

517416 Sequence Listing
SEQUENCE LISTING

<110> Nuseed Pty Ltd
Grain Research and Development Corporation
Commonwealth Scientific and Industrial Research
Organisation

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<150> AU 2014902471

<151> 2014-06-27

<150> US 14/575,756

<151> 2014-12-18

<150> AR 20140104761

<151> 2014-12-18

<150> PCT/AU2014/050433

<151> 2014-12-18

<160> 58

<170> PatentIn version 3.5

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517416 Sequence Listing

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517416 Sequence Listing

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517416 Sequence Listing

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517416 Sequence Listing

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517416 Sequence Listing

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Ser Ser Asn Thr Glu Gln Glu Val Pro Lys Val Ala Ile Asp Thr Asn
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Gly Asn Val Phe Ser Val Pro Asp Phe Thr Ile Lys Asp Ile Leu Gly
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Ala Ile Pro His Glu Cys Tyr Glu Arg Arg Leu Ala Thr Ser Leu Tyr
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Tyr Val Phe Arg Asp Ile Phe Cys Met Leu Thr Thr Gly Tyr Leu Thr
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His Lys Ile Leu Tyr Pro Leu Leu Ile Ser Tyr Thr Ser Asn Ser Ile
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517416 Sequence Listing

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130 135 140

Tyr Leu Met Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Gly Lys His
145 150 155 160

His Lys Ala Thr Gly His Met Thr Arg Asp Met Val Phe Val Pro Ala
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Thr Lys Glu Glu Phe Lys Lys Ser Arg Asn Phe Phe Gly Asn Leu Ala
180 185 190

Glu Tyr Ser Glu Asp Ser Pro Leu Arg Thr Leu Tyr Glu Leu Leu Val
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Gln Pro Tyr Pro Asp Val Pro Ser Trp Lys Trp Asn His Phe Trp Leu
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Thr Ser Pro Leu Phe Glu Gln Arg Asp Ala Leu Tyr Ile Phe Leu Ser
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Asp Leu Gly Ile Leu Thr Gln Gly Ile Val Leu Thr Leu Trp Tyr Lys
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Lys Phe Gly Gly Trp Ser Leu Phe Ile Asn Trp Phe Val Pro Tyr Ile
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Pro Thr Met Pro His Tyr Asn Ala Glu Glu Trp Thr Phe Ala Lys Gly
305 310 315 320

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Phe His Asp Ile Ile Glu Thr His Val Leu His His Tyr Cys Ser Arg
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517416 Sequence Listing

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<211> 415
<212> PRT
<213> Pichia pastoris

<400> 6

517416 Sequence Listing

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

517416 Sequence Listing

Val Phe Gly Phe Trp Pro Thr Phe Ile Thr Trp Phe Cys Pro Trp Ile
275 280 285

Leu Val Asn His Trp Leu Val Phe Val Thr Phe Leu Gln His Thr Asp
290 295 300

Ser Ser Met Pro His Tyr Asp Ala Gln Glu Trp Thr Phe Ala Lys Gly
305 310 315 320

Ala Ala Ala Thr Ile Asp Arg Glu Phe Gly Ile Leu Gly Ile Ile Phe
325 330 335

His Asp Ile Ile Glu Thr His Val Leu His His Tyr Val Ser Arg Ile
340 345 350

Pro Phe Tyr His Ala Arg Glu Ala Thr Glu Cys Ile Lys Lys Val Met
355 360 365

Gly Glu His Tyr Arg His Thr Asp Glu Asn Met Trp Val Ser Leu Trp
370 375 380

Lys Thr Trp Arg Ser Cys Gln Phe Val Glu Asn His Asp Gly Val Tyr
385 390 395 400

Met Phe Arg Asn Cys Asn Asn Val Gly Val Lys Pro Lys Asp Thr
405 410 415

<210> 7
<211> 1392
<212> DNA
<213> Micromonas pusilla

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ctcgagccgc acgagctcgc ggcgacgttc gagacgcgat ggggtgcgct ggaggacgtc 180
gagtacgacg tcacaaactt caaacacccg ggaggcagcg tgatattcta catgctcgcg 240
aacacgggcg cggacgccac ggaggcggtc aaggagttcc acatgcgatc gcttaaggcg 300
tggaagatgc tcagagcgct gccgtcgcgc cccgcggaga tcaaacgcag cgagagcgag 360
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tcggtctacg tcgacaagcg cctccaagcg atgacgtgcg gggtcgggct gtccacgagc 660
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517416 Sequence Listing

