

<110> SOLAZYME, INC.

<120> OLEAGINOUS MICROALGAE HAVING AN LPAAT ABLATION

<130> SOLAP070WO / 1503X01WO

<140> PCT/US2016/026265

<141> 2016-04-06

<150> 62/145,723

<151> 2015-04-10

<150> 62/143,711

<151> 2015-04-06

<160> 180

<170> PatentIn version 3.5

<210> 1

<211> 726

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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tgcgccgggt gagccactgc ttcgtccggg cggccaagag gagcatgagg gaggactcct	180
ggtccaggggt cctgacgtgg tcgcggctct gggagcgggc cagcatcatc tggctctgcc	240
gcaccgaggc cgcctccaac tggtcctcca gcagccgcag tcgccgccga ccctggcaga	300
ggaagacagg tgaggggggt atgaattgta cagaacaacc acgagccttg tctaggcaga	360
atccctacca gtcattggctt tacctggatg acggcctgcg aacagctgtc cagcgaccct	420
cgctgccgcc gcttctcccg cacgcttctt tccagcaccg tgatggcgcg agccagcgcc	480
gcacgctggc gctgcgcttc gccgatctga ggacagtcgg ggaactctga tcagtctaaa	540
cccccttgcg cgttagtgtt gccatccttt gcagaccggt gagagccgac ttgttgtgcg	600
ccacccccca caccacctcc tcccagacca attctgtcac ctttttggcg aaggcatcgg	660
cctcggcctg cagagaggac agcagtgcc agccgctggg ggttggcgga tgcacgtca	720
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<210> 2

<211> 749

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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acttgccgct caaaccgcgt acctctgctt tcgcgcaatc tgccctgttg aaatcgccac      240
cacattcata ttgtgacgct tgagcagtct gtaattgcct cagaatgtgg aatcatctgc      300
cccctgtgcg agcccatgcc aggcattgtc cgggcgagga caccgcccac tcgtacagca      360
gaccattatg ctacctcaca atagttcata acagtgacca tattttctcga agctcccaa      420
cgagcacctc catgctctga gtggccaccc cccggccctg gtgcttgcgg agggcaggtc      480
aaccggcatg gggctaccga aatccccgac cggatccac cccccgcg atgggaagaa      540
tctctccccg ggatgtgggc ccaccaccag cacaacctgc tggcccaggc gagcgtcaaa      600
ccataccaca caaatatcct tggcatcggc cctgaattcc ttctgccgct ctgctacccg      660
gtgcttctgt ccgaagcagg ggttgctagg gatcgctccg agtccgcaaa cccttgtcgc      720
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<210> 3

<211> 532

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 3

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Phe Thr Pro Asn Lys Gly Trp Met Asn Asp Pro Asn Gly Leu Trp Tyr
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Asp Glu Lys Asp Ala Lys Trp His Leu Tyr Phe Gln Tyr Asn Pro Asn
50           55           60

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Asp Thr Val Trp Gly Thr Pro Leu Phe Trp Gly His Ala Thr Ser Asp
65           70           75           80

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Asp Leu Thr Asn Trp Glu Asp Gln Pro Ile Ala Ile Ala Pro Lys Arg
          85           90           95

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Asn Asp Ser Gly Ala Phe Ser Gly Ser Met Val Val Asp Tyr Asn Asn
          100          105          110

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Thr Ser Gly Phe Phe Asn Asp Thr Ile Asp Pro Arg Gln Arg Cys Val
          115          120          125

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Ala Ile Trp Thr Tyr Asn Thr Pro Glu Ser Glu Glu Gln Tyr Ile Ser
          130          135          140

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

420

425

430

Ala Ser Ser Phe Phe Leu Asp Arg Gly Asn Ser Lys Val Lys Phe Val
 435 440 445

Lys Glu Asn Pro Tyr Phe Thr Asn Arg Met Ser Val Asn Asn Gln Pro
 450 455 460

Phe Lys Ser Glu Asn Asp Leu Ser Tyr Tyr Lys Val Tyr Gly Leu Leu
 465 470 475 480

Asp Gln Asn Ile Leu Glu Leu Tyr Phe Asn Asp Gly Asp Val Val Ser
 485 490 495

Thr Asn Thr Tyr Phe Met Thr Thr Gly Asn Ala Leu Gly Ser Val Asn
 500 505 510

Met Thr Thr Gly Val Asp Asn Leu Phe Tyr Ile Asp Lys Phe Gln Val
 515 520 525

Arg Glu Val Lys
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<210> 4

<211> 1599

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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aacgacccca acggcctgtg gtacgacgag aaggacgcca agtggcacct gtacttccag	180
tacaaccgga acgacaccgt ctggggggacg cccttgttct gggggccacgc cacgtccgac	240
gacctgacca actgggagga ccagcccatc gccatcgccc cgaagcgcaa cgactccggc	300
gccttctccg gctccatggt ggtggactac aacaacacct ccggcttctt caacgacacc	360
atcgacccgc gccagcgctg cgtggccatc tggacctaca acaccccgga gtccgaggag	420
cagtacatct cctacagcct ggacggcggc tacaccttca ccgagtacca gaagaacccc	480
gtgctggccg ccaactccac ccagttccgc gacccgaagg tcttctggta cgagccctcc	540
cagaagtgga tcatgaccgc ggccaagtcc caggactaca agatcgagat ctactcctcc	600
gacgacctga agtcctggaa gctggagtcc gcgttcgcca acgagggctt cctcggctac	660
cagtacgagt gccccggcct gatcgaggtc cccaccgagc aggaccccgag caagtcctac	720
tgggtgatgt tcatctccat caaccccggc gccccggccg gcggctcctt caaccagtac	780
ttcgtcggca gcttcaacgg caccacttc gaggccttcg acaaccagtc ccgctggtg	840
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agcgccctgg gcatcgctg ggcctccaac tgggagtact ccgccttcgt gcccaccaac      960
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aaccgggaga cggagctgat caacctgaag gccgagccga tcctgaacat cagcaacgcc      1080
ggcccctgga gccggttcgc caccaacacc acgttgacga aggccaacag ctacaacgtc      1140
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cagacgatct ccaagtccgt gttcgcggac ctctccctct ggttcaaggg cctggaggac      1260
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gggaacagca aggtgaagtt cgtgaaggag aaccctact tcaccaaccg catgagcgtg      1380
aacaaccagc ctttcaagag cgagaacgac ctgtcctact acaagggtgta cggcttgctg      1440
gaccagaaca tcctggagct gtacttcaac gacggcgacg tcgtgtccac caacacctac      1500
ttcatgacca ccgggaacgc cctgggctcc gtgaacatga cgacgggggt ggacaacctg      1560
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<210> 5
<211> 312
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"

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gctccgatgc cgctccaggg cgagcgctgt ttaaatagcc aggccccga ttgcaaagac      180
attatagcga gttaccaaag ccatattcaa acacctagat cactaccact tctacacagg      240
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<210> 6
<211> 408
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"

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tgtgtttgat cttgtgtgta cgcgcttttg cgagttgcta gctgcttggt ctatttgcca      180
ataccacccc cagcatcccc ttccctcgtt tcatatcgct tgcaccccaa ccgcaactta      240
tctacgctgt cctgctatcc ctacgcgctg ctctgctcc tgctcactgc ccctcgaca      300

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gccttggttt gggctccgcc tgtattctcc tggtagtgca acctgtaaac cagcactgca 360

atgctgatgc acggaagta gtgggatggg aacacaaatg gaaagctt 408

<210> 7

<211> 2333

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 7

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gctccgatgc cgctccagg cgagcgctgt ttaaataagc agggccccga ttgcaaagac 180

attatagcga gctaccaaag ccatattcaa acacctagat cactaccact tctacacagg 240

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cccccaacaa gggctggatg aacgaccca acggcctgtg gtacgacgag aaggacgcca 480

agtggcacct gtacttccag tacaacccga acgacaccgt ctgggggacg cccttgttct 540

ggggccacgc cacgtccgac gacctgacca actgggagga ccagcccatc gccatcgccc 600

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ccgagtacca gaagaacccc gtgctggccg ccaactccac ccagttccgc gacccgaagg 840

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<210> 8

<211> 1065

<212> DNA

<213> Prototheca moriformis

<400> 8

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tactgatggc	cctagattct	tcatcaaaaa	cgctgagac	acttgcccag	gattgaaact	420
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aggctgtacc	tgtgatcgag	gctggcggga	aaataggctt	cgtgtgctca	ggcatggga	540
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taatatcagc	ccgactgcct	gacgccagcg	tccacttttg	tgcacacatt	ccattcgtgc	960
ccaagacatt	tcattgtggg	gcgaagcgctc	cccagttacg	ctcacctgtt	tcccgcacctc	1020
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<211> 120

<212> DNA

<213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<210> 10
 <211> 1236
 <212> DNA
 <213> Cuphea wrightii

<400> 10
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 agcaacccca acggccgctt ccagggtgaag gccaacgtga gccccacgg gcgcgcccc 180
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<210> 11
 <211> 408
 <212> PRT
 <213> Cuphea wrightii

<400> 11
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Pro Arg Pro Thr Pro Lys Pro Gly Lys Phe Gly Asn Trp Pro Ser Ser
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 Leu Ser Gln Pro Phe Lys Pro Lys Ser Asn Pro Asn Gly Arg Phe Gln
 35 40 45
 Val Lys Ala Asn Val Ser Pro His Pro Lys Ala Asn Gly Ser Ala Val
 50 55 60
 Ser Leu Lys Ser Gly Ser Leu Asn Thr Leu Glu Asp Pro Pro Ser Ser
 65 70 75 80
 Pro Pro Pro Arg Thr Phe Leu Asn Gln Leu Pro Asp Trp Ser Arg Leu
 85 90 95
 Arg Thr Ala Ile Thr Thr Val Phe Val Ala Ala Glu Lys Gln Phe Thr
 100 105 110
 Arg Leu Asp Arg Lys Ser Lys Arg Pro Asp Met Leu Val Asp Trp Phe
 115 120 125
 Gly Ser Glu Thr Ile Val Gln Asp Gly Leu Val Phe Arg Glu Arg Phe
 130 135 140
 Ser Ile Arg Ser Tyr Glu Ile Gly Ala Asp Arg Thr Ala Ser Ile Glu
 145 150 155 160
 Thr Leu Met Asn His Leu Gln Asp Thr Ser Leu Asn His Cys Lys Ser
 165 170 175
 Val Gly Leu Leu Asn Asp Gly Phe Gly Arg Thr Pro Glu Met Cys Thr
 180 185 190
 Arg Asp Leu Ile Trp Val Leu Thr Lys Met Gln Ile Val Val Asn Arg
 195 200 205
 Tyr Pro Thr Trp Gly Asp Thr Val Glu Ile Asn Ser Trp Phe Ser Gln
 210 215 220
 Ser Gly Lys Ile Gly Met Gly Arg Glu Trp Leu Ile Ser Asp Cys Asn
 225 230 235 240
 Thr Gly Glu Ile Leu Val Arg Ala Thr Ser Ala Trp Ala Met Met Asn
 245 250 255
 Gln Lys Thr Arg Arg Phe Ser Lys Leu Pro Cys Glu Val Arg Gln Glu
 260 265 270
 Ile Ala Pro His Phe Val Asp Ala Pro Pro Val Ile Glu Asp Asn Asp
 275 280 285
 Arg Lys Leu His Lys Phe Asp Val Lys Thr Gly Asp Ser Ile Cys Lys
 290 295 300

Gly Leu Thr Pro Gly Trp Asn Asp Phe Asp Val Asn Gln His Val Ser
 305 310 315 320

Asn Val Lys Tyr Ile Gly Trp Ile Leu Glu Ser Met Pro Thr Glu Val
 325 330 335

Leu Glu Thr Gln Glu Leu Cys Ser Leu Thr Leu Glu Tyr Arg Arg Glu
 340 345 350

Cys Gly Arg Glu Ser Val Val Glu Ser Val Thr Ser Met Asn Pro Ser
 355 360 365

Lys Val Gly Asp Arg Ser Gln Tyr Gln His Leu Leu Arg Leu Glu Asp
 370 375 380

Gly Ala Asp Ile Met Lys Gly Arg Thr Glu Trp Arg Pro Lys Asn Ala
 385 390 395 400

Gly Thr Asn Arg Ala Ile Ser Thr
 405

<210> 12
 <211> 933
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 12
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 cccgccgacg ccgacgactt cgtggacgac gaccgctgga tcaccgtgat cctgtccgtg 180
 gtgcgcatcg ccgcctgctt cctgtccatg atggtgacca ccatcgtgtg gaacatgatc 240
 atgctgatcc tgctgccctg gccctacgcc cgcattccgc agggcaacct gtacggccac 300
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 ttctccaaca cccgcgccat ctacatctgc aaccacgcct ccctggtgga catcttcctg 420
 atcatgtggc tgatcccaaa gggcaccgtg accatcgcca agaaggagat catctggtat 480
 cccctgttcg gccagctgta cgtgctggcc aaccaccagc gcatcgaccg ctccaacccc 540
 tccgccgcca tcgagtccat caaggagggtg gcccgcgccg tggatgaagaa gaacctgtcc 600
 ctgatcatct tccccgaggg caccgctcc aagaccggcc gcctgctgcc cttcaagaag 660
 ggcttcatcc acatcgccct ccagacccgc ctgcccacg tgccgatggt gctgaccggc 720
 acccacctgg cctggcgcaa gaactccctg cgcgtgcgcc ccgcccccat caccgtgaag 780
 tacttctccc ccatcaagac cgacgactgg gaggaggaga agatcaacca ctacgtggag 840
 atgatccacg ccctgtacgt ggaccacctg cccgagtccc agaagcccct ggtgtccaag 900
 ggccgcgacg cctccggccg ctccaactcc tga 933

<210> 13
 <211> 563
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 13
 gctcttcgct aacggagggtc tgtcaccaaa tggaccccggt ctattgcggg aaaccacggc 60
 gatggcacgt ttcaaaactt gatgaaatac aatattcagt atgtcgcggg cggcgacggc 120
 ggggagctga tgtcgcgctg ggtattgctt aatcgccagc ttcgcccccg tcttggcgcg 180
 aggcgtgaac aagccgaccg atgtgcacga gcaaattcctg aactagaag ggctgactcg 240
 cccggcacgg ctgaattaca caggcttgca aaaataccag aatttgcacg caccgtattc 300
 gcggtatttt gttggacagt gaatagcgat gcggcaatgg cttgtggcgt tagaagggtgc 360
 gacgaagggtg gtgccaccac tgtgccagcc agtcctggcg gctcccaggg ccccgatcaa 420
 gagccaggac atccaaacta cccacagcat caacgccccg gcctatactc gaacccact 480
 tgcactctgc aatgggtatgg gaaccacggg gcagtcttgt gtgggtcgcg cctatcgcg 540
 tcggcgaaga ccgggaagggt acc 563

<210> 14
 <211> 465
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 14
 gagctcagcg gcgacgggtcc tgctaccgta cgacgttggg cacgcccattg aaagtttgta 60
 taccgagctt gttgagcgaa ctgcaagcgc ggctcaagga tacttgaact cctggattga 120
 tatcgggtcca ataattgatg gaaaatccga acctcgtgca agaactgagc aaacctcgtt 180
 acatggatgc acagtcgcca gtccaatgaa cattgaagtg agcgaactgt tcgcttcggt 240
 ggcagtacta ctcaaagaat gagctgctgt taaaaatgca ctctcgttct ctcaagtgag 300
 tggcagatga gtgctcacgc cttgcacttc gctgcccgtg tcatgccctg cgccccaaaa 360
 tttgaaaaaa gggatgagat tattgggcaa tggacgacgt cgtcgctccg ggagtcagga 420
 ccggcggaata ataagaggca acacactccg cttcttagct cttcc 465

<210> 15
 <211> 1533
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 15
ctttcttgcg ctatgacact tccagcaaaa ggtagggcgg gctgcgagac ggcttcccgg 60
cgctgcatgc aacaccgatg atgcttcgac cccccgaagc tccttcgggg ctgcatgggc 120
gctccgatgc cgctccaggg cgagcgctgt ttaaatagcc aggccccga ttgcaaagac 180
attatagcga gctaccaaag ccatattcaa acacctagat cactaccact tctacacagg 240
ccactcgagc ttgtgatcgc actccgctaa gggggcgcct cttcctcttc gtttcagtca 300
caaccgcaa actctagaat atcaatgatc gagcaggacg gcctccacgc cggctcccc 360
gccgcctggg tggagcgcct gttcggctac gactgggccc agcagaccat cggctgctcc 420
gacgccgccc tggtccgcct gtccgcccag ggccgcccc tgctgttcgt gaagaccgac 480
ctgtccggcg ccctgaacga gctgcaggac gaggccgccc gcctgtcctg gctggccacc 540
accggcgtgc cctgcgccgc cgtgctggac gtggtgaccg aggccggccg cgactggctg 600
ctgctgggcg aggtgcccgg ccaggacctg ctgtcctccc acctggcccc cgccgagaag 660
gtgtccatca tggccgacgc catgcgccgc ctgcacaccc tggacccgc cacctgcccc 720
ttcgaccacc aggccaaagca ccgcatcgag cgcgcccga cccgcatgga ggccggcctg 780
gtggaccagg acgacctgga cgaggagcac cagggcctgg cccccgccga gctgttcgcc 840
cgcctgaagg cccgcatgcc cgacggcgag gacctgggtg tgaccacgg cgacgcctgc 900
ctgccaaca tcatggtgga gaacggccgc ttctccggct tcatcgactg cggccgcctg 960
ggcgtggccg accgctacca ggacatcgc ctggccaccc gcgacatcgc cgaggagctg 1020
ggcggcgagt gggccgaccg cttcctggtg ctgtacggca tcgccgcccc cgactcccag 1080
cgcacgcct tctaccgcct gctggacgag ttcttctgac aattggcagc agcagctcgg 1140
atagtatcga cactctctgg acgctggtcg tgtgatggac tgttgccgcc acacttgctg 1200
ccttgacctg tgaatatccc tgccgctttt atcaaacagc ctcagtgtgt ttgatcttgt 1260
gtgtacgcgc ttttgcgagt tgctagctgc ttgtgctatt tgcgaatacc acccccagca 1320
tccccctccc tcgtttcata tcgcttgcat cccaaccgca acttatctac gctgtcctgc 1380
tatccctcag cgctgctcct gtcctgctc actgcccctc gcacagcctt ggtttgggct 1440
ccgcctgtat tctcctggta ctgcaacctg taaaccagca ctgcaatgct gatgcacggg 1500
aagtagtggg atgggaacac aaatggagga tcc 1533

<210> 16
<211> 310
<212> PRT
<213> Cocos nucifera

<400> 16
Met Asp Ala Ser Gly Ala Ser Ser Phe Leu Arg Gly Arg Cys Leu Glu
1 5 10 15
Ser Cys Phe Lys Ala Ser Phe Gly Tyr Val Met Ser Gln Pro Lys Asp
20 25 30
Ala Ala Gly Gln Pro Ser Arg Arg Pro Ala Asp Ala Asp Asp Phe Val
35 40 45

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

<210> 17

<211> 1476

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 17

atggccaccg catccacttt ctcggcggtc aatgcccgt gcggcgacct gcgtcgctcg	60
gcggggtccg ggccccggcg cccagcgagg cccctccccg tgcgcgggcg cgccgccgcc	120
gccgccgacg ccaaccccg cgcgccgag cgccgcgtgg tgatcaccgg ccagggcgtg	180
gtgacctccc tgggcccagac catcgagcag ttctactcct ccctgctgga gggcgtgtcc	240
ggcatctccc agatccagaa gttcgacacc accgggtaca ccaccaccat cgccggcgag	300
atcaagtccc tgcagctgga cccctacgtg cccaagcgct gggccaagcg cgtggacgac	360
gtgatcaagt acgtgtacat cgccggcaag caggccctgg agtccgccgg cctgcccata	420
gaggccgccc gcctggccgg cgccggcctg gaccccgccc tgtgcggcgt gctgatcggc	480
accgccatgg ccggcatgac ctcttcgcc gccggcggtg aggccctgac ccgcggcggc	540
gtgcgcaaga tgaacccctt ctgcatcccc ttctccatct ccaacatggg cggcgccatg	600
ctggccatgg acatcggcct catgggcccc aactactcca tctccaccgc ctgcgccacc	660
ggcaactact gcatcctggg cgccgccgac cacatccgcc gcggcgacgc caacgtgatg	720
ctggccggcg gcgccgacgc cgccatcatc ccctccggca tcggcggtt catgcctgc	780
aaggccctgt ccaagcgcaa cgacgagccc gagcgcgcct cccgcccctg ggacgccgac	840
cgcgacggct tcgtgatggg cgagggcgcc ggcgtgctgg tgctggagga gctggagcac	900
gccaagcgcc gcggcgccac catcctggcc gagctggtgg gcggcgccgc cacctccgac	960
gcccaccaca tgaccgagcc cgacccccag ggccgcggcg tgcgcctgtg cctggagcgc	1020
gccctggagc gcgcccgcct ggcccccgag cgcgtgggct acgtgaacgc ccacggcacc	1080
tccacccccg ccggcgacgt ggccgagtac cgcgccatcc gcgccgtgat ccccaggac	1140
tccctgcgca tcaactccac caagtccatg atcggccacc tgctggggcg cgccggcgcc	1200
gtggaggccg tggccgccat ccaggccctg cgcaccggct ggctgcaccc caacctgaac	1260
ctggagaacc ccgcccccg cgtggacccc gtggtgctgg tgggcccccg caaggagcgc	1320
gccgaggacc tggacgtggt gctgtccaac tccttcggct tcggcggcc caactcctgc	1380
gtgatcttcc gcaagtacga cgagatggac tacaaggacc acgacggcga ctacaaggac	1440
cacgacatcg actacaagga cgacgacgac aagtga	1476

<210> 18

<211> 491

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 18

Met Ala Thr Ala Ser Thr Phe Ser Ala Phe Asn Ala Arg Cys Gly Asp
 1 5 10 15

 Leu Arg Arg Ser Ala Gly Ser Gly Pro Arg Arg Pro Ala Arg Pro Leu
 20 25 30

 Pro Val Arg Gly Arg Ala Ala Ala Ala Asp Ala Asn Pro Ala Arg
 35 40 45

 Pro Glu Arg Arg Val Val Ile Thr Gly Gln Gly Val Val Thr Ser Leu
 50 55 60

 Gly Gln Thr Ile Glu Gln Phe Tyr Ser Ser Leu Leu Glu Gly Val Ser
 65 70 75 80

 Gly Ile Ser Gln Ile Gln Lys Phe Asp Thr Thr Gly Tyr Thr Thr Thr
 85 90 95

 Ile Ala Gly Glu Ile Lys Ser Leu Gln Leu Asp Pro Tyr Val Pro Lys
 100 105 110

 Arg Trp Ala Lys Arg Val Asp Asp Val Ile Lys Tyr Val Tyr Ile Ala
 115 120 125

 Gly Lys Gln Ala Leu Glu Ser Ala Gly Leu Pro Ile Glu Ala Ala Gly
 130 135 140

 Leu Ala Gly Ala Gly Leu Asp Pro Ala Leu Cys Gly Val Leu Ile Gly
 145 150 155 160

 Thr Ala Met Ala Gly Met Thr Ser Phe Ala Ala Gly Val Glu Ala Leu
 165 170 175

 Thr Arg Gly Gly Val Arg Lys Met Asn Pro Phe Cys Ile Pro Phe Ser
 180 185 190

 Ile Ser Asn Met Gly Gly Ala Met Leu Ala Met Asp Ile Gly Phe Met
 195 200 205

 Gly Pro Asn Tyr Ser Ile Ser Thr Ala Cys Ala Thr Gly Asn Tyr Cys
 210 215 220

 Ile Leu Gly Ala Ala Asp His Ile Arg Arg Gly Asp Ala Asn Val Met
 225 230 235 240

 Leu Ala Gly Gly Ala Asp Ala Ala Ile Ile Pro Ser Gly Ile Gly Gly
 245 250 255

 Phe Ile Ala Cys Lys Ala Leu Ser Lys Arg Asn Asp Glu Pro Glu Arg
 260 265 270

 Ala Ser Arg Pro Trp Asp Ala Asp Arg Asp Gly Phe Val Met Gly Glu
 275 280 285

Gly Ala Gly Val Leu Val Leu Glu Glu Leu Glu His Ala Lys Arg Arg
 290 295 300
 Gly Ala Thr Ile Leu Ala Glu Leu Val Gly Gly Ala Ala Thr Ser Asp
 305 310 315 320
 Ala His His Met Thr Glu Pro Asp Pro Gln Gly Arg Gly Val Arg Leu
 325 330 335
 Cys Leu Glu Arg Ala Leu Glu Arg Ala Arg Leu Ala Pro Glu Arg Val
 340 345 350
 Gly Tyr Val Asn Ala His Gly Thr Ser Thr Pro Ala Gly Asp Val Ala
 355 360 365
 Glu Tyr Arg Ala Ile Arg Ala Val Ile Pro Gln Asp Ser Leu Arg Ile
 370 375 380
 Asn Ser Thr Lys Ser Met Ile Gly His Leu Leu Gly Gly Ala Gly Ala
 385 390 395 400
 Val Glu Ala Val Ala Ala Ile Gln Ala Leu Arg Thr Gly Trp Leu His
 405 410 415
 Pro Asn Leu Asn Leu Glu Asn Pro Ala Pro Gly Val Asp Pro Val Val
 420 425 430
 Leu Val Gly Pro Arg Lys Glu Arg Ala Glu Asp Leu Asp Val Val Leu
 435 440 445
 Ser Asn Ser Phe Gly Phe Gly Gly His Asn Ser Cys Val Ile Phe Arg
 450 455 460
 Lys Tyr Asp Glu Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp
 465 470 475 480
 His Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys
 485 490

<210> 19

<211> 1590

<212> DNA

<213> Artificial Sequence

<220>

<221> source

 <223> /note="Description of Artificial Sequence: Synthetic
 polynucleotide"

<400> 19

atggactccc gcgcccagaa ccgcgacggc ggcgaggacg tgaagcagga gctgctgtcc 60

gccggcgacg acggcaaggt gccctgcccc accgtggcca tcggcatccg ccagcgcctg 120

cccgaattcc tgagttccgt gaacatgaag tacgtgaagc tgggctacca ctacctgatc 180

acccacgcca tgttcctgct gacctgccc gccttcttcc tggtagccgc cgagatcggc 240
 cgctggggcc acgagcgcat ctaccgag ctgtggaccc acctgcacct gaacctggtg 300
 tccatcatgg cctgctcctc cgccctggtg gccggcgcca ccctgtactt catgtcccgc 360
 ccccgccccg tgtacctggt ggagttcgcc tgctaccgcc ccgacgagcg cctgaagggtg 420
 tccaaggact tcttcctgga catgtcccgc cgaccgggcc tgttctcctc ctctccatg 480
 gacttccaga ccaagatcac ccagcgctcc ggcctgggagc acgagaccta cctgcccccc 540
 gccatcctgg cctccccccc caaccctgc atgcgagagg cccgcgagga ggccgccatg 600
 gtgatgttcg gcgccctgga cgagctgttc gagcagaccg gcgtgaagcc caaggagatc 660
 ggcgtgctgg tggtagactg ctccctgttc aacccaccc cctccatgtc cgccatgatc 720
 gtgaaccact accacatgcg cggcaacatc aagtccctga acctgggagg catgggctgc 780
 tccgccggcc tgatctccat cgacctggcc cgcgacctgc tgcagggtgca cggcaacacc 840
 tacgccgtgg tgggtgtccac cgagaacatc accctgaact ggtacttcgg cgacgaccgc 900
 tccaagctga tgtccaactg catcttccgc atggggcgcg ccgccgtgct gctgtccaac 960
 aagcgccgcg agcgccgccg cgccaagtac gagctgctgc acaccgtgcg caccacaag 1020
 ggcgccgacg acaagtgtt ccgctgctg taccaggagg aggactccac cggctccctg 1080
 ggcgtgtccc tgtcccgca gctgatggcc gtggccggca acgccctgaa ggccaacatc 1140
 accacctg gccccctggt gctgcccctg tccgagcaga tcctgttctt cgctccctg 1200
 gtggcccgca agttcctgaa catgaagatg aagccctaca tccccgactt caagctggcc 1260
 ttcgagcact tctgcatcca cgccggcgcc cgcgccgtgc tggacgagct ggagaagaac 1320
 ctggacctga ccgagtggca catggagccc tccgcatga ccctgtaccg cttcggcaac 1380
 acctcctcct cctccctgtg gtacgagctg gcctacaccg agggccaggg ccgctgaag 1440
 cgcgcgacc gcctgtggca gatcgcttc ggctccggct tcaagtgcaa ctccgccgtg 1500
 tggcgcgcg tgcgaccgt gaagcccccc gtgaacaacg cctggtccga cgtgatcgac 1560
 cgcttccccg tgaagctgcc ccagttctga 1590

<210> 20

<211> 529

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 20

Met Asp Ser Arg Ala Gln Asn Arg Asp Gly Gly Glu Asp Val Lys Gln
 1 5 10 15

Glu Leu Leu Ser Ala Gly Asp Asp Gly Lys Val Pro Cys Pro Thr Val
 20 25 30

Ala Ile Gly Ile Arg Gln Arg Leu Pro Asp Phe Leu Gln Ser Val Asn
 35 40 45

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

Arg Thr His Lys Gly Ala Asp Asp Lys Cys Phe Arg Cys Val Tyr Gln
 340 345 350
 Glu Glu Asp Ser Thr Gly Ser Leu Gly Val Ser Leu Ser Arg Glu Leu
 355 360 365
 Met Ala Val Ala Gly Asn Ala Leu Lys Ala Asn Ile Thr Thr Leu Gly
 370 375 380
 Pro Leu Val Leu Pro Leu Ser Glu Gln Ile Leu Phe Phe Ala Ser Leu
 385 390 395 400
 Val Ala Arg Lys Phe Leu Asn Met Lys Met Lys Pro Tyr Ile Pro Asp
 405 410 415
 Phe Lys Leu Ala Phe Glu His Phe Cys Ile His Ala Gly Gly Arg Ala
 420 425 430
 Val Leu Asp Glu Leu Glu Lys Asn Leu Asp Leu Thr Glu Trp His Met
 435 440 445
 Glu Pro Ser Arg Met Thr Leu Tyr Arg Phe Gly Asn Thr Ser Ser Ser
 450 455 460
 Ser Leu Trp Tyr Glu Leu Ala Tyr Thr Glu Ala Gln Gly Arg Val Lys
 465 470 475 480
 Arg Gly Asp Arg Leu Trp Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys
 485 490 495
 Asn Ser Ala Val Trp Arg Ala Leu Arg Thr Val Lys Pro Pro Val Asn
 500 505 510
 Asn Ala Trp Ser Asp Val Ile Asp Arg Phe Pro Val Lys Leu Pro Gln
 515 520 525

Phe

<210> 21
 <211> 906
 <212> DNA
 <213> Trypanosoma brucei

<400> 21
 atgctgatga acttcggcgg ctctacgac gcctacatca acaacttcca gggcaccttc 60
 ctggccgagt ggatgctgga ccaccctcc gtgccctaca tcgccggcgt gatgtacctg 120
 atcctggtgc tgtacgtgcc caagtccatc atggcctccc agccccccct gaacctgcgc 180
 gccgcaaca tcgtgtggaa cctgttcctg accctgttct ccatgtgcgg cgcctactac 240
 accgtgccct acctggtgaa ggccttcattg aaccccgaga tcgtgatggc cgcctccggc 300
 atcaagctgg acgccaacac ctcccccatc atcaccact cgggcttcta caccaccacc 360

tgcgccctgg ccgactcctt ctacttcaac ggcgacgtgg gcttctgggt ggccctgttc 420
 gccctgtcca agatccccga gatgatcgac accgccttcc tgggtgttcca gaagaagccc 480
 gtgatcttcc tgcactggta ccaccacctg accgtgatgc tgttctgctg gttcgcttac 540
 gtgcagaaga tctcctccgg cctgtgggtc gcctccatga actactccgt gcactccatc 600
 atgtacctgt actacttcgt gtgcgcctgc ggccaccgcc gcctgggtgcg ccccttcgcc 660
 cccatcatca ccttcgtgca gatcttccag atggtgggtg gcaccatcgt ggtgtgctac 720
 acctacaccg tgaagcacgt gctggggccg tcctgcaccg tgaccgactt ctccctgcac 780
 accggcctgg tgatgtacgt gtcctacctg ctgctgttct cccagctgtt ctaccgctcc 840
 tacctgtccc cccgcgacaa ggcctccatc cccacgtgg ccgccgagat caagaagaag 900
 gagtga 906

