Tyr	Ser Ala Thr Asp			
	675	680	685			
Ser Lys Thr Asp	Asn Ile Gly Lys	Leu Pro Ser Glu	Ile Asp Asp Asn			
	690	695	700			
Thr Gly Ala Tyr	Ala Val Pro Phe Thr	Arg Thr Leu Thr	Asn Asp Ile			
705	710	715	720			
Pro Asp Lys Lys	Ser Asn Ile Thr	Val Lys Tyr Ile	Asp Ile Ser Gly			
	725	730	735			
Asn Thr Ile Ser	Asp Asn Ile Val	Lys Ala Gly Asn	Val Gly Asp Ser			
	740	745	750			
Tyr Thr Thr Glu	Gln Lys Ala Ile	Pro Gly Tyr Thr	Phe Lys Ala Val			
	755	760	765			
Gln Gly Asn Pro	Thr Gly Gln Phe Thr	Ser Asp Ala Gln	Thr Val Thr			
	770	775	780			
Tyr Val Tyr Thr	Lys Asp Pro Val	Ala Gly Gly Ser	Val Thr Ala Lys			
785	790	795	800			
Tyr Val Asp Thr	Ser Gly Asn Ala	Ile Ser Asp Asn	Val Val Lys Thr			
	805	810	815			
Gly Asn Ile Gly	Asp Thr Tyr Ser	Thr Lys Gln Lys	Thr Ile Pro Gly			
	820	825	830			

Tyr Thr Phe Lys Glu Val Gln Gly Ser Val Ser Gly Gln Phe Thr Asn
835 840 845

Gln Glu Gln Thr Val Thr Tyr Val Tyr Thr Lys Asp Pro Val Ala Gly
850 855 860

Ala His Ile Ile Ala Lys Tyr Val Asp Glu Asn Gly Asn Thr Ile Ser
865 870 875 880

Asp Asn Val Val Lys Ser Gly Asn Ile Gly Asp Ser Tyr Thr Thr Glu
885 890 895

Gln Lys Ala Ile Pro Gly Tyr Thr Phe Lys Ala Val Gln Gly Asn Pro
900 905 910

Thr Gly Gln Phe Thr Ser Asp Ala Gln Thr Val Thr Tyr Ile Tyr Thr
915 920 925

Lys Val Lys Thr Ser Gly Gly Ser Glu Thr Pro Thr Pro Ser Lys Thr
930 935 940

Ile Ala Thr Lys Ser Ser Thr Asn Thr Ile Ser Ser Ser Thr Leu Pro
945 950 955 960

Lys Thr Gly Asp Ser Gln Val Ser Thr Leu Phe Gly Met Val Val Gly
965 970 975

Phe Phe Ile Phe Gly Ala Gly Thr Leu Ser Leu Phe Phe Asn Ser Lys
980 985 990

Arg Lys Arg Lys Ser Lys
995

<210> 17

<211> 3240

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<221> CDS

<222> (208)..(3201)

<400> 17

agcttttagaa gaagaaaaaag cagctgttga attagagggt tcagaaactg cctgatggat 60

atTTTTtata aatctggttt gaacaaatta tattgacatc tctTTTTtcta tcctgataat 120

tctgagagggt tatttttggga aatactattg aaccatatcg aggtgggtgtg gtataatgaa 180

gggaattaaa aaagatagga aaatttc atg gtg tca aag aat aac gtg cag ttt 234
Met Val Ser Lys Asn Asn Val Gln Phe
1 5

tac gac aag aaa aat gat aat caa cag cga tgg ggc ttg aga aaa act 282
Tyr Asp Lys Lys Asn Asp Asn Gln Gln Arg Trp Gly Leu Arg Lys Thr
10 15 20 25

tca ttt ggt tta gcg agc ctt ttg ctt ggc acg tct ttc gtt tta ttc 330
Ser Phe Gly Leu Ala Ser Leu Leu Leu Gly Thr Ser Phe Val Leu Phe
30 35 40

aat gga gcg gtc gtg cac gcg gat aca ccg agc aat gac aaa cct gtg 378
Asn Gly Ala Val Val His Ala Asp Thr Pro Ser Asn Asp Lys Pro Val
45 50 55

gtt gta aca acc att gcg tca aac tca tct gcc gtt gaa gct gag act 426
Val Val Thr Thr Ile Ala Ser Asn Ser Ser Ala Val Glu Ala Glu Thr
60 65 70

gcc agc agt tct tca tca agt gcc gta aaa gcg gaa acg acc agc gcc 474
Ala Ser Ser Ser Ser Ser Ser Ala Val Lys Ala Glu Thr Thr Ser Ala
75 80 85

tct tct tca agt gct gta aaa gct gag aca gcc tct agc agt tca agc 522
Ser Ser Ser Ser Ala Val Lys Ala Glu Thr Ala Ser Ser Ser Ser Ser
90 95 100 105

tca gcc gta aag gca gaa act acg agt gca tca tct tca tca gcg gta 570
Ser Ala Val Lys Ala Glu Thr Thr Ser Ala Ser Ser Ser Ser Ala Val
110 115 120

aag gcg gag acc gct agc tct tct tct agt agt gct gtg aaa gcc gag 618
Lys Ala Glu Thr Ala Ser Ser Ser Ser Ser Ser Ala Val Lys Ala Glu

125	130	135	
acg acg agc gca tct tca tct tct gct gtt aag gcg gaa aca aca agc Thr Thr Ser Ala Ser Ser Ser Ser Ala Val Lys Ala Glu Thr Thr Ser 140 145 150			666
gct tct agc tca agc gcc gtc aaa gca gaa aca gcg agt tca tct tct Ala Ser Ser Ser Ser Ala Val Lys Ala Glu Thr Ala Ser Ser Ser Ser 155 160 165			714
agt agt gca gtt aaa gcc gaa act acc tct gcc agc tca tct tca gca Ser Ser Ala Val Lys Ala Glu Thr Thr Ser Ala Ser Ser Ser Ser Ala 170 175 180 185			762
gca aag gcg gat acc acc agc gca gct agt tca tct gcg gca aag agc Ala Lys Ala Asp Thr Thr Ser Ala Ala Ser Ser Ala Ala Lys Ser 190 195 200			810
gac agt tca ctt gtg aaa ggg cgt gtt tat gcc tct acg tat tta gag Asp Ser Ser Leu Val Lys Gly Arg Val Tyr Ala Ser Thr Tyr Leu Glu 205 210 215			858
tca aac aag aac tat tat acc gat ccg gct atc agt cgt ggc ttt tta Ser Asn Lys Asn Tyr Tyr Thr Asp Pro Ala Ile Ser Arg Gly Phe Leu 220 225 230			906
gac agt ccg ata tct aaa gag tta ctt ggt gat caa aat tgg aat atg Asp Ser Pro Ile Ser Lys Glu Leu Leu Gly Asp Gln Asn Trp Asn Met 235 240 245			954
ttt caa gtt gct gtc agc aag aac ctt gtc tca tat aat cca gga atg Phe Gln Val Ala Val Ser Lys Asn Leu Val Ser Tyr Asn Pro Gly Met 250 255 260 265			1002
acg ttt aac caa tat tac ttg gcg aat aat atc tca cca gaa gat aat Thr Phe Asn Gln Tyr Tyr Leu Ala Asn Asn Ile Ser Pro Glu Asp Asn 270 275 280			1050
ttc atc gtt tat cct cgt tta acc aat caa ata gta aga tta aag agt Phe Ile Val Tyr Pro Arg Leu Thr Asn Gln Ile Val Arg Leu Lys Ser 285 290 295			1098
gga gcc tat ttg aac gcg aac cct aac cct aag ggg gcg aaa gac gat Gly Ala Tyr Leu Asn Ala Asn Pro Asn Pro Lys Gly Ala Lys Asp Asp 300 305 310			1146
agt ggc aac ata gtc gac tac ata act tat gtt ggc cct acg gac gat Ser Gly Asn Ile Val Asp Tyr Ile Thr Tyr Val Gly Pro Thr Asp Asp 315 320 325			1194

