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Commonwealth Scientific and Industrial Research
Organisation

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<151> 2014-12-18

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<160> 58

<170> PatentIn version 3.5

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Phe His Asp Ile Ile Glu Thr His Val Leu His His Tyr Cys Ser Arg
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Phe Leu Arg Phe Ala Ala Trp Ser Ala Tyr Val Phe Ser Ile Ser Cys
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Phe Gly Phe Gly Ile Trp Ile Leu Gly His Glu Cys Gly His Ser Ala
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Phe Ser Asn Tyr Gly Trp Val Asn Asp Thr Val Gly Trp Val Leu His
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Ser Leu Val Met Val Pro Tyr Phe Ser Trp Lys Phe Ser His Ala Lys
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His His Lys Ala Thr Gly His Met Thr Arg Asp Met Val Phe Val Pro
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Tyr Thr Ala Glu Glu Phe Lys Glu Lys His Gln Val Thr Ser Leu His
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Gln Gln Leu Gly Gly Leu Ser Leu Tyr Leu Ala Thr Asn Ala Thr Gly
210 215 220

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Ser Ser Met Pro His Tyr Asp Ala Gln Glu Trp Thr Phe Ala Lys Gly
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catcacctgt tcccggacat gccgcagttt cgccagccgg aggtgagccg gcggttcgtc	1260

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ccgttcgcga agaagtgggg gctgaactac aaggtgctgt cctattacgg cgcctggaag	1320
gcgacgttct cgaacttgga taaggtcggg cagcactact acgtcaacgg caaggcggag	1380
aaggcgcaact ga	1392

<210> 8
 <211> 1395
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Codon-optimized open reading frame for expression of *Micromonas pusilla* 6 desaturase in plants (version 1)

<400> 8	
atgtgccctc ctaagactga tggaagatct tctcctagat ctccacttac caggtctaaa	60
tcttctgctg aggctcttga tgctaaggat gcttctactg ctctgttga tcttaagact	120
cttgagcctc atgagcttgc tgctactttc gagactagat gggtagagt tgaggacgtt	180
gagtacgatg tgactaactt caagcaccct ggtggatctg tgatcttcta catgcttgct	240
aacactgggtg ctgatgctac tgaggctttc aaagaattcc acatgcgttc tctcaaggct	300
tggaagatgc ttagagcttt gccttctaga cctgctgaga tcaagagatc tgagtctgag	360
gatgctccta tgcttgagga tttcgctaga tggcgtgctg agcttgagag agatggattc	420
ttcaagcctt ctatcaccca tgtggcttac agacttctcg agcttcttgc tacattcgct	480
cttggaaactg ctcttatgta cgctggatac cctatcattg cttctgttgt ttacggtgct	540
ttcttcggag ctagatgtgg atgggttcaa catgagggtg gacataactc tcttaccgga	600
tctgtttacg tggacaagag acttcaggct atgacttggtg gattcggact ttctacttct	660
ggtgagatgt ggaaccagat gcataacaag caccatgcta cccctcaaaa ggtagacac	720
gatatggatc ttgataccac tcctgctgtg gctttcttca acactgctgt tgaggataac	780
agacctagag gattctctag agcttgggct agacttcaag cttggacttt cgttcctgtt	840
acctctggac ttcttgttca agctttctgg atctacgttc tccaccctag acaagtctc	900

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cgtaagaaga actacgaaga ggcttccttg atgctcggtt ctcattgttg tagaaccgct 960
 gttatcaagc ttgtactagg atactccttg cctgttgctt actggtgggt cactttcgga 1020
 aactggatcg cttacatgta ccttttcgct cacttctcta cttctcatac tcacctccct 1080
 gttgttccat ctgataagca cctttccttg gttactacg ctgttgatca caccgttgat 1140
 atcgatcctt ctagaggata cgtgaactgg cttatgggat accttaactg tcagggtatc 1200
 caccacctct tccctgatat gcctcaattc agacagcctg aggttagcag aagattcggt 1260
 cctttcgcta agaagtgggg actcaactac aagggtgctt cttactacgg tgcttggaag 1320
 gctactttct ctaaccttga taagggtgga cagcactact acgttaacgg aaaggctgag 1380
 aaggctcact aatga 1395

<210> 9
 <211> 463
 <212> PRT
 <213> *Micromonas pusilla*

<400> 9

Met Cys Pro Pro Lys Thr Asp Gly Arg Ser Ser Pro Arg Ser Pro Leu
 1 5 10 15

Thr Arg Ser Lys Ser Ser Ala Glu Ala Leu Asp Ala Lys Asp Ala Ser
 20 25 30

Thr Ala Pro Val Asp Leu Lys Thr Leu Glu Pro His Glu Leu Ala Ala
 35 40 45

Thr Phe Glu Thr Arg Trp Val Arg Val Glu Asp Val Glu Tyr Asp Val
 50 55 60

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

Asn Thr Gly Ala Asp Ala Thr Glu Ala Phe Lys Glu Phe His Met Arg
 85 90 95

Ser Leu Lys Ala Trp Lys Met Leu Arg Ala Leu Pro Ser Arg Pro Ala
100 105 110

Glu Ile Lys Arg Ser Glu Ser Glu Asp Ala Pro Met Leu Glu Asp Phe
115 120 125

Ala Arg Trp Arg Ala Glu Leu Glu Arg Asp Gly Phe Phe Lys Pro Ser
130 135 140

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

Leu Gly Thr Ala Leu Met Tyr Ala Gly Tyr Pro Ile Ile Ala Ser Val
165 170 175

Val Tyr Gly Ala Phe Phe Gly Ala Arg Cys Gly Trp Val Gln His Glu
180 185 190

Gly Gly His Asn Ser Leu Thr Gly Ser Val Tyr Val Asp Lys Arg Leu
195 200 205

Gln Ala Met Thr Cys Gly Phe Gly Leu Ser Thr Ser Gly Glu Met Trp
210 215 220

Asn Gln Met His Asn Lys His His Ala Thr Pro Gln Lys Val Arg His
225 230 235 240

Asp Met Asp Leu Asp Thr Thr Pro Ala Val Ala Phe Phe Asn Thr Ala
245 250 255

Val Glu Asp Asn Arg Pro Arg Gly Phe Ser Arg Ala Trp Ala Arg Leu
260 265 270

Gln Ala Trp Thr Phe Val Pro Val Thr Ser Gly Leu Leu Val Gln Ala
275 280 285

Phe Trp Ile Tyr Val Leu His Pro Arg Gln Val Leu Arg Lys Lys Asn
290 295 300

Tyr Glu Glu Ala Ser Trp Met Leu Val Ser His Val Val Arg Thr Ala
305 310 315 320

Val Ile Lys Leu Ala Thr Gly Tyr Ser Trp Pro Val Ala Tyr Trp Trp
325 330 335

Phe Thr Phe Gly Asn Trp Ile Ala Tyr Met Tyr Leu Phe Ala His Phe
340 345 350

Ser Thr Ser His Thr His Leu Pro Val Val Pro Ser Asp Lys His Leu
355 360 365

Ser Trp Val Asn Tyr Ala Val Asp His Thr Val Asp Ile Asp Pro Ser
370 375 380

Arg Gly Tyr Val Asn Trp Leu Met Gly Tyr Leu Asn Cys Gln Val Ile
385 390 395 400

His His Leu Phe Pro Asp Met Pro Gln Phe Arg Gln Pro Glu Val Ser
405 410 415

Arg Arg Phe Val Pro Phe Ala Lys Lys Trp Gly Leu Asn Tyr Lys Val
420 425 430

Leu Ser Tyr Tyr Gly Ala Trp Lys Ala Thr Phe Ser Asn Leu Asp Lys
435 440 445

Val Gly Gln His Tyr Tyr Val Asn Gly Lys Ala Glu Lys Ala His
450 455 460

<210> 10

<211> 1449

<212> DNA

<213> *Ostreococcus lucimarinus*

<400> 10

atgtgcgtcg aaacgaccga aggcacatcg cgaacgatgg cgaacgaacg cacgagctcg	60
tcgtcgtcgc tgagcgaagg cggaacgccg acggtgacgg tcgggatggg aagcgaagac	120
gcggggaaga agactcgaaa cgcgagcgtc acggcgtgga cgaaagagtt ggagccgcac	180
gcgatcgcga agacgttcga acggcgggtac gtgacgatcg aaggcgtgga atacgatgtg	240
acggatttta agcatcccgaggatcggtt atttattaca tgctgtcgaa cacgggagcg	300
gacgcgacgg aggcttttaa agagtttcat tatcggtcga aaaaggcgcg caaggcgttg	360
gcggcgttgc cgcataagcc agtggacgcg gcgacgcggg aaccgatcga agatgaggcg	420
atgctgaagg atttcgcgca gtggcgcaag gaattggagc gtgagggatt ttttaagccc	480
tcgccggcgc acgtggcgta tcgattcgcc gagctcgcgg cgatgttcgc gctcggcacg	540
gcgttgatgc acgcgcgttg gcacgtcgct tccgtgatcg tgtactcgtg tttcttcggc	600
gcgcgatgcg gttgggtgca gcacgagggt gggcacaatt cgttgactgg aaacatttgg	660
tgggacaagc gaatccaagc cttcgccgcg gggttcggct tggcgtcgag tggcgacatg	720
tggaacaaca tgcacaacaa gcatcacgcg acgccccaaa aggtgcgaca cgatatggat	780
ctcgacacca ctcccacggt ggcgttcttc aactccgcgg ttgaagaaaa tcgcccgcgg	840
ggattcagta agttgtgggt gcgccttcaa gcgtggacct tcgtgcccgt gacgtccggt	900
atggttttgt tcttctggat gttcgtcttg caccgcgta acgcgctgcg acgcaaaagc	960
ttcgaagaag cggcttggat gttttccgcg cacgtcattc gcacggcgggt tatcaaagcc	1020
gtcaccggct actcctggat cgcctcgta ggcttgttcg cggcgacgat gtgggcgagc	1080
ggatgttact tgttcgcgca cttttccacg tctcacacgc acttggatgt cgtgccgagc	1140
gataaacacc tctcgtgggt gcgatacgcc gtcgatcaca cgatcgacat caatccgaac	1200
aacagcgtcg tcaactgggt gatgggctac ttgaactgcc aagtcatcca tcacctgttc	1260
ccggatatgc ctgagttccg ccaacccgaa gtctcccgcc gattcgtccc gtttgcgaag	1320

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aagtggaact taaactacaa ggtcttgacg tattatgggg cctggaaggc gacgttcggc	1380
aacttgaacg acgtcgggaa gcactattac gtgcacggat ctcagcgcgt caaatcaaag	1440
tcggcgtga	1449

<210> 11
 <211> 1449
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Codon-optimized open reading frame for expression of *Ostreococcus lucimarinus* 6-desaturase in plants