<210> 22
 <211> 322
 <212> PRT
 <213> Trypanosoma brucei

<400> 22
 Met Tyr Pro Thr His Arg Asp Leu Ile Leu Asn Asn Tyr Ser Asp Ile
 1 5 10 15
 Tyr Arg Ser Pro Thr Cys His Tyr His Thr Trp His Thr Leu Ile His
 20 25 30
 Thr Pro Ile Asn Glu Leu Leu Phe Pro Asn Leu Pro Arg Glu Cys Asp
 35 40 45
 Phe Gly Tyr Asp Ile Pro Tyr Phe Arg Gly Gln Ile Asp Val Phe Asp
 50 55 60
 Gly Trp Ser Met Ile His Phe Thr Ser Ser Asn Trp Cys Ile Pro Ile
 65 70 75 80
 Thr Val Cys Leu Cys Tyr Ile Met Met Ile Ala Gly Leu Lys Lys Tyr
 85 90 95
 Met Gly Pro Arg Asp Gly Gly Arg Ala Pro Ile Gln Ala Lys Asn Tyr
 100 105 110
 Ile Ile Ala Trp Asn Leu Phe Leu Ser Phe Phe Ser Phe Ala Gly Val
 115 120 125
 Tyr Tyr Thr Val Pro Tyr His Leu Phe Asp Pro Glu Asn Gly Leu Phe
 130 135 140
 Ala Gln Gly Phe Tyr Ser Thr Val Cys Asn Asn Gly Ala Tyr Tyr Gly
 145 150 155 160
 Asn Gly Asn Val Gly Phe Phe Val Trp Leu Phe Ile Tyr Ser Lys Ile
 165 170 175

Phe Glu Leu Val Asp Thr Phe Phe Leu Leu Ile Arg Lys Asn Pro Val
 180 185 190
 Ile Phe Leu His Trp Tyr His His Leu Thr Val Leu Leu Tyr Cys Trp
 195 200 205
 His Ala Tyr Ser Val Arg Ile Gly Thr Gly Ile Trp Phe Ala Thr Met
 210 215 220
 Asn Tyr Ser Val His Ser Val Met Tyr Leu Tyr Phe Ala Met Thr Gln
 225 230 235 240
 Tyr Gly Pro Ser Thr Lys Lys Phe Ala Lys Lys Phe Ser Lys Phe Ile
 245 250 255
 Thr Thr Ile Gln Ile Leu Gln Met Val Val Gly Ile Ile Val Thr Phe
 260 265 270
 Ala Ala Met Leu Tyr Val Thr Phe Asp Val Pro Cys Tyr Thr Ser Leu
 275 280 285
 Ala Asn Ser Val Leu Gly Leu Met Met Tyr Ala Ser Tyr Phe Val Leu
 290 295 300
 Phe Val Gln Leu Tyr Val Ser His Tyr Val Ser Pro Lys His Val Lys
 305 310 315 320
 Gln Glu

<210> 23
 <211> 933
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polynucleotide"

<400> 23
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 gaccgcccct tcttcaacat ctacctgtgg gactacttca accgcgccgt gggctgggcc 120
 accgccggcc gcttccagcc caaggacttc gagttcacccg tgggcaagca gccctgtcc 180
 gagccccgcc ccgtgctgct gttcatcgcc atgtactacg tggatgattt cggcggccgc 240
 tccctggtga agtcctgcaa gccctgaag ctgcgcttca tctcccagggt gcacaacctg 300
 atgctgacct ccgtgtcctt cctgtggctg atcctgatgg tggagcagat gctgcccac 360
 gtgtaccgcc acggcctgta cttcgccgtg tgcaacgtgg agtcctggac ccagcccatg 420
 gagacctgt actacctgaa ctacatgacc aagttcgtgg agttcgccga caccgtgctg 480
 atggtgctga agcaccgcaa gctgaccttc ctgcacacct accaccacgg cgccaccgcc 540
 ctgctgtgct acaaccagct ggtgggctac accgccgtga cctgggtgcc cgtgaccctg 600

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aacctggccg tgcacgtgct gatgtactgg tactacttcc tgtccgcctc cggcatccgc      660
gtgtggtgga aggcctgggt gacccgcctg cagatcgtgc agttcatgct ggacctgac      720
gtggtgtact acgtgctgta ccagaagatc gtggccgcct acttcaagaa cgcctgcacc      780
ccccagtgcg aggactgcct gggctccatg accgccatcg ccgccggcgc cgccatcctg      840
acctcctacc tgttcctgtt catctccttc tacatcgagg tgtacaagcg cggctccgcc      900
tccggcaaga agaagatcaa caagaacaac tga                                  933

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<210> 24

<211> 310

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 24

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Met Val Ser Asp Trp Lys Asn Phe Cys Leu Glu Lys Ala Ser Arg Phe
1          5          10          15

```

```

Arg Pro Thr Ile Asp Arg Pro Phe Phe Asn Ile Tyr Leu Trp Asp Tyr
          20          25          30

```

```

Phe Asn Arg Ala Val Gly Trp Ala Thr Ala Gly Arg Phe Gln Pro Lys
          35          40          45

```

```

Asp Phe Glu Phe Thr Val Gly Lys Gln Pro Leu Ser Glu Pro Arg Pro
          50          55          60

```

```

Val Leu Leu Phe Ile Ala Met Tyr Tyr Val Val Ile Phe Gly Gly Arg
65          70          75          80

```

```

Ser Leu Val Lys Ser Cys Lys Pro Leu Lys Leu Arg Phe Ile Ser Gln
          85          90          95

```

```

Val His Asn Leu Met Leu Thr Ser Val Ser Phe Leu Trp Leu Ile Leu
          100          105          110

```

```

Met Val Glu Gln Met Leu Pro Ile Val Tyr Arg His Gly Leu Tyr Phe
          115          120          125

```

```

Ala Val Cys Asn Val Glu Ser Trp Thr Gln Pro Met Glu Thr Leu Tyr
          130          135          140

```

```

Tyr Leu Asn Tyr Met Thr Lys Phe Val Glu Phe Ala Asp Thr Val Leu
          145          150          155          160

```

```

Met Val Leu Lys His Arg Lys Leu Thr Phe Leu His Thr Tyr His His
          165          170          175

```