cgt ggt gcg tac tgg ggg gac aaa gag ctt gaa gat ccg gtg ctt ttc Arg Gly Ala Tyr Trp Gly Asp Lys Glu Leu Glu Asp Pro Val Leu Phe 330 335 340 345	1242
tct cga ctt act gtg ggt gag ttg ccg agt gct tct gag ggc acg ctt Ser Arg Leu Thr Val Gly Glu Leu Pro Ser Ala Ser Glu Gly Thr Leu 350 355 360	1290
ggc ttg ttt aac agt gga aca tat ctt ttc cct aca caa ata ggc tac Gly Leu Phe Asn Ser Gly Thr Tyr Leu Phe Pro Thr Gln Ile Gly Tyr 365 370 375	1338
ggc gaa aac gcc aca gtt aac gat tac atg ctt acc cct ggt aat gac Gly Glu Asn Ala Thr Val Asn Asp Tyr Met Leu Thr Pro Gly Asn Asp 380 385 390	1386
ttc atc ata cca act cga ttt aat acg atc cgt aat gac gtg tac tta Phe Ile Ile Pro Thr Arg Phe Asn Thr Ile Arg Asn Asp Val Tyr Leu 395 400 405	1434
acg atg cga tct cgt gca tac ttc ggg gct gga tta caa ggg gca cag Thr Met Arg Ser Arg Ala Tyr Phe Gly Ala Gly Leu Gln Gly Ala Gln 410 415 420 425	1482
gca agt tta acc gca acc tct aat gga aaa ccg gta gtg ggg tca tca Ala Ser Leu Thr Ala Thr Ser Asn Gly Lys Pro Val Val Gly Ser Ser 430 435 440	1530
gag aac agc aaa ttt tac ata gac aca gac agt aat gtc tat ctt aca Glu Asn Ser Lys Phe Tyr Ile Asp Thr Asp Ser Asn Val Tyr Leu Thr 445 450 455	1578
aaa cag ggg ttt gat caa ctt ggt aac ttt ggt aaa ata atg gct cca Lys Gln Gly Phe Asp Gln Leu Gly Asn Phe Gly Lys Ile Met Ala Pro 460 465 470	1626
ttc gtt tat acg agc gct tca aac gat ttg aag aag gtc gga ata gac Phe Val Tyr Thr Ser Ala Ser Asn Asp Leu Lys Lys Val Gly Ile Asp 475 480 485	1674
aaa ttc tca gcc atg atg aac caa ggg ttg agt agc ata caa agc aag Lys Phe Ser Ala Met Met Asn Gln Gly Leu Ser Ser Ile Gln Ser Lys 490 495 500 505	1722
tct ggg gca aac acc atc gta tca ggg aac ggc ggc cag att caa ttg Ser Gly Ala Asn Thr Ile Val Ser Gly Asn Gly Gly Gln Ile Gln Leu 510 515 520	1770
agc ggt ttc aat aga gaa aca gac ttg gat gga gca ttc tca tct tca Ser Gly Phe Asn Arg Glu Thr Asp Leu Asp Gly Ala Phe Ser Ser Ser 530 535 540 545	1818

525	530	535	
ata agc gat cgt gag aac gat gca tta aag aat aca gat gtc aac ttc Ile Ser Asp Arg Glu Asn Asp Ala Leu Lys Asn Thr Asp Val Asn Phe 540 545 550			1866
tat atg tat acg aaa ggc aac aca gaa act aat gtg acg acg ccg ttg Tyr Met Tyr Thr Lys Gly Asn Thr Glu Thr Asn Val Thr Thr Pro Leu 555 560 565			1914
gcc ccg aat ggg tac cac ctt tac tca cca aac gta tct gaa ttc aag Ala Pro Asn Gly Tyr His Leu Tyr Ser Pro Asn Val Ser Glu Phe Lys 570 575 580 585			1962
ata cag act acc aga cct tac ttc tca tgg acg gga gac ata agt aat Ile Gln Thr Thr Arg Pro Tyr Phe Ser Trp Thr Gly Asp Ile Ser Asn 590 595 600			2010
gct ata aaa att tct gaa gcc aat gcg gat ttc gat gat tta ctt ggt Ala Ile Lys Ile Ser Glu Ala Asn Ala Asp Phe Asp Asp Leu Leu Gly 605 610 615			2058
agt aac tca tta cag gtt act gat aat ggg gtg gac agc gac ggt acc Ser Asn Ser Leu Gln Val Thr Asp Asn Gly Val Asp Ser Asp Gly Thr 620 625 630			2106
cct ata tct gtc gac ctt aat cgt gtc aga ata aga ata tct gag gac Pro Ile Ser Val Asp Leu Asn Arg Val Arg Ile Arg Ile Ser Glu Asp 635 640 645			2154
gga ggg agt aca tat tct aac gat tct tat acg ctt aat gac tta aaa Gly Gly Ser Thr Tyr Ser Asn Asp Ser Tyr Thr Leu Asn Asp Leu Lys 650 655 660 665			2202
gcc tta ttg acc agc gga aac atc act gtc cct aag ata gtt atc gct Ala Leu Leu Thr Ser Gly Asn Ile Thr Val Pro Lys Ile Val Ile Ala 670 675 680			2250
tat acc tac tct gcg act gat tca aaa act gat aac atc ggt aag tta Tyr Thr Tyr Ser Ala Thr Asp Ser Lys Thr Asp Asn Ile Gly Lys Leu 685 690 695			2298
ccg tct gaa att gac gac aac aca ggc gcg tac gcc gtt ccg ttc aca Pro Ser Glu Ile Asp Asp Asn Thr Gly Ala Tyr Ala Val Pro Phe Thr 700 705 710			2346
cgt acg ttg acg aat gac att cca gat aaa aaa agt aac att acg gtc Arg Thr Leu Thr Asn Asp Ile Pro Asp Lys Lys Ser Asn Ile Thr Val 715 720 725			2394