<400> 11	
atgtgtgttg agactactga gggaacctct agaactatgg ctaacgagag gacctcttct	60
tcttcttcac tctctgaggg tggaaactcct actgttactg tgggaatggg atctgaggat	120
gctggaaaaga aaaccagaaa cgcttctgtt actgcttgga ccaaagagct tgagcctcac	180
gctatcgcta agaccttcga gagaagatac gttaccatcg aggggtgttg gtacgatgtg	240
accgatttca aacaccctgg tggatctgtg atctactaca tgctctctaa cactgggtgct	300
gatgctactg aggctttcaa agagttccac taccgttcta agaaggctag aaaggctctt	360
gctgctcttc ctcaacaagg tggtgatgct gctactagag agcctattga ggacgaggct	420
atgcttaagg atttcgctca gtggagaaaa gagttggaga gagagggatt cttcaagcct	480
tctcctgctc atgttgctta ccgtttcgct gaactcgctg ctatgttcgc tcttggaacc	540
gctcttatgc atgctagatg gcacgttgct agcgttatcg tgtactcctg tttcttcgga	600
gctagatgtg gatgggttca acatgagggt ggacacaact ctcttaccgg aaacatctgg	660
tgggataaga gaatccaagc tttcgctgct ggattcggac ttgcttcttc tgggtgacatg	720
tggacaaca tgcacaaca gcaccatgct actcctcaga aagtgagaca cgatatggat	780
cttgatacca cccctaccgt tgctttcttc aactctgctg tggaggaaaa cagacctagg	840
ggattctcta agctttggct cagacttcaa gcttggacct tcgttcctgt tacctctgga	900
atgggtgctct tcttctggat gttcgttctc catcctagaa acgctctccg tcgtaagtct	960

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ttcgaagagg ctgcttggat gttctctgct cacgttatca gaaccgctgt tatcaaggct 1020
 gttaccggat actcttggat cgctagctac ggacttttcg ctgctactat gtgggcttct 1080
 ggatgctacc ttttcgctca cttctctact tctcacaccc acctcgatgt tgttccatct 1140
 gataagcacc ttagctgggt taggtacgct gttgatcaca ccatcgacat caaccctaac 1200
 aactctgttg tgaactggct tatgggatac cttaactgcc aggttatcca ccatctcttc 1260
 cctgatatgc ctcaattcag acagcctgag gtgtcaagaa gattcgtccc tttcgctaag 1320
 aagtggaacc tcaactacaa ggtgctcact tactacggtg cttggaaggc tactttcgga 1380
 aacctcaacg atgttggaag gcactactac gttcacggat ctgagagagt gaagagcaag 1440
 agcgcttga 1449

<210> 12
 <211> 482
 <212> PRT
 <213> *Ostreococcus lucimarinus*

<400> 12

Met Cys Val Glu Thr Thr Glu Gly Thr Ser Arg Thr Met Ala Asn Glu
 1 5 10 15

Arg Thr Ser Ser Ser Ser Leu Ser Glu Gly Gly Thr Pro Thr Val
 20 25 30

Thr Val Gly Met Gly Ser Glu Asp Ala Gly Lys Lys Thr Arg Asn Ala
 35 40 45

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

Thr Phe Glu Arg Arg Tyr Val Thr Ile Glu Gly Val Glu Tyr Asp Val
 65 70 75 80

Thr Asp Phe Lys His Pro Gly Gly Ser Val Ile Tyr Tyr Met Leu Ser

85

90

95

Asn Thr Gly Ala Asp Ala Thr Glu Ala Phe Lys Glu Phe His Tyr Arg
 100 105 110

Ser Lys Lys Ala Arg Lys Ala Leu Ala Ala Leu Pro His Lys Pro Val
 115 120 125

Asp Ala Ala Thr Arg Glu Pro Ile Glu Asp Glu Ala Met Leu Lys Asp
 130 135 140

Phe Ala Gln Trp Arg Lys Glu Leu Glu Arg Glu Gly Phe Phe Lys Pro
 145 150 155 160

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

Ala Leu Gly Thr Ala Leu Met His Ala Arg Trp His Val Ala Ser Val
 180 185 190

Ile Val Tyr Ser Cys Phe Phe Gly Ala Arg Cys Gly Trp Val Gln His
 195 200 205

Glu Gly Gly His Asn Ser Leu Thr Gly Asn Ile Trp Trp Asp Lys Arg
 210 215 220

Ile Gln Ala Phe Ala Ala Gly Phe Gly Leu Ala Ser Ser Gly Asp Met
 225 230 235 240

Trp Asn Asn Met His Asn Lys His His Ala Thr Pro Gln Lys Val Arg
 245 250 255

His Asp Met Asp Leu Asp Thr Thr Pro Thr Val Ala Phe Phe Asn Ser
 260 265 270

Ala Val Glu Glu Asn Arg Pro Arg Gly Phe Ser Lys Leu Trp Leu Arg

275

280

285

Leu Gln Ala Trp Thr Phe Val Pro Val Thr Ser Gly Met Val Leu Phe
 290 295 300

Phe Trp Met Phe Val Leu His Pro Arg Asn Ala Leu Arg Arg Lys Ser
 305 310 315 320

Phe Glu Glu Ala Ala Trp Met Phe Ser Ala His Val Ile Arg Thr Ala
 325 330 335

Val Ile Lys Ala Val Thr Gly Tyr Ser Trp Ile Ala Ser Tyr Gly Leu
 340 345 350

Phe Ala Ala Thr Met Trp Ala Ser Gly Cys Tyr Leu Phe Ala His Phe
 355 360 365

Ser Thr Ser His Thr His Leu Asp Val Val Pro Ser Asp Lys His Leu
 370 375 380

Ser Trp Val Arg Tyr Ala Val Asp His Thr Ile Asp Ile Asn Pro Asn
 385 390 395 400

Asn Ser Val Val Asn Trp Leu Met Gly Tyr Leu Asn Cys Gln Val Ile
 405 410 415

His His Leu Phe Pro Asp Met Pro Gln Phe Arg Gln Pro Glu Val Ser
 420 425 430

Arg Arg Phe Val Pro Phe Ala Lys Lys Trp Asn Leu Asn Tyr Lys Val
 435 440 445

Leu Thr Tyr Tyr Gly Ala Trp Lys Ala Thr Phe Gly Asn Leu Asn Asp
 450 455 460

Val Gly Lys His Tyr Tyr Val His Gly Ser Gln Arg Val Lys Ser Lys

465 470 475 480

Ser Ala

<210> 13
 <211> 456
 <212> PRT
 <213> *Ostreococcus tauri*

<400> 13

Met Cys Val Glu Thr Glu Asn Asn Asp Gly Ile Pro Thr Val Glu Ile
 1 5 10 15

Ala Phe Asp Gly Glu Arg Glu Arg Ala Glu Ala Asn Val Lys Leu Ser
 20 25 30

Ala Glu Lys Met Glu Pro Ala Ala Leu Ala Lys Thr Phe Ala Arg Arg
 35 40 45

Tyr Val Val Ile Glu Gly Val Glu Tyr Asp Val Thr Asp Phe Lys His
 50 55 60

Pro Gly Gly Thr Val Ile Phe Tyr Ala Leu Ser Asn Thr Gly Ala Asp
 65 70 75 80

Ala Thr Glu Ala Phe Lys Glu Phe His His Arg Ser Arg Lys Ala Arg
 85 90 95

Lys Ala Leu Ala Ala Leu Pro Ser Arg Pro Ala Lys Thr Ala Lys Val
 100 105 110

Asp Asp Ala Glu Met Leu Gln Asp Phe Ala Lys Trp Arg Lys Glu Leu
 115 120 125

Glu Arg Asp Gly Phe Phe Lys Pro Ser Pro Ala His Val Ala Tyr Arg
 130 135 140

Phe Ala Glu Leu Ala Ala Met Tyr Ala Leu Gly Thr Tyr Leu Met Tyr
145 150 155 160

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

Ala Arg Cys Gly Trp Val Gln His Glu Gly Gly His Ser Ser Leu Thr
180 185 190

Gly Asn Ile Trp Trp Asp Lys Arg Ile Gln Ala Phe Thr Ala Gly Phe
195 200 205

Gly Leu Ala Gly Ser Gly Asp Met Trp Asn Ser Met His Asn Lys His
210 215 220

His Ala Thr Pro Gln Lys Val Arg His Asp Met Asp Leu Asp Thr Thr
225 230 235 240

Pro Ala Val Ala Phe Phe Asn Thr Ala Val Glu Asp Asn Arg Pro Arg
245 250 255

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

Val Thr Ser Gly Leu Val Leu Leu Phe Trp Met Phe Phe Leu His Pro
275 280 285

Ser Lys Ala Leu Lys Gly Gly Lys Tyr Glu Glu Leu Val Trp Met Leu
290 295 300

Ala Ala His Val Ile Arg Thr Trp Thr Ile Lys Ala Val Thr Gly Phe
305 310 315 320

Thr Ala Met Gln Ser Tyr Gly Leu Phe Leu Ala Thr Ser Trp Val Ser
325 330 335

Gly Cys Tyr Leu Phe Ala His Phe Ser Thr Ser His Thr His Leu Asp
340 345 350

Val Val Pro Ala Asp Glu His Leu Ser Trp Val Arg Tyr Ala Val Asp
355 360 365

His Thr Ile Asp Ile Asp Pro Ser Gln Gly Trp Val Asn Trp Leu Met
370 375 380

Gly Tyr Leu Asn Cys Gln Val Ile His His Leu Phe Pro Ser Met Pro
385 390 395 400

Gln Phe Arg Gln Pro Glu Val Ser Arg Arg Phe Val Ala Phe Ala Lys
405 410 415

Lys Trp Asn Leu Asn Tyr Lys Val Met Thr Tyr Ala Gly Ala Trp Lys
420 425 430

Ala Thr Leu Gly Asn Leu Asp Asn Val Gly Lys His Tyr Tyr Val His
435 440 445

Gly Gln His Ser Gly Lys Thr Ala
450 455

<210> 14
<211> 894
<212> DNA
<213> Pyramimonas cordata

<400> 14
atggagttcg ctcagcctct tgtggctatg gcacaggagc agtatgccgc aattgacgcg 60
gtggtagccc ctgcaatttt ctcagctacc gacagcatcg gttgggggtct taagcccatt 120
agcagcgcga caaaggatct tcctctcggt gagagtccga cgccgctcat actgagcctg 180
ttggcctatt ttgcgatcgt cggctctggg ctggtgtacc gcaaagtatt ccctcgaca 240