```

Gly Ala Thr Ala Leu Leu Cys Tyr Asn Gln Leu Val Gly Tyr Thr Ala
          180          185          190

```

Val Thr Trp Val Pro Val Thr Leu Asn Leu Ala Val His Val Leu Met
 195 200 205
 Tyr Trp Tyr Tyr Phe Leu Ser Ala Ser Gly Ile Arg Val Trp Trp Lys
 210 215 220
 Ala Trp Val Thr Arg Leu Gln Ile Val Gln Phe Met Leu Asp Leu Ile
 225 230 235 240
 Val Val Tyr Tyr Val Leu Tyr Gln Lys Ile Val Ala Ala Tyr Phe Lys
 245 250 255
 Asn Ala Cys Thr Pro Gln Cys Glu Asp Cys Leu Gly Ser Met Thr Ala
 260 265 270
 Ile Ala Ala Gly Ala Ala Ile Leu Thr Ser Tyr Leu Phe Leu Phe Ile
 275 280 285
 Ser Phe Tyr Ile Glu Val Tyr Lys Arg Gly Ser Ala Ser Gly Lys Lys
 290 295 300
 Lys Ile Asn Lys Asn Asn
 305 310

<210> 25

<211> 573

<212> DNA

<213> Prototheca moriformis

<400> 25

tggtgaagaa tgagccggcg acttaaaata aatggcaggc taagagaatt aataactcga	60
aacctaagcg aaagcaagtc ttaatagggc gctaatttaa caaacatta aataaaatct	120
aaagtcattt attttagacc cgaacctgag tgatctaacc atggtcagga tgaaacttgg	180
gtgacaccaa gtggaagtcc gaaccgaccg atgttgaaaa atcggcggat gaactgtggt	240
tagtggtgaa ataccagtcg aactcagagc tagctggttc tccccgaaat gcgttgaggc	300
gcagcaatat atctcgtcta tctaggggta aagcactgtt tcggtgcggg ctatgaaaat	360
ggtaccaaact cgtggcaaac tctgaatact agaaatgacg atatattagt gagactatgg	420
gggataagct ccatagtcga gagggaaaca gccagacca ccagttaagg ccccaaaatg	480
ataatgaagt ggtaaaggag gtgaaaatgc aaatacaacc aggaggttgg cttagaagca	540
gccatccttt aaagagtgcg taatagctca ctg	573

<210> 26

<211> 384

<212> PRT

<213> Cuphea wrightii

<400> 26

Met Ala Ile Ala Ala Ala Val Ile Phe Leu Phe Gly Leu Ile Phe	
1 5 10 15	

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

Leu Ile Arg Pro Leu Ser Lys Asn Ala Tyr Arg Arg Ile Asn Arg Val
 35 40 45

Phe Ala Glu Leu Leu Leu Ser Glu Leu Leu Cys Leu Phe Asp Trp Trp
 50 55 60

Ala Gly Ala Lys Leu Lys Leu Phe Thr Asp Pro Glu Thr Phe Arg Leu
 65 70 75 80

Met Gly Lys Glu His Ala Leu Val Ile Ile Asn His Met Thr Glu Leu
 85 90 95

Asp Trp Met Val Gly Trp Val Met Gly Gln His Phe Gly Cys Leu Gly
 100 105 110

Ser Ile Ile Ser Val Ala Lys Lys Ser Thr Lys Phe Leu Pro Val Leu
 115 120 125

Gly Trp Ser Met Trp Phe Ser Glu Tyr Leu Tyr Leu Glu Arg Ser Trp
 130 135 140

Ala Lys Asp Lys Ser Thr Leu Lys Ser His Ile Glu Arg Leu Ile Asp
 145 150 155 160

Tyr Pro Leu Pro Phe Trp Leu Val Ile Phe Val Glu Gly Thr Arg Phe
 165 170 175

Thr Arg Thr Lys Leu Leu Ala Ala Gln Gln Tyr Ala Val Ser Ser Gly
 180 185 190

Leu Pro Val Pro Arg Asn Val Leu Ile Pro Arg Thr Lys Gly Phe Val
 195 200 205

Ser Cys Val Ser His Met Arg Ser Phe Val Pro Ala Val Tyr Asp Val
 210 215 220

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

Phe Glu Gly Gln Ser Ile Met Leu His Val His Ile Lys Arg His Ala
 245 250 255

Met Lys Asp Leu Pro Glu Ser Asp Asp Ala Val Ala Glu Trp Cys Arg
 260 265 270

Asp Lys Phe Val Glu Lys Asp Ala Leu Leu Asp Lys His Asn Ala Glu
 275 280 285

Asp Thr Phe Ser Gly Gln Glu Val Cys His Ser Gly Ser Arg Gln Leu
 290 295 300

Lys Ser Leu Leu Val Val Ile Ser Trp Val Val Val Thr Thr Phe Gly
305 310 315 320

Ala Leu Lys Phe Leu Gln Trp Ser Ser Trp Lys Gly Lys Ala Phe Ser
325 330 335

Ala Ile Gly Leu Gly Ile Val Thr Leu Leu Met His Val Leu Ile Leu
340 345 350

Ser Ser Gln Ala Glu Arg Ser Asn Pro Ala Glu Val Ala Gln Ala Lys
355 360 365

Leu Lys Thr Gly Leu Ser Ile Ser Lys Lys Val Thr Asp Lys Glu Asn
370 375 380

<210> 27
<211> 387
<212> PRT
<213> Cuphea wrightii

<400> 27
Met Ala Ile Ala Ala Ala Val Ile Val Pro Leu Ser Leu Leu Phe
1 5 10 15

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

Leu Ile Arg Pro Leu Ser Lys Asn Thr Tyr Arg Arg Ile Asn Arg Val
35 40 45

Val Ala Glu Leu Leu Trp Leu Glu Leu Val Trp Leu Ile Asp Trp Trp
50 55 60

Ala Gly Val Lys Ile Lys Val Phe Thr Asp His Glu Thr Phe His Leu
65 70 75 80

Met Gly Lys Glu His Ala Leu Val Ile Cys Asn His Lys Ser Asp Ile
85 90 95

Asp Trp Leu Val Gly Trp Val Leu Gly Gln Arg Ser Gly Cys Leu Gly
100 105 110

Ser Thr Leu Ala Val Met Lys Lys Ser Ser Lys Phe Leu Pro Val Leu
115 120 125

Gly Trp Ser Met Trp Phe Ser Glu Tyr Leu Phe Leu Glu Arg Ser Trp
130 135 140

Ala Lys Asp Glu Ile Thr Leu Lys Ser Gly Leu Asn Arg Leu Lys Asp
145 150 155 160

Tyr Pro Leu Pro Phe Trp Leu Ala Leu Phe Val Glu Gly Thr Arg Phe
165 170 175

Thr Arg Ala Lys Leu Leu Ala Ala Gln Gln Tyr Ala Ala Ser Ser Gly
 180 185 190

Leu Pro Val Pro Arg Asn Val Leu Ile Pro Arg Thr Lys Gly Phe Val
 195 200 205

Ser Ser Val Ser His Met Arg Ser Phe Val Pro Ala Ile Tyr Asp Val
 210 215 220

Thr Val Ala Ile Pro Lys Thr Ser Pro Pro Pro Thr Leu Ile Arg Met
 225 230 235 240

Phe Lys Gly Gln Ser Ser Val Leu His Val His Leu Lys Arg His Leu
 245 250 255

Met Lys Asp Leu Pro Glu Ser Asp Asp Ala Val Ala Gln Trp Cys Arg
 260 265 270

Asp Ile Phe Val Glu Lys Asp Ala Leu Leu Asp Lys His Asn Ala Glu
 275 280 285

Asp Thr Phe Ser Gly Gln Glu Leu Gln Glu Thr Gly Arg Pro Ile Lys
 290 295 300

Ser Leu Leu Val Val Ile Ser Trp Ala Val Leu Glu Val Phe Gly Ala
 305 310 315 320

Val Lys Phe Leu Gln Trp Ser Ser Leu Leu Ser Ser Trp Lys Gly Leu
 325 330 335

Ala Phe Ser Gly Ile Gly Leu Gly Val Ile Thr Leu Leu Met His Ile
 340 345 350

Leu Ile Leu Phe Ser Gln Ser Glu Arg Ser Thr Pro Ala Lys Val Ala
 355 360 365

Pro Ala Lys Pro Lys Asn Glu Gly Glu Ser Ser Lys Thr Glu Met Glu
 370 375 380

Lys Glu Lys
 385

<210> 28
 <211> 327
 <212> PRT
 <213> Cuphea wrightii

<400> 28
 Met Glu Ile Pro Pro His Cys Leu Cys Ser Pro Ser Pro Ala Pro Ser
 1 5 10 15

Gln Leu Tyr Tyr Lys Lys Lys Lys His Ala Ile Leu Gln Thr Gln Thr
 20 25 30

Pro Tyr Arg Tyr Arg Val Ser Pro Thr Cys Phe Ala Pro Pro Arg Leu

35

40

Arg Lys Gln His Pro Tyr Pro Leu Pro Val Leu Cys Tyr Pro Lys Leu
50 55 60

Leu His Phe Ser Gln Pro Arg Tyr Pro Leu Val Arg Ser His Leu Ala
65 70 75 80

Glu Ala Gly Val Ala Tyr Arg Pro Gly Tyr Glu Leu Leu Gly Lys Ile
85 90 95

Arg Gly Val Cys Phe Tyr Ala Val Thr Ala Ala Val Ala Leu Leu Leu
100 105 110

Phe Gln Cys Met Leu Leu Leu His Pro Phe Val Leu Leu Phe Asp Pro
115 120 125

Phe Pro Arg Lys Ala His His Thr Ile Ala Lys Leu Trp Ser Ile Cys
130 135 140

Ser Val Ser Leu Phe Tyr Lys Ile His Ile Lys Gly Leu Glu Asn Leu
145 150 155 160

Pro Pro Pro His Ser Pro Ala Val Tyr Val Ser Asn His Gln Ser Phe
165 170 175

Leu Asp Ile Tyr Thr Leu Leu Thr Leu Gly Arg Thr Phe Lys Phe Ile
180 185 190

Ser Lys Thr Glu Ile Phe Leu Tyr Pro Ile Ile Gly Trp Ala Met Tyr
195 200 205

Met Leu Gly Thr Ile Pro Leu Lys Arg Leu Asp Ser Arg Ser Gln Leu
210 215 220

Asp Thr Leu Lys Arg Cys Met Asp Leu Ile Lys Lys Gly Ala Ser Val
225 230 235 240

Phe Phe Phe Pro Glu Gly Thr Arg Ser Lys Asp Gly Lys Leu Gly Ala
245 250 255

Phe Lys Lys Gly Ala Phe Ser Ile Ala Ala Lys Ser Lys Val Pro Val
260 265 270

Val Pro Ile Thr Leu Ile Gly Thr Gly Lys Ile Met Pro Pro Gly Ser
275 280 285

Glu Leu Thr Val Asn Pro Gly Thr Val Gln Val Ile Ile His Lys Pro
290 295 300

Ile Glu Gly Ser Asp Ala Glu Ala Met Cys Asn Glu Ala Arg Ala Thr
305 310 315 320

Ile Ser His Ser Leu Asp Asp
325

<210> 29
<211> 984
<212> DNA
<213> Cuphea wrightii

<400> 29
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aagaagaaga agcatgccat tctccaaact caaactccct atagatatag agtttccccg 120
acatgctttg ccccccccg attgaggaag cagcatcctt accctctccc tgcctctgc 180
tatccaaaac tcctccactt cagccagcct aggtaccctc tggtttagatc tcatttggct 240
gaagctggtg ttgcttatcg tccaggatac gaattattag gaaaaataag gggagtgtgt 300
ttctatgctg tcaactgctgc cgttgccttg cttctatttc agtgcattgct cctcctccat 360
ccctttgtgc tcctcttcga tccatttcca agaaaggctc accataccat cgccaaactc 420
tgggtctatct gctctgtttc tcttttttac aagattcaca tcaaggggtt ggaaaatctt 480
ccccacccc actctcctgc cgtctatgtc tctaatacctc agagtcttct cgacatctat 540
actctcctca ctctcggtag aaccttcaag ttcattcagca agactgagat ctttctctat 600
ccaattatcg gttgggccat gtatatgttg ggtaccattc ctctcaagcg gttggacagc 660
agaagccaat tggacactct taagcgatgt atggatctca tcaagaaggg agcatccgtc 720
ttttcttcc cagagggaaac acgaagtaaa gatgggaaac tgggtgcttt caagaaagg 780
gcattcagca tcgcagcaaa aagcaagggt cctgttgtgc cgatcacctt tattggaact 840
ggcaagatta tgccacctgg gagcgaactt actgtcaatc caggaactgt gcaagtaatc 900
atacataaac ctatcgaagg aagtgatgca gaagcaatgt gcaatgaagc tagagccacg 960
atttctcact cacttgatga ttaa 984

<210> 30
<211> 1155
<212> DNA
<213> Cuphea wrightii

<400> 30
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ctcataatca atctcttcca ggcgctttgc tttgtcctta ttcggcctct ttcgaaaaac 120
gcctacmga gaataaacag agtttttgca gaattgttgt tgcggagct tttatgccta 180
ttcgattggt gggctggtgc taagctcaaa ttatttaccg accctgaaac ctttcgcctt 240
atgggcaagg aacatgctct tgtcataatt aatcacatga ctgaacttga ctggatgggt 300
ggatgggtta tgggtcagca ttttggttgc cttgggagca taatatctgt tgcgaagaaa 360
tcaacaaaat ttcttccggt attggggtgg tcaatgtggt tttcagagta cctatatctt 420
gagagaagct gggccaagga taaaagtaca ttaaagtcac atatcgagag gctgatagac 480
taccctctgc ctttctgggt ggtaattttt gtggaaggaa ctcggtttac tcggacaaaa 540
ctcttggcag cccagcagta tgctgtctca tctgggctac cagtgccgag aaatgttttg 600

atccacgta ctaaggggtt tgtttcatgt gtaagtcaca tgcgatcatt tgttccagca	660
gtatatgatg tcacagtggc attccctaag acttcacctc caccaacggt gctaaatctt	720
ttcgaggggtc agtccataat gcttcacgtt cacatcaagc gacatgcaat gaaagattta	780
ccagaatccg atgatgcagt agcagagtgg ttagagagaca aatttgtgga aaaggatgct	840
ttgttggaca agcataatgc tgaggacact ttcagtgggtc aagaagtttg tcatagcggc	900
agccgccagt taaagtctct tctgggtgga atatcttggg tggttgtaac aacatttggg	960
gctctaaagt tccttcagt gtcacatggt aaggggaaag cattttcagc tatcgggctg	1020
ggcatcgtca ctctacttat gcacgtattg attctatcct cacaagcaga gcggtctaac	1080
cctgcggagg tggcacaggc aaagctaaag accgggttgt cgatctcaaa gaaggtaacg	1140
gacaaggaaa actag	1155

<210> 31

<211> 1164

<212> DNA

<213> Cuphea wrightii

<400> 31

atggcgattg ctgcggcagc tgtcatcgtc ccgctcagcc tcctcttctt cgtctccggc	60
ctcatcgtca atctcgtaca ggcagtttgc tttgtactga ttaggcctct gtcgaaaaac	120
acttacagaa gaataaacag agtgggtgca gaattgttgt ggttggagtt ggtatggctg	180
attgattggt gggctggtgt caagataaaa gtattcacgg atcatgaaac ctttcacctt	240
atgggcaaag aacatgctct tgtcatttgt aatcacaaga gtgacataga ctggctggtt	300
gggtgggttc tgggacagcg gtcaggttgc cttggaagca cattagctgt tatgaagaaa	360
tcatcaaagt ttctcccgtt attaggggtg tcaatgtggt tctcagagta tctattcctt	420
gaaagaagct gggccaagga tgaaattaca ttaaagtcag gtttgaatag gctgaaagac	480
tatcccttac ctttctggtt ggcacttttt gtggaaggaa ctcggttcac tcgagcaaaa	540
ctcttggcag cccagcagta tgctgcctct tcggggctac ctgtgccgag aaatgttctg	600
atccgcgta ctaaggggtt tgtttcttct gtgagtcaca tgcgatcatt tgttccagcc	660
atatatgatg ttacagtggc aatcccaaag acgtcacctc caccaacatt gataagaatg	720
ttcaagggtc agtcctcagt gcttcacgtc cacctcaagc gacacctaata gaaagattta	780
cctgaatcag atgatgctgt tgctcagtgg tgcagagata tattcgtcga gaaggatgct	840
ttgttggata agcataatgc tgaggacact ttcagtggcc aagaacttca agaaactggc	900
cgccaataa agtctcttct ggttgtaatc tcttgggcgg tggtggaggt atttggagct	960
gtgaagtttc ttcaatgggt atcgctgtta tcatcatgga agggacttgc attttcggga	1020
ataggactgg gtgtcatcac gctactcatg cacatactga ttttattctc acaatccgag	1080
cgggtctacc ctgcaaaagt ggcaccagca aagccaaaga atgagggaga gtcctccaag	1140
acgggaaatgg aaaaggaaaa gtag	1164

<210> 32

<211> 984

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 32

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atggagatcc cccccactg cctgtgctcc ccctcccccg ccccctccca gctgtactac      60
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acctgcttcg ccccccccg cctgcgcaag cagcaccctt accccctgcc cgtgctgtgc      180
taccccaagc tgctgcactt ctcccagccc cgctaccccc tggcgcgctc ccacctggcc      240
gaggccggcg tggcctaccg ccccggtac gagctgctgg gcaagatccg cggcgtgtgc      300
ttctacgccg tgaccgccgc cgtggccctg ctgctgttcc agtgcattgt gctgctgcac      360
cccttcgtgc tgctgttcga ccccttcccc cgcaaggccc accacaccat cgccaagctg      420
tgggtccatct gctccgtgtc cctgttttac aagatccaca tcaagggcct ggagaacctg      480
ccccccccc actccccgc cgtgtacgtg tccaaccacc agtccttcct ggacatctac      540
accctgctga ccctgggccc caccttcaag ttcatctcca agaccgagat cttcctgtac      600
cccatcatcg gctgggcat gtacatgctg ggcaccatcc ccctgaagcg cctggactcc      660
cgctcccagc tggacaccct gaagcgctgc atggacctga tcaagaaggc cgctccgtg      720
ttcttcttcc ccgagggcac ccgctccaag gacggcaagc tgggcgcctt caagaagggc      780
gccttctcca tcgccgcaa gtccaaggct cccgtggtgc ccatcacctt gatcggcacc      840
ggcaagatca tgcccccg ctccgagctg accgtgaacc ccggcaccgt gcaggatgac      900
atccacaagc ccatcgaggc ctccgacgcc gaggccatgt gcaacgaggc ccgcgccacc      960
atctcccact ccctggacga ctga                                     984

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<210> 33

<211> 1155

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 33

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atggcgatcg cggccgcggc ggtgatcttc ctgttcggcc tgatcttctt cgcctccggc      60
ctgatcatca acctgttcca ggcgctgtgc ttcgtcctga tccgccccct gtccaagaac      120
gcctaccgcc gcatcaaccg cgtgttcgcg gagctgctgc tgtccgagct gctgtgcctg      180
ttcgactggt gggcgggccc gaagctgaag ctgttcaccg accccgagac gttccgcctg      240
atgggcaagg agcacgccct ggtcatcatc aaccacatga ccgagctgga ctggatggtg      300
ggctgggtga tgggccagca cttcggctgc ctgggtccca tcatctccgt cgccaagaag      360
tccacgaagt tcctgcccgt gctgggctgg tccatgtggt tctccgagta cctgtacctg      420
gagcgctcct gggccaagga caagtccacc ctgaagtccc acatcgagcg cctgatcgac      480
taccctctgc cttctggct ggtcatcttc gtcgagggca cccgcttcac gcgcacgaag      540

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ctgctggcgg	cccagcagta	cgcggtctcc	tccggcctgc	ccgtcccccg	caacgtcctg	600
atcccccgca	cgaagggctt	cgtctcctgc	gtgtcccaca	tgcgctcctt	cgtccccgcg	660
gtgtacgacg	tcacggtggc	gttccccaag	acgtcccccc	ccccacgct	gctgaacctg	720
ttcgagggcc	agtccatcat	gctgcacgtg	cacatcaagc	gccacgccat	gaaggacctg	780
cccgagtccg	acgacgccgt	cgcggtggtg	tgccgcgaca	agttcgtcga	gaaggacgcc	840
ctgctggaca	agcacaacgc	ggaggacacg	ttctccggcc	aggaggtgtg	ccactccggc	900
tcccgccagc	tgaagtccct	gctggtcgtg	atctcctggg	tcgtggtgac	gacgttcggc	960
gccctgaagt	tcctgcagtg	gtcctcctgg	aagggaagg	cgttctccgc	catcggcctg	1020
ggcatcgtca	ccctgctgat	gcacgtgctg	atcctgtcct	cccaggccga	gcgctccaac	1080
cccgccgagg	tggcccaggc	caagctgaag	accggcctgt	ccatctccaa	gaaggtgacg	1140
gacaaggaga	actga					1155

<210> 34

<211> 1164

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 34

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ctgatcgtca	acctggtgca	ggccgtctgc	ttcgtcctga	tccgccccct	gtccaagaac	120
acgtaccgcc	gcatcaaccg	cgtggtcgcg	gagctgctgt	ggctggagct	ggtgtggctg	180
atcgactggg	gggcggggcg	gaagatcaag	gtcttcacgg	accacgagac	gttccacctg	240
atgggcaagg	agcacgccct	ggtcatctgc	aaccacaagt	ccgacatcga	ctggctggtc	300
ggctgggtcc	tgggccagcg	ctccggctgc	ctgggtcca	ccctggcggt	catgaagaag	360
tcctccaagt	tcctgcccgt	cctgggctgg	tccatgtggt	tctccgagta	cctgttcctg	420
gagcgtcct	gggccaagga	cgagatcacg	ctgaagtccg	gcctgaaccg	cctgaaggac	480
taccctctgc	ccttctggct	ggcgctgttc	gtggagggca	cgcgcttcac	ccgcgcgaag	540
ctgctggcgg	cgacgagta	cgccgcgtcc	tccggcctgc	ccgtgccccg	caacgtgctg	600
atcccccgca	cgaagggctt	cgtgtcctcc	gtgtcccaca	tgcgctcctt	cgtgcccgcg	660
atctacgacg	tcaccgtggc	catccccaag	acgtcccccc	ccccacgct	gatccgcatg	720
ttcaagggcc	agtccctccg	gctgcacgtg	cacctgaagc	gccacctgat	gaaggacctg	780
cccgagtccg	acgacgccgt	cgcgagtggt	tgccgcgaca	tcttcgtgga	gaaggacgcg	840
ctgctggaca	agcacaacgc	cgaggacacc	ttctccggcc	aggagctgca	ggagaccggc	900
cgccccatca	agtcctgtct	ggtcgtcatc	tcctggggccg	tcctggagggt	gttcggcgcc	960
gtcaagttcc	tgagtggttc	ctccctgctg	tcctcctgga	agggcctggc	gttctccggc	1020
atcggcctgg	gcgtgatcac	cctgctgatg	cacatcctga	tcctgttctc	ccagtccgag	1080

cgctccaccc ccgccaaggt ggccccgcg aagcccaaga acgagggcga gtcctccaag 1140
accgagatgg agaaggagaa gtga 1164

<210> 35
<211> 7041
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 35
gctcttcgcc gccgccactc ctgctcgagc gcgcccgcg gtgcgccgcc agcgccttgg 60
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tgcgccggct gagccactgc ttcgtccggg cggccaagag gagcatgagg gaggactcct 180
ggtccagggt cctgacgtgg tcgcggctct gggagcgggc cagcatcatc tggctctgcc 240
gcaccgaggc cgctccaac tggctcctca gcagccgcag tcgccgccga ccctggcaga 300
ggaagacagg tgaggggggt atgaattgta cagaacaacc acgagccttg tctaggcaga 360
atccctacca gtcattggctt tacctggatg acggcctgcg aacagctgtc cagcgaccct 420
cgctgccgcc gcttctcccc cagcttctt tccagaccg tgatggcgcg agccagcgcc 480
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<210> 36

<211> 1530

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 36

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<210> 37

<211> 1533

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 37

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<210> 38

<211> 1524

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 38

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<210> 39

<211> 1530

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 39

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cgcaccaca	ccggcgccga	cgacaagtcc	ttccgctgcy	tgacgagggg	cgacgacgag	960
aacggccaga	ccggcggtgc	cctgtccaag	gacatcaccg	acgtggccgg	ccgcaccgtg	1020
aagaagaaca	tcgccaccct	gggccccctg	atcctgcccc	tgtccgagaa	gctgctgttc	1080
ttcgtgacct	tcatgggcaa	gaagctgttc	aaggacgaga	tcaagcacta	ctacgtgccc	1140
gacttcaagc	tggccatcga	ccacttctgc	atccacgccg	gcggcaaggc	cgtgatcgac	1200
gtgctggaga	agaacctggg	cctggcccc	atcgacgtgg	aggcctcccc	ctccaccctg	1260

caccgcttcg gcaacacctc ctctcctcc atctggtacg agctggccta catcgagccc	1320
aagggccgca tgaagaaggg caacaagggtg tggcagatcg ccctgggctc cggcttcaag	1380
tgcaactccg ccgtgtgggt ggccctgaac aacgtgaagg cctccaccaa ctccccctgg	1440
gagcactgca tcgaccgcta ccccgtagaag atcgactccg actccggcaa gtccgagacc	1500
cgctgcccc aacggccgctc ctgacttaag	1530

<210> 40

<211> 1599

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 40

actagtatgg agcgcaccaa ctccatcgag atggaccagg agcgccctgac cgccgagatg	60
gccttcaagg actcctcctc cgccgtgatc cgcattccgc gccgcctgcc cgacttcctg	120
acctccgtga agctgaagta cgtgaagctg ggccctgcaca actccttcaa cttcaccacc	180
ttcctgttcc tgctgatcat cctgcccctg accggcaccg tgctggtgca gctgaccggc	240
ctgaccttcg agaccttctc cgagctgtgg tacaaccacg ccgcccagct ggacggcgtg	300
acccgcctgg cctgcctgggt gtccctgtgc ttcgtgctga tcattctacgt gaccaaccgc	360
tccaagcccc tgtacctggt ggacttctcc tgctacaagc ccgaggacga gcgcaagatg	420
tccgtggact ccttcctgaa gatgaccgag cagaacggcg ccttcaccga cgacaccgtg	480
cagttccagc agcgcatctc caaccgcgc gccctgggag acgagaccta cctgccccgc	540
ggcatcacct ccaccccccc caagctgaac atgtccgagg cccgcgccga ggccgaggcc	600
gtgatgttcg gcgcccctga ctccctgttc gagaagaccg gcatcaagcc cgccgagggtg	660
ggcatcctga tcgtgtcctg ctccctgttc aacccacccc cctccctgtc cgccatgatc	720
gtgaaccact acaagatgcy cgaggacatc aagtccctaca acctgggagc catgggctgc	780
tccgccggcc tgatctccat cgacctggcc aacaacctgc tgaaggccaa ccccaactcc	840
tacgccgtgg tgggtgtccac cgagaacatc accctgaact ggtacttcgg caacgaccgc	900
tccatgctgc tgtgcaactg catcttccgc atgggcggcg ccgccatcct gctgtccaac	960
cgccgccagg accgctccaa gtccaagtac gagctggtga acgtggtgcy caccacaag	1020
ggctccgacg acaagaacta caactgcgtg taccagaagg aggacgagcy cggcaccatc	1080
ggcgtgtccc tggcccgcg gctgatgtcc gtggccggcg acgccctgaa gaccaacatc	1140
accaccttg gcccattggt gctgcccctg tccggccagc tgatgttctc cgtgtcccctg	1200
gtgaagcgca agctgctgaa gctgaagggt aagccctaca tccccgactt caagctggcc	1260
ttcgagcact tctgcatcca cgccggcggc cgcgccgtgc tggacgaggt gcagaagaac	1320
ctggacctgg aggactggca catggagccc tcccgcatga ccctgcaccg cttcggcaac	1380
acctcctcct cctccctgtg gtacgagatg gcctacaccg aggccaaagg ccgctggaag	1440

gccggcgacc gcctgtggca gatcgccctt ggctccggct tcaagtgcaa ctccgccgtg 1500
 tggaaggccc tgcgcgtggt gtccaccgag gagctgaccg gcaacgcctg ggccggctcc 1560
 atcgagaact acccctgtaa gatcgtgcag tgacttaag 1599

<210> 41
 <211> 5851
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 41
 gctcttcgga gtcactgtgc cactgagttc gactggtagc tgaatggagt cgctgctcca 60
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 cgcgccatgg caccgaccag cctgcttgcc agtactggcg tctcttccgc ttctctgtgg 180
 tcctctgcmc gctccagcmc gtgcgctttt ccggtggatc atgcgggtccg tggcgccaccg 240
 cagcggccgc tgcccatgca gcgccgctgc ttccgaacag tggcggtcag ggccgcaccc 300
 gcggtagccg tccgtccgga acccgccaa gagttttggg agcagcttga gccctgcaag 360
 atggcggagg acaagcgcac cttcctggag gagcaccggg gcgtggagggt ccggggctga 420
 ccggccgtcg cattcaacgt aatcaatcmc atgatgatca gaggacacga agtcttggtg 480
 gcggtggcca gaaacactgt ccattgcaag ggcataggga tgcgttcctt cacctctcat 540
 ttctcatttc tgaatccctc cctgctcact ctttctcctc ctccctcccg ttcacgcagc 600
 attcggggta ccgcggtgag aatcgaaaat gcatcgtttc taggttcgga gacggtcaat 660
 tccctgtctc ggcaaatctg tcggtcaagc tggccagtgg acaatgttgc tatggcagcc 720
 cgcgcacatg ggctcccgga cgcgcccatc aggagcccaa acagcgtgtc aggggtatgtg 780
 aaactcaaga ggtccctgct gggcactccg gcccactcc gggggcggga cgccaggcat 840
 tcgcggtcgg tcccgcgcga cgagcgaat gatgattcgg ttacgagacc aggacgtcgt 900
 cgaggctcag aggcagctc ggacacgtct cgctagggca acgccccgag tcccgcgag 960
 ggccgtaaac attgtttctg ggtgtcggag tgggcatttt gggcccgatc caatcmcctc 1020
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 cacgtggtgt tgccccgcca ttggcgcca cgtttcaaag tccccggcca gaaatgcaca 1140
 ggaccggccc ggctcgaca ggccatgctg aacgcccaga tttcgacagc aacaccatct 1200
 agaataatcg caaccatccg cgttttgaac gaaacgaaac ggcgctgttt agcatgtttc 1260
 cgacatcgtg gggggcgaag catgctccgg ggggagggaa gcgtggcaca gcggtagccc 1320
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 ccgcacatat aaagccggac gcctaaccgg tttcgtggtt atgactagta tgttcgcgtt 1440
 ctacttctg acggcctgca tctccctgaa gggcgtgttc ggcgtctccc cctcctacaa 1500
 cggcctgggc ctgacgcccc agatgggctg ggacaactgg aacacgttcg cctgcgacgt 1560
 ctccgagcag ctgctgctgg acacggccga ccgcatctcc gacctgggcc tgaaggacat 1620

gggctacaag	tacatcatcc	tggacgactg	ctggctctcc	ggccgcgact	ccgacggctt	1680
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caacaactcc	ttcctgttcg	gcatgtactc	ctccgcgggc	gagtacacgt	gcgccggcta	1800
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ccaccgctac	aaggccatgt	ccgacgccct	gaacaagacg	ggccgcccc	tcttctactc	1980
cctgtgcaac	tggggccagg	acctgacctt	ctactggggc	tccggcatcg	cgaactcctg	2040
gcgcatgtcc	ggcgacgtca	cggcggagtt	cacgcgcccc	gactcccgt	gccctgcga	2100
cggcgacgag	tacgactgca	agtacgccgg	cttccactgc	tccatcatga	acatcctgaa	2160
caaggccgcc	cccatggggc	agaacgcggg	cgtcggcggc	tggaaacgacc	tggacaacct	2220
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cgtgtccccg	cccatgaaca	cgaccctgga	ggagatcttc	ttcgactcca	acctgggctc	2580
caagaagctg	acctccacct	gggacatcta	cgacctgtgg	gcgaaccgcg	tcgacaactc	2640
cacggcgtcc	gccatcctgg	gccgcaacaa	gaccgccacc	ggcatcctgt	acaacgccac	2700
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gctcctgctc	ctgctcactg	cccctcgac	agccttggtt	tgggctccgc	ctgtattctc	3180
ctgggtactgc	aacctgtaaa	ccagcactgc	aatgctgatg	cacgggaagt	agtggtgatg	3240
gaacacaaat	ggagatatcg	cgaggggtct	gcctgggcca	gccgctccct	ctaaacacgg	3300
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tcgtgacct	gcttaatgaa	cccagccggg	cctgtagcac	cgctaagag	gttttgatta	3540
tttcattata	ccaatctatt	cgccactagt	atggccatca	agaccaaccg	ccagcccgtg	3600
gagaagcccc	ccttcacat	cggcaccctg	cgcaaggcca	tccccgcca	ctgcttcgag	3660
cgctccgccc	tgcgctcctc	catgtacctg	gccttcgaca	tcgccgtgat	gtccctgctg	3720

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cacgagtgcg	gccaccaggc	cttctcctcc	tcccaggcca	tcaacgacgg	cgtgggcctg	3900
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cgcttcgcca	accacttcga	cccctggtcc	cccatcttct	ccaagcgcg	gcgcatcgag	4200
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accatcccc	actaccacgc	cgaggaggcc	tccgccgcca	tccgccccat	cctgggcaag	4560
tactaccagt	ccgactcccc	ctgggtgggc	cgcgccctgt	gggaggactg	gcgcgactgc	4620
cgctacgtgg	tgcccgcgac	ccccgaggac	gactccgccc	tgtggttcca	caagtagatc	4680
gatcttaagg	cagcagcagc	tcggatagta	tcgacacact	ctggacgctg	gtcgtgtgat	4740
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tatttgcgaa	taccaccccc	agcatcccc	tccctcgttt	catatcgctt	gcatcccaac	4920
cgcaacttat	ctacgctgtc	ctgctatccc	tcagcgctgc	tcctgctcct	gctcactgcc	4980
cctcgcacag	ccttggtttg	ggctccgcct	gtattctcct	ggtactgcaa	cctgtaaacc	5040
agcactgcaa	tgctgatgca	cggaagtag	tgggatggga	acacaaatgg	aaagcttaat	5100
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acctccaaag	ccgctcta	tggtggaggg	gttcgaattt	aaaagcttgg	aatgttggtt	5220
cgtgcgtctg	gaacaagccc	agacttggtg	ctcactggga	aaaggaccat	cagctccaaa	5280
aaacttgccg	ctcaaaccgc	gtacctctgc	tttcgcgcaa	tctgccctgt	tgaaatcgcc	5340
accacattca	tattgtgacg	cttgagcagt	ctgtaattgc	ctcagaatgt	ggaatcatct	5400
gccccctgtg	cgagcccatg	ccaggcatgt	cgcgggcgag	gacacccgcc	actcgtacag	5460
cagaccatta	tgctacctca	caatagttca	taacagtgc	catatttctc	gaagctcccc	5520
aacgagcacc	tcatgtctct	gagtggccac	ccccgggcc	tggtgcttgc	ggagggcagg	5580
tcaaccggca	tggggctacc	gaaatccccg	accggatccc	accacccccg	cgatgggaag	5640
aatctctccc	cgggatgtgg	gcccaccacc	agcacaacct	gctggcccag	gcgagcgtca	5700
aaccatacca	cacaaatatt	cttggcatcg	gccctgaatt	ccttctgccg	ctctgtacc	5760
cggtgcttct	gtccgaagca	ggggttgcta	gggatcgctc	cgagtccgca	aacccttgtc	5820
gcgtggcggg	gcttgttcga	gcttgaagag	c			5851

<210> 42
 <211> 186
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 42
 tacaacttat tacgtaacgg agcgtcgtgc gggagggagt gtgccgagcg gggagtcccc 60
 gtctgtgcga ggcccggcag ctgacgttg cgagccgtac gcccggagg tccccctccc 120
 ctgcaccctc ttccccctcc ctctgacggc cgcgcctgtt cttgcatgtt cagcgacgag 180
 gatatc 186

<210> 43
 <211> 305
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 43
 gcgaggggtc tgcctgggcc agccgctccc tctgaacacg ggacgcgtgg tccaattcgg 60
 gcttcggggac cttttggcgg tttgaacgcc tgggagaggg cgcccgcgag cctgggggacc 120
 ccggcaacgg cttccccaga gcctgccttg caatctcgcg cgtcctctcc ctcagcacgt 180
 ggcggttcca cgtgtggtcg ggcgtcccgg actagctcac gtcgtgacct agcttaatga 240
 acccagccgg gcctgcagca ccaccttaga ggttttgatt atttgattag accaatctat 300
 tcacc 305

<210> 44
 <211> 305
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 44
 ggcgaaataga ttggtataat gaaataatca aaacctctta ggcggtgcta caggcccggc 60