aag tat atc gat atc tct ggt aat acc ata tct gat aac ata gtt aaa Lys Tyr Ile Asp Ile Ser Gly Asn Thr Ile Ser Asp Asn Ile Val Lys 730 735 740 745	2442
gcc ggt aat gtt ggc gat tca tat aca aca gaa caa aaa gca ata ccg Ala Gly Asn Val Gly Asp Ser Tyr Thr Thr Glu Gln Lys Ala Ile Pro 750 755 760	2490
gga tac acc ttc aaa gcc gta caa ggt aat cca acc ggt caa ttc acg Gly Tyr Thr Phe Lys Ala Val Gln Gly Asn Pro Thr Gly Gln Phe Thr 765 770 775	2538
tct gat gct caa aca gtg acg tac gtt tac acg aag gat cca gtg gca Ser Asp Ala Gln Thr Val Thr Tyr Val Tyr Thr Lys Asp Pro Val Ala 780 785 790	2586
ggc ggc agc gtc acc gct aag tat gtc gat acc agt ggg aac gcc atc Gly Gly Ser Val Thr Ala Lys Tyr Val Asp Thr Ser Gly Asn Ala Ile 795 800 805	2634
tct gat aac gtt gtt aaa acc ggt aac atc ggc gat acc tac agt act Ser Asp Asn Val Val Lys Thr Gly Asn Ile Gly Asp Thr Tyr Ser Thr 810 815 820 825	2682
aag cag aag acc ata ccg gga tat act ttc aaa gag gtt caa gga tct Lys Gln Lys Thr Ile Pro Gly Tyr Thr Phe Lys Glu Val Gln Gly Ser 830 835 840	2730
gtt agc gga caa ttt acc aat cag gaa caa acg gtc act tat gta tac Val Ser Gly Gln Phe Thr Asn Gln Glu Gln Thr Val Thr Tyr Val Tyr 845 850 855	2778
act aaa gat ccg gtc gct ggt gcc cat atc ata gca aaa tac gta gac Thr Lys Asp Pro Val Ala Gly Ala His Ile Ile Ala Lys Tyr Val Asp 860 865 870	2826
gag aat ggt aac acg ata tca gac aac gtt gtg aag tca ggt aac att Glu Asn Gly Asn Thr Ile Ser Asp Asn Val Val Lys Ser Gly Asn Ile 875 880 885	2874
ggg gat tct tac act act gag caa aag gca att cct gga tac act ttt Gly Asp Ser Tyr Thr Thr Glu Gln Lys Ala Ile Pro Gly Tyr Thr Phe 890 895 900 905	2922
aaa gct gtt cag gga aac cca acg gga caa ttc acc agt gac gcc cag Lys Ala Val Gln Gly Asn Pro Thr Gly Gln Phe Thr Ser Asp Ala Gln 910 915 920	2970
acg gtg acc tac ata tac act aaa gtg aaa aca tct ggt ggg agc gaa Thr Val Thr Tyr Ile Tyr Thr Lys Val Lys Thr Ser Gly Gly Ser Glu	3018

925	930	935	
acc cca acg ccg tca aaa acg att gca acc aag tca agt aca aac aca			3066
Thr Pro Thr Pro Ser Lys Thr Ile Ala Thr Lys Ser Ser Thr Asn Thr			
940	945	950	
atc tct agt tct aca ctt ccg aag acg ggc gat agt caa gtg tct act			3114
Ile Ser Ser Ser Thr Leu Pro Lys Thr Gly Asp Ser Gln Val Ser Thr			
955	960	965	
tta ttc ggc atg gtg gtg ggg ttc ttc ata ttt ggg gcg gga acc ttg			3162
Leu Phe Gly Met Val Val Gly Phe Phe Ile Phe Gly Ala Gly Thr Leu			
970	975	980	985
agc tta ttt ttt aac agt aag cga aaa aga aag tca aag taaattaatc			3211
Ser Leu Phe Phe Asn Ser Lys Arg Lys Arg Lys Ser Lys			
990	995		
tataagttac tgacaaaact gtcagtaac			3240

<210> 18
 <211> 262
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 18
 Met Lys Lys Lys Ile Ile Ser Ala Ile Leu Met Ser Thr Val Ile Leu
 1 5 10 15

Ser Ala Ala Ala Pro Leu Ser Gly Val Tyr Ala Ser Ser Ala Val Asn
 20 25 30

Ser Glu Leu Val His Lys Gly Glu Leu Thr Ile Gly Leu Glu Gly Thr
 35 40 45

Tyr Ser Pro Tyr Ser Tyr Arg Lys Asn Asn Lys Leu Thr Gly Phe Glu
 50 55 60

Val Asp Leu Gly Lys Ala Val Ala Lys Lys Met Gly Leu Lys Ala Asn
 65 70 75 80

Phe Val Pro Thr Lys Trp Asp Ser Leu Ile Ala Gly Leu Gly Ser Gly
85 90 95

Lys Phe Asp Val Val Met Asn Asn Ile Thr Gln Thr Pro Glu Arg Ala
100 105 110

Lys Gln Tyr Asn Phe Ser Thr Pro Tyr Ile Lys Ser Arg Phe Ala Leu
115 120 125

Ile Val Pro Thr Asp Ser Asn Ile Lys Ser Leu Lys Asn Ile Lys Gly
130 135 140

Lys Lys Ile Ile Ala Gly Thr Gly Thr Asn Asn Ala Asn Val Val Lys
145 150 155 160

Lys Tyr Lys Gly Asn Leu Thr Pro Asn Gly Asp Phe Ala Ser Ser Leu
165 170 175

Asp Met Ile Lys Gln Gly Arg Ala Ala Gly Thr Ile Asn Ser Arg Glu
180 185 190

Ala Trp Tyr Ala Tyr Ser Lys Lys Asn Ser Thr Lys Gly Leu Lys Met
195 200 205

Ile Asp Val Ser Ser Glu Gln Asp Pro Ala Lys Ile Ser Ala Leu Phe
210 215 220

Asn Lys Lys Asp Thr Ala Ile Gln Ser Ser Tyr Asn Lys Ala Leu Lys
225 230 235 240

Glu Leu Gln Gln Asp Gly Thr Val Lys Lys Leu Ser Glu Lys Tyr Phe
245 250 255

Gly Ala Asp Ile Thr Glu
260

<211> 957
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> CDS
<222> (153)..(938)