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gtaaaggggc aagacccctt cctgctgaag gcgctcatgc ttgcgcacaa cgtgttcctc	300
attggcctca gtctatacat gtgcttgaag cttgtctacg aggcttacgt caacaagtac	360
tccttctggg gaaacgccta caaccccgca cagaccgaga tggcgaaggt catctggatt	420
ttctacgtct ccaagatcta tgagttcatg gacacgttca tcatgctctt gaagggcaac	480
gtcaaccagg tctctttcct gcatgtgtac catcatggct ccatctctgg tatctgggtg	540
atgatcacct acgctgcccc tggcgggtgac gcgtacttct cggcggcgct caactcgtgg	600
gtgcacgtgt gcatgtacac gtactacttc atggcggcgg tgctgcccac ggacgagaag	660
accaagcgca agtacctctg gtggggccgc tacctgaccc agatgcagat gttccagttc	720
ttcatgaacc tgctccaggc ggtctacctc ctctactcct ctagccccta ccccaagttc	780
atcgcccagc tgctgggtgg gtacatgggtc acgctgctga tgctcttcgg caacttctac	840
tacatgaagc accacgcgag caagaagcag aagctggcca gcaagaagca gtag	894

<210> 15

<211> 870

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon-optimized open reading frame for expression of Pyramimonas cordata 6 elongase in plants (truncated at 3' end and encoding functional elongase) (version 1)

<400> 15

atggaattcg cccagcctct tggtgctatg gctcaagagc aatacgtgc tatcgtatgct	60
gttgttgctc ctgctatctt ctctgctact gattctatcg gatggggact taagcctatc	120
tcttctgcta ctaaggactt gcctcttggt gagtctccta cacctctcat cttttctttg	180
cttgcttact tcgctatcgt tggatctgga ctcgtttaca gaaaggtttt ccctagaacc	240
gtgaaggagc aagatccatt ctttttgaag gctcttatgc ttgctcacia cgtgttcctt	300
atcggacttt ctctttacat gtgcctcaag cttgtgtacg aggcttacgt taacaagtac	360
tctttctggg gaaacgctta caaccctgct caaactgaga tggctaaggt tatctggatc	420

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ttctacgtga gcaagatcta cgagttcatg gataccttca tcatgctcct caagggaaat	480
gttaaccagg ttagcttcct tcacgtttac catcacggat ctatctctgg aatctggtgg	540
atgattactt acgctgctcc tgggtggtgat gcttacttct ctgctgctct taactcttgg	600
gttcacgtgt gtatgtacac ctactatttt atggctgccg tgcttcctaa ggacgagaaa	660
actaagagaa agtacctctg gtggggaaga taccttactc aaatgcagat gttccagttc	720
ttcatgaacc ttctccaggc tgtttacctt ctctactctt catctcctta ccctaagttt	780
atcgctcagc tcctcgtggg gtacatgggt actctttctca tgcttttcgg aaacttctac	840
tacatgaagc accacgctag caagtgatga	870

<210> 16
 <211> 297
 <212> PRT
 <213> *Pyramimonas cordata*

<400> 16

Met	Glu	Phe	Ala	Gln	Pro	Leu	Val	Ala	Met	Ala	Gln	Glu	Gln	Tyr	Ala
1			5					10						15	

Ala	Ile	Asp	Ala	Val	Val	Ala	Pro	Ala	Ile	Phe	Ser	Ala	Thr	Asp	Ser
		20					25						30		

Ile	Gly	Trp	Gly	Leu	Lys	Pro	Ile	Ser	Ser	Ala	Thr	Lys	Asp	Leu	Pro
	35					40						45			

Leu	Val	Glu	Ser	Pro	Thr	Pro	Leu	Ile	Leu	Ser	Leu	Leu	Ala	Tyr	Phe
	50					55					60				

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

Val	Lys	Gly	Gln	Asp	Pro	Phe	Leu	Leu	Lys	Ala	Leu	Met	Leu	Ala	His
			85						90					95	

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Asn Val Phe Leu Ile Gly Leu Ser Leu Tyr Met Cys Leu Lys Leu Val
100 105 110

Tyr Glu Ala Tyr Val Asn Lys Tyr Ser Phe Trp Gly Asn Ala Tyr Asn
115 120 125

Pro Ala Gln Thr Glu Met Ala Lys Val Ile Trp Ile Phe Tyr Val Ser
130 135 140

Lys Ile Tyr Glu Phe Met Asp Thr Phe Ile Met Leu Leu Lys Gly Asn
145 150 155 160

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

Gly Ile Trp Trp Met Ile Thr Tyr Ala Ala Pro Gly Gly Asp Ala Tyr
180 185 190

Phe Ser Ala Ala Leu Asn Ser Trp Val His Val Cys Met Tyr Thr Tyr
195 200 205

Tyr Phe Met Ala Ala Val Leu Pro Lys Asp Glu Lys Thr Lys Arg Lys
210 215 220

Tyr Leu Trp Trp Gly Arg Tyr Leu Thr Gln Met Gln Met Phe Gln Phe
225 230 235 240

Phe Met Asn Leu Leu Gln Ala Val Tyr Leu Leu Tyr Ser Ser Ser Pro
245 250 255

Tyr Pro Lys Phe Ile Ala Gln Leu Leu Val Val Tyr Met Val Thr Leu
260 265 270

Leu Met Leu Phe Gly Asn Phe Tyr Tyr Met Lys His His Ala Ser Lys
275 280 285

Lys Gln Lys Leu Ala Ser Lys Lys Gln
 290 295

<210> 17
 <211> 288
 <212> PRT
 <213> *Pyramimonas cordata*

<400> 17

Met Glu Phe Ala Gln Pro Leu Val Ala Met Ala Gln Glu Gln Tyr Ala
 1 5 10 15

Ala Ile Asp Ala Val Val Ala Pro Ala Ile Phe Ser Ala Thr Asp Ser
 20 25 30

Ile Gly Trp Gly Leu Lys Pro Ile Ser Ser Ala Thr Lys Asp Leu Pro
 35 40 45

Leu Val Glu Ser Pro Thr Pro Leu Ile Leu Ser Leu Leu Ala Tyr Phe
 50 55 60

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

Val Lys Gly Gln Asp Pro Phe Leu Leu Lys Ala Leu Met Leu Ala His
 85 90 95

Asn Val Phe Leu Ile Gly Leu Ser Leu Tyr Met Cys Leu Lys Leu Val
 100 105 110

Tyr Glu Ala Tyr Val Asn Lys Tyr Ser Phe Trp Gly Asn Ala Tyr Asn
 115 120 125

Pro Ala Gln Thr Glu Met Ala Lys Val Ile Trp Ile Phe Tyr Val Ser
 130 135 140

Lys Ile Tyr Glu Phe Met Asp Thr Phe Ile Met Leu Leu Lys Gly Asn

Leu Met Leu Phe Gly Asn Phe Tyr Tyr Met Lys His His Ala Ser Lys
275 280 285

<213> Pavlova salina

gcgacggacg cgtacaagca gttccatgtg cggctctgcca aggcgggacaa gatgctcaag 240

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tcgctgcctt cgcgcccggg gcacaagggc tactcgcccc gccgcgctga cctcattgcc	300
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cacgtggcat accgcctggc ggaggtgatc gcgatgcacg tggccggcgc cgcgctcatc	420
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<210> 19

<211> 1281

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon-optimized open reading frame for expression of Pavlova salina 5 desaturase in plants (version 1)

<400> 19

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<210> 20
 <211> 425
 <212> PRT

<213> Pavlova salina

<400> 20

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Leu His Glu Val Asp Thr Pro Gln Glu His Asp Lys Lys Glu Leu Val
 20 25 30

Ile Gly Asp Arg Ala Tyr Asp Val Thr Asn Phe Val Lys Arg His Pro
 35 40 45

Gly Gly Lys Ile Ile Ala Tyr Gln Val Gly Thr Asp Ala Thr Asp Ala
 50 55 60

Tyr Lys Gln Phe His Val Arg Ser Ala Lys Ala Asp Lys Met Leu Lys
 65 70 75 80

Ser Leu Pro Ser Arg Pro Val His Lys Gly Tyr Ser Pro Arg Arg Ala
 85 90 95

Asp Leu Ile Ala Asp Phe Gln Glu Phe Thr Lys Gln Leu Glu Ala Glu
 100 105 110

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

Val Ile Ala Met His Val Ala Gly Ala Ala Leu Ile Trp His Gly Tyr
 130 135 140

Thr Phe Ala Gly Ile Ala Met Leu Gly Val Val Gln Gly Arg Cys Gly
 145 150 155 160

Trp Leu Met His Glu Gly Gly His Tyr Ser Leu Thr Gly Asn Ile Ala
 165 170 175

PCTAU2015050340-seql-000001-EN-20150624 (1)

Phe Asp Arg Ala Ile Gln Val Ala Cys Tyr Gly Leu Gly Cys Gly Met
180 185 190

Ser Gly Ala Trp Trp Arg Asn Gln His Asn Lys His His Ala Thr Pro
195 200 205

Gln Lys Leu Gln His Asp Val Asp Leu Asp Thr Leu Pro Leu Val Ala
210 215 220

Phe His Glu Arg Ile Ala Ala Lys Val Lys Ser Pro Ala Met Lys Ala
225 230 235 240

Trp Leu Ser Met Gln Ala Lys Leu Phe Ala Pro Val Thr Thr Leu Leu
245 250 255

Val Ala Leu Gly Trp Gln Leu Tyr Leu His Pro Arg His Met Leu Arg
260 265 270

Thr Lys His Tyr Asp Glu Leu Ala Met Leu Gly Ile Arg Tyr Gly Leu
275 280 285

Val Gly Tyr Leu Ala Ala Asn Tyr Gly Ala Gly Tyr Val Leu Ala Cys
290 295 300

Tyr Leu Leu Tyr Val Gln Leu Gly Ala Met Tyr Ile Phe Cys Asn Phe
305 310 315 320

Ala Val Ser His Thr His Leu Pro Val Val Glu Pro Asn Glu His Ala
325 330 335

Thr Trp Val Glu Tyr Ala Ala Asn His Thr Thr Asn Cys Ser Pro Ser
340 345 350

Trp Trp Cys Asp Trp Trp Met Ser Tyr Leu Asn Tyr Gln Ile Glu His
355 360 365

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His Leu Tyr Pro Ser Met Pro Gln Phe Arg His Pro Lys Ile Ala Pro
370 375 380

Arg Val Lys Gln Leu Phe Glu Lys His Gly Leu His Tyr Asp Val Arg
385 390 395 400

Gly Tyr Phe Glu Ala Met Ala Asp Thr Phe Ala Asn Leu Asp Asn Val
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Ala His Ala Pro Glu Lys Lys Met Gln
420 425

<210> 21
<211> 1329
<212> DNA
<213> Pyramimonas cordata

<400> 21
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ggttctgggtg ctgacgccac cgcttcctac cgcgagttcc acgttaggtc agcgaaggca 180
gacaagttct tgaagacgct gccctccgc gaagccactc cccaggagct gaagcaggcg 240
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tatagtctta ctgggaagat ctccattgat aggcgtctgc aggagtcaat ttacggattc 600
ggctgtggaa tgtccggcgc ctggtggcgc aaccagcaca acaagcacca cgcaacccca 660
cagaagctgc agcatgacgt cgacctggag acccttcctc tgatggcttt caacaacgct 720
gttaccgata gacgcaaggt gaagcctggt agtctccagg ctctgtggct caagtaccag 780

