

SEQUENCE LISTING

<110> BASF Plant Science GmbH

<120> Plants having enhanced yield-related traits and a method for making the same

<130> PF60629

<160> 200

<170> PatentIn version 3.3

<210> 1

<211> 1149

<212> DNA

<213> Chlamydomonas reinhardtii

<400> 1

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gagtatgtgt ggatcggcgg ctccatgcac gacgtgcgct ccaagtcgcg caccctgtcc      180
accatcccca cgaagcccgga ggacctgccc cactggaact acgacggctc ctccaccggc      240
caggcccccg gccacgactc agaggtctat ctcatcctcc gctccatctt caaggacccc      300
ttccgcggcg gcgacaacat cctgggtcatg tgcgactgct acgagccgcc caaggtcaac      360
cccgacggca ccctggccgc gcccaagccg atccccacga acaccgctt tgccctgcgc      420
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<210> 2

<211> 382
<212> PRT
<213> Chlamydomonas reinhardtii

<400> 2

Met Ala Ala Gly Ser Val Gly Val Phe Ala Thr Asp Glu Lys Ile Gly
1 5 10 15

Ser Leu Leu Asp Gln Ser Ile Thr Arg His Phe Leu Ser Thr Val Thr
20 25 30

Asp Gln Gln Gly Lys Ile Cys Ala Glu Tyr Val Trp Ile Gly Gly Ser
35 40 45

Met His Asp Val Arg Ser Lys Ser Arg Thr Leu Ser Thr Ile Pro Thr
50 55 60

Lys Pro Glu Asp Leu Pro His Trp Asn Tyr Asp Gly Ser Ser Thr Gly
65 70 75 80

Gln Ala Pro Gly His Asp Ser Glu Val Tyr Leu Ile Pro Arg Ser Ile
85 90 95

Phe Lys Asp Pro Phe Arg Gly Gly Asp Asn Ile Leu Val Met Cys Asp
100 105 110

Cys Tyr Glu Pro Pro Lys Val Asn Pro Asp Gly Thr Leu Ala Ala Pro
115 120 125

Lys Pro Ile Pro Thr Asn Thr Arg Phe Ala Cys Ala Glu Val Met Glu
130 135 140

Lys Ala Lys Lys Glu Glu Pro Trp Phe Gly Ile Glu Gln Glu Tyr Thr
145 150 155 160

Leu Leu Asn Ala Ile Thr Lys Trp Pro Leu Gly Trp Pro Lys Gly Gly
165 170 175

Tyr Pro Ala Pro Gln Gly Pro Tyr Tyr Cys Ser Ala Gly Ala Gly Val
180 185 190

Ala Ile Gly Arg Asp Val Ala Glu Val His Tyr Arg Leu Cys Leu Ala
195 200 205

Ala Gly Val Asn Ile Ser Gly Val Asn Ala Glu Val Leu Pro Ser Gln
210 215 220

Trp Glu Tyr Gln Val Gly Pro Cys Glu Gly Ile Thr Met Gly Asp His
225 230 235 240

Met Trp Met Ser Arg Tyr Ile Met Tyr Arg Val Cys Glu Met Phe Asn
245 250 255

Val Glu Val Ser Phe Asp Pro Lys Pro Ile Pro Gly Asp Trp Asn Gly
260 265 270

Ser Gly Gly His Thr Asn Tyr Ser Thr Lys Ala Thr Arg Thr Ala Pro
275 280 285

Asp Gly Trp Lys Val Ile Gln Glu His Cys Ala Lys Leu Glu Ala Arg
290 295 300

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

Thr Gly Lys His Glu Thr Ser Ser Met Ser Asp Phe Ser Trp Gly Val
325 330 335

Ala Asn Arg Gly Cys Ser Ile Arg Val Gly Arg Met Val Pro Val Glu
340 345 350

Lys Ser Gly Tyr Tyr Glu Asp Arg Arg Pro Ala Ser Asn Leu Asp Ala
355 360 365

Tyr Val Val Thr Arg Leu Ile Val Glu Thr Thr Ile Leu Leu
370 375 380

<210> 3
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> motif 1

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<220>
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<222> (4)..(4)
<223> /replace = "Thr"

<220>

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<223> /replace = "Ser" /replace = "Pro"

<220>
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<223> /replace = "Ser"

<220>
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<222> (11)..(11)
<223> /replace = "Asp"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace = "Leu" /replace = "Ala" /replace = "Met"

<220>
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<222> (14)..(14)
<223> /replace = "Ala"

<400> 3

Gly Tyr Tyr Glu Asp Arg Arg Pro Ala Ala Asn Val Asp Pro Tyr
1 5 10 15

<210> 4
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> motif 2

<220>
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<220>
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<222> (6)..(6)
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"Gly" /replace = "Leu" /replace = "Val"

<220>
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<222> (7)..(7)
<223> /replace = "Asn" /replace = "Asp"

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<221> VARIANT
<222> (9)..(9)
<223> /replace = "Ile"

<220>
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<222> (10)..(10)
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<220>
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<222> (12)..(12)
<223> /replace = "Ile" /replace = "Met"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace = "Thr" /replace = "Ala"

<400> 4

Asp Pro Ile Arg Gly Ala Pro His Val Leu Val Leu Cys
1 5 10

<210> 5
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> motif 3

<220>
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<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace = "Ser" /replace = "Ile" /replace = "Val" /replace =
"Phe"

<220>
<221> VARIANT
<222> (5)..(5)
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<220>
<221> VARIANT
<222> (6)..(6)
<223> /replace = "Tyr" /replace = "Val"

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace = "Ser" /replace = "Asn"

<400> 5

Gly Ala His Thr Asn Phe Ser Thr
1 5

<210> 6
<211> 1179
<212> DNA
<213> *Oryza sativa*

<400> 6
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cattaccact ttacctgaca ttttggacag agattagaaa tagtttcgta ctacctgcaa 180
gttgcaactt gaaaagtga atttgttcct tgctaataata ttggcgtgta attcttttat 240
gcgttagcgt aaaaagttga aatttgggtc agtttactgg tcagattaac cagtaactgg 300
ttaaagttga aagatggtct tttagtaatg gagggagtag tacactatcc tcagctgatt 360
taaactttat tccgtcgggtg gtgatttcgt caatctccca acttagtttt tcaatatatt 420
cataggatag agtgtgcata tgtgtgttta tagggatgag tctacgcgcc ttatgaacac 480
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cagaccaat gggcctttcc tacgtgtctc ggccacagcc agtcgtttac cgacggttca 660
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acgcccacac accgcacacg ggtcgcgata gccacgaccc aatcacacaa cgccacgtca 840
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ttacgaaaaa atatcccacc acgtgtcgtc ttacacaggac aatatctcga aggaaaaaaa 960
tcgtagcggg aaatccgagg cagagctgc gattggctgg gaggcgtcca gcgtggtggg 1020
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<210> 7
<211> 53
<212> DNA
<213> Artificial sequence

<220>
<223> primer: prm08458

<400> 7

ggggacaagt ttgtacaaaa aagcaggctt aaacaatggc cgcgggatct gtt 53

<210> 8
<211> 50
<212> DNA
<213> Artificial sequence

<220>
<223> primer: prm08459

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<210> 9
<211> 357
<212> PRT
<213> Aureococcus anophagefferens

<400> 9

Met Ala Ser Met Asp Gln Ala Val Leu Gly Lys Tyr Met Gly Leu Asp
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Thr Gly Asp Asp Cys Gln Val Glu Tyr Val Phe Leu Asp Lys Asp Gln
20 25 30

Val Ala Arg Ser Lys Cys Arg Thr Leu Pro Leu Lys Lys Val Gln Gly
35 40 45

Pro Val Asp Ala Tyr Pro Lys Trp Asn Tyr Asp Gly Ser Ser Thr Gly
50 55 60

Gln Ala Pro Gly Asp Asp Ser Glu Val Met Ile Val Pro Arg Ala Lys
65 70 75 80

Tyr Pro Asp Pro Phe Arg Gly Gly Asn His Val Leu Val Leu Cys Asp
85 90 95

Thr Tyr Glu Pro Asp Gly Thr Pro Leu Pro Thr Asn Thr Arg Ala Pro
100 105 110

Ala Val Ala Arg Phe Glu Ser Gly Gly Ala Lys Glu Gln Val Pro Trp
115 120 125

Tyr Gly Leu Glu Gln Glu Tyr Thr Leu Phe Asn Leu Asp Gly Val Thr
130 135 140

Pro Leu Gly Trp Pro Val Gly Gly Phe Pro Lys Pro Gln Gly Pro Tyr
145 150 155 160

Tyr Cys Gly Ala Gly Ala Asp Arg Ala Phe Gly Arg Ala Val Ser Glu
165 170 175

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

Asn Ala Glu Val Met Pro Gly Gln Trp Glu Tyr Gln Ile Gly Pro Ser
195 200 205

Ile Gly Ile Asp Ala Ala Asp Gln Leu Thr Ile Ser Arg Tyr Ile Leu
210 215 220

Ser Arg Val Cys Glu Asp Leu Gly Val Ile Val Thr Ile Asp Pro Lys
225 230 235 240

Pro Ile Ala Gly Asp Trp Asn Gly Ala Gly Met His Ile Asn Phe Ser
245 250 255

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

Cys Glu Lys Leu Gly Ala Lys His Thr Glu His Ile Ala Ala Tyr Gly
275 280 285

Glu Gly Asn Glu Arg Arg Leu Thr Gly Asp Cys Glu Thr Ala Ser Ile
290 295 300

Asp Gln Phe Ser Tyr Gly Val Ala Asp Arg Gly Cys Ser Ile Arg Ile
305 310 315 320

Pro Arg Asp Thr Ala Ala Asp Lys Lys Gly Tyr Leu Glu Asp Arg Arg
325 330 335

Pro Ala Ser Asn Val Asp Pro Tyr Val Ala Thr Ser Leu Ile Phe Ala
340 345 350

Thr Cys Thr Ser Ala
355

<210> 10
<211> 380
<212> PRT
<213> Chlamydomonas reinhardtii

<400> 10

Met Ala Phe Ala Leu Arg Gly Val Thr Ala Lys Ala Ser Gly Arg Thr

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

Ser Thr Phe Asn Pro Lys Pro Val Arg Thr Gly Asp Trp Asn Gly Thr
260 265 270

Gly Ala His Thr Asn Phe Ser Thr Lys Gly Met Arg Val Pro Gly Gly
275 280 285

Met Lys Val Ile Glu Glu Ala Val Glu Lys Leu Ser Lys Thr His Ile
290 295 300

Glu His Ile Thr Gln Tyr Gly Ile Gly Asn Glu Ala Arg Leu Thr Gly
305 310 315 320

Lys His Glu Thr Cys Asp Ile Asn Thr Phe Lys His Gly Val Ala Asp
325 330 335

Arg Gly Ser Ser Ile Arg Ile Pro Leu Pro Val Met Leu Lys Gly Tyr
340 345 350

Gly Tyr Leu Glu Asp Arg Arg Pro Ala Ala Asn Val Asp Pro Tyr Thr
355 360 365

Val Ala Arg Leu Leu Ile Lys Thr Val Leu Lys Gly
370 375 380

<210> 11
<211> 375
<212> PRT
<213> Chlamydomonas reinhardtii

<400> 11

Met Arg Leu Asn Thr Gln Val Ser Gly Arg Ala Thr Gly Ala Pro Arg
1 5 10 15

Gln Gly Arg Arg Leu Thr Val Arg Val Gln Ala Tyr Gly Met Lys Ala
20 25 30

Glu Tyr Ile Trp Ala Asp Gly Asn Glu Gly Lys Ala Glu Lys Gly Met
35 40 45

Ile Phe Asn Glu Met Arg Ser Lys Thr Lys Cys Phe Glu Ala Pro Leu
50 55 60

Gly Leu Asp Ala Ser Glu Tyr Pro Asp Trp Ser Phe Asp Gly Ser Ser
65 70 75 80

Thr Gly Gln Ala Glu Gly Asn Asn Ser Asp Cys Ile Leu Arg Pro Val
85 90 95

Arg Val Val Thr Asp Pro Ile Arg Gly Ala Pro His Val Leu Val Met
100 105 110

Cys Glu Val Phe Ala Pro Asp Gly Lys Pro His Ser Thr Asn Thr Arg
115 120 125

Ala Lys Leu Arg Glu Ile Ile Asp Asp Lys Val Thr Ala Glu Asp Cys
130 135 140

Trp Tyr Gly Phe Glu Gln Glu Tyr Thr Met Leu Ala Lys Thr Ser Gly
145 150 155 160

His Ile Tyr Gly Trp Pro Ala Gly Gly Phe Pro Ala Pro Gln Gly Pro
165 170 175

Phe Tyr Cys Gly Val Gly Ala Glu Ser Ala Phe Gly Arg Pro Leu Ala
180 185 190

Glu Ala His Met Glu Ala Cys Met Lys Ala Gly Leu Val Ile Ser Gly
195 200 205

Ile Asn Ala Glu Val Met Pro Gly Gln Trp Glu Tyr Gln Ile Gly Pro
210 215 220

Val Gly Pro Leu Ala Leu Gly Asp Glu Val Met Leu Ser Arg Trp Leu
225 230 235 240

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

Lys Pro Val Arg Thr Gly Asp Trp Asn Gly Thr Gly Ala His Thr Asn
260 265 270

Phe Ser Thr Lys Gly Met Arg Val Pro Gly Gly Met Lys Val Ile Glu
275 280 285

Glu Ala Val Glu Lys Leu Ser Lys Thr His Ile Glu His Ile Thr Gln
290 295 300

Tyr Gly Ile Gly Asn Glu Ala Arg Leu Thr Gly Lys His Glu Thr Cys
305 310 315 320

Asp Ile Asn Thr Phe Lys His Gly Val Ala Asp Arg Gly Ser Ser Ile

325

330

335

Arg Ile Pro Leu Pro Val Met Leu Lys Gly Tyr Gly Tyr Leu Glu Asp
 340 345 350

Arg Arg Pro Ala Ala Asn Val Asp Pro Tyr Thr Val Ala Arg Leu Leu
 355 360 365

Ile Lys Thr Val Leu Lys Gly
 370 375

<210> 12

<211> 577

<212> PRT

<213> Chlamydomonas reinhardtii

<400> 12

Met Asp Leu Ala Thr Ala Leu Gly Leu Gly Ile Ala Pro Pro Pro Pro
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Ala Asp Asp Ser Ser His His Ser Thr Thr Glu Ala Cys Thr Leu Pro
 20 25 30

Ala Tyr Leu Arg Ala Pro Glu Val Thr Ala Gln Val Met Ala Glu Tyr
 35 40 45

Ile Trp Leu Met Gly Gly Thr Gly Gln Leu Arg Ser Lys Thr Lys Val
 50 55 60

Leu Asp Ala Lys Pro Ser Cys Ala Glu Glu Ala Pro Ile Met Ile Val
 65 70 75 80

Glu Ser Asn Pro Asp Gly Gln Leu Ala Glu Pro Asn His Glu Leu Phe
 85 90 95

Leu Lys Pro Arg Lys Ile Phe Arg Asp Pro Phe Arg Gly Gly Asp His
 100 105 110

Ile Leu Val Leu Cys Asp Thr Phe Ile Val Ala Gln Val Val Ala Glu
 115 120 125

Ala Gly Ala Ala Pro Ser Thr Val Leu Gln Pro Ser Glu Thr Asn Ser
 130 135 140

Arg Val Ala Cys Glu Asn Val Leu Arg Val Ala Glu Gln Gln Glu Pro
 145 150 155 160

Val Phe Ala Val Glu Gln Glu Tyr Ala Ile Ile His Pro Ala Tyr Pro
165 170 175

Thr Lys Val Pro Leu Gly Pro Arg Arg Pro Ser Thr Ser Arg Ala Ser
180 185 190

Ser Cys His Ser Gly Ser Arg Arg Ser Ser Tyr Val Ser Ser Gly Ser
195 200 205

Ala Arg Gly Gly Ile Gly Lys Asn Ser Ser His His Gly Gly Lys Gln
210 215 220

Ser His Ala Ala Ala Ala Ala Ala Ala Ala Val Ala Gly Ile Pro
225 230 235 240

Trp Pro Ser Pro Asp Ala Cys Glu Gln Thr Ala Gln Glu Ala Ser Ala
245 250 255

Ala Arg Gln Lys Ala Ser Arg Gln Leu Ala Asp Ser His Leu Arg Cys
260 265 270

Cys Leu Phe Ala Gly Val Arg Val Thr Gly Ala Asp Val His Ser Leu
275 280 285

Asp Gly Leu His Ser Tyr Lys Ile Gly Pro Ser Pro Gly Val Asp Leu
290 295 300

Gly Asp Asp Leu Trp Thr Ser Arg Tyr Leu Leu Gln Arg Val Ala Glu
305 310 315 320

Gln His Ser Ala Ser Val Ser Trp Glu Pro Asp Ser Met Pro Ser Glu
325 330 335

Arg Pro Leu Gly Cys His Phe Lys Tyr Ser Thr Ala Ser Thr Arg Gln
340 345 350

Ala Pro His Gly Leu Asn Ala Ile Glu Gln Gln Leu Val Arg Leu Gln
355 360 365

Ala Thr His Val Gln His Gln Val Ala Tyr Asn Asp Gly Arg Leu Asp
370 375 380

Arg Leu Ser Ser Pro Glu Ala Ser Thr Phe Thr His Ala Val Gly Ser
385 390 395 400

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

Gly Tyr Phe Thr Asp Arg Arg Pro Pro Ser Asp Ala Asp Pro Tyr Lys
420 425 430

Val Thr Leu Leu Leu Ala Ala Thr Thr Leu Asp Ile Pro Leu Pro Lys
435 440 445

Leu Pro Ala Ser Ser Ser Ala Gly Asn Thr Ala Ala Asn Cys Ser Gly
450 455 460

Gly Met Ser Ala Gly Pro Ser Ser Cys Pro Ala Ala Ala Ala Leu Pro
465 470 475 480

Phe Gly Ser Pro Met Gln Ser Tyr Leu Leu Ala Ala Ala Ala Ala Gln
485 490 495

Arg Gln Gln Gln Gln Gln His Leu Met Phe Asp Thr Glu Ser Glu Glu
500 505 510

Cys Asp Ser Val Asp Glu Asp Asp Ala Met Thr Glu Asp Ser Ala Ala
515 520 525

Leu Leu Ala Lys Met Asp Asp Asp Gly Gly Ala Ala Glu Ala Ser Ser
530 535 540

Cys Asp Ser Asp Phe Glu Asp Gln Asp Asp Ala Ser Ser Ser Pro Ile
545 550 555 560

Thr Gly Thr Trp Ala Asp Asn Asp Cys Thr His Met Leu Gly Ala Gly
565 570 575

Ile

<210> 13
<211> 386
<212> PRT
<213> Helicosporidium sp.

<400> 13

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Thr Gln Gly Gln Ile Thr Gln Leu Leu Asp Pro Ile Met Ala Glu Arg
20 25 30