<400> 19
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ataattctga gaggttattt tgggaaatac tattgaacca tatcgagggtg gtgtggtata 120
atgaaggggaa ttaaaaaaga taggaaaatt tc atg aaa aaa aag att atc tca 173
Met Lys Lys Lys Ile Ile Ser
1 5
gct att tta atg tct aca gtg ata ctt tct gct gca gcc ccg ttg tca 221
Ala Ile Leu Met Ser Thr Val Ile Leu Ser Ala Ala Ala Pro Leu Ser
10 15 20
ggg gtt tac gct tca tca gct gtt aat tca gaa tta gtt cat aag gga 269
Gly Val Tyr Ala Ser Ser Ala Val Asn Ser Glu Leu Val His Lys Gly
25 30 35
gaa tta aca att ggt ctt gag gga acg tac tct ccg tac tct tat cgt 317
Glu Leu Thr Ile Gly Leu Glu Gly Thr Tyr Ser Pro Tyr Ser Tyr Arg
40 45 50 55
aaa aat aac aaa tta act ggc ttt gaa gta gat ctt ggt aaa gca gtt 365
Lys Asn Asn Lys Leu Thr Gly Phe Glu Val Asp Leu Gly Lys Ala Val
60 65 70
gct aaa aag atg ggc tta aaa gct aac ttt gta cca act aaa tgg gat 413
Ala Lys Lys Met Gly Leu Lys Ala Asn Phe Val Pro Thr Lys Trp Asp
75 80 85
tcg cta att gcc ggt ctt ggt tca ggt aag ttt gat gta gta atg aac 461
Ser Leu Ile Ala Gly Leu Gly Ser Gly Lys Phe Asp Val Val Met Asn
90 95 100
aac att aca cag aca cct gaa cgg gcc aag caa tat aat ttc tct acc 509
Asn Ile Thr Gln Thr Pro Glu Arg Ala Lys Gln Tyr Asn Phe Ser Thr
105 110 115

cca tat atc aag tcc cgg ttt gca tta att gtt cct act gat agt aac	557
Pro Tyr Ile Lys Ser Arg Phe Ala Leu Ile Val Pro Thr Asp Ser Asn	
120 125 130 135	
atc aaa agc ttg aag aat att aaa ggc aag aag att att gct ggt acg	605
Ile Lys Ser Leu Lys Asn Ile Lys Gly Lys Lys Ile Ile Ala Gly Thr	
140 145 150	
gga act aat aat gcg aat gtg gta aaa aaa tat aag ggt aac ctt aca	653
Gly Thr Asn Asn Ala Asn Val Val Lys Lys Tyr Lys Gly Asn Leu Thr	
155 160 165	
cca aat ggc gat ttt gct agt tcc tta gat atg atc aag caa ggt cgg	701
Pro Asn Gly Asp Phe Ala Ser Ser Leu Asp Met Ile Lys Gln Gly Arg	
170 175 180	
gct gcc ggg aca att aac tcc cgt gaa gct tgg tac gct tac agc aag	749
Ala Ala Gly Thr Ile Asn Ser Arg Glu Ala Trp Tyr Ala Tyr Ser Lys	
185 190 195	
aag aac agt act aag ggt ctc aag atg att gat gtt tct agt gaa caa	797
Lys Asn Ser Thr Lys Gly Leu Lys Met Ile Asp Val Ser Ser Glu Gln	
200 205 210 215	
gat cca gct aag att tca gca ctt ttt aac aag aaa gat act gct att	845
Asp Pro Ala Lys Ile Ser Ala Leu Phe Asn Lys Lys Asp Thr Ala Ile	
220 225 230	
caa tct tcc tac aac aag gca ctt aag gaa ctt caa caa gac gga aca	893
Gln Ser Ser Tyr Asn Lys Ala Leu Lys Glu Leu Gln Gln Asp Gly Thr	
235 240 245	
gtc aag aag cta tct gaa aag tac ttc ggt gca gat att act gaa	938
Val Lys Lys Leu Ser Glu Lys Tyr Phe Gly Ala Asp Ile Thr Glu	
250 255 260	
taaattaatc tataagtta	957

<210> 20

<211> 263

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 20

Met Lys Phe Trp Lys Lys Ala Leu Leu Thr Ile Val Ala Leu Thr Val

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

Met Ile Asp Val Ser Ser Glu Gln Asp Pro Ala Lys Ile Ser Ala Leu
 210 215 220

Phe Asn Lys Lys Asp Thr Ala Ile Gln Ser Ser Tyr Asn Lys Ala Leu
 225 230 235 240

Lys Glu Leu Gln Gln Asp Gly Thr Val Lys Lys Leu Ser Glu Lys Tyr
 245 250 255

Phe Gly Ala Asp Ile Thr Glu
 260

<210> 21

<211> 960

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<220>

<221> CDS

<222> (153)..(941)

<400> 21

tggatatttt ttataaatct ggtttgaaca aattatattg acatctcttt ttctatcctg 60

ataattctga gaggttattt tgggaaatac tattgaacca tatcgagggtg gtgtggtata 120

atgaagggaa ttaaaaaaga taggaaaatt tc atg aaa ttt tgg aag aaa gca 173
 Met Lys Phe Trp Lys Lys Ala
 1 5

cta tta aca att gta gcc tta acg gtc ggt acc cct gca gga atc aca 221
 Leu Leu Thr Ile Val Ala Leu Thr Val Gly Thr Pro Ala Gly Ile Thr
 10 15 20

agt gtt tct gct gct tca tca gct gtt aat tca gaa tta gtt cat aag 269
 Ser Val Ser Ala Ala Ser Ser Ala Val Asn Ser Glu Leu Val His Lys
 25 30 35

gga gaa tta aca att ggt ctt gag gga acg tac tct ccg tac tct tat 317
 Gly Glu Leu Thr Ile Gly Leu Glu Gly Thr Tyr Ser Pro Tyr Ser Tyr