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<210> 22

<211> 442

<212> PRT

<213> Pyramimonas cordata

<400> 22

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Leu Ile Glu Gly Lys Phe Tyr Asp Val Thr Asp Phe Arg His Pro Gly
 20 25 30

Gly Ser Ile Ile Lys Phe Leu Ser Gly Ser Gly Ala Asp Ala Thr Ala
 35 40 45

Ser Tyr Arg Glu Phe His Val Arg Ser Ala Lys Ala Asp Lys Phe Leu
 50 55 60

Lys Thr Leu Pro Ser Arg Glu Ala Thr Pro Gln Glu Leu Lys Gln Ala
 65 70 75 80

PCTAU2015050340-seql-000001-EN-20150624 (1)

Val Glu Phe Ser Lys Leu Asn Pro Pro Ser Ala Glu Ser Ala Ser Ala
85 90 95

Pro Leu Thr Asp Leu Ala Lys Val Glu Ala Leu Asn Lys Asp Phe Glu
100 105 110

Ala Phe Arg Glu Gln Leu Ile Gln Glu Gly Phe Phe Lys Pro Asn Ile
115 120 125

Pro His Val Val Lys Arg Ile Thr Glu Val Val Ala Met Met Ala Val
130 135 140

Ala Ser Trp Met Met Val Gln Thr Asn Ala Leu Val Val Thr Leu Gly
145 150 155 160

Val Leu Ile Arg Gly Ile Ala Gln Gly Arg Cys Gly Trp Leu Met His
165 170 175

Glu Gly Gly His Tyr Ser Leu Thr Gly Lys Ile Ser Ile Asp Arg Arg
180 185 190

Leu Gln Glu Ser Ile Tyr Gly Phe Gly Cys Gly Met Ser Gly Ala Trp
195 200 205

Trp Arg Asn Gln His Asn Lys His His Ala Thr Pro Gln Lys Leu Gln
210 215 220

His Asp Val Asp Leu Glu Thr Leu Pro Leu Met Ala Phe Asn Asn Ala
225 230 235 240

Val Thr Asp Arg Arg Lys Val Lys Pro Gly Ser Leu Gln Ala Leu Trp
245 250 255

Leu Lys Tyr Gln Ala Phe Leu Phe Phe Pro Val Thr Ser Leu Leu Val
260 265 270

PCTAU2015050340-seql-000001-EN-20150624 (1)

Gly Leu Gly Trp Thr Thr Val Leu His Pro Arg His Ser Leu Arg Thr
275 280 285

Lys His Tyr Phe Glu Leu Leu Cys Met Ala Ala Arg Tyr Ala Ser Phe
290 295 300

Ala Ala Leu Phe Ala Pro Lys Tyr Gly Leu Ala Gly Ala Ala Gly Leu
305 310 315 320

Tyr Leu Ala Thr Phe Ala Val Gly Cys Asn Tyr Ile Phe Ile Asn Phe
325 330 335

Ser Val Ser His Thr His Leu Pro Val Ser Gly Ala Ser Glu Tyr Leu
340 345 350

His Trp Val Val Tyr Ser Ala Ile His Thr Thr Asn Ile Lys Ser Ser
355 360 365

Met Leu Cys Asp Trp Trp Met Ser Phe Leu Asn Phe Gln Ile Glu His
370 375 380

His Leu Phe Pro Ser Met Pro Gln Phe Arg His Lys Ile Ile Ser Pro
385 390 395 400

Arg Val Lys Ala Leu Phe Glu Lys His Gly Leu Val Tyr Asp Val Arg
405 410 415

Pro Tyr Trp Gly Ala Met Ala Asp Thr Phe Lys Asn Leu Asn Asp Val
420 425 430

Gly Thr His Ala Ser His Ser Lys Ala His
435 440

<210> 23

<211> 804

<212> DNA

<213> Pyramimonas cordata

<400> 23

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tattggggggc caacgattgg gaccatcggg tatcttctgt tcatctactt tggtaaacgg      180
attatgcaaa acaggagcca gccgtttggc ctgaagaacg ctatgctggg gtacaacttc      240
tatcagactt tcttcaactc gtactgcata tacctttttg tcacgtcgca ccgcgctcag      300
gggctgaaag tttggggaaa catccccgat atgactgcca acagctgggg gatctcacag      360
gtgatctggc tgcactacaa caacaagtac gttgagctgc tggacacgtt cttcatggtc      420
atgcbgaaga agtttgacca gctttcgctc ctgcacattt accatcatac cctgttgatc      480
tggtcttggt tcgtgggtgat gaaattggag cccgttgggg actgctactt tggctctagc      540
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<210> 24

<211> 807

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon-optimized open reading frame for expression of Pyramimonas
cordata 5 elongase in plants (version 1)

<400> 24

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tactgggggac ctactatcgg aactattgga tacctcctct tcatctactt cggaaaagcgt      180
atcatgcaga acagatctca acctttcgga ctcaagaacg ctatgctcgt ttacaacttc      240

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<210> 25
 <211> 267
 <212> PRT
 <213> Pyramimonas cordata

<400> 25

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			20					25					30		

Pro	Ala	Tyr	Phe	Met	Gln	Val	Glu	Tyr	Trp	Gly	Pro	Thr	Ile	Gly	Thr
		35					40					45			

Ile	Gly	Tyr	Leu	Leu	Phe	Ile	Tyr	Phe	Gly	Lys	Arg	Ile	Met	Gln	Asn
	50					55					60				

Arg	Ser	Gln	Pro	Phe	Gly	Leu	Lys	Asn	Ala	Met	Leu	Val	Tyr	Asn	Phe
65					70					75					80

Tyr Gln Thr Phe Phe Asn Ser Tyr Cys Ile Tyr Leu Phe Val Thr Ser
85 90 95

His Arg Ala Gln Gly Leu Lys Val Trp Gly Asn Ile Pro Asp Met Thr
100 105 110

Ala Asn Ser Trp Gly Ile Ser Gln Val Ile Trp Leu His Tyr Asn Asn
115 120 125

Lys Tyr Val Glu Leu Leu Asp Thr Phe Phe Met Val Met Arg Lys Lys
130 135 140

Phe Asp Gln Leu Ser Phe Leu His Ile Tyr His His Thr Leu Leu Ile
145 150 155 160

Trp Ser Trp Phe Val Val Met Lys Leu Glu Pro Val Gly Asp Cys Tyr
165 170 175

Phe Gly Ser Ser Val Asn Thr Phe Val His Val Ile Met Tyr Ser Tyr
180 185 190

Tyr Gly Leu Ala Ala Leu Gly Val Asn Cys Phe Trp Lys Lys Tyr Ile
195 200 205

Thr Gln Ile Gln Met Leu Gln Phe Cys Ile Cys Ala Ser His Ser Ile
210 215 220

Tyr Thr Ala Tyr Val Gln Asn Thr Ala Phe Trp Leu Pro Tyr Leu Gln
225 230 235 240

Leu Trp Val Met Val Asn Met Phe Val Leu Phe Ala Asn Phe Tyr Arg
245 250 255

Lys Arg Tyr Lys Ser Lys Gly Ala Lys Lys Gln
260 265

<210> 26

<211> 1344

<212> DNA

<213> Pavlova salina

<400> 26

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gacagcgtgt acgatgcgaa ggcgttccgc tccgagcatc cgggtggcgc gcactttgtg	180
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aggccgcgca gcaaggcgga gtga 1344

<210> 27

<211> 1347

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon-optimized open reading frame for expression of Pavlova salina 4 desaturase in plants (version 1)

<400> 27

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gattctgttt acgatgctaa ggctttcaga tctgagcatc ctgggtgggtgc tcatttcggtt 180

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cctaagtcta gaatgtctag attccacgtt ggatctcttg cttctactga ggaacctgtt 300

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<210> 28

<211> 447

<212> PRT

<213> Pavlova salina

<400> 28

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		20					25					30			

Arg	Pro	Asp	Leu	Thr	Ile	Val	Gly	Asp	Ser	Val	Tyr	Asp	Ala	Lys	Ala
		35				40					45				

Phe	Arg	Ser	Glu	His	Pro	Gly	Gly	Ala	His	Phe	Val	Ser	Leu	Phe	Gly
	50					55				60					

Gly	Arg	Asp	Ala	Thr	Glu	Ala	Phe	Met	Glu	Tyr	His	Arg	Arg	Ala	Trp
65				70					75					80	

Pro	Lys	Ser	Arg	Met	Ser	Arg	Phe	His	Val	Gly	Ser	Leu	Ala	Ser	Thr
			85					90						95	

Glu	Glu	Pro	Val	Ala	Ala	Asp	Glu	Gly	Tyr	Leu	Gln	Leu	Cys	Ala	Arg
			100					105					110		

Ile Ala Lys Met Val Pro Ser Val Ser Ser Gly Phe Ala Pro Ala Ser
115 120 125

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

Ala Tyr Met Leu Tyr Ala Gly Lys Arg Leu Leu Pro Ser Ile Val Leu
145 150 155 160

Gly Trp Leu Phe Ala Leu Ile Gly Leu Asn Ile Gln His Asp Ala Asn
165 170 175

His Gly Ala Leu Ser Lys Ser Ala Ser Val Asn Leu Ala Leu Gly Leu
180 185 190

Cys Gln Asp Trp Ile Gly Gly Ser Met Ile Leu Trp Leu Gln Glu His
195 200 205

Val Val Met His His Leu His Thr Asn Asp Val Asp Lys Asp Pro Asp
210 215 220

Gln Lys Ala His Gly Ala Leu Arg Leu Lys Pro Thr Asp Ala Trp Ser
225 230 235 240

Pro Met His Trp Leu Gln His Leu Tyr Leu Leu Pro Gly Glu Thr Met
245 250 255

Tyr Ala Phe Lys Leu Leu Phe Leu Asp Ile Ser Glu Leu Val Met Trp
260 265 270

Arg Trp Glu Gly Glu Pro Ile Ser Lys Leu Ala Gly Tyr Leu Phe Met
275 280 285

Pro Ser Leu Leu Leu Lys Leu Thr Phe Trp Ala Arg Phe Val Ala Leu
290 295 300

Pro Leu Tyr Leu Ala Pro Ser Val His Thr Ala Val Cys Ile Ala Ala
305 310 315 320

Thr Val Met Thr Gly Ser Phe Tyr Leu Ala Phe Phe Phe Phe Ile Ser
325 330 335

His Asn Phe Glu Gly Val Ala Ser Val Gly Pro Asp Gly Ser Ile Thr
340 345 350

Ser Met Thr Arg Gly Ala Ser Phe Leu Lys Arg Gln Ala Glu Thr Ser
355 360 365

Ser Asn Val Gly Gly Pro Leu Leu Ala Thr Leu Asn Gly Gly Leu Asn
370 375 380

Tyr Gln Ile Glu His His Leu Phe Pro Arg Val His His Gly Phe Tyr
385 390 395 400

Pro Arg Leu Ala Pro Leu Val Lys Ala Glu Leu Glu Ala Arg Gly Ile
405 410 415

Glu Tyr Lys His Tyr Pro Thr Ile Trp Ser Asn Leu Ala Ser Thr Leu
420 425 430

Arg His Met Tyr Ala Leu Gly Arg Arg Pro Arg Ser Lys Ala Glu
435 440 445

<210> 29

<211> 263

<212> PRT

<213> Isochrysis galbana

<400> 29

Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr
1 5 10 15

Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro
20 25 30

Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg
35 40 45

Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu
50 55 60

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

Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
85 90 95

Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
100 105 110

Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
115 120 125

Val Leu Lys Gly Lys Arg Val Ser Phe Leu Gln Ala Phe His His Phe
130 135 140

Gly Ala Pro Trp Asp Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly
145 150 155 160