 tgggttcatt aagctaggtc acgacgcgag ctagtccggg aagcccgacc acacgtggaa 120
 ccgccacgtg ctgagggaga ggacgcgca gattgcaagg caggctctgg ggaagccgtt 180
 gccggggtcc ccaggctcgc gggcgcccca tccctggcgt tcaaaccgcc aaagggtccc 240
 gaagcccga ttggaccacg cgtcccgtgt ttagagggag cggctggccc aggcagaccc 300
 ctgc 305

<210> 45

<211> 305
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 45
 ggtgaataga ttggtctaata caaataatca aaacctctaa ggtggtgctg caggcccggc 60
 tgggttcatt aagctaggtc acgacgtgag ctatgccggg acgcccgacc acacgtggaa 120
 ccgccacgtg ctgagggaga ggacgcgcga gattgcaagg caggctctgg ggaagccgtt 180
 gccggggtcc ccaggctcgc gggcgccctc tcccaggcgt tcaaaccgcc aaagggtccc 240
 gaagcccga ttggaccacg cgtcccgtgt tcagagggag cggctggccc aggcagaccc 300
 ctgc 305

<210> 46
 <211> 1322
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 46
 gtgatgggt ctttagacga tccagcccag gatcatgtgt tgcccacatg gagcctatcc 60
 acgctggcct agaaggcaag cacatttcaa ggtgaaccca cgtccatgga gcatggcgc 120
 caatatctcg cctctagacc aagcgggttct caccccaact gcgtcatttg tatgtatggc 180
 tgcaaagttg tcggtacgat agaggccgcc aacctggcgg cgagggcgag gagctggtg 240
 ccgatctgtg cccaagcatg tgtcggagct cggctgtctc ggacgcgagc tcctgtgcaa 300
 ggggcttgca tcgagaatgt caggcgatag aactgcacg ttggggacac ggaggtgccc 360
 ctgtggcgtg tcctggatgc ctcgggtcc gtcgcgagaa gctctggcga ccagcaccgc 420
 gccacaaccg cagcaggcgt tcaccacaa gaatcttcca gatcgtgatg cgcattgatc 480
 gtgacacgat tggcgaggtc cgcaggacgc acacggactc gtccactcat cagaactggt 540
 cagggcaccc atctgcgtcc cttttcagga accaccacc gctgccaggc accttcgcca 600
 gcggcggaact ccacacagag aatgccttgc tgtgagagac catggccggc aagtgtgtc 660
 ggatctgccc gcatacggtc agtccccagc acaaggaagc caagagtaca ggctgttggt 720
 gtcgatggag gaggggcgt tcccacaagt agtgagcggc agctgctcaa cggcttcccc 780
 ctgttcatct tggcaaagcc agtgacttcc tacaagtatg tgatgcagat cggcactgca 840
 atctgtcggc atgcgtacag aacatcggct cgccagggca gcgttgctcg ctctggatga 900
 gctgcttggg aggaatcatc ggcacacgcc cgtgccgtgc ccgcgccccg cgcccgctcg 960
 gaaaggcccc cggtaggac actgccgcgt cagccagtcg tgggatcgat cggacgtggc 1020
 gaatcctcgc ccggacaccc tcatcacacc ccacatttcc ctgcaagcaa tcttgccgac 1080
 aaaatagtca agatccattg ggtttaggga acacgtgcga gactgggcag ctgtatctgt 1140

ccttgccccg	cgtaaattc	ctgggctga	cgagtcaca	ggagaatcta	ttagaccctg	1200
gacttgacgc	tcagtcattg	gcgtgagtg	ctaaagcacc	taggtcaggc	gagtaccgcc	1260
ccttccccag	gattcactct	tctgcgattg	acgttgagcc	tgcatcgggc	tgcttcgtca	1320
cc						1322

<210> 47
 <211> 841
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 47	
tcggagctaa	agcagagact
ggacaagact	tgcgttcgca
tactggtgac	acagaatagc
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tcccatctat	tcatacgcct
ttgggaaaag	gaacgagcct
tgtggcctct	gcattgctgc
	120
ctgctttgag	gccgaggacg
gtgcgggacg	ctcagatcca
tcagcgatcg	ccccaccctc
	180
agagcacctc	cgatccaagg
caatactatc	aggcaaagtt
tccaaattca	aacattccaa
	240
aatcacgcca	gggactggat
cacacacgca	gatcagcgcc
gttttgctct	ttgcctacgg
	300
gcgactgtgc	catttgtcga
cccctggtga	cgggaggac
cacgcctgcg	gttggcatcc
	360
acttcgacgg	accagggac
ggtttctcat	gccaaacctg
agatttgagc	accagatga
	420
gcacattatg	cgtttttagga
tgcctgagca	gcgggctg
aggaatctgg	tctcgccaga
	480
ttcaccgaag	atgcgccc
cggagcgagg	cgagggttt
gtgaccacgc	aaggcagtgt
	540
gaggcaaaca	catagggaca
cctgctctt	tcaatgcaca
gacatctatg	gtgccc
	600
atataaaatg	ggctacttct
gagtcaaacc	aacgcaaact
gcgctatggc	aaggccggcc
	660
aaggttggaa	tcccgtctg
tctggatttg	agtttggtg
ggctatcacg	tgacaatccc
	720
tgggattggg	cggcagcagc
gcacggcctg	ggtggcaatg
gcgcactaat	actgctgaaa
	780
gcacggctct	gcatcccttt
ctcttgacct	gcgattggc
cttttcgcaa	gcgtgatcat
	840
c	841

<210> 48
 <211> 841
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 48	
tcggagctaa	agcagaaact
gaacaagact	tgcgttcgca
tacttgtgac	actgaatagg
	60
ttcaatctat	tcatacgcct
ttgggaaaact	gaacgagcct
tgtggcctct	gcattgctgc
	120
ctgctttgag	gccgaggacg
gcgcggaacg	cacagatcca
tcagcgatcg	ccccaccctc
	180
agagtacatc	cgatccaagg
caatactatc	aggcaaagtt
tccaaattca	aacattccaa
	240

aattacgtca gggactggat cacacacgca gatcagcgcc gttttgctct ttgcctacgg 300
gcgactgtgc cacttgtcga cgcttggtga cgggagggac cacgcctgcg gttggcatcc 360
acttcgacgg acccagggac ggtctcacat gccaaacctg agatttgagc accaagatga 420
gcacattatg cgttttttga tgcctgagca gcgggctgtc aggaatctgg tctcgccaga 480
ttcaccgaag atgcggccat cggagcgagg cgagggctgt gtggccacgc caggcagtgt 540
gaggcaaaca cacagggaca tctgcttctt tcgatgcaca gacatctatg ttgcccgtgc 600
atataaaatg ggctacttct gaatcaaacc aacgcaaact tcgctatggc aaggccggcc 660
aaggttggaa tcccggctctg tctggatttg agtttggtgg ggctatcacg tgacaatccc 720
tgggattggg cggcagcagc gcacggcctg gatggcaatg gcgcactaat actgctgaaa 780
gcacggctct gcatcccttt ctcttgacct gcgattggct cttttcgcaa gcgtgatcat 840
c 841

<210> 49
<211> 512
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 49
caccgatcac tccgtcgccg cccaagagaa atcaacctcg atggagggcg aggtggatca 60
gaggtattgg ttatcgttcg ttcttagtct caatcaatcg tacaccttgc agttgcccga 120
gtttctccac acatacagca cctcccgtc ccagcccatt cgagcgaccc aatccgggcg 180
atcccagcga tcgtcgtcgc ttcagtgtg accggtggaa agcaggagat ctcgggagcag 240
caggaccaca tccagcccag gatcttcgac tggctcagag ctgacctca cgcggcacag 300
caaaagtagc acgcacgcgt tatgcaaact ggttacaacc tgtccaacag tgttgcgacg 360
ttgactggct acattgtctg tctgtcgcga gtgcgcctgg gcccttacgg tgggacactg 420
gaactccgcc ccgagtcgaa cacctagggc gacgcccga gcttggcatg acagctctcc 480
ttgtgttcta aataccttgc gcgtgtggga ga 512

<210> 50
<211> 516
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 50
atccaccgat cactccgtcg ccgccaaga gaattcaacc tcgatggagg gcaaggtgga 60
tcagaggtat tggttatcgt tcgctattag tctcaatcaa tcgtgcacct tgcatgtgct 120
cgagtttctc cacacataca gcacctccc ctcccagccc attcgagcga cccaatccgg 180
gcgatcccag cgatcgtcgt cgcttcagt ctgaccggtg gaaagcagga gatctcgggc 240

gagcaggacc acatccagca caggatcttc gactgggtca gagctgaccc tcacgcggca 300
 cagcaaaagt agcccgacg cgttatgcaa acagggtaca acctgtccaa cactgttgcg 360
 acgttgactg gctacattgt ctgtctgtcg cgagtacgcc tggaccctta cgggtgggaca 420
 ctggaactcc gccccgagtc gaacacctag ggcgacgccc gcagcttggc atgacagctc 480
 tccttgatt ctaaatacct cgcgctgtg ggagaa 516

<210> 51
 <211> 335
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 51
 atgatgcgcg tgtacgacta tcaaggaaga aagaggactt aatttcttac cttctaacca 60
 ccatattctt tttgctggat gcttgctcgt ctcgatgaca attgtgaacc tcttggtga 120
 ccctgaccct gctgcaaggc tctccgaccg cacgcaaggc gcagccggcg cgtccggagg 180
 cgatcggatc caatccagtc gtcctccgc agcccgggca cgtttgcca tgcaggccct 240
 tccacaccgc tcaagagact cccgaacacc gccactcgg cactcgcttc ggctgccgag 300
 tgcgcgtttg agtttgcct gccacagaag acacc 335

<210> 52
 <211> 335
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 52
 atgatgcgcg tgtacgacta tcaaggaaga aagaggactt aatttcttac cttctaacca 60
 ccatattctt tttgctggat gcttgctcgt ctcgatgaca attgtgaacc tcttggtga 120
 ccctgaccct gctgcaaggc tctccgaccg cacgcaaggc gcagccggcg cgtccggagg 180
 cgatcggatc caatccagtc gtcctccgc agcccgggca cgtttgcca tgcaggccct 240
 tccacaccgc tcaagagact cccgaacacc gccactcgg cactcgcttc ggctgccgag 300
 tgcgcgtttg agtttgcct gccacaggag acatc 335

<210> 53
 <211> 1097
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 53

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ccccgggagag ctgtacgcct acggagcgag gcctgggtgtg accgttgcca tctcgccagc      60
agacgtcgcg gagcctcgtc ccaaaggccc tttctgatcg agcttgctgt ccactggagc      120
ctttaagttg cgcgcgcgat gggataaccg agctgatctg cactcagatt ttggttttgtt      180
ttcgcgcatg gtgcagcgag gggagggtact acgctgggggt acgagatcct ccggattccc      240
agaccgtgtt gccggcattt acccggtcat cgccagcgat tcgggacgac aaggccttat      300
cctgtgctga gacgctcgag cacgtttata aaattgtggg taccgcggtg tgcacagcgt      360
tcaacacgcg ccacgccgaa attggttggg gggggagcac gtatgggact gacgtatggc      420
cagcagcgaa cactcaccga acaagtgcc aatgtatacct tgcataaatg atgctccggc      480
agcttcgatt gactgtctcg aaaaagtgtg agcaagcaga tcatgtggcc gctctgtcgc      540
gcagcacctg acgcattcga caccacggc aatgccagg ccagggaata gagagtaaga      600
caactcccat tgttcagcaa aacattgcac tgcaagtgcct tcacaactat acaatgaatg      660
ggagggaata tgggctctgc atgggacagc ttagctggga cattcggcta ctgaacaaga      720
aaaccccgag agaaccaatt ggcgaaacct gccggggagga ggtgatcgtt tctgtaaagt      780
gcttacgcat tcccccccg cggtcacga ggggtgtggg gaaccctgcc agctgatcaa      840
gtgcttgctg acgtcggcca gggagggtga tgtgattggg ccgtggggcg tgagttatcc      900
taccgccgga cccgcgaagt cacatgacga atggccgtgc gggatgacga gagcacgact      960
cgctctttct tcgccggccc ggcttcattg aggacaataa taaaggggtg ccaccggcaa     1020
cagccctcca tacctgaacc gattccagac ccaaacctct tgaattttga gggatccagt     1080
tcaccggtat agtcacg                                     1097

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<210> 54

<211> 1105

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 54

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atccccgggc gagctgtacg cctacggagc gaggcctggt gtgaccgttg cgatctcgcc      60
agcagacgtc gcggagcctc gtcccaaagg ccctttctga tcgagcttgt cgtccactgg      120
acgctttaag ttgcgcgcg gatgggataa ccgagctgat ctgcactcag attttggttt      180
gttttcgcg atggtgcagc gaggggagg actacgctgg ggtacgagat cctccggatt      240
cccagaccgt gttgccggca tttaaccggt catcgccagc gattcgggac gacaaggcct      300
tatcctgtgc tgagacgctc gagcacgttt ataaaattgt ggtcaccgtg gtacgcacag      360
cgtccaacac gcgccacgcc gaaattcgtt ggtgggggag cacgtatcgg actgacgtat      420
ggccagcagc gaacactcac caaacagggt ccaatgtata gcttgcatca atgatgctct      480
ggcagcttcg attgactgtc tcgaaaaagt gtgtgcaaac agattatgtg gccgctctgt      540
ggccgcgag cacctgacgc actcgacacc cacggcaatg ccaggccaa ggaacagaga      600
gtaagacaac tcccattgtt cagtaaaaca ttgactgca gtgccttcac aaacatacaa      660

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cgaatgggag ggaatatggg cttcgaatgg gacagcttag ctgggacatt cggttactga	720
acaagaaaac cccacgagaa ccaactggcg aaacctgccg ggaggaggtg atcgtttttg	780
taaatggctt acgcattccc cccccggcgg ctcacggggg gtgtggtgaa ccctgccagc	840
tgatcaagtg cttgctgacg tcggccaggg aggtgtatgt gatttggccg tggggcgtga	900
gttatcctac cgccggaccc gcgaagtcac atgacgaatg gccgtgcggg atgacgagag	960
cagggctcgc tctttcttcg ccggcccggc ttcattggagg acaataataa aggggtggcca	1020
ccggcaacag ccctccatac ctgaaccgat tccagacca aacctcttga attttgaggg	1080
atccagttca ccggtatagt cacga	1105

<210> 55

<211> 754

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 55

gcgagtgggt ttgctgccgg gaagggagtg gggagcgtcg agcgagggac gcggcgctcg	60
aggcgcacgt cgtctgtcaa cgcgcgcggc cctcgcggcc gcgggccccca cccagctcta	120
atcatcgaaa actaagaggc tccacacgcc tgctgtagaa tgcattgggat tcgccagtag	180
accacgatct gcgccgaaga agctgggtcta cccgacgttt tttgttgctc ctttattctg	240
aatgatatga agatagtgtg cgcagtgccca cgcattaggca tcaggagcaa gggaggacgg	300
gtcaacttga aagaacaaaa ccatccatcc gagaaatgcg catcatcttt gtagtaccat	360
caaacgcctt ggccaatgtc ttctgcatgg acaacacaac ctgctcctgg ccacacggtc	420
gacttggagc gccccatgcy cccaggtcgc cacgacccgc ggcccagcgc gcggcgattc	480
gcctcacgag atcccggcgg acccggcacg cccgcggggc gacggtgcgc ttggcgatgc	540
tgctcattaa cccacggccg tcacccgatc cacatgctct ttttcaacac atccacattg	600
gaatagagct ctaccagggt gactactgca ttctttgggg ctgggaggac cccactcgac	660
acctggtcct tcacggccg aaagcccga cctgagcgt tccccgccc gttcctcatc	720
cccgactttc cgatggccca ttgcagtttc aaac	754

<210> 56

<211> 318

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 56

atctgggtgg aggactggga gtaagatgta aggatattaa ttaaacttc tagtttgttg	60
atggcacaac agtcaatgca tttcagtcgt cttgctcctt ataacctatg cgtgtgccat	120

cgccggccat gcacctgtgg cgtggtaccg accatcgggg agaggcccga gattcggagg 180
 tacctcccgc cctgggagag cccttcacgt gacggcaciaa gtcccttgca tcggcccgcg 240
 agcacggaat acagagcccc gtgccccca cgggccctca catcatccac tccattgttc 300
 ttgccacacc gatcagca 318

<210> 57
 <211> 316
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 57
 tgggtggagg actgggaaga agatgtaagg atatcaattt aacattctag tttgttgatg 60
 gcacaacagt cactgaatac cgggcgtctg gctgctaaaa tagccggagc gtgtgccatc 120
 gccggccatg catctgtggc gtggtaccga ccatcaggga gaggcccag attcggaggt 180
 acctcccgcc ctgggagagc ccttcacgtg acggcacaag tcccttgcat cggcccgcga 240
 gcacggaata cagagccccg tgctccccac gggccctcac atcatccact ccattgttct 300
 tgccacaccg atcagc 316

<210> 58
 <211> 350
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 58
 ataacgaggc acaatgatcg atatttctat cgaacaactg tatttagccc tgtacgtacc 60
 ccgctcttgg gccagcccgt ccgtgcttgc cttcggaaaa ttgcatggcg cctcatgcaa 120
 actcgcgctc tcacagcaga tctcgcccag ctccggggag agcaatcgcg ggtggggccc 180
 ggggcgaatc caggacgcgc cccgcggggc cgctccactc gccagggcca atgggcggct 240
 tatagtcctg gcatgggctc tgcatgcaca gtatcgcagt ttgggagagg ttttgcccc 300
 gcgatttcga atacgcgacg cccggtactc gtgcgagaac aggttcttg 350

<210> 59
 <211> 818
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 59
 atcgcgatgg tgcgcactcg tgcgcaatga atatgggggtc acgcggtgga cgaacgcgga 60
 gggggcctgg ccgaatctag gcttgcatc ctcagatcac tttctgccgg cgggtccgggg 120

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tttgcgcgtc gcgcaacgct ccgtctccct agccgctgcg caccgcgcggt gcgacgcgaa 180
ggtcattttc cagaacaacg accatggctt gtcttagcga tcgctcgaat gactgctagt 240
gagtcgtacg ctcgaccag tcgctcgag gagaacgcgg caactgccga gcttcggctt 300
gccagtcgtg actcgtatgt gatcaggaat cattggcatt ggtagcatta taattcggct 360
tccgcgctgt ttatgggcat ggcaatgtct catgcagtcg accttagtca accaattctg 420
ggtagccagc tccgggagc cgggctccgt gtcgccgggc accacctcct gccatgagta 480
acagggccgc cctctcctcc cgacgttggc cactgaata ccgtgtcttg gggccctaca 540
tgatgggctg cctagtcggg cgggacgcgc aactgcccgc gcaatctggg acgtggtctg 600
aatcctccag gcgggtttcc ccgagaaaaga aagggtgccg atttcaaagc agagccatgt 660
gccgggcccct gtggcctgtg ttggcgcccta ttagtcacc cccctcacc caattgtcgc 720
cagtttgcg aatccataaa ctcaaaactg cagcttctga gctgcgctgt tcaagaacac 780
ctctgggggt tgctacccc cgaggtcgac gccagca 818

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<210> 60

<211> 819

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 60

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atcacgatgg tgcgcattcg tgcaaagtga atatggggtc acgcggtgga cgaacgcgga 60
gggggcatga ccgaatctag gtcgcattc ctcatcac ttcattgccg cggtccgggg 120
tttgcgcgtc gcgcaaggct acgtctccct agccgctgcg caccacgcgt gcgacgcgga 180
ggccatcttc cggagcaacg accatggatt gtcttagcga tcgcacgaat gactgctagt 240
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accagtcgtg actcgtatgt gatcaggaat cattggcatt ggtagcatta taattcggct 360
tccgcgctgc gtatgggcat ggcaatgtct catgcagtcg atcttagtca accaattttg 420
ggtagccagg tccgggagc cgggctccgt gtcgccgggc accacctcct gccaggagta 480
gcagggccgc cctctcgtcc cgacgttggc cactgaata ccgtggcttc gagccctaca 540
tgatgggctg cctagtcggg cgggacgcgc aactgcccgc gcgatctggg ggctggtctg 600
aatccttcag gcgggtgta cccgagaaag aaagggtgcc gatttcaaag cagacccatg 660
tgccggggccc tgtggcctgt gttggcgccct atgtagtcac cccctcacc ccaattgtcg 720
ccagtttgcg cactccataa actcaaaaca gcagcttctg agctgcgctg ttcaagaaca 780
cctctgggggt ttgctacccc gcgaggtcga cgccagca 819

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<210> 61

<211> 7081

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 61

gctcttcgcc gccgccactc ctgctcgagc gcgcccgcg	gtgcgccgcc agcgcccttg	60
ccttttcgcc gcgctcgtgc gcgtcgtga tgtccatcac	caggtccatg aggtctgcct	120
tgcgccggct gagccactgc ttcgtccggg cggccaagag	gagcatgagg gaggactcct	180
ggtccaggggt cctgacgtgg tcgcggtctt gggagcgggc	cagcatcatc tggctctgcc	240
gcaccgaggc cgctccaac tggctctcca gcagccgcag	tcgccgccga ccctggcaga	300
ggaagacagg tgaggggggt atgaattgta cagaacaacc	acgagccttg tctaggcaga	360
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cgctgccgcc gcttctccc cagccttctt tccagaccg	tgatggcgcg agccagcgcc	480
gcacgctggc gctgcgctt gccgatctga ggacagtcgg	ggaactctga tcagtctaaa	540
cccccttgcg cgtagtggt gccatcctt gcagaccggt	gagagccgac ttgttgtg	600
ccacccccca caccacctc tcccagacca attctgtcac	ctttttggcg aaggcatcgg	660
cctcggcctg cagagaggac agcagtgccc agccgctggg	ggttggcgga tgcacgtca	720
ggtacccttt cttgcgctat gacacttcca gcaaaaggta	ggcggggctg cgagacggct	780
tcccggcgct gcatgcaaca ccgatgatgc ttcgaccccc	cgaagctcct tcggggctgc	840
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aaagacatta tagcgagcta ccaaagccat attcaaacac	ctagatcact accacttcta	960
cacaggccac tcgagcttgt gatcgactc cgctaagggg	gcgcctcttc ctcttcgttt	1020
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gccggcttcg ccgccaagat cagcgctcc atgacgaacg	agacgtccga ccgccccctg	1140
gtgcacttca cccccaacaa gggctggatg aacgaccccc	acggcctgtg gtacgacgag	1200
aaggacgcca agtggcacct gtacttccag tacaaccgga	acgacaccgt ctgggggacg	1260
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gacccgaagg tcttctggta cgagccctcc cagaagtgga	tcatgaccgc ggccaagtcc	1620
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gaggccttcg acaaccagtc ccgcgtggtg gacttcggca	aggactacta cgccctgcag	1920
accttcttca acaccgaccc gacctacggg agcgccctgg	gcatcgctg ggcctccaac	1980

tgaggagtact	ccgccttcgt	gccaccaac	ccctggcgct	cctccatgtc	cctcgtgcgc	2040
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gccgagccga	tcctgaacat	cagcaacgcc	ggcccctgga	gccggttcgc	caccaacacc	2160
acgttgacga	aggccaacag	ctacaacgtc	gacctgtcca	acagcaccgg	caccctggag	2220
ttcgagctgg	tgtacgccgt	caacaccacc	cagacgatct	ccaagtccgt	gttcgcggac	2280
ctctccctct	ggttcaaggg	cctggaggac	cccgaggagt	acctccgcat	gggcttcgag	2340
gtgtccgcgt	cctccttctt	cctggaccgc	gggaacagca	aggatgaagt	cgtgaaggag	2400
aacccctact	tcaccaaccg	catgagcgtg	aacaaccagc	ccttcaagag	cgagaacgac	2460
ctgtcctact	acaaggtgta	cggcttgctg	gaccagaaca	tcctggagct	gtacttcaac	2520
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tcccgcgtct	cgaacagagc	gcgcagagga	acgctgaagg	tctcgcctct	gtcgcacctc	3120
agcgcgcat	acaccacaat	aaccacctga	cgaatgcgct	tggttcttcg	tccattagcg	3180
aagcgtccgg	ttcacacacg	tgccacgttg	gcgaggtggc	aggatgacaat	gatcgggtgga	3240
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acgcgtaaaa	gttgggggtg	tgccagtgcg	tcattgccagg	catgatgtgc	tcctgcacat	3540
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gagggaggag	agagaggggg	gggggggggg	gggatgatta	cacgccagtc	tcacaacgca	3780
tgcaagaccc	gtttgattat	gagtacaatc	atgcactact	agatggatga	gcgccaggca	3840
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195 200 205

Ala Val Ser Asn Met Arg Ser Phe Val Pro Ala Ile Tyr Asp Met Thr
210 215 220

Val Ala Ile Pro Lys Thr Ser Pro Pro Pro Thr Met Leu Arg Leu Phe
225 230 235 240

Lys Gly Gln Pro Ser Val Val His Val His Ile Lys Cys His Ser Met
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Gln Phe Val Ala Lys Asp Ala Leu Leu Asp Lys His Ile Ala Ala Asp
275 280 285

Thr Phe Pro Gly Gln Lys Glu Gln Asn Ile Gly Arg Pro Ile Lys Ser
290 295 300

Leu Ala Val Val Val Ser Trp Ala Cys Leu Leu Thr Leu Gly Ala Met
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Lys Phe Leu His Trp Ser Asn Leu Phe Ser Ser Trp Lys Gly Ile Ala
325 330 335

Leu Ser Ala Phe Gly Leu Gly Ile Ile Thr Leu Cys Met Gln Ile Leu
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Ile Arg Ser Ser Gln Ser Glu Arg Ser Thr Pro Ala Lys Val Ala Pro
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 <213> *Protheca moriformis*

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 Gln Lys Phe Asp Thr Thr Gly Tyr Thr Thr Thr Ile Ala Gly Glu Ile
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 Val Asp Asp Val Ile Lys Tyr Val Tyr Ile Ala Gly Lys Gln Ala Leu
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 Glu Ser Ala Gly Leu Pro Ile Glu Ala Ala Gly Leu Ala Gly Ala Gly
 100 105 110
 Leu Asp Pro Ala Leu Cys Gly Val Leu Ile Gly Thr Ala Met Ala Gly
 115 120 125
 Met Thr Ser Phe Ala Ala Gly Val Glu Ala Leu Thr Arg Gly Gly Val
 130 135 140
 Arg Lys Met Asn Pro Phe Cys Ile Pro Phe Ser Ile Ser Asn Met Gly
 145 150 155 160
 Gly Ala Met Leu Ala Met Asp Ile Gly Phe Met Gly Pro Asn Tyr Ser
 165 170 175
 Ile Ser Thr Ala Cys Ala Thr Gly Asn Tyr Cys Ile Leu Gly Ala Ala
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 Asp His Ile Arg Arg Gly Asp Ala Asn Val Met Leu Ala Gly Gly Ala
 195 200 205
 Asp Ala Ala Ile Ile Pro Ser Gly Ile Gly Gly Phe Ile Ala Cys Lys
 210 215 220
 Ala Leu Ser Lys Arg Asn Asp Glu Pro Glu Arg Ala Ser Arg Pro Trp
 225 230 235 240
 Asp Ala Asp Arg Asp Gly Phe Val Met Gly Glu Gly Ala Gly Val Leu
 245 250 255

Val Leu Glu Glu Leu Glu His Ala Lys Arg Arg Gly Ala Thr Ile Leu
260 265 270

Ala Glu Leu Val Gly Gly Ala Ala Thr Ser Asp Ala His His Met Thr
275 280 285

Glu Pro Asp Pro Gln Gly Arg Gly Val Arg Leu Cys Leu Glu Arg Ala
290 295 300

Leu Glu Arg Ala Arg Leu Ala Pro Glu Arg Val Gly Tyr Val Asn Ala
305 310 315 320

His Gly Thr Ser Thr Pro Ala Gly Asp Val Ala Glu Tyr Arg Ala Ile
325 330 335

Arg Ala Val Ile Pro Gln Asp Ser Leu Arg Ile Asn Ser Thr Lys Ser
340 345 350

Met Ile Gly His Leu Leu Gly Gly Ala Gly Ala Val Glu Ala Val Ala
355 360 365

Ala Ile Gln Ala Leu Arg Thr Gly Trp Leu His Pro Asn Leu Asn Leu
370 375 380

Glu Asn Pro Ala Pro Gly Val Asp Pro Val Val Leu Val Gly Pro Arg
385 390 395 400

Lys Glu Arg Ala Glu Asp Leu Asp Val Val Leu Ser Asn Ser Phe Gly
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Phe Gly Gly His Asn Ser Cys Val Ile Phe Arg Lys Tyr Asp Glu
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<210> 65

<211> 387

<212> PRT

<213> Prototheca moriformis

<400> 65

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Gln Arg Pro Ser Pro Val Val Tyr Ser Lys Leu Asp Lys Gln His Arg
35 40 45

Leu Thr Pro Glu Arg Leu Glu Leu Val Gln Ser Met Gly Gln Phe Ala
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Glu Glu Arg Val Leu Pro Val Leu His Pro Val Asp Lys Leu Trp Gln
65 70 75 80

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 Val Val Leu₁₁₅ Val Gly Asp Met Ile₁₂₀ Thr Glu Glu Ala Leu₁₂₅ Pro Thr Tyr
 Met Ala₁₃₀ Met Leu Asn Thr Leu₁₃₅ Asp Gly Val Arg Asp₁₄₀ Asp Thr Gly Ala
 Ala₁₄₅ Asp His Pro Trp Ala₁₅₀ Arg Trp Thr Arg Gln₁₅₅ Trp Val Ala Glu Glu₁₆₀
 Asn Arg His Gly Asp₁₆₅ Leu Leu Asn Lys Tyr₁₇₀ Cys Trp Leu Thr Gly₁₇₅ Arg
 Val Asn Met Arg₁₈₀ Ala Val Glu Val Thr₁₈₅ Ile Asn Asn Leu Ile₁₉₀ Lys Ser
 Gly Met Asn₁₉₅ Pro Gln Thr Asp Asn₂₀₀ Asn Pro Tyr Leu Gly₂₀₅ Phe Val Tyr
 Thr Ser₂₁₀ Phe Gln Glu Arg Ala₂₁₅ Thr Lys Tyr Ser His₂₂₀ Gly Asn Thr Ala
 Arg₂₂₅ Leu Ala Ala Glu His₂₃₀ Gly Asp Lys Gly Leu₂₃₅ Ser Lys Ile Cys Gly₂₄₀
 Leu Ile Ala Ser Asp₂₄₅ Glu Gly Arg His Glu₂₅₀ Ile Ala Tyr Thr Arg₂₅₅ Ile
 Val Asp Glu Phe₂₆₀ Phe Arg Leu Asp Pro₂₆₅ Glu Gly Ala Val Ala₂₇₀ Ala Tyr
 Ala Asn Met₂₇₅ Met Arg Lys Gln Ile₂₈₀ Thr Met Pro Ala His₂₈₅ Leu Met Asp
 Asp Met₂₉₀ Gly His Gly Glu Ala₂₉₅ Asn Pro Gly Arg Asn₃₀₀ Leu Phe Ala Asp
 Phe₃₀₅ Ser Ala Val Ala Glu₃₁₀ Lys Ile Asp Val Tyr₃₁₅ Asp Ala Glu Asp Tyr₃₂₀
 Cys Arg Ile Leu Glu₃₂₅ His Leu Asn Ala Arg₃₃₀ Trp Lys Val Asp Glu₃₃₅ Arg
 Gln Val Ser Gly₃₄₀ Gln Ala Ala Ala Asp₃₄₅ Gln Glu Tyr Val Leu₃₅₀ Gly Leu
 Pro Gln Arg₃₅₅ Phe Arg Lys Leu Ala₃₆₀ Glu Lys Thr Ala Ala₃₆₅ Lys Arg Lys

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<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<211> 1003

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<210> 68

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<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 69
gtcctgaaca acgcttttcgg aggtcctcag gaagctggca tccccgcgcc gtatgctcat 60
ccgcgcagcc ccgattcatt cgcacccgtt cgtcccctgt cccaccttcc gctggcactc 120
cccgccacgc ggtgccggcc cggcgcccat tgactcccat cccaatcgct acccaccac 180
actctcaccg cgtgtccctg ttcctgcttc gccgcagttc cagcgctccc gcgcgccctg 240
cctccctccc gcgcgcggga catgtcccta ttctgctcat aaccttgcct cacgcatccc 300
ttggtccacc tgtatctcca tagtacacac aggtcgcaaa aagaggtcaa aaatcagacg 360
ggtgcgagcc ggccagtgcc cttcgggtcat cccttggaa ccagaacgaa tcagcagggc 420
cgccccacgt gatatttgct ggggatcgcg cgatgacgat gcacaagacc atccaatgaa 480
caagccagcg ggcagccacg gaaaaccccc caatgccaac actctggccg ttctctcact 540
ttgttcccac cactcgcgc ggtcgaccag cagcgcaaca tggccatgat g 591

<210> 70
<211> 624
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 70
gaggaacccg catggtggca gagcaatgcc gaatgattga tcaactgcgcc acgtgccggg 60
ttatacaatt ggtgcaacgg atggcgaggt cacggagggg gccccaaata acccccgtgc 120
cagccgtaca caagattcta tcggctctga aacattctga cgctcattaa gtagcatgat 180
gagacgcgaa aaacgacgga gtcgggtgga tgacaagggg ggcatcgggtg acacgatgct 240
gccaaggatg cttatatctg gattcgcact ggtaccagcg gctagctcaa tgacagaaca 300
acaggcaacg ggcaccacct tgacaatcat gatgcgcaat actggcctgc tttcgtactt 360
ttacttgcat gtcattcagt tgagaaacgc catctcgatt gattcactca gttgtgtcac 420
caagtatggg cctggatcac ctgcccttcc gcgcccttcg ttagtcaactg ccccttcctt 480
tcttcgggca caaacgcccg gcgcccccg gcccgtaggg gctccctttg agtacgcatt 540
catccccaag acgctcccct ctttcgatca gcgtgtcttc ctccgcttac ccgtttccct 600
tgattgaaca taggcgcagc ggcg 624

<210> 71
<211> 529
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 71
cctggatgtg agagtctcga agaaccattc ccaagacccg tatcaggacg ccacgcctat 60
tccatcaaac agaccatcg tcgggcatca agacaatacc ttttgcgac atagaaatgc 120

ttacggcggg	atgacataca	taagccctcc	cccaactagc	ctgacaaaagg	cttccaaaga	180
gcgatcagcc	caagcaccaa	aactatccaa	agcacaattc	ccgactctga	agcaatcagt	240
tagacgtagc	acgcacattt	atatatgtac	acaagtcaaa	ttggtaaaac	aatcgcaacc	300
tgaccaagtt	cagcccgttg	tgctccgtct	gggccctgag	cgagcgaggg	cagagggtca	360
gaccaggccc	agtttgtccc	aggcgtgata	ttcgtggcgc	gacccgggca	agaggagggg	420
gccccctaga	agcctcggcc	gccctcgag	gaataaacgg	cctctctgca	gccgggatcg	480
ccctcttcca	catttctgaa	aacgctgtac	gtgcgcttca	acttgaaga		529

<210> 72

<211> 529

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 72

cctggatgtg	agagtctcga	agaaccactc	ccaagacccg	tatcaggatg	ccacgcaaaa	60
tccagcgaac	aaacccatca	tcgggcacca	agacaatacc	ttttgccaac	atagaaatgc	120
atatggcggg	atgacataca	tacgccctcc	cctaactagc	ctgaccactg	cttcccaaga	180
gcgatcagcc	caagcaccaa	tactaaccaa	agcacaactc	ccgactctga	agcaatcagt	240
tcggcgtagc	tcgcacattc	agatatgtac	acacgtcgaa	ttggtaaaac	aatcgcaacc	300
tgaccgagtt	cagcccgttg	ttctccgtct	gggccctgag	cgagcgaggg	cagagggtca	360
gaccaggccc	agtttgtccc	aggcgtgata	ttcgtggcgc	gacccgggca	agaggagggg	420