40	45	50	55	
cgt aaa aat aac aaa tta act ggc ttt gaa gta gat ctt ggt aaa gca				365
Arg Lys Asn Asn Lys Leu Thr Gly Phe Glu Val Asp Leu Gly Lys Ala	60	65	70	
gtt gct aaa aag atg ggc tta aaa gct aac ttt gta cca act aaa tgg				413
Val Ala Lys Lys Met Gly Leu Lys Ala Asn Phe Val Pro Thr Lys Trp	75	80	85	
gat tcg cta att gcc ggt ctt ggt tca ggt aag ttt gat gta gta atg				461
Asp Ser Leu Ile Ala Gly Leu Gly Ser Gly Lys Phe Asp Val Val Met	90	95	100	
aac aac att aca cag aca cct gaa cgg gcc aag caa tat aat ttc tct				509
Asn Asn Ile Thr Gln Thr Pro Glu Arg Ala Lys Gln Tyr Asn Phe Ser	105	110	115	
acc cca tat atc aag tcc cgg ttt gca tta att gtt cct act gat agt				557
Thr Pro Tyr Ile Lys Ser Arg Phe Ala Leu Ile Val Pro Thr Asp Ser	120	125	130	135
aac atc aaa agc ttg aag aat att aaa ggc aag aag att att gct ggt				605
Asn Ile Lys Ser Leu Lys Asn Ile Lys Gly Lys Lys Ile Ile Ala Gly	140	145	150	
acg gga act aat aat gcg aat gtg gta aaa aaa tat aag ggt aac ctt				653
Thr Gly Thr Asn Asn Ala Asn Val Val Lys Lys Tyr Lys Gly Asn Leu	155	160	165	
aca cca aat ggc gat ttt gct agt tcc tta gat atg atc aag caa ggt				701
Thr Pro Asn Gly Asp Phe Ala Ser Ser Leu Asp Met Ile Lys Gln Gly	170	175	180	
cgg gct gcc ggg aca att aac tcc cgt gaa gct tgg tac gct tac agc				749
Arg Ala Ala Gly Thr Ile Asn Ser Arg Glu Ala Trp Tyr Ala Tyr Ser	185	190	195	
aag aag aac agt act aag ggt ctc aag atg att gat gtt tct agt gaa				797
Lys Lys Asn Ser Thr Lys Gly Leu Lys Met Ile Asp Val Ser Ser Glu	200	205	210	215
caa gat cca gct aag att tca gca ctt ttt aac aag aaa gat act gct				845
Gln Asp Pro Ala Lys Ile Ser Ala Leu Phe Asn Lys Lys Asp Thr Ala	220	225	230	
att caa tct tcc tac aac aag gca ctt aag gaa ctt caa caa gac gga				893
Ile Gln Ser Ser Tyr Asn Lys Ala Leu Lys Glu Leu Gln Gln Asp Gly	235	240	245	

aca gtc aag aag cta tct gaa aag tac ttc ggt gca gat att act gaa	941
Thr Val Lys Lys Leu Ser Glu Lys Tyr Phe Gly Ala Asp Ile Thr Glu	
250 255 260	

taaattaatc tataagtta	960
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<210> 22
 <211> 271
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 22
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Ser Ala Ala Ala Pro Leu Ser Gly Val Tyr Ala Glu Ala Gln Thr Glu
20 25 30

Thr Cys Thr Val Ala Pro Arg Glu Arg Gln Asn Cys Gly Phe Pro Gly
35 40 45

Val Thr Pro Ser Gln Cys Ala Asn Lys Gly Cys Cys Phe Asp Asp Thr
50 55 60

Val Arg Gly Val Pro Trp Cys Phe Tyr Pro Asn Thr Ile Asp Val Pro
65 70 75 80

Pro Glu Glu Glu Cys Glu Phe Asp Pro Lys Glu Glu Asp Asn Asn Lys
85 90 95

Pro Gly Lys Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Gly Asn Lys
100 105 110

Pro Gly Lys Glu Asp Asn Lys Lys Pro Gly Lys Glu Asp Gly Asn Lys
115 120 125

Pro Gly Lys Glu Asp Asn Lys Lys Pro Gly Lys Glu Asp Gly Asn Lys

130

135

140

Pro Gly Lys Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Gly Asn Lys
145 150 155 160

Pro Gly Lys Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Gly Asn Gly
165 170 175

Val His Val Val Lys Pro Gly Asp Thr Val Asn Asp Ile Ala Lys Ala
180 185 190

Asn Gly Thr Thr Ala Asp Lys Ile Ala Ala Asp Asn Lys Leu Ala Asp
195 200 205

Lys Asn Met Ile Lys Pro Gly Gln Glu Leu Val Val Asp Lys Lys Gln
210 215 220

Pro Ala Asn His Ala Asp Ala Asn Lys Ala Gln Ala Leu Pro Glu Thr
225 230 235 240

Gly Glu Glu Asn Pro Phe Ile Gly Thr Thr Val Phe Gly Gly Leu Ser
245 250 255

Leu Ala Leu Gly Ala Ala Leu Leu Ala Gly Arg Arg Arg Glu Leu
260 265 270

<210> 23

<211> 1020

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>

<221> CDS

<222> (153)..(965)

<400> 23

tggaatatttt ttataaatct ggtttgaaca aattatattg acatctcttt ttctatcctg	60
ataattctga gaggttattt tgggaaatac tattgaacca tatcgagggtg gtgtggtata	120
atgaaggggaa ttaaaaaaga taggaaaatt tc atg aaa aaa aag att atc tca	173
Met Lys Lys Lys Ile Ile Ser	
1 5	
gct att tta atg tct aca gtg ata ctt tct gct gca gcc ccg ttg tca	221
Ala Ile Leu Met Ser Thr Val Ile Leu Ser Ala Ala Ala Pro Leu Ser	
10 15 20	
ggg gtt tac gcc gaa gct caa act gaa act tgt act gtt gct cca cgt	269
Gly Val Tyr Ala Glu Ala Gln Thr Glu Thr Cys Thr Val Ala Pro Arg	
25 30 35	
gaa cgt caa aac tgt ggt ttt cca ggt gtt act cca tca caa tgt gct	317
Glu Arg Gln Asn Cys Gly Phe Pro Gly Val Thr Pro Ser Gln Cys Ala	
40 45 50 55	
aac aaa ggt tgt tgt ttt gat gat act gtt cgt ggt gtt cca tgg tgt	365
Asn Lys Gly Cys Cys Phe Asp Asp Thr Val Arg Gly Val Pro Trp Cys	
60 65 70	
ttt tac cca aac act atc gat gtt cca cca gaa gaa gaa tgt gaa ttt	413
Phe Tyr Pro Asn Thr Ile Asp Val Pro Pro Glu Glu Glu Cys Glu Phe	
75 80 85	
gat cca aaa gag gaa gac aac aac aag cct ggt aaa gaa gac ggc aac	461
Asp Pro Lys Glu Glu Asp Asn Asn Lys Pro Gly Lys Glu Asp Gly Asn	
90 95 100	
aaa cct ggt aaa gaa gac ggc aac aaa cct ggt aaa gaa gac aac aaa	509
Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Asn Lys	
105 110 115	
aaa cct ggc aaa gaa gac ggc aac aaa cct ggt aaa gaa gac aac aaa	557
Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Asn Lys	
120 125 130 135	
aaa cct ggc aaa gaa gat ggc aac aaa cct ggt aaa gaa gac ggc aac	605
Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Gly Asn	
140 145 150	
aag cct ggt aaa gaa gat ggc aac aag cct ggt aaa gaa gat ggc aac	653
Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Gly Asn	
155 160 165	
aag cct ggt aaa gaa gac ggc aac gga gta cat gtc gtt aaa cct ggt	701
Lys Pro Gly Lys Glu Asp Gly Asn Gly Val His Val Val Lys Pro Gly	