Val Trp Ile Phe Met Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr
165 170 175

Thr Tyr Tyr Gly Leu Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro
180 185 190

Leu Ile Thr Ala Met Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu
195 200 205

Val Trp Asp Tyr Ile Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys
210 215 220

Leu Phe Ser Trp Ala Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu
225 230 235 240

Leu Phe Cys His Phe Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser
245 250 255

Ala Lys Ala Gly Lys Gln Leu
260

<210> 30
<211> 801
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized open reading frame for expression of Emilia
huxleyi 9 elongase in plants

<400> 30
atgcttgata gagcttcatc tgatgctgct atttggagcg ctgtttctga tcctgagatc 60
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gatgagagaa agggagctta ccgtacttct atgatctggt acaacgttgt tcttgctctt 180
ttctctgcta cctctttcta cgttactgct actgctcttg gatgggataa gggaactggt 240
gagtggctta gatctcttac tgggtattct cctcaacaac tttggcagtg cccttctaga 300
gtttgggaca gcaaactctt cttgtggact gctaaagcct tctactactc caagtacgtt 360
gagtaccttg atactgcttg gcttggtctc aagggaaga aggtttcatt cctccaggga 420
ttccatcatt tcggtgctcc atgggatgtt taccttgga tcaggcttaa gaacgaggga 480
gtttggatct tcatgttctt caacagcttc atccacactg ttatgtacac ttactacgga 540
cttactgctg ctggatacaa gatcagagga aagcctatca tcaccgctat gcaaactctt 600
caattcgttg gtggattcgt tcttgtgtgg gactacatca acgttccttg tttccatgct 660

gatgctggac aagttttctc ttgggtgttc aactacgctt atgtgggatc tgttttcctt 720
 cttttctgcc acttcttcta catggacaac attgctaagg ctaaggctaa aaaggctgtt 780
 gctaccagaa aggctctttg a 801

<210> 31
 <211> 266
 <212> PRT
 <213> *Emiliana huxleyi*
 <400> 31

Met Leu Asp Arg Ala Ser Ser Asp Ala Ala Ile Trp Ser Ala Val Ser
 1 5 10 15

Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro
 20 25 30

Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Arg Lys Gly Ala Tyr Arg
 35 40 45

Thr Ser Met Ile Trp Tyr Asn Val Val Leu Ala Leu Phe Ser Ala Thr
 50 55 60

Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Lys Gly Thr Gly
 65 70 75 80

Glu Trp Leu Arg Ser Leu Thr Gly Asp Ser Pro Gln Gln Leu Trp Gln
 85 90 95

Cys Pro Ser Arg Val Trp Asp Ser Lys Leu Phe Leu Trp Thr Ala Lys
 100 105 110

Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
 115 120 125

Val Leu Lys Gly Lys Lys Val Ser Phe Leu Gln Gly Phe His His Phe

130

135

140

Gly Ala Pro Trp Asp Val Tyr Leu Gly Ile Arg Leu Lys Asn Glu Gly
 145 150 155 160

Val Trp Ile Phe Met Phe Phe Asn Ser Phe Ile His Thr Val Met Tyr
 165 170 175

Thr Tyr Tyr Gly Leu Thr Ala Ala Gly Tyr Lys Ile Arg Gly Lys Pro
 180 185 190

Ile Ile Thr Ala Met Gln Ile Ser Gln Phe Val Gly Gly Phe Val Leu
 195 200 205

Val Trp Asp Tyr Ile Asn Val Pro Cys Phe His Ala Asp Ala Gly Gln
 210 215 220

Val Phe Ser Trp Val Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu
 225 230 235 240

Leu Phe Cys His Phe Phe Tyr Met Asp Asn Ile Ala Lys Ala Lys Ala
 245 250 255

Lys Lys Ala Val Ala Thr Arg Lys Ala Leu
 260 265

<210> 32

<211> 819

<212> DNA

<213> Pavlova pinguis

<400> 32

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ttcgggtgggg aggtgctcta cttctccatt gcctacctgt ttcttgcgcc cattttgaag 120

cgcaccccggt tgggtggacac gcggaagggc gcgtataaga gtggtatgat cgcgtacaac 180

gtgatcatgt gcgtgttctc gctggtgtgc ttcatctgcc agctcgcagc cctgggctat 240

gacatgggct acttgacgtg ggtgcgtgac ctcacagggg acgagattgt cccctctac 300
 caggacgtgt ccccgctccc cgccttctcc aacaagctct tcaagtattc gtctattgcc 360
 ttccactact ccaagtatgt tgagtacatg gacaccgcat ggctgggtgat gaagggcaag 420
 cccgtgtcct tgctccaggg cttccaccac tttggcgccg cctgggacac ctactttggc 480
 atcaccttcc agaacgaggg catctacgtg ttcgtgggtgc tcaacgcctt catccacacg 540
 atcatgtacg catactacgc ggccactgcg gcgggtctca agttctcact gaagttcgtc 600
 atcacgctca tgcagatcac ccaattcaac gtgggcttcg taatgggtgta tcactacatc 660
 accctggagt acttccgcaa ctcaccggag ctcgtcttct cctacctttt caactatgcg 720
 tacgtctgca cggttctcct cctcttcatg cagttcttct acatggacaa ctttggcaag 780
 aagaaggccg ctgccgccgc gggcaagaag aagaagtag 819

<210> 33
 <211> 272
 <212> PRT
 <213> Pavlova pinguis

<400> 33

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

Lys Asp Ala Val Phe Gly Gly Glu Val Leu Tyr Phe Ser Ile Ala Tyr
 20 25 30

Leu Phe Leu Ala Pro Ile Leu Lys Arg Thr Pro Leu Val Asp Thr Arg
 35 40 45

Lys Gly Ala Tyr Lys Ser Gly Met Ile Ala Tyr Asn Val Ile Met Cys
 50 55 60

Val Phe Ser Leu Val Cys Phe Ile Cys Gln Leu Ala Ala Leu Gly Tyr
 65 70 75 80

Asp Met Gly Tyr Leu Gln Trp Val Arg Asp Leu Thr Gly Asp Glu Ile
85 90 95

Val Pro Leu Tyr Gln Asp Val Ser Pro Ser Pro Ala Phe Ser Asn Lys
100 105 110

Leu Phe Lys Tyr Ser Ser Ile Ala Phe His Tyr Ser Lys Tyr Val Glu
115 120 125

Tyr Met Asp Thr Ala Trp Leu Val Met Lys Gly Lys Pro Val Ser Leu
130 135 140

Leu Gln Gly Phe His His Phe Gly Ala Ala Trp Asp Thr Tyr Phe Gly
145 150 155 160

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

Phe Ile His Thr Ile Met Tyr Ala Tyr Tyr Ala Ala Thr Ala Ala Gly
180 185 190

Leu Lys Phe Ser Leu Lys Phe Val Ile Thr Leu Met Gln Ile Thr Gln
195 200 205

Phe Asn Val Gly Phe Val Met Val Tyr His Tyr Ile Thr Leu Glu Tyr
210 215 220

Phe Arg Asn Ser Pro Glu Leu Val Phe Ser Tyr Leu Phe Asn Tyr Ala
225 230 235 240

Tyr Val Cys Thr Val Leu Leu Leu Phe Met Gln Phe Phe Tyr Met Asp
245 250 255

Asn Phe Gly Lys Lys Lys Ala Ala Ala Ala Ala Gly Lys Lys Lys Lys
260 265 270

<210> 34

<211> 840

<212> DNA

<213> Pavlova salina

<400> 34

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atcctcaagc gctcaccgtt tgtggacaag cgcaagggcg cataaccgcaa cggcatgatc      180
gcgtacaaca tcctcatgtg cggtttctcg ctggtatgct tcgtgtgcca gatggcggcg      240
ctcggccttg atcgcggcc cctgcagttt gtccgcgacc tcacgggcga cagcgtggtg      300
cagctctacc aggacgtgag cccatcccct gcattcgcga acaagctctt ccggtactca      360
gcggtggcgt tccactactc aaagtacgtg gagtacatgg acacagcgtg gcttgtgctg      420
aagggcaagc ccgtctcggt cctgcagggc ttccaccact tcggcgccgc gtgggacacc      480
tactttggca tcacgtttca gaacgagggc acctacgtct ttgtgctgct caacgcattc      540
atccacacaa tcatgtacac ctactacggc gcgacggcag cgggcatcaa aatctcgatg      600
aagccgctga tcaccctcat gcagatcacg cagttcctgc tgggcttcgc gctcgtctac      660
ccgtacattg acctcggcta cttccgtgcg tcgcccgagc tcgtgtggag ctacctgttc      720
aactatgcgt acgtactcat ggtgctcttc ctcttcatgc gcttcttcta ccacgacaac      780
ttagcaagc acaagccaat ctcgcgcata gactccagca accgcatgaa aaccgagtag      840

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<210> 35

<211> 279

<212> PRT

<213> Pavlova salina

<400> 35

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Met Ala Thr Glu Gly Met Pro Ala Ile Thr Leu Asp Trp Leu Leu Ser
1           5           10          15

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Pro Gly Leu Lys Asp Ala Val Ile Gly Gly Glu Val Leu Tyr Phe Ser

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20

25

30

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

Asp Lys Arg Lys Gly Ala Tyr Arg Asn Gly Met Ile Ala Tyr Asn Ile
 50 55 60

Leu Met Cys Gly Phe Ser Leu Val Cys Phe Val Cys Gln Met Ala Ala
 65 70 75 80

Leu Gly Leu Asp Arg Gly His Leu Gln Phe Val Arg Asp Leu Thr Gly
 85 90 95

Asp Ser Val Val Gln Leu Tyr Gln Asp Val Ser Pro Ser Pro Ala Phe
 100 105 110

Ala Asn Lys Leu Phe Arg Tyr Ser Ala Val Ala Phe His Tyr Ser Lys
 115 120 125

Tyr Val Glu Tyr Met Asp Thr Ala Trp Leu Val Leu Lys Gly Lys Pro
 130 135 140

Val Ser Phe Leu Gln Gly Phe His His Phe Gly Ala Ala Trp Asp Thr
 145 150 155 160

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

Leu Asn Ala Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Ala Thr
 180 185 190