gccccctaga	agcctcggcc	gccctcgag	gaataaacgg	cctctctgca	gccgggatcg	480
ccctcttcca	catttctgaa	aacgctgtac	gtgcgcttca	acttgaaga		529

<210> 73

<211> 570

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 73

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agacggacga	ggccgcctct	gccctgtttg	aactgagcgt	cagcgctggc	taaggggagg	120
gagactcatc	cccaggctcg	cgccagggtc	ctgatcccg	ctcgggcggg	gatcggcgcg	180
catgactacg	acccaacgac	gtacgagact	gatgtcggtc	ccgacgagga	gcgccgcgag	240
gcactcccgg	gccaccgacc	atgtttacac	cgaccgaaag	cactcgctcg	tatccattcc	300
gtgcgcccgc	acatgcatca	tcttttggtg	ccgacttcgg	tcttgtttta	cccctacgac	360
ctgccttcca	aggtgtgagc	aactcgcccc	gacatgaccg	agggatgatca	tccggatccc	420
caggccccag	cagcccctgc	cagaatggct	cgcgctttcc	agcctgcagg	cccgtctccc	480

aggctcgacgc aacctacatg accaccccaa tctgtcccag accccaaaca ccctccttcc 540
ctgcttctct gtgatcgctg atcagcaaca 570

<210> 74
<211> 574
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 74
gcctgctcaa gcgggcgctc aacatgcaga gcgtcagcga gacgggctgt ggagatcggg 60
agacggacga ggccgcctct gccctgtttg aactgagcgt cagcgctggc taaggggagg 120
gagactcatc cccacgcccg cgccagggtct ctgatcccggt ctcgggcggt gatcggcgcg 180
catgactacg acccaacgac gtacgagact gatgtcggtc ccgacgagga gcgccgcgag 240
gcactcccgg gccaccgacc atgtttacac cgaccgaaag cactcgctcg tatccattcc 300
gtgcgcccg acatgcatca tcttttggtta ccgacttcgg tcttgtttta cccctacgac 360
ctgccttttc caaggtgtga gcaactcgcc cgggacatga ccgaggatgg atcatccgga 420
tcccaggcc ccagcagccc ctgccagaat ggctcgcgct ttccagcctg caggcccgtc 480
tcccaggctg acgcaacctg catgaccacc ccaatctgtc ccagacccca aacaccctcc 540
ttccctgctt ctctgtgatc gctgatcagc aaca 570

<210> 75
<211> 377
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 75
gcgccgagtt tgcgcgatcg aatacgataa ccaataaaag cacgctctaa gcaaaaacta 60
gcgatgcatt gtttatagtc agctgcatga atgtagacag cctgggcaat catgtgtcgg 120
gtgatcggcg ggcaccggct cccgataaca tcagggcgct cgatcgagcg tgctccgctg 180
cagaccccat ctcccctcac tctcgctcgg gcgaggaccc ggccctgcacg accagtctgt 240
gcagaaccgc ggtcttgcaa atcctattgc gagagccagg tgccgtatag gtcaagggtg 300
gtccgttttt cgctagccag cgccggtgtt ggcacgacta tcccaccagc ccgggcgcac 360
ggaggcaggc cagcagg 377

<210> 76
<211> 573
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 76
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ctagtagtac agtactgcaa gcaccaactt gaacctcaag atggtccgtc gacctcagctc 120
cagtttgcaa cgaagggtcgg gcgggtattg gagatccaga tcaaagcgta aatgcgaccc 180
tctcccgaag agacttcattg cgtgtgtcct gaagtgcattg aaaacattcc aggagcgcac 240
tcgtgctcca ggctggcggtt ctttgcgact tgttggtcccg cttcgagctc ggacctaggg 300
gcctgattcc gcgggtcgcgt tgatgacaca gaaaccaacg gacgacctat gtgacaccgg 360
ggactgaatc acagctgccc ccaggggcta gggcattcga gctgatacat tgataacgct 420
agacgaagtg cactgcggcg gtaaaaagct ctattttgtgc catcacagcg ccttgctgtg 480
cttcaggagc gcttgacgcg ctgcatttct gaagtcgaaa gccctagtcg ccaggaggag 540
ggtcgactcg cccgcagttc gggaacgttt gga 573

<210> 77
<211> 569
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 77
gagtgcgcag ggcccggccg accctttgat gccgcaacca cacatacgtg ttttttagagt 60
ctagtaatac agtactgcaa gcaccaactt gaacctcaag atggtccgtc gacctcagctc 120
cagtttgcaa cgaagggtcgg gcagggtattg gagatccaga tcaaagctga catgcgaccc 180
tcccgaagag acttcattgcg tgtgtcctga agtgcatgaa aacattccag gcagcgactc 240
gtgctccagg ctggcgactt ttgcgacttg ttggcccgtc tcgcggtcga acctggggggc 300
ctgattccgg tcgctgtgat gacacagaaa ccaacggacg acctatgtga caccggggac 360
tgaatcacag ctgccccag gggctagggc attcgggctg atacattgat aacgccagac 420
gaagtgcacg gcggcggtaa aaagctctat ttgtgccatc acagcgcctt gcgtggcttc 480
aggagcgctt gacgcgctgc atttttgaag tccaaagccc tagtcgccag gaggagggtc 540
gactcgcccg cagctcggga acgttttga 569

<210> 78
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 78
gatagtttat attttcgtgg tcgaagcggg tggggaaggg tgcgtagggt ttggcaagta 60
tgaggcatgt gtgcccagcg ttgcacccag gcgggggttc atggccgaca ggacgcgtgt 120

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caaagggtgct ggtcgtgtat gccctggccg gcaggtcgtt gctgctgctg gttagtgtatt 180
ccgcaaccct gatttttggcg tcttatttttgc gctggtgcaaa cgctggcgcc cgcgagccgg 240
gccggcggcg atgcggtgccc ccacggctgc cggaatccaa gggaggcaag agcgcccggg 300
tcagttgaag ggctttacgc gcaagggtaca gccgctcctg caaggctgcg tgggtggaatt 360
ggacgtgcag gtcctgctga agttcctcca ccgcctcacc agcggacaaa gcaccggtgt 420
atcagggtccg tgtcatccac tctaaagagc tcgactacga cctactgatg gccctagatt 480
cttcatcaaa aacgcctgag acaacttggc aggattgaaa ctccctgaag ggaccaccag 540
gggccctgag ttgttccttc cccccgtggc gagctgccag ccaggctgta cctgtgatcg 600
gggctggcgg gaaaacaggc ttcgtgtgct cagggttatgg gaggtgcagg acagctcatt 660
aaacgccaac aatcgacaaa ttcattggca gctaatacgt tatttcccat taacgagcta 720
taattgtccc aaaatttctg tctaccgggg gtgatccttc gtgtacgggc ccttccctca 780
accctaggta tgcgcacatg cggtcgccgc gcaacgcgcg cgagggccga gggtttggga 840
cgggccgtcc cgaaatgcag ttgcacccgg atgcgtggca ctttttttgc gataatttat 900
gcaatggact gctctgcaaa attctggctc tgcgccaaac cctaggatca gcggtgtagg 960
atttcgtaat cattcgtcct gatggggagc taccgactgc cctagtatca gcccgactgc 1020
ctgacgccag cgtccacttt tgtgcacaca ttccattcgt gcccaagaca tttcattgtg 1080
gtgcaagcg tccccagta cgctcacctg atccccaacc tccttattgt tctgtcgaca 1140
gagtgggccc agaggccggt cgca 1164

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<210> 79

<211> 1173

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 79

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atggtttaca tccttgtggt tgaggcatct ggggaagggg gcgtgggggt tggcgagtat 60
gaggcgtgtg tgcccagcgc tgcacccagg cgggggggtca tggccgacag gacgcgcgtc 120
aaagggtgctg ggcgtgtatg ccctggctcg caggctcgtt ctgttgctgc gctcgtgggt 180
ccgcaaccct gatttttggcg tcttattctg gcgtggcaag cgctgacgcc cgcgagccgg 240
gccggcggcg atgcggtgtc tcacggctgc cgagctccaa gggaggcaag agcgcccgga 300
tcagctgaag ggctttacac gcaagggtaca gccgctcctg caaggctgcg tgggtggactt 360
gaacctgtag gtcctctgct gaagtccctc cactacctca ccaggcccag cagaccaaag 420
cacaggcttt tcagggtccgt gtcattccact ctaaaacact cgactacgac ctactgatgg 480
ccctagattc ttcattcaaca atgcctgaga cacttgctca gaattgaaac tccctgaagg 540
gaccaccaga ggccctgagt tgttccttcc ccccggtggc agctgccagc caggctgtac 600
ctgtgatcga ggctggcggg aaaataggct tcgtgtgctc aggtcatggg aggtgcagga 660

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cagctcatga aacgccaaca atcgcacaaat tcatgtcaag ctaatcagct atttcctctt	720
cacgagctgt aattgtccca aaattctggt ctaccggggg tgatccttcg tgtacggggc	780
cttcctcaa ccctaggtat gcgcgcatgc ggtcgccgcg caactcgcg gagggccgag	840
ggtttgggac gggccgtccc gaaatgcagt tgcacccgga tgcgcggcg ctttcttgcg	900
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cggcgtagga tttcgtaatc attcgtcctg atggggagct accgactacc ctaatatcag	1020
cccggctgcc tgacgccagc gtccactttt gcgtacacat tccattcgtg cccaagacat	1080
ttcattgtgg tgcgaagcgt cccagttac gtcacctgt ttcccgcact cttactgtt	1140
ctgtcgacag agcgggcca caggccggtc gca	1173

<210> 80

<211> 9619

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 80

gctcttcgcg aaggctatctt tccagaacaa cgaccatggc ttgtcttagc gatcgctcga	60
atgactgcta gtgagtcgta cgctcgaccc agtcgctcgc aggagaacgc ggcaactgcc	120
gagcttcggc ttgccagtcg tgactcgatg gtgatcagga atcattggca ttggtagcat	180
tataattcgg cttccgcgct gtttatgggc atggcaatgt ctcatgcagt cgaccttagt	240
caaccaattc tgggtggcca gctccgggcg accgggctcc gtgtcgccgg gcaccacctc	300
ctgccatgag taacagggcc gccctctcct cccgacgttg gccactgaa taccgtgtct	360
tggggcccta catgatgggc tgcctagtcg ggcgggacgc gcaactgccc gcgcaatctg	420
ggacgtggtc tgaatcctcc aggcggggtt ccccgagaaa gaaagggtgc cgatttcaaa	480
gcagagccat gtgccgggccc ctgtggcctg tgttggcgcc tatgtagtca cccccctca	540
cccaattgtc gccagtttgc gcaatccata aactcaaaac tgcagcttct gagctgcgct	600
gttcaagaac acctctgggg tttgctcacc cgcgaggtcg acggtacccc gctcccgtct	660
ggtcctcacg ttcgtgtacg gcctggatcc cggaaagggc ggatgcacgt ggtgttgccc	720
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cgttgatggc	atgagcaact	cccgcacat	atttcctatt	gtcctcacgc	caagccggtc	3840
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ctttctgctg	tcaccacgac	ccacgatgca	acgcgacacg	acccggtggg	actgatcggg	4020
tcactgcacc	tgcatgcaat	tgtcacaagc	gcatactcca	atcgtatccg	tttgatttct	4080
gtgaaaactc	gctcgaccgc	ccgcgtcccc	caggcagcga	tgacgtgtgc	gtgacctggg	4140
tgtttcgtcg	aaaggccagc	aaccccaa	cgaggcgat	ccggagattg	ggatctgatc	4200
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ccagctttcg	taaatgccag	attggtgtcc	gataccttga	tttgccatca	gcgaaacaag	4320
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<210> 81
<211> 566

<212> DNA

<213> *Protheca moriformis*

<400> 81

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cgcgtgcatg gtgtgtgtgt ctgttttcgg ctgcacaatt tcaatagtcg gatgggcgac      420
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<210> 82

<211> 281

<212> PRT

<213> *Limnanthes douglasii*

<400> 82

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Pro Ala Val Ala Ala Thr Ala Asp Asp Asp Lys Asp Gly Val Phe Met
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Val Leu Leu Ser Cys Phe Lys Ile Phe Val Cys Phe Ala Ile Val Leu
      35      40      45

Ile Thr Ala Val Ala Trp Gly Leu Ile Met Val Leu Leu Leu Pro Trp
      50      55      60

Pro Tyr Met Arg Ile Arg Leu Gly Asn Leu Tyr Gly His Ile Ile Gly
      65      70      75      80

Gly Leu Val Ile Trp Ile Tyr Gly Ile Pro Ile Lys Ile Gln Gly Ser
      85      90      95

Glu His Thr Lys Lys Arg Ala Ile Tyr Ile Ser Asn His Ala Ser Pro
      100      105      110

Ile Asp Ala Phe Phe Val Met Trp Leu Ala Pro Ile Gly Thr Val Gly
      115      120      125

Val Ala Lys Lys Glu Val Ile Trp Tyr Pro Leu Leu Gly Gln Leu Tyr
      130      135      140

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

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Ile Gln Ser Met Lys Glu Ala Val Arg Val Ile Thr Glu Lys Asn Leu
165 170 175

Ser Leu Ile Met Phe Pro Glu Gly Thr Arg Ser Arg Asp Gly Arg Leu
180 185 190

Leu Pro Phe Lys Lys Gly Phe Val His Leu Ala Leu Gln Ser His Leu
195 200 205

Pro Ile Val Pro Met Ile Leu Thr Gly Thr His Leu Ala Trp Arg Lys
210 215 220

Gly Thr Phe Arg Val Arg Pro Val Pro Ile Thr Val Lys Tyr Leu Pro
225 230 235 240

Pro Ile Asn Thr Asp Asp Trp Thr Val Asp Lys Ile Asp Asp Tyr Val
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Lys Met Ile His Asp Val Tyr Val Arg Asn Leu Pro Ala Ser Gln Lys
260 265 270

Pro Leu Gly Ser Thr Asn Arg Ser Asn
275 280

<210> 83

<211> 281

<212> PRT

<213> Limnanthus alba

<400> 83

Met Ala Lys Thr Arg Thr Ser Ser Leu Arg Asn Arg Arg Gln Leu Lys
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Thr Ala Val Ala Ala Thr Ala Asp Asp Asp Lys Asp Gly Ile Phe Met
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Val Leu Leu Ser Cys Phe Lys Ile Phe Val Cys Phe Ala Ile Val Leu
35 40 45

Ile Thr Ala Val Ala Trp Gly Leu Ile Met Val Leu Leu Leu Pro Trp
50 55 60

Pro Tyr Met Arg Ile Arg Leu Gly Asn Leu Tyr Gly His Ile Ile Gly
65 70 75 80

Gly Leu Val Ile Trp Leu Tyr Gly Ile Pro Ile Glu Ile Gln Gly Ser
85 90 95

Glu His Thr Lys Lys Arg Ala Ile Tyr Ile Ser Asn His Ala Ser Pro
100 105 110

Ile Asp Ala Phe Phe Val Met Trp Leu Ala Pro Ile Gly Thr Val Gly
115 120 125

Val Ala Lys Lys Glu Val Ile Trp Tyr Pro Leu Leu Gly Gln Leu Tyr

130

135

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

Ile Gln Ser Met Lys Glu Ala Val Arg Val Ile Thr Glu Lys Asn Leu
165 170 175

Ser Leu Ile Met Phe Pro Glu Gly Thr Arg Ser Gly Asp Gly Arg Leu
180 185 190

Leu Pro Phe Lys Lys Gly Phe Val His Leu Ala Leu Gln Ser His Leu
195 200 205

Pro Ile Val Pro Met Ile Leu Thr Gly Thr His Leu Ala Trp Arg Lys
210 215 220

Gly Thr Phe Arg Val Arg Pro Val Pro Ile Thr Val Lys Tyr Leu Pro
225 230 235 240

Pro Ile Asn Thr Asp Asp Trp Thr Val Asp Lys Ile Asp Asp Tyr Val
245 250 255

Lys Met Ile His Asp Ile Tyr Val Arg Asn Leu Pro Ala Ser Gln Lys
260 265 270

Pro Leu Gly Ser Thr Asn Arg Ser Lys
275 280

<210> 84
<211> 506
<212> PRT
<213> Crambe abyssinica

<400> 84
Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
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Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
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Ala Ser Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
35 40 45

Leu Gln His Asn Val Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
50 55 60

Phe Gly Ser Ile Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu
65 70 75 80

Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr Gln Cys Arg Ser Ser Ile
85 90 95

Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Phe
100 105 110

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

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

420

425

430

Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Ala
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Trp Gln Ile Ala Val Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp
 450 455 460

Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Glu His
 465 470 475 480

Cys Ile His Lys Tyr Pro Val Gln Met Tyr Ser Gly Ser Ser Lys Ser
 485 490 495

Glu Thr Arg Ala Gln Asn Gly Arg Ser
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<210> 86

<211> 462

<212> PRT

<213> Arabidopsis thaliana

<400> 86

Met Asp Met Ser Ser Met Ala Gly Ser Ile Gly Val Ser Val Ala Val
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Leu Arg Phe Leu Leu Cys Phe Val Ala Thr Ile Pro Val Ser Phe Ala
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Cys Arg Ile Val Pro Ser Arg Leu Gly Lys His Leu Tyr Ala Ala Ala
 35 40 45

Ser Gly Ala Phe Leu Ser Tyr Leu Ser Phe Gly Phe Ser Ser Asn Leu
 50 55 60

His Phe Leu Val Pro Met Thr Ile Gly Tyr Ala Ser Met Ala Ile Tyr
 65 70 75 80

Arg Pro Lys Cys Gly Ile Ile Thr Phe Phe Leu Gly Phe Ala Tyr Leu
 85 90 95

Ile Gly Cys His Val Phe Tyr Met Ser Gly Asp Ala Trp Lys Glu Gly
 100 105 110

Gly Ile Asp Ser Thr Gly Ala Leu Met Val Leu Thr Leu Lys Val Ile
 115 120 125

Ser Cys Ser Met Asn Tyr Asn Asp Gly Met Leu Lys Glu Glu Gly Leu
 130 135 140

Arg Glu Ala Gln Lys Lys Asn Arg Leu Ile Gln Met Pro Ser Leu Ile
 145 150 155 160

Glu Tyr Phe Gly Tyr Cys Leu Cys Cys Gly Ser His Phe Ala Gly Pro
 165 170 175

Val Tyr Glu Met Lys Asp Tyr Leu Glu Trp Thr Glu Gly Lys Gly Ile
 180 185 190
 Trp Asp Thr Thr Glu Lys Arg Lys Lys Pro Ser Pro Tyr Gly Ala Thr
 195 200 205
 Ile Arg Ala Ile Leu Gln Ala Ala Ile Cys Met Ala Leu Tyr Leu Tyr
 210 215 220
 Leu Val Pro Gln Tyr Pro Leu Thr Arg Phe Thr Glu Pro Val Tyr Gln
 225 230 235 240
 Glu Trp Gly Phe Leu Arg Lys Phe Ser Tyr Gln Tyr Met Ala Gly Phe
 245 250 255
 Thr Ala Arg Trp Lys Tyr Tyr Phe Ile Trp Ser Ile Ser Glu Ala Ser
 260 265 270
 Ile Ile Ile Ser Gly Leu Gly Phe Ser Gly Trp Thr Asp Asp Ala Ser
 275 280 285
 Pro Lys Pro Lys Trp Asp Arg Ala Lys Asn Val Asp Ile Leu Gly Val
 290 295 300
 Glu Leu Ala Lys Ser Ala Val Gln Ile Pro Leu Val Trp Asn Ile Gln
 305 310 315 320
 Val Ser Thr Trp Leu Arg His Tyr Val Tyr Glu Arg Leu Val Gln Asn
 325 330 335
 Gly Lys Lys Ala Gly Phe Phe Gln Leu Leu Ala Thr Gln Thr Val Ser
 340 345 350
 Ala Val Trp His Gly Leu Tyr Pro Gly Tyr Met Met Phe Phe Val Gln
 355 360 365
 Ser Ala Leu Met Ile Ala Gly Ser Arg Val Ile Tyr Arg Trp Gln Gln
 370 375 380
 Ala Ile Ser Pro Lys Met Ala Met Leu Arg Asn Ile Met Val Phe Ile
 385 390 395 400
 Asn Phe Leu Tyr Thr Val Leu Val Leu Asn Tyr Ser Ala Val Gly Phe
 405 410 415
 Met Val Leu Ser Leu His Glu Thr Leu Thr Ala Tyr Gly Ser Val Tyr
 420 425 430
 Tyr Ile Gly Thr Ile Ile Pro Val Gly Leu Ile Leu Leu Ser Tyr Val
 435 440 445
 Val Pro Ala Lys Pro Ser Arg Pro Lys Pro Arg Lys Glu Glu

450

455

<210> 87
<211> 465
<212> PRT
<213> Arabidopsis thaliana

<400> 87
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35 40 45
Ser Ala Ala Ser Gly Ala Phe Leu Ser Tyr Leu Ser Phe Gly Phe Ser
50 55 60
Ser Asn Leu His Phe Leu Val Pro Met Thr Ile Gly Tyr Ala Ser Met
65 70 75 80
Ala Ile Tyr Arg Pro Leu Ser Gly Phe Ile Thr Phe Phe Leu Gly Phe
85 90 95
Ala Tyr Leu Ile Gly Cys His Val Phe Tyr Met Ser Gly Asp Ala Trp
100 105 110
Lys Glu Gly Gly Ile Asp Ser Thr Gly Ala Leu Met Val Leu Thr Leu
115 120 125
Lys Val Ile Ser Cys Ser Ile Asn Tyr Asn Asp Gly Met Leu Lys Glu
130 135 140
Glu Gly Leu Arg Glu Ala Gln Lys Lys Asn Arg Leu Ile Gln Met Pro
145 150 155 160
Ser Leu Ile Glu Tyr Phe Gly Tyr Cys Leu Cys Cys Gly Ser His Phe
165 170 175
Ala Gly Pro Val Phe Glu Met Lys Asp Tyr Leu Glu Trp Thr Glu Glu
180 185 190
Lys Gly Ile Trp Ala Val Ser Glu Lys Gly Lys Arg Pro Ser Pro Tyr
195 200 205
Gly Ala Met Ile Arg Ala Val Phe Gln Ala Ala Ile Cys Met Ala Leu
210 215 220
Tyr Leu Tyr Leu Val Pro Gln Phe Pro Leu Thr Arg Phe Thr Glu Pro
225 230 235 240
Val Tyr Gln Glu Trp Gly Phe Leu Lys Arg Phe Gly Tyr Gln Tyr Met
245 250 255

Ala Gly Phe Thr Ala Arg Trp Lys Tyr Tyr Phe Ile Trp Ser Ile Ser
260 265 270

Glu Ala Ser Ile Ile Ile Ser Gly Leu Gly Phe Ser Gly Trp Thr Asp
275 280 285

Glu Thr Gln Thr Lys Ala Lys Trp Asp Arg Ala Lys Asn Val Asp Ile
290 295 300

Leu Gly Val Glu Leu Ala Lys Ser Ala Val Gln Ile Pro Leu Phe Trp
305 310 315 320

Asn Ile Gln Val Ser Thr Trp Leu Arg His Tyr Val Tyr Glu Arg Ile
325 330 335

Val Lys Pro Gly Lys Lys Ala Gly Phe Phe Gln Leu Leu Ala Thr Gln
340 345 350

Thr Val Ser Ala Val Trp His Gly Leu Tyr Pro Gly Tyr Ile Ile Phe
355 360 365

Phe Val Gln Ser Ala Leu Met Ile Asp Gly Ser Lys Ala Ile Tyr Arg
370 375 380

Trp Gln Gln Ala Ile Pro Pro Lys Met Ala Met Leu Arg Asn Val Leu
385 390 395 400

Val Leu Ile Asn Phe Leu Tyr Thr Val Val Val Leu Asn Tyr Ser Ser
405 410 415

Val Gly Phe Met Val Leu Ser Leu His Glu Thr Leu Val Ala Phe Lys
420 425 430

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Glu
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 35 40 45
 Ala Ala Ala Ser Gly Val Phe Leu Ser Tyr Leu Ser Phe Gly Phe Ser
 50 55 60
 Ser Asn Leu His Phe Leu Val Pro Met Thr Ile Gly Tyr Ala Ser Met
 65 70 75 80
 Ala Met Tyr Arg Pro Lys Cys Gly Ile Ile Thr Phe Phe Leu Gly Phe
 85 90 95
 Ala Tyr Leu Ile Gly Cys His Val Phe Tyr Met Ser Gly Asp Ala Trp
 100 105 110
 Lys Glu Gly Gly Ile Asp Ser Thr Gly Ala Leu Met Val Leu Thr Leu
 115 120 125
 Lys Val Ile Ser Cys Ala Val Asn Tyr Asn Asp Gly Met Leu Lys Glu
 130 135 140
 Glu Gly Leu Arg Glu Ala Gln Lys Lys Asn Arg Leu Ile Glu Met Pro
 145 150 155 160
 Ser Leu Ile Glu Tyr Phe Gly Tyr Cys Leu Cys Cys Gly Ser His Phe
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 Ala Gly Pro Val Tyr Glu Met Lys Asp Tyr Leu Gln Trp Thr Glu Gly
 180 185 190
 Thr Gly Ile Trp Asp Ser Ser Glu Lys Arg Lys Gln Pro Ser Pro Tyr
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 225 230 235 240
 Val Tyr Gln Glu Trp Gly Phe Trp Lys Lys Phe Gly Tyr Gln Tyr Met
 245 250 255
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 260 265 270
 Glu Ala Ser Ile Ile Ile Ser Gly Leu Gly Phe Ser Gly Trp Thr Asp
 275 280 285
 Asp Glu Ala Ser Pro Lys Pro Lys Trp Asp Arg Ala Lys Asn Val Asp
 290 295 300
 Ile Leu Gly Val Glu Leu Ala Lys Ser Ala Val Gln Ile Pro Leu Val
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Trp Asn Ile Gln Val Ser Thr Trp Leu Arg His Tyr Val Tyr Glu Arg
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 340 345 350
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 355 360 365
 Phe Phe Val Gln Ser Ala Leu Met Ile Ala Gly Ser Arg Val Ile Tyr
 370 375 380
 Arg Trp Gln Gln Ala Ile Ser Pro Lys Leu Gly Val Leu Arg Ser Met
 385 390 395 400
 Met Val Phe Ile Asn Phe Leu Tyr Thr Val Leu Val Leu Asn Tyr Ser
 405 410 415
 Ala Val Gly Phe Met Val Leu Ser Leu His Glu Thr Leu Thr Ala Tyr
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 35 40 45
 Ala Ala Ala Ser Gly Val Phe Leu Ser Tyr Leu Ser Phe Gly Phe Ser
 50 55 60
 Ser Asn Leu His Phe Leu Val Pro Met Thr Ile Gly Tyr Ala Ser Met
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 Ala Met Tyr Arg Pro Lys Cys Gly Ile Ile Thr Phe Phe Leu Gly Phe
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Ala Tyr Leu Ile Gly Cys His Val Phe Tyr Met Ser Gly Asp Ala Trp
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Lys Glu Gly Gly Ile Asp Ser Thr Gly Ala Leu Met Val Leu Thr Leu
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Lys Val Ile Ser Cys Ala Val Asn Tyr Asn Asp Gly Met Leu Lys Glu
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Glu Gly Leu Arg Glu Ala Gln Lys Lys Asn Arg Leu Ile Glu Met Pro
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Thr Gly Ile Trp Asp Ser Ser Glu Lys Arg Lys Gln Pro Ser Pro Tyr
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Tyr Leu Tyr Leu Val Pro Gln Phe Pro Leu Thr Arg Phe Thr Glu Pro
225 230 235 240

Val Tyr Gln Glu Trp Gly Phe Trp Lys Lys Phe Gly Tyr Gln Tyr Met
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Ala Gly Gln Thr Ala Arg Trp Lys Tyr Tyr Phe Ile Trp Ser Ile Ser
260 265 270

Glu Ala Ser Ile Ile Ile Ser Gly Leu Gly Phe Ser Gly Trp Thr Asp
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Asp Asp Ala Ser Pro Lys Pro Lys Trp Asp Arg Ala Lys Asn Val Asp
290 295 300

Ile Leu Gly Val Glu Leu Ala Lys Ser Ala Val Gln Ile Pro Leu Val
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Trp Asn Ile Gln Val Ser Thr Trp Leu Arg His Tyr Val Tyr Glu Arg
325 330 335

Leu Val Lys Ser Gly Lys Lys Ala Gly Phe Phe Gln Leu Leu Ala Thr
340 345 350

Gln Thr Val Ser Ala Val Trp His Gly Leu Tyr Pro Gly Tyr Met Met
355 360 365

Phe Phe Val Gln Ser Ala Leu Met Ile Ala Gly Ser Arg Val Ile Tyr
370 375 380

Arg Trp Gln Gln Ala Ile Ser Pro Lys Leu Gly Val Leu Arg Ser Met
 385 390 395 400
 Met Val Phe Ile Asn Phe Leu Tyr Thr Val Leu Val Leu Asn Tyr Ser
 405 410 415
 Ala Val Gly Phe Met Val Leu Ser Leu His Glu Thr Leu Thr Ala Tyr
 420 425 430
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 Glu Glu
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 Ala Ala Ala Ser Gly Val Phe Leu Ser Tyr Leu Ser Phe Gly Phe Ser
 50 55 60
 Ser Asn Leu His Phe Leu Val Pro Met Thr Ile Gly Tyr Ala Ser Met
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 Ala Met Tyr Arg Pro Lys Cys Gly Ile Ile Thr Phe Phe Leu Gly Phe
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 Ala Tyr Leu Ile Gly Cys His Val Phe Tyr Met Ser Gly Asp Ala Trp
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 130 135 140
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Ser Leu Ile Glu Tyr Phe Gly Tyr Cys Leu Cys Cys Gly Ser His Phe
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 Lys Gly Ile Trp Asp Ser Ser Glu Lys Arg Lys Gln Pro Ser Pro Tyr
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 Gly Ala Thr Leu Arg Ala Ile Phe Gln Ala Gly Ile Cys Met Ala Leu
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 Tyr Leu Tyr Leu Val Pro Gln Phe Pro Leu Thr Arg Phe Thr Glu Pro
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 Val Tyr Gln Glu Trp Gly Phe Leu Lys Lys Phe Gly Tyr Gln Tyr Met
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 Trp Asn Ile Gln Val Ser Thr Trp Leu Arg His Tyr Val Tyr Glu Arg
 325 330 335
 Leu Val Lys Ser Gly Lys Lys Ala Gly Phe Phe Gln Leu Leu Ala Thr
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 Phe Phe Val Gln Ser Ala Leu Met Ile Ala Gly Ser Arg Val Ile Tyr
 370 375 380
 Arg Trp Gln Gln Ala Ile Ser Pro Lys Leu Ala Met Leu Arg Asn Ile
 385 390 395 400
 Met Val Phe Ile Asn Phe Leu Tyr Thr Val Leu Val Leu Asn Tyr Ser
 405 410 415
 Ala Val Gly Phe Met Val Leu Ser Leu His Glu Thr Leu Thr Ala Tyr
 420 425 430
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Leu Ser Tyr Val Val Pro Ala Lys Pro Ser Arg Pro Lys Pro Arg Lys
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Glu Glu
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 <213> Limnanthes douglasii

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Ala Ala Thr Gly Ala Phe Leu Ser Tyr Leu Ser Phe Gly Phe Ser Ser
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Asn Ile His Phe Leu Ile Pro Met Thr Leu Gly Tyr Ala Ser Met Ala
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Leu Tyr Arg Ala Lys Cys Gly Ile Val Thr Phe Phe Leu Ala Phe Gly
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Tyr Leu Ile Gly Cys His Val Tyr Tyr Met Ser Gly Asp Ala Trp Lys
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Glu Gly Gly Ile Asp Ala Thr Gly Ala Leu Met Val Leu Thr Leu Lys
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Val Ile Ser Cys Ser Val Asn Tyr Asn Asp Gly Leu Leu Lys Glu Glu
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Gly Leu Arg Pro Ser Gln Lys Lys Asn Arg Leu Ser Ser Leu Pro Ser
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Phe Ile Glu Tyr Val Gly Tyr Cys Leu Cys Cys Gly Thr His Phe Ala
 165 170 175

Gly Pro Val Tyr Glu Met Lys Asp Tyr Leu Glu Trp Thr Ala Gly Lys
 180 185 190

Gly Ile Trp Ala Lys Ser Glu Lys Ala Lys Ser Pro Ser Pro Phe Leu
 195 200 205

Pro Ala Leu Arg Ala Leu Leu Gln Gly Ala Val Cys Met Val Leu Tyr
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Leu Tyr Leu Val Pro Gln Tyr Pro Leu Ser Gln Phe Thr Ser Pro Val
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 Tyr Gln Glu Trp Gly Phe Trp Lys Arg Leu Ser Tyr Gln Tyr Met Ala
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 Gly Phe Thr Ala Arg Trp Lys Tyr Tyr Phe Ile Trp Ser Ile Ser Glu
 260 265 270
 Ala Ser Val Ile Leu Ser Gly Leu Gly Phe Ser Gly Trp Thr Asp Ser
 275 280 285
 Ser Pro Pro Lys Pro Arg Trp Asp Arg Ala Lys Asn Val Asp Ile Leu
 290 295 300
 Gly Val Glu Phe Ala Thr Ser Gly Ala Gln Val Pro Leu Val Trp Asn
 305 310 315 320
 Ile Gln Val Ser Thr Trp Leu Arg His Tyr Val Tyr Asp Arg Leu Val
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 Lys Thr Gly Lys Lys Pro Gly Phe Phe Gln Leu Leu Ala Thr Gln Thr
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 Thr Ser Ala Val Trp His Gly Leu Tyr Pro Gly Tyr Leu Phe Phe Phe