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cgaagaaga	actacgagga	ggcgtagtg	atgctcgtct	ctcacgtcgt	caggaccgcg	960
gtgattaaac	tcgcgacggg	gtactcgtgg	cccgtagcgt	actggtaggt	caccttcggc	1020
aactggatcg	cgtacatgta	cctcttcgcg	cacttctcca	cgagccacac	gcacctcccg	1080
gtcgtgccct	cggataagca	cctgagctgg	gtgaactacg	cggtagatca	caccgtggac	1140
atcgaccgt	cgcgcgggta	cgtgaactgg	ttgatgggat	atctgaactg	ccaggtcatt	1200
catcacctgt	tcccggacat	gccgcagttt	cgccagccgg	aggtgagccg	gcggttcgtc	1260
ccgttcgcga	agaagtgggg	gctgaactac	aaggtagctgt	cctattacgg	cgcttggaag	1320
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<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)

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gagtacgatg	tgactaactt	caagcaccct	ggtggatctg	tgatcttcta	catgcttgct	240
aacactgggtg	ctgatgctac	tgaggctttc	aaagaattcc	acatgcgttc	tctcaaggct	300
tggaagatgc	ttagagcttt	gccttctaga	cctgctgaga	tcaagagatc	tgagtctgag	360
gatgctccta	tgcttgagga	tttcgctaga	tgccgtgctg	agcttgagag	agatggattc	420
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cttggaaactg	ctcttatgta	cgctggatac	cctatcattg	cttctgttgt	ttacgggtgct	540
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ggtgagatgt	ggaaccagat	gcataacaag	caccatgcta	cccctcaaaa	ggtagacac	720
gatatggatc	ttgataccac	tcctgctgtg	gctttcttca	acactgctgt	tgaggataac	780
agacctagag	gattctctag	agcttgggct	agacttcaag	cttggacttt	cgttcctgtt	840
acctctggac	ttcttggtca	agctttctgg	atctacgttc	tccaccctag	acaagttctc	900
cgtaagaaga	actacgaaga	ggcttcttgg	atgctcgttt	ctcatgttgt	tagaaccgct	960
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517416 Sequence Listing

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aaggctcact aatga 1395

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

<400> 9

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Thr Arg Ser Lys Ser Ser Ala Glu Ala Leu Asp Ala Lys Asp Ala Ser
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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

517416 Sequence Listing

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
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517416 Sequence Listing

<210> 10
 <211> 1449
 <212> DNA
 <213> *Ostreococcus lucimarinus*

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 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

517416 Sequence Listing

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aagtgaacc tcaactacaa ggtgctcact tactacggtg cttggaaggc tactttcgga 1380
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agcgcttga 1449

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

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<400> 12

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1 5 10 15

Arg Thr Ser 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
Page 33

517416 Sequence Listing

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
Page 34

517416 Sequence Listing

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

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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

517416 Sequence Listing

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

517416 Sequence Listing

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

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

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tccttctggg gaaacgccta caaccccgca cagaccgaga tggcgaaggc catctggatt	420
ttctacgtct ccaagatcta tgagttcatg gacacgttca tcatgctctt gaagggaac	480
gtcaaccagg tctctttcct gcatgtgtac catcatggct ccatctctgg tatctggtgg	540
atgatcacct acgctgcccc tggcgggtgac gcgtacttct cggcggcgct caactcgtgg	600
gtgcacgtgt gcatgtacac gtactacttc atggcggcgg tgctgcccaa ggacgagaag	660
accaagcgca agtacctctg gtggggccgc tacctgaccc agatgcagat gttccagttc	720
ttcatgaacc tgctccaggc ggtctacctc ctctactcct ctagccccta cccaagttc	780
atcgcccagc tgctggtggg gtacatgggc acgctgctga tgctcttcgg caacttctac	840