Phe Lys Asp Leu Ser Gln His Gly Lys Val Met Ala Glu Tyr Val Trp
35 40 45

Ile Gly Gly Thr Gly Ser Asp Leu Arg Cys Lys Thr Arg Val Leu Asp
50 55 60

Ser Val Pro Asn Ser Val Glu Asp Leu Pro Val Trp Asn Tyr Asp Gly
65 70 75 80

Ser Ser Thr Gly Gln Ala Pro Gly Asp Asp Ser Glu Val Phe Leu Ile
85 90 95

Pro Arg Ala Ile Tyr Arg Asp Pro Phe Arg Gly Gly Asp Asn Ile Leu
100 105 110

Val Leu Ala Asp Thr Tyr Glu Pro Pro Arg Val Leu Pro Asn Gly Lys
115 120 125

Val Ser Pro Pro Val Pro Leu Pro Thr Asn Ser Arg His Ala Cys Ala
130 135 140

Glu Ala Met Asp Lys Ala Ala Ala His Glu Pro Trp Phe Gly Ile Glu
145 150 155 160

Gln Glu Tyr Thr Val Leu Asp Ala Arg Thr Lys Trp Pro Leu Gly Trp
165 170 175

Pro Ser Asn Gly Phe Pro Gly Pro Gln Gly Pro Tyr Tyr Cys Ala Ala
180 185 190

Gly Ala Gly Cys Ala Ile Gly Arg Asp Leu Ile Glu Ala His Leu Lys
195 200 205

Ala Cys Leu Phe Ala Gly Ile Asn Val Ser Gly Val Asn Ala Glu Val
210 215 220

Met Pro Ser Gln Trp Glu Tyr Gln Val Gly Pro Cys Thr Gly Ile Glu
225 230 235 240

Ser Gly Asp Gln Met Trp Met Ser Arg Tyr Ile Leu Ile Arg Cys Ala
245 250 255

Glu Leu Tyr Asn Val Glu Val Ser Phe Asp Pro Lys Pro Val Pro Gly
260 265 270

Asp Trp Asn Gly Ala Gly Gly His Val Asn Tyr Ser Asn Lys Ala Thr
275 280 285

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

Leu Gly Lys Arg His Ala Val His Ile Ala Ala Tyr Gly Glu Gly Asn
305 310 315 320

Glu Arg Arg Leu Thr Gly Lys His Glu Thr Ser Ser Met Asn Asp Phe
325 330 335

Ser Trp Gly Val Ala Asn Arg Gly Ala Ser Val Arg Val Gly Arg Leu
340 345 350

Val Pro Val Glu Lys Cys Gly Tyr Tyr Glu Asp Arg Arg Pro Ala Ser
355 360 365

Asn Leu Asp Pro Tyr Val Val Thr Arg Leu Leu Val Glu Thr Thr Leu
370 375 380

Leu Met
385

<210> 14
<211> 416
<212> PRT
<213> Thalassiosira pseudonana

<400> 14

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

Phe Ala Pro Ser Leu Thr Thr Pro Ser Arg Thr Thr Ser Leu Ser Met
20 25 30

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

Val Ile Asp Arg Phe Asn Ala Leu Pro Tyr Pro Ala Asp Lys Val Leu
50 55 60

Ala Glu Tyr Val Trp Val Asp Ala Lys Gly Glu Cys Arg Ser Lys Thr
65 70 75 80

Arg Thr Leu Pro Val Ala Arg Thr Thr Ala Val Asp Asn Leu Pro Arg

85

90

95

Trp Asn Phe Asp Gly Ser Ser Thr Gly Gln Ala Pro Gly Asp Asp Ser
 100 105 110

Glu Val Ile Leu Arg Pro Cys Arg Ile Phe Lys Asp Pro Phe Arg Pro
 115 120 125

Arg Asn Asp Gly Val Asp Asn Ile Leu Val Met Cys Asp Thr Tyr Thr
 130 135 140

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

Ala Phe Glu Gly Lys Glu Asp Glu Glu Ile Trp Phe Gly Leu Glu Gln
 165 170 175

Glu Phe Thr Leu Phe Asn Leu Asp Gln Arg Thr Pro Leu Gly Trp Pro
 180 185 190

Lys Gly Gly Val Pro Ala Arg Ala Gln Gly Pro Tyr Tyr Cys Ser Val
 195 200 205

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

Ala Cys Leu Tyr Ala Gly Ile Glu Ile Ser Gly Thr Asn Gly Glu Val
 225 230 235 240

Met Pro Gly Gln Gln Glu Tyr Gln Val Gly Pro Cys Val Gly Ile Asp
 245 250 255

Ala Gly Asp Gln Leu Gln Met Ser Arg Tyr Ile Leu Gln Arg Val Cys
 260 265 270

Glu Glu Phe Gln Val Tyr Cys Thr Leu His Pro Lys Pro Ile Val Glu
 275 280 285

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

Met Arg Glu Glu Gly Gly Leu Glu Val Ile Lys Lys Ala Ile Tyr Lys
 305 310 315 320

Leu Gly Ala Lys His Gln Glu His Ile Ala Val Tyr Gly Glu Gly Asn
 325 330 335

Glu Leu Arg Leu Thr Gly Lys His Glu Thr Ala Ser Ile Asp Gln Phe
340 345 350

Ser Phe Gly Val Ala Asn Arg Gly Ala Ser Val Arg Ile Gly Arg Asp
355 360 365

Thr Glu Ala Glu Gly Lys Gly Tyr Phe Glu Asp Arg Arg Pro Ser Ser
370 375 380

Asn Ala Asp Pro Tyr Leu Val Thr Gly Lys Ile Met Ala Thr Ile Met
385 390 395 400

Glu Asp Val Asp Val Pro Glu Ile Ser Ala Leu Asp Arg Ala Glu Ala
405 410 415

<210> 15
<211> 379
<212> PRT
<213> Volvox carterii

<400> 15

Met Ala Thr Met Arg Met Ser Thr Lys Ala Gln Gly Arg Val Gly Ile
1 5 10 15

Val Arg Asn Thr Arg Thr Leu Thr Val Arg Val Arg Ala Tyr Gly Met
20 25 30

Lys Ala Glu Tyr Ile Trp Ala Asp Gly Asn Glu Gly Arg Pro Glu Lys
35 40 45

Gly Met Ile Phe Asn Glu Met Arg Ser Lys Thr Lys Val Phe Asp Glu
50 55 60

Ala Leu Pro Leu Glu Ala Gly Gln Tyr Pro Asp Trp Ser Phe Asp Gly
65 70 75 80

Ser Ser Thr Gly Gln Ala Ala Gly Asn Asn Ser Asp Cys Ile Leu Arg
85 90 95

Pro Val Arg Val Ile Lys Asp Pro Ile Arg Gly Glu Pro His Val Leu
100 105 110

Val Met Cys Glu Val Phe Ala Pro Asp Gly Thr Pro His Pro Thr Asn
115 120 125

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

Asp Cys Trp Tyr Gly Leu Glu Gln Glu Tyr Thr Met Leu Gln Lys Thr
145 150 155 160

Thr Gly Gln Ile Tyr Gly Trp Pro Ser Gly Gly Tyr Pro Ala Pro Gln
165 170 175

Gly Pro Phe Tyr Cys Gly Val Gly Ala Glu Ser Ala Phe Gly Arg Pro
180 185 190

Leu Ala Glu Ala His Met Glu Ala Cys Met Lys Ala Gly Leu Lys Ile
195 200 205

Ser Gly Ile Asn Ala Glu Val Met Pro Gly Gln Trp Glu Tyr Gln Ile
210 215 220

Gly Pro Val Gly Pro Leu Glu Met Gly Asp Glu Val Met Leu Ser Arg
225 230 235 240

Trp Leu Leu His Arg Leu Gly Glu Asp Phe Gly Ile Val Cys Thr Phe
245 250 255

Asn Pro Lys Pro Val Arg Thr Gly Asp Trp Asn Gly Thr Gly Ala His
260 265 270

Thr Asn Phe Ser Thr Lys Ser Met Arg Gln Pro Gly Gly Met Lys Val
275 280 285

Ile Glu Asp Ala Val Glu Lys Leu Ser Lys Thr His Ile Glu His Ile
290 295 300

Thr Gln Tyr Gly Leu Gly Asn Glu Ala Arg Leu Thr Gly Lys His Glu
305 310 315 320

Thr Cys Asp Ile Asn Thr Phe Lys His Gly Val Ala Asp Arg Gly Ser
325 330 335

Ser Ile Arg Ile Pro Leu Pro Val Met Leu Lys Gly Tyr Gly Tyr Leu
340 345 350

Glu Asp Arg Arg Pro Ala Ala Asn Val Asp Pro Tyr Thr Val Ala Arg
355 360 365

Leu Leu Ile Lys Ser Ile Leu Lys Gly Pro Gln

370

375

<210> 16
 <211> 382
 <212> PRT
 <213> Volvox carterii

<400> 16

Met Ala Ala Gly Ser Ile Gly Val Phe Ala Thr Asp Glu Lys Ile Gly
 1 5 10 15

Ser Leu Leu Asp Gln Ser Ile Thr Arg His Phe Leu Thr Asn Val Thr
 20 25 30

Asp Gln Cys Gly Lys Ile Thr Ala Glu Tyr Val Trp Ile Gly Gly Ser
 35 40 45

Met Gln Asp Leu Arg Ser Lys Ser Arg Thr Leu Thr Ser Val Pro Thr
 50 55 60

Lys Pro Glu Asp Leu Pro His Trp Asn Tyr Asp Gly Ser Ser Thr Gly
 65 70 75 80

Gln Ala Pro Gly His Asp Ser Glu Val Tyr Leu Ile Pro Arg Arg Ile
 85 90 95

Phe Arg Asp Pro Phe Arg Gly Gly Asp Asn Ile Leu Val Met Cys Asp
 100 105 110

Cys Tyr Glu Pro Pro Lys Ala Asn Ala Asp Gly Ile Leu Gln Pro Pro
 115 120 125

Lys Pro Ile Pro Thr Asn Thr Arg Tyr Ala Cys Ala Glu Ala Met Glu
 130 135 140

Lys Ala Lys Asp Glu Glu Pro Trp Phe Gly Ile Glu Gln Glu Tyr Thr
 145 150 155 160

Leu Leu Asn Ala Ile Thr Lys Trp Pro Leu Gly Trp Pro Lys Gly Gly
 165 170 175

Tyr Pro Ala Pro Gln Gly Pro Tyr Tyr Cys Ser Ala Gly Ala Gly Val
 180 185 190

Ala Ile Gly Arg Asp Val Ala Glu Val His Tyr Arg Leu Cys Leu Tyr
 195 200 205

Ala Gly Val Asn Ile Ser Gly Val Asn Ala Glu Val Leu Pro Ser Gln
210 215 220

Trp Glu Tyr Gln Val Gly Pro Cys Glu Gly Ile Glu Met Gly Asp His
225 230 235 240

Met Trp Met Ser Arg Tyr Ile Met Tyr Arg Val Cys Glu Met Phe Asn
245 250 255

Val Glu Val Ser Phe Asp Pro Lys Pro Ile Pro Gly Asp Trp Asn Gly
260 265 270

Ser Gly Gly His Thr Asn Tyr Ser Thr Lys Ala Thr Arg Thr Ala Pro
275 280 285

Asn Gly Trp Lys Ala Ile Gln Glu His Cys Gln Lys Leu Glu Ala Arg
290 295 300

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

Thr Gly Lys His Glu Thr Ser Ser Met Asn Asp Phe Ser Trp Gly Val
325 330 335

Ala Asn Arg Gly Cys Ser Ile Arg Val Gly Arg Met Val Pro Val Glu
340 345 350

Lys Cys Gly Tyr Tyr Glu Asp Arg Arg Pro Ala Ser Asn Leu Asp Pro
355 360 365

Tyr Val Val Thr Lys Leu Ile Val Glu Thr Thr Val Leu Leu
370 375 380

<210> 17
<211> 356
<212> PRT
<213> Arabidopsis thaliana

<400> 17

Met Ser Leu Leu Ala Asp Leu Val Asn Leu Asp Ile Ser Asp Asn Ser
1 5 10 15

Glu Lys Ile Ile Ala Glu Tyr Ile Trp Val Gly Gly Ser Gly Met Asp
20 25 30

Met Arg Ser Lys Ala Arg Thr Leu Pro Gly Pro Val Thr Asp Pro Ser

35

40

45

Lys Leu Pro Lys Trp Asn Tyr Asp Gly Ser Ser Thr Gly Gln Ala Pro
 50 55 60

Gly Gln Asp Ser Glu Val Ile Leu Tyr Pro Gln Ala Ile Phe Lys Asp
 65 70 75 80

Pro Phe Arg Arg Gly Asn Asn Ile Leu Val Met Cys Asp Ala Tyr Thr
 85 90 95

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

Ile Phe Ala Asn Pro Asp Val Ile Ala Glu Val Pro Trp Tyr Gly Ile
 115 120 125

Glu Gln Glu Tyr Thr Leu Leu Gln Lys Asp Val Asn Trp Pro Leu Gly
 130 135 140

Trp Pro Ile Gly Gly Phe Pro Gly Pro Gln Gly Pro Tyr Tyr Cys Ser
 145 150 155 160

Ile Gly Ala Asp Lys Ser Phe Gly Arg Asp Ile Val Asp Ala His Tyr
 165 170 175

Lys Ala Ser Leu Tyr Ala Gly Ile Asn Ile Ser Gly Ile Asn Gly Glu
 180 185 190

Val Met Pro Gly Gln Trp Glu Phe Gln Val Gly Pro Ser Val Gly Ile
 195 200 205

Ser Ala Ala Asp Glu Ile Trp Ile Ala Arg Tyr Ile Leu Glu Arg Ile
 210 215 220

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

Gly Asp Trp Asn Gly Ala Gly Ala His Thr Asn Tyr Ser Thr Lys Ser
 245 250 255

Met Arg Glu Glu Gly Gly Tyr Glu Ile Ile Lys Lys Ala Ile Glu Lys
 260 265 270

Leu Gly Leu Arg His Lys Glu His Ile Ser Ala Tyr Gly Glu Gly Asn
 275 280 285

Glu Arg Arg Leu Thr Gly His His Glu Thr Ala Asp Ile Asn Thr Phe
290 295 300

Leu Trp Gly Val Ala Asn Arg Gly Ala Ser Ile Arg Val Gly Arg Asp
305 310 315 320

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

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

Leu Trp Asn Pro
355

<210> 18
<211> 430
<212> PRT
<213> Arabidopsis thaliana

<400> 18

Met Ala Gln Ile Leu Ala Ala Ser Pro Thr Cys Gln Met Arg Val Pro
1 5 10 15

Lys His Ser Ser Val Ile Ala Ser Ser Ser Lys Leu Trp Ser Ser Val
20 25 30

Val Leu Lys Gln Lys Lys Gln Ser Asn Asn Lys Val Arg Gly Phe Arg
35 40 45

Val Leu Ala Leu Gln Ser Asp Asn Ser Thr Val Asn Arg Val Glu Thr
50 55 60

Leu Leu Asn Leu Asp Thr Lys Pro Tyr Ser Asp Arg Ile Ile Ala Glu
65 70 75 80

Tyr Ile Trp Ile Gly Gly Ser Gly Ile Asp Leu Arg Ser Lys Ser Arg
85 90 95

Thr Ile Glu Lys Pro Val Glu Asp Pro Ser Glu Leu Pro Lys Trp Asn
100 105 110

Tyr Asp Gly Ser Ser Thr Gly Gln Ala Pro Gly Glu Asp Ser Glu Val
115 120 125

Ile Leu Tyr Pro Gln Ala Ile Phe Arg Asp Pro Phe Arg Gly Gly Asn
130 135 140

Asn Ile Leu Val Ile Cys Asp Thr Trp Thr Pro Ala Gly Glu Pro Ile
145 150 155 160

Pro Thr Asn Lys Arg Ala Lys Ala Ala Glu Ile Phe Ser Asn Lys Lys
165 170 175

Val Ser Gly Glu Val Pro Trp Phe Gly Ile Glu Gln Glu Tyr Thr Leu
180 185 190

Leu Gln Gln Asn Val Lys Trp Pro Leu Gly Trp Pro Val Gly Ala Phe
195 200 205

Pro Gly Pro Gln Gly Pro Tyr Tyr Cys Gly Val Gly Ala Asp Lys Ile
210 215 220

Trp Gly Arg Asp Ile Ser Asp Ala His Tyr Lys Ala Cys Leu Tyr Ala
225 230 235 240

Gly Ile Asn Ile Ser Gly Thr Asn Gly Glu Val Met Pro Gly Gln Trp
245 250 255

Glu Phe Gln Val Gly Pro Ser Val Gly Ile Asp Ala Gly Asp His Val
260 265 270

Trp Cys Ala Arg Tyr Leu Leu Glu Arg Ile Thr Glu Gln Ala Gly Val
275 280 285

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

Gly Cys His Thr Asn Tyr Ser Thr Lys Ser Met Arg Glu Glu Gly Gly
305 310 315 320

Phe Glu Val Ile Lys Lys Ala Ile Leu Asn Leu Ser Leu Arg His Lys
325 330 335

Glu His Ile Ser Ala Tyr Gly Glu Gly Asn Glu Arg Arg Leu Thr Gly
340 345 350

Lys His Glu Thr Ala Ser Ile Asp Gln Phe Ser Trp Gly Val Ala Asn
355 360 365

Arg Gly Cys Ser Ile Arg Val Gly Arg Asp Thr Glu Ala Lys Gly Lys

370

375

380

Gly Tyr Leu Glu Asp Arg Arg Pro Ala Ser Asn Met Asp Pro Tyr Ile
 385 390 395 400

Val Thr Ser Leu Leu Ala Glu Thr Thr Leu Leu Trp Glu Pro Thr Leu
 405 410 415

Glu Ala Glu Ala Leu Ala Ala Gln Lys Leu Ser Leu Asn Val
 420 425 430

<210> 19

<211> 356

<212> PRT

<213> Brassica napus

<400> 19

Met Ser Leu Leu Thr Asp Leu Val Asn Leu Asp Leu Ser Asp Asn Thr
 1 5 10 15

Glu Lys Ile Ile Ala Glu Tyr Ile Trp Val Gly Gly Ser Gly Met Asp
 20 25 30

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

Lys Leu Pro Lys Trp Asn Tyr Asp Gly Ser Ser Thr Gly Gln Ala Pro
 50 55 60

Gly Glu Asp Ser Glu Val Ile Leu Tyr Pro Gln Ala Ile Phe Lys Asp
 65 70 75 80

Pro Phe Arg Arg Gly Asn Asn Ile Leu Val Met Cys Asp Thr Tyr Thr
 85 90 95

Pro Ala Gly Glu Pro Ile Pro Thr Asn Lys Arg His Ala Ala Ala Gln
 100 105 110

Ile Phe Ser Asn Pro Asp Val Val Ala Glu Val Pro Trp Tyr Gly Ile
 115 120 125

Glu Gln Glu Tyr Thr Leu Leu Gln Lys Asp Val Asn Trp Pro Val Gly
 130 135 140

Trp Pro Ile Gly Gly Phe Pro Gly Pro Gln Gly Pro Tyr Tyr Cys Ser
 145 150 155 160

Val Gly Ala Asp Lys Ser Phe Gly Arg Asp Ile Val Asp Ala His Tyr
165 170 175

Lys Ala Cys Leu Tyr Ala Gly Ile Asn Ile Ser Gly Ile Asn Gly Glu
180 185 190

Val Met Pro Gly Gln Trp Glu Phe Gln Val Gly Pro Ser Val Gly Ile
195 200 205

Ser Ala Ala Asp Glu Val Trp Ile Ala Arg Tyr Ile Leu Glu Arg Ile
210 215 220

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

Gly Asp Trp Asn Gly Ala Gly Ala His Thr Asn Tyr Ser Thr Lys Ser
245 250 255

Met Arg Glu Glu Gly Gly Tyr Glu Ile Ile Lys Lys Ala Ile Asp Lys
260 265 270

Leu Gly Leu Arg His Lys Glu His Ile Ser Ala Tyr Gly Glu Gly Asn
275 280 285

Glu Arg Arg Leu Thr Gly His His Glu Thr Ala Asp Ile Asn Thr Phe
290 295 300

Lys Trp Gly Val Ala Asn Arg Gly Ala Ser Ile Arg Val Gly Arg Asp
305 310 315 320

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

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

Leu Trp Asn Pro
355

<210> 20
<211> 428
<212> PRT
<213> Brassica napus

<400> 20

Met Ala Gln Ile Leu Ala Ala Ser Pro Thr Cys Gln Met Arg Leu Thr

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

Gln Val Gly Pro Ser Val Gly Ile Glu Ala Gly Asp His Val Trp Cys
260 265 270

Ala Arg Tyr Leu Leu Glu Arg Ile Thr Glu Gln Ala Gly Val Val Leu
275 280 285

Thr Leu Asp Pro Lys Pro Ile Glu Gly Asp Trp Asn Gly Ala Gly Cys
290 295 300

His Thr Asn Tyr Ser Thr Lys Ser Met Arg Glu Asp Gly Gly Phe Glu
305 310 315 320

Val Ile Lys Lys Ala Ile Leu Asn Leu Ser Leu Arg His Met Glu His
325 330 335

Ile Ser Ala Tyr Gly Glu Gly Asn Glu Arg Arg Leu Thr Gly Lys His
340 345 350

Glu Thr Ala Ser Ile Asp Gln Phe Ser Trp Gly Val Ala Asn Arg Gly
355 360 365

Cys Ser Ile Arg Val Gly Arg Asp Thr Glu Lys Lys Gly Lys Gly Tyr
370 375 380

Leu Glu Asp Arg Arg Pro Ala Ser Asn Met Asp Pro Tyr Ile Val Thr
385 390 395 400

Ser Leu Leu Ala Glu Thr Thr Leu Leu Trp Glu Pro Thr Leu Glu Ala
405 410 415

Glu Ala Leu Ala Ala Gln Lys Leu Ser Leu Lys Val
420 425

<210> 21

<211> 364

<212> PRT

<213> Hordeum vulgare

<400> 21

Met Ala Ala Ala Thr Thr Asn Val Ser Tyr Thr Thr Asn Leu Leu Lys
1 5 10 15

Tyr Met Gly Leu Asp Gln Lys Gly Ser Ala Met Ala Glu Tyr Ile Trp
20 25 30

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

Ile Pro Pro Ser Gly Glu Phe Thr Val Asp Asp Leu Pro Glu Trp Asn
50 55 60

Phe Asp Gly Ser Ser Thr Gly Gln Ala Pro Gly Asp Asn Ser Asp Val
65 70 75 80

Tyr Leu Arg Pro Val Ala Val Phe Pro Asp Pro Phe Arg Gly Ala Pro
85 90 95

Asn Ile Leu Val Ile Thr Glu Cys Trp Asp Pro Asp Gly Thr Pro Asn
100 105 110

Lys Tyr Asn His Arg His Glu Ala Ala Lys Leu Met Glu Ala His Lys
115 120 125

Ala Gln Lys Pro Trp Phe Gly Leu Glu Gln Glu Tyr Thr Leu Leu Asp
130 135 140

Met His Asp Arg Pro Tyr Gly Trp Pro Ala Gly Gly Phe Pro Gly Pro
145 150 155 160

Gln Gly Pro Tyr Tyr Cys Gly Val Gly Ser Gly Lys Val Tyr Cys Arg
165 170 175

Asp Ile Val Glu Ala His Tyr Lys Ala Cys Leu Phe Ala Gly Val Lys
180 185 190

Ile Ser Gly Thr Asn Ala Glu Val Met Pro Ala Gln Trp Glu Phe Gln
195 200 205

Val Gly Pro Cys Glu Gly Ile Glu Leu Gly Asp Gln Leu Trp Leu Ala
210 215 220

Arg Phe Leu Leu His Arg Ile Ala Glu Glu Phe Gly Ala Lys Ile Ser
225 230 235 240

Phe His Pro Lys Pro Ile Pro Gly Asp Trp Asn Gly Ala Gly Leu His
245 250 255

Ser Asn Phe Ser Ser Glu Glu Met Arg Lys Pro Gly Gly Met Lys Ala
260 265 270

Ile Glu Ala Ala Met Lys Lys Leu Glu Ala Arg His Lys Glu His Ile

275

280

285

Ala Val Tyr Gly Glu Asp Asn Thr Met Arg Leu Thr Gly Arg His Glu
 290 295 300

Thr Gly Asn Ile Asp Ser Phe Thr Tyr Gly Val Ala Asn Arg Gly Thr
 305 310 315 320

Ser Ile Arg Ile Pro Arg Glu Val Ser Gln Lys Gly Phe Gly Tyr Phe
 325 330 335

Glu Asp Arg Arg Pro Ala Ser Asn Ala Asp Pro Tyr Gln Ile Thr Gly
 340 345 350

Ile Met Val Glu Thr Ile Phe Gly Gly Leu Asp Lys
 355 360

<210> 22
 <211> 356
 <212> PRT
 <213> Oryza sativa

<400> 22

Met Ala Ser Leu Thr Asp Leu Val Asn Leu Asn Leu Ser Asp Thr Thr
 1 5 10 15

Glu Lys Ile Ile Ala Glu Tyr Ile Trp Ile Gly Gly Ser Gly Met Asp
 20 25 30

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

Lys Leu Pro Lys Trp Asn Tyr Asp Gly Ser Ser Thr Gly Gln Ala Pro
 50 55 60

Gly Glu Asp Ser Glu Val Ile Leu Tyr Pro Gln Ala Ile Phe Lys Asp
 65 70 75 80

Pro Phe Arg Lys Gly Asn Asn Ile Leu Val Met Cys Asp Cys Tyr Thr
 85 90 95

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

Ile Phe Ser Ser Pro Glu Val Ala Ser Glu Glu Pro Trp Tyr Gly Ile
 115 120 125

Glu Gln Glu Tyr Thr Leu Leu Gln Lys Asp Ile Asn Trp Pro Leu Gly
130 135 140

Trp Pro Val Gly Gly Phe Pro Gly Pro Gln Gly Pro Tyr Tyr Cys Gly
145 150 155 160

Ile Gly Ala Asp Lys Ser Phe Gly Arg Asp Ile Val Asp Ser His Tyr
165 170 175

Lys Ala Cys Leu Tyr Ala Gly Ile Asn Ile Ser Gly Ile Asn Gly Glu
180 185 190

Val Met Pro Gly Gln Trp Glu Phe Gln Val Gly Pro Ser Val Gly Ile
195 200 205

Ser Ala Gly Asp Gln Val Trp Val Ala Arg Tyr Ile Leu Glu Arg Ile
210 215 220

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

Gly Asp Trp Asn Gly Ala Gly Ala His Thr Asn Tyr Ser Thr Lys Ser
245 250 255

Met Arg Asn Asp Gly Gly Tyr Glu Ile Ile Lys Ser Ala Ile Glu Lys
260 265 270

Leu Lys Leu Arg His Lys Glu His Ile Ser Ala Tyr Gly Glu Gly Asn
275 280 285

Glu Arg Arg Leu Thr Gly Arg His Glu Thr Ala Asp Ile Asn Thr Phe
290 295 300

Ser Trp Gly Val Ala Asn Arg Gly Ala Ser Val Arg Val Gly Arg Glu
305 310 315 320

Thr Glu Gln Asn Gly Lys Gly Tyr Phe Glu Asp Arg Arg Pro Ala Ser
325 330 335

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

Ile Trp Lys Pro
355

<210> 23
<211> 428
<212> PRT
<213> Oryza sativa

<400> 23

Met Ala Gln Ala Val Val Pro Ala Met Gln Cys Gln Val Gly Ala Val
1 5 10 15

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

Gly Val Arg Arg Thr Gly Arg Gly Thr Ser Gly Phe Arg Val Met Ala
35 40 45

Val Ser Thr Glu Thr Thr Gly Val Val Thr Arg Met Glu Gln Leu Leu
50 55 60

Asn Met Asp Thr Thr Pro Phe Thr Asp Lys Ile Ile Ala Glu Tyr Ile
65 70 75 80

Trp Val Gly Gly Thr Gly Ile Asp Leu Arg Ser Lys Ser Arg Thr Ile
85 90 95

Ser Lys Pro Val Glu Asp Pro Ser Glu Leu Pro Lys Trp Asn Tyr Asp
100 105 110

Gly Ser Ser Thr Gly Gln Ala Pro Gly Glu Asp Ser Glu Val Ile Leu
115 120 125

Tyr Pro Gln Ala Ile Phe Lys Asp Pro Phe Arg Gly Gly Asn Asn Ile
130 135 140

Leu Val Met Cys Asp Thr Tyr Thr Pro Ala Gly Glu Pro Ile Pro Thr
145 150 155 160

Asn Lys Arg Asn Arg Ala Ala Gln Val Phe Ser Asp Pro Lys Val Val
165 170 175

Ser Gln Val Pro Trp Phe Gly Ile Glu Gln Glu Tyr Thr Leu Leu Gln
180 185 190

Arg Asp Val Asn Trp Pro Leu Gly Trp Pro Val Gly Gly Tyr Pro Gly
195 200 205

Pro Gln Gly Pro Tyr Tyr Cys Ala Val Gly Ser Asp Lys Ser Phe Gly
210 215 220

Arg Asp Ile Ser Asp Ala His Tyr Lys Ala Cys Leu Tyr Ala Gly Ile
225 230 235 240

Asn Ile Ser Gly Thr Asn Gly Glu Val Met Pro Gly Gln Trp Glu Tyr
245 250 255

Gln Val Gly Pro Ser Val Gly Ile Glu Ala Gly Asp His Ile Trp Ile
260 265 270

Ser Arg Tyr Ile Leu Glu Arg Ile Thr Glu Gln Ala Gly Val Val Leu
275 280 285

Thr Leu Asp Pro Lys Pro Ile Gln Gly Asp Trp Asn Gly Ala Gly Cys
290 295 300

His Thr Asn Tyr Ser Thr Lys Ser Met Arg Glu Asp Gly Gly Phe Glu
305 310 315 320

Val Ile Lys Lys Ala Ile Leu Asn Leu Ser Leu Arg His Asp Leu His
325 330 335

Ile Ser Ala Tyr Gly Glu Gly Asn Glu Arg Arg Leu Thr Gly Leu His
340 345 350

Glu Thr Ala Ser Ile Asp Asn Phe Ser Trp Gly Val Ala Asn Arg Gly
355 360 365

Cys Ser Ile Arg Val Gly Arg Asp Thr Glu Ala Lys Gly Lys Gly Tyr
370 375 380

Leu Glu Asp Arg Arg Pro Ala Ser Asn Met Asp Pro Tyr Val Val Thr
385 390 395 400

Ala Leu Leu Ala Glu Thr Thr Ile Leu Trp Glu Pro Thr Leu Glu Ala
405 410 415

Glu Val Leu Ala Ala Lys Lys Leu Ala Leu Lys Val
420 425

<210> 24
<211> 346
<212> PRT
<213> Physcomitrella patens

<400> 24

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

245

250

255

Ala Ile His Ala Ala Ile Glu Lys Leu Ser Lys Lys His Val Glu His
260 265 270

Ile Ser Ser Tyr Gly Leu Gly Asn Glu Arg Arg Leu Thr Gly Lys His
275 280 285

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

Ala Ser Ile Arg Ile Pro Leu Gly Val Ser Leu Asp Gly Lys Gly Tyr
305 310 315 320

Leu Glu Asp Arg Arg Pro Ala Ala Asn Val Asp Pro Tyr Val Val Ala
325 330 335

Arg Met Leu Ile Gln Thr Thr Leu Lys Asn
340 345

<210> 25

<211> 346

<212> PRT

<213> Physcomitrella patens

<400> 25

Met Ala Leu Ala Gln Lys Ala Glu Tyr Ile Trp Met Asp Gly Gln Glu
1 5 10 15

Gly Gln Lys Gly Ile Arg Phe Asn Glu Met Arg Ser Lys Thr Lys Val
20 25 30

Ile Gln Glu Pro Ile Lys Ala Gly Ser Leu Asp Phe Pro Lys Trp Ser
35 40 45

Phe Asp Gly Ser Ser Thr Gly Gln Ala Glu Gly Arg Phe Ser Asp Cys
50 55 60

Ile Leu Asn Pro Val Phe Ser Cys Pro Asp Pro Ile Arg Gly Asp Asn
65 70 75 80

His Val Leu Val Leu Cys Glu Val Leu Asn Pro Asp Ser Thr Pro His
85 90 95

Glu Thr Asn Thr Arg Arg Lys Ile Glu Glu Leu Leu Thr Pro Asp Val
100 105 110

Leu Ala Glu Glu Thr Leu Phe Gly Phe Glu Gln Glu Tyr Thr Met Phe
115 120 125

Asn Lys Ala Ala Lys Val Tyr Gly Trp Pro Glu Gly Gly Phe Pro His
130 135 140

Pro Gln Gly Pro Phe Tyr Cys Gly Val Gly Leu Glu Ala Val Tyr Gly
145 150 155 160

Arg Pro Leu Val Glu Ala His Met Asp Ala Cys Ile Lys Ala Gly Leu
165 170 175

Lys Ile Ser Gly Ile Asn Ala Glu Val Met Pro Gly Gln Trp Glu Phe
180 185 190

Gln Ile Gly Pro Ala Gly Pro Leu Glu Val Gly Asp His Val Met Val
195 200 205

Ala Arg Trp Leu Leu His Arg Leu Gly Glu Asp Phe Gly Ile Thr Cys
210 215 220

Thr Phe Glu Pro Lys Pro Met Glu Gly Asp Trp Asn Gly Ala Gly Ala
225 230 235 240

His Thr Asn Tyr Ser Thr Lys Ser Met Arg Val Asp Gly Gly Ile Lys
245 250 255

Ala Ile His Ala Ala Ile Glu Lys Leu Ser Lys Lys His Ala Glu His
260 265 270

Ile Ser Ser Tyr Gly Leu Gly Asn Glu Arg Arg Leu Thr Gly Lys His
275 280 285

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

Ala Ser Ile Arg Ile Pro Leu Gly Val Ser Leu Glu Gly Lys Gly Tyr
305 310 315 320

Leu Glu Asp Arg Arg Pro Ala Ala Asn Val Asp Pro Tyr Val Val Ala
325 330 335

Arg Met Leu Ile Gln Thr Thr Leu Lys Asn
340 345

<210> 26
<211> 371
<212> PRT
<213> Pinus taeda

<400> 26

Met Ala Thr Pro Ile Thr Ser Arg Thr Glu Thr Leu Gln Lys Tyr Leu
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Lys Leu Asp Gln Lys Gly Met Ile Met Ala Glu Tyr Val Trp Val Asp
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Ala Asp Gly Gly Thr Arg Ser Lys Ser Arg Thr Leu Pro Glu Lys Glu
35 40 45