170	175	180	
gat aca gta aat gac att gca aaa gca aac ggc act act gct gac aaa			749
Asp Thr Val Asn Asp Ile Ala Lys Ala Asn Gly Thr Thr Ala Asp Lys			
185	190	195	
att gct gca gat aac aaa tta gct gat aaa aac atg atc aaa cct ggt			797
Ile Ala Ala Asp Asn Lys Leu Ala Asp Lys Asn Met Ile Lys Pro Gly			
200	205	210	215
caa gaa ctt gtt gtt gat aag aag caa cca gca aac cat gca gat gct			845
Gln Glu Leu Val Val Asp Lys Lys Gln Pro Ala Asn His Ala Asp Ala			
220	225	230	
aac aaa gct caa gca tta cca gaa act ggt gaa gaa aat cca ttc atc			893
Asn Lys Ala Gln Ala Leu Pro Glu Thr Gly Glu Glu Asn Pro Phe Ile			
235	240	245	
ggt aca act gta ttt ggt gga tta tca tta gcg tta ggt gca gcg tta			941
Gly Thr Thr Val Phe Gly Gly Leu Ser Leu Ala Leu Gly Ala Ala Leu			
250	255	260	
tta gct gga cgt cgt cgc gaa cta taaaattaat ctataagtta ctgacaaaac			995
Leu Ala Gly Arg Arg Arg Glu Leu			
265	270		
tgtcagtaac tttttttgtg ggaaa			1020

<210> 24

<211> 716

<212> PRT

<213> Petroselinum crispum

<400> 24

Met	Glu	Asn	Gly	Asn	Gly	Ala	Thr	Thr	Asn	Gly	His	Val	Asn	Gly	Asn
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Gly	Met	Asp	Phe	Cys	Met	Lys	Thr	Glu	Asp	Pro	Leu	Tyr	Trp	Gly	Ile
			20					25					30		

Ala	Ala	Glu	Ala	Met	Thr	Gly	Ser	His	Leu	Asp	Glu	Val	Lys	Lys	Met
		35				40						45			

Val	Ala	Glu	Tyr	Arg	Lys	Pro	Val	Val	Lys	Leu	Gly	Gly	Glu	Thr	Leu
	50					55					60				

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

Thr Val Glu Leu Ser Glu Ala Ala Arg Ala Gly Val Lys Ala Ser Ser
85 90 95

Asp Trp Val Met Asp Ser Met Asn Lys Gly Thr Asp Ser Tyr Gly Val
100 105 110

Thr Thr Gly Phe Gly Ala Thr Ser His Arg Arg Thr Lys Gln Gly Gly
115 120 125

Ala Leu Gln Lys Glu Leu Ile Arg Phe Leu Asn Ala Gly Ile Phe Gly
130 135 140

Asn Gly Ser Asp Asn Thr Leu Pro His Ser Ala Thr Arg Ala Ala Met
145 150 155 160

Leu Val Arg Ile Asn Thr Leu Leu Gln Gly Tyr Ser Gly Ile Arg Phe
165 170 175

Glu Ile Leu Glu Ala Ile Thr Lys Phe Leu Asn Gln Asn Ile Thr Pro
180 185 190

Cys Leu Pro Leu Arg Gly Thr Ile Thr Ala Ser Gly Asp Leu Val Pro
195 200 205

Leu Ser Tyr Ile Ala Gly Leu Leu Thr Gly Arg Pro Asn Ser Lys Ala
210 215 220

Val Gly Pro Thr Gly Val Ile Leu Ser Pro Glu Glu Ala Phe Lys Leu
225 230 235 240

Ala Gly Val Glu Gly Gly Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu
245 250 255

Ala Leu Val Asn Gly Thr Ala Val Gly Ser Gly Met Ala Ser Met Val

260

265

270

Leu Phe Glu Ala Asn Ile Leu Ala Val Leu Ala Glu Val Met Ser Ala
 275 280 285

Ile Phe Ala Glu Val Met Gln Gly Lys Pro Glu Phe Thr Asp His Leu
 290 295 300

Thr His Lys Leu Lys His His Pro Gly Gln Ile Glu Ala Ala Ala Ile
 305 310 315 320

Met Glu His Ile Leu Asp Gly Ser Ala Tyr Val Lys Ala Ala Gln Lys
 325 330 335

Leu His Glu Met Asp Pro Leu Gln Lys Pro Lys Gln Asp Arg Tyr Ala
 340 345 350

Leu Arg Thr Ser Pro Gln Trp Leu Gly Pro Gln Ile Glu Val Ile Arg
 355 360 365

Ser Ser Thr Lys Met Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn
 370 375 380

Pro Leu Ile Asp Val Ser Arg Asn Lys Ala Ile His Gly Gly Asn Phe
 385 390 395 400

Gln Gly Thr Pro Ile Gly Val Ser Met Asp Asn Thr Arg Leu Ala Ile
 405 410 415

Ala Ala Ile Gly Lys Leu Met Phe Ala Gln Phe Ser Glu Leu Val Asn
 420 425 430

Asp Phe Tyr Asn Asn Gly Leu Pro Ser Asn Leu Ser Gly Gly Arg Asn
 435 440 445

Pro Ser Leu Asp Tyr Gly Phe Lys Gly Ala Glu Ile Ala Met Ala Ser
 450 455 460

Tyr Cys Ser Glu Leu Gln Phe Leu Ala Asn Pro Val Thr Asn His Val
465 470 475 480

Gln Ser Ala Glu Gln His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile
485 490 495

Ser Ser Arg Lys Thr Ser Glu Ala Val Glu Ile Leu Lys Leu Met Ser
500 505 510

Thr Thr Phe Leu Val Gly Leu Cys Gln Ala Ile Asp Leu Arg His Leu
515 520 525

Glu Glu Asn Leu Lys Ser Thr Val Lys Asn Thr Val Ser Ser Val Ala
530 535 540

Lys Arg Val Leu Thr Met Gly Val Asn Gly Glu Leu His Pro Ser Arg
545 550 555 560

Phe Cys Glu Lys Asp Leu Leu Arg Val Val Asp Arg Glu Tyr Ile Phe
565 570 575

Ala Tyr Ile Asp Asp Pro Cys Ser Ala Thr Tyr Pro Leu Met Gln Lys
580 585 590

Leu Arg Gln Thr Leu Val Glu His Ala Leu Lys Asn Gly Asp Asn Glu
595 600 605

Arg Asn Leu Ser Thr Ser Ile Phe Gln Lys Ile Ala Thr Phe Glu Asp
610 615 620

Glu Leu Lys Ala Leu Leu Pro Lys Glu Val Glu Ser Ala Arg Ala Ala
625 630 635 640

Leu Glu Ser Gly Asn Pro Ala Ile Pro Asn Arg Ile Glu Glu Cys Arg
645 650 655

Ser Tyr Pro Leu Tyr Lys Phe Val Arg Lys Glu Leu Gly Thr Glu Tyr

660

665

670

Leu Thr Gly Glu Lys Val Thr Ser Pro Gly Glu Glu Phe Glu Lys Val
 675 680 685

Phe Ile Ala Met Ser Lys Gly Glu Ile Ile Asp Pro Leu Leu Glu Cys
 690 695 700

Leu Glu Ser Trp Asn Gly Ala Pro Leu Pro Ile Cys
 705 710 715

<210> 25

<211> 3300

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<220>

<221> CDS

<222> (1091)..(3238)