Ala Ala Gly Ile Lys Ile Ser Met Lys Pro Leu Ile Thr Leu Met Gln
 195 200 205

Ile Thr Gln Phe Leu Leu Gly Phe Ala Leu Val Tyr Pro Tyr Ile Asp

210

215

220

Leu Gly Tyr Phe Arg Ala Ser Pro Glu Leu Val Trp Ser Tyr Leu Phe
 225 230 235 240

Asn Tyr Ala Tyr Val Leu Met Val Leu Phe Leu Phe Met Arg Phe Phe
 245 250 255

Tyr His Asp Asn Phe Ser Lys His Lys Pro Ile Ser Arg Ile Asp Ser
 260 265 270

Ser Asn Arg Met Lys Thr Glu
 275

<210> 36

<211> 1284

<212> DNA

<213> Pavlova salina

<400> 36

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 agcgaccgcg cggagggtgag caacgctgac agcaaagcgc tgcacatcgt gctgtatggc 120
 aagcgcgtgg atgtgaccaa gttccaacgc acgcacccgg gtggtagcaa ggtcttccgg 180
 atcttccagg accgcgatgc gacggagcag ttcgagtcct accactcgaa gcgcgcgatc 240
 aagatgatgg agggcatgct caagaagtct gaggatgctc ccgccgacac gcccttgccc 300
 tcccagtcac cgatggggaa ggacttcaag gcgatgatcg agcggcacgt tgcagcgggt 360
 tactacgatc catgcccgtc cgatgagctg ttcaagctca gcctcgtgct cctcccgacc 420
 tttgcgggca tgtacatgct caaggcgggc gtcggctccc cgctctgcgg cgccctcatg 480
 gtgagctttg gctggtacct cgatggctgg ctcgcgcacg actatctgca ccaactccgtc 540
 ttcaaggggt ccgtcgcacg caccgtcggg tggaacaacg cggcgggcta cttcctcggc 600
 ttcgtgcagg ggtatgcggt cgagtgggtg gcgcgcgggc ataacacgca ccacgtgtgc 660
 accaatgagg acggctcgga ccccgacatc aaaacggcgc cgctgctcat atacgtgcgc 720

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aacaagccga gcatcgccaa gcgcctgaac gccttccagc gctaccagca gtactactat 780
 gtgccgggtga tggcaatcct cgacctgtac tggcgggctcg agtcgatcgc ctacgtcgcg 840
 atgcgcctgc cgaagatgct gccgcaggcc ctcgcactcg tcgcgcacta cgccatcgtc 900
 gcgtgggtct ttgcgggcaa ctaccacctg ctcccgtcg tgacgggttct gcgcgggttt 960
 ggcaactggga tcaccgtttt cgcgacgcac tacggtgagg acattctcga cgcggaccag 1020
 gtgcgtcaca tgacgtcgt cgagcagacg gcactcacct cgcgcaacat ctcgggcggc 1080
 tggctcgtga acgtgctcac cggcttcac tcaactgcaga cggagcacca cctgttcccg 1140
 atgatgccaa ccggcaacct catgactatc cagcccagg tgccgcctt cttcaagaag 1200
 cacggacttg agtaccgca gggcaacctc attgagtgcg tgcggcagaa catccgtgcg 1260
 cttgcattcg agcacctgct ttga 1284

<210> 37

<211> 427

<212> PRT

<213> Pavlova salina

<400> 37

Met Gly Arg Gly Gly Asp Ser Ser Gly Gln Ala His Pro Ala Ala Glu
 1 5 10 15

Leu Ala Val Pro Ser Asp Arg Ala Glu Val Ser Asn Ala Asp Ser Lys
 20 25 30

Ala Leu His Ile Val Leu Tyr Gly Lys Arg Val Asp Val Thr Lys Phe
 35 40 45

Gln Arg Thr His Pro Gly Gly Ser Lys Val Phe Arg Ile Phe Gln Asp
 50 55 60

Arg Asp Ala Thr Glu Gln Phe Glu Ser Tyr His Ser Lys Arg Ala Ile
 65 70 75 80

Lys Met Met Glu Gly Met Leu Lys Lys Ser Glu Asp Ala Pro Ala Asp
85 90 95

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

Ile Glu Arg His Val Ala Ala Gly Tyr Tyr Asp Pro Cys Pro Leu Asp
115 120 125

Glu Leu Phe Lys Leu Ser Leu Val Leu Leu Pro Thr Phe Ala Gly Met
130 135 140

Tyr Met Leu Lys Ala Gly Val Gly Ser Pro Leu Cys Gly Ala Leu Met
145 150 155 160

Val Ser Phe Gly Trp Tyr Leu Asp Gly Trp Leu Ala His Asp Tyr Leu
165 170 175

His His Ser Val Phe Lys Gly Ser Val Ala Arg Thr Val Gly Trp Asn
180 185 190

Asn Ala Ala Gly Tyr Phe Leu Gly Phe Val Gln Gly Tyr Ala Val Glu
195 200 205

Trp Trp Arg Ala Arg His Asn Thr His His Val Cys Thr Asn Glu Asp
210 215 220

Gly Ser Asp Pro Asp Ile Lys Thr Ala Pro Leu Leu Ile Tyr Val Arg
225 230 235 240

Asn Lys Pro Ser Ile Ala Lys Arg Leu Asn Ala Phe Gln Arg Tyr Gln
245 250 255

Gln Tyr Tyr Tyr Val Pro Val Met Ala Ile Leu Asp Leu Tyr Trp Arg
260 265 270

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Leu Glu Ser Ile Ala Tyr Val Ala Met Arg Leu Pro Lys Met Leu Pro
275 280 285

Gln Ala Leu Ala Leu Val Ala His Tyr Ala Ile Val Ala Trp Val Phe
290 295 300

Ala Gly Asn Tyr His Leu Leu Pro Leu Val Thr Val Leu Arg Gly Phe
305 310 315 320

Gly Thr Gly Ile Thr Val Phe Ala Thr His Tyr Gly Glu Asp Ile Leu
325 330 335

Asp Ala Asp Gln Val Arg His Met Thr Leu Val Glu Gln Thr Ala Leu
340 345 350

Thr Ser Arg Asn Ile Ser Gly Gly Trp Leu Val Asn Val Leu Thr Gly
355 360 365

Phe Ile Ser Leu Gln Thr Glu His His Leu Phe Pro Met Met Pro Thr
370 375 380

Gly Asn Leu Met Thr Ile Gln Pro Glu Val Arg Ala Phe Phe Lys Lys
385 390 395 400

His Gly Leu Glu Tyr Arg Glu Gly Asn Leu Ile Glu Cys Val Arg Gln
405 410 415

Asn Ile Arg Ala Leu Ala Phe Glu His Leu Leu
420 425

<210> 38
<211> 116
<212> PRT
<213> Tomato yellow leaf curl virus

<400> 38

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Met Trp Asp Pro Leu Leu Asn Glu Phe Pro Glu Ser Val His Gly Phe
1 5 10 15

Arg Cys Met Leu Ala Ile Lys Tyr Leu Gln Ser Val Glu Glu Thr Tyr
20 25 30

Glu Pro Asn Thr Leu Gly His Asp Leu Ile Arg Asp Leu Ile Ser Val
35 40 45

Val Arg Ala Arg Asp Tyr Val Glu Ala Thr Arg Arg Tyr Asn His Phe
50 55 60

His Ala Arg Leu Glu Gly Ser Pro Lys Ala Glu Leu Arg Gln Pro Ile
65 70 75 80

Gln Gln Pro Cys Cys Cys Pro His Cys Pro Arg His Lys Gln Ala Thr
85 90 95

Ile Met Asp Val Gln Ala His Val Pro Glu Ala Gln Asn Ile Gln Asn
100 105 110

Val Ser Lys Pro
115

<210> 39

<211> 351

<212> DNA

<213> Tomato yellow leaf curl virus

<400> 39

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ttaattaggg atcttatatc tgttgtaagg gcccgtagct atgtcgaagc gaccaggcga 180

tataatcatt tccacgcccc cctcgaaggt tcgccgaagg ctgaacttcg acagcccata 240

cagcagccgt gctgctgtcc ccattgtcca aggcacaaac aagcgacgat catggacgta 300

caggcccatg taccggaagc ccagaatata cagaatgtat cgaagccctg a

351

<210> 40

<211> 389

<212> PRT

<213> Arabidopsis thaliana

<400> 40

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

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

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

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

Gly Val Lys Ile Gln Val Phe Ala Asp Asn Glu Thr Phe Asn Arg Met
 65 70 75 80

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

Trp Leu Val Gly Trp Ile Leu Ala Gln Arg Ser Gly Cys Leu Gly Ser
 100 105 110

Ala Leu Ala Val Met Lys Lys Ser Ser Lys Phe Leu Pro Val Ile Gly
 115 120 125

Trp Ser Met Trp Phe Ser Glu Tyr Leu Phe Leu Glu Arg Asn Trp Ala
 130 135 140

Lys Asp Glu Ser Thr Leu Lys Ser Gly Leu Gln Arg Leu Ser Asp Phe
 145 150 155 160

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

Glu Ala Lys Leu Lys Ala Ala Gln Glu Tyr Ala Ala Ser Ser Glu Leu
180 185 190

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

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

Val Thr 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
245 250 255

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

Gln Phe Val Ala Lys Asp Ala Leu Leu Asp Lys His Ile Ala Ala Asp
275 280 285

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

Leu Ala Val Val Leu Ser Trp Ala Cys Val Leu Thr Leu Gly Ala Ile
305 310 315 320

Lys Phe Leu His Trp Ala Gln Leu Phe Ser Ser Trp Lys Gly Ile Thr
325 330 335

Ile Ser Ala Leu Gly Leu Gly Ile Ile Thr Leu Cys Met Gln Ile Leu
340 345 350

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

Ala Lys Pro Lys Asp Asn His His Pro Glu Ser Ser Ser Gln Thr Glu
370 375 380

Thr Glu Lys Glu Lys
385

<210> 41
<211> 281
<212> PRT
<213> Limnanthes alba

<400> 41

Met Ala Lys Thr Arg Thr Ser Ser Leu Arg Asn Arg Arg Gln Leu Lys
1 5 10 15

Thr Ala Val Ala Ala Thr Ala Asp Asp Asp Lys Asp Gly Ile Phe Met
20 25 30

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

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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

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> 42
<211> 303
<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 42