Tyr Lys Pro Glu Asp Leu Pro Val Trp Asn Phe Asp Gly Ser Ser Thr
50 55 60

Asn Gln Ala Pro Gly Asp Asn Ser Asp Val Tyr Leu Arg Pro Cys Ala
65 70 75 80

Val Tyr Pro Asp Pro Phe Arg Gly Ser Pro Asn Ile Ile Val Leu Ala
85 90 95

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

Asp Cys Val Lys Val Met Asp Thr Tyr Ala Asp Asp Glu Pro Trp Phe
115 120 125

Gly Leu Glu Gln Glu Tyr Thr Leu Leu Gly Ser Asp Asn Arg Pro Tyr
130 135 140

Gly Trp Pro Ala Gly Gly Phe Pro Ala Pro Gln Gly Glu Tyr Tyr Cys
145 150 155 160

Gly Val Gly Thr Gly Lys Val Val Gln Arg Asp Ile Val Glu Ala His
165 170 175

Tyr Lys Ala Cys Leu Tyr Ala Gly Ile Gln Ile Ser Gly Thr Asn Ala
180 185 190

Glu Val Met Pro Ala Gln Trp Glu Tyr Gln Val Gly Pro Cys Thr Gly
195 200 205

Ile Ala Met Gly Asp Gln Leu Trp Ile Ser Arg Phe Phe Leu His Arg
210 215 220

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

Ala Gly Asp Trp Asn Gly Ala Leu Ser Phe Pro Gly Leu Cys Phe Ile
245 250 255

Ser Val Ile Leu Ile Ser Leu Gln Gly Leu His Ser Asn Phe Ser Thr
260 265 270

Lys Ala Met Arg Glu Glu Gly Gly Met Lys Val Ile Glu Glu Ala Leu
275 280 285

Lys Lys Leu Glu Pro His His Val Glu Cys Ile Ala Glu Tyr Gly Glu
290 295 300

Asp Asn Glu Leu Arg Leu Thr Gly Arg His Glu Thr Gly Ser Ile Asp
305 310 315 320

Ser Phe Ser Trp Gly Val Ala Asn Arg Gly Thr Ser Ile Arg Val Pro
325 330 335

Arg Glu Thr Ala Ala Lys Gly Tyr Gly Tyr Phe Glu Asp Arg Arg Pro
340 345 350

Ala Ser Asn Ala Asp Pro Tyr Arg Val Thr Lys Val Leu Leu Gln Phe
355 360 365

Ser Met Ala
370

<210> 27
<211> 354
<212> PRT
<213> Pinus taeda

<400> 27

Met Ala Tyr Ala Tyr Arg Pro Glu Leu Leu Ala Pro Tyr Leu Ser Leu
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Pro Gln Gly Glu Lys Val Gln Ala Glu Tyr Val Trp Val Asp Gly Asp
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Gly Gly Leu Arg Ser Lys Thr Cys Thr Val Asp Lys Lys Val Thr Asp
35 40 45

Ile Gly Gln Leu Arg Val Trp Asp Phe Asp Gly Ser Ser Thr Asn Gln
50 55 60

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

Lys Asp Pro Phe Arg Gly Gly Asp Asn Ile Leu Val Leu Ala Glu Cys
85 90 95

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

Ala Lys Val Met Glu Leu Ala Lys Asp Gln Lys Pro Trp Phe Gly Leu
115 120 125

Glu Gln Glu Tyr Thr Leu Phe Asp Val Asp Gly Thr Pro Phe Gly Trp
130 135 140

Pro Lys Gly Gly Phe Pro Gly Pro Gln Gly Pro Tyr Tyr Cys Gly Ala
145 150 155 160

Gly Ala Gly Lys Val Tyr Ala Arg Asp Leu Ile Glu Ala His Tyr Arg
165 170 175

Val Cys Leu Tyr Ala Gly Ile Lys Ile Ser Gly Val Asn Ala Glu Val
180 185 190

Met Pro Ala Gln Trp Glu Phe Gln Val Gly Pro Cys Glu Gly Ile Glu
195 200 205

Met Gly Asp His Leu Trp Met Ala Arg Tyr Leu Leu Ile Arg Leu Ala
210 215 220

Glu Gln Trp Gly Ile Lys Val Ser Phe His Pro Lys Pro Leu Ala Gly
225 230 235 240

Asp Trp Asn Gly Ser Gly Cys His Thr Asn Tyr Ser Thr Ala Pro Met
245 250 255

Arg Glu Glu Gly Gly Met Lys His Ile Glu Ala Ala Ile Glu Lys Leu
260 265 270

Ala Gln Lys His Asp Glu His Ile Ala Val Tyr Gly Asp Asp Asn Asp
275 280 285

Met Arg Leu Thr Gly Arg His Glu Thr Gly His Ile Gly Thr Phe Ser

290

295

300

Ser Gly Val Ala Asn Arg Gly Ala Ser Ile Arg Ile Pro Arg His Val
 305 310 315 320

Ala Ala Lys Gly Tyr Gly Tyr Leu Glu Asp Arg Arg Pro Ala Ser Asn
 325 330 335

Val Asp Pro Tyr Arg Val Thr Ser Ile Ile Val Glu Thr Thr Val Thr
 340 345 350

Asn Ala

<210> 28
 <211> 416
 <212> PRT
 <213> *Phaedactylum tricornutum*

<400> 28

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

Val Ile Glu Arg Tyr Ala Ala Leu Pro Tyr Pro Asp Asp Thr Val Leu
 50 55 60

Ala Glu Tyr Val Trp Val Asp Ala Val Gly Asn Thr Arg Ser Lys Thr
 65 70 75 80

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

Trp Asn Phe Asp Gly Ser Ser Thr Asp Gln Ala Pro Gly Asp Asp Ser
 100 105 110

Glu Val Ile Leu Arg Pro Cys Arg Ile Phe Lys Asp Pro Phe Arg Pro
 115 120 125

Arg Asn Asp Gly Leu Asp Asn Val Leu Val Met Cys Asp Cys Tyr Thr
 130 135 140

Pro Asn Gly Glu Ala Ile Pro Thr Asn His Arg Ala Lys Ala Met Glu
145 150 155 160

Ser Phe Glu Ser Arg Glu Asp Glu Glu Ile Trp Phe Gly Leu Glu Gln
165 170 175

Glu Phe Thr Leu Phe Asn Leu Asp Lys Arg Thr Pro Leu Gly Trp Pro
180 185 190

Glu Gly Gly Met Pro Asn Arg Pro Gln Gly Pro Tyr Tyr Cys Ser Val
195 200 205

Gly Pro Glu Asn Asn Phe Gly Arg His Ile Thr Glu Ser Met Tyr Arg
210 215 220

Ala Cys Leu Tyr Ala Gly Ile Asn Ile Ser Gly Thr Asn Gly Glu Val
225 230 235 240

Met Pro Gly Gln Gln Glu Tyr Gln Val Gly Pro Cys Val Gly Ile Asp
245 250 255

Ala Gly Asp Gln Leu Met Met Ser Arg Tyr Ile Leu Gln Arg Val Cys
260 265 270

Glu Asp Phe Gln Val Tyr Cys Thr Leu His Pro Lys Pro Ile Val Asp
275 280 285

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

Met Arg Glu Glu Gly Gly Leu Glu Val Ile Lys Lys Ala Ile Tyr Lys
305 310 315 320

Leu Gly Ala Lys His Leu Glu His Ile Ala Val Tyr Gly Glu Gly Asn
325 330 335

Glu Leu Arg Leu Thr Gly Lys His Glu Thr Ala Ser Met Asp Lys Phe
340 345 350

Cys Tyr Gly Val Ala Asn Arg Gly Ala Ser Ile Arg Ile Gly Arg Asp
355 360 365

Thr Glu Ala Glu Gly Lys Gly Tyr Phe Glu Asp Arg Arg Pro Ser Ser
370 375 380

Asn Ala Asp Pro Tyr Ile Val Thr Gly Lys Ile Met Asn Thr Ile Met
385 390 395 400

Glu Asp Val Glu Val Pro Asp Ile Ala Pro Met Asp Lys Ala Val Ala
405 410 415

<210> 29
<211> 423
<212> PRT
<213> Zea mays

<400> 29

Met Ala Gln Ala Val Val Pro Ala Met Gln Cys Arg Val Gly Val Lys
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Ala Ala Ala Gly Arg Val Trp Ser Ala Gly Arg Thr Arg Thr Gly Arg
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Gly Gly Ala Ser Pro Gly Phe Lys Val Met Ala Val Ser Thr Gly Ser
35 40 45

Thr Gly Val Val Pro Arg Leu Glu Gln Leu Leu Asn Met Asp Thr Thr
50 55 60

Pro Tyr Thr Asp Lys Val Ile Ala Glu Tyr Ile Trp Val Gly Gly Ser
65 70 75 80

Gly Ile Asp Ile Arg Ser Lys Ser Arg Thr Ile Ser Lys Pro Val Glu
85 90 95

Asp Pro Ser Glu Leu Pro Lys Trp Asn Tyr Asp Gly Ser Ser Thr Gly
100 105 110

Gln Ala Pro Gly Glu Asp Ser Glu Val Ile Leu Tyr Pro Gln Ala Ile
115 120 125

Phe Lys Asp Pro Phe Arg Gly Gly Asn Asn Val Leu Val Ile Cys Asp
130 135 140

Thr Tyr Thr Pro Gln Gly Glu Pro Leu Pro Thr Asn Lys Arg His Arg
145 150 155 160

Ala Ala Gln Ile Phe Ser Asp Pro Lys Val Ala Glu Gln Val Pro Trp
165 170 175

Phe Gly Ile Glu Gln Glu Tyr Thr Leu Leu Gln Lys Asp Val Asn Trp
180 185 190

Pro Leu Gly Trp Pro Val Gly Gly Phe Pro Gly Pro Gln Gly Pro Tyr
195 200 205

Tyr Cys Ala Val Gly Ala Asp Lys Ser Phe Gly Arg Asp Ile Ser Asp
210 215 220

Ala His Tyr Lys Ala Cys Leu Tyr Ala Gly Ile Asn Ile Ser Gly Thr
225 230 235 240

Asn Gly Glu Val Met Pro Gly Gln Trp Glu Tyr Gln Val Gly Pro Ser
245 250 255

Val Gly Ile Glu Ala Gly Asp His Ile Trp Ile Ser Arg Tyr Ile Leu
260 265 270

Glu Arg Ile Thr Glu Gln Ala Gly Val Val Leu Thr Leu Asp Pro Lys
275 280 285

Pro Ile Gln Gly Asp Trp Asn Gly Ala Gly Cys His Thr Asn Tyr Ser
290 295 300

Thr Lys Thr Met Arg Glu Asp Gly Gly Phe Glu Glu Ile Lys Arg Ala
305 310 315 320

Ile Leu Asn Leu Ser Leu Arg His Asp Leu His Ile Ser Ala Tyr Gly
325 330 335

Glu Gly Asn Glu Arg Arg Leu Thr Gly Lys His Glu Thr Ala Ser Ile
340 345 350

Gly Thr Phe Ser Trp Gly Val Ala Asn Arg Gly Cys Ser Ile Arg Val
355 360 365

Gly Arg Asp Thr Glu Ala Lys Gly Lys Gly Tyr Leu Glu Asp Arg Arg
370 375 380

Pro Ala Ser Asn Met Asp Pro Tyr Ile Val Thr Gly Leu Leu Ala Glu
385 390 395 400

Thr Thr Ile Leu Trp Gln Pro Ser Leu Glu Ala Glu Ala Leu Ala Ala
405 410 415

Lys Lys Leu Ala Leu Lys Val
420

<210> 30
<211> 356
<212> PRT
<213> Zea mays

<400> 30

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

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

Lys Leu Pro Lys Trp Asn Tyr Asp Gly Ser Ser Thr Gly Gln Ala Pro
50 55 60

Gly Glu Asp Ser Glu Val Ile Leu Tyr Pro Gln Ala Ile Phe Lys Asp
65 70 75 80

Pro Phe Arg Arg Gly Asn Asn Ile Leu Val Met Cys Asp Cys Tyr Thr
85 90 95

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

Ile Phe Ser Ser Leu Glu Val Ala Ala Glu Glu Pro Trp Tyr Gly Ile
115 120 125

Glu Gln Glu Tyr Thr Leu Leu Gln Lys Asp Thr Asn Trp Pro Leu Gly
130 135 140

Trp Pro Ile Gly Gly Phe Pro Gly Pro Gln Gly Pro Tyr Tyr Cys Gly
145 150 155 160

Ile Gly Ala Glu Lys Ser Phe Gly Arg Asp Ile Val Asp Ala His Tyr
165 170 175

Lys Ala Cys Leu Tyr Ala Gly Ile Asn Ile Ser Gly Ile Asn Gly Glu
180 185 190

Val Met Pro Gly Gln Trp Glu Phe Gln Val Gly Pro Ser Val Gly Ile
195 200 205

Ser Ser Gly Asp Gln Val Trp Val Ala Arg Tyr Ile Leu Glu Arg Ile

210

215

220

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

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

Met Arg Lys Glu Gly Gly Tyr Glu Val Ile Lys Ala Ala Ile Glu Lys
 260 265 270

Leu Lys Leu Arg His Lys Glu His Ile Ala Ala Tyr Gly Glu Gly Asn
 275 280 285

Glu Arg Arg Leu Thr Gly Arg His Glu Thr Ala Asp Ile Asn Thr Phe
 290 295 300

Ser Trp Gly Val Ala Asn Arg Gly Ala Ser Val Arg Val Gly Arg Glu
 305 310 315 320

Thr Glu Gln Asn Gly Lys Gly Tyr Phe Glu Asp Arg Arg Pro Ala Ser
 325 330 335

Asn Met Asp Pro Tyr Val Val Thr Ser Met Ile Ala Glu Thr Thr Ile
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Val Trp Lys Pro
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 <212> DNA
 <213> Aureococcus anophagefferens

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 <211> 2031
 <212> DNA
 <213> Chlamydomonas reinhardtii

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<210> 33

<211> 3248

<212> DNA

<213> Chlamydomonas reinhardtii

<400> 33

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 <213> Chlamydomonas reinhardtii

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<210> 42
<211> 1555
<212> DNA
<213> Brassica napus

<400> 42
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aacatgtcaa atgagattga ctaaaccag ctccattgca tcgtcaaagt tatggaactc 180
ggttggtgtg aaacagaaga aacagagcag cagcaaagtc agaagcttca aagtgatggc 240
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<210> 43
 <211> 1456
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> misc_feature
 <222> (1237)..(1237)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (1240)..(1240)
 <223> n is a, c, g, or t

<220>

<221> misc_feature
<222> (1324)..(1324)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1405)..(1405)
<223> n is a, c, g, or t

<400> 43
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gagtacatat ggatcggcgg atctggcatg gatctcagga gcaaggccag gcacctcccc 180
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ggtctcgtgt aatctc 1456

<210> 44
 <211> 1495
 <212> DNA
 <213> *Oryza sativa*

<400> 44
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 gtcacgcgcc agtacatatg ggttggtggt actgggatgg atgtgaggag caaagccaga 240
 acgttgctctg gacctgttga tgaccaagc aagcttccaa agtggaactt tgatggctcc 300
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 agagacccat tcaggaaggg gaagaacatc ctgggtcatgt gtgactgtta tgcgccgaat 420
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 gaggccatca cctgcagcat ctcatgaaat agatctattg caatgacaat accaatggca 1440
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<210> 45
 <211> 1677
 <212> DNA
 <213> *Oryza sativa*

<400> 45
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gattatctgt aggggggtgaa aatggcgag gcggtggtgc cggcgatgca gtgccaggtc 120
ggggccgtgc gggcgaggcc ggcggcggtt ggcggcggtt cgggggggag ggtgtgggga 180
gtcaggagga ccgggcgcgg cacgtcgggg ttccagggtga tggccgtgag cacggagacc 240
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<210> 46
<211> 1041

<212> DNA
<213> Physcomitrella patens

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tctttggact tccccaaagtg gtcattcgac ggttccagca ctgggcaagc agaggggcca 180
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gcagacagag gtgcatcgat ccgtatccct ctggagtgt ctcttgacgg caagggttat 960
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cagacgactt tgaagaacta g 1041

<210> 47
<211> 1041
<212> DNA
<213> Physcomitrella patens

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cacgtgctgg ttctgtgcga ggtggtgaac cccgacagca caccatga aaccaacacc 300
cggcgcaaga tcgaggaact attgaccccg gatgtgctgg cagaggagac actgttcgga 360
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attaatgccg aggtgatgcc gggacagtgg gagttccaga tcggccccgc tggacctctg	600
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gccattgaga agctgtccaa gaagcacgcg gagcacatct cctcatacgg gttgggcaat	840
gagcgtcgtc tgacaggcaa gcacgagacc gccaacatca acacattcaa gtcgggagtt	900
gcggaacagag gtgcgtcgat ccgtattccg cttggagtgt ccctggaggg caaaggttac	960
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caaacgactt tgaagaacta g	1041

<210> 48
 <211> 1584
 <212> DNA
 <213> Pinus taeda

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gatctctctg atgtcactga gaagatcatc gctgagtaca tatggatcgg aggcctctggc	300
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cgtggagctt	ctattcgagt	tggacgtgac	acggaacgtg	aaggcaaagg	gtacttcgaa	1200
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tctcatttga	atttctttat	gtgcctaaag	tatttcccct	atttctgtta	ataagaacat	1440
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attttcattg	ttccatgact	ctgatatgat	tggtgtgcaa	ttgaatttaa	tgaattcaga	1560
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<210> 49
 <211> 1304
 <212> DNA
 <213> Pinus taeda

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ctccagaagt	atctcaagct
120	
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tggctgagta	cgtctggggt
gatgccgatg	gtggcactcg
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gaggatcttc	ccgtttggaa
240	
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tccgatgtct	acctccgtcc
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ccttccgcgg	ctctcccaac
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aggaggccct	gaagaagctt
gaacctcacc	acgtcgagtg
960	

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<210> 50
 <211> 1251
 <212> DNA
 <213> *Phaedactylum tricornutum*

<400> 50	
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<212> DNA
<213> Zea mays

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ccgcaggcca tcttcaagga cccattcagg aggggcaaca acatccttgt catgtgcgat	360
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<212> PRT
<213> Hordeum vulgare

<400> 53

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

Gln Leu Pro Lys Trp Asn Tyr Asp Gly Ser Ser Thr Gly Gln Ala Pro
50 55 60

Gly Glu Asp Ser Glu Val Ile Leu Tyr Pro Gln Ala Ile Phe Lys Asp
65 70 75 80

Pro Phe Arg Arg Gly Asp Asn Ile Leu Val Met Cys Asp Cys Tyr Thr
85 90 95

Pro Gln Gly Val Pro Ile Pro Thr Asn Lys Arg His Asn Ala Ala Lys
100 105 110

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

Glu Gln Glu Tyr Thr Leu Leu Gln Lys Asp Val Asn Trp Pro Leu Gly
130 135 140

Trp Pro Ile Gly Gly Tyr Pro Gly Pro Gln Gly Pro Tyr Tyr Cys Ala
145 150 155 160

Ala Gly Ala Asp Lys Ala Phe Gly Arg Asp Ile Val Asp Ala His Tyr
165 170 175

Lys Ala Cys Leu Tyr Ala Gly Ile Asn Ile Ser Gly Ile Asn Gly Glu
180 185 190

Val Met Pro Gly Gln Trp Glu Phe Gln Val Gly Pro Ser Val Gly Ile

195

200

205

Ala Ala Ser Asp Gln Leu Trp Val Ala Arg Tyr Ile Leu Glu Arg Ile
 210 215 220

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

Gly Asp Trp Asn Gly Ala Gly Ala His Thr Asn Tyr Ser Thr Lys Ser
 245 250 255

Met Arg Gln Ala Gly Gly Tyr Glu Val Ile Lys Lys Ala Ile Glu Lys
 260 265 270

Leu Gly Lys Arg His Met Gln His Ile Ala Ala Tyr Gly Glu Gly Asn
 275 280 285

Glu Arg Arg Leu Thr Gly His His Glu Thr Ala Asp Ile Asn Thr Phe
 290 295 300

Lys Trp Gly Val Ala Asp Arg Gly Ala Ser Ile Arg Val Gly Arg Asp
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Thr Glu Lys Asp Gly Lys Gly Tyr Phe Glu Asp Arg Arg Pro Ala Ser
 325 330 335

Asn Met Asp Pro Tyr Val Val Thr Ser Met Ile Ala Glu Thr Thr Leu
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Leu Leu

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<211> 427

<212> PRT

<213> Hordeum vulgare

<400> 54

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Val Arg Arg Ala Ala Arg Ala Thr Ser Gly Phe Lys Val Leu Ala Leu
 35 40 45