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 Val Gln Ser Ala Leu Met Ile Ala Gly Ser Lys Val Ile Tyr Arg Trp
 370 375 380
 Lys Gln Ala Leu Pro Pro Ser Ala Ser Val Leu Gln Lys Ile Leu Val
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 Gly Phe Met Val Leu Ser Met His Glu Thr Ile Ala Ala Tyr Gly Ser
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 Arg Ser Lys Cys Gly Ile Leu Thr Phe Val Leu Gly Phe Thr Tyr Leu
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 Ile Gly Cys His Phe Tyr Tyr Met Ser Gly Asp Ala Trp Lys Asp Gly
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 Gly Met Asp Ala Thr Gly Ser Leu Met Val Leu Thr Leu Lys Val Ile
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 Ser Cys Ala Ile Asn Tyr Asn Asp Gly Leu Leu Lys Glu Glu Gly Leu
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 Arg Glu Ala Gln Lys Lys Asn Arg Leu Ile Asn Leu Pro Ser Val Val
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 Glu Tyr Val Gly Tyr Cys Leu Cys Cys Gly Ser His Phe Ala Gly Pro
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 Val Phe Glu Met Lys Asp Tyr Leu Gln Trp Thr Lys Lys Lys Gly Ile
 180 185 190
 Trp Ala Ala Lys Glu Arg Ser Pro Ser Pro Tyr Val Ala Thr Ile Arg
 195 200 205
 Ala Leu Leu Gln Ala Ala Ile Cys Met Val Val Tyr Met Tyr Leu Val
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 Pro Arg Phe Pro Leu Ser Thr Leu Ala Glu Pro Ile Tyr Gln Glu Trp
 225 230 235 240
 Gly Phe Trp Lys Lys Leu Ser Tyr Gln Tyr Ile Thr Gly Phe Ser Ser
 245 250 255
 Arg Trp Lys Tyr Phe Phe Val Trp Ser Ile Ser Glu Ala Ser Met Ile
 260 265 270
 Ile Ser Gly Leu Gly Phe Ser Gly Trp Thr Asp Thr Ser Pro Gln Asn
 275 280 285
 Pro Gln Trp Asp Arg Ala Lys Asn Val Asp Ile Leu Arg Ala Glu Leu
 290 295 300

Pro Glu Ser Ala Val Val Leu Pro Leu Val Trp Asn Ile His Val Ser
305 310 315 320

Thr Trp Leu Arg His Tyr Val Tyr Glu Arg Leu Ile Lys Asn Gly Lys
325 330 335

Lys Pro Gly Phe Phe Glu Leu Leu Ala Thr Gln Thr Val Ser Ala Val
340 345 350

Trp His Gly Leu Tyr Pro Gly Tyr Ile Ile Phe Phe Val His Thr Ala
355 360 365

Leu Met Ile Ala Gly Ser Arg Val Ile Tyr Arg Trp Arg Gln Ala Val
370 375 380

Pro Pro Asn Met Ala Leu Val Lys Lys Met Leu Thr Phe Met Asn Leu
385 390 395 400

Leu Tyr Thr Val Leu Ile Leu Asn Tyr Ser Tyr Val Gly Phe Arg Val
405 410 415

Leu Asn Leu His Glu Thr Leu Ala Ala His Arg Ser Val Tyr Tyr Val
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Ala Lys Pro Ser Arg Pro Lys Pro Arg Lys Gln Gln
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<210> 94

<211> 6402

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 94

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<210> 95

<211> 1191

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 95

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<210> 96

<211> 1191

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 96

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<210> 97

<211> 12759

<212> DNA

<213> Artificial Sequence

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<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 97

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 <213> Brassica juncea

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 <213> Limnanthes douglasii

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<210> 102

<211> 1383

<212> DNA

<213> *Limnanthes douglasii*

<400> 102

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<210> 103

<211> 6630

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 103

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<210> 104

<211> 6078

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 104

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<210> 105

<211> 725

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 105

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<210> 106

<211> 723

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 106

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<210> 107

<211> 858

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 107

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<210> 108

<211> 1413

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 108

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<210> 109

<211> 1413

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 109

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<210> 110
 <211> 6633
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 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<400> 110
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<210> 111
 <211> 725
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 111	
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gtacc	725

<210> 112
 <211> 723
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 112
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<210> 113
<211> 1407
<212> DNA
<213> Artificial Sequence
<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 113
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<210> 114

<211> 1395

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 114

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 cagcagtgc ttaag 1395

<210> 115
 <211> 1400
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 115
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 gcaaggagga gtgacttaag 1400

<210> 116
 <211> 1410
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 116
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 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<210> 118

<211> 725

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 118

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<210> 119

<211> 723

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 119

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gtgggagacg attccggcca agtggcacat cttcctgatg ctctgccacc cccgccacaa 240

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<210> 120
 <211> 1410
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<210> 121

<211> 1413

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 121

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<210> 122

<211> 1413

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 122

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<210> 123

<211> 1413

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 123

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gtgctgcgct tcctgctgtg cttcgtggcc accatccccg tgtccttcgc ctggcgcata 120
gtgccctccc gcctgggcaa gcacatctac gccgccgcct ccggcgtgtt cctgtcctac 180
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tccatggcca tgtaccgccc caagtgcggc atcatcacct tcttcctggg cttgcctac 300
ctgatcggct gccacgtgtt ctacatgtcc ggcgacgcct ggaaggaggg cggcatcgac 360

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tccaccggcg	ccctgatggt	gctgaccctg	aaggtgatct	cctgcgccgt	gaactacaac	420
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atgccctccc	tgatcgagta	cttcggctac	tgctgtgtct	gcggctccca	cttcgccggc	540
cccgtgtacg	agatgaagga	ctacctgcag	tggaccgagg	gcaagggcat	ctgggactcc	600
tccgagaagc	gcaagcagcc	ctccccctac	ggcgccaccc	tgcgcgccat	cttccaggcc	660
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<210> 124

<211> 1407

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 124

actagtatgg	acctggacat	ggactccatg	gcctcctcca	tcggcgtgtc	ctgccccgtg	60
ctgcgcttcc	tgctgtgcta	cgccgccacc	atccccgtgt	ccttcactctg	ccgcttcgtg	120
cccggcaaga	cccccaagaa	cgtgttctcc	gccgccaccg	gcgccttcct	gtcctacctg	180
tccttcgggt	tctcctccaa	catccacttc	ctgatcccca	tgaccctggg	ctacgcctcc	240
atggccctgt	accgcgccaa	gtgcggcatc	gtgaccttct	tcctggcctt	cggctacctg	300
atcggctgcc	acgtgtacta	catgtccggc	gacgcctgga	aggagggcgg	catcgacgcc	360
accggcgccc	tgatgggtgt	gacctgaag	gtgatctcct	gctccgtgaa	ctacaacgac	420
ggcctgctga	aggaggaggg	cctgcgcccc	tcccagaaga	agaaccgcct	gtcctccctg	480
ccctccttca	tcgagtacgt	gggctactgc	ctgtgctgcy	gcacccactt	cgccggcccc	540
gtgtacgaga	tgaaggacta	cctggagtgg	accgccggca	agggcatctg	ggccaagtcc	600
gagaaggcca	agtccccctc	ccccttcctg	cccgccttgc	gcgccctgct	gcagggcgcc	660
gtgtgcatgg	tgctgtacct	gtacctgggtg	ccccagtacc	ccctgtccca	gttcacctcc	720

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cccggtgtacc aggagtgggg cttctggaag cgcctgtcct accagtacat ggccggcttc      780
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ggcctggggct tctccggctg gaccgactcc tccccccca agccccgctg ggaccgcgcc      900
aagaacgtgg acatcctggg cgtggagttc gccacctccg gcgcccaggt gcccctggtg      960
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atggtgctgt ccatgcacga gaccatcgcc gcctacggct ccgtgtacta cgtgggcacc     1320
atcgtgcca tcgtgctgac catcctgggc tccatcatcc ccgtgaagcc ccgccgcacc     1380
aaggtgcaga aggagcagtg acttaag                                           1407

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<210> 125

<211> 1395

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 125

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aacctgggca agcacgtgta cgccgccggc tccggcgccc tgctgtcctg cctggccttc      180
ggcctgctgt ccaacctgca cttcctggtg ctgatggtga tgggctactg ctccatggtg      240
ttctaccgct ccaagtgcgg catcctgacc ttcgtgctgg gcttcaccta cctgatcggc      300
tgccacttct actacatgtc cggcgacgcc tggaaggacg gcggcatgga cgccaccggc      360
tccctgatgg tgctgaccct gaaggatgac tcctgcgcca tcaactacaa cgacggcctg      420
ctgaaggagg agggcctgcg cgaggcccag aagaagaacc gcctgatcaa cctgccctcc      480
gtggtggagt acgtgggcta ctgcctgtgc tgcggctccc acttcgccgg ccccggtgtc      540
gagatgaagg actacctgca gtggaccaag aagaagggca tctgggccgc caaggagcgc      600
tccccctccc cctacgtggc caccatccgc gccctgctgc aggccgcat ctgcatggtg      660
gtgtacatgt acctggtgcc ccgcttcccc ctgtccaccc tggccgagcc catctaccag      720
gagtggggct tctggaagaa gctgtcctac cagtacatca ccggcttctc ctcccgtgg      780
aagtacttct tcgtgtggtc catctccgag gcctccatga tcatctccgg cctgggcttc      840
tccggctgga ccgacacctc cccccagaac cccagtgagg accgcgcaa gaacgtggac      900
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ggcttcttcg agctgctggc caccagacc gtgtccgccg tgtggcacgg cctgtacccc	1080
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cgctggcgcc aggccgtgcc cccaacatg gccctggtga agaagatgct gaccttcacg	1200
aacctgctgt acaccgtgct gatcctgaac tactcctacg tgggcttccg cgtgctgaac	1260
ctgcacgaga ccctggccgc ccaccgctcc gtgtactacg tgggcacat cctgcccac	1320
atcttcacatc tcctgggcta catcttcccc gccaaagcct cccgccccaa gccccgcaag	1380
cagcagtgc ttaag	1395

<210> 126

<211> 6138

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 126

gctcttctgc ttcggattcc actacatcaa gtgggtgaac ctggcgggcg cggaggaggg	60
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gtccgattcc ttccccgcct ttgtggcgcg ccagtcgacg gccaaagctgc cttttatcgg	180
catcatcagg tgcgtgaaag tgggggctgc tgtggtcgtg gtgggcgggg tcacaaatga	240
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gggatcacaa atctcaccac cactcgtcca ccttgcctgg gccttgacgc caaattatga	360
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tgaagcagcg catgcaggac gaggccgagg ggaagacccc gcccgagtac cggccgctgc	480
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gtcgtcgacc agaagagc	6138

<210> 127

<211> 725

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 127

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gctcgaaatc agagccagcc tgggtcatggg atcacagagc tcaccaccac tcgtccacct	360
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<210> 128

<211> 723

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 128

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<210> 129

<211> 6138

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 129

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<210> 130

<211> 725

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 130

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<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 131

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<210> 132

<211> 6402

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 132

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<210> 133

<211> 725

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 133

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catcatcagg	tgctgtgaaag	cgggggctgc	tgtggccgtg	gtgggcaggg	ttgcgaaggg	240
gggcaggcgt	aggcgtgcag	tgtgagcggg	cattgatgcc	gtcgtttgcc	ggtcaggaga	300
gctcgaaatc	agagccagcc	tggtcatggg	atcacagagc	tcaccaccac	tcgtccacct	360

cgctgcgcc ttgcagccaa atcatgagct gcctctacgt gaaccgcgac cgctcggggc 420
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cattgcctc tcaaccccggt ctctcctttc ctccatcgcc agggcaccac ctccaacggc 660
gactacctgc ttcccttcaa gaccggcgcc ttcctggccg gggtgcccgt ccagcccgtg 720
gtacc 725

<210> 134

<211> 723

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 134

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cccactcacc cttgctgcc a tcgctcccca cccttttccc cagggaaccc tgtggcccac 180
gtgggagacg attccggcca agtggcacat cttcctgatg ctctgccacc cccgccacaa 240
agtgaccgtg atgaaggtag gaacaagggt cgggccccga ttctggatat cacgtctggg 300
gtgtgtttct cgcgcacgcg tccccgatg cgctgcacag tctccctcac accctcacc 360
ctaacgctcg cagttgcccg tgtacgtccc caatgaggag gaaaaggccg accccaagct 420
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gtgggcgggg cggtcttagc gaattggcg attggccctc accgaggcag cacatcggac 540
accaatcgtc acccggcgag caattccgcc ccctctgtct tctcgagat ggaggtcgcc 600
gggaccaagg acacgacggc ggtgtttgag gacaagatgc gctacctgaa ctccctgaag 660
agaaagtacg gcaagcctgt gcctaagaaa attgagtga ccccgctcgt cgaccagaag 720
agc 723

<210> 135

<211> 1191

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 135

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tgcgacgccc	tggcctgcgc	cttcgaggcc	atggccttcg	gctccaccgc	catgtgcggc	420
cgcgacacct	tctggttctg	ggtgatctcc	gccatcccct	tctacggcgc	cacctgggag	480
cactacttca	ccaacaccct	gatcctgccc	gtgatcaacg	gccccaccga	gggcctggcc	540
ctgatctacg	tgtcccactt	cttcaccgcc	ctggtgggcg	ccgagtgggtg	ggcccagcag	600
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<210> 136

<211> 1191

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 136

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gtgacctcct	ccctgctggg	ctacatctac	tccccccagc	tggactcccc	ccccccccgc	240
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<210> 137

<211> 6630

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 137

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<210> 140

<211> 5108

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 140

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<211> 10051

<212> DNA

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<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 141

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caccaggcgc agacggagga acgcatggtg agtgcgcac acaagatgca tgtcttggtg	6840
tctgtactat aatgctagag catcaccagg ggcttagtca tcgcacctgc tttggtcatt	6900
acagaaattg cacaagggcg tcctccggga tgaggagatg taccagctca agctggagcg	6960
gcttcgagcc aagcaggagc gcggcgcatg acgacctacc cacatgcgaa gagcctctag	7020
a	7021

<210> 143

<211> 678

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 143

actagtatgg cgggctccct gtcgtttgtg cggcgctgt acctcacct gtacaactgg	60
atcgtgttcg ccggctgggc ccagggtgctg tactttgccg tcaagacgct caaggagtcc	120
ggccacgaga acgtgtacga cgccgtggag aagcccctcc agctggcgca aaccgccgcg	180
gtcctggaga tcctccacgg cctggtcggc ctcgtcagga gcccggtctc ggccaccctg	240
ccgcagatcg ggagccgcct ctttctgacc tggggcattc tgtattcctt cccggaggtc	300
cagagccact ttctggtgac ctccctcgtg atcagctggt cgatcacgga aatcatccgc	360
tacagcttct tcggcctgaa ggaggcgctg ggcttcgcgc ccagctggca cctgtggctc	420
cgctattcga gctttctggt gctctacccc accggcatca cctccgaggc cggcctcatc	480
tacctggccc tgccgcacat caagacgtcg gagatgtact ccgtccgcat gcccaacacc	540
ttgaactttt ctttcgactt tttctacgcc acgattctcg tcctcgcgat ctacgtcccc	600
ggttcgcccc acatgtaccg ctacatgctg ggccagcgga agcgggccct gagcaagtcc	660
aagcgcgagt gactcgag	678

<210> 144

<211> 969

<212> DNA

<213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 144
 actagtatgg agatctgcac gtacttcaag tcccaaccca gctggctgct gtcctgttt 60
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 tacttctctgc gccccggcaa gaacctccgc cgctacgggt cctgggccat tatcaccggc 180
 ccgaccgacg gcatcggcaa ggccttttgcg ttccagctgg ccacaaaggg cctgaacctg 240
 gtgctggtgg cgcgcaaccc ggacaagctg aaggacgtct ccgacagcat caggccaag 300
 catagcaacg tgcagatcaa gacggtgatc atggacttta gcggcgacgt tgacgacggc 360
 gtccgccgca tcaaggagac catcgagggg ctggagggtg gcatcctgat caacaatgcc 420
 ggcatgtcct acccgtagcg gaagtacttt cacgaggtcg acgaggagct cgtcaacggc 480
 ctcacaaaaa tcaacgtcga gggcacgacc aagggtgaccc aggccgtgct gccgggcatg 540
 ctggagcgca agcgcggcgc catcgtaac atgggcagcg gcgcggccgc cctgatcccg 600
 tcgtaccctt tctacagcgt gtatgccggc gcgaagacgt acgtggacca gttcaccggg 660
 tgcctgcacg tcgagtacaa gaagagcggc attgacgtcc agtgccagggt cccgctctac 720
 gtggccacga agatgacgaa gatccgccgc gcctccttcc tggtcgcctc ccccgagggc 780
 tacgccaagg ccgccctgcg gttcgtgggg tacgaggccc ggtgcacccc ctactggccg 840
 cacgccctga tgggctacgt cgtctccgcc ctgccccagt ccgtgttcga gtccttcaac 900
 atcaagcgct gcctgcagat ccgcaagaag ggcatgctga aggattcgcg gaagaaggag 960
 tgactcgag 969

<210> 145
 <211> 5319
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 145
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 ttgttgttcc ctgtttttac accttgccag agcctggtca aagcttgaca gtttgaccaa 120
 attcagggtg cctcatctct ctgcactga tagacattgc agatttggaa gaccagtc 180
 gtacactaca tgcacagccg tttgtccttg cgccatgaac ttgccacttt tgtgcgccgg 240
 tcgggggtga tagctcggca gccgccgatc ccaaagggtc cgcggccag gggcacgaga 300
 acccccgaca cgattaaata gccaaaatca gttagaacgg cacctccacc ctaccggaat 360
 ctgacagggg catcaagcgc gcgaaacaac ggcgaggggt cgttcgggaa gcgcgcgtag 420
 ttgacgcaag aagcctgggt caggctggga gggccgcgag aagatcgctt cctgccgagt 480
 ctgacccac gcctcgagcg caccgtccgc gaacaaccaa cccctttgcg cgagccctga 540

cattctttca	attgccaagg	atgcacatgt	gacacgtata	gccattcggc	tttgtttgtg	600
cctgcttgac	tcgcgtcatt	taattgattt	gtgccggtga	gccgggagtc	ggccactcgt	660
ctccgagccg	cagtcccggc	gccagtcccc	cggcctctga	tctgggtccg	gaagggttgg	720
tataggagcg	gtctcggcta	tctgaagccc	attacccgac	actttggccg	gctgctttcc	780
aggcagccgt	gtactcttgc	gcagtcggta	ccccgctccc	gtctggtcct	cacgttcgtg	840
tacggcctgg	atcccggaaa	gggcggatgc	acgtggtgtt	gccccgcat	tggcgccac	900
gtttcaaagt	ccccggccag	aaatgcacag	gaccggcccc	gctcgcacag	gccatgacga	960
atgccagat	ttcgacagca	aaacaatctg	gaataatcgc	aaccattcgc	gttttgaacg	1020
aaacgaaaag	acgctgttta	gcacgtttcc	gatatcgtgg	gggccgaagc	atgattgggg	1080
ggaggaaaagc	gtggcccaa	ggtagcccat	tctgtgccac	acgccgacga	ggaccaatcc	1140
ccggcatcag	ccttcatcga	cggctgcgcc	gcacatataa	agccggacgc	cttcccga	1200
cgttcaaaca	gttttatttc	ctccacttcc	tgaatcaaac	aaatcttcaa	ggaagatcct	1260
gctcttgagc	aactagtatg	ttcgcgttct	acttcctgac	ggcctgcatc	tccctgaagg	1320
gcgtgttcgg	cgtctcccc	tcctacaacg	gcctgggcct	gacgccccag	atgggctggg	1380
acaactggaa	cacgttcgcc	tgcgacgtct	ccgagcagct	gctgctggac	acggccgacc	1440
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ggtcctccgg	ccgcgactcc	gacggcttcc	tggtcgccga	cgagcagaag	ttccccaacg	1560
gcatgggcca	cgtcgccgac	cacctgcaca	acaactcctt	cctgttcggc	atgtactcct	1620
ccgcggggcga	gtacacgtgc	gccggctacc	ccggctccct	gggccgcgag	gaggaggacg	1680
cccagttctt	cgcaacaac	cgcggtggact	acctgaagta	cgacaactgc	tacaacaagg	1740
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acaagacggg	ccgccccatc	ttctactccc	tgtgcaactg	gggccaggac	ctgaccttct	1860
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acgtgaacaa	cctgaaggcc	tcctcctact	ccatctactc	ccaggcgtcc	gtcatcgcca	2220
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cggacgagta	cggccagggc	gagatccaga	tgtgggtccg	ccccctggac	aacggcgacc	2340
aggtcgtggc	gctgctgaac	ggcggctccg	tgtcccgccc	catgaacacg	accctggagg	2400
agatcttctt	cgactccaac	ctgggctcca	agaagctgac	ctccacctgg	gacatctacg	2460
acctgtgggc	gaaccgcgtc	gacaactcca	cggcgtccgc	catcctgggc	cgcaacaaga	2520
ccgccaccgg	catcctgtac	aacgccaccg	agcagtccta	caaggacggc	ctgtccaaga	2580
acgacacccg	cctgttcggc	cagaagatcg	gctccctgtc	ccccaacgcg	atcctgaaca	2640
cgaccgtccc	cgcccacggc	atcgcgttct	accgcctgcg	cccctcctcc	tgatacaact	2700

tattacgtat	tctgaccggc	gctgatgtgg	cgcggaacgc	gtcgtactct	ttcagacttt	2760
actcttgagg	aattgaacct	ttctcgcttg	ctggcatgta	aacattggcg	caattaattg	2820
tgtgatgaag	aaaggggtggc	acaagatgga	tcgcgaatgt	acgagatcga	caacgatggg	2880
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cccgggtcga	tcaatgttct	gagcggagg	cgaagcgtca	ggaaatcgtc	tcggcagctg	3120
gaagcgcgtg	gaatgcggag	cggagatcga	atcaggatcc	cgctgtctga	acagagcgcg	3180
cagaggaacg	ctgaaggtct	cgcctctgtc	gcacctcagc	gcggcataca	ccacaataac	3240
cacctgacga	atgcgcttgg	ttcttcgtcc	attagcgaag	cgtccggttc	acacacgtgc	3300
cacgttggcg	aggtggcagg	tgacaatgat	cgggtggagct	gatggtcgaa	acgttcacag	3360
cctagggaaat	tcggccgaca	ggacgcgcgt	caaaggtgct	ggtcgtgtat	gccctggccg	3420
gcaggtcgtt	gctgctgctg	gttagtgatt	ccgcaaccct	gattttggcg	tcttattttg	3480
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gccgctcctg	caaggctgcg	tggtggaatt	ggacgtgcag	gtcctgctga	agttcctcca	3660
ccgcctcacc	agcggacaaa	gcaccggtgt	atcagggtccg	tgtcatccac	tctaaagaac	3720
tcgactacga	cctactgatg	gccctagatt	cttcatcaaa	aacgcctgag	acacttgccc	3780
aggattgaaa	ctccctgaag	ggaccaccag	gggccctgag	ttgttccttc	ccccgtggc	3840
gagctgccag	ccaggctgta	cctgtgatcg	aggctggcgg	gaaaataggc	ttcgtgtgct	3900
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gctaatacagc	tatttcctct	tcacgagctg	taattgtccc	aaaattctgg	tctaccgggg	4020
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tgtcgccaac	cctaggatca	gcggcgtagg	atttcgtaat	cattcgtcct	gatggggagc	4260
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tcctaccggg	agctctcgcg	ttccaagtgc	gtgcaggggc	gggggcacct	tttgttggtg	4620
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tcggcggttt	aagatgtaat	gcgccaattt	cttgctgatg	cattcctaga	cacaaagagt	4740
ctctcattcg	agtctcatcg	cggttgtgcg	ctcctcactc	cgtgcagcca	gcagtcgcgg	4800

tcgttcactt	cgcggggggt	gccagggagg	acggacgttt	cggatgagct	ggagcgccgc	4860
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gttgggggtca	ggtcagaagt	cgtgaagtta	caggcctgca	tttgacatc	ctgcgcgcgc	4980
ctctggccgc	ttgtcttaag	acccttgcac	tcgcttcctc	atgaaccccc	atgaactccc	5040
tcctgcaccc	cacagcgtgc	tggtggccaa	caacgggtctg	gcggcgggtca	agttcatccg	5100
gtcgatccgg	tcgtggtcgt	acaagacgtt	tgggaacgag	cgtgcgggtga	agctgatcgc	5160
gatggcgacg	cccgaggaca	tgcgcgcgga	cgcgggagcac	atccgcatgg	cggaccagtt	5220
tgtggaggtc	cccggcggca	agaacgtgca	gaactacgcc	aacgtggggc	tgatcacctc	5280
ggtggcggtg	cgcaccgggg	tggacgcggt	gcctgcagg			5319

<210> 146

<211> 811

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 146

gattcatatc	atcaaatttc	gcatatgttt	cacgagttgc	tcacaacatc	ggcaaagtgcg	60
ttgtttgtcc	ctgtttttac	accttgccag	ggcctgggtca	aagcttgaca	gtttgaccaa	120
attcaggtgg	cctcatctct	ttcgactga	tagacattgc	agatttggaa	gacccagcca	180
gtacattaca	tgcacagcca	tttgctcctg	caccatgaac	ttgccacttt	tgtgcgccgg	240
tcgggggtga	tagctcggca	gccgccgatc	ccaaagggtcc	cgcgggcccag	gggcacgaga	300
ccccccgaca	cgattaaata	gccaaaatca	gtcagaacgg	cacctccacc	ctacccgaat	360
ctgacaaggt	catcaaacgc	gcgaaacaac	ggcgaggggtg	cgttcgggaa	gcgcgcgtag	420
ttgacgcaag	aagcctgggt	caggctggag	ggccgcgaga	agatcgcttc	ctgccgagtc	480
tgcacccacg	cctcgagcgc	accgtccgcg	aacaaccaac	cccttttcgc	gagccctggc	540
attctttcaa	ttgccaagga	tgcacatgtg	acacgtatag	ccattcgggt	ttgtttgtgc	600
ctgcttgact	cgcgccattt	aattgttttg	tgccggtgag	ccgggagtcg	gccactcgtc	660
tccgagccgc	agtcccggcg	ccagtcccc	ggcctctgat	ctgggtccgg	aagggttggt	720
ataggagcag	tctcggtat	ctgaagccc	ttaccagaca	ctttggccgg	ctgctttcca	780
ggcagccgtg	tactcttgcg	cagtcggtac	c			811

<210> 147

<211> 884

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 147

actagtatga	cggtggccaa	tccccggaa	gccccgttcg	acagcgaggg	ttcctcgctg	60
------------	------------	-----------	------------	------------	------------	----

gcgcccgaca atgggtccag caagcccacc aagctgagct ccacccggtc cctgctgtcc	120
atctcctacc gggagctctc gcgttccaag tgcgtacagg ggcgagggca ccttttgttg	180
gtgttgtttg ggcgggcctc ggtactggga ggaggaggaa tgcgtgcaca cctctgcggt	240
tttagatgca atgcgacaag tgcctgctga tgcattttct agacatgaag catctcgtat	300
tcgagtctca acgcgggtgt gcgctcctca ctccgtgcag ccagcagtcg cggtcgttca	360
cttcgcgggg ggtgccaggg aggacggacg tttcggatga gctggagcgc cgcacccctc	420
agtggcaggg cgatcgcgcc atccacaggt cggttgggtg ggaaaggggg agtaccgggg	480
tcaggtcaga agtcgtgcat ttacaggcat gcatctgcac atcgtgcgca cgcgcacgtc	540
tttggccgct tgtctcaaga ctcttgact cgtttcctca tgcaccataa tcaattccct	600
ccccctcgc aaactcacag cgtgctggtg gccacaacg gtctggcggc ggtcaagttc	660
atccggtcga tccggtcgtg gtcgtacaag acgtttggga acgagcgcgc ggtgaagctg	720
attgcgatgg cgacgcccga gggcatgcgc gcggacgcgg agcacatccg catggcggac	780
cagtttgtgg aggtccccgg cggcaagaac gtgcagaact acgccaacgt gggcctgac	840
acctcggtgg cggtcgcac cggggtggac gcggtgcctg cagg	884

<210> 148

<211> 2734

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 148

ggtaccgtaa tcccagaggtt ggccccgctt ccgctggaca cccatcgcat cttccggctc	60
gcccgtgtc gagcaagcgc cctcgtgcgc gcaacccttg tggcgcctgc ccgagagcc	120
gggcataaag gcgagacca caccgaacc agtccaattt gctttctgca ttcactcacc	180
aactttttaca tccacacatc gtactaccac acctgcccag tcggggtttga tttctattgc	240
aaagggtgcgg ggggggttggc gactgcgtg ggttgtgcag ccggccgccg cggctgtacc	300
cagcgatcag gtagcttggg ctgtatcttc tcaagcatta ccttgcctg ggcgtaggtt	360
tgccgctagc accatggcca ccgcatccac tttctcggcg ttcaatgccc gctgcggcga	420
cctgcgtcgc tcggcgggct ccgggccccg gcgcccagcg aggccccctc ccgtgcgcgg	480
gcgcgccgtc caggccgcgg ccacccgctt caagaaggag acgacgacca cccgcgccac	540
gctgacgttc gaccccccca cgaccaactc cgagcgcgcc aagcagcgca agcacaccat	600
cgacccctcc tccccgact tccagcccat cccctccttc gaggagtgtt tcccaagtc	660
cacgaaggag cacaaggagg tggcgcacga ggagtccggc cacgtcctga aggtgccctt	720
ccgccgcgtg cacctgtccg gcggcgagcc cgcttcgac aactacgaca cgtccggccc	780