517416 Sequence Listing

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 tgttgctatg gctcaagagc aatacgctgc tatcgatgct 60
 gttgttgctc ctgctatctt ctctgctact gattctatcg gatggggact taagcctatc 120
 tctttctgcta ctaaggactt gcctcttggt gagtctccta cacctctcat cctttctttg 180
 cttgcttact tcgctatcgt tggatctgga ctcgtttaca gaaagggttt ccctagaacc 240
 gtgaagggac aagatccatt cttttgaag gctcttatgc ttgctcaciaa cgtgttcctt 300
 atcggacttt ctctttacat gtgcctcaag cttgtgtacg aggcttacgt taacaagtac 360
 tctttctggg gaaacgctta caaccctgct caaactgaga tggctaagggt tatctggatc 420
 ttctacgtga gcaagatcta cgagttcatg gataccttca tcatgctcct caagggaaat 480
 gttaaccagg ttagcttcct tcacgtttac catcacggat ctatctctgg aatctggtgg 540
 atgattactt acgctgctcc tgggtggtgat gcttacttct ctgctgctct taactcttgg 600
 gttcacgtgt gtatgtacac ctactatctt atggctgccg tgcttcctaa ggacgagaaa 660
 actaagagaa agtacctctg gtggggaaga taccttactc aaatgcagat gttccagttc 720
 ttcatgaacc ttctccaggc tgtttacctt ctctactctt catctcctta ccctaagttt 780
 atcgtcagc tcctcggtgt gtacatgggt actcttctca 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

517416 Sequence Listing

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
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
Page 39

517416 Sequence Listing

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
 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
 Page 40

<210> 18
 <211> 1278
 <212> DNA
 <213> Pavlova salina

<400> 18
 atgccgccgc gcgatagcta ctcgtacgcc gccccgccgt cggcccagct gcacgaggtc 60
 gataccccgc aggagcatga taagaaggag ctcgtcatcg gtgaccgcgc gtacgacgtg 120
 accaactttg tgaagcgcca cccgggtggc aagatcatcg cataccaggt tggcacagat 180
 gcgacggacg cgtacaagca gttccatgtg cggctctgcc aggcggaaca gatgctcaag 240
 tcgctgcctt cgcgcccggg gcacaagggc tactcgcccc gccgcgctga cctcattgcc 300
 gacttccagg agttcaccaa gcagctggag gcggagggca tgtttgagcc gtcgctgccg 360
 cacgtggcat accgcctggc ggaggtgatc gcgatgcacg tggccggcgc cgcgctcatc 420
 tggcacgggt acaccttcgc gggcattgcc atgctcggcg ttgtgcaggg ccgctgcggc 480
 tggctcatgc acgagggcgg cactactcg ctcacgggca acattgcttt tgaccgtgcc 540
 atccaagtcg cgtgctacgg ccttggtgc ggcatgtcgg gcgcgtggtg gcgcaaccag 600
 cacaacaagc accacgcgac gccgcagaag ttgcagcacg acgtcgacct cgacaccctc 660
 ccgctcgtcg ccttccacga gcggatagcc gccaaaggta agagccccgc gatgaaggcg 720
 tggcttagta tgcaggcgaa gctcttcgcg ccagtgaaca cgctgctggt cgcgctgggc 780
 tggcagctgt acctgcaccc gcgccatatg ctgcgcacca agcactacga cgagctcgcg 840
 atgctcggca ttcgctacgg ccttgctggc tacctcgcgg cgaactacgg cgcggggtac 900
 gtgctcgcgt gctacctgct gtacgtgcag ctcggcgcca tgtacatctt ctgcaacttt 960
 gccgtgtcgc acacacacct gccggttgtc gagcctaacg agcacgcaac gtgggtggag 1020
 tacgccgcga accacacgac caactgctcg ccctcgtggt ggtgcgactg gtggatgtcg 1080
 tacctcaact accagatcga gcaccacctc taccgtcca tgccgcagtt ccgccacccg 1140
 aagattgcgc cgcgggtgaa gcagctcttc gagaagcacg gcctgcacta cgacgtgcgt 1200
 ggctacttcg aggccatggc ggacacgttt gccaaccttg acaacgtcgc gcacgcgccg 1260
 gagaagaaga tgcagtga 1278

<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
 atgcctccaa gggactctta ctcttatgct gtcctcctt ctgctcaact tcacgaagtt 60
 gatactcctc aagagcacga caagaaagag cttgttatcg gagatagggc ttacgatgtt 120