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

Met Asp Thr Thr Pro Phe Thr Asp Lys Ile Ile Ala Glu Tyr Ile Trp
65 70 75 80

Val Gly Gly Ser Gly Ile Asp Leu Arg Ser Lys Ser Arg Thr Ile Ser
85 90 95

Lys Pro Val Glu Asp Pro Ser Glu Leu Pro Lys Trp Asn Tyr Asp Gly
100 105 110

Ser Ser Thr Gly Gln Ala Pro Gly Glu Asp Ser Glu Val Ile Leu Tyr
115 120 125

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

Val Ile Cys Asp Thr Tyr Thr Pro Gln Gly Glu Pro Ile Pro Thr Asn
145 150 155 160

Lys Arg His Met Ala Ala Gln Ile Phe Ser Asp Pro Lys Val Thr Ser
165 170 175

Gln Val Pro Trp Phe Gly Ile Glu Gln Glu Tyr Thr Leu Met Gln Arg
180 185 190

Asp Val Asn Trp Pro Leu Gly Trp Pro Val Gly Gly Tyr Pro Gly Pro
195 200 205

Gln Gly Pro Tyr Tyr Cys Ala Val Gly Ser Asp Lys Ser Phe Gly Arg
210 215 220

Asp Ile Ser Asp Ala His Tyr Lys Ala Cys Leu Tyr Ala Gly Ile Glu
225 230 235 240

Ile Ser Gly Thr Asn Gly Glu Val Met Pro Gly Gln Trp Glu Tyr Gln
245 250 255

Val Gly Pro Ser Val Gly Ile Asp Ala Gly Asp His Ile Trp Ala Ser
260 265 270

Arg Tyr Ile Leu Glu Arg Ile Thr Glu Gln Ala Gly Val Val Leu Thr
275 280 285

Leu Asp Pro Lys Pro Ile Gln Gly Asp Trp Asn Gly Ala Gly Cys His
290 295 300

Thr Asn Tyr Ser Thr Leu Ser Met Arg Glu Asp Gly Gly Phe Asp Val
305 310 315 320

Ile Lys Lys Ala Ile Leu Asn Leu Ser Leu Arg His Asp Leu His Ile
325 330 335

Ala Ala Tyr Gly Glu Gly Asn Glu Arg Arg Leu Thr Gly Leu His Glu
340 345 350

Thr Ala Ser Ile Ser Asp Phe Ser Trp Gly Val Ala Asn Arg Gly Cys
355 360 365

Ser Ile Arg Val Gly Arg Asp Thr Glu Ala Lys Gly Lys Gly Tyr Leu
370 375 380

Glu Asp Arg Arg Pro Ala Ser Asn Met Asp Pro Tyr Thr Val Thr Ala
385 390 395 400

Leu Leu Ala Glu Thr Thr Ile Leu Trp Glu Pro Thr Leu Glu Ala Glu
405 410 415

Ala Leu Ala Ala Lys Lys Leu Ala Leu Lys Val
420 425

<210> 55
<211> 1455
<212> PRT
<213> Hordeum vulgare

<400> 55

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35 40 45

Cys Gly Ala Cys Cys Thr Cys Cys Cys Thr Cys Cys Cys Thr Gly Cys
50 55 60

Gly Ala Gly Cys Ala Gly Cys Ala Gly Cys Ala Gly Cys Ala Gly Cys
65 70 75 80

Ala Ala Thr Gly Gly Cys Cys Ala Gly Cys Cys Thr Cys Gly Cys Cys
85 90 95

Gly Ala Cys Cys Thr Cys Gly Thr Thr Ala Ala Thr Cys Thr Cys Ala
100 105 110

Ala Cys Cys Thr Cys Ala Gly Cys Gly Ala Cys Thr Gly Cys Ala Cys
115 120 125

Gly Gly Ala Cys Ala Ala Gly Gly Thr Cys Ala Thr Cys Gly Thr Cys
130 135 140

Gly Ala Gly Thr Ala Cys Cys Thr Cys Thr Gly Gly Gly Thr Thr Gly
145 150 155 160

Gly Ala Gly Gly Ala Thr Cys Thr Gly Gly Thr Ala Thr Cys Gly Ala
165 170 175

Cys Ala Thr Cys Ala Gly Gly Ala Gly Cys Ala Ala Ala Gly Cys Ala
180 185 190

Ala Gly Gly Ala Cys Gly Gly Thr Gly Ala Ala Cys Gly Gly Ala Cys
195 200 205

Cys Cys Ala Thr Cys Ala Cys Cys Gly Ala Cys Gly Cys Gly Ala Gly
210 215 220

Cys Cys Ala Gly Cys Thr Gly Cys Cys Cys Ala Ala Gly Thr Gly Gly
225 230 235 240

Ala Ala Cys Thr Ala Cys Gly Ala Cys Gly Gly Cys Thr Cys Cys Ala
245 250 255

Gly Cys Ala Cys Cys Gly Gly Cys Cys Ala Gly Gly Cys Thr Cys Cys
260 265 270

Cys Gly Gly Ala Gly Ala Gly Gly Ala Cys Ala Gly Cys Gly Ala Ala
275 280 285

Gly Thr Cys Ala Thr Cys Cys Thr Cys Thr Ala Cys Cys Cys Cys Cys
290 295 300

Ala Gly Gly Cys Cys Ala Thr Thr Thr Thr Cys Ala Ala Gly Gly Ala
305 310 315 320

Cys Cys Cys Gly Thr Thr Cys Ala Gly Gly Ala Gly Gly Gly Gly Thr
325 330 335

Gly Ala Cys Ala Ala Cys Ala Thr Cys Cys Thr Thr Gly Thr Thr Ala
340 345 350

Thr Gly Thr Gly Cys Gly Ala Cys Thr Gly Cys Thr Ala Cys Ala Cys
355 360 365

Ala Cys Cys Ala Cys Ala Ala Gly Gly Thr Gly Thr Gly Cys Cys Ala
370 375 380

Ala Thr Thr Cys Cys Cys Ala Cys Thr Ala Ala Cys Ala Ala Gly Ala
385 390 395 400

Gly Gly Cys Ala Cys Ala Ala Thr Gly Cys Thr Gly Cys Cys Ala Ala
405 410 415

Gly Ala Thr Cys Thr Thr Cys Ala Ala Cys Ala Gly Cys Gly Cys Thr
420 425 430

Ala Ala Gly Gly Thr Thr Gly Cys Ala Gly Cys Thr Gly Ala Gly Gly
435 440 445

Ala Gly Ala Cys Ala Thr Gly Gly Thr Ala Thr Gly Gly Thr Ala Thr
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Thr Gly Ala Gly Cys Ala Gly Gly Ala Gly Thr Ala Cys Ala Cys Ala
465 470 475 480

Cys Thr Cys Cys Thr Cys Cys Ala Gly Ala Ala Gly Gly Ala Thr Gly
485 490 495

Thr Gly Ala Ala Cys Thr Gly Gly Cys Cys Thr Cys Thr Thr Gly Gly
500 505 510

Cys Thr Gly Gly Cys Cys Ala Ala Thr Thr Gly Gly Thr Gly Gly Cys
515 520 525

Thr Ala Cys Cys Cys Thr Gly Gly Thr Cys Cys Thr Cys Ala Gly Gly
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Gly Ala Cys Cys Ala Thr Ala Cys Thr Ala Cys Thr Gly Cys Gly Cys
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Cys Gly Cys Cys Gly Gly Thr Gly Cys Cys Gly Ala Cys Ala Ala Gly
565 570 575

Gly Cys Gly Thr Thr Cys Gly Gly Gly Cys Gly Thr Gly Ala Cys Ala
580 585 590

Thr Cys Gly Thr Gly Gly Ala Cys Gly Cys Cys Cys Ala Cys Thr Ala
595 600 605

Cys Ala Ala Gly Gly Cys Gly Thr Gly Cys Cys Thr Cys Thr Ala Cys
610 615 620

Gly Cys Cys Gly Gly Gly Ala Thr Cys Ala Ala Cys Ala Thr Cys Ala
625 630 635 640

Gly Cys Gly Gly Cys Ala Thr Cys Ala Ala Cys Gly Gly Gly Gly Ala
645 650 655

Gly Gly Thr Cys Ala Thr Gly Cys Cys Cys Gly Gly Cys Cys Ala Gly
660 665 670

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675 680 685

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690 695 700

Cys Gly Cys Cys Gly Cys Cys Thr Cys Cys Gly Ala Cys Cys Ala Gly
705 710 715 720

Cys Thr Gly Thr Gly Gly Gly Thr Gly Gly Cys Gly Cys Gly Cys Thr
725 730 735

Ala Cys Ala Thr Cys Cys Thr Cys Gly Ala Gly Ala Gly Gly Ala Thr
740 745 750

Cys Ala Cys Ala Gly Ala Gly Gly Thr Thr Gly Cys Cys Gly Gly Gly
755 760 765

Gly Thr Gly Gly Thr Gly Cys Thr Gly Thr Cys Cys Cys Thr Gly Gly
770 775 780

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785 790 795 800

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805

810

815

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 820 825 830

Ala Cys Thr Ala Cys Ala Gly Cys Ala Cys Cys Ala Ala Gly Thr Cys
 835 840 845

Cys Ala Thr Gly Ala Gly Gly Cys Ala Gly Gly Cys Cys Gly Gly Cys
 850 855 860

Gly Gly Cys Thr Ala Cys Gly Ala Gly Gly Thr Gly Ala Thr Cys Ala
 865 870 875 880

Ala Gly Ala Ala Gly Gly Cys Cys Ala Thr Cys Gly Ala Gly Ala Ala
 885 890 895

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 900 905 910

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 915 920 925

Cys Cys Thr Ala Cys Gly Gly Cys Gly Ala Gly Gly Gly Cys Ala Ala
 930 935 940

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 945 950 955 960

Gly Gly Cys Cys Ala Cys Cys Ala Cys Gly Ala Gly Ala Cys Cys Gly
 965 970 975

Cys Cys Gly Ala Cys Ala Thr Cys Ala Ala Cys Ala Cys Cys Thr Thr
 980 985 990

Cys Ala Ala Ala Thr Gly Gly Gly Gly Cys Gly Thr Gly Gly Cys Gly
 995 1000 1005

Gly Ala Cys Cys Gly Cys Gly Gly Cys Gly Cys Gly Thr Cys Cys
 1010 1015 1020

Ala Thr Cys Cys Gly Cys Gly Thr Gly Gly Gly Gly Cys Gly Cys
 1025 1030 1035

Gly Ala Cys Ala Cys Gly Gly Ala Gly Ala Ala Gly Gly Ala Cys
 1040 1045 1050

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	1085					1090					1095			
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	1175					1180					1185			
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	1190					1195					1200			
Cys	Thr	Cys	Gly	Ala	Cys	Thr	Cys	Thr	Cys	Thr	Cys	Gly	Ala	Thr
	1205					1210					1215			
Cys	Gly	Ala	Gly	Gly	Gly	Thr	Gly	Gly	Thr	Gly	Ala	Thr	Thr	Gly
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<211> 1428
<212> DNA
<213> *Arabidopsis thaliana*

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<210> 58
<211> 475
<212> PRT
<213> *Arabidopsis thaliana*

<400> 58

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

Val Phe Gly Glu Gly Tyr Val Ser Thr Gly Gly Phe Glu Thr Thr Lys
245 250 255

Glu Phe Val Ala Lys Met Asp Leu Lys Pro Gly Gln Lys Val Leu Asp
260 265 270

Val Gly Cys Gly Ile Gly Gly Asp Phe Tyr Met Ala Glu Asn Phe
275 280 285

Asp Val His Val Val Gly Ile Asp Leu Ser Val Asn Met Ile Ser Phe
290 295 300

Ala Leu Glu Arg Ala Ile Gly Leu Lys Cys Ser Val Glu Phe Glu Val
305 310 315 320

Ala Asp Cys Thr Thr Lys Thr Tyr Pro Asp Asn Ser Phe Asp Val Ile
325 330 335

Tyr Ser Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro Ala Leu Phe
340 345 350

Arg Thr Phe Phe Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Thr
355 360 365

Asp Tyr Cys Arg Ser Ala Glu Thr Pro Ser Pro Glu Phe Ala Glu Tyr
370 375 380

Ile Lys Gln Arg Gly Tyr Asp Leu His Asp Val Gln Ala Tyr Gly Gln
385 390 395 400

Met Leu Lys Asp Ala Gly Phe Asp Asp Val Ile Ala Glu Asp Arg Thr
405 410 415

Asp Gln Phe Val Gln Val Leu Arg Arg Glu Leu Glu Lys Val Glu Lys
420 425 430

Glu Lys Glu Glu Phe Ile Ser Asp Phe Ser Glu Glu Asp Tyr Asn Asp
435 440 445

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Gln Lys Trp Gly Leu Phe Ile Ala Asp Lys Lys
465 470 475

<211> 1428
<212> DNA
<213> Arabidopsis thaliana

<400> 59
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<210> 60
<211> 475
<212> PRT
<213> Arabidopsis thaliana

<400> 60

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

Gly Arg Phe Thr Gly Glu Leu Ala Gln Lys Ala Gly Glu Val Ile Ala
50 55 60

Leu Asp Phe Ile Glu Ser Ala Ile Gln Lys Asn Glu Ser Val Asn Gly
65 70 75 80

His Tyr Lys Asn Ile Lys Phe Met Cys Ala Asp Val Thr Ser Pro Asp
85 90 95

Leu Lys Ile Lys Asp Gly Ser Ile Asp Leu Ile Phe Ser Asn Trp Leu
100 105 110

Leu Met Tyr Leu Ser Asp Lys Glu Val Glu Leu Met Ala Glu Arg Met
115 120 125

Ile Gly Trp Val Lys Pro Gly Gly Tyr Ile Phe Phe Arg Glu Ser Cys
130 135 140

Phe His Gln Ser Gly Asp Ser Lys Arg Lys Ser Asn Pro Thr His Tyr
145 150 155 160

Arg Glu Pro Arg Phe Tyr Thr Lys Val Phe Gln Glu Cys Gln Thr Arg
165 170 175

Asp Ala Ser Gly Asn Ser Phe Glu Leu Ser Met Val Gly Cys Lys Cys
180 185 190

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

Ile Trp Gln Lys Val Ser Val Glu Asn Asp Lys Asp Phe Gln Arg Phe
210 215 220

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

Val Phe Gly Glu Gly Tyr Val Ser Thr Gly Gly Phe Glu Thr Thr Lys

				245					250					255			
Glu	Phe	Val	Ala	Lys	Met	Asp	Leu	Lys	Pro	Gly	Gln	Lys	Val	Leu	Asp		
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		275					280					285					
Asp	Val	His	Val	Val	Gly	Ile	Asp	Leu	Ser	Val	Asn	Met	Ile	Ser	Phe		
	290					295					300						
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305					310					315					320		
Ala	Asp	Cys	Thr	Thr	Lys	Thr	Tyr	Pro	Asp	Asn	Ser	Phe	Asp	Val	Ile		
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Tyr	Ser	Arg	Asp	Thr	Ile	Leu	His	Ile	Gln	Asp	Lys	Pro	Ala	Leu	Phe		
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Asp	Tyr	Cys	Arg	Ser	Ala	Glu	Thr	Pro	Ser	Pro	Glu	Phe	Ala	Glu	Tyr		
	370					375					380						
Ile	Lys	Gln	Arg	Gly	Tyr	Asp	Leu	His	Asp	Val	Gln	Ala	Tyr	Gly	Gln		
385					390					395					400		
Met	Leu	Lys	Asp	Ala	Gly	Phe	Asp	Asp	Val	Ile	Ala	Glu	Asp	Arg	Thr		
				405					410					415			
Asp	Gln	Phe	Val	Gln	Val	Leu	Arg	Arg	Glu	Leu	Glu	Lys	Val	Glu	Lys		
			420					425					430				
Glu	Lys	Glu	Glu	Phe	Ile	Ser	Asp	Phe	Ser	Glu	Glu	Asp	Tyr	Asn	Asp		
		435					440					445					
Ile	Val	Gly	Gly	Trp	Ser	Ala	Lys	Leu	Glu	Arg	Thr	Ala	Ser	Gly	Glu		
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Gln	Lys	Trp	Gly	Leu	Phe	Ile	Ala	Asp	Lys	Lys							
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<210> 61
 <211> 1668

<212> DNA
<213> *Arabidopsis thaliana*

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ttctcgaaag aggattacga ggatattata ggcgggtgga agtcaaagct acttaggagc 1620
tcaagtggtg agcagaagtg gggtttgttc atcgccaaga gaaactga 1668

<210> 62
<211> 555
<212> PRT
<213> Arabidopsis thaliana

<400> 62

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Ile Glu Arg Glu Ser Asn Leu Gly Ser Ala Ser Val Leu Met Gln Ser
20 25 30

Lys Val Ile Ser Val Ser Asn Phe Phe Ser Ile His Arg Phe His Tyr
35 40 45

Pro Arg Glu Lys Ile Val Ser Phe Leu Phe Pro Ser Val Phe Ser Arg
50 55 60

Ile Met Ala Ser Tyr Gly Glu Glu Arg Glu Ile Gln Lys Asn Tyr Trp
65 70 75 80

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

Lys Ala Ser Asp Leu Asp Lys Glu Glu Arg Pro Glu Ile Leu Ala Phe
100 105 110

Leu Pro Pro Ile Glu Gly Thr Thr Val Leu Glu Phe Gly Ala Gly Ile
115 120 125

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

Val Asp Phe Ile Glu Ser Val Ile Lys Lys Asn Glu Asn Ile Asn Gly
145 150 155 160

His Tyr Lys Asn Val Lys Phe Leu Cys Ala Asp Val Thr Ser Pro Asn
165 170 175

Met Asn Phe Pro Asn Glu Ser Met Asp Leu Ile Phe Ser Asn Trp Leu
180 185 190

Leu Met Tyr Leu Ser Asp Gln Glu Val Glu Asp Leu Ala Lys Lys Met
195 200 205

Leu Gln Trp Thr Lys Val Gly Gly Tyr Ile Phe Phe Arg Glu Ser Cys
210 215 220

Phe His Gln Ser Gly Asp Asn Lys Arg Lys Tyr Asn Pro Thr His Tyr
225 230 235 240

Arg Glu Pro Lys Phe Tyr Thr Lys Leu Phe Lys Glu Cys His Met Asn
245 250 255

Asp Glu Asp Gly Asn Ser Tyr Glu Leu Ser Leu Val Ser Cys Lys Cys
260 265 270

Ile Gly Ala Tyr Val Arg Asn Lys Lys Asn Gln Asn Gln Ile Cys Trp
275 280 285

Leu Trp Gln Lys Val Ser Ser Asp Asn Asp Arg Gly Phe Gln Arg Phe
290 295 300

Leu Asp Asn Val Gln Tyr Lys Ser Ser Gly Ile Leu Arg Tyr Glu Arg
305 310 315 320

Val Phe Gly Glu Gly Phe Val Ser Thr Gly Gly Leu Glu Thr Thr Lys
325 330 335

Glu Phe Val Asp Met Leu Asp Leu Lys Pro Gly Gln Lys Val Leu Asp
340 345 350

Val Gly Cys Gly Ile Gly Gly Gly Asp Phe Tyr Met Ala Glu Asn Phe
355 360 365

Asp Val Asp Val Val Gly Ile Asp Leu Ser Val Asn Met Ile Ser Phe
370 375 380

Ala Leu Glu His Ala Ile Gly Leu Lys Cys Ser Val Glu Phe Glu Val
385 390 395 400

Ala Asp Cys Thr Lys Lys Glu Tyr Pro Asp Asn Thr Phe Asp Val Ile
405 410 415

Tyr Ser Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro Ala Leu Phe
420 425 430

Arg Arg Phe Tyr Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Thr
435 440 445

Asp Tyr Cys Arg Ser Pro Lys Thr Pro Ser Pro Asp Phe Ala Ile Tyr
450 455 460

Ile Lys Lys Arg Gly Tyr Asp Leu His Asp Val Gln Ala Tyr Gly Gln
 465 470 475 480

Met Leu Arg Asp Ala Gly Phe Glu Glu Val Ile Ala Glu Asp Arg Thr
 485 490 495

Asp Gln Phe Met Lys Val Leu Lys Arg Glu Leu Asp Ala Val Glu Lys
 500 505 510

Glu Lys Glu Glu Phe Ile Ser Asp Phe Ser Lys Glu Asp Tyr Glu Asp
 515 520 525

Ile Ile Gly Gly Trp Lys Ser Lys Leu Leu Arg Ser Ser Ser Gly Glu
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Gln Lys Trp Gly Leu Phe Ile Ala Lys Arg Asn
 545 550 555

<210> 63
 <211> 1476
 <212> DNA
 <213> Arabidopsis thaliana

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<211> 491
<212> PRT
<213> Arabidopsis thaliana

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35 40 45

Leu Pro Pro Tyr Glu Gly Lys Ser Val Leu Glu Leu Gly Ala Gly Ile
50 55 60

Gly Arg Phe Thr Gly Glu Leu Ala Gln Lys Ala Gly Glu Leu Ile Ala
65 70 75 80

Leu Asp Phe Ile Asp Asn Val Ile Lys Lys Asn Glu Ser Ile Asn Gly
85 90 95

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

Leu Lys Ile Thr Asp Gly Ser Leu Asp Leu Ile Phe Ser Asn Trp Leu
115 120 125

Leu Met Tyr Leu Ser Asp Lys Glu Val Glu Leu Leu Ala Glu Arg Met

130

135

140

Val Gly Trp Ile Lys Val Gly Gly Tyr Ile Phe Phe Arg Glu Ser Cys
 145 150 155 160

Phe His Gln Ser Gly Asp Ser Lys Arg Lys Ser Asn Pro Thr His Tyr
 165 170 175

Arg Glu Pro Arg Phe Tyr Ser Lys Val Phe Gln Glu Cys Gln Thr Arg
 180 185 190

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

Ile Gly Ala Tyr Val Lys Asn Lys Lys Asn Gln Asn Gln Ile Cys Trp
 210 215 220

Ile Trp Gln Lys Val Ser Ser Glu Asn Asp Arg Gly Phe Gln Arg Phe
 225 230 235 240

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

Val Phe Gly Gln Gly Phe Val Ser Thr Gly Gly Leu Glu Thr Thr Lys
 260 265 270

Glu Phe Val Glu Lys Met Asn Leu Lys Pro Gly Gln Lys Val Leu Asp
 275 280 285

Val Gly Cys Gly Ile Gly Gly Gly Asp Phe Tyr Met Ala Glu Lys Phe
 290 295 300

Asp Val His Val Val Gly Ile Asp Leu Ser Val Asn Met Ile Ser Phe
 305 310 315 320

Ala Leu Glu Arg Ala Ile Gly Leu Ser Cys Ser Val Glu Phe Glu Val
 325 330 335

Ala Asp Cys Thr Thr Lys His Tyr Pro Asp Asn Ser Phe Asp Val Ile
 340 345 350

Tyr Ser Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro Ala Leu Phe
 355 360 365

Arg Thr Phe Phe Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Ser
 370 375 380

Asp Tyr Cys Arg Ser Pro Lys Thr Pro Ser Ala Glu Phe Ser Glu Tyr
 385 390 395 400

Ile Lys Gln Arg Gly Tyr Asp Leu His Asp Val Gln Ala Tyr Gly Gln
 405 410 415

Met Leu Lys Asp Ala Gly Phe Thr Asp Val Ile Ala Glu Asp Arg Thr
 420 425 430

Asp Gln Phe Met Gln Val Leu Lys Arg Glu Leu Asp Arg Val Glu Lys
 435 440 445

Glu Lys Glu Lys Phe Ile Ser Asp Phe Ser Lys Glu Asp Tyr Asp Asp
 450 455 460

Ile Val Gly Gly Trp Lys Ser Lys Leu Glu Arg Cys Ala Ser Asp Glu
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<210> 65
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 <212> DNA
 <213> Oryza sativa

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 acagaagatc gggggtttca aagatTTTTg gacaatgtgc agtacaagc cagtgggaata 780

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ttacgctatg aacgcatctt tggagaaggc tttgtgagca ctggtggaat tgaaactaca      840
aaagaatttg tggacaggct ggatctcaaa cctggccaga acgttcttga tgttggaatgt      900
ggaattgggg gcggtgattt ttatatggct gacaagtatg atgttcatgt tgttggtatt      960
gatctttcga taaacatggt ttcttttgca cttgagcgtg ctattgggcg taagtgtca      1020
gttgagtttg aagtcgctga ttgcaccaa aagacatacc cagacaacac gtttgacgtc      1080
atctacagtc gtgatactat ccttcacata caagataaac cctcactatt taaaagtttc      1140
ttcaagtggc tcaaacctgg gggtaaggtc ctaattagtg attactgcaa gtgccctggg      1200
aaaccttcag aagagttcgc agcttacatt aagcaaaggg gttatgacct tcacgacgtc      1260
agggcttacg gacagatgct tgagaatgct ggtttccatg atgtcattgc tgaagaccgc      1320
accgatcagt tcctcgatgt tctagagagg gagcttgcta aagttgaaaa gaacaaaaaac      1380
gagttcgtct ctgatttcag ccaggaggac tacgacgcca ttgtgaatgg atggaaggca      1440
aaacttcaaa ggagttctgc tggtagcag aggtgggggc tgttcacgcg gaccaagtga      1500

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<210> 66
<211> 499
<212> PRT
<213> Oryza sativa

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<400> 66
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Met Asp Ala Ala Ala Ala Thr Ala Val Asn Gly Val Leu Glu Val Glu
1           5           10           15

```

```

Glu Arg Lys Ala Gln Lys Ser Tyr Trp Glu Glu His Ser Lys Asp Leu
          20           25           30

```

```

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

```

```

Glu Glu Arg Pro Glu Ile Leu Ser Leu Leu Pro Pro Tyr Glu Gly Lys
          50           55           60

```

```

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

```

```

Val Lys Thr Ala Gly His Val Leu Ala Met Asp Phe Ile Glu Ser Val
          85           90           95

```