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

Val Leu Ala Leu Ala Gly Cys Gly Phe Tyr Gly Val Ile Ala Ser Ile
 20 25 30

Leu Cys Thr Leu Ile Gly Lys Gln His Leu Ala Gln Trp Ile Thr Ala
 35 40 45

Arg Cys Phe Tyr His Val Met Lys Leu Met Leu Gly Leu Asp Val Lys
 50 55 60

Val Val Gly Glu Glu Asn Leu Ala Lys Lys Pro Tyr Ile Met Ile Ala
 65 70 75 80

Asn His Gln Ser Thr Leu Asp Ile Phe Met Leu Gly Arg Ile Phe Pro
 85 90 95

Pro Gly Cys Thr Val Thr Ala Lys Lys Ser Leu Lys Tyr Val Pro Phe
 100 105 110

Leu Gly Trp Phe Met Ala Leu Ser Gly Thr Tyr Phe Leu Asp Arg Ser
 115 120 125

Lys Arg Gln Glu Ala Ile Asp Thr Leu Asn Lys Gly Leu Glu Asn Val
 130 135 140

Lys Lys Asn Lys Arg Ala Leu Trp Val Phe Pro Glu Gly Thr Arg Ser
 145 150 155 160

Tyr Thr Ser Glu Leu Thr Met Leu Pro Phe Lys Lys Gly Ala Phe His
 165 170 175

PCTAU2015050340-seq1-000001-EN-20150624 (1)

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

Thr Ser Thr Leu Val Ser Pro Lys Tyr Gly Val Phe Asn Arg Gly Cys
195 200 205

Met Ile Val Arg Ile Leu Lys Pro Ile Ser Thr Glu Asn Leu Thr Lys
210 215 220

Asp Lys Ile Gly Glu Phe Ala Glu Lys Val Arg Asp Gln Met Val Asp
225 230 235 240

Thr Leu Lys Glu Ile Gly Tyr Ser Pro Ala Ile Asn Asp Thr Thr Leu
245 250 255

Pro Pro Gln Ala Ile Glu Tyr Ala Ala Leu Gln His Asp Lys Lys Val
260 265 270

Asn Lys Lys Ile Lys Asn Glu Pro Val Pro Ser Val Ser Ile Ser Asn
275 280 285

Asp Val Asn Thr His Asn Glu Gly Ser Ser Val Lys Lys Met His
290 295 300

<210> 43

<211> 373

<212> PRT

<213> Micromonas pusilla

<400> 43

Met Thr Pro Tyr Gln Trp Phe Asn Val Val Ser Ser Leu Gly Tyr Val
1 5 10 15

Leu Phe Thr Ala Thr Thr Ser Thr Val Thr Met Leu Val Pro Ala Ile
20 25 30

Ile Leu Leu Arg Pro Val Ser Ala Asn Leu Tyr Ala Arg Cys Thr Ser

35

40

45

Trp Ile Phe Ala Cys Trp Trp Thr Ser Cys Leu Phe Ile Thr Glu Arg
 50 55 60

Leu Asn Gly Val Lys Val Arg Val Thr Gly Asp Ala Leu Pro Leu Asn
 65 70 75 80

Ala Pro Leu Leu Ile Met Ser Asn His Lys Cys Asn Leu Asp Trp Met
 85 90 95

Phe Leu Trp Ser Ser Ala Ile Arg Thr Gly Ser Met Phe His Val Gly
 100 105 110

Val Phe Lys Ala Val Ala Lys Ser Glu Ile Arg Val Ile Pro Ile Phe
 115 120 125

Gly Trp Gly Cys Lys Leu Asn Gly Phe Ala Tyr Val Arg Arg Arg Trp
 130 135 140

Ser Ser Asp Ala Ser His Leu Thr Ser Trp Ile Gln Ser Gln Ile Arg
 145 150 155 160

Arg Arg Leu Asn Ala Asn Trp Thr Leu Ile Phe Pro Glu Gly Thr Arg
 165 170 175

Tyr Thr Asp Arg Asn Lys Glu Arg Ser Asp Leu Ser Cys Ala Lys Asp
 180 185 190

Gly Leu Glu Pro Met Ala Gly Glu Ile Leu Arg Pro Arg Thr Lys Gly
 195 200 205

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

Lys Ile Val Asp Met Thr Ile Gln Tyr Thr Asp Ala Asp Gly Lys Pro

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225 230 235 240

Leu Lys Gly Ala Ala Leu Gly Thr Arg Cys Phe Gly Gln Leu Ala Lys
245 250 255

Gly Gln Leu Pro Val Ala Thr Cys His Val His Phe Asp Val Phe Ser
260 265 270

His Lys Asp Val Pro Ala Gly Glu Asp Glu Asp Glu Val Glu Ala Trp
275 280 285

Val Trp Lys Arg Trp Arg Lys Lys Ala Asn Met Leu Glu Ala Cys Ala
290 295 300

Ser Ala Gly Gln Phe Glu Gly Val Arg Glu Trp Ser Thr Ser Gly Thr
305 310 315 320

Ala Val Pro Leu Lys Thr Gln Thr Ala Leu Arg Cys Phe Phe Val Leu
325 330 335

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

Ala Tyr Val Ala Cys Ala Ala Val Gly Ala Ala Val Ile Ala Gln Thr
355 360 365

Asp Pro Ala Trp Trp
370

<210>	44
<211>	314
<212>	PRT
<213>	Mortierella alpina

<400> 44

Met Ser Ile Gly Ser Ser Asn Pro Val Leu Leu Ala Ala Ile Pro Phe
1 5 10 15

Val Tyr Leu Phe Val Leu Pro Arg Val Leu Ala Phe Leu Pro Gln Lys
20 25 30

Ala Gln Phe Leu Ala Lys Cys Ile Val Val Leu Ile Ala Thr Leu Ile
35 40 45

Met Ser Val Ala Gly Cys Phe Ile Ser Ile Val Cys Ala Leu Leu Asp
50 55 60

Lys Arg Tyr Val Ile Asn Tyr Val Val Ser Arg Leu Phe Ser Phe Leu
65 70 75 80

Ala Ala Arg Pro Cys Gly Val Thr Tyr Lys Ile Val Gly Glu Glu His
85 90 95

Leu Asp Lys Tyr Pro Ala Ile Val Val Cys Asn His Gln Ser Ser Met
100 105 110

Asp Met Met Val Leu Gly Arg Val Phe Pro Lys His Cys Val Val Met
115 120 125

Ala Lys Lys Glu Leu Leu Tyr Phe Pro Phe Leu Gly Met Phe Met Lys
130 135 140

Leu Ser Asn Ala Ile Phe Ile Asp Arg Lys Asn His Lys Lys Ala Ile
145 150 155 160

Glu Ser Thr Thr Gln Ala Val Ala Asp Met Lys Lys His Asn Ser Gly
165 170 175

Ile Trp Ile Phe Pro Glu Gly Thr Arg Ser Arg Leu Asp Lys Ala Asp
180 185 190

Leu Leu Pro Phe Lys Lys Gly Ala Phe His Leu Ala Ile Gln Ala Gln
195 200 205

Leu Pro Ile Leu Pro Ile Ile Ser Gln Gly Tyr Ser His Ile Tyr Asp
210 215 220

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

Glu Pro Ile Pro Thr Thr Gly Leu Thr Thr Asp Asp Val Asn Asp Leu
245 250 255

Met Asp Lys Thr Arg Asn Leu Met Leu Lys His Leu Lys Glu Met Asp
260 265 270

Ser Gln Tyr Ser Ser Ser Thr Ala Glu Asn Gly Ser Thr His Ile Asp
275 280 285

Ala Asp Ile Ala Lys Ser Thr Ala Thr Ser Ile Gly Asn Thr Asp Asp
290 295 300

Ala Ile Thr Lys Arg Arg Thr Pro Lys Glu
305 310

<210> 45

<211> 391

<212> PRT

<213> Braccisa napus

<400> 45

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

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

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

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

Ala Gly Val Lys Ile Gln Val Phe Ala Asp Asp Glu Thr Phe Asn Arg
65 70 75 80

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

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

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

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

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

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

Thr Glu Ala Lys Leu Lys Ala Ala Gln Glu Tyr Ala Ala Ser Ser Gln
180 185 190

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

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

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

PCTAU2015050340-seq1-000001-EN-20150624 (1)

Phe Lys Gly Gln Pro Ser Val Val His Val His Ile Lys Cys His Ser
245 250 255

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

Asp Gln Phe Val Ala Lys Asp Ala Leu Leu Asp Lys His Ile Ala Ala
275 280 285

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

Ser Leu Ala Val Val Val Ser Trp Ala Cys Leu Leu Thr Leu Gly Ala
305 310 315 320

Met Lys Phe Leu His Trp Ser Asn Leu Phe Ser Ser Leu Lys Gly Ile
325 330 335

Ala Leu Ser Ala Leu Gly Leu Gly Ile Ile Thr Leu Cys Met Gln Ile
340 345 350

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

Pro Ala Lys Pro Lys Asp Lys His Gln Ser Gly Ser Ser Ser Gln Thr
370 375 380

Glu Val Glu Glu Lys Gln Lys
385 390

<210> 46

<211> 390

<212> PRT

<213> Braccisa napus

<400> 46

PCTAU2015050340-seq1-000001-EN-20150624 (1)

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

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

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

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

Gly Val Lys Ile Gln Val Phe Ala Asp Asn Glu Thr Phe Asn Arg Met
65 70 75 80

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

Trp Leu Val Gly Trp Ile Leu Ala Gln Arg Ser Gly Cys Leu Gly Ser
100 105 110

Ala Leu Ala Val Met Lys Lys Ser Ser Lys Phe Leu Pro Val Ile Gly
115 120 125

Trp Ser Met Trp Phe Ser Glu Tyr Leu Phe Leu Glu Arg Asn Trp Ala
130 135 140

Lys Asp Glu Ser Thr Leu Lys Ser Gly Leu Gln Arg Leu Asn Asp Phe
145 150 155 160

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

Glu Ala Lys Leu Lys Ala Ala Gln Glu Tyr Ala Ala Ser Ser Glu Leu
180 185 190

PCTAU2015050340-seql-000001-EN-20150624 (1)