517416 Sequence Listing

accaacttcg ttaagagaca ccctggtgga aagatcattg cttaccaagt tggaactgat 180
 gctaccgatg cttacaagca gttccatggt agatctgcta aggctgacaa gatgcttaag 240
 tctcttcctt ctcgtcctgt tcacaagggga tactctccaa gaagggctga tcttatcgct 300
 gatttccaag agttcaccaa gcaacttgag gctgagggaa tggtcgagcc ttctcttcct 360
 catgttgctt acagacttgc tgaggttatc gctatgcatg ttgctggtgc tgctcttattc 420
 tggcatggat acactttcgc tggaatcgct atgcttgagg ttgttcaggg aagatgtgga 480
 tggcttatgc atgaggggtg acattactct ctactggaa acattgcttt cgacagagct 540
 atccaagttg cttgttacgg acttggaatg ggaatgtctg gtgcttggtg gcgtaaccag 600
 cataacaagc accatgctac tcctcaaaag cttcagcacg atgttgatct tgataccctt 660
 cctctcgttg ctttccatga gagaatcgct gctaagggtta agtctcctgc tatgaaggct 720
 tggctttcta tgcaagctaa gcttttcgct cctgttacca ctcttcttgt tgctcttgga 780
 tggcagcttt accttcatcc tagacacatg cttaggacta agcactacga tgagcttgct 840
 atgctcggaa tcagatacgg acttggtgga taccttgctg ctaactacgg tgctggatac 900
 gttctcgctt gttaccttct ttacgttcag cttggagcta tgtacatctt ctgcaacttc 960
 gctgtttctc atactcacct ccctgttggt gagcctaacg agcatgctac ttgggttgag 1020
 tacgctgcta accacactac taactgttct ccatcttggt ggtgtgattg gtggatgtct 1080
 taccttaact accagatcga gcaccacctt tacccttcta tgcctcaatt cagacaccct 1140
 aagatcgctc ctagagttaa gcagcttttc gagaagcacg gacttcacta cgatgttaga 1200
 ggatacttcg aggctatggc tgatactttc gctaaccttg ataacgttgc ccatgctcct 1260
 gagaagaaaa tgcagtaatg a 1281

<210> 20
 <211> 425
 <212> PRT
 <213> Pavlova salina

<400> 20

Met Pro Pro Arg Asp Ser Tyr Ser Tyr Ala Ala Pro Pro Ser Ala Gln
 1 5 10 15

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

517416 Sequence Listing

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

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

517416 Sequence Listing
 Trp Trp Cys Asp Trp Trp Met Ser Tyr Leu Asn Tyr Gln Ile Glu His
 355 360 365

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
 405 410 415

Ala His Ala Pro Glu Lys Lys Met Gln
 420 425

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

<400> 21
 atgggaaagg gaggcaatgc tagcgctcct actgcgaaga aggaggtggt gatcgagggg 60
 aagttttacg atgtcaccga cttcaggcac cccgggtggt cgatcatcaa gtttctctcg 120
 ggttctggtg ctgacgccac cgcttcctac cgcgagttcc acgtaggtc agcgaaggca 180
 gacaagttct tgaagacgct gccctcccg cgaagccactc cccaggagct gaagcaggcg 240
 gttgagttct ccaagctcaa cccgccctcc gcggagagtg cctctgctcc cctgaccgac 300
 cttgccaagg tggaagcgct gaacaaggac ttcgaggctt tccgtgagca gctcattcag 360
 gagggcttct ttaagcccaa tatcccgcat gtggtcaagc gcatcacgga agtcgtggcg 420
 atgatggccg tagcctcctg gatgatggtg cagaccaacg ctcttggtgt gaccctcgga 480
 gttctgatcc gcggcattgc acagggccgg tgcggttggc ttatgcacga gggcggccac 540
 tatagtctta ctgggaagat ctccattgat aggcgtctgc aggagtcaat ttacggattc 600
 ggctgtggaa tgtccggcgc ctggtggcgc aaccagcaca acaagcacca cgcaacccca 660
 cagaagctgc agcatgacgt cgacctggag acccttcctc tgatggcttt caacaacgct 720
 gttaccgata gacgcaagg tgaagcctggt agtctccagg ctctgtggct caagtaccag 780
 gccttcctct tcttccccgt gacctccctt ctggtcggcc tcggttggac caccgtcctc 840
 caccacaggc acagcttgcg caccaagcac tatttcgagc tgctctgcat ggctgctcgt 900
 tacgcgagtt tcgctgctct tttcgctccc aagtacggac ttgcaggagc tgccgggctc 960
 tacctcgcca ccttcgctgt cgggtgcaac tatatatttca tcaacttctc ggtctctcac 1020
 actcacctgc ccgtgagcgg tgcgagcgag tacctgcatt gggctgtgta ttcggccatc 1080
 cacaccacta acatcaaata cagcatgctg tgcgattggt ggatgtcatt cctcaacttc 1140
 cagatcgagc atcacctggt ccttcaatg cccagttcc gccacaagat tatctccccg 1200
 cgtgtaaagg ccttggttga gaagcacggt cttgtgtatg atgtgcgccc ctattggggg 1260