```

Ile Lys Lys Asn Glu Ser Ile Asn Gly His His Lys Asn Ala Ser Phe
          100          105          110

```

Met Cys Ala Asp Val Thr Cys Pro Asp Leu Met Ile Glu Asp Asn Ser
115 120 125

Ile Asp Leu Ile Phe Ser Asn Trp Leu Leu Met Tyr Leu Ser Asp Glu
130 135 140

Glu Val Glu Lys Leu Val Lys Arg Met Val Arg Trp Leu Lys Val Gly
145 150 155 160

Gly Tyr Ile Phe Phe Arg Glu Ser Cys Phe His Gln Ser Gly Asp Ser
165 170 175

Lys Arg Lys Val Asn Pro Thr His Tyr Arg Glu Pro Arg Phe Tyr Thr
180 185 190

Lys Val Phe Lys Glu Cys Gln Ala Leu Asp Gln Asp Gly Asn Ser Phe
195 200 205

Glu Leu Ser Val Leu Thr Cys Lys Cys Val Gly Ala Tyr Val Lys Ser
210 215 220

Lys Lys Asn Gln Asn Gln Ile Cys Trp Leu Trp Gln Lys Val Asp Ser
225 230 235 240

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

Ala Ser Gly Ile Leu Arg Tyr Glu Arg Ile Phe Gly Glu Gly Phe Val
260 265 270

Ser Thr Gly Gly Ile Glu Thr Thr Lys Glu Phe Val Asp Arg Leu Asp
275 280 285

Leu Lys Pro Gly Gln Asn Val Leu Asp Val Gly Cys Gly Ile Gly Gly
290 295 300

Gly Asp Phe Tyr Met Ala Asp Lys Tyr Asp Val His Val Val Gly Ile
305 310 315 320

Asp Leu Ser Ile Asn Met Val Ser Phe Ala Leu Glu Arg Ala Ile Gly
325 330 335

Arg Lys Cys Ser Val Glu Phe Glu Val Ala Asp Cys Thr Lys Lys Thr
340 345 350

Tyr Pro Asp Asn Thr Phe Asp Val Ile Tyr Ser Arg Asp Thr Ile Leu

355

360

365

His Ile Gln Asp Lys Pro Ser Leu Phe Lys Ser Phe Phe Lys Trp Leu
 370 375 380

Lys Pro Gly Gly Lys Val Leu Ile Ser Asp Tyr Cys Lys Cys Pro Gly
 385 390 395 400

Lys Pro Ser Glu Glu Phe Ala Ala Tyr Ile Lys Gln Arg Gly Tyr Asp
 405 410 415

Leu His Asp Val Arg Ala Tyr Gly Gln Met Leu Glu Asn Ala Gly Phe
 420 425 430

His Asp Val Ile Ala Glu Asp Arg Thr Asp Gln Phe Leu Asp Val Leu
 435 440 445

Glu Arg Glu Leu Ala Lys Val Glu Lys Asn Lys Asn Glu Phe Val Ser
 450 455 460

Asp Phe Ser Gln Glu Asp Tyr Asp Ala Ile Val Asn Gly Trp Lys Ala
 465 470 475 480

Lys Leu Gln Arg Ser Ser Ala Gly Glu Gln Arg Trp Gly Leu Phe Ile
 485 490 495

Ala Thr Lys

<210> 67
 <211> 1476
 <212> DNA
 <213> Oryza sativa

<400> 67
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 tccaaggacc tcaccgtcga ggccatgatg ctcgactccc gcgccgccga cctcgacaag 120
 gaggagcgcc ccgaggtcct gtctgtactc ctttcttaca aagggaaatc agtactggag 180
 cttggtgctg gaataggacg ctttactggg gaactggcaa aagaagctgg ccatgtttta 240
 gccctagact tcattgaaag tgtgattaag aagaatgaga acataaatgg gcatcacaag 300
 aacataacct ttatgtgcgc tgatgtcacg tctccggacc tgacgatcga agataactct 360
 attgatctca tattctcaaa ctggctacta atgtaccttt cagatgagga ggtcgagaag 420
 ctagtaggaa gaatggtgaa atggctgaag gtaggtggcc atatattctt tagggagtca 480

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tgctttcacc aatctggaga ttccaaaagg aaggtgaatc caacacatta ccgggagcca      540
aggttctata caaagatatt taaagaatgc cattcctatg ataaagatgg gggttcttat      600
gaactttctc tagaaacatg caagtgcatt ggggcttatg tgaaaagcaa gaaaaatcaa      660
aatcagttat gttggctatg ggaaaagggt aagtcaacag aagacagagg attccaaaga      720
ttcctggaca atgtgcagta caaaaccact ggaatcttac gctatgagcg tgtcttcgga      780
gaggggttatg tcagcactgg tggaattgaa accacaaagg aatttgtgga taagctggat      840
cttaaacctg gacagaaagt gcttgatggt ggggtcggaa ttggaggcgg cgacttctat      900
atggctgaaa actacgatgc ccatgttctt ggtattgatc tttcaatcaa catggtttca      960
tttgcaatcg aacgtgccat tggacgcaag tgttcggttg agtttgaagt agctgattgc     1020
accacaaaga cctacgcacc aaatacattt gatgtgatct acagccgtga caccattctt     1080
cacatacatg ataaacctgc tttgttcaga agtttcttca agtggctgaa acctgggggc     1140
aaagtcctca tcagtgatta ctgtaggaat cctgggaaac catcagaaga atttgctgct     1200
tacattaagc agagaggcta tgacctccac gatgtgaaga cttacggaaa gatgcttgag     1260
gatgctggtt tccatcatgt cattgctgaa gaccgcacgg accagttcct gcgtgttctt     1320
caaagggagc ttgctgaagt tgagaagaac aaagaagcct tcatggcaga cttcaccag      1380
gaggactacg atgacattgt gaacggctgg aacgcgaagc tgaagcggag ctctgccggt      1440
gagcagaggt gggggctggt cattgcaacc aaatga                                1476

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<210> 68
<211> 491
<212> PRT
<213> Oryza sativa

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<400> 68
```

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Met Arg Ala Gly Ile Gly Glu Val Glu Arg Lys Ala Gln Arg Ser Tyr
1           5           10          15

```

```

Trp Glu Glu His Ser Lys Asp Leu Thr Val Glu Ala Met Met Leu Asp
          20          25          30

```

```

Ser Arg Ala Ala Asp Leu Asp Lys Glu Glu Arg Pro Glu Val Leu Ser
          35          40          45

```

```

Val Leu Pro Ser Tyr Lys Gly Lys Ser Val Leu Glu Leu Gly Ala Gly
50           55           60

```

```

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

```

Ala Leu Asp Phe Ile Glu Ser Val Ile Lys Lys Asn Glu Asn Ile Asn
85 90 95

Gly His His Lys Asn Ile Thr Phe Met Cys Ala Asp Val Thr Ser Pro
100 105 110

Asp Leu Thr Ile Glu Asp Asn Ser Ile Asp Leu Ile Phe Ser Asn Trp
115 120 125

Leu Leu Met Tyr Leu Ser Asp Glu Glu Val Glu Lys Leu Val Gly Arg
130 135 140

Met Val Lys Trp Leu Lys Val Gly Gly His Ile Phe Phe Arg Glu Ser
145 150 155 160

Cys Phe His Gln Ser Gly Asp Ser Lys Arg Lys Val Asn Pro Thr His
165 170 175

Tyr Arg Glu Pro Arg Phe Tyr Thr Lys Ile Phe Lys Glu Cys His Ser
180 185 190

Tyr Asp Lys Asp Gly Gly Ser Tyr Glu Leu Ser Leu Glu Thr Cys Lys
195 200 205

Cys Ile Gly Ala Tyr Val Lys Ser Lys Lys Asn Gln Asn Gln Leu Cys
210 215 220

Trp Leu Trp Glu Lys Val Lys Ser Thr Glu Asp Arg Gly Phe Gln Arg
225 230 235 240

Phe Leu Asp Asn Val Gln Tyr Lys Thr Thr Gly Ile Leu Arg Tyr Glu
245 250 255

Arg Val Phe Gly Glu Gly Tyr Val Ser Thr Gly Gly Ile Glu Thr Thr
260 265 270

Lys Glu Phe Val Asp Lys Leu Asp Leu Lys Pro Gly Gln Lys Val Leu
275 280 285

Asp Val Gly Cys Gly Ile Gly Gly Gly Asp Phe Tyr Met Ala Glu Asn
290 295 300

Tyr Asp Ala His Val Leu Gly Ile Asp Leu Ser Ile Asn Met Val Ser
305 310 315 320

Phe Ala Ile Glu Arg Ala Ile Gly Arg Lys Cys Ser Val Glu Phe Glu
325 330 335

Val Ala Asp Cys Thr Thr Lys Thr Tyr Ala Pro Asn Thr Phe Asp Val
340 345 350

Ile Tyr Ser Arg Asp Thr Ile Leu His Ile His Asp Lys Pro Ala Leu
355 360 365

Phe Arg Ser Phe Phe Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile
370 375 380

Ser Asp Tyr Cys Arg Asn Pro Gly Lys Pro Ser Glu Glu Phe Ala Ala
385 390 395 400

Tyr Ile Lys Gln Arg Gly Tyr Asp Leu His Asp Val Lys Thr Tyr Gly
405 410 415

Lys Met Leu Glu Asp Ala Gly Phe His His Val Ile Ala Glu Asp Arg
420 425 430

Thr Asp Gln Phe Leu Arg Val Leu Gln Arg Glu Leu Ala Glu Val Glu
435 440 445

Lys Asn Lys Glu Ala Phe Met Ala Asp Phe Thr Gln Glu Asp Tyr Asp
450 455 460

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

Glu Gln Arg Trp Gly Leu Phe Ile Ala Thr Lys
485 490

<210> 69
<211> 1488
<212> DNA
<213> Oryza sativa

<400> 69
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tgggaggagc actccaagga cctcaccgtc gaggccatga tgctcgactc ccgcgccgcc 120
gacctcgaca aggaggagcg ccccgaggtc ctgtctgtac tcccttctta caaagggaaa 180
tcagtactgg agcttggtgc tggaatagga cgctttactg gggaactggc aaaagaagct 240
ggccatgttt tagccctaga cttcattgaa agtgtgatta agaagaatga gaacataaat 300
gggcatcaca agaacataac ctttatgtgc gctgatgtca cgtctccgga cctgacgac 360

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gaagataact ctattgatct catattctca aactggctac taatgtacct ttcagatgag      420
gaggtcgaga agctagtagg aagaatggtg aaatggctga aggtaggtgg ccatatattc      480
tttagggagt catgctttca ccaatctgga gattccaaaa ggaaggtgaa tccaacacat      540
taccgggagc caaggttcta tacaagata tttaaagaat gccattccta tgataaagat      600
gggggttctt atgaactttc tctagaaaca tgcaagtgca ttggggctta tgtgaaaagc      660
aagaaaaatc aaaatcagtt atgttggtc tgggaaaagg ttaagtcaac agaagacaga      720
ggattccaaa gattcctgga caatgtgcag taaaaacca ctggaatctt acgctatgag      780
cgtgtcttcg gagaggggta tgtcagcact ggtggaattg aaaccacaaa ggaatttgtg      840
gataagctgg atcttaaacc tggacagaaa gtgcttgatg ttgggtgcgg aattggaggc      900
ggcgacttct atatggctga aaactacgat gcccatgttc ttggtattga tctttcaatc      960
aacatggttt catttgcaat cgaacgtgcc attggacgca agtggtcggg tgagtttgaa    1020
gtagctgatt gcaccacaaa gacctacgca ccaaatacat ttgatgtgat ctacagccgt    1080
gacaccattc ttcacataca tgataaacct gctttgttca gaagtttctt caagtggctg    1140
aaacctgggg gcaaagtcct catcagtgat tactgtagga atcctgggaa accatcagaa    1200
gaatttgctg cttacattaa gcagagaggc tatgacctcc acgatgtgaa gacttacgga    1260
aagatgcttg aggatgctgg tttccatcat gtcattgctg aagaccgcac ggaccagttc    1320
ctgcggtgtc ttcaaagga gcttgctgaa gttgagaaga acaaagaagc cttcatggca    1380
gacttcaccc aggaggacta cgatgacatt gtgaacggct ggaacgcgaa gctgaagcgg    1440
agctctgccg gtgagcagag gtgggggctg ttcattgcaa ccaaatga                    1488

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<210> 70
<211> 495
<212> PRT
<213> Oryza sativa

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<400> 70
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Met Asp Ala Val Ala Ala Asn Gly Ile Gly Glu Val Glu Arg Lys Ala
1           5           10           15

```

```

Gln Arg Ser Tyr Trp Glu Glu His Ser Lys Asp Leu Thr Val Glu Ala
          20           25           30

```

```

Met Met Leu Asp Ser Arg Ala Ala Asp Leu Asp Lys Glu Glu Arg Pro
          35           40           45

```

```

Glu Val Leu Ser Val Leu Pro Ser Tyr Lys Gly Lys Ser Val Leu Glu
          50           55           60

```

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

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

Glu Asn Ile Asn Gly His His Lys Asn Ile Thr Phe Met Cys Ala Asp
100 105 110

Val Thr Ser Pro Asp Leu Thr Ile Glu Asp Asn Ser Ile Asp Leu Ile
115 120 125

Phe Ser Asn Trp Leu Leu Met Tyr Leu Ser Asp Glu Glu Val Glu Lys
130 135 140

Leu Val Gly Arg Met Val Lys Trp Leu Lys Val Gly Gly His Ile Phe
145 150 155 160

Phe Arg Glu Ser Cys Phe His Gln Ser Gly Asp Ser Lys Arg Lys Val
165 170 175

Asn Pro Thr His Tyr Arg Glu Pro Arg Phe Tyr Thr Lys Ile Phe Lys
180 185 190

Glu Cys His Ser Tyr Asp Lys Asp Gly Gly Ser Tyr Glu Leu Ser Leu
195 200 205

Glu Thr Cys Lys Cys Ile Gly Ala Tyr Val Lys Ser Lys Lys Asn Gln
210 215 220

Asn Gln Leu Cys Trp Leu Trp Glu Lys Val Lys Ser Thr Glu Asp Arg
225 230 235 240

Gly Phe Gln Arg Phe Leu Asp Asn Val Gln Tyr Lys Thr Thr Gly Ile
245 250 255

Leu Arg Tyr Glu Arg Val Phe Gly Glu Gly Tyr Val Ser Thr Gly Gly
260 265 270

Ile Glu Thr Thr Lys Glu Phe Val Asp Lys Leu Asp Leu Lys Pro Gly
275 280 285

Gln Lys Val Leu Asp Val Gly Cys Gly Ile Gly Gly Gly Asp Phe Tyr
290 295 300

Met Ala Glu Asn Tyr Asp Ala His Val Leu Gly Ile Asp Leu Ser Ile
305 310 315 320

Asn Met Val Ser Phe Ala Ile Glu Arg Ala Ile Gly Arg Lys Cys Ser
325 330 335

Val Glu Phe Glu Val Ala Asp Cys Thr Thr Lys Thr Tyr Ala Pro Asn
340 345 350

Thr Phe Asp Val Ile Tyr Ser Arg Asp Thr Ile Leu His Ile His Asp
355 360 365

Lys Pro Ala Leu Phe Arg Ser Phe Phe Lys Trp Leu Lys Pro Gly Gly
370 375 380

Lys Val Leu Ile Ser Asp Tyr Cys Arg Asn Pro Gly Lys Pro Ser Glu
385 390 395 400

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

Lys Thr Tyr Gly Lys Met Leu Glu Asp Ala Gly Phe His His Val Ile
420 425 430

Ala Glu Asp Arg Thr Asp Gln Phe Leu Arg Val Leu Gln Arg Glu Leu
435 440 445

Ala Glu Val Glu Lys Asn Lys Glu Ala Phe Met Ala Asp Phe Thr Gln
450 455 460

Glu Asp Tyr Asp Asp Ile Val Asn Gly Trp Asn Ala Lys Leu Lys Arg
465 470 475 480

Ser Ser Ala Gly Glu Gln Arg Trp Gly Leu Phe Ile Ala Thr Lys
485 490 495

<210> 71
<211> 1164
<212> DNA
<213> Oryza sativa

<400> 71
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ttctcaaaact ggctactaat gtacctttca gatgaggagg tcgagaagct agtaggaaga 120
atggtgaaat ggctgaaggt aggtggccat atattcttta gggagtcatg ctttcaccaa 180

tctggagatt ccaaaaggaa ggtgaatcca acacattacc gggagccaag gttctataca	240
aagatattta aagaatgccca ttcctatgat aaagatgggg gttcttatga actttctcta	300
gaaacatgca agtgcattgg ggcttatgtg aaaagcaaga aaaatcaaaa tcagttatgt	360
tggctatggg aaaaggttaa gtcaacagaa gacagaggat tccaaagatt cctggacaat	420
gtgcagtaca aaaccactgg aatcttacgc tatgagcgtg tcttcggaga gggttatgtc	480
agcactggtg gaattgaaac cacaaaggaa tttgtggata agctggatct taaacctgga	540
cagaaagtgc ttgatgttgg gtgcggaatt ggaggcggcg acttctatat ggctgaaaac	600
tacgatgccc atgttcttgg tattgatctt tcaatcaaca tggtttcatt tgcaatcgaa	660
cgtgccattg gacgcaagtg ttcggttgag tttgaagtag ctgattgcac cacaaagacc	720
tacgcaccaa atacatttga tgtgatctac agccgtgaca ccattcttca catacatgat	780
aaacctgctt tgttcagaag tttcttcaag tggctgaaac ctggggggcaa agtcctcatc	840
agtgattact gtaggaatcc tgggaaacca tcagaagaat ttgctgctta cattaagcag	900
agaggctatg acctccacga tgtgaagact tacggaaaga tgcttgagga tgctggtttc	960
catcatgtca ttgctgaaga cgcacggac cagttcctgc gtgttcttca aaggagctt	1020
gctgaagttg agaagaacaa agaagccttc atggcagact tcaccagga ggactacgat	1080
gacattgtga acggctggaa cgcgaagctg aagcggagct ctgccggtga gcagaggtgg	1140
gggctgttca ttgcaaccaa atga	1164

<210> 72
 <211> 387
 <212> PRT
 <213> Oryza sativa

 <400> 72

Met Cys Ala Asp Val Thr Ser Pro Asp Leu Thr Ile Glu Asp Asn Ser	
1 5 10 15	
Ile Asp Leu Ile Phe Ser Asn Trp Leu Leu Met Tyr Leu Ser Asp Glu	
20 25 30	
Glu Val Glu Lys Leu Val Gly Arg Met Val Lys Trp Leu Lys Val Gly	
35 40 45	
Gly His Ile Phe Phe Arg Glu Ser Cys Phe His Gln Ser Gly Asp Ser	
50 55 60	
Lys Arg Lys Val Asn Pro Thr His Tyr Arg Glu Pro Arg Phe Tyr Thr	
65 70 75 80	

Lys Ile Phe Lys Glu Cys His Ser Tyr Asp Lys Asp Gly Gly Ser Tyr
85 90 95

Glu Leu Ser Leu Glu Thr Cys Lys Cys Ile Gly Ala Tyr Val Lys Ser
100 105 110

Lys Lys Asn Gln Asn Gln Leu Cys Trp Leu Trp Glu Lys Val Lys Ser
115 120 125

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

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

Ser Thr Gly Gly Ile Glu Thr Thr Lys Glu Phe Val Asp Lys Leu Asp
165 170 175

Leu Lys Pro Gly Gln Lys Val Leu Asp Val Gly Cys Gly Ile Gly Gly
180 185 190

Gly Asp Phe Tyr Met Ala Glu Asn Tyr Asp Ala His Val Leu Gly Ile
195 200 205

Asp Leu Ser Ile Asn Met Val Ser Phe Ala Ile Glu Arg Ala Ile Gly
210 215 220

Arg Lys Cys Ser Val Glu Phe Glu Val Ala Asp Cys Thr Thr Lys Thr
225 230 235 240

Tyr Ala Pro Asn Thr Phe Asp Val Ile Tyr Ser Arg Asp Thr Ile Leu
245 250 255

His Ile His Asp Lys Pro Ala Leu Phe Arg Ser Phe Phe Lys Trp Leu
260 265 270

Lys Pro Gly Gly Lys Val Leu Ile Ser Asp Tyr Cys Arg Asn Pro Gly
275 280 285

Lys Pro Ser Glu Glu Phe Ala Ala Tyr Ile Lys Gln Arg Gly Tyr Asp
290 295 300

Leu His Asp Val Lys Thr Tyr Gly Lys Met Leu Glu Asp Ala Gly Phe
305 310 315 320

His His Val Ile Ala Glu Asp Arg Thr Asp Gln Phe Leu Arg Val Leu
 325 330 335

Gln Arg Glu Leu Ala Glu Val Glu Lys Asn Lys Glu Ala Phe Met Ala
 340 345 350

Asp Phe Thr Gln Glu Asp Tyr Asp Asp Ile Val Asn Gly Trp Asn Ala
 355 360 365

Lys Leu Lys Arg Ser Ser Ala Gly Glu Gln Arg Trp Gly Leu Phe Ile
 370 375 380

Ala Thr Lys
 385

<210> 73
 <211> 1446
 <212> DNA
 <213> Populus trichocarpa

<400> 73
 atggctactc atgtggaaga acgcgatatt cagaagaagt attggatgga taacatttcc 60
 gatttgagtg tgaatgcaat gatgcttgac tcgaaagcat ccgaacttga caaggaagaa 120
 cgacctgaga tacttttctct gcttccacct tatgaaggaa aaacagtttt ggaactcgga 180
 gctggtattg gccgtttcac aggggaatta gcacagaagg ctggccaagt agtggctttg 240
 gacttcattg agagtgcaat aaaaaagaat gaaaatatca acggacacta taagaatgtc 300
 aagtttatgt gcgctgatgt gacatcccca gatctgaata tttcagaggg gtcggtggat 360
 ttgatattct caaattggct tctcatgtat ctctctgaca aagaggtgga gaatctggta 420
 gaaaggatgg tcaaattgggt gaaggttgat gggtttattt tcttcagaga gtcttggttt 480
 catcaatctg gagattctaa gcgaaaatac aaccacaacc attaccggga acccagattc 540
 tacacgaagg tgtttaaaga atgccatacg cgtgatgggt ctggagattc tttcgaactc 600
 tctcttggtg gctgcaaatt catctcagct tatatttggt ggatatggca gaaagttagt 660
 tcatatgagg ataagggggt ccagcgattc ttagataatg ttcagtataa atccaatggc 720
 atattacgtt atgagcgtgt ctttggacaa ggttatgtga gtacaggagg aattgaaaca 780
 actaaagaat ttgtgggaaa actggatctt aagcctggcc agaaagtcct agatgttggc 840
 tgtgggattg ggggaggtga cttttacatg gctgagaact ttgatgtgga gggtgtaggc 900
 attgacctct ccataaatat gatttcgttt gcccttgaac gtgccattgg gctcaaatgt 960
 tctgtggagt ttgaagttgc tgattgtact acaaagacat atcctgacaa cacatttgat 1020
 gttatctaca gccgtgacac ctttttgac attcaagaca aacctgcatt atttagatct 1080

ttcttcaagt ggttgaagcc tggaggtaaa gtacttatca gtgattactg caagtgtgat	1140
ggaactccat caccagaatt cgccgagtac attaaacaga gaggatatga tcttcatgat	1200
gtaaaagcat atggccagat gcttagggat gctggttttg atgaggtcgt tgcagaggac	1260
cgaactgata agttcaacaa agttctgcaa agggagttaa atgctataga gaaggacaag	1320
gatgagttca tccacgactt ttccgaaggg gactataatg atatagttgg tggatggaag	1380
gcaaagctga tcaggagttc atctggggag cagcgatggg gcctgttcat cgccaagaaa	1440
aaatga	1446

<210> 74
 <211> 481
 <212> PRT
 <213> Populus trichocarpa

<400> 74

Met	Ala	Thr	His	Val	Glu	Glu	Arg	Asp	Ile	Gln	Lys	Lys	Tyr	Trp	Met
1				5					10					15	

Asp	Asn	Ile	Ser	Asp	Leu	Ser	Val	Asn	Ala	Met	Met	Leu	Asp	Ser	Lys
			20					25					30		

Ala	Ser	Glu	Leu	Asp	Lys	Glu	Glu	Arg	Pro	Glu	Ile	Leu	Ser	Leu	Leu
		35					40					45			

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

Arg	Phe	Thr	Gly	Glu	Leu	Ala	Gln	Lys	Ala	Gly	Gln	Val	Val	Ala	Leu
65					70					75					80

Asp	Phe	Ile	Glu	Ser	Ala	Ile	Lys	Lys	Asn	Glu	Asn	Ile	Asn	Gly	His
				85					90					95	

Tyr	Lys	Asn	Val	Lys	Phe	Met	Cys	Ala	Asp	Val	Thr	Ser	Pro	Asp	Leu
			100					105						110	

Asn	Ile	Ser	Glu	Gly	Ser	Val	Asp	Leu	Ile	Phe	Ser	Asn	Trp	Leu	Leu
		115					120					125			

Met	Tyr	Leu	Ser	Asp	Lys	Glu	Val	Glu	Asn	Leu	Val	Glu	Arg	Met	Val
	130					135					140				

Lys	Trp	Val	Lys	Val	Asp	Gly	Phe	Ile	Phe	Phe	Arg	Glu	Ser	Cys	Phe
145					150					155					160