ccagaacgtc aacgcccaca tcggcctggc gaagctgcgc aaggagtgga tcgaccgccg	840
cgagaagctg ggcacgcccc gctacacgca gatgtactac gcgaagcagg gcatcatcac	900

ggaggagatg	ctgtactgcg	cgacgcgcga	gaagctggac	cccgagttcg	tccgctccga	960
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gatcgtgggc	cgcaagttcc	tgggtgaagg	gaacgcgaac	atcggcaact	ccgccgtggc	1080
ctcctccatc	gaggaggagg	tctacaagg	gcagtggggc	accatgtggg	gcgccgacac	1140
catcatggac	ctgtccacgg	gccgccacat	ccacgagacg	cgcgagtggg	tcctgcgcaa	1200
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cgcgggagaac	ctgaactggg	agggtgttccg	cgagacgctg	atcgagcagg	ccgagcaggg	1320
cgtggactac	ttcacgatcc	acgcggggcgt	gctgctgcgc	tacatcccc	tgaccgccaa	1380
gcgcatgacg	ggcatcgtgt	cccgcggcgg	ctccatccac	gcgaagtgg	gcctggccta	1440
ccacaaggag	aacttcgcct	acgagcactg	ggacgacatc	ctggacatct	gcaaccagta	1500
cgacgtcgcc	ctgtccatcg	gcgacggcct	gcgccccggc	tccatctacg	acgccaacga	1560
cacggcccag	ttcgccgagc	tgctgacca	gggcgagctg	acgcgccgcg	cgtgggagaa	1620
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catgcagaag	cagctggagt	ggtgcaacga	ggcgcccttc	tacaccctgg	gccccctgac	1740
gaccgacatc	gcgcccggct	acgaccacat	cacctccgcc	atcggcgcgg	ccaacatcgg	1800
cgccctgggc	accgccctgc	tgtgctacgt	gacgcccga	gagcacctgg	gcctgcccga	1860
ccgcgacgac	gtgaaggcgg	gcgtcatcgc	ctacaagatc	gccgcccacg	cggccgacct	1920
ggccaagcag	cacccccacg	cccaggcgtg	ggacgacgcg	ctgtccaagg	cgcgcttcga	1980
gttccgctgg	atggaccagt	tcgcgctgtc	cctggacccc	atgacggcga	tgctcttcca	2040
cgacgagacg	ctgcccgcgg	acggcgcgaa	ggtcgccac	ttctgctcca	tgtgcggccc	2100
caagtcttgc	tccatgaaga	tcacggagga	catccgcaag	tacgccgagg	agaacggcta	2160
cggctccgcc	gaggaggcca	tccgccaggg	catggacgcc	atgtccgagg	agttcaacat	2220
cgccaagaag	acgatctccg	gcgagcagca	cggcgaggtc	ggcggcgaga	tctacctgcc	2280
cgagtcctac	gtcaaggccg	cgcagaagtg	ataccttatt	acgtaacaga	cgaccttggc	2340
aggcgtcggg	tagggagggt	gtgggtgatg	cgtctcgatg	ccatcgcacg	catccaacga	2400
ccgtatacgc	atcgtccaat	gaccgtcgg	gtcctctctg	cctccgtttt	gtgagatgtc	2460
tcaggcttgg	tgcatcctcg	ggtggccagc	cacgttgcgc	gtcgtgctgc	ttgcctctct	2520
tgcgctctg	tggactgga	aaatatcatc	gaggccggtt	tttttgcctc	catttccttt	2580
ccgctacatc	ttgaaagcaa	acgacaaacg	aagcagcaag	caaagagcac	gaggacggtg	2640
aacaagtctg	tcacctgtat	acatctat	ccccgcgggt	gcacctactc	tctctcctgc	2700
cccggcagag	tcagctgcct	tacgtgacgg	atcc			2734

<210> 149

<211> 9618

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 149

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atccggtcga tccggtcgtg gtcgtacaag acgtttggga acgagcgcg cgtgaagctg 720
attgcgatgg cgacgcccga gggcatgcgc gcggacgcgg agcacatccg catggcggac 780
cagtttgtgg aggtccccgg cggcaagaac gtgcagaact acgccaacgt gggcctgac 840
acctcggtgg cggtgcgcac cggggtggac gcggtgcctg cagg 884

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<210> 153
 <211> 310
 <212> PRT
 <213> *Alliaria petiolata*

<400> 153
 Met Lys Val Thr Val Val Ser Arg Ser Gly Arg Glu Val Leu Lys Ala
 1 5 10 15
 Pro Leu Asp Leu Pro Asp Ser Ala Thr Val Ala Asp Leu Gln Glu Ala
 20 25 30
 Phe His Lys Arg Ala Lys Lys Phe Tyr Pro Ser Arg Gln Arg Leu Thr
 35 40 45
 Leu Pro Val Ala Pro Gly Ser Lys Glu Lys Pro Val Val Leu Asn Ser
 50 55 60
 Lys Lys Ser Leu Lys Glu Tyr Cys Asp Gly Asn Thr Asp Ser Leu Thr
 65 70 75 80
 Val Val Phe Lys Asp Leu Gly Thr Gln Val Ser Tyr Arg Thr Leu Phe
 85 90 95
 Phe Phe Glu Tyr Leu Gly Pro Leu Leu Ile Tyr Pro Val Phe Tyr Tyr
 100 105 110
 Phe Pro Val Tyr Lys Phe Leu Gly Tyr Gly Glu Asp Arg Val Ile His
 115 120 125
 Pro Val Gln Thr Tyr Ala Met Tyr Tyr Trp Cys Phe His Tyr Phe Lys
 130 135 140
 Arg Ile Leu Glu Thr Phe Phe Val His Arg Phe Ser His Ala Thr Ser
 145 150 155 160
 Pro Ile Ala Asn Val Phe Arg Asn Cys Ala Tyr Tyr Trp Thr Phe Gly
 165 170 175
 Ala Tyr Ile Ala Tyr Tyr Val Asn His Pro Leu Tyr Thr Pro Val Ser
 180 185 190

Asp Leu Gln Met Lys Ile Gly Phe Gly Phe Gly Leu Val Cys Gln Val
 195 200 205
 Ala Asn Phe Tyr Cys His Ile Leu Leu Lys Asn Leu Arg Asp Pro Asn
 210 215 220
 Gly Ser Gly Gly Tyr Gln Ile Pro Arg Gly Phe Leu Phe Asn Ile Val
 225 230 235 240
 Thr Cys Ala Asn Tyr Thr Thr Glu Ile Tyr Gln Trp Leu Gly Phe Asn
 245 250 255
 Ile Ala Thr Gln Thr Val Ala Gly Tyr Val Phe Leu Thr Val Ala Ala
 260 265 270
 Leu Ile Met Thr Asn Trp Ala Leu Gly Lys His Ser Arg Leu Arg Lys
 275 280 285
 Ile Phe Asp Gly Lys Asp Gly Lys Pro Lys Tyr Pro Arg Arg Trp Val
 290 295 300
 Ile Leu Pro Pro Phe Leu
 305 310
 <210> 154
 <211> 310
 <212> PRT
 <213> Arabidopsis thaliana
 <400> 154
 Met Lys Val Thr Val Val Ser Arg Ser Gly Arg Glu Val Leu Lys Ala
 1 5 10 15
 Pro Leu Asp Leu Pro Asp Ser Ala Thr Val Ala Asp Leu Gln Glu Ala
 20 25 30
 Phe His Lys Arg Ala Lys Lys Phe Tyr Pro Ser Arg Gln Arg Leu Thr
 35 40 45
 Leu Pro Val Thr Pro Gly Ser Lys Asp Lys Pro Val Val Leu Asn Ser
 50 55 60
 Lys Lys Ser Leu Lys Glu Tyr Cys Asp Gly Asn Asn Asn Ser Leu Thr
 65 70 75 80
 Val Val Phe Lys Asp Leu Gly Ala Gln Val Ser Tyr Arg Thr Leu Phe
 85 90 95
 Phe Phe Glu Tyr Leu Gly Pro Leu Leu Ile Tyr Pro Val Phe Tyr Tyr
 100 105 110
 Phe Pro Val Tyr Lys Phe Leu Gly Tyr Gly Glu Asp Cys Val Ile His
 115 120 125

Pro Val Gln Thr Tyr Ala Met Tyr Tyr Trp Cys Phe His Tyr Phe Lys
 130 135 140

Arg Ile Leu Glu Thr Phe Phe Val His Arg Phe Ser His Ala Thr Ser
 145 150 155 160

Pro Ile Gly Asn Val Phe Arg Asn Cys Ala Tyr Tyr Trp Ser Phe Gly
 165 170 175

Ala Tyr Ile Ala Tyr Tyr Val Asn His Pro Leu Tyr Thr Pro Val Ser
 180 185 190

Asp Leu Gln Met Lys Ile Gly Phe Gly Phe Gly Leu Val Cys Gln Val
 195 200 205

Ala Asn Phe Tyr Cys His Ile Leu Leu Lys Asn Leu Arg Asp Pro Ser
 210 215 220

Gly Ala Gly Gly Tyr Gln Ile Pro Arg Gly Phe Leu Phe Asn Ile Val
 225 230 235 240

Thr Cys Ala Asn Tyr Thr Thr Glu Ile Tyr Gln Trp Leu Gly Phe Asn
 245 250 255

Ile Ala Thr Gln Thr Ile Ala Gly Tyr Val Phe Leu Ala Val Ala Ala
 260 265 270

Leu Ile Met Thr Asn Trp Ala Leu Gly Lys His Ser Arg Leu Arg Lys
 275 280 285

Ile Phe Asp Gly Lys Asp Gly Lys Pro Lys Tyr Pro Arg Arg Trp Val
 290 295 300

Ile Leu Pro Pro Phe Leu
 305 310

<210> 155
 <211> 310
 <212> PRT
 <213> Crambe abyssinica

<400> 155
 Met Lys Val Thr Val Val Ser Arg Ser Gly Arg Glu Val Leu Lys Ala
 1 5 10 15

Pro Leu Asp Leu Pro Asp Ser Ala Thr Val Ala Asp Leu Gln Glu Ala
 20 25 30

Phe His Lys Arg Ala Lys Lys Phe Tyr Pro Ser Arg Gln Arg Leu Thr
 35 40 45

Leu Pro Val Ala Pro Gly Ser Lys Asp Lys Pro Val Val Leu Asn Ser
 50 55 60

Lys Lys Ser Leu Lys Glu Tyr Cys Asp Gly Asn Thr Asp Ser Leu Thr

<400> 156
Met Lys Val Thr Val Val Ser Arg Ser Gly Arg Glu Val Leu Lys Ala
1 5 10 15

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

290

295

Ile Leu Pro Pro Phe Leu
305 310

<210> 157
<211> 310
<212> PRT
<213> Erysimum allioni

<400> 157
Met Lys Val Thr Val Val Ser Arg Ser Gly Arg Glu Val Leu Lys Ala
1 5 10 15

Pro Leu Asp Leu Pro Asp Ser Ala Thr Val Ala Asp Leu Gln Glu Ala
20 25 30

Phe His Lys Arg Ala Lys Lys Phe Tyr Pro Ser Arg Gln Arg Leu Thr
35 40 45

Leu Pro Val Ala Pro Gly Ser Lys Asp Lys Pro Val Val Leu Asn Ser
50 55 60

Lys Lys Ser Leu Lys Glu Tyr Cys Asp Gly Asn Thr Asp Ser Leu Thr
65 70 75 80

Val Val Phe Lys Asp Leu Gly Ala Gln Val Ser Tyr Arg Thr Leu Phe
85 90 95

Phe Phe Glu Tyr Leu Gly Pro Leu Leu Ile Tyr Pro Val Phe Tyr Tyr
100 105 110

Leu Pro Val Tyr Lys Phe Leu Gly Tyr Gly Glu Asp Arg Val Ile His
115 120 125

Pro Val Gln Thr Tyr Ala Met Tyr Tyr Trp Cys Phe His Tyr Phe Lys
130 135 140

Arg Ile Leu Glu Thr Phe Phe Val His Arg Phe Ser His Ala Thr Ser
145 150 155 160

Pro Ile Gly Asn Val Phe Arg Asn Cys Ala Tyr Tyr Trp Ser Phe Gly
165 170 175

Ala Phe Ile Ala Tyr Tyr Val Asn His Pro Leu Tyr Thr Pro Val Ser
180 185 190

Asp Leu Gln Met Lys Ile Gly Phe Gly Phe Gly Leu Val Cys Gln Val
195 200 205

Ala Asn Phe Tyr Cys His Ile Leu Leu Lys Asn Leu Arg Asp Pro Asn
210 215 220

Gly Ser Gly Gly Tyr Gln Ile Pro Arg Gly Phe Leu Phe Asn Ile Val
225 230 235 240

Thr Cys Ala Asn Tyr Thr Thr Glu Ile Tyr Gln Trp Leu Gly Phe Asn
 245 250 255

 Ile Ala Thr Gln Thr Ile Ala Gly Tyr Val Phe Leu Ala Val Ala Ala
 260 265 270

 Leu Ile Met Thr Asn Trp Ala Leu Gly Lys His Ser Arg Leu Arg Lys
 275 280 285

 Ile Phe Asp Gly Lys Asp Gly Lys Pro Lys Tyr Pro Arg Arg Trp Val
 290 295 300

 Ile Leu Pro Pro Phe Leu
 305 310

 <210> 158
 <211> 305
 <212> PRT
 <213> Prototheca moriformis

 <400> 158
 Met Pro Leu Glu Ile Leu Ile Lys Thr Arg Asp Gly Arg Pro Ala Phe
 1 5 10 15

 Ser Arg Asp Gly Gly Ala Ile Thr Val Asp Ser Thr Ser Ala Thr Val
 20 25 30

 Gln Glu Val Lys Gly Leu Ile Ala Arg Ala Lys Lys Leu Ser Pro Ala
 35 40 45

 Arg Leu Arg Leu Thr Leu Pro Ala Pro Ala Gly Thr Arg Pro Thr Val
 50 55 60

 Leu Glu Asp Lys Lys Thr Leu Gly Asp Tyr Gly Leu His Asp Gly Ala
 65 70 75 80

 Ser Leu Val Leu Lys Asp Leu Gly Pro Gln Ile Gly Tyr Gln Met Val
 85 90 95

 Phe Phe Trp Glu Tyr Phe Gly Pro Leu Ala Ile Tyr Pro Leu Phe Tyr
 100 105 110

 Phe Leu Pro Ser Leu Ile Tyr Gly Arg Ser Thr Glu His Val Phe Ala
 115 120 125

 Gln Lys Ala Ala Leu Ala Phe Trp Thr Phe His Tyr Ala Lys Arg Ile
 130 135 140

 Leu Glu Thr Phe Phe Val His Lys Phe Gly His Ala Thr Met Pro Val
 145 150 155 160

 Arg Asn Leu Val Lys Asn Cys Ser Tyr Tyr Trp Ser Phe Gly Ala Phe
 165 170 175

Ile Ser Tyr Phe Val Asn His Pro Leu Tyr Ala Ala Pro Pro Ala Ala
180 185 190

Gln Thr Ala Val Ala Phe Val Ala Thr Leu Cys Thr Leu Ser Asn
195 200 205

Phe Lys Cys His Leu Ile Leu Ser Asn Leu Arg Ala Pro Gly Gly Ser
210 215 220

Gly Tyr Val Ile Pro Arg Gly Phe Leu Phe Asp Tyr Val Thr Cys Ala
225 230 235 240

Asn Tyr Thr Ala Glu Ile Trp Ser Trp Ile Phe Phe Ser Ile Gly Thr
245 250 255

Gln Cys Leu Pro Ala Leu Ile Phe Thr Val Ala Gly Ala Ala Gln Met
260 265 270

Ala Ile Trp Ala Gly Gly Lys His Arg Arg Leu Lys Lys Leu Phe Asp
275 280 285

Gly Lys Glu Gly Arg Glu Arg Tyr Pro Lys Arg Tyr Ile Met Leu Pro
290 295 300

Pro
305

<210> 159

<211> 305

<212> PRT

<213> Prototheca moriformis

<400> 159

Met Pro Leu Glu Ile Leu Val Lys Thr Arg Asn Gly Arg Pro Ala Phe
1 5 10 15

Ser Arg Asp Gly Gly Ala Ile Thr Val Asp Ser Thr Ser Ala Thr Val
20 25 30

Gln Glu Val Lys Gly Leu Ile Ala Arg Ala Lys Lys Leu Ser Pro Ala
35 40 45

Arg Leu Arg Leu Thr Leu Pro Ala Pro Ala Gly Thr Arg Pro Thr Val
50 55 60

Leu Glu Asp Lys Lys Thr Leu Gly Asp Tyr Gly Leu His Asp Gly Ala
65 70 75 80

Ser Leu Val Leu Lys Asp Leu Gly Pro Gln Ile Gly Tyr Gln Met Val
85 90 95

Phe Phe Trp Glu Tyr Phe Gly Pro Leu Ala Ile Tyr Pro Leu Phe Tyr
100 105 110

Phe Leu Pro Ser Leu Ile Tyr Gly Arg Pro Thr Glu His Val Phe Ala
115 120 125

Gln Lys Ala Ala Leu Ala Phe Trp Thr Phe His Tyr Gly Lys Arg Ile
130 135 140

Leu Glu Ser Phe Phe Val His Lys Phe Gly His Ala Thr Met Pro Val
145 150 155 160

Arg Asn Leu Val Lys Asn Cys Ser Tyr Tyr Trp Ser Phe Gly Ala Phe
165 170 175

Ile Ser Tyr Phe Val Asn His Pro Leu Tyr Ser Ala Pro Pro Ala Ala
180 185 190

Gln Thr Ala Val Ala Phe Val Ala Ala Thr Leu Cys Thr Leu Ser Asn
195 200 205

Phe Lys Cys His Leu Ile Leu Ser Asn Leu Arg Ala Pro Gly Gly Ser
210 215 220

Gly Tyr Val Ile Pro Arg Gly Phe Leu Phe Asp Tyr Val Thr Cys Ala
225 230 235 240

Asn Tyr Thr Ala Glu Ile Trp Ser Trp Ile Phe Phe Ser Ile Gly Thr
245 250 255

Gln Cys Leu Pro Ala Leu Val Phe Thr Val Ala Gly Ala Ala Gln Met
260 265 270

Ala Ile Trp Ala Gly Gly Lys His Cys Arg Leu Lys Lys Leu Phe Asp
275 280 285

Gly Lys Glu Gly Arg Glu Arg Tyr Pro Lys Arg Tyr Ile Met Phe Pro
290 295 300

Pro
305

<210> 160
<211> 221
<212> PRT
<213> Alliaria petiolata

<400> 160
Met Ala Gly Phe Leu Ser Val Val Arg Arg Val Tyr Leu Thr Leu Tyr
1 5 10 15

Asn Trp Ile Val Phe Ala Gly Trp Ala Gln Val Leu Phe Leu Ala Ile
20 25 30

Lys Thr Leu Lys Glu Thr Gly His Glu Asn Val Tyr Asp Ala Ile Glu
35 40 45

Lys Pro Leu Gln Leu Ala Gln Thr Ala Ala Val Leu Glu Ile Leu His

50

55

Gly Leu Val Gly Leu Val Arg Ser Pro Val Ser Ala Thr Leu Pro Gln
65 70 75 80

Ile Gly Ser Arg Leu Phe Leu Thr Trp Gly Ile Leu Tyr Ser Phe Pro
85 90 95

Glu Val Arg Ser His Phe Leu Val Thr Ser Leu Val Ile Ser Trp Ser
100 105 110

Ile Thr Glu Ile Ile Arg Tyr Ser Phe Phe Gly Phe Lys Glu Ala Leu
115 120 125

Gly Phe Ala Pro Ala Trp His Leu Trp Leu Arg Tyr Ser Ser Phe Leu
130 135 140

Leu Leu Tyr Pro Thr Gly Ile Thr Ser Glu Val Gly Leu Ile Tyr Leu
145 150 155 160

Ala Leu Pro His Ile Lys Thr Ser Glu Met Tyr Ser Val Arg Met Pro
165 170 175

Asn Thr Leu Asn Phe Ser Phe Asp Tyr Phe Tyr Ala Thr Ile Leu Val
180 185 190

Leu Ala Ile Tyr Val Pro Gly Ser Pro His Met Tyr Arg Tyr Met Leu
195 200 205

Gly Gln Arg Lys Arg Ala Leu Ser Lys Ser Lys Arg Glu
210 215 220

<210> 161
<211> 221
<212> PRT
<213> Arabidopsis thaliana

<400> 161
Met Ala Gly Phe Leu Ser Val Val Arg Arg Val Tyr Leu Thr Leu Tyr
1 5 10 15

Asn Trp Ile Val Phe Ala Gly Trp Ala Gln Val Leu Tyr Leu Ala Ile
20 25 30

Thr Thr Leu Lys Glu Thr Gly Tyr Glu Asn Val Tyr Asp Ala Ile Glu
35 40 45

Lys Pro Leu Gln Leu Ala Gln Thr Ala Ala Val Leu Glu Ile Leu His
50 55 60

Gly Leu Val Gly Leu Val Arg Ser Pro Val Ser Ala Thr Leu Pro Gln
65 70 75 80

Ile Gly Ser Arg Leu Phe Leu Thr Trp Gly Ile Leu Tyr Ser Phe Pro
85 90 95

Glu Val Arg Ser His Phe Leu Val Thr Ser Leu Val Ile Ser Trp Ser
 100 105 110
 Ile Thr Glu Ile Ile Arg Tyr Ser Phe Phe Gly Phe Lys Glu Ala Leu
 115 120 125
 Gly Phe Ala Pro Ser Trp His Leu Trp Leu Arg Tyr Ser Ser Phe Leu
 130 135 140
 Leu Leu Tyr Pro Thr Gly Ile Thr Ser Glu Val Gly Leu Ile Tyr Leu
 145 150 155 160
 Ala Leu Pro His Ile Lys Thr Ser Glu Met Tyr Ser Val Arg Met Pro
 165 170 175
 Asn Ile Leu Asn Phe Ser Phe Asp Phe Phe Tyr Ala Thr Ile Leu Val
 180 185 190
 Leu Ala Ile Tyr Val Pro Gly Ser Pro His Met Tyr Arg Tyr Met Leu
 195 200 205
 Gly Gln Arg Lys Arg Ala Leu Ser Lys Ser Lys Arg Glu
 210 215 220
 <210> 162
 <211> 221
 <212> PRT
 <213> Crambe abyssinica
 <400> 162
 Met Ala Gly Ser Leu Ser Phe Val Arg Arg Val Tyr Leu Thr Leu Tyr
 1 5 10 15
 Asn Trp Ile Val Phe Ala Gly Trp Ala Gln Val Leu Tyr Phe Ala Val
 20 25 30
 Lys Thr Leu Lys Glu Ser Gly His Glu Asn Val Tyr Asp Ala Val Glu
 35 40 45
 Lys Pro Leu Gln Leu Ala Gln Thr Ala Ala Val Leu Glu Ile Leu His
 50 55 60
 Gly Leu Val Gly Leu Val Arg Ser Pro Val Ser Ala Thr Leu Pro Gln
 65 70 75 80
 Ile Gly Ser Arg Leu Phe Leu Thr Trp Gly Ile Leu Tyr Ser Phe Pro
 85 90 95
 Glu Val Gln Ser His Phe Leu Val Thr Ser Leu Val Ile Ser Trp Ser
 100 105 110
 Ile Thr Glu Ile Ile Arg Tyr Ser Phe Phe Gly Leu Lys Glu Ala Leu
 115 120 125

Gly Phe Ala Pro Ser Trp His Leu Trp Leu Arg Tyr Ser Ser Phe Leu
 130 135 140

Val Leu Tyr Pro Thr Gly Ile Thr Ser Glu Val Gly Leu Ile Tyr Leu
 145 150 155 160

Ala Leu Pro His Ile Lys Thr Ser Glu Met Tyr Ser Val Arg Met Pro
 165 170 175

Asn Thr Leu Asn Phe Ser Phe Asp Phe Phe Tyr Ala Thr Ile Leu Val
 180 185 190

Leu Ala Ile Tyr Val Pro Gly Ser Pro His Met Tyr Arg Tyr Met Leu
 195 200 205

Gly Gln Arg Lys Arg Ala Leu Ser Lys Ser Lys Arg Glu
 210 215 220

<210> 163

<211> 221

<212> PRT

<213> Crambe cordifolia

<400> 163

Met Ala Gly Ser Phe Ser Phe Ile Arg Arg Val Tyr Leu Thr Leu Tyr
 1 5 10 15

Asn Trp Ile Val Phe Ala Gly Trp Ala Gln Val Leu Tyr Phe Ala Val
 20 25 30

Lys Thr Leu Lys Glu Thr Gly His Glu Asn Val Tyr Asp Ala Val Glu
 35 40 45

Lys Pro Leu Gln Leu Ala Gln Thr Ala Ala Val Leu Glu Ile Leu His
 50 55 60

Gly Leu Val Gly Leu Val Arg Ser Pro Val Ser Ala Thr Leu Pro Gln
 65 70 75 80

Ile Gly Ser Arg Leu Phe Leu Thr Trp Gly Ile Leu Tyr Ser Phe Pro
 85 90 95

Glu Val Gln Ser His Phe Leu Val Thr Ser Leu Val Ile Ser Trp Ser
 100 105 110

Ile Thr Glu Ile Ile Arg Tyr Ser Phe Phe Gly Leu Lys Glu Ala Leu
 115 120 125

Gly Phe Ala Pro Ser Trp His Leu Trp Leu Arg Tyr Ser Ser Phe Leu
 130 135 140

Val Leu Tyr Pro Thr Gly Ile Thr Ser Glu Val Gly Leu Ile Tyr Leu
 145 150 155 160

Ala Leu Pro His Ile Lys Thr Ser Glu Met Tyr Ser Val Arg Met Pro
 165 170 175

Asn Thr Leu Asn Phe Ser Phe Asp Phe Phe Tyr Ala Thr Ile Leu Val
 180 185 190

Leu Ala Ile Tyr Val Pro Gly Ser Pro His Met Tyr Arg Tyr Met Leu
 195 200 205

Gly Gln Arg Lys Arg Ala Leu Ser Lys Ser Lys Arg Glu
 210 215 220

<210> 164
 <211> 221
 <212> PRT
 <213> Erysimum allioni

<400> 164
 Met Ala Gly Phe Leu Ser Val Val Arg Arg Val Tyr Leu Thr Leu Tyr
 1 5 10 15

Asn Trp Ile Val Phe Ala Gly Trp Ala Gln Val Leu Phe Leu Ala Ile
 20 25 30

Lys Thr Leu Lys Glu Thr Gly His Glu Asn Val Phe Asp Ala Ile Glu
 35 40 45

Lys Pro Leu Gln Leu Ala Gln Thr Ala Ala Val Leu Glu Ile Leu His
 50 55 60

Gly Leu Val Gly Leu Val Arg Ser Pro Val Ser Ala Thr Leu Pro Gln
 65 70 75 80

Ile Gly Ser Arg Leu Phe Leu Thr Trp Gly Ile Leu Tyr Ser Phe Pro
 85 90 95

Glu Val Arg Ser His Phe Leu Val Thr Ser Leu Val Ile Ser Trp Ser
 100 105 110

Ile Thr Glu Ile Ile Arg Tyr Ser Phe Phe Gly Phe Lys Glu Ala Leu
 115 120 125

Gly Phe Ala Pro Ala Trp His Leu Trp Leu Arg Tyr Ser Ser Phe Leu
 130 135 140

Leu Leu Tyr Pro Thr Gly Ile Thr Ser Glu Val Gly Leu Ile Tyr Leu
 145 150 155 160

Ala Leu Pro His Met Lys Thr Ser Glu Met Tyr Ser Val Arg Met Pro
 165 170 175

Asn Thr Leu Asn Phe Ser Phe Asp Tyr Phe Tyr Ala Thr Ile Leu Val
 180 185 190

Leu Ala Ile Tyr Val Pro Gly Ser Pro His Met Tyr Arg Tyr Met Leu

195

200

Gly Gln Arg Lys Arg Ala Leu Ser Lys Ser Lys Arg Glu
210 215 220

<210> 165
<211> 221
<212> PRT
<213> Erysimum sp.

<220>
<221> source
<223> /note="Erysimum golden gem"

<400> 165
Met Ala Gly Phe Leu Ser Val Val Arg Arg Val Tyr Leu Thr Leu Tyr
1 5 10 15

Asn Trp Ile Val Phe Ala Gly Trp Ala Gln Val Leu Phe Leu Ala Ile
20 25 30

Lys Thr Leu Lys Glu Thr Gly His Glu Asn Val Tyr Asp Ala Ile Glu
35 40 45

Lys Pro Leu Gln Leu Ala Gln Thr Ala Ala Val Leu Glu Ile Leu His
50 55 60

Gly Leu Val Gly Leu Val Arg Ser Pro Val Ser Ala Thr Leu Pro Gln
65 70 75 80

Ile Gly Ser Arg Leu Phe Leu Thr Trp Gly Ile Leu Tyr Ser Phe Pro
85 90 95

Glu Val Arg Ser His Phe Leu Val Thr Ser Leu Val Ile Ser Trp Ser
100 105 110

Ile Thr Glu Ile Ile Arg Tyr Ser Phe Phe Gly Phe Lys Glu Ala Leu
115 120 125

Gly Phe Ala Pro Ala Trp His Leu Trp Leu Arg Tyr Ser Ser Phe Leu
130 135 140

Leu Leu Tyr Pro Thr Gly Ile Thr Ser Glu Val Gly Leu Ile Tyr Leu
145 150 155 160

Ala Leu Pro His Met Lys Thr Ser Glu Met Tyr Asn Val Arg Met Pro
165 170 175

Asn Thr Leu Asn Phe Ser Phe Asp Tyr Phe Tyr Ala Thr Ile Leu Val
180 185 190

Leu Ala Ile Tyr Val Pro Gly Ser Pro His Met Tyr Arg Tyr Met Leu
195 200 205

Gly Gln Arg Lys Arg Ala Leu Ser Lys Ser Lys Arg Glu
210 215 220

<210> 166
 <211> 221
 <212> PRT
 <213> Erysimum sp.

<220>
 <221> source
 <223> /note="Erysimum helveticum"

<400> 166
 Met Ala Gly Phe Leu Ser Val Val Arg Arg Val Tyr Leu Thr Leu Tyr
 1 5 10 15
 Asn Trp Ile Val Phe Ala Gly Trp Ala Gln Val Leu Phe Leu Ala Ile
 20 25 30
 Lys Thr Leu Lys Glu Thr Gly His Glu Asn Val Tyr Asp Ala Ile Glu
 35 40 45
 Lys Pro Leu Gln Leu Ala Gln Thr Ala Ala Val Leu Glu Ile Leu His
 50 55 60
 Gly Leu Val Gly Leu Val Arg Ser Pro Val Ser Ala Thr Leu Pro Gln
 65 70 75 80
 Ile Gly Ser Arg Leu Phe Leu Thr Trp Gly Ile Leu Tyr Ser Phe Pro
 85 90 95
 Glu Val Arg Ser His Phe Leu Val Thr Ser Leu Val Ile Ser Trp Ser
 100 105 110
 Ile Thr Glu Ile Ile Arg Tyr Ser Phe Phe Gly Phe Lys Glu Ala Leu
 115 120 125
 Gly Phe Ala Pro Ala Trp His Leu Trp Leu Arg Tyr Ser Ser Phe Leu
 130 135 140
 Leu Leu Tyr Pro Thr Gly Ile Thr Ser Glu Val Gly Leu Ile Tyr Leu
 145 150 155 160
 Ala Leu Pro His Ile Lys Thr Ser Glu Met Tyr Ser Val Arg Met Pro
 165 170 175
 Asn Thr Leu Asn Phe Ser Phe Asp Tyr Phe Tyr Ala Thr Ile Leu Val
 180 185 190
 Leu Ala Ile Tyr Val Pro Gly Ser Pro His Met Tyr Arg Tyr Met Leu
 195 200 205
 Gly Gln Arg Lys Arg Ala Leu Ser Lys Ser Lys Arg Glu
 210 215 220

<210> 167
 <211> 235
 <212> PRT

<213> *Prototheca moriformis*

<400> 167

Met Ser Leu Arg Ser Ala Tyr Leu Thr Ile Tyr Asn Gly Ser Leu Ala
1 5 10 15

Leu Gly Trp Ala Tyr Leu Leu Trp Leu Ser Val Ser Val Leu Ala Ala
20 25 30

Gly Gly Ser Leu Trp Asp Leu Trp Lys Thr Val Glu Val Pro Leu Lys
35 40 45

Ile Ile Gln Thr Ala Ala Ile Ala Glu Val Val His Ala Ser Val Gly
50 55 60

Ile Val Arg Ser Pro Pro Leu Val Thr Ala Leu Gln Val Ala Ser Arg
65 70 75 80

Val Phe Leu Val Trp Gly Val Val Asn Leu Ala Pro Glu Val Ala Thr
85 90 95

Gly Ser Gln Val Ala Ala Val Pro Ile Pro Gly Val Gly Arg Val Gly
100 105 110

Leu Ser Phe Ala Thr Leu Val Ile Ala Trp Ala Leu Ser Glu Ile Ile
115 120 125

Arg Tyr Gly His Phe Ala Ala Lys Glu Ala Gly Ile Ala Ser Lys Leu
130 135 140

Leu Leu Trp Leu Arg Tyr Thr Gly Phe Leu Val Leu Tyr Pro Leu Gly
145 150 155 160

Val Ser Ser Glu Leu Thr Met Val Tyr Leu Val Ala Pro Tyr Val Lys
165 170 175

Lys His Gly Ile Leu Ser Leu Glu Met Pro Asn Ala Ala Asn Phe Ala
180 185 190

Phe Ser Tyr Tyr Ala Ala Leu Trp Ile Val Ser Leu Thr Tyr Ile Pro
195 200 205

Gly Phe Pro Met Leu Tyr Gly Tyr Met Leu Lys Gln Arg Lys Lys Met
210 215 220

Leu Gly Gly Gly Ala Lys Ala Lys Lys Leu Ala
225 230 235

<210> 168

<211> 318

<212> PRT

<213> *Alliaria petiolata*

<400> 168

Met Glu Ile Cys Thr Tyr Phe Lys Ser Gln Pro Thr Trp Leu Leu Ile
1 5 10 15

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

290

295

Ile Arg Lys Lys Gly Leu Gln Lys Asp Ser Met Lys Lys Glu
305 310 315

<210> 169
<211> 318
<212> PRT
<213> Arabidopsis thaliana

<400> 169
Met Glu Ile Cys Thr Tyr Phe Lys Ser Gln Pro Thr Trp Leu Leu Ile
1 5 10 15

Leu Phe Val Leu Gly Ser Ile Ser Ile Phe Lys Phe Ile Phe Thr Leu
20 25 30

Leu Arg Ser Phe Tyr Ile Tyr Phe Leu Arg Pro Ser Lys Asn Leu Arg
35 40 45

Arg Tyr Gly Ser Trp Ala Ile Ile Thr Gly Pro Thr Asp Gly Ile Gly
50 55 60

Lys Ala Phe Ala Phe Gln Leu Ala Gln Lys Gly Leu Asn Leu Ile Leu
65 70 75 80

Val Ala Arg Asn Pro Asp Lys Leu Lys Asp Val Ser Asp Ser Ile Arg
85 90 95

Ser Lys Tyr Ser Gln Thr Gln Ile Leu Thr Val Val Met Asp Phe Ser
100 105 110

Gly Asp Ile Asp Glu Gly Val Lys Arg Ile Lys Glu Ser Ile Glu Gly
115 120 125

Leu Asp Val Gly Ile Leu Ile Asn Asn Ala Gly Met Ser Tyr Pro Tyr
130 135 140

Ala Lys Tyr Phe His Glu Val Asp Glu Glu Leu Ile Asn Asn Leu Ile
145 150 155 160

Lys Ile Asn Val Glu Gly Thr Thr Lys Val Thr Gln Ala Val Leu Pro
165 170 175

Asn Met Leu Lys Arg Lys Lys Gly Ala Ile Ile Asn Met Gly Ser Gly
180 185 190

Ala Ala Ala Leu Ile Pro Ser Tyr Pro Phe Tyr Ser Val Tyr Ala Gly
195 200 205

Ala Lys Thr Tyr Val Asp Gln Phe Thr Lys Cys Leu His Val Glu Tyr
210 215 220

Lys Lys Ser Gly Ile Asp Val Gln Cys Gln Val Pro Leu Tyr Val Ala
225 230 235 240

Thr Lys Met Thr Lys₂₄₅ Ile Arg Arg Ala Ser₂₅₀ Phe Leu Val Ala Ser₂₅₅ Pro
 Glu Gly Tyr Ala₂₆₀ Lys Ala Ala Leu Arg₂₆₅ Phe Val Gly Tyr Glu₂₇₀ Ala Gln
 Cys Thr Pro₂₇₅ Tyr Trp Pro His Ala₂₈₀ Leu Met Gly Ala Val₂₈₅ Val Ser Ala
 Leu Pro₂₉₀ Glu Ser Val Phe Glu₂₉₅ Ser Phe Asn Ile Lys₃₀₀ Arg Cys Leu Gln
 Ile Arg Lys Lys Gly Leu₃₁₀ Gln Lys Asp Ser Met₃₁₅ Lys Lys Glu
 305
 <210> 170
 <211> 319
 <212> PRT
 <213> Brassica napus
 <400> 170
 Met Glu Ile Cys₅ Thr Tyr Phe Lys Ser Gln₁₀ Pro Thr Trp Leu₁₅ Val
 1
 Leu Phe Ser Leu₂₀ Gly Ser Ile Ser Ile₂₅ Leu Arg Phe Thr Phe₃₀ Thr Leu
 Leu Thr Ser₃₅ Leu Tyr Ile Tyr Phe Leu Arg Pro Gly Lys₄₅ Asn Leu Arg
 Arg Tyr Gly Ser Trp Ala Ile₅₅ Ile Thr Gly Pro Thr₆₀ Asp Gly Ile Gly
 50
 Lys Ala Phe Ala Phe Gln₇₀ Leu Ala Gln Lys Gly₇₅ Leu Asn Leu Val Leu₈₀
 65
 Val Ala Arg Asn₈₅ Pro Asp Lys Leu Lys Asp₉₀ Val Ser Asp Ser Ile₉₅ Gln
 Ala Lys Tyr Ser₁₀₀ Asn Thr Gln Ile Lys₁₀₅ Thr Val Val Met Asp₁₁₀ Phe Ser
 Gly Asp Ile₁₁₅ Asp Gly Gly Val Arg₁₂₀ Arg Ile Lys Glu Ala₁₂₅ Ile Glu Gly
 Leu Glu Val Gly Ile Leu Ile₁₃₅ Asn Asn Ala Gly Val₁₄₀ Ser Tyr Pro Tyr
 130
 Ala Lys Tyr Phe His Glu₁₅₀ Val Asp Glu Glu Met₁₅₅ Leu Gly Asn Leu Ile₁₆₀
 145
 Lys Ile Asn Val Glu₁₆₅ Gly Thr Thr Lys Val₁₇₀ Thr Gln Ala Val Leu₁₇₅ Val
 165

Asn Met Leu Lys Arg Lys Arg Gly Ala Ile Val Asn Met Gly Ser Gly
 180 185 190
 Ala Ala Ala Leu Ile Pro Ser Tyr Pro Phe Tyr Ser Val Tyr Ala Gly
 195 200 205
 Ala Lys Thr Tyr Val Asp Gln Phe Ser Arg Cys Leu His Val Glu Tyr
 210 215 220
 Lys Lys Ser Gly Ile Asp Val Gln Cys Gln Val Pro Leu Tyr Val Ala
 225 230 235 240
 Thr Lys Met Thr Lys Ile Arg Arg Ala Ser Phe Leu Val Ala Ser Pro
 245 250 255
 Glu Gly Tyr Ala Lys Ala Ala Leu Arg Phe Val Gly Tyr Glu Pro Arg
 260 265 270
 Cys Thr Pro Tyr Trp Pro His Ala Leu Met Gly Tyr Val Val Ser Ala
 275 280 285
 Leu Pro Glu Ser Val Phe Glu Ser Phe Asn Ile Lys Arg Cys Leu Gln
 290 295 300
 Ile Arg Lys Lys Gly Met Leu Lys Asp Ser Ile Ser Lys Lys Glu
 305 310 315
 <210> 171
 <211> 319
 <212> PRT
 <213> Brassica napus
 <400> 171
 Met Glu Ile Cys Thr Tyr Phe Lys Ser Gln Pro Thr Trp Leu Leu Val
 1 5 10 15
 Leu Phe Ser Leu Gly Ser Ile Ser Ile Leu Arg Phe Thr Leu Thr Leu
 20 25 30
 Leu Thr Ser Leu Tyr Ile Tyr Phe Leu Arg Pro Gly Lys Asn Leu Arg
 35 40 45
 Arg Tyr Gly Ser Trp Ala Ile Ile Thr Gly Pro Thr Asp Gly Ile Gly
 50 55 60
 Lys Ala Phe Ala Phe Gln Leu Ala Gln Lys Gly Leu His Leu Val Leu
 65 70 75 80
 Val Ala Arg Asn Pro Asp Lys Leu Lys Ala Val Ser Asp Ser Ile Gln
 85 90 95
 Ala Lys His Ser Thr Thr Gln Ile Lys Thr Val Leu Met Asp Phe Ser
 100 105 110

Gly Asp Ile Asp Ala Gly Val Arg Arg Ile Lys Glu Ala Ile Glu Gly
115 120 125

Leu Glu Val Gly Ile Leu Ile Asn Asn Ala Gly Val Ser Tyr Pro Tyr
130 135 140

Ala Lys Tyr Phe His Glu Val Asp Glu Glu Leu Leu Gly Asn Leu Ile
145 150 155 160

Lys Ile Asn Val Glu Gly Thr Thr Lys Val Thr Gln Ala Val Leu Val
165 170 175

Asn Met Leu Lys Arg Lys Arg Gly Ala Ile Val Asn Met Gly Ser Gly
180 185 190

Ala Ala Ala Leu Ile Pro Ser Tyr Pro Phe Tyr Ser Val Tyr Ala Gly
195 200 205

Ala Lys Thr Tyr Val Asp Gln Phe Ser Arg Cys Leu His Val Glu Tyr
210 215 220

Lys Lys Ser Gly Ile Asp Val Gln Cys Gln Val Pro Leu Tyr Val Ala
225 230 235 240

Thr Lys Met Thr Lys Ile Arg Arg Ala Ser Phe Leu Val Ala Ser Pro
245 250 255

Glu Gly Tyr Ala Lys Ala Ala Leu Arg Phe Val Gly Tyr Glu Pro Arg
260 265 270

Cys Thr Pro Tyr Trp Pro His Ala Leu Met Gly Tyr Val Val Ser Ala
275 280 285

Leu Pro Glu Ser Val Phe Glu Ser Phe Asn Ile Lys Arg Cys Leu Gln