<220>

<221> misc_feature

<222> (1091)..(3241)

<223> PAL

<220>

<221> misc_feature

<222> (3239)..(3241)

<223> Stop codon

<400> 25

ttgttaactt agtcaattta aaagggtttgc cttttataaaa atctaattccc tataaggagg 60

aaactactaa tggtagttaa agttggtatt aacggtttcg gtcgtatcgg tcgtcttgct 120

ttccgtcgta ttcaaaatgt tgaagggtgtt gaagttgttg caatcaacga cttgacagat 180

ccagcaatgc ttgtcactt gcttaaatac gatacaactc aaggtcgttt tgatggtaaa 240

gttgaagtta aagatggtgg ttttgaagtt aacggtaaatt tcgttaaagt tactgctgaa 300

tctaaccag ctaacatcaa ctgggctgaa gttgggtgcag aaatcgttct tgaagcaact	360
ggttttcttcg caactaaaga aaaagctgaa caacacttgc acgctaattgg tgctaagaaa	420
gttggttatca ctgcacctgg tggatcagat gttaaaacaa tcgttttcaa cactaaccac	480
gaagtacttg atggaactga aacagtaatt tcagctgggt catgtacaac caactgtctt	540
gctccaatgg ctgatacttt gaacaaacaa ttcggtatca aagttggtac aatgactaca	600
gttcacgggt acactgggtga ccaaagtact cttgatggcc cacaccgtgg tggagatttc	660
cgtcgcgcac gtgctgcagc tgaaaacatc gtacctaaact caacagggtgc tgctaaagcc	720
atcgggtcttg tattgccaga acttcaaggt aaacttcaag gacatgctca acgtgtacca	780
gttccaactg gttcattgac tgaacttggt actatccttg ataaagaagt tacagttgac	840
gaaatcaacg cagctatgaa agctgcttca aatgaatcat ttggttaca cgaagaccaa	900
atcgtttcat ctgatatcgt tggatatctca aactcttcac tctttgatgc tactcaaact	960
gaagttactt cagctaacgg agctcaactt gttaaaactg tatcttggtg cgataacgaa	1020
atgtcataca cttcaaacct tgttcgtaca cttgcatact tcgctaaaat cgctaaataa	1080
ggaggaaaaa atg gaa aat ggt aat ggt gca act acg aat ggg cat gtg	1129
Met Glu Asn Gly Asn Gly Ala Thr Thr Asn Gly His Val	
1 5 10	
aac ggg aat gga atg gac ttc tgt atg aag aca gaa gat cct ctt tat	1177
Asn Gly Asn Gly Met Asp Phe Cys Met Lys Thr Glu Asp Pro Leu Tyr	
15 20 25	
tgg ggt att gca gct gaa gcg atg act ggt tca cac ttg gat gaa gta	1225
Trp Gly Ile Ala Ala Glu Ala Met Thr Gly Ser His Leu Asp Glu Val	
30 35 40 45	
aaa aaa atg gtc gcc gag tac aga aaa cct gtc gtt aaa tta gga gga	1273
Lys Lys Met Val Ala Glu Tyr Arg Lys Pro Val Val Lys Leu Gly Gly	
50 55 60	
gag aca ctt aca att agt cag gtt gct gct att agt gcg cga gat gga	1321
Glu Thr Leu Thr Ile Ser Gln Val Ala Ala Ile Ser Ala Arg Asp Gly	
65 70 75	
agt ggt gta act gtg gaa ctt agt gag gca gca cgc gct gga gtt aaa	1369
Ser Gly Val Thr Val Glu Leu Ser Glu Ala Ala Arg Ala Gly Val Lys	
80 85 90	

gct tct tct gat tgg gta atg gac agt atg aat aaa gga act gat tca	1417
Ala Ser Ser Asp Trp Val Met Asp Ser Met Asn Lys Gly Thr Asp Ser	
95 100 105	
tac ggt gta aca act ggt ttc ggc gct act tct cat cgt cgt acg aaa	1465
Tyr Gly Val Thr Thr Gly Phe Gly Ala Thr Ser His Arg Arg Thr Lys	
110 115 120 125	
cag gga gga gct ctt caa aaa gaa ctt att aga ttt ctt aac gca gga	1513
Gln Gly Gly Ala Leu Gln Lys Glu Leu Ile Arg Phe Leu Asn Ala Gly	
130 135 140	
att ttc ggt aat ggc tca gat aat act ctt cca cat tct gca aca cga	1561
Ile Phe Gly Asn Gly Ser Asp Asn Thr Leu Pro His Ser Ala Thr Arg	
145 150 155	
gct gca atg ctt gtc aga att aat act tta ctt caa gga tac tca ggc	1609
Ala Ala Met Leu Val Arg Ile Asn Thr Leu Leu Gln Gly Tyr Ser Gly	
160 165 170	
att cgt ttt gaa ata ctt gaa gca att aca aaa ttt ttg aac caa aat	1657
Ile Arg Phe Glu Ile Leu Glu Ala Ile Thr Lys Phe Leu Asn Gln Asn	
175 180 185	
att act cct tgc tta cca ctt cgt gga aca att aca gct tca ggt gat	1705
Ile Thr Pro Cys Leu Pro Leu Arg Gly Thr Ile Thr Ala Ser Gly Asp	
190 195 200 205	
tta gtt cca tta tct tac att gct ggt ctt ctt act ggt cga cct aat	1753
Leu Val Pro Leu Ser Tyr Ile Ala Gly Leu Leu Thr Gly Arg Pro Asn	
210 215 220	
agt aaa gct gta ggt cct acg ggg gtt att tta tct cca gaa gag gca	1801
Ser Lys Ala Val Gly Pro Thr Gly Val Ile Leu Ser Pro Glu Glu Ala	
225 230 235	
ttc aag tta gct ggt gtt gaa ggt ggg ttt ttc gaa ttg caa cca aag	1849
Phe Lys Leu Ala Gly Val Glu Gly Gly Phe Phe Glu Leu Gln Pro Lys	
240 245 250	
gaa gga ctt gca ttg gtg aat ggc aca gct gtt ggc tct gga atg gct	1897
Glu Gly Leu Ala Leu Val Asn Gly Thr Ala Val Gly Ser Gly Met Ala	
255 260 265	
agt atg gtt tta ttt gaa gct aat att ctt gcg gta tta gct gaa gta	1945
Ser Met Val Leu Phe Glu Ala Asn Ile Leu Ala Val Leu Ala Glu Val	
270 275 280 285	
atg tct gca att ttt gcc gaa gtc atg caa gga aaa cca gaa ttt act	1993
Met Ser Ala Ile Phe Ala Glu Val Met Gln Gly Lys Pro Glu Phe Thr	