His Gln Ser Gly Asp Ser Lys Arg Lys Tyr Asn Pro Thr His Tyr Arg
165 170 175

Glu Pro Arg Phe Tyr Thr Lys Val Phe Lys Glu Cys His Thr Arg Asp
180 185 190

Gly Ser Gly Asp Ser Phe Glu Leu Ser Leu Val Gly Cys Lys Cys Ile
195 200 205

Ser Ala Tyr Ile Cys Trp Ile Trp Gln Lys Val Ser Ser Tyr Glu Asp
210 215 220

Lys Gly Phe Gln Arg Phe Leu Asp Asn Val Gln Tyr Lys Ser Asn Gly
225 230 235 240

Ile Leu Arg Tyr Glu Arg Val Phe Gly Gln Gly Tyr Val Ser Thr Gly
245 250 255

Gly Ile Glu Thr Thr Lys Glu Phe Val Gly Lys Leu Asp Leu Lys Pro
260 265 270

Gly Gln Lys Val Leu Asp Val Gly Cys Gly Ile Gly Gly Gly Asp Phe
275 280 285

Tyr Met Ala Glu Asn Phe Asp Val Glu Val Val Gly Ile Asp Leu Ser
290 295 300

Ile Asn Met Ile Ser Phe Ala Leu Glu Arg Ala Ile Gly Leu Lys Cys
305 310 315 320

Ser Val Glu Phe Glu Val Ala Asp Cys Thr Thr Lys Thr Tyr Pro Asp
325 330 335

Asn Thr Phe Asp Val Ile Tyr Ser Arg Asp Thr Ile Leu His Ile Gln
340 345 350

Asp Lys Pro Ala Leu Phe Arg Ser Phe Phe Lys Trp Leu Lys Pro Gly
355 360 365

Gly Lys Val Leu Ile Ser Asp Tyr Cys Lys Cys Asp Gly Thr Pro Ser
370 375 380

Pro Glu Phe Ala Glu Tyr Ile Lys Gln Arg Gly Tyr Asp Leu His Asp
385 390 395 400

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

Val Ala Glu Asp Arg Thr Asp Gln Phe Asn Lys Val Leu Gln Arg Glu
420 425 430

Leu Asn Ala Ile Glu Lys Asp Lys Asp Glu Phe Ile His Asp Phe Ser
435 440 445

Glu Gly Asp Tyr Asn Asp Ile Val Gly Gly Trp Lys Ala Lys Leu Ile
450 455 460

Arg Ser Ser Ser Gly Glu Gln Arg Trp Gly Leu Phe Ile Ala Lys Lys
465 470 475 480

Lys

<210> 75
<211> 1038
<212> DNA
<213> Populus trichocarpa

<400> 75
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tgcaagtgtg ctggaactcc atcaccagaa ttgacagagt acattaaaca gagaggatat 780
gatcttcatg atgtgaaagc atatggccag atgcttaggg atgctgggtt tgatgaggtc 840
attgcagaag accgaactga tcagttcaac caagttctgc taagggaatt aaaagctata 900

gaaaaggaga aggatgaatt tatccatgac ttctctgaag aagactataa tgatatagtt 960
 ggtggatgga aggcaaagct gatcaggagt tcctctggcg agcagcgatg gggcctgttc 1020
 attgccaaga aaaaatga 1038

<210> 76
 <211> 345
 <212> PRT
 <213> Populus trichocarpa

<400> 76

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

Glu Arg Met Val Lys Trp Leu Lys Val Gly Gly Phe Ile Phe Phe Arg
 35 40 45

Glu Ser Cys Phe His Gln Ser Gly Asp Ser Lys Arg Lys Tyr Asn Pro
 50 55 60

Thr His Tyr Arg Glu Pro Arg Phe Tyr Thr Lys Ile Cys Trp Ile Trp
 65 70 75 80

Gln Lys Val Ser Ser Asn Asp Asp Lys Gly Phe Gln Arg Phe Leu Asp
 85 90 95

Asn Val Gln Tyr Lys Ser Asn Gly Ile Leu Arg Tyr Glu Arg Val Phe
 100 105 110

Gly Gln Gly Phe Val Ser Thr Gly Gly Met Glu Thr Thr Lys Glu Phe
 115 120 125

Val Glu Lys Leu Asp Leu Lys Pro Gly Gln Lys Val Leu Asp Val Gly
 130 135 140

Cys Gly Ile Gly Gly Gly Asp Phe Tyr Met Ala Glu Asn Phe Glu Val
 145 150 155 160

Glu Val Val Gly Ile Asp Leu Ser Val Asn Met Ile Ser Phe Ala Leu
 165 170 175

Glu Arg Ala Ile Gly Leu Lys Cys Ser Val Glu Phe Glu Val Ala Asp
 180 185 190

Cys Thr Thr Lys Thr Tyr Pro Asp Asn Thr Phe Asp Val Ile Tyr Ser
195 200 205

Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro Ala Leu Phe Arg Ser
210 215 220

Phe Phe Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Ser Asp Tyr
225 230 235 240

Cys Lys Cys Ala Gly Thr Pro Ser Pro Glu Phe Ala Glu Tyr Ile Lys
245 250 255

Gln Arg Gly Tyr Asp Leu His Asp Val Lys Ala Tyr Gly Gln Met Leu
260 265 270

Arg Asp Ala Gly Phe Asp Glu Val Ile Ala Glu Asp Arg Thr Asp Gln
275 280 285

Phe Asn Gln Val Leu Leu Arg Glu Leu Lys Ala Ile Glu Lys Glu Lys
290 295 300

Asp Glu Phe Ile His Asp Phe Ser Glu Glu Asp Tyr Asn Asp Ile Val
305 310 315 320

Gly Gly Trp Lys Ala Lys Leu Ile Arg Ser Ser Ser Gly Glu Gln Arg
325 330 335

Trp Gly Leu Phe Ile Ala Lys Lys Lys
340 345

<210> 77
<211> 1506
<212> DNA
<213> Zea Mays

<400> 77
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ctcgactccc gcgccgccga cctcgacaag gaagagcgac ccgagatcct gtctttgctt 180
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gatctggcaa aagaagctgg gcacgttctg gcactagact ttattgaaag tgtgattaag 300
aagaaccaa gcataaatgg gcatacacaag aacataacct tcaggtgtgc cgatgtgaca 360
tctaacgact tgaagattga agataactct gttgatctga ttttttcaaa ctggctatta 420

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atgtatcttt cagatgagga ggtccaaaag cttgtgggga aaatggtaaa atggttaaag    480
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aaggtgaacc caacacacta tcgagaacca aggttttata ccaaggtatt taaagagggc    600
cattcatttg atcaagatgg aggttcgttt gaactttctc tagtgacctg taaatgcatt    660
ggggcttatg tcaaaaacaa gaagaatcaa aaccagatat gctgggttatg ggaaaaggta    720
aaatcaacag aagacagaga ttttcaaaga ttcttggaaca acgtgcaata caaaacaagt    780
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gacgtgaagg cttatggaca gatgctgaag gatgctgggt ttcataatgt catcgcgga   1320
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aagtga                                           1506

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<210> 78
<211> 501
<212> PRT
<213> Zea Mays

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<400> 78
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Met Asp Thr Val Gly Val Pro Val Val Ala Val Ala Asn Gly Ile Gly
1          5          10         15

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Glu Val Glu Arg Lys Val Gln Lys Ser Tyr Trp Glu Glu His Ser Lys
          20          25          30

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Cys Leu Thr Val Glu Ser Met Met Leu Asp Ser Arg Ala Ala Asp Leu
          35          40          45

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Asp Lys Glu Glu Arg Pro Glu Ile Leu Ser Leu Leu Pro Ser Tyr Lys
          50          55          60

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

Asp Leu Ala Lys Glu Ala Gly His Val Leu Ala Leu Asp Phe Ile Glu
85 90 95

Ser Val Ile Lys Lys Asn Gln Ser Ile Asn Gly His His Lys Asn Ile
100 105 110

Thr Phe Arg Cys Ala Asp Val Thr Ser Asn Asp Leu Lys Ile Glu Asp
115 120 125

Asn Ser Val Asp Leu Ile Phe Ser Asn Trp Leu Leu Met Tyr Leu Ser
130 135 140

Asp Glu Glu Val Gln Lys Leu Val Gly Lys Met Val Lys Trp Leu Lys
145 150 155 160

Val Gly Gly His Ile Phe Phe Arg Glu Ser Cys Phe His Gln Ser Gly
165 170 175

Asp Ser Lys Arg Lys Val Asn Pro Thr His Tyr Arg Glu Pro Arg Phe
180 185 190

Tyr Thr Lys Val Phe Lys Glu Gly His Ser Phe Asp Gln Asp Gly Gly
195 200 205

Ser Phe Glu Leu Ser Leu Val Thr Cys Lys Cys Ile Gly Ala Tyr Val
210 215 220

Lys Asn Lys Lys Asn Gln Asn Gln Ile Cys Trp Leu Trp Glu Lys Val
225 230 235 240

Lys Ser Thr Glu Asp Arg Asp Phe Gln Arg Phe Leu Asp Asn Val Gln
245 250 255

Tyr Lys Thr Ser Gly Ile Leu Arg Tyr Glu Arg Val Phe Gly Glu Gly
260 265 270

Phe Val Ser Thr Gly Gly Ile Glu Thr Thr Lys Glu Phe Val Gly Met
275 280 285

Leu Asp Leu Lys Pro Gly Gln Lys Val Leu Asp Val Gly Cys Gly Ile
290 295 300

Gly Gly Gly Asp Phe Tyr Met Ala Ala Asn Tyr Asp Val His Val Leu
 305 310 315 320

Gly Ile Asp Leu Ser Val Asn Met Val Ser Phe Ala Ile Glu Arg Ala
 325 330 335

Ile Gly Arg Lys Cys Ser Val Glu Phe Glu Val Ala Asp Cys Thr Thr
 340 345 350

Lys Asp Tyr Pro Glu Asn Ser Phe Asp Val Ile Tyr Ser Arg Asp Thr
 355 360 365

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

Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Ser Asp Tyr Cys Lys Asn
 385 390 395 400

Pro Gly Lys Pro Ser Glu Glu Phe Ala Ala Tyr Ile Lys Gln Arg Gly
 405 410 415

Tyr Asp Leu His Asp Val Lys Ala Tyr Gly Gln Met Leu Lys Asp Ala
 420 425 430

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

Val Leu Gln Arg Glu Leu Gly Glu Val Glu Lys Asn Lys Asp Ala Phe
 450 455 460

Leu Ala Asp Phe Thr Gln Glu Asp Tyr Asp Asp Ile Val Asn Gly Trp
 465 470 475 480

Asn Ala Lys Leu Lys Arg Ser Ser Ala Gly Glu Gln Arg Trp Gly Leu
 485 490 495

Phe Ile Ala Thr Lys
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<210> 79
 <211> 1488
 <212> DNA
 <213> Zea Mays

<400> 79
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gggcatgttt	ttgcagtgga	tttcgttgaa	agtgtgatta	aaaagaatgg	aagtataaat	300
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gagattgaca	agttggtaga	aagaatggta	aaatggttga	aggtcggtgg	ttatatcttc	480
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aagaaagatc	aaaaccagat	atgttggcta	tggaaaaaag	taaactcatc	agaagatggg	720
ggatttcaaa	gttttttgga	caatgtgcag	tacaaagcca	ctggaatact	acgctatgaa	780
cgtatctttg	gagatggcta	cgtgagtact	ggaggagctg	agactacaaa	agaatttgtg	840
gagaaactga	atcttaagcc	tgggcagaag	gtgcttgatg	ttggatgtgg	aattggggga	900
ggtgactttt	atatggctga	gaagtatgg	acacatgtcg	ttggtattga	cctttccatt	960
aacatgataa	tgtttgccct	tgagcgttcc	attgggtgta	agtgcctagt	tgagtttgaa	1020
gttgctgatt	gcaccacaaa	gacataccca	gaccacatgt	ttgatgtcat	ctacagtcgt	1080
gacactatcc	ttcatataca	agataaaccc	tccttgttta	aaagtttctt	caaattggctg	1140
aaacctgggg	gaaaggttct	aatcagtgat	tactgcaaga	gtcctggaaa	accatcagaa	1200
gagtttgcaa	catacattaa	gcagaggggt	tatgatctcc	atgacgtgga	ggcttatgga	1260
cagatgctga	aggatgctgg	ttttcataat	gtcatcgcg	aagatcgcac	tgagcagttc	1320
ttgaatgttc	tacagaggga	gataggtgaa	gttgaaaaga	acaaagacgc	tttcctggca	1380
gacttcaccc	aggaggacta	tgacgacatt	gtgaacggct	ggaacgcgaa	gctgaaacgg	1440
agctctggcg	gtgagcagag	gtgggggttg	ttcattgcca	ccaagtga		1488

<210> 80
 <211> 495
 <212> PRT
 <213> Zea Mays

<400> 80

Met	Ala	Ala	Ala	Val	Asn	Gly	Ser	Leu	Asp	Val	His	Glu	Arg	Lys	Ala
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Gln	Lys	Ser	Tyr	Trp	Glu	Glu	His	Ser	Gly	Glu	Leu	Asn	Leu	Glu	Ala
			20					25					30		

Ile Met Leu Asp Ser Arg Ala Ala Glu Leu Asp Lys Glu Glu Arg Pro
35 40 45

Glu Val Leu Ser Leu Leu Pro Ser Tyr Glu Gly Lys Ser Ile Leu Glu
50 55 60

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

Gly His Val Phe Ala Val Asp Phe Val Glu Ser Val Ile Lys Lys Asn
85 90 95

Gly Ser Ile Asn Asp His Tyr Gly Asn Thr Ser Phe Met Cys Ala Asp
100 105 110

Val Thr Ser Pro Asp Leu Met Ile Glu Ala Asn Ser Ile Asp Leu Ile
115 120 125

Phe Ser Asn Trp Leu Leu Met Tyr Leu Ser Asp Glu Glu Ile Asp Lys
130 135 140

Leu Val Glu Arg Met Val Lys Trp Leu Lys Val Gly Gly Tyr Ile Phe
145 150 155 160

Phe Arg Glu Ser Cys Phe His Gln Ser Gly Asp Thr Glu Arg Lys Phe
165 170 175

Asn Pro Thr His Tyr Arg Glu Pro Arg Phe Tyr Thr Lys Val Phe Lys
180 185 190

Glu Cys Gln Thr Phe Asn Gln Asp Gly Thr Ser Phe Lys Leu Ser Leu
195 200 205

Ile Thr Phe Lys Cys Ile Gly Ala Tyr Val Asn Ile Lys Lys Asp Gln
210 215 220

Asn Gln Ile Cys Trp Leu Trp Lys Lys Val Asn Ser Ser Glu Asp Gly
225 230 235 240

Gly Phe Gln Ser Phe Leu Asp Asn Val Gln Tyr Lys Ala Thr Gly Ile
245 250 255

Leu Arg Tyr Glu Arg Ile Phe Gly Asp Gly Tyr Val Ser Thr Gly Gly
260 265 270

Ala Glu Thr Thr Lys Glu Phe Val Glu Lys Leu Asn Leu Lys Pro Gly
275 280 285

Gln Lys Val Leu Asp Val Gly Cys Gly Ile Gly Gly Gly Asp Phe Tyr
290 295 300

Met Ala Glu Lys Tyr Gly Thr His Val Val Gly Ile Asp Leu Ser Ile
305 310 315 320

Asn Met Ile Met Phe Ala Leu Glu Arg Ser Ile Gly Cys Lys Cys Leu
325 330 335

Val Glu Phe Glu Val Ala Asp Cys Thr Thr Lys Thr Tyr Pro Asp His
340 345 350

Met Phe Asp Val Ile Tyr Ser Arg Asp Thr Ile Leu His Ile Gln Asp
355 360 365

Lys Pro Ser Leu Phe Lys Ser Phe Phe Lys Trp Leu Lys Pro Gly Gly
370 375 380

Lys Val Leu Ile Ser Asp Tyr Cys Lys Ser Pro Gly Lys Pro Ser Glu
385 390 395 400

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

Glu Ala Tyr Gly Gln Met Leu Lys Asp Ala Gly Phe His Asn Val Ile
420 425 430

Ala Glu Asp Arg Thr Glu Gln Phe Leu Asn Val Leu Gln Arg Glu Ile
435 440 445

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

Glu Asp Tyr Asp Asp Ile Val Asn Gly Trp Asn Ala Lys Leu Lys Arg
465 470 475 480

Ser Ser Gly Gly Glu Gln Arg Trp Gly Leu Phe Ile Ala Thr Lys
485 490 495

<210> 81
<211> 1086
<212> DNA
<213> Zea Mays

<400> 81
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<210> 82
<211> 361
<212> PRT
<213> Zea Mays

<400> 82

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20 25 30

His Gln Ser Gly Asp Ser Lys Arg Lys Val Asn Pro Thr His Tyr Arg
35 40 45

Glu Pro Ser Phe Tyr Thr Lys Val Phe Lys Glu Cys His Thr Phe Asp

50

55

60

Gln Asp Gly Asn Ser Phe Glu Leu Ser Leu Val Thr Cys Lys Cys Ile
65 70 75 80

Gly Ala Tyr Val Lys Asn Lys Lys Asn Gln Asn Gln Ile Cys Trp Leu
85 90 95

Trp Gln Lys Val His Ser Thr Glu Asp Lys Gly Phe Gln Arg Phe Leu
100 105 110

Asp Asn Val Gln Tyr Lys Ala Ser Gly Ile Leu Arg Tyr Glu Arg Ile
115 120 125

Phe Gly Glu Gly Tyr Val Ser Thr Gly Gly Val Glu Thr Thr Lys Glu
130 135 140

Phe Val Asp Lys Leu Asp Leu Lys Pro Gly His Lys Val Leu Asp Val
145 150 155 160

Gly Cys Gly Ile Gly Gly Gly Asp Phe Tyr Met Ala Glu Lys Tyr Asp
165 170 175

Ala His Val Val Gly Ile Asp Leu Ser Ile Asn Met Val Ser Phe Ala
180 185 190

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

Asp Cys Thr Thr Lys Thr Tyr Pro Asp Asn Thr Phe Asp Val Ile Tyr
210 215 220

Ser Arg Asp Thr Ile Leu His Ile His Asp Lys Pro Ser Leu Phe Lys
225 230 235 240

Ser Phe Phe Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Ser Asp
245 250 255

Tyr Cys Arg Ser Pro Gly Lys Pro Ser Glu Glu Phe Ala Ala Tyr Ile
260 265 270

Lys Gln Arg Gly Tyr Asp Leu His Ala Val Glu Ala Tyr Gly Gln Met
275 280 285

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

Gln Phe Leu Gly Val Leu Asp Lys Glu Leu Ala Glu Phe Glu Lys Asn
305 310 315 320

Lys Asp Asp Phe Leu Ser Asp Phe Thr Gln Glu Asp Tyr Asp Asp Ile
325 330 335

Val Asn Gly Trp Lys Ala Lys Leu Gln Arg Ser Ser Ala Gly Glu Gln
340 345 350

Arg Trp Gly Leu Phe Ile Ala Thr Lys
355 360

<210> 83
<211> 56
<212> DNA
<213> Artificial sequence

<220>
<223> primer 1

<400> 83
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<210> 84
<211> 50
<212> DNA
<213> Artificial sequence

<220>
<223> primer 2

<400> 84
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<210> 85
<211> 2194
<212> DNA
<213> Oryza sativa

<400> 85
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tccgcaacaa ctttttaaca gcaggctttg cggccaggag agaggaggag aggcaaagaa	960
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<211> 110
<212> PRT
<213> Artificial sequence

<220>
<223> Methyltransferase type 11 domain

<400> 86

Pro Pro Tyr Glu Gly Lys Ser Val Leu Glu Leu Gly Ala Gly Ile Gly
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Arg Phe Thr Gly Glu Leu Ala Gln Lys Ala Gly Glu Val Ile Ala Leu
20 25 30

Asp Ile Ile Glu Ser Ala Ile Gln Lys Asn Glu Ser Val Asn Gly His
35 40 45

Tyr Lys Asn Ile Lys Phe Met Cys Ala Asp Val Thr Ser Pro Asp Leu
50 55 60

Lys Ile Lys Asp Gly Ser Ile Asp Leu Ile Phe Ser Asn Trp Leu Leu
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Met Tyr Leu Ser Asp Lys Glu Val Glu Leu Met Ala Glu Arg Met Ile
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Gly Trp Val Lys Pro Gly Gly Tyr Ile Phe Phe Arg Glu Ser
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<210> 87
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<212> PRT
<213> Artificial sequence

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<223> Methyltransferase type 11 domain

<400> 87

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

Ile Asp Leu Ser Val Asn Met Ile Ser Phe Ala Leu Glu Arg Ala Ile
35 40 45

Gly Leu Lys Cys Ser Val Glu Phe Glu Val Ala Asp Cys Thr Thr Lys
50 55 60

Thr Tyr Pro Asp Asn Ser Phe Asp Val Ile Tyr Ser Arg Asp Thr Ile
65 70 75 80

Leu His Ile Gln Asp Lys Pro Ala Leu Phe Arg Thr Phe Phe Lys Trp
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Leu Lys Pro Gly Gly Lys Val Leu Ile Thr Asp Tyr
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<210> 88

<211> 180

<212> PRT

<213> Artificial sequence

<220>

<223> ubiE/COQ5 methyltransferase domain

<400> 88

Glu Arg Val Phe Gly Glu Gly Tyr Val Ser Thr Gly Gly Phe Glu Thr
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Thr Lys Glu Phe Val Ala Lys Met Asp Leu Lys Pro Gly Gln Lys Val
20 25 30

Leu Asp Val Gly Cys Gly Ile Gly Gly Gly Asp Phe Tyr Met Ala Glu
35 40 45

Asn Phe Asp Val His Val Val Gly Ile Asp Leu Ser Val Asn Met Ile
50 55 60

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

Glu Val Ala Asp Cys Thr Thr Lys Thr Tyr Pro Asp Asn Ser Phe Asp
85 90 95

Val Ile Tyr Ser Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro Ala
100 105 110

Leu Phe Arg Thr Phe Phe Lys Trp Leu Lys Pro Gly Gly Lys Val Leu
115 120 125

Ile Thr Asp Tyr Cys Arg Ser Ala Glu Thr Pro Ser Pro Glu Phe Ala
130 135 140

Glu Tyr Ile Lys Gln Arg Gly Tyr Asp Leu His Asp Val Gln Ala Tyr
145 150 155 160

Gly Gln Met Leu Lys Asp Ala Gly Phe Asp Asp Val Ile Ala Glu Asp
165 170 175

Arg Thr Asp Gln
180

<210> 89
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> motif 5

<400> 89

Ile Phe Phe Arg Glu Ser Cys Phe His Gln Ser Gly Asp
1 5 10

<210> 90
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> motif 6

<400> 90

Glu Tyr Ile Lys Gln Arg
1 5

<210> 91
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> motif 7

<400> 91

Trp Gly Leu Phe Ile Ala
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<210> 92
<211> 1239
<212> DNA
<213> Arabidopsis thaliana

<400> 92

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<210> 93
<211> 412
<212> PRT
<213> Arabidopsis thaliana

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<400> 93
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Ser Leu Asp Pro Asn Gly Lys Gly Asn Lys Ile Gly Ser Thr Asn Leu
20           25           30

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Ala Gly Leu Asn Ser Ala Pro Asn Ser Gly Arg Met Lys Val Lys Pro
35           40           45

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Asn Ala Gln Ala Pro Pro Lys Ile Asn Gly Lys Lys Val Gly Leu Pro
50 55 60

Gly Ser Val Asp Ile Val Arg Thr Asp Thr Glu Thr Ser Ser His Pro
65 70 75 80

Ala Pro Arg Thr Phe Ile Asn Gln Leu Pro Asp Trp Ser Met Leu Leu
85 90 95

Ala Ala Ile Thr Thr Ile Phe Leu Ala Ala Glu Lys Gln Trp Met Met
100 105 110

Leu Asp Trp Lys Pro Arg Arg Ser Asp Met Leu Val Asp Pro Phe Gly
115 120 125

Ile Gly Arg Ile Val Gln Asp Gly Leu Val Phe Arg Gln Asn Phe Ser
130 135 140

Ile Arg Ser Tyr Glu Ile Gly Ala Asp Arg Ser Ala Ser Ile Glu Thr
145 150 155 160

Val Met Asn His Leu Gln Glu Thr Ala Leu Asn His Val Lys Thr Ala
165 170 175

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

Asn Leu Ile Trp Val Val Thr Arg Met Gln Val Val Val Asp Lys Tyr
195 200 205

Pro Thr Trp Gly Asp Val Val Glu Val Asp Thr Trp Val Ser Gln Ser
210 215 220

Gly Lys Asn Gly Met Arg Arg Asp Trp Leu Val Arg Asp Cys Asn Thr
225 230 235 240

Gly Glu Thr Leu Thr Arg Ala Ser Ser Val Trp Val Met Met Asn Lys
245 250 255

Leu Thr Arg Arg Leu Ser Lys Ile Pro Glu Glu Val Arg Gly Glu Ile
260 265 270

Glu Pro Tyr Phe Val Asn Ser Asp Pro Val Leu Ala Glu Asp Ser Arg
275 280 285

Lys Leu Thr Lys Ile Asp Asp Lys Thr Ala Asp Tyr Val Arg Ser Gly
 290 295 300

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

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

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

Gly Arg Asp Ser Val Leu Gln Ser Leu Thr Ala Val Thr Gly Cys Asp
 355 360 365

Ile Gly Asn Leu Ala Thr Ala Gly Asp Val Glu Cys Gln His Leu Leu
 370 375 380

Arg Leu Gln Asp Gly Ala Glu Val Val Arg Gly Arg Thr Glu Trp Ser
 385 390 395 400

Ser Lys Thr Pro Thr Thr Thr Trp Gly Thr Ala Pro
 405 410

<210> 94
 <211> 1245
 <212> DNA
 <213> Aquilegia formosa x Aquilegia pubescens

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 aaacctactt cttctggagg ttgaaagtt aaggctaata cacaagcaac tctctaaaatt 180
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<210> 95
 <211> 414
 <212> PRT
 <213> Aquilegia formosa x Aquilegia pubescens