517416 Sequence Listing

gccatggctg acaccttcaa gaacttgaat gacgttggca ctcacgcatc tcactccaag 1320
gcgcactag 1329

<210> 22
<211> 442
<212> PRT
<213> Pyramimonas cordata
<400> 22

Met Gly Lys Gly Gly Asn Ala Ser Ala Pro Thr Ala Lys Lys Glu Val
1 5 10 15

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

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

517416 Sequence Listing

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
 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
 atggcgtcta ttgcgattcc ggctgcgctg gcagggactc ttggttatgt gacgtacaat 60
 gtcgcaaacc cagatattcc tgcattccgag aaggtgcctg cttactttat gcaggtcgag 120
 tattggggggc caacgattgg gaccatcggg tatcttctgt tcattctactt tggtaaacgg 180

517416 Sequence Listing

attatgcaaa acaggagcca gccgtttggc ctgaagaacg ctatgctggg	gtacaacttc	240
tatcagactt tcttcaactc gtactgcata tacctttttg tcacgtcgca ccgcgctcag		300
gggctgaaag tttggggaaa catccccgat atgactgccca acagctgggg gatctcacag		360
gtgatctggc tgcactacaa caacaagtac gttgagctgc tggacacggt cttcatggtc		420
atgcgcaaga agtttgacca gctttcgttc ctgcacattt accatcatac cctgttgatc		480
tggtcttggg tcgtgggtgat gaaattggag cccgttgggg actgctactt tggctctagc		540
gtcaacacgt ttgtgcacgt cattatgtac tcgtactatg gccttgccgc gctcgggggtg		600
aattgcttct ggaagaagta cattacgcag attcagatgc tgcagttctg tatctgcgct		660
tcgcactcga ttataaccgc ctatgtgcag aacaccgcgt tctgggtgcc ttacttgtag		720
ctgtgggtga tgggtgaacat gttcgtgttg ttcgccaaact tctatcgcaa gcgctacaag		780
agcaagggtg ccaagaagca gtaa		804

<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	
atggcctcta tcgctatccc tgctgctctt gctggaactc ttggatacgt tacctacaat	60
gtggctaacc ctgatatccc agcttctgag aaagttcctg cttacttcat gcaggttgag	120
tactggggac ctactatcgg aactattgga tacctcctct tcatctactt cggaaagcgt	180
atcatgcaga acagatctca acctttcgga ctcaagaacg ctatgctcgt ttacaacttc	240
taccagacct tcttcaacag ctactgcata tacctttttc ttactttctca tagggctcag	300
ggacttaagg tttggggaaa catccctgat atgactgcta actcttgggg aatctctcag	360
gttatctggc ttcactacaa caacaagtac gttgagcttc tcgacacctt cttcatgggtg	420
atgaggaaga agttcgacca gctttctttc cttcacatct accaccacac tcttctcatc	480
tggtcatggg tcgttggtat gaagcttgag cctgttgagg attgctactt cggatcttct	540
gttaacacct tcgtgcacgt gatcatgtac tcttactacg gacttgctgc tcttgaggtt	600
aactgtttct ggaagaagta catcaccag atccagatgc ttcagttctg tatctgtgct	660
tctcactcta tctacaccgc ttacgttcag aataccgctt tctggcttcc ttaccttcaa	720
ctctgggtta tgggtgaacat gttcgttctc ttcgccaaact tctaccgtaa gaggtacaag	780
tctaagggtg ctaagaagca gtgataa	807