290	295	300	
gat cat tta act cac aaa ttg aaa cac cat cct gga caa atc gaa gca Asp His Leu Thr His Lys Leu Lys His His Pro Gly Gln Ile Glu Ala 305 310 315			2041
gct gca att atg gaa cat ata tta gat ggg tca gct tat gtt aaa gct Ala Ala Ile Met Glu His Ile Leu Asp Gly Ser Ala Tyr Val Lys Ala 320 325 330			2089
gct cag aaa ctt cac gaa atg gat cct tta caa aaa cct aag caa gat Ala Gln Lys Leu His Glu Met Asp Pro Leu Gln Lys Pro Lys Gln Asp 335 340 345			2137
cgt tat gct ctt aga acg agt cca caa tgg ttg ggg cca caa att gag Arg Tyr Ala Leu Arg Thr Ser Pro Gln Trp Leu Gly Pro Gln Ile Glu 350 355 360 365			2185
gtt att cgc tca tca act aaa atg att gaa aga gaa atc aat tca gtt Val Ile Arg Ser Ser Thr Lys Met Ile Glu Arg Glu Ile Asn Ser Val 370 375 380			2233
aat gac aat cct tta att gat gtt tca cgt aat aaa gcg att cat ggt Asn Asp Asn Pro Leu Ile Asp Val Ser Arg Asn Lys Ala Ile His Gly 385 390 395			2281
ggt aac ttc caa gga aca cca atc ggt gtt tca atg gat aat act aga Gly Asn Phe Gln Gly Thr Pro Ile Gly Val Ser Met Asp Asn Thr Arg 400 405 410			2329
tta gct att gcg gct att gga aaa ctt atg ttt gca caa ttt tct gaa Leu Ala Ile Ala Ala Ile Gly Lys Leu Met Phe Ala Gln Phe Ser Glu 415 420 425			2377
ctt gtt aac gat ttc tat aac aac gga tta cca tca aat tta agt ggc Leu Val Asn Asp Phe Tyr Asn Asn Gly Leu Pro Ser Asn Leu Ser Gly 430 435 440 445			2425
ggg cgc aat cca agt ttg gat tat ggt ttt aaa ggt gct gaa att gcc Gly Arg Asn Pro Ser Leu Asp Tyr Gly Phe Lys Gly Ala Glu Ile Ala 450 455 460			2473
atg gca tct tat tgt tca gaa ctt caa ttt tta gcc aat cca gtt aca Met Ala Ser Tyr Cys Ser Glu Leu Gln Phe Leu Ala Asn Pro Val Thr 465 470 475			2521
aac cac gta caa agt gcg gaa caa cat aat caa gat gtc aac tct ttg Asn His Val Gln Ser Ala Glu Gln His Asn Gln Asp Val Asn Ser Leu 480 485 490			2569

ggc ctt att tct tca cga aaa aca agt gag gcc gtc gag ata tta aaa	2617
Gly Leu Ile Ser Ser Arg Lys Thr Ser Glu Ala Val Glu Ile Leu Lys	
495 500 505	
tta atg tca aca aca ttt ctt gtc ggc ctt tgc caa gca att gat tta	2665
Leu Met Ser Thr Thr Phe Leu Val Gly Leu Cys Gln Ala Ile Asp Leu	
510 515 520 525	
cgt cat ctt gaa gaa aat tta aaa tca act gtt aaa aac aca gta tct	2713
Arg His Leu Glu Glu Asn Leu Lys Ser Thr Val Lys Asn Thr Val Ser	
530 535 540	
tct gtt gct aaa cga gtt tta acc atg gga gtt aat ggt gaa tta cat	2761
Ser Val Ala Lys Arg Val Leu Thr Met Gly Val Asn Gly Glu Leu His	
545 550 555	
cca tca cgc ttt tgt gaa aaa gat ctt tta cgc gtc gtc gat cgt gaa	2809
Pro Ser Arg Phe Cys Glu Lys Asp Leu Leu Arg Val Val Asp Arg Glu	
560 565 570	
tat att ttt gca tat att gat gac cca tgt agt gca aca tat cct tta	2857
Tyr Ile Phe Ala Tyr Ile Asp Asp Pro Cys Ser Ala Thr Tyr Pro Leu	
575 580 585	
atg cag aaa ctt aga caa aca tta gtt gag cat gcc ttg aag aat ggt	2905
Met Gln Lys Leu Arg Gln Thr Leu Val Glu His Ala Leu Lys Asn Gly	
590 595 600 605	
gat aat gag cgt aat ctt tct aca tca att ttt caa aaa att gca acc	2953
Asp Asn Glu Arg Asn Leu Ser Thr Ser Ile Phe Gln Lys Ile Ala Thr	
610 615 620	
ttc gag gac gaa ctt aaa gca tta tta cct aaa gaa gtg gaa tca gct	3001
Phe Glu Asp Glu Leu Lys Ala Leu Leu Pro Lys Glu Val Glu Ser Ala	
625 630 635	
aga gcc gct ttg gaa agt gga aac cca gcc att cca aat cga att gaa	3049
Arg Ala Ala Leu Glu Ser Gly Asn Pro Ala Ile Pro Asn Arg Ile Glu	
640 645 650	
gaa tgt cgt tca tat cct ctt tat aaa ttt gtt cga aaa gag ctt ggt	3097
Glu Cys Arg Ser Tyr Pro Leu Tyr Lys Phe Val Arg Lys Glu Leu Gly	
655 660 665	
acg gaa tat ctt act ggc gaa aag gta aca tca cct ggt gaa gag ttt	3145
Thr Glu Tyr Leu Thr Gly Glu Lys Val Thr Ser Pro Gly Glu Glu Phe	
670 675 680 685	
gaa aaa gtt ttt att gcc atg agt aaa ggt gaa att att gat cct tta	3193
Glu Lys Val Phe Ile Ala Met Ser Lys Gly Glu Ile Ile Asp Pro Leu	

690	695	700	
ctt gaa tgt ctt gag tca tgg aat gga gcc cct tta cct atc tgt			3238
Leu Glu Cys Leu Glu Ser Trp Asn Gly Ala Pro Leu Pro Ile Cys			
705	710	715	
taattttccg attttaacgg tataaaaacc agtcttcggg ctggtttttt tattttataa			3298
ag			3300