<400> 95

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 20 25 30

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

Lys Val Lys Ala Asn Ala Gln Ala Thr Pro Lys Ile Asn Gly Thr Ser
 50 55 60

Ile His Tyr Pro Pro Ser Ser Glu Arg Leu Lys Asn Ser Asp Glu Thr
 65 70 75 80

Ser Ile Ala Pro Ala Arg Thr Phe Ile Asn Gln Leu Pro Asp Trp Ser
 85 90 95

Val Leu Leu Thr Ala Ile Thr Ala Met Phe Leu Ala Ala Glu Lys Gln
 100 105 110

Trp Thr Leu Leu Asp Trp Lys Pro Arg Arg Ser Asp Met Leu Val Asp
 115 120 125

Pro Phe Gly Leu Gly Lys Ile Val Gln Asp Gly Leu Val Phe Gln Gln
 130 135 140

Asn Phe Ser Ile Arg Ser Tyr Glu Ile Gly Val Asp Gly Thr Thr Ser
145 150 155 160

Ile Glu Ser Phe Met Asn His Leu Gln Glu Thr Ala Leu Asn His Ala
165 170 175

Lys Thr Val Gly Leu Leu Gly Asp Gly Phe Gly Ser Thr Glu Ala Met
180 185 190

Ser Lys Arg Asn Leu Ile Trp Val Val Ala Arg Met Gln Ile Leu Val
195 200 205

Asn Arg Tyr Pro Thr Trp Gly Asp Thr Val Gln Val Asp Thr Trp Val
210 215 220

Ala Ala Asn Gly Lys Asn Gly Met Arg Arg Asp Trp Leu Val Arg Asp
225 230 235 240

Gly Asn Ser Gly Glu Thr Leu Ala Arg Ala Ser Ser Lys Trp Val Met
245 250 255

Met Asn Thr Ser Thr Arg Lys Leu Ser Lys Met Pro Asp Asp Val Arg
260 265 270

Val Glu Ile Glu Pro Tyr Phe Met Asp Cys Ala Pro Ile Val Glu Glu
275 280 285

Asp Gly Arg Lys Leu Pro Lys Leu Asp Glu Ser Thr Ser Asp Tyr Val
290 295 300

Arg Asn Gly Leu Thr Pro Arg Trp Asn Asp Leu Asp Leu Asn Gln His
305 310 315 320

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

Met Leu Glu Asn His Glu Leu Ala Gly Ile Thr Leu Glu Tyr Arg Lys
340 345 350

Glu Cys Arg Lys Asp Asn Val Leu Gln Ser Leu Thr Ala Val Ser Lys
355 360 365

Asp Ala Lys Gly Trp Pro Glu Cys Val His Leu Leu Arg Leu Asp Ser
370 375 380

Gly Ala Glu Val Val Arg Gly Ser Thr Met Trp Arg Pro Lys Arg Ile
 385 390 395 400

Asn Asn Phe Gly Ser Val Gly Arg Ile Pro Thr Asp Gly Met
 405 410

<210> 96
 <211> 1242
 <212> DNA
 <213> *Arachis hypogaea*

<400> 96
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<210> 97
 <211> 413
 <212> PRT

<213> Arachis hypogaea

<400> 97

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Pro Asp Ala Gly Ala Asp Gly Asn Lys Leu Val Gly Gly Ser Val Lys
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Leu Gln Gly Leu Lys Ser Lys His Ala Ser Ser Gly Gly Leu Gln Val
35 40 45

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

Ser Leu Lys His Asp Asp Asp Leu Pro Ser Pro Pro Pro Arg Thr Phe
65 70 75 80

Ile Asn Gln Leu Pro Asp Trp Ser Met Leu Leu Ala Ala Ile Thr Thr
85 90 95

Ile Phe Leu Ala Ala Glu Lys Gln Trp Met Met Leu Asp Trp Lys Pro
100 105 110

Arg Arg Ser Asp Met Leu Ile Asp Pro Phe Gly Ile Gly Arg Ile Val
115 120 125

Gln Asp Gly Leu Val Phe Arg Gln Asn Phe Ser Ile Arg Ser Tyr Glu
130 135 140

Ile Gly Ala Asp Arg Thr Ala Ser Ile Glu Thr Val Met Asn His Leu
145 150 155 160

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

Gly Phe Gly Ser Thr Pro Glu Met Cys Lys Lys Asn Leu Ile Trp Val
180 185 190

Val Thr Arg Met Gln Val Val Val Asp Arg Tyr Pro Thr Trp Gly Asp
195 200 205

Val Val Gln Val Asp Thr Trp Val Ser Ala Ser Gly Lys Asn Gly Met
210 215 220

Arg Arg Asp Trp Leu Leu Arg Asp Cys Lys Thr Gly Glu Val Leu Thr

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Arg Ala Ser Ser Val Trp Val Met Met Asn Lys Leu Thr Arg Arg Leu						
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Ser Lys Ile Pro Glu Glu Val Arg Ala Glu Ile Ala Ser Tyr Phe Val						
	260		265		270	
Asn Ser Ala Pro Ile Leu Glu Glu Asp Asn Arg Lys Leu Ser Lys Leu						
	275		280		285	
Asp Asp Asn Thr Ala Asp Tyr Ile Arg Thr Gly Leu Ser Pro Arg Trp						
	290		295		300	
Asn Asp Leu Asp Val Asn Gln His Val Asn Asn Val Lys Tyr Ile Gly						
305		310		315		320
Trp Ile Leu Glu Ser Ala Pro Gln Pro Ile Leu Glu Ser His Glu Leu						
	325		330		335	
Ser Ala Met Thr Leu Glu Tyr Arg Arg Glu Cys Gly Arg Asp Ser Val						
	340		345		350	
Leu Gln Ser Leu Thr Ala Val Ser Ala Ala Asp Val Gly Asn Leu Ala						
	355		360		365	
His Arg Gly Gln Leu Glu Cys Lys His Leu Leu Arg Leu Glu Asp Gly						
	370		375		380	
Ala Glu Ile Val Arg Gly Arg Thr Glu Trp Arg Pro Lys Pro Val Ser						
385		390		395		400
Asn Phe Asp Ile Val Asn Gln Val Pro Ala Glu Ser Ile						
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<210> 98
 <211> 1236
 <212> DNA
 <213> Brassica juncea

<400> 98	
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aactctggcg gcaggatgaa ggttaaacca aacgcccagg ctccrcccaa gatcaacggs	180
aagaaagttg gtctccctgg ctcggtagag atcgagacct cacaacaaca acaaccgcga	240

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<210> 99
<211> 411
<212> PRT
<213> Brassica juncea

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<222> (22)..(22)
<223> Unknown amino acid

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<220>
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<222> (171)..(171)
<223> Unknown amino acid

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<220>
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<222> (192)..(192)
<223> Unknown amino acid

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<400> 99

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20 25 30

Phe Ala Gly Leu Gly Pro Thr Pro Asn Ser Gly Gly Arg Met Lys Val
35 40 45

Lys Pro Asn Ala Gln Ala Pro Pro Lys Ile Asn Gly Lys Lys Val Gly
50 55 60

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

Pro Arg Thr Phe Ile Asn Gln Leu Pro Asp Trp Ser Met Leu Leu Ala
85 90 95

Ala Ile Thr Thr Val Phe Leu Ala Ala Glu Lys Gln Trp Met Met Leu
100 105 110

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

Gly Arg Ile Val Gln Asp Gly Leu Val Phe Arg Gln Asn Phe Ser Ile
130 135 140

Arg Ser Tyr Glu Ile Gly Ala Asp Arg Ser Ala Ser Ile Glu Thr Val
145 150 155 160

Met Asn His Leu Gln Glu Thr Ala Leu Asn Xaa Val Lys Thr Ala Gly
165 170 175

Leu Leu Gly Asp Gly Phe Gly Ser Thr Pro Glu Met Val Lys Lys Xaa
180 185 190

Leu Ile Trp Val Val Thr Arg Met Gln Val Val Val Asp Thr Tyr Pro
195 200 205

Thr Trp Gly Asp Val Val Glu Val Asp Thr Trp Val Ser Lys Ser Gly
210 215 220

Lys Asn Gly Met Arg Arg Asp Trp Leu Val Arg Asp Gly Asn Thr Gly
225 230 235 240

Gln Ile Leu Thr Arg Ala Ser Ser Val Trp Val Met Met Asn Lys Leu
245 250 255

Thr Arg Arg Leu Ser Lys Ile Pro Glu Glu Val Arg Gly Glu Ile Glu
260 265 270

Pro Tyr Phe Val Asp Phe Asp Pro Val Leu Ala Glu Asp Ser Arg Lys
275 280 285

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

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

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

Ser Gln Lys Leu Lys Ser Met Thr Leu Glu Tyr Arg Arg Glu Cys Gly
340 345 350

Arg Asp Ser Val Leu Gln Ser Leu Thr Ala Val Ser Gly Cys Asp Ile
355 360 365

Gly Asn Leu Gly Thr Ala Gly Glu Val Glu Cys Gln His Leu Leu Arg
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Leu Gln Asp Gly Ala Glu Val Val Arg Gly Arg Thr Glu Trp Ser Ser
385 390 395 400

Lys Thr Pro Thr Thr Thr Trp Asp Ile Thr Pro
405 410

<210> 100
<211> 1287
<212> DNA
<213> Brachypodium sylvaticum

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cttgcaactg tcacgaccat cttcctggcc gcagagaagc agtggacaat gcttgattgg 360
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gcttctatag agacattaat gaatcattta caggaaacag ctcttaacca tgtcaagact      540
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cgtgactaca attcggggca aacgatcttg agagctacaa gtgtttgggt tacgatgaat      780
aagaacacta gaaaactttc aaaaatgcct gatgaagtta gggctgaaat aggcccgac      840
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aggaaaggtg gtgacctgc taccaaacag ttcataagga aggggcttac cccaaaatgg      960
ggtgaccttg atgtcaacca acatgtgaac aatgtgaagt atattgggtg gattcttgag     1020
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aaggagtgtg gccgtgacag cgtgctgcag tctcttacca atgtcatagg tgagtgcacc     1140
gacggcagcc cagagtctgc tatccagtgc agccatctgc tccagctgga gtctggaact     1200
gacatcgtga aggctcacac aaagtggcga ccgaagagag cgcagggcga aggaaacaca     1260
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```

```

<210> 101
<211> 428
<212> PRT
<213> Brachypodium sylvaticum

```

```
<400> 101
```

```

Met Ala Gly Ser Leu Ala Ala Ser Ala Phe Phe Pro Ser Pro Gly Ser
1           5           10           15

```

```

Ser Pro Ala Ala Leu Ala Lys Ser Ser Lys Asn Thr Ser Gly Glu Leu
          20           25           30

```

```

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

```

```

Pro Ala Ser Met Gln Val Lys Thr Lys Ala Gln Ala Leu Pro Lys Val
          50           55           60

```

```

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

```

```

Thr Val Pro Tyr Ser Ser Ser Lys Thr Phe Tyr Asn Gln Leu Pro Asp
          85           90           95

```

Trp Ser Met Leu Leu Ala Ala Val Thr Thr Ile Phe Leu Ala Ala Glu
100 105 110

Lys Gln Trp Thr Met Leu Asp Trp Lys Pro Lys Arg Pro Asp Met Leu
115 120 125

Val Asp Thr Phe Gly Phe Gly Arg Ile Ile Gln Asp Gly Met Val Phe
130 135 140

Arg Gln Asn Phe Leu Ile Arg Ser Tyr Glu Ile Gly Ala Asp Arg Thr
145 150 155 160

Ala Ser Ile Glu Thr Leu Met Asn His Leu Gln Glu Thr Ala Leu Asn
165 170 175

His Val Lys Thr Ala Gly Leu Leu Gly Asp Gly Phe Gly Ala Thr Gln
180 185 190

Glu Met Ser Lys Arg Asn Leu Ile Trp Val Val Ser Lys Ile Gln Leu
195 200 205

Leu Val Glu Arg Tyr Pro Ser Trp Glu Asp Met Val Gln Val Asp Thr
210 215 220

Trp Val Ala Ser Ser Gly Lys Asn Gly Met Arg Arg Asp Trp His Ile
225 230 235 240

Arg Asp Tyr Asn Ser Gly Gln Thr Ile Leu Arg Ala Thr Ser Val Trp
245 250 255

Val Thr Met Asn Lys Asn Thr Arg Lys Leu Ser Lys Met Pro Asp Glu
260 265 270

Val Arg Ala Glu Ile Gly Pro His Phe Asn Asn Asp Arg Ser Ala Leu
275 280 285

Thr Glu Glu His Ser Asp Lys Leu Ala Lys Pro Gly Arg Lys Gly Gly
290 295 300

Asp Pro Ala Thr Lys Gln Phe Ile Arg Lys Gly Leu Thr Pro Lys Trp
305 310 315 320

Gly Asp Leu Asp Val Asn Gln His Val Asn Asn Val Lys Tyr Ile Gly
325 330 335

Trp Ile Leu Glu Ser Ala Pro Ile Ser Ile Leu Glu Lys His Glu Leu

340

345

350

Ala Ser Met Thr Leu Glu Tyr Arg Lys Glu Cys Gly Arg Asp Ser Val
 355 360 365

Leu Gln Ser Leu Thr Asn Val Ile Gly Glu Cys Thr Asp Gly Ser Pro
 370 375 380

Glu Ser Ala Ile Gln Cys Ser His Leu Leu Gln Leu Glu Ser Gly Thr
 385 390 395 400

Asp Ile Val Lys Ala His Thr Lys Trp Arg Pro Lys Arg Ala Gln Gly
 405 410 415

Glu Gly Asn Thr Gly Leu Phe Pro Ala Ser Ser Ala
 420 425

<210> 102
 <211> 1257
 <212> DNA
 <213> Citrus sinensis

<400> 102
 atggttgcta ctgccgcagc ttctgcgttc ttcccagttt cctcaccatc tggggattct 60
 gttgcaaaga ccaaaaatct cggatctgct aatctgggag gtattaagtc aaaatcctct 120
 tctgggagtt tgcaggttaa ggctaattgc caagcacctt ccaagataaa tggtaacttca 180
 gttggtttga caacaccagc agaaagtttg aagaatgggtg atatctccac gtcacacct 240
 cctcctagga cttttattaa ccagttacct gactggagta tgcttcttgc tgctataaca 300
 acaatcttct tggcagcaga gaagcagtggt atgatgcttg attggaaacc aaggcgatct 360
 gacatgcttg tggaccatt tgggattggg aaaatagttc aggatgggtt cattttccgg 420
 caaaatttct caattagatc atatgagata ggtgctgatg gtactgcatc tatagagaca 480
 ttaatgaatc atttacagga aacagcgctt aatcatgtta tgactgctgg tcttctagat 540
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gtgaagtaca ttggctggat cctagagagt gtcctcagc agatcttgga gagtcacag 1020
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<210> 103
<211> 418
<212> PRT
<213> Citrus sinensis

<400> 103

Met Val Ala Thr Ala Ala Ala Ser Ala Phe Phe Pro Val Ser Ser Pro
1 5 10 15

Ser Gly Asp Ser Val Ala Lys Thr Lys Asn Leu Gly Ser Ala Asn Leu
20 25 30

Gly Gly Ile Lys Ser Lys Ser Ser Ser Gly Ser Leu Gln Val Lys Ala
35 40 45

Asn Ala Gln Ala Pro Ser Lys Ile Asn Gly Thr Ser Val Gly Leu Thr
50 55 60

Thr Pro Ala Glu Ser Leu Lys Asn Gly Asp Ile Ser Thr Ser Ser Pro
65 70 75 80

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

Ala Ala Ile Thr Thr Ile Phe Leu Ala Ala Glu Lys Gln Trp Met Met
100 105 110

Leu Asp Trp Lys Pro Arg Arg Ser Asp Met Leu Val Asp Pro Phe Gly
115 120 125

Ile Gly Lys Ile Val Gln Asp Gly Phe Ile Phe Arg Gln Asn Phe Ser
130 135 140

Ile Arg Ser Tyr Glu Ile Gly Ala Asp Gly Thr Ala Ser Ile Glu Thr
145 150 155 160

Leu Met Asn His Leu Gln Glu Thr Ala Leu Asn His Val Met Thr Ala
165 170 175

Gly Leu Leu Asp Ala Gly Phe Gly Ala Thr Pro Ala Met Ala Lys Lys
180 185 190

Asn Leu Ile Trp Val Val Thr Arg Met Gln Val Val Val Asp Arg Tyr
195 200 205

Pro Thr Trp Asn Asp Val Val Asn Val Glu Thr Trp Val Ser Ala Ser
210 215 220

Gly Lys Asn Gly Met Arg Arg Asp Trp Leu Ile Arg Asn Ala Lys Thr
225 230 235 240

Gly Glu Thr Leu Thr Arg Ala Thr Ser Leu Trp Val Met Met Asn Lys
245 250 255

Leu Thr Arg Arg Leu Ser Lys Met Pro Asp Glu Val Arg Gln Glu Ile
260 265 270

Glu Pro Tyr Phe Leu Asn Ser Asp Pro Val Val Asp Glu Asp Ser Arg
275 280 285

Lys Leu Pro Lys Leu Gly Asp Ser Thr Ala Asp Tyr Val Arg Arg Gly
290 295 300

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

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

Glu Ser His Gln Leu Ala Ser Val Thr Leu Glu Tyr Arg Arg Glu Cys
340 345 350

Gly Arg Asp Ser Val Leu Gln Ser Leu Thr Ala Val Ser Asp Lys Asp
355 360 365

Ile Gly Asn Leu Val Asn Leu Gly Ser Val Glu Cys Gln His Leu Leu
370 375 380

Arg Leu Glu Glu Gly Ala Glu Val Leu Arg Ala Arg Thr Glu Trp Arg
385 390 395 400

Pro Lys Asp Ala His Asn Phe Gly Asn Val Gly Pro Ile Pro Ala Glu
405 410 415

Ser Thr

<210> 104
<211> 1254
<212> DNA
<213> *Elaeis guineensis*

<400> 104
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tcagcaaaag cttcgaagac cattggtgaa ggctccgaga atttgaatgt tcgggggtatc 120
atagccaaac ccacttcttc ttcggcggct aagcagggtta aggtgatggc ccaagccgtc 180
ccaagatca atggcgcgaa ggttggcctg aaagctgaat cccaaaaggc cgaggaagat 240
gctgccccctt cctcagcccc gaggacattc tataatcaac tacctgactg gagcgtgctc 300
cttgccgccc taacaacgat ctttttggct gccgagaagc agtggaccct tcttgattgg 360
aagccacggc gtcccgacat gcttactggg gcatttagcc ttgggaagat tgtgcaggat 420
ggactagttt tcaggcagaa cttttccatc aggtcatatg agattggggc tgatcggacg 480
gcttctatag aaacgttaat gaaccattta caggaaacag cacttaatca tgtgaggaat 540
gctgggcttc tgggcgatgg ttttggtgcc acaccagaga tgagtaaaag aaatttgatt 600
tgggttgcca ctaaaatgca ggtcctgatt gagcactatc cttcctgggg ggatgttggt 660
gaagtagata catgggttgg tgcactcggg aaaaatggga tgcgtcgtga ttggcatggt 720
cgtgactacc gaacaggcca aactatattg agagccacca gtatctgggt gatgatggat 780
aaacacacta ggaagtgtgc taaaatgcc gaagaagtca gagcagagat agggccttac 840
tttatggaac atgctgctat tgtggacgag gacagcagaa agcttccaaa gcttgatgat 900
gatactgcag attatattaa atggggcctg actcctcgat ggagtgattt agatgtgaat 960
cagcatgtga acaatgtcaa atatataggc tggattcttg agagcgctcc aatatcaatc 1020
ctggagaatc acgagctggc gagtatgact ctggaatata ggagggagtg tgggagggac 1080
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agcatcgagt gccagcatct gctgcagctg gaatgcgggg ccgagattgt taggggacgg 1200
acacagtgga ggcccaggcg tgcctccggt cccacttcag ctggaagtgc ttga 1254

<210> 105
<211> 417
<212> PRT
<213> *Elaeis guineensis*

<400> 105

Met Val Ala Ser Ile Val Ala Trp Ala Phe Phe Pro Thr Pro Ser Phe

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

Val Met Met Asp Lys His Thr Arg Lys Leu Ser Lys Met Pro Glu Glu
260 265 270

Val Arg Ala Glu Ile Gly Pro Tyr Phe Met Glu His Ala Ala Ile Val
275 280 285

Asp Glu Asp Ser Arg Lys Leu Pro Lys Leu Asp Asp Asp Thr Ala Asp
290 295 300

Tyr Ile Lys Trp Gly Leu Thr Pro Arg Trp Ser Asp Leu Asp Val Asn
305 310 315 320

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

Pro Ile Ser Ile Leu Glu Asn His Glu Leu Ala Ser Met Thr Leu Glu
340 345 350

Tyr Arg Arg Glu Cys Gly Arg Asp Ser Val Leu Gln Ser Leu Thr Ala
355 360 365

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

Gln His Leu Leu Gln Leu Glu Cys Gly Ala Glu Ile Val Arg Gly Arg
385 390 395 400

Thr Gln Trp Arg Pro Arg Arg Ala Ser Gly Pro Thr Ser Ala Gly Ser
405 410 415

Ala

<210> 106

<211> 1221

<212> DNA

<213> Garcinia mangostana

<400> 106

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aaatcgggca atccccgaaa agggtcggtg agttttgggt caatgaagtc gaaatccgcg 120

gcttcctcga ggggtttaca agtgaaggcc aatgcacagg caccactaa gatcaatgga 180

tccacggatg atgctcaatt gcctgccccg aggactttta ttaaccagtt gcctgattgg 240

agcatgcttc ttgctgctat tactaccgtg tttttggcag ccgagaagca gtggatgatg 300

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ttggattgga agcctaggag gcccgacatg cttattgaca cgtttggttt ggggaggatt      360
gtgcaggatg gtcttggttt tcgacagaat ttctcgatta ggtcctatga aattggtgct      420
gatcgtactg cgtctataga gacggttatg aatcatctgc aagaaactgc cctcaatcat      480
gttaagactg caggacttct gggatgatgga ttcggttcaa caccagagat gtctaaaagg      540
aatctcatat gggttgttac taagatgcag gtcgaagtcg atcggtatcc tacatggggg      600
gacgttggtc aggtagatac ttgggtgagt gcatcaggaa agaattggaat gcgtcgagat      660
tggcttcttc gtgatggtaa tactggggag acattaacca gagcttcaag tgtgtgggtg      720
atgatgaata aactgacaag gagattgtct aaaattcccg aagaagttcg ggaggaaata      780
ggatcttact ttgtgaattc tgatcctgtt gtggaggagg atggtagaaa ggtgacaaaa      840
cttgatgaca aactgcaga ttttgttcgc aaaggggttaa ctctaaatg gaatgacttg      900
gacatcaatc agcatgtgaa taatgtgaag tatattggct ggatccttga gacgctcca      960
cagccaatcc tggaaacccg tgagctctca gcggtgactt tggagtatag gagggagtgt     1020
ggaagggaca gtgtgctgcg gtctctgacc gccgtttctg gcggtggcgt tggtgattta     1080
ggacacgctg gtaacgtcga gtgccagcac gtgcttcgct tggaggatgg agctgagatt     1140
gttcgtggaa ggaccgagtg gaggcccaaa tacattaaca acttcagtat catgggccag     1200
attccgacag atgcttctta g                                     1221

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```

<210> 107
<211> 406
<212> PRT
<213> Garcinia mangostana

```

```
<400> 107
```

```

Met Val Ala Thr Ala Ala Thr Ser Ser Phe Phe Pro Leu Thr Ser Pro
1              5              10              15

```

```

Ser Gly Asp Ala Lys Ser Gly Asn Pro Gly Lys Gly Ser Val Ser Phe
                20              25              30

```

```

Gly Ser Met Lys Ser Lys Ser Ala Ala Ser Ser Arg Gly Leu Gln Val
          35              40              45

```

```

Lys Ala Asn Ala Gln Ala Pro Thr Lys Ile Asn Gly Ser Thr Asp Asp
50              55              60

```