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

<400> 25

517416 Sequence Listing

Met Ala Ser Ile Ala Ile Pro Ala Ala Leu Ala Gly Thr Leu Gly Tyr
1 5 10 15
Val Thr Tyr Asn Val Ala Asn Pro Asp Ile Pro Ala Ser Glu Lys Val
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

517416 Sequence Listing

<210> 26
 <211> 1344
 <212> DNA
 <213> Pavlova salina

 <400> 26
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 gattcgtcgg ccttcacgcg caaggatgtc gccgacaggc cggacctcac gatcgtgggt 120
 gacagcgtgt acgatgcgaa ggcgttccgc tccgagcatc cgggtggcgc gcactttgtg 180
 tcgctgttcg gcgggcgca tgccacggag gcgttcatgg agtaccaccg gcgcgcctgg 240
 cccaagtcgc gcatgtcgcg cttccacgtc ggctctctgg catcgaccga ggagcccgtc 300
 gccgccgatg agggctacct ccagctgtgc gctcgcacgc ccaagatggt gccgtcggtc 360
 agcagcgggt tcgcgccggc gtcgtactgg gtgaaggccg ggctgaccta cggctccgcg 420
 atcgcgctcg aggcgtacat gctgtacgcg ggcaagcgcc tgctcccgtc gatcgtgctc 480
 ggggtggctgt ttgcgtgat tggcctgaac atccagcacg atgccaacca cggcgcgctc 540
 tccaagtcgg cctcggtaaa cctggcgctc gggttgtgcc aggactggat cggcgggagc 600
 atgacctaata ggctgcagga gcacgttggt atgcaccact tgcacaccaa cgacgttgac 660
 aaggacccgg accagaaggc gcacggcgcc ctgcggctca agccgaccga cgcgtggagc 720
 ccgatgcact ggctgcagca cctctacctg ctgcctgggg agacgatgta cgccttcaag 780
 ctgctgtttc tcgacatcag cgagctgggt atgtggcggt gggagggcga gcccatcagc 840
 aagctggccg ggtacctctt catgccctcg ctgctcctca agctcacctt ctgggcgcgc 900
 tttgtcgcgc tgccgctgta cctcgcgccc agcgtgcaca cggcgggtgt catcgcggcg 960
 acggtaataa cggggagctt ctacctcgcc ttcttcttct tcatctcgca caacttcgag 1020
 ggcgtggcga gcgtcggacc ggacggcagc atcaccagca tgacgcgcgg cgcatacttc 1080
 ctcaagcggc aggccgagac ctcgtccaac gtgggcggcc cgctgctcgc cacgctcaac 1140
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 cctcgcctcg cgccgttggg caaggcggag ctcgagggcg gcggcattga gtacaagcac 1260
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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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 gactcttctg ctttcaccag aaaggatggt gctgatagac ctgatctcac catcgttgga 120

517416 Sequence Listing

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cctaagtcta gaatgtctag attccacggt ggatctcttg cttctactga ggaacctggt 300
gctgctgatg agggatacct tcaactttgt gctaggatcg ctaagatggt gccttctggt 360
tcttctggat tcgctcctgc ttcttactgg gttaaggctg gacttatcct tggatctgct 420
atcgctcttg aggcctacat gctttacgct ggaaagagac ttctcccttc tatcggttctt 480
ggatggcttt tcgctcttat cggctttaac atccagcatg atgctaacca tggtgctttg 540
tctaagtctg cttctgttaa ccttgctctt ggactttgtc aggattggat cggaggatct 600
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aaggatcctg atcaaaaggc tcacggtgct cttagactca agcctactga tgcttgggtca 720
cctatgcatt ggcttcagca tctttacctt ttgcctgggt agactatgta cgctttcaag 780
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aggcctagat ctaaggctga gtaatga 1347

<210> 28
<211> 447
<212> PRT
<213> Pavlova salina
<400> 28

Met Pro Pro Ser Ala Ala Lys Gln Met Gly Ala Ser Thr Gly Val His
1 5 10 15

Ala Gly Val Thr Asp Ser Ser Ala Phe Thr Arg Lys Asp Val Ala Asp
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