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

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

Gln Phe Val Ala Lys Asp Ala Leu Leu Asp Lys His Ile Ala Ala Asp
275 280 285

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

Leu Ala Val Val Leu Ser Trp Ser Cys Leu Leu Ile Leu Gly Ala Met
305 310 315 320

Lys Phe Leu His Trp Ser Asn Leu Phe Ser Ser Trp Lys Gly Ile Ala
325 330 335

Phe Ser Ala Leu Gly Leu Gly Ile Ile Thr Leu Cys Met Gln Ile Leu
340 345 350

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

Ala Lys Pro Lys Asp Asn His Asn Asp Ser Gly Ser Ser Ser Gln Thr
370 375 380

Glu Val Glu Lys Gln Lys
385 390

<210> 47
<211> 361
<212> PRT
<213> Phytophthora infestans

<400> 47

Met Ala Thr Lys Glu Ala Tyr Val Phe Pro Thr Leu Thr Glu Ile Lys
1 5 10 15

Arg Ser Leu Pro Lys Asp Cys Phe Glu Ala Ser Val Pro Leu Ser Leu
20 25 30

Tyr Tyr Thr Val Arg Cys Leu Val Ile Ala Val Ala Leu Thr Phe Gly
35 40 45

Leu Asn Tyr Ala Arg Ala Leu Pro Glu Val Glu Ser Phe Trp Ala Leu
50 55 60

Asp Ala Ala Leu Cys Thr Gly Tyr Ile Leu Leu Gln Gly Ile Val Phe
65 70 75 80

Trp Gly Phe Phe Thr Val Gly His Asp Ala Gly His Gly Ala Phe Ser
85 90 95

Arg Tyr His Leu Leu Asn Phe Val Val Gly Thr Phe Met His Ser Leu
100 105 110

Ile Leu Thr Pro Phe Glu Ser Trp Lys Leu Thr His Arg His His His
115 120 125

Lys Asn Thr Gly Asn Ile Asp Arg Asp Glu Val Phe Tyr Pro Gln Arg
130 135 140

Lys Ala Asp Asp His Pro Leu Ser Arg Asn Leu Ile Leu Ala Leu Gly

145 150 155 160

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

Asn His Phe Asn Pro Phe Glu Pro Leu Phe Val Arg Gln Val Ser Ala
180 185 190

Val Val Ile Ser Leu Leu Ala His Phe Phe Val Ala Gly Leu Ser Ile
195 200 205

Tyr Leu Ser Leu Gln Leu Gly Leu Lys Thr Met Ala Ile Tyr Tyr Tyr
210 215 220

Gly Pro Val Phe Val Phe Gly Ser Met Leu Val Ile Thr Thr Phe Leu
225 230 235 240

His His Asn Asp Glu Glu Thr Pro Trp Tyr Ala Asp Ser Glu Trp Thr
245 250 255

Tyr Val Lys Gly Asn Leu Ser Ser Val Asp Arg Ser Tyr Gly Ala Leu
260 265 270

Ile Asp Asn Leu Ser His Asn Ile Gly Thr His Gln Ile His His Leu
275 280 285

Phe Pro Ile Ile Pro His Tyr Lys Leu Lys Lys Ala Thr Ala Ala Phe
290 295 300

His Gln Ala Phe Pro Glu Leu Val Arg Lys Ser Asp Glu Pro Ile Ile
305 310 315 320

Lys Ala Phe Phe Arg Val Gly Arg Leu Tyr Ala Asn Tyr Gly Val Val
325 330 335

Asp Gln Glu Ala Lys Leu Phe Thr Leu Lys Glu Ala Lys Ala Ala Thr

340

345

350

Glu Ala Ala Ala Lys Thr Lys Ser Thr
 355 360

<210> 48

<211> 418

<212> PRT

<213> *Thalassiosira pseudonana*

<400> 48

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

Ser Ile Asn Ala Phe Ser Pro Gln Arg Pro Pro Arg Thr Ile Thr Lys
 20 25 30

Ser Lys Val Gln Ser Thr Val Leu Pro Ile Pro Thr Lys Asp Asp Leu
 35 40 45

Asn Phe Leu Gln Pro Gln Leu Asp Glu Asn Asp Leu Tyr Leu Asp Asp
 50 55 60

Val Asn Thr Pro Pro Arg Ala Gly Thr Ile Met Lys Met Leu Pro Lys
 65 70 75 80

Glu Thr Phe Asn Ile Asp Thr Ala Thr Ser Leu Gly Tyr Phe Gly Met
 85 90 95

Asp Met Ala Ala Val Val Ser Ser Met Thr Leu Leu Asn Ala Ile Val
 100 105 110

Thr Ser Asp Gln Tyr His Ala Leu Pro Leu Pro Leu Gln Ala Ala Thr
 115 120 125

Val Ile Pro Phe Gln Leu Leu Ala Gly Phe Ala Met Trp Cys Met Trp
 130 135 140

Cys Ile Gly His Asp Ala Gly His Ser Thr Val Ser Lys Thr Lys Trp
 145 150 155 160

Ile Asn Arg Val Val Gly Glu Val Ala His Ser Val Val Cys Leu Thr
 165 170 175

Pro Phe Val Pro Trp Gln Met Ser His Arg Lys His His Leu Asn His
 180 185 190

Asn His Ile Glu Lys Asp Tyr Ser His Lys Trp Tyr Ser Arg Asp Glu
 195 200 205

Phe Asp Asp Ile Pro Gln Leu Tyr Lys Thr Phe Gly Tyr Asn Pro Arg
 210 215 220

Met Met Gln Leu Pro Phe Leu Tyr Phe Met Tyr Leu Ala Leu Gly Ile
 225 230 235 240

Pro Asp Gly Gly His Val Val Phe Tyr Gly Arg Met Trp Glu Gly Val
 245 250 255

Ser Leu Gln Lys Lys Phe Asp Ala Ala Ile Ser Val Ala Val Ser Cys
 260 265 270

Ala Thr Ala Gly Ser Leu Trp Met Asn Met Gly Thr Ala Asp Phe Thr
 275 280 285

Val Val Cys Met Val Pro Trp Leu Val Leu Ser Trp Trp Leu Phe Met
 290 295 300

Val Thr Tyr Leu Gln His His Ser Glu Asp Gly Lys Leu Tyr Thr Asp
 305 310 315 320

Glu Thr Phe Thr Phe Glu Lys Gly Ala Phe Glu Thr Val Asp Arg Ser
 325 330 335

Tyr Gly Lys Leu Ile Asn Arg Met Ser His His Met Met Asp Gly His
340 345 350

Val Val His His Leu Phe Phe Glu Arg Val Pro His Tyr Arg Leu Glu
355 360 365

Ala Ala Thr Glu Ala Leu Val Lys Gly Met Asp Glu Thr Gly Gln Lys
370 375 380

His Leu Tyr Lys Tyr Ile Asp Thr Pro Asp Phe Asn Ala Glu Ile Val
385 390 395 400

Asn Gly Phe Arg Asp Asn Trp Phe Leu Val Glu Glu Glu Asn Ile Lys
405 410 415

Arg Glu

<210> 49
<211> 363
<212> PRT
<213> Pythium irregulare

<400> 49

Met Ala Ser Thr Ser Ala Ala Gln Asp Ala Ala Pro Tyr Glu Phe Pro
1 5 10 15

Ser Leu Thr Glu Ile Lys Arg Ala Leu Pro Ser Glu Cys Phe Glu Ala
20 25 30

Ser Val Pro Leu Ser Leu Tyr Tyr Thr Ala Arg Ser Leu Ala Leu Ala
35 40 45

Gly Ser Leu Ala Val Ala Leu Ser Tyr Ala Arg Ala Leu Pro Leu Val
50 55 60

Gln Ala Asn Ala Leu Leu Asp Ala Thr Leu Cys Thr Gly Tyr Val Leu
65 70 75 80

Leu Gln Gly Ile Val Phe Trp Gly Phe Phe Thr Val Gly His Asp Cys
85 90 95

Gly His Gly Ala Phe Ser Arg Ser His Val Leu Asn Phe Ser Val Gly
100 105 110

Thr Leu Met His Ser Ile Ile Leu Thr Pro Phe Glu Ser Trp Lys Leu
115 120 125

Ser His Arg His His His Lys Asn Thr Gly Asn Ile Asp Lys Asp Glu
130 135 140

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

Leu Val Met Ser Leu Gly Ser Ala Trp Phe Ala Tyr Leu Phe Ala Gly
165 170 175

Phe Pro Pro Arg Thr Met Asn His Phe Asn Pro Trp Glu Ala Met Tyr
180 185 190

Val Arg Arg Val Ala Ala Val Ile Ile Ser Leu Gly Val Leu Phe Ala
195 200 205

Phe Ala Gly Leu Tyr Ser Tyr Leu Thr Phe Val Leu Gly Phe Thr Thr
210 215 220

Met Ala Ile Tyr Tyr Phe Gly Pro Leu Phe Ile Phe Ala Thr Met Leu
225 230 235 240

Val Val Thr Thr Phe Leu His His Asn Asp Glu Glu Thr Pro Trp Tyr
245 250 255

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Ala Asp Ser Glu Trp Thr Tyr Val Lys Gly Asn Leu Ser Ser Val Asp
260 265 270

Arg Ser Tyr Gly Ala Leu Ile Asp Asn Leu Ser His Asn Ile Gly Thr
275 280 285

His Gln Ile His His Leu Phe Pro Ile Ile Pro His Tyr Lys Leu Asn
290 295 300

Asp Ala Thr Ala Ala Phe Ala Lys Ala Phe Pro Glu Leu Val Arg Lys
305 310 315 320

Asn Ala Ala Pro Ile Ile Pro Thr Phe Phe Arg Met Ala Ala Met Tyr
325 330 335

Ala Lys Tyr Gly Val Val Asp Thr Asp Ala Lys Thr Phe Thr Leu Lys
340 345 350

Glu Ala Lys Ala Ala Ala Lys Thr Lys Ser Ser
355 360

<210> 50
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 50
gcgaagcaca tcgagtca

18

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 51
ggttgaggtg gtagctgagg 20

<210> 52
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<220>
<221> misc_feature
<222> (1)..(1)
<223> N = Hex

<220>
<221> misc_feature
<222> (9)..(9)
<223> N = Zen

<220>
<221> misc_feature
<222> (26)..(26)
<223> N = 3IABkFQ

<400> 52
ntctctacnc cgtctcacat gacgcn 26

<210> 53
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 53
atacaagcac ggtggatgg 19

<210> 54
<211> 22
<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer

<400> 54

tggtctaaca ggtctaggag ga

22

<210> 55

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer

<220>

<221> misc_feature

<222> (1)..(1)

<223> N = FAM

<220>

<221> misc_feature

<222> (11)..(11)

<223> N = Zen

<220>

<221> misc_feature

<222> (29)..(29)

<223> N = 3IABkFQ

<400> 55

ntggcaaaga ngatttcgag cttcctgcn

29

<210> 56

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer

<400> 56

caagcaccgt agtaagagag ca

22

<210> 57
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer

<400> 57
 cagacagcct gaggttagca 20

<210> 58
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer

<220>
 <221> misc_feature
 <222> (1)..(1)
 <223> N = FAM

<220>
 <221> misc_feature
 <222> (11)..(11)
 <223> N = Zen

<220>
 <221> misc_feature
 <222> (29)..(29)
 <223> N = 3IABkFQ

<400> 58
 ntccccactt ncttagcgaa aggaacgan 29