290 295 300

Ile Arg Lys Lys Gly Met Leu Lys Asp Ser Ser Ser Lys Lys Glu
305 310 315

<210> 172

<211> 318

<212> PRT

<213> Crambe abyssinica

<400> 172

Met Glu Ile Cys Thr Tyr Phe Lys Ser Gln Pro Ser Trp Leu Leu Leu
1 5 10 15

Leu Phe Phe Leu Gly Ser Leu Gln Ile Leu Lys Ser Thr Phe Ser Leu
20 25 30

Leu Lys Ser Leu Tyr Ile Tyr Phe Leu Arg Pro Gly Lys Asn Leu Arg
35 40 45

Arg Tyr Gly Ser Trp Ala Ile Ile Thr Gly Pro Thr Asp Gly Ile Gly

50

55

Lys Ala Phe Ala Phe Gln Leu Ala His Lys Gly Leu Asn Leu Val Leu
65 70 75 80

Val Ala Arg Asn Pro Asp Lys Leu Lys Asp Val Ser Asp Ser Ile Arg
85 90 95

Ser Lys His Ser Asn Val Gln Ile Lys Thr Val Ile Met Asp Phe Ser
100 105 110

Gly Asp Val Asp Asp Gly Val Arg Arg Ile Lys Glu Thr Ile Glu Gly
115 120 125

Leu Glu Val Gly Ile Leu Ile Asn Asn Ala Gly Met Ser Tyr Pro Tyr
130 135 140

Ala Lys Tyr Phe His Glu Val Asp Glu Glu Leu Val Asn Gly Leu Ile
145 150 155 160

Lys Ile Asn Val Glu Gly Thr Thr Lys Val Thr Gln Ala Val Leu Pro
165 170 175

Gly Met Leu Glu Arg Lys Arg Gly Ala Ile Val Asn Met Gly Ser Gly
180 185 190

Ala Ala Ala Leu Ile Pro Ser Tyr Pro Phe Tyr Ser Val Tyr Ala Gly
195 200 205

Ala Lys Thr Tyr Val Asp Gln Phe Thr Arg Cys Leu His Val Glu Tyr
210 215 220

Lys Lys Ser Gly Ile Asp Val Gln Cys Gln Val Pro Leu Tyr Val Ala
225 230 235 240

Thr Lys Met Thr Lys Ile Arg Arg Ala Ser Phe Leu Val Ala Ser Pro
245 250 255

Glu Gly Tyr Ala Lys Ala Ala Leu Arg Phe Val Gly Tyr Glu Ala Arg
260 265 270

Cys Thr Pro Tyr Trp Pro His Ala Leu Met Gly Tyr Val Val Ser Ala
275 280 285

Leu Pro Gln Ser Val Phe Glu Ser Phe Asn Ile Lys Arg Cys Leu Gln
290 295 300

Ile Arg Lys Lys Gly Met Leu Lys Asp Ser Arg Lys Lys Glu
305 310 315

<210> 173

<211> 318

<212> PRT

<213> Crambe cordifolia

<400> 173

Met Glu Ile Cys Thr Tyr Phe Lys Ser Gln Pro Ser Trp Leu Leu Val
 1 5 10 15

 Leu Phe Ala Leu Gly Ser Leu Gln Ile Leu Lys Phe Thr Phe Ser Leu
 20 25 30

 Leu Thr Ser Leu Tyr Ile Tyr Phe Leu Arg Pro Gly Lys Asn Leu Arg
 35 40 45

 Arg Tyr Gly Ser Trp Ala Ile Ile Thr Gly Pro Thr Asp Gly Ile Gly
 50 55 60

 Lys Ala Phe Ala Phe Gln Leu Ala His Lys Gly Leu Asn Leu Val Leu
 65 70 75 80

 Val Ala Arg Asn Pro Asp Lys Leu Arg Asp Val Ser Asp Ser Ile Arg
 85 90 95

 Ser Lys Tyr Ser Asn Val Glu Ile Lys Thr Val Leu Met Asp Phe Ser
 100 105 110

 Gly Asp Val Asp Asp Gly Val Arg Arg Ile Lys Glu Thr Ile Glu Gly
 115 120 125

 Leu Glu Val Gly Ile Leu Ile Asn Asn Ala Gly Met Ser Tyr Pro Tyr
 130 135 140

 Ala Lys Tyr Phe His Glu Val Asp Glu Glu Leu Val Asn Gly Leu Ile
 145 150 155 160

 Lys Ile Asn Val Glu Gly Thr Thr Lys Val Thr Gln Ala Val Leu Pro
 165 170 175

 Gly Met Leu Lys Arg Lys Arg Gly Ala Ile Val Asn Met Gly Ser Gly
 180 185 190

 Ala Ala Ala Leu Ile Pro Ser Tyr Pro Phe Tyr Ser Val Tyr Ala Gly
 195 200 205

 Ala Lys Thr Tyr Val Asp Gln Phe Thr Arg Cys Leu His Val Glu Tyr
 210 215 220

 Lys Lys Ser Gly Ile Asp Val Gln Cys Gln Val Pro Leu Tyr Val Ala
 225 230 235 240

 Thr Lys Met Thr Ser Ile Arg Arg Ala Ser Phe Leu Val Ala Ser Pro
 245 250 255

 Glu Gly Tyr Ala Lys Ala Ala Leu Arg Phe Val Gly Tyr Glu Ala Arg
 260 265 270

 Cys Thr Pro Tyr Trp Pro His Ala Leu Met Gly Tyr Val Val Ser Ala

275

280

Leu Pro Glu Ser Val Phe Glu Ser Phe Asn Ile Lys Arg Cys Leu Gln
290 295 300

Ile Arg Lys Lys Gly Met Leu Lys Asp Ser Arg Lys Lys Glu
305 310 315

<210> 174

<211> 318

<212> PRT

<213> Erysimum allioni

<400> 174

Met Glu Ile Cys Thr Tyr Phe Lys Ser Gln Pro Thr Trp Leu Leu Phe
1 5 10 15

Leu Phe Ala Leu Gly Ser Ile Ser Ile Phe Lys Phe Ile Phe Ser Leu
20 25 30

Leu Arg Ser Phe Tyr Ile Tyr Phe Leu Arg Pro Ala Lys Asn Leu Arg
35 40 45

Arg Tyr Gly Ser Trp Ala Ile Val Thr Gly Pro Thr Asp Gly Ile Gly
50 55 60

Lys Ala Phe Ala Phe Gln Leu Ala Gln Lys Gly Leu Asn Leu Val Leu
65 70 75 80

Val Ala Arg Asn Pro Asp Lys Leu Asn Asp Val Ser Asp Ser Ile Arg
85 90 95

Ser Lys Tyr Ser Asn Ile Gln Ile Lys Thr Val Ile Met Asp Phe Ser
100 105 110

Gly Asp Ile Asp Glu Gly Val Lys Arg Ile Lys Glu Thr Ile Glu Gly
115 120 125

Leu Glu Ile Gly Ile Leu Ile Asn Asn Ala Gly Met Ser Tyr Pro Tyr
130 135 140

Ala Lys Tyr Phe His Glu Val Asp Glu Glu Met Leu Thr Asn Leu Ile
145 150 155 160

Lys Ile Asn Val Glu Gly Thr Thr Lys Val Thr Gln Ala Val Leu Pro
165 170 175

Ile Met Leu Gln Arg Lys Arg Gly Ala Ile Val Asn Met Gly Ser Gly
180 185 190

Ala Ala Ala Leu Ile Pro Ser Tyr Pro Phe Tyr Ser Val Tyr Ala Gly
195 200 205

Ala Lys Thr Tyr Val Asp Gln Phe Thr Arg Cys Leu His Val Glu Tyr
210 215 220

Lys Lys Ser Gly Ile Asp Val Gln Cys Gln Val Pro Leu Tyr Val Ala
 225 230 235 240
 Thr Lys Met Thr Ser Ile Arg Arg Ala Ser Phe Leu Val Ala Ser Pro
 245 250 255
 Glu Gly Tyr Ala Lys Ala Ala Leu Arg Phe Val Gly Tyr Glu Ala Arg
 260 265 270
 Cys Thr Pro Tyr Trp Pro His Ala Leu Met Gly Phe Val Val Ser Ala
 275 280 285
 Leu Pro Glu Ser Val Phe Glu Ser Phe Asn Ile Lys Arg Cys Leu Gln
 290 295 300
 Ile Arg Lys Lys Gly Leu Leu Lys Asp Ser Arg Lys Lys Glu
 305 310 315
 <210> 175
 <211> 339
 <212> PRT
 <213> Prototheca moriformis
 <400> 175
 Met Asp Ala Gln Gly Tyr Leu Val Lys Ala Ser Glu Ser Pro Ala Trp
 1 5 10 15
 Thr Tyr Leu Val Leu Leu Ala Ser Ala Leu Phe Ala Ile Lys Val Val
 20 25 30
 Gly Phe Val Leu Thr Val Leu Gly Gly Leu Tyr Ala His Phe Leu Arg
 35 40 45
 Lys Gly Lys Lys Leu Arg Arg Tyr Gly Asp Trp Ala Val Val Thr Gly
 50 55 60
 Ala Thr Asp Gly Ile Gly Lys Ala Tyr Ala Glu Ala Leu Ala Lys Gln
 65 70 75 80
 Lys Leu Arg Leu Val Leu Ile Ser Arg Thr Glu Ser Arg Leu Glu Glu
 85 90 95
 Glu Ala Arg Leu Leu Gln Asp Lys Phe Gly Val Glu Val Lys Ile Ile
 100 105 110
 Pro Ala Asp Leu Ser Ser Ser Asp Glu Ala Val Phe Ala Arg Ile Gly
 115 120 125
 Lys Gly Leu Glu Gly Leu Asp Ile Gly Ile Leu Val Asn Asn Ala Gly
 130 135 140
 Met Ser Tyr Pro His Pro Glu Tyr Leu His Leu Val Asp Asp Glu Thr
 145 150 155 160

Leu Thr Asn Leu Ile Asn Leu Asn Val Ala Thr Leu Thr Lys Leu Cys
165 170 175

Lys Met Val Leu Gly Gly Met Lys Glu Arg Gly Arg Gly Leu Val Val
180 185 190

Asn Val Gly Ser Gly Val Ala Ser Ala Ile Pro Ser Gly Pro Leu Leu
195 200 205

Ser Ala Tyr Thr Ala Ser Lys Ala Tyr Val Asp Gln Leu Ser Glu Ser
210 215 220

Leu Asn Asp Glu Tyr Lys Glu Phe Gly Val Gln Val Gln Asn Gln Ala
225 230 235 240

Pro Leu Phe Val Ala Thr Lys Met Ser Lys Ile Arg Lys Pro Arg Ile
245 250 255

Asp Ala Pro Thr Pro Gly Thr Trp Ala Ala Ala Ala Val Arg Ala Met
260 265 270

Gly Phe Glu Thr Leu Ser Phe Pro Tyr Trp Phe His Ala Leu Gln Ala
275 280 285

Ala Val Val Glu Arg Leu Pro Glu Ala Met Ile Arg Tyr Gln Val Met
290 295 300

Gln Ile His Arg Ser Leu Arg Arg Ala Ala Tyr Lys Lys Lys Ala Arg
305 310 315 320

Ala Ser Ala Ala Ala Leu Ala Asp Glu Gly Val Ser Ala Glu Pro Lys
325 330 335

Lys Asp Leu

<210> 176

<211> 326

<212> PRT

<213> Zea mays

<400> 176

Met Ala Gly Thr Cys Ala His Val Glu Phe Leu Arg Ala Gln Pro Ala
1 5 10 15

Trp Ala Leu Ala Leu Ala Ala Val Gly Leu Leu Val Ala Val Arg Ala
20 25 30

Ala Ala Arg Phe Ala Leu Trp Val Tyr Ala Ala Phe Leu Arg Pro Gly
35 40 45

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

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

Leu Gly Leu Val Leu Val Gly Arg Asn Gln Glu Lys Leu Ala Ala Val
85 90 95

Ala Ala Glu Ile Lys Ala Arg His Pro Lys Val Pro Glu Val Arg Thr
100 105 110

Phe Val Leu Asp Phe Ala Gly Glu Gly Leu Ala Ala Ala Val Glu Ala
115 120 125

Leu Lys Asp Ser Ile Arg Gly Leu Asp Val Gly Val Leu Val Asn Asn
130 135 140

Ala Gly Val Ser Tyr Pro Tyr Ala Arg Tyr Phe His Glu Val Asp Glu
145 150 155 160

Glu Leu Met Arg Thr Leu Ile Arg Val Asn Val Glu Gly Val Thr Arg
165 170 175

Val Thr His Ala Val Leu Pro Ala Met Val Glu Arg Lys Arg Gly Ala
180 185 190

Ile Val Asn Ile Gly Ser Gly Ala Ala Ser Val Val Pro Ser Asp Pro
195 200 205

Leu Tyr Ser Val Tyr Ala Ala Thr Lys Ala Tyr Val Asp Gln Phe Ser
210 215 220

Arg Cys Leu Tyr Val Glu Tyr Lys Ser Lys Gly Ile Asp Val Gln Cys
225 230 235 240

Gln Val Pro Leu Tyr Val Ala Thr Lys Met Ala Ser Ile Arg Lys Ser
245 250 255

Ser Phe Met Val Pro Ser Ala Asp Thr Tyr Ala Arg Ala Ala Val Arg
260 265 270

His Ile Gly Tyr Glu Pro Arg Cys Thr Pro Tyr Trp Pro His Ser Val
275 280 285

Val Trp Phe Leu Ile Ser Ile Leu Pro Glu Ser Leu Ile Asp Ser Val
290 295 300

Arg Leu Gly Met Cys Ile Lys Ile Arg Lys Lys Gly Leu Ala Lys Asp
305 310 315 320

Ala Lys Lys Lys Ala Leu
325

<210> 177
<211> 1145
<212> PRT

<213> Prototheca moriformis

<400> 177

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

Pro Val Phe Ala Met Lys Leu Ala Pro Gln Ser Arg His Leu Glu Val
 275 280 285

Gln Leu Leu Cys Asp Ala His Gly Gln Val Cys Ser Leu Tyr Ser Arg
 290 295 300

Asp Cys Ser Val Gln Arg Arg His Gln Lys Val Val Glu Glu Gly Pro
 305 310 315 320

Val Thr Ala Ala Pro Pro Glu Val Leu Glu Gly Met Glu Arg Cys Ala
 325 330 335

Arg Ser Leu Ala Arg Ala Val Gly Tyr Val Gly Ala Ala Thr Val Glu
 340 345 350

Tyr Leu Tyr Met Val Glu Thr Arg Glu Tyr Cys Phe Leu Glu Leu Asn
 355 360 365

Pro Arg Leu Gln Val Glu His Pro Val Thr Glu Met Ile Thr Gly Val
 370 375 380

Asn Ile Pro Ala Ala Gln Leu Leu Val Ala Ala Gly Val Pro Leu His
 385 390 395 400

Arg Ile Pro Asp Ile Arg Arg Leu Tyr Arg Ala Pro Leu Ala Glu Asp
 405 410 415

Gly Pro Ile Asp Phe Glu Asp Asp Ala Ala Arg Leu Pro Pro Asn Gly
 420 425 430

His Val Leu Ala Val Arg Val Thr Ala Glu Asn Ala His Asp Gly Phe
 435 440 445

Lys Pro Thr Ser Gly Ala Ile Glu Glu Ile Ser Phe Arg Ser Thr Pro
 450 455 460

Asp Val Trp Gly Tyr Phe Ser Val Lys Gly Gly Ser Ala Val His Glu
 465 470 475 480

Phe Ala Asp Ser Gln Phe Gly His Leu Phe Ala Arg Gly Asp Ser Arg
 485 490 495

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

Arg Gly Glu Ile Gln Thr Pro Val Asp Tyr Val Ala Arg Met Ile Gln
 515 520 525

Thr Asp Asp Phe Leu Gly Asn Arg His His Thr Gly Trp Leu Asp Ala
 530 535 540

Arg Ile Ala Ala Gln Val Gly Ala Glu Arg Pro Pro Trp Phe Leu Val
 545 550 555 560

Val Ile Ala Gly Ala Val Leu Arg Ala Thr Arg Ala Val Asn Glu Arg
 565 570 575

Ala Ala Ala Phe Leu Asp His Leu Arg Lys Gly Gln Leu Pro Pro Ser
 580 585 590

Glu Val Pro Leu Thr Arg Val Ala Glu Glu Phe Val Val Asp Gly Thr
 595 600 605

Lys Tyr Ala Val Asp Val Thr Arg Thr Gly Pro Gln Ala Tyr Arg Val
 610 615 620

Ala Leu Arg Asp Pro Glu Ala Arg Ala Pro Gly His Ala Arg Arg Glu
 625 630 635 640

Ser Leu Ala Ser Ala Ala Gly Ala Ala Ser Ser Val Asp Val Ile Ala
 645 650 655

Arg Thr Leu Gln Asp Gly Gly Leu Leu Leu Gln Val Asp Gly Arg Val
 660 665 670

His Val Leu His Ser Glu Glu Glu Ala Leu Gly Thr Arg Leu Val Ile
 675 680 685

Asp Ser Ala Thr Cys Leu Leu Ser Asn Glu His Asp Pro Ser Gln Leu
 690 695 700

Val Ala Val Ser Thr Gly Lys Leu Val Arg His Leu Val Ala Glu Gly
 705 710 715 720

Glu His Val Arg Ala Asp Glu Pro Tyr Ala Glu Val Glu Val Met Lys
 725 730 735

Met Met Met Thr Leu Leu Ala Pro Ala Ala Gly Ala Val Arg Trp Glu
 740 745 750

Val Ala Glu Gly Ala Ala Leu Ala Pro Gly Leu Leu Leu Ala Arg Leu
 755 760 765

Glu Leu Asp Asp Pro Ala Ala Ala Ala Gln Asp Val Leu Asp Gly Phe
 770 775 780

Glu Gly Asp Val Pro Ala Val Val Ala Ala Leu Leu Ala Ala Leu Asp
 785 790 795 800

Asp Pro Ala Leu Ser Leu Val Leu Leu Asp Glu Ala Leu Ala Val Ala
 805 810 815

Ser Thr Pro Arg Phe Val Val Lys Arg Arg Leu Thr Pro Ala Ala Arg
 820 825 830

Cys Thr Ala Arg Phe Glu Glu Ala Ala Arg Ala Ala Leu Ala Ser Ala
 835 840 845

Ala Ser Glu Glu Ala Arg Ala Ala Leu Asp Pro Leu Leu Thr Pro Leu
 850 855 860
 Leu Glu Leu Thr Ala Ala His Arg Tyr Leu Asp Val Glu Glu Arg Phe
 865 870 875 880
 Glu Ser Gly Gly Ala Lys Thr Asp Gln Glu Val Ile Asp Gly Leu Arg
 885 890 895
 Gly Thr His Ser Ala Asp Pro Gly Lys Val Leu Glu Ile Val Val Ala
 900 905 910
 His Gln Ser Ala Gly Pro Arg Ala Asp Leu Val His Arg Leu Leu Asn
 915 920 925
 Ala Leu Arg Ala Arg Arg Leu Leu Glu Arg Ser Leu Leu Gly Glu Leu
 930 935 940
 Arg Val Leu Val Ala Arg Ala Leu Ser Gly Leu Asp Met Phe Ser Asp
 945 950 955 960
 Ala Thr Leu Arg Gly Leu Cys Leu Gly Glu Ser Pro Gly Glu Pro Val
 965 970 975
 Ser Pro Arg Ala Glu Leu Ala Ser Ala Leu Ala Ala Glu Ser Ser Val
 980 985 990
 Ala Ser Pro Thr Ser Arg Arg Ser Thr Leu Ala Glu Gly Leu Tyr Val
 995 1000 1005
 Gly Leu Gly Asn Leu Ala Ala Ala Ala Ala Ser Ser Val Glu Ala
 1010 1015 1020
 Arg Met Ala Met Leu Val Glu Ala Pro Ala Ala Val Asp Asp Ala
 1025 1030 1035
 Leu Ala Thr Leu Leu Asp His Pro Asp Pro Val Leu Gln Arg Arg
 1040 1045 1050
 Ala Leu Ser Thr Tyr Val Arg Arg Ile Tyr Phe Pro Gly Val Leu
 1055 1060 1065
 His Glu Pro Gln Val Val Gly Leu Gly Arg Arg Gly Ser Val Ala
 1070 1075 1080
 Ala Val Trp Ala His Ala Gly Ala Arg Pro Ala Arg Pro Arg Ala
 1085 1090 1095
 Thr Ala Ala Arg Ser Ser Met Ala Gly Leu Ala Pro Gly Thr Leu
 1100 1105 1110
 His Val Val Leu Thr Ala Glu Gly Ala Ala Ala Leu Gln Leu Asp

1115

1120

Ala Ala Ala Gln Ala Ala Leu Gly Thr Leu Asp Val Ser Gly Tyr
1130 1135 1140

Val Ala
1145

<210> 178
<211> 1182
<212> PRT
<213> Prototheca moriformis

<400> 178
Met Thr Val Ala Asn Pro Pro Glu Ala Pro Phe Asp Ser Glu Ala Leu
1 5 10 15

Ala Phe Gln Pro Ala Val Ala Val Val His Phe Ala Gly Val Pro Gly
20 25 30

Arg Thr Asp Val Ser Asp Glu Leu Glu Arg Arg Ile Leu Glu Trp Gln
35 40 45

Gly Asp Arg Ala Ile His Ser Val Leu Val Ala Asn Asn Gly Leu Ala
50 55 60

Ala Val Lys Phe Ile Arg Ser Ile Arg Ser Trp Ser Tyr Lys Thr Phe
65 70 75 80

Gly Asn Glu Arg Ala Val Lys Leu Ile Ala Met Ala Thr Pro Glu Asp
85 90 95

Met Arg Ala Asp Ala Glu His Ile Arg Met Ala Asp Gln Phe Val Glu
100 105 110

Val Pro Gly Gly Lys Asn Val Gln Asn Tyr Ala Asn Val Gly Leu Ile
115 120 125

Thr Ser Val Ala Val Arg Thr Gly Val Asp Ala Val Trp Pro Gly Trp
130 135 140

Gly His Ala Ser Glu Phe Pro Glu Leu Pro Glu Ser Leu Gly Ala Thr
145 150 155 160

Pro Ser Gln Ile Arg Phe Val Gly Pro Pro Ala Gly Pro Met Ala Ala
165 170 175

Leu Gly Asp Lys Val Gly Ser Thr Ile Leu Ala Gln Ala Ala Gly Val
180 185 190

Pro Thr Leu Ala Trp Ser Gly Ser Gly Val Ser Ile Ala Tyr Ala Asp
195 200 205

Cys Pro Arg Gly Glu Ile Pro Pro Glu Val Tyr Arg Arg Ala Cys Ile
210 215 220

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

500

505

510

Lys Glu Ile Lys Ile Arg Gly Glu Ile Gln Thr Pro Val Asp Tyr Val
 515 520 525
 Ala Arg Met Ile Gln Thr Asp Asp Phe Leu Gly Asn Arg His His Thr
 530 535 540
 Gly Trp Leu Asp Ala Arg Ile Ala Ala Gln Val Gly Ala Glu Arg Pro
 545 550 555 560
 Pro Trp Phe Leu Val Val Ile Ala Gly Ala Val Leu Arg Ala Thr Arg
 565 570 575
 Ala Val Asn Glu Arg Ala Ala Ala Phe Leu Asp His Leu Arg Lys Gly
 580 585 590
 Gln Leu Pro Pro Ser Glu Val Pro Leu Thr Arg Val Ala Glu Glu Phe
 595 600 605
 Val Val Asp Gly Thr Lys Tyr Ala Val Asp Val Thr Arg Thr Gly Pro
 610 615 620
 Gln Ala Tyr Arg Ser Leu Ala Ser Ala Ala Gly Ala Ala Ser Ser Val
 625 630 635 640
 Asp Val Ile Ala Arg Thr Leu Gln Asp Gly Gly Leu Leu Leu Gln Val
 645 650 655
 Asp Gly Arg Val His Val Leu His Ser Glu Glu Glu Ala Leu Gly Thr
 660 665 670
 Arg Leu Val Ile Asp Ser Ala Thr Cys Leu Leu Ser Asn Glu His Asp
 675 680 685
 Pro Ser Gln Leu Val Ala Val Ser Thr Gly Lys Leu Val Arg His Leu
 690 695 700
 Val Ala Glu Gly Glu His Val Arg Ala Asp Glu Pro Tyr Ala Glu Val
 705 710 715 720
 Glu Val Met Lys Met Met Met Thr Leu Leu Ala Pro Ala Ala Gly Ala
 725 730 735
 Val Arg Trp Glu Val Ala Glu Gly Ala Ala Leu Ala Pro Gly Leu Leu
 740 745 750
 Leu Ala Arg Leu Glu Leu Asp Asp Pro Ala Ala Val Arg Arg Ala Glu
 755 760 765
 Pro Phe Arg Gly Ala Phe Pro Asp Leu Gly Pro Pro Ser Pro Asp Phe
 770 775 780

Asp Gly Leu Ala Ala Arg Tyr Arg Ser Ala Leu Glu Ala Ala Gln Asp
 785 790 795 800

Val Leu Asp Gly Phe Glu Gly Asp Val Pro Ala Val Val Ala Ala Leu
 805 810 815

Leu Ala Ala Leu Asp Asp Pro Ala Leu Ser Leu Val Leu Leu Asp Glu
 820 825 830

Ala Leu Ala Val Ala Ser Thr Pro Arg Phe Val Val Lys Arg Arg Leu
 835 840 845

Thr Pro Ala Ala Arg Cys Thr Ala Arg Phe Glu Glu Ala Ala Arg Ala
 850 855 860

Ala Leu Ala Ser Ala Ala Ser Glu Glu Ala Arg Ala Ala Leu Asp Pro
 865 870 875 880

Leu Leu Thr Pro Leu Leu Glu Leu Thr Ala Ala His Val Gly Gly Pro
 885 890 895

Glu Gly His Ala Arg Arg Val Ala Arg Gln Leu Leu Glu Arg Tyr Leu
 900 905 910

Asp Val Glu Glu Arg Phe Glu Ser Gly Gly Ala Lys Thr Asp Gln Glu
 915 920 925

Val Ile Asp Gly Leu Arg Gly Thr His Ser Ala Asp Pro Gly Lys Val
 930 935 940

Leu Glu Ile Val Val Ala His Gln Ser Ala Gly Pro Arg Ala Asp Leu
 945 950 955 960

Val His Arg Leu Leu Asn Ala Leu Arg Ala Arg Arg Leu Leu Glu Arg
 965 970 975

Ser Leu Leu Gly Glu Leu Arg Val Leu Val Ala Arg Ala Leu Ser Gly
 980 985 990

Leu Asp Met Phe Ser Asp Ala Thr Leu Arg Gly Leu Cys Leu Gly Glu
 995 1000 1005

Ser Pro Gly Glu Pro Val Ser Pro Arg Ala Glu Leu Ala Ser Ala
 1010 1015 1020

Leu Ala Ala Glu Ser Ser Val Ala Ser Pro Thr Ser Arg Arg Ser
 1025 1030 1035

Thr Leu Ala Glu Gly Leu Tyr Val Gly Leu Gly Asn Leu Ala Ala
 1040 1045 1050

Ala Ala Ala Ser Ser Val Glu Ala Arg Met Ala Met Leu Arg Arg
 1055 1060 1065

Ala Leu Ser Thr Tyr Val Arg Arg Ile Tyr Phe Pro Gly Val Leu
1070 1075 1080

His Glu Pro Gln Val Val Gly Leu Gly Arg Arg Gly Ser Val Ala
1085 1090 1095

Ala Val Trp Ala His Ala Gly Ala Arg Pro Gly Ala Pro Ala Arg
1100 1105 1110

His Gly Gly Ala Leu Val Val Pro Ala Leu Arg Ala Leu Pro Asp
1115 1120 1125

Ala Leu Ala Glu Leu Ala His Leu Arg Ala Gln Thr Ser Met Ala
1130 1135 1140

Gly Leu Ala Pro Gly Thr Leu His Val Ala Leu Thr Ala Glu Gly
1145 1150 1155

Ala Ala Ala Leu Gln Leu Asp Ala Ala Ala Gln Ala Ala Leu Gly
1160 1165 1170

Thr Leu Asp Val Ser Gly Tyr Val Ala
1175 1180

<210> 179

<211> 1105

<212> PRT

<213> Prototheca moriformis

<400> 179

Pro Glu His Gln Gln Gln Pro Gly Leu Pro Asp Ala Thr Val Val Ala
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Ala Ser Ala Ala Ala Ala Val Ser Ala Leu Ala Pro Ala Leu Arg Glu
20 25 30

Ala Gly Tyr Asn Ala Val Ser Phe Leu Thr Lys Arg Gly Gly Val Glu
35 40 45

Pro Leu Arg Val Val Phe Tyr Asp Gly Thr Ser Ser Gly Ser Ala Ala
50 55 60

Ala Ser Asp Ala Ser Ser Thr Gln Thr Ala Thr Gly Trp Ser Leu Asp
65 70 75 80

Pro Val Leu Gly Thr Val Glu Pro Pro Thr Ala Glu Ala Leu Glu Leu
85 90 95

Ala Cys Leu Ala Gly Arg Ala Gly Ala Ser His Asp Ala Ser Arg Asn
100 105 110

Arg Gln Trp His Met Trp Thr Val Ala Glu Arg Ala Gly Lys Arg Ser
115 120 125

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

Thr Leu Ala Thr Pro Glu Cys Pro Arg Gly Arg Ala Val Val Ala Ile
 420 425 430
 Ala Asn Asp Ile Thr Tyr Asn Ser Gly Ser Phe Gly Pro Arg Glu Asp
 435 440 445
 Ala Phe Phe Lys Ala Ala Thr Glu Tyr Ala Leu Ala Glu Arg Leu Pro
 450 455 460
 Val Val Tyr Leu Ala Ala Asn Ser Gly Ala Arg Val Gly Leu Ala Glu
 465 470 475 480
 Glu Val Lys Arg Cys Leu Arg Val Glu Trp Ser Val Pro Gly Asp Pro
 485 490 495
 Thr Lys Gly His Lys Tyr Leu Tyr Leu Asp Asp Glu Asp Tyr Arg Ser
 500 505 510
 Ile Thr Ser Arg Ala Ala Gly Arg Thr Leu Pro Val Ser Cys Ser Ala
 515 520 525
 Lys Val Gly Ala Asp Gly Arg Thr Arg His Val Leu His Asp Val Ile
 530 535 540
 Gly Leu Glu Asp Gly Leu Gly Val Glu Cys Leu Ser Gly Ser Gly Ala
 545 550 555 560
 Ile Ala Gly Ala Phe Ala Arg Ala Phe Arg Glu Gly Phe Thr Val Thr
 565 570 575
 Leu Val Ser Gly Arg Thr Val Gly Ile Gly Ala Tyr Leu Ala Arg Leu
 580 585 590
 Gly Arg Arg Cys Val Gln Arg Arg Glu Gln Pro Ile Ile Leu Thr Gly
 595 600 605
 Phe Ala Ala Leu Asn Lys Leu Leu Gly Arg Glu Val Tyr Thr Ser Gln
 610 615 620
 Gln Gln Leu Gly Gly Pro Arg Val Met Gly Ala Asn Gly Val Ser His
 625 630 635 640
 His Val Val Asp Asp Asp Leu Gln Gly Val His Thr Val Leu Arg Trp
 645 650 655
 Leu Ala Tyr Thr Pro Ala Arg Val Gly Glu Leu Pro Pro Thr Leu Arg
 660 665 670
 Ala Ala Asp Pro Val Asp Arg Arg Val Thr Tyr Ala Pro Val Glu Asn
 675 680 685
 Glu Lys Leu Asp Pro Arg Leu Ala Val Ala Gly Gly Asp Ala Pro Glu
 690 695 700

Pro Val Thr Gly Leu Phe Asp Arg Gly Ser Trp Thr Glu Ala Gln Ala
 705 710 715 720
 Gly Trp Ala Gln Thr Val Val Thr Gly Arg Ala Arg Leu Gly Gly Ile
 725 730 735
 Pro Val Gly Val Val Ala Val Glu Val Asn Ala Val Ser Leu His Ile
 740 745 750
 Pro Ala Asp Pro Gly Met Pro Asp Ser Ala Glu Arg Thr Ile Pro Gln
 755 760 765
 Ala Gly Gln Val Trp Phe Pro Asp Ser Ala Leu Lys Thr Ala Gln Ala
 770 775 780
 Ile Glu Glu Phe Gly Leu Glu Gly Leu Pro Leu Phe Ile Leu Ala Asn
 785 790 795 800
 Trp Arg Gly Phe Ser Gly Gly Gln Arg Asp Leu Phe Glu Gly Val Leu
 805 810 815
 Gln Ala Gly Ser Gln Ile Val Glu Met Leu Arg Thr Tyr Arg Arg Pro
 820 825 830
 Val Thr Val Tyr Leu Gly Pro Gly Cys Glu Leu Arg Gly Gly Ala Trp
 835 840 845
 Val Val Leu Asp Ser Gln Ile Asn Pro Ala Ser Ile Glu Met Tyr Ala
 850 855 860
 Asp Pro Thr Ala Gln Gly Ala Val Leu Glu Pro Gln Gly Val Val Glu
 865 870 875 880
 Ile Lys Phe Arg Thr Pro Asp Leu Leu Ala Ala Met His Arg Leu Asp
 885 890 895
 Glu Lys Ile Ile Ala Leu Lys Ser Asp Asp Ser Pro Ser Ala Leu Ala
 900 905 910
 Ala Ile Lys Ala Arg Glu Ala Glu Leu Leu Pro Val Tyr Ser Gln Val
 915 920 925
 Ala His Gln Phe Ala Gln Met His Asp Gly Pro Val Arg Met Leu Ala
 930 935 940
 Lys Gly Val Leu Arg Gly Ile Val Pro Trp Ser Ala Ala Arg Ala Phe
 945 950 955 960
 Leu Ala Thr Arg Leu Arg Arg Arg Leu Ala Glu Glu Ala Leu Leu Arg
 965 970 975
 Gln Ile Ala Ala Ala Asp Ala Ser Val Glu His Ala Asp Ala Leu Ala

980

985

990

Met Leu Arg Ser Trp Phe Leu Ser Ser Pro Pro Thr Gly Gly Ala Pro
 995 1000 1005

Gly Ala Pro Gly Ala Leu Gly Ala Leu Leu Lys Glu Thr Val Val
 1010 1015 1020

Ala Pro Pro Asp Ala Gly Glu Ala Pro Leu Ala Leu Trp Gln Asp
 1025 1030 1035

Asp Leu Ala Phe Leu Asp Trp Ser Glu Ala Glu Ala Gly Ala Ser
 1040 1045 1050

Arg Val Ala Leu Glu Leu Lys Ser Leu Arg Val Asn Val Ala Met
 1055 1060 1065

Arg Ser Val Asp Arg Leu Cys Gln Thr Pro Glu Gly Thr Ala Gly
 1070 1075 1080

Leu Val Lys Gly Leu Asp Glu Ala Ile Lys Ser Asn Pro Ser Leu
 1085 1090 1095

Leu Leu Cys Leu Arg Ser Leu
 1100 1105

<210> 180

<211> 1067

<212> PRT

<213> Prototheca moriformis

<400> 180

Pro Glu His Gln Gln Gln Pro Gly Cys Arg Thr Pro Pro Ser Ala Val
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Ser Phe Leu Thr Lys Arg Gly Gly Val Glu Pro Leu Arg Val Val Phe
 20 25 30

Tyr Asp Gly Thr Ser Ser Gly Ser Ala Ala Ala Ser Asp Ser Ser Ser
 35 40 45

Thr Gln Thr Gly Pro Ser Thr Gly Trp Ser Leu Asp Pro Val Leu Gly
 50 55 60

Thr Val Glu Pro Pro Thr Ala Glu Ala Leu Glu Leu Ala Cys Leu Ala
 65 70 75 80

Gly Arg Ala Gly Ala Ser His Asp Ala Ser Arg Asn Arg Gln Trp His
 85 90 95

Met Trp Thr Val Ala Glu Arg Ala Gly Lys Arg Ser Ala Val Leu Arg
 100 105 110

Arg Thr Phe Leu Arg Gly Ala Val Arg Ser Leu Gly Arg Pro Ala Leu
 115 120 125

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

405

410

415

Thr Tyr Asn Ser₄₂₀ Gly Ser Phe Gly Pro₄₂₅ Arg Glu Asp Ala Phe₄₃₀ Phe Lys
 Ala Ala Thr₄₃₅ Glu Tyr Ala Leu Ala₄₄₀ Glu Arg Leu Pro Val₄₄₅ Val Tyr Leu
 Ala Ala Asn Ser Gly Ala Arg₄₅₅ Val Gly Leu Ala Glu₄₆₀ Glu Val Lys Arg
 Cys₄₆₅ Leu Arg Val Glu Trp₄₇₀ Ser Val Pro Gly Asp₄₇₅ Pro Thr Lys Gly His₄₈₀
 Lys Tyr Leu Tyr Leu₄₈₅ Asp Asp Glu Asp Tyr₄₉₀ Arg Ser Ile Thr Ser₄₉₅ Arg
 Ala Ala Gly Arg₅₀₀ Thr Leu Pro Val Ser₅₀₅ Cys Ser Ala Lys Val₅₁₀ Gly Ala
 Asp Gly Arg₅₁₅ Thr Arg His Val Leu₅₂₀ His Asp Val Ile Gly₅₂₅ Leu Glu Asp
 Gly Leu₅₃₀ Gly Val Glu Cys Leu₅₃₅ Ser Gly Ser Gly Ala₅₄₀ Ile Ala Gly Ala
 Phe₅₄₅ Ala Arg Ala Phe Arg₅₅₀ Glu Gly Phe Thr Val₅₅₅ Thr Leu Val Ser Gly₅₆₀
 Arg Thr Val Gly Ile₅₆₅ Gly Ala Tyr Leu Ala₅₇₀ Arg Leu Gly Arg Arg₅₇₅ Cys
 Val Gln Arg Arg₅₈₀ Glu Gln Pro Ile Ile₅₈₅ Leu Thr Gly Phe Ala₅₉₀ Ala Leu
 Asn Lys Leu₅₉₅ Leu Gly Arg Glu Val₆₀₀ Tyr Thr Ser Gln Gln₆₀₅ Gln Leu Gly
 Gly Pro₆₁₀ Arg Val Met Gly Ala₆₁₅ Asn Gly Val Ser His₆₂₀ His Val Val Asp
 Asp₆₂₅ Asp Leu Gln Gly Val₆₃₀ His Thr Val Leu Arg₆₃₅ Trp Leu Ala Tyr Thr₆₄₀
 Pro Ala Arg Val Gly₆₄₅ Glu Leu Pro Pro Thr₆₅₀ Leu Arg Ala Ala Asp₆₅₅ Pro
 Val Asp Arg Arg₆₆₀ Val Thr Tyr Ala Pro₆₆₅ Val Glu Asn Glu Lys₆₇₀ Leu Asp
 Pro Arg Leu₆₇₅ Ala Val Ala Gly Gly₆₈₀ Asp Ala Pro Glu Pro₆₈₅ Val Thr Gly

Leu Phe Asp Arg Gly Ser Trp Thr Glu Ala Gln Ala Gly Trp Ala Gln
 690 695 700
 Thr Val Val Asn Ala Val Ser Leu His Ile Pro Ala Asp Pro Gly Met
 705 710 715 720
 Pro Asp Ser Ala Glu Arg Thr Ile Pro Gln Ala Gly Gln Val Trp Phe
 725 730 735
 Pro Asp Ser Ala Leu Lys Thr Ala Gln Ala Ile Glu Glu Phe Gly Leu
 740 745 750
 Glu Gly Leu Pro Leu Phe Ile Leu Ala Asn Trp Arg Gly Phe Ser Gly
 755 760 765
 Gly Gln Arg Asp Leu Phe Glu Gly Val Leu Gln Ala Gly Ser Gln Ile
 770 775 780
 Val Glu Met Leu Arg Thr Tyr Arg Arg Pro Val Thr Val Tyr Leu Gly
 785 790 795 800
 Pro Gly Cys Glu Leu Arg Gly Gly Ala Trp Val Val Leu Asp Ser Gln
 805 810 815
 Ile Asn Pro Ala Ser Ile Glu Met Tyr Ala Asp Pro Thr Ala Gln Gly
 820 825 830
 Ala Val Leu Glu Pro Gln Gly Val Val Glu Ile Lys Phe Arg Thr Pro
 835 840 845
 Asp Leu Leu Ala Ala Met His Arg Leu Asp Glu Lys Ile Ile Ala Leu
 850 855 860
 Lys Ser Asp Asp Ser Pro Ser Ala Leu Ala Ala Ile Lys Ala Arg Glu
 865 870 875 880
 Ser Glu Leu Leu Pro Val Tyr Ser Gln Val Ala His Gln Phe Ala Gln
 885 890 895
 Met His Asp Gly Pro Val Arg Met Leu Ala Lys Gly Val Leu Arg Gly
 900 905 910
 Ile Val Pro Trp Ser Ala Ala Arg Ala Phe Leu Ala Thr Arg Leu Arg
 915 920 925
 Arg Arg Leu Ala Glu Glu Ala Leu Leu Arg Gln Ile Ala Ala Ala Asp
 930 935 940
 Ala Ser Val Glu His Ala Asp Ala Leu Ala Met Leu Arg Ser Trp Phe
 945 950 955 960
 Leu Ser Ser Pro Pro Thr Gly Gly Ala Pro Gly Ala Pro Gly Ala Leu
 965 970 975

Gly Ala Leu Leu Lys Glu Thr Val Val Ala Pro Pro Asp Ala Gly Glu
 980 985 990

Ala Pro Leu Ala Leu Trp Gln Asp Asp Leu Ala Phe Leu Asp Trp Ser
 995 1000 1005

Glu Ala Glu Ala Gly Ala Ser Arg Val Ala Leu Glu Leu Lys Ser
 1010 1015 1020

Leu Arg Val Asn Val Ala Met Arg Ser Val Asp Arg Leu Cys Gln
 1025 1030 1035

Thr Pro Glu Gly Thr Ala Gly Leu Val Lys Gly Leu Asp Glu Ala
 1040 1045 1050

Ile Lys Ser Asn Pro Ser Leu Leu Leu Cys Leu Arg Ser Leu
 1055 1060 1065