517416 Sequence Listing

Pro Lys Ser Arg Met₈₅ Ser Arg Phe His Val₉₀ Gly Ser Leu Ala Ser₉₅ Thr
 Glu Glu Pro Val₁₀₀ Ala Ala Asp Glu Gly₁₀₅ Tyr Leu Gln Leu Cys₁₁₀ Ala Arg
 Ile Ala Lys₁₁₅ Met Val Pro Ser Val₁₂₀ Ser Ser Gly Phe Ala₁₂₅ Pro Ala Ser
 Tyr Trp Val₁₃₀ Lys Ala Gly Leu₁₃₅ Ile Leu Gly Ser Ala₁₄₀ Ile Ala Leu Glu
 Ala Tyr Met Leu Tyr Ala₁₅₀ Gly Lys Arg Leu Leu₁₅₅ Pro Ser Ile Val Leu₁₆₀
 Gly Trp Leu Phe Ala₁₆₅ Leu Ile Gly Leu Asn₁₇₀ Ile Gln His Asp Ala₁₇₅ Asn
 His Gly Ala Leu₁₈₀ Ser Lys Ser Ala Ser₁₈₅ Val Asn Leu Ala Leu₁₉₀ Gly Leu
 Cys Gln Asp Trp Ile Gly Gly Ser₂₀₀ Met Ile Leu Trp Leu₂₀₅ Gln Glu His
 Val Val₂₁₀ Met His His Leu His₂₁₅ Thr Asn Asp Val Asp₂₂₀ Lys Asp Pro Asp
 Gln Lys Ala His Gly Ala₂₃₀ Leu Arg Leu Lys Pro₂₃₅ Thr Asp Ala Trp Ser₂₄₀
 Pro Met His Trp Leu₂₄₅ Gln His Leu Tyr Leu₂₅₀ Leu Pro Gly Glu Thr₂₅₅ Met
 Tyr Ala Phe Lys₂₆₀ Leu Leu Phe Leu Asp₂₆₅ Ile Ser Glu Leu Val₂₇₀ Met Trp
 Arg Trp Glu₂₇₅ Gly Glu Pro Ile Ser₂₈₀ Lys Leu Ala Gly Tyr₂₈₅ Leu Phe Met
 Pro Ser Leu Leu Leu Lys Leu₂₉₅ Thr Phe Trp Ala Arg₃₀₀ Phe Val Ala Leu
 Pro Leu Tyr Leu Ala Pro₃₁₀ Ser Val His Thr Ala₃₁₅ Val Cys Ile Ala Ala₃₂₀
 Thr Val Met Thr Gly₃₂₅ Ser Phe Tyr Leu Ala₃₃₀ Phe Phe Phe Phe Ile₃₃₅ Ser
 His Asn Phe Glu₃₄₀ Gly Val Ala Ser Val₃₄₅ Gly Pro Asp Gly Ser₃₅₀ Ile Thr

517416 Sequence Listing

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

517416 Sequence Listing

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 Emiliania
huxleyi 9 elongase in plants

<400> 30
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cttatcgga cttctctta cttttgctt aagcctctcc tcagaaactc tggacttggt 120
gatgagagaa agggagctta ccgtacttct atgatctggt acaacgttgt tcttgctctt 180
ttctctgcta cctctttcta cgttactgct actgctcttg gatgggataa gggaactggt 240
gagtggctta gatctcttac tgggtattct cctcaacaac tttggcagt cccttctaga 300
gtttgggaca gcaaactctt cttgtggact gctaaagcct tctactactc caagtacgtt 360
gagtaccttg atactgcttg gcttgttctc aagggaaga aggtttcatt cctccaggga 420
ttccatcatt tcggtgctcc atgggatggt taccttggaa tcaggcttaa gaacgaggga 480
gtttggatct tcatgttctt caacagcttc atccacactg ttatgtacac ttactacgga 540
cttactgctg ctggatacaa gatcagagga aagcctatca tcaccgctat gcaaactctt 600
caattcggtg gtggattcgt tcttggtggt gactacatca acgttccttg tttccatgct 660
gatgctggac aagttttctc ttgggtgttc aactacgctt atgtgggatc tgttttcctt 720
cttttctgcc acttcttcta catggacaac attgctaagg ctaaggctaa aaaggctggt 780

517416 Sequence Listing

801

gctaccagaa aggctctttg a

<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
 Page 54

517416 Sequence Listing

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
260 265 270

<210> 34

<211> 840

<212> DNA

<213> Pavlova salina

<400> 34

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gatgccgtaa ttggcgggga ggtgctctac ttttcgcttg ggtatctgct gctcgagccc 120

atcctcaagc gctcaccgtt tgtggacaag cgcaagggcg cataccgcaa cggcatgatc 180

gcgtacaaca tcctcatgtg cggtttctcg ctggtatgct tcgtgtgcca gatggcggcg 240

ctcggccttg atcgcgcca cctgcagttt gtccgcgacc tcacgggcga cagcgtggtg 300

517416 Sequence Listing

cagctctacc aggacgtgag cccatcccct gcattcgcga acaagctctt ccggtactca 360
gcggtggcgt tccactactc aaagtacgtg gagtacatgg acacagcgtg gcttgctgctg 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
tttagcaagc acaagccaat ctcgcgcacg gactccagca accgcatgaa aaccgagtag 840

<210> 35
<211> 279
<212> PRT
<213> Pavlova salina

<400> 35

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

Pro Gly Leu Lys Asp Ala Val Ile Gly Gly Glu Val Leu Tyr Phe Ser
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
Page 57

517416 Sequence Listing

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 ccactccgtc	540
ttcaaggggt ccgtcgcacg caccgtcggg tggaacaacg cggcgggcta cttcctcggc	600
ttcgtgcagg ggtatgcggt cgagtggtag cgcgcgcggc ataacacgca ccacgtgtgc	660
accaatgagg acggctcgga ccccgacatc aaaacggcgc cgctgctcat atacgtgcgc	720
aacaagccga gcatcgccaa gcgcctgaac gccttccagc gctaccagca gtactactat	780
gtgccggtga tggcaatcct cgacctgtac tggcggctcg agtcgatcgc ctacgtcgcg	840
atgcgcctgc cgaagatgct gccgcaggcc ctcgcactcg tcgcgcacta cgccatcgtc	900
gcgtgggtct ttgcgggcaa ctaccacctg ctcccgtcgc tgacgggttct gcgcgggttt	960

517416 Sequence Listing

ggcactggga tcaccgtttt cgcgacgcac tacggtgagg acattctcga cgcggaccag 1020
 gtgcgtcaca tgacgctcgt cgagcagacg gcactcacct cgcgcaacat ctcgggcggc 1080
 tggctcgtga acgtgctcac cggcttcac tcaactgcaga cggagcacca cctgttcccg 1140
 atgatgcaa cccgcaacct catgactatc cagcccgagg tgcgcgcctt cttcaagaag 1200
 cacggacttg agtaccgcga 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

517416 Sequence Listing

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
 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

517416 Sequence Listing

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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gctattaaat atttgcagtc cggtgaggaa acttacgagc ccaatacatt gggccacgat 120
ttaattaggg atcttatatc tggtgtaagg gcccgtgact atgtcgaagc gaccaggcga 180
tataatcatt tccacgcccg 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

517416 Sequence Listing

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

517416 Sequence Listing

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

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

517416 Sequence Listing

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

517416 Sequence Listing

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

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
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517416 Sequence Listing

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
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
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517416 Sequence Listing
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

517416 Sequence Listing

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

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

517416 Sequence Listing

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
 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

517416 Sequence Listing

Glu Val Glu Glu Lys Gln Lys
385 390

<210> 46
<211> 390
<212> PRT
<213> Braccisa napus

<400> 46

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

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

517416 Sequence Listing

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
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517416 Sequence Listing

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

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

517416 Sequence Listing

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

517416 Sequence Listing

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
 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

517416 Sequence Listing

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
ggttgagggtg gtagctgagg 20

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

<220>
<223> oligonucleotide primer

<220>
<221> misc_feature
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<223> N = Hex

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<223> N = Zen

<220>
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<223> N = 3IABkFQ

<400> 52
ntctctacnc cgtctcacat gacgcn 26

517416 Sequence Listing

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<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>
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<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

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517416 Sequence Listing

<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

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<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