```

Ala Gln Leu Pro Ala Pro Arg Thr Phe Ile Asn Gln Leu Pro Asp Trp
65              70              75              80

```

Ser Met Leu Leu Ala Ala Ile Thr Thr Val Phe Leu Ala Ala Glu Lys
85 90 95

Gln Trp Met Met Leu Asp Trp Lys Pro Arg Arg Pro Asp Met Leu Ile
100 105 110

Asp Thr Phe Gly Leu Gly Arg Ile Val Gln Asp Gly Leu Val Phe Arg
115 120 125

Gln Asn Phe Ser Ile Arg Ser Tyr Glu Ile Gly Ala Asp Arg Thr Ala
130 135 140

Ser Ile Glu Thr Val Met Asn His Leu Gln Glu Thr Ala Leu Asn His
145 150 155 160

Val Lys Thr Ala Gly Leu Leu Gly Asp Gly Phe Gly Ser Thr Pro Glu
165 170 175

Met Ser Lys Arg Asn Leu Ile Trp Val Val Thr Lys Met Gln Val Glu
180 185 190

Val Asp Arg Tyr Pro Thr Trp Gly Asp Val Val Gln Val Asp Thr Trp
195 200 205

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

Asp Gly Asn Thr Gly Glu Thr Leu Thr Arg Ala Ser Ser Val Trp Val
225 230 235 240

Met Met Asn Lys Leu Thr Arg Arg Leu Ser Lys Ile Pro Glu Glu Val
245 250 255

Arg Glu Glu Ile Gly Ser Tyr Phe Val Asn Ser Asp Pro Val Val Glu
260 265 270

Glu Asp Gly Arg Lys Val Thr Lys Leu Asp Asp Asn Thr Ala Asp Phe
275 280 285

Val Arg Lys Gly Leu Thr Pro Lys Trp Asn Asp Leu Asp Ile Asn Gln
290 295 300

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

Gln Pro Ile Leu Glu Thr Arg Glu Leu Ser Ala Val Thr Leu Glu Tyr

325

330

335

Arg Arg Glu Cys Gly Arg Asp Ser Val Leu Arg Ser Leu Thr Ala Val
 340 345 350

Ser Gly Gly Gly Val Gly Asp Leu Gly His Ala Gly Asn Val Glu Cys
 355 360 365

Gln His Val Leu Arg Leu Glu Asp Gly Ala Glu Ile Val Arg Gly Arg
 370 375 380

Thr Glu Trp Arg Pro Lys Tyr Ile Asn Asn Phe Ser Ile Met Gly Gln
 385 390 395 400

Ile Pro Thr Asp Ala Ser
 405

<210> 108
 <211> 1251
 <212> DNA
 <213> Glycine max

<400> 108
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 ggtggagcag gcagcaaact tgggtggtggg cctgcaaacc ttggaggact aaaatccaaa 120
 tctgcgtctt ctggtggctt gaaggcaaag gcgcaagccc cttcgaaaat taatggaacc 180
 acagttgtta catctaaaga aagcttcaag catgatgatg atctaccttc gcctcccccc 240
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 aaaattccag aagaagtcag acaggagata ggatcttatt ttgtggattc tgatccaatt 840
 ctggaagagg ataacagaaa actgactaaa cttgacgaca acacagcgga ttatatctgt 900
 accggtttta gtcctaggtg gagtgatcta gatatcaatc agcatgtcaa caatgtgaag 960

tacattggct ggattctgga gagtgctcca cagccaatct tggagagtca tgagctttct 1020
 tccatgactt tagagtatag gagagagtgt ggtagggaca gtgtgctgga ttccctgact 1080
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 cctgtgaaca actttggtgt tgtgaaccag gttccagcag aaagcaccta a 1251

<210> 109
 <211> 416
 <212> PRT
 <213> Glycine max

<400> 109

Met Val Ala Thr Ala Ala Thr Ser Ser Phe Phe Pro Val Thr Ser Pro
 1 5 10 15

Ser Pro Asp Ser Gly Gly Ala Gly Ser Lys Leu Gly Gly Gly Pro Ala
 20 25 30

Asn Leu Gly Gly Leu Lys Ser Lys Ser Ala Ser Ser Gly Gly Leu Lys
 35 40 45

Ala Lys Ala Gln Ala Pro Ser Lys Ile Asn Gly Thr Thr Val Val Thr
 50 55 60

Ser Lys Glu Ser Phe Lys His Asp Asp Asp Leu Pro Ser Pro Pro Pro
 65 70 75 80

Arg Thr Phe Ile Asn Gln Leu Pro Asp Trp Ser Met Leu Leu Ala Ala
 85 90 95

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

Trp Lys Pro Arg Arg Pro Asp Met Leu Ile Asp Pro Phe Gly Ile Gly
 115 120 125

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

Ser Tyr Glu Ile Gly Ala Asp Arg Thr Ala Ser Ile Glu Thr Val Met
 145 150 155 160

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

Leu Gly Asp Gly Phe Gly Ser Thr Pro Glu Met Cys Lys Lys Asn Leu
180 185 190

Ile Trp Val Val Thr Arg Met Gln Val Val Val Glu Arg Tyr Pro Thr
195 200 205

Trp Gly Asp Ile Val Gln Val Asp Thr Trp Val Ser Gly Ser Gly Lys
210 215 220

Asn Gly Met Arg Arg Asp Trp Leu Leu Arg Asp Cys Lys Thr Gly Glu
225 230 235 240

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

Arg Arg Leu Ser Lys Ile Pro Glu Glu Val Arg Gln Glu Ile Gly Ser
260 265 270

Tyr Phe Val Asp Ser Asp Pro Ile Leu Glu Glu Asp Asn Arg Lys Leu
275 280 285

Thr Lys Leu Asp Asp Asn Thr Ala Asp Tyr Ile Arg Thr Gly Leu Ser
290 295 300

Pro Arg Trp Ser Asp Leu Asp Ile Asn Gln His Val Asn Asn Val Lys
305 310 315 320

Tyr Ile Gly Trp Ile Leu Glu Ser Ala Pro Gln Pro Ile Leu Glu Ser
325 330 335

His Glu Leu Ser Ser Met Thr Leu Glu Tyr Arg Arg Glu Cys Gly Arg
340 345 350

Asp Ser Val Leu Asp Ser Leu Thr Ala Val Ser Gly Ala Asp Met Gly
355 360 365

Asn Leu Ala His Ser Gly His Val Glu Cys Lys His Leu Leu Arg Leu
370 375 380

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

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

<210> 110
 <211> 1242
 <212> DNA
 <213> *Gossypium hirsutum*

<400> 110
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 gactcgaaaa acaagaagct cggaagcatc aagtcgaagc catcggtttc ttctggaagt 120
 ttgcaagtca aggcaaatgc tcaagcacct ccgaaaataa acggcactgt ggcgtcgacg 180
 actcccgtgg aagggttcaa gaacgatgac ggtgcaagtt cccctcctcc taggacgttt 240
 atcaaccagt tacctgattg gagcatgctt cttgctgcta tcacaacat tttcttggt 300
 gctgagaagc agtggatgat gcttgattgg aagccgaggc ggctgacat ggtcattgat 360
 ccgtttgcca tagggaagat tgttcaggat ggtcttggtt tcagtcagaa cttctcgatt 420
 agatcatatg agataggcgc tgatcaaaca gcatccatag agacactaat gaatcattta 480
 caggaaacag ctataaatca ttgtcgaagt gctggactgc ttggagaagg ttttggtgca 540
 acacctgaga tgtgcaagaa gaacctaata tgggttggtc cacggatgca agttgtggtt 600
 gatcgctatc ctacttgggg tgatgttggt caagtcgaca cttgggtcag tgcacgggg 660
 aagaatggca tgcgaagaga ttggcttggt agcaatagtg aaactggtga aattttaaca 720
 cgagccacaa gtgtatgggt gatgatgaat aaactgacta gaagggtatc taaaatccca 780
 gaagagggtc gaggggaaat agaacctttt tttatgaatt cagatcctgt tctggctgag 840
 gatagccaga aactagttaa actcgatgac agcacagctg aacacgtgtg caaagggtta 900
 actcctaaat ggagcgactt ggatgtcaac cagcatgtca ataatgtgaa gtacattggc 960
 tggatccttg agagtgtcc attaccaatc ttggagagtc acgagctttc cgccttgact 1020
 ctggaatata ggaggagtg cgggagggac agcgtgctgc agtcactgac cactgtgtct 1080
 gattccaata cggaaaatgc agtaaatgtt ggtgaattta attgccaaca tttgctccga 1140
 ctcgacgatg gagctgagat tgtgagaggc aggacccgat ggaggcctaa acatgccaaa 1200
 agttccgcta acatggatca aattaccgca aaaagggcat ag 1242

<210> 111
 <211> 413
 <212> PRT
 <213> *Gossypium hirsutum*

<400> 111
 Met Val Ala Thr Ala Val Thr Ser Ala Phe Phe Pro Val Thr Ser Ser
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 Pro Asp Ser Ser Asp Ser Lys Asn Lys Lys Leu Gly Ser Ile Lys Ser

20

25

30

Lys Pro Ser Val Ser Ser Gly Ser Leu Gln Val Lys Ala Asn Ala Gln
 35 40 45

Ala Pro Pro Lys Ile Asn Gly Thr Val Ala Ser Thr Thr Pro Val Glu
 50 55 60

Gly Ser Lys Asn Asp Asp Gly Ala Ser Ser Pro Pro Pro Arg Thr Phe
 65 70 75 80

Ile Asn Gln Leu Pro Asp Trp Ser Met Leu Leu Ala Ala Ile Thr Thr
 85 90 95

Ile Phe Leu Ala Ala Glu Lys Gln Trp Met Met Leu Asp Trp Lys Pro
 100 105 110

Arg Arg Pro Asp Met Val Ile Asp Pro Phe Gly Ile Gly Lys Ile Val
 115 120 125

Gln Asp Gly Leu Val Phe Ser Gln Asn Phe Ser Ile Arg Ser Tyr Glu
 130 135 140

Ile Gly Ala Asp Gln Thr Ala Ser Ile Glu Thr Leu Met Asn His Leu
 145 150 155 160

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

Gly Phe Gly Ala Thr Pro Glu Met Cys Lys Lys Asn Leu Ile Trp Val
 180 185 190

Val Thr Arg Met Gln Val Val Val Asp Arg Tyr Pro Thr Trp Gly Asp
 195 200 205

Val Val Gln Val Asp Thr Trp Val Ser Ala Ser Gly Lys Asn Gly Met
 210 215 220

Arg Arg Asp Trp Leu Val Ser Asn Ser Glu Thr Gly Glu Ile Leu Thr
 225 230 235 240

Arg Ala Thr Ser Val Trp Val Met Met Asn Lys Leu Thr Arg Arg Leu
 245 250 255

Ser Lys Ile Pro Glu Glu Val Arg Gly Glu Ile Glu Pro Phe Phe Met
 260 265 270

Asn Ser Asp Pro Val Leu Ala Glu Asp Ser Gln Lys Leu Val Lys Leu
275 280 285

Asp Asp Ser Thr Ala Glu His Val Cys Lys Gly Leu Thr Pro Lys Trp
290 295 300

Ser Asp Leu Asp Val Asn Gln His Val Asn Asn Val Lys Tyr Ile Gly
305 310 315 320

Trp Ile Leu Glu Ser Ala Pro Leu Pro Ile Leu Glu Ser His Glu Leu
325 330 335

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

Leu Gln Ser Leu Thr Thr Val Ser Asp Ser Asn Thr Glu Asn Ala Val
355 360 365

Asn Val Gly Glu Phe Asn Cys Gln His Leu Leu Arg Leu Asp Asp Gly
370 375 380

Ala Glu Ile Val Arg Gly Arg Thr Arg Trp Arg Pro Lys His Ala Lys
385 390 395 400

Ser Ser Ala Asn Met Asp Gln Ile Thr Ala Lys Arg Ala
405 410

<210> 112
<211> 1293
<212> DNA
<213> Helianthus annuus

<400> 112
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ggagccaaga catctgataa gcttggaggt gaaccaggta gtgttgctgt gcgcggaatc 120
aagacaaaat ctgttaattc cgggtggtatg aaagttaagg ctaacgcaca ggctcctact 180
gaggtgaatg ggagtagatc acgtatcacg catggcttca aaaccgatga ttattctaca 240
tcacctgccc cgagaacctt tatcaaccaa ttgcccgatt ggagcatgct tcttgctgca 300
atcacaacaa tcttcttggc tgcagagaag caatggatga tgctggaatg gaagacccaaa 360
cgccccgata tgattgctga tatggatcct ttcggtttag ggaggattgt tcaagatggc 420
cttgattcc gtcaaaactt ctctattaga tcatatgaaa taggggctga tcgaactgca 480
tcgatagaaa ccctaataa tcatttataa gaaacggccc ttaatcatgt aaagtctgcg 540

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ggctcttctgg gcgatggatt cggttcaaca ccagaaatgt gcaagaagaa tctattttgg      600
gtggtgacaa agatgcaggt gatagttgac cgttatccaa cttgggggtga tgttgttcaa      660
gtagatactt gggtagcccc aaatgggaaa aatgggatgc gccgtgattg gctcgttcgc      720
gattataaaa caggcgagat ttttaacaaga gcctcaagta actgggttat gatgaataaa      780
gagacaagga ggttatcgaa aatcccagat gaagttcgag gtgaaataga gcattacttt      840
gtagatgcac ctccggttgt ggaggatgat tctagaaaat tatctaaact tgacgaaagc      900
actgctgact atgttcgcga cggtttgatt ccaagatgga gtgatttgga tgtcaaccag      960
catgttaaca atgtgaagta tattggctgg atccttgaga gtgctccaca agttgtggag     1020
aagtacgagc ttgctcgcat tactctcgag taccgtagag aatgtaggaa ggatagtgtg     1080
gtgaaatcac tgacctcggc attaggtggc ggcgacgacg acaatgggtg aataggcgat     1140
tctggccgtg ttgattgcca acatgtgctc ttgtttgcgg gtggyggaga tgggtactcct     1200
ggtggcgaga ttgtgaaggg aaggaccagc tggcgccga aatatgagaa acaagatggg     1260
agtgttgatc acttctctgc tggaaatgtt taa                                     1293

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```

<210> 113
<211> 430
<212> PRT
<213> Helianthus annuus

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<400> 113
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Met Val Ala Met Ser Ala Thr Ala Ser Leu Phe Pro Val Ser Ser Pro
1           5           10           15

```

```

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

```

```

Gly Ser Val Ala Val Arg Gly Ile Lys Thr Lys Ser Val Asn Ser Gly
          35           40           45

```

```

Gly Met Lys Val Lys Ala Asn Ala Gln Ala Pro Thr Glu Val Asn Gly
          50           55           60

```

```

Ser Arg Ser Arg Ile Thr His Gly Phe Lys Thr Asp Asp Tyr Ser Thr
65           70           75           80

```

```

Ser Pro Ala Pro Arg Thr Phe Ile Asn Gln Leu Pro Asp Trp Ser Met
          85           90           95

```

```

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

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Met Met Leu Glu Trp Lys Thr Lys Arg Pro Asp Met Ile Ala Asp Met
115 120 125

Asp Pro Phe Gly Leu Gly Arg Ile Val Gln Asp Gly Leu Val Phe Arg
130 135 140

Gln Asn Phe Ser Ile Arg Ser Tyr Glu Ile Gly Ala Asp Arg Thr Ala
145 150 155 160

Ser Ile Glu Thr Leu Met Asn His Leu Gln Glu Thr Ala Leu Asn His
165 170 175

Val Lys Ser Ala Gly Leu Leu Gly Asp Gly Phe Gly Ser Thr Pro Glu
180 185 190

Met Cys Lys Lys Asn Leu Phe Trp Val Val Thr Lys Met Gln Val Ile
195 200 205

Val Asp Arg Tyr Pro Thr Trp Gly Asp Val Val Gln Val Asp Thr Trp
210 215 220

Val Ala Pro Asn Gly Lys Asn Gly Met Arg Arg Asp Trp Leu Val Arg
225 230 235 240

Asp Tyr Lys Thr Gly Glu Ile Leu Thr Arg Ala Ser Ser Asn Trp Val
245 250 255

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

Arg Gly Glu Ile Glu His Tyr Phe Val Asp Ala Pro Pro Val Val Glu
275 280 285

Asp Asp Ser Arg Lys Leu Ser Lys Leu Asp Glu Ser Thr Ala Asp Tyr
290 295 300

Val Arg Asp Gly Leu Ile Pro Arg Trp Ser Asp Leu Asp Val Asn Gln
305 310 315 320

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

Gln Val Val Glu Lys Tyr Glu Leu Ala Arg Ile Thr Leu Glu Tyr Arg
340 345 350

Arg Glu Cys Arg Lys Asp Ser Val Val Lys Ser Leu Thr Ser Val Leu
 355 360 365

Gly Gly Gly Asp Asp Asp Asn Gly Gly Ile Gly Asp Ser Gly Arg Val
 370 375 380

Asp Cys Gln His Val Leu Leu Phe Ala Gly Gly Gly Asp Gly Thr Pro
 385 390 395 400

Gly Gly Glu Ile Val Lys Gly Arg Thr Gln Trp Arg Pro Lys Tyr Glu
 405 410 415

Lys Gln Asp Gly Ser Val Asp His Phe Ser Ala Gly Asn Val
 420 425 430

<210> 114
 <211> 1275
 <212> DNA
 <213> Iris tectorum

<400> 114
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 gatgccctcg atgcccgggg cctcgtggcc aaaccgcgat ccaattccgg cagcttacia 180
 gtaaaggtca atgccaagc cgccaccagg gttaattgat ccaaggtcgg gttgaaaacc 240
 gataccaaca agcttgagga cacacccttt ttctcttctt ccgccccgag gactttctac 300
 aaccaattgc cagactggag cgtctccttt gctgccatca ccaccatctt cttggctgct 360
 gagaagcaat ggacgcttat cgattggaag ccaaggcggc ccgacatgct cgccgatgca 420
 ttcggccttg gaaagattat tgagaatgga cttgtctaca ggcagaactt ctccataagg 480
 tcatatgaga ttggggcgga tcagacggca tctatagaga cgttaatgaa tcatttacag 540
 gaaacggcgt taaacatgt gaagtgtgcc ggactcttgg gtaatgggtt tggttccacg 600
 ccggagatga gtaaaaagaa tttaatatgg gtcgtcacca aaatgcaggt ccttgtggag 660
 cattatcctt cctgggggaa tgttattgaa gtagatacat gggctgcggg atctggaaag 720
 aatggaatgc ggcgtgattg gcatgttcgg gactgccaaa ccggtcaaac tatcatgaga 780
 agctccagca attgggtgat gatgaacaag gacaccagga ggttgtctaa atttcctgaa 840
 gaagttagag ctgaaataga accctacttc atggagcgtg ttcctgtcat tgatgatgac 900
 aacaggaagc tccctaagct tgatgatgat actgctgatc atgttcgcaa gggcttaact 960
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atccttgaga gtgctccaat ctccatcctg gagagtcatg agcttgcaag catgactctt 1080
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gattgcactg atgggctcgg cgagcttccc attgaatgtc agcatctact ccgctcgagg 1200
gtgggcctga atgtgaaagg acgaactgag tggaggccca agaaacgtgc ccccttccct 1260
gttgggagcc catga 1275

<210> 115
<211> 424
<212> PRT
<213> Iris tectorum

<400> 115

Met Val Ala Ser Val Ser Ala Ser Ala Phe Phe Pro Val Pro Ser Ser
1 5 10 15

Ser Ser Ser Ser Ser Ser Ser Ser Thr Gly Ser Thr Lys Pro Ser
20 25 30

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

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

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

Asp Thr Asn Lys Leu Glu Asp Thr Pro Phe Phe Pro Ser Ser Ala Pro
85 90 95

Arg Thr Phe Tyr Asn Gln Leu Pro Asp Trp Ser Val Ser Phe Ala Ala
100 105 110

Ile Thr Thr Ile Phe Leu Ala Ala Glu Lys Gln Trp Thr Leu Ile Asp
115 120 125

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

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

Ser Tyr Glu Ile Gly Ala Asp Gln Thr Ala Ser Ile Glu Thr Leu Met
165 170 175

Asn His Leu Gln Glu Thr Ala Leu Asn His Val Lys Cys Ala Gly Leu
180 185 190

Leu Gly Asn Gly Phe Gly Ser Thr Pro Glu Met Ser Lys Lys Asn Leu
195 200 205

Ile Trp Val Val Thr Lys Met Gln Val Leu Val Glu His Tyr Pro Ser
210 215 220

Trp Gly Asn Val Ile Glu Val Asp Thr Trp Ala Ala Val Ser Gly Lys
225 230 235 240

Asn Gly Met Arg Arg Asp Trp His Val Arg Asp Cys Gln Thr Gly Gln
245 250 255

Thr Ile Met Arg Ser Ser Ser Asn Trp Val Met Met Asn Lys Asp Thr
260 265 270

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

Tyr Phe Met Glu Arg Val Pro Val Ile Asp Asp Asp Asn Arg Lys Leu
290 295 300

Pro Lys Leu Asp Asp Asp Thr Ala Asp His Val Arg Lys Gly Leu Thr
305 310 315 320

Pro Arg Trp Ser Asp Leu Asp Val Asn Gln His Val Asn Asn Val Lys
325 330 335

Tyr Ile Gly Trp Ile Leu Glu Ser Ala Pro Ile Ser Ile Leu Glu Ser
340 345 350

His Glu Leu Ala Ser Met Thr Leu Glu Tyr Arg Arg Glu Cys Gly Arg
355 360 365

Asp Ser Met Leu Gln Ser Leu Thr Ser Leu Ser Asn Asp Cys Thr Asp
370 375 380

Gly Leu Gly Glu Leu Pro Ile Glu Cys Gln His Leu Leu Arg Ser Arg
385 390 395 400

Val Gly Leu Asn Val Lys Gly Arg Thr Glu Trp Arg Pro Lys Lys Arg
405 410 415

Ala Pro Phe Pro Val Gly Ser Pro
420

<210> 116
<211> 1257
<212> DNA
<213> *Jatropha curcas*

<400> 116
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tcttctgggg gcttgcaagt caaggcaaata gcccaagccc ctccaagat aaatggatcc 180
acagtaggct atacaacacc tgtggacagt gtgaaaaatg agggtgacac gccatcaccc 240
cccccaagga ctttatcaa ccaattacct gattggagca tgcttcttgc tgctattaca 300
actatattct tggcagcaga gaagcagtgg atgatgcttg actggaaacc acggcgacct 360
gacatgctta ttgacccttt tgggtctaggg agaattgttc aggatggcct tgtgttcagg 420
cagaacttct ccatccgata atatgaaatt ggcgcggata ggacagcata catagagaca 480
ttgatgaata atttacaaga aacagccctc aaccatgtta agactgctgg acttcttggg 540
gaggggtttg gttcaacacc agagatgagt aaaaggaacc tgatatgggt gggtactcgg 600
atgcagggtc tgggtggatcg ttatccaacg tggggtgatg ttgttgaagt agatacttgg 660
gtgagtgcac caggaaaaaa tggcatgcgc cgcgattggc ttgttcgtga cagtaaaacc 720
ggtgaaactc taacaagagc ctccagtgtg tgggtaata tgaataaact gactaggaga 780
ttatctaaaa ttcctgaaga ggtaggggg gaaatagagc ctacttttt gaattctgat 840
cctattgtgg atgaggatgg cagaaaactg caaaacttg atgacaacac tgcggattat 900
gtttgcaaag gtttaactcc tagatggagt gatttagatg tcaaccaaca tgttaacaat 960
gtgaagtaca ttggctggat ccttgagagt gtcctgctgc cgatcctgga gagtcatgag 1020
ctatcatcca ttattatgga atataggagg gagtgtggaa gggatagtgt gcttcagtcg 1080
ctgactgctg tctctggcac cggcttagga aatttaggaa atgctgggtga aattgagtgt 1140
cagcacttgc ttcgactgga ggaagggtgct gagatagtaa ggggaaggac tgcgtggagg 1200
ccaaagtata gcagcaactt tggaattatg ggtcagattc cagttgaaag tgccata 1257

<210> 117
<211> 418
<212> PRT
<213> *Jatropha curcas*

<400> 117

Met Val Ala Thr Ala Ala Thr Ser Ser Phe Phe Pro Val Pro Thr Ser

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

Leu Thr Arg Arg Leu Ser Lys Ile Pro Glu Glu Val Arg Gly Glu Ile
260 265 270

Glu Pro Tyr Phe Leu Asn Ser Asp Pro Ile Val Asp Glu Asp Gly Arg
275 280 285

Lys Leu Pro Lys Leu Asp Asp Asn Thr Ala Asp Tyr Val Cys Lys Gly
290 295 300

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

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

Glu Ser His Glu Leu Ser Ser Ile Ile Met Glu Tyr Arg Arg Glu Cys
340 345 350

Gly Arg Asp Ser Val Leu Gln Ser Leu Thr Ala Val Ser Gly Thr Gly
355 360 365

Leu Gly Asn Leu Gly Asn Ala Gly Glu Ile Glu Cys Gln His Leu Leu
370 375 380

Arg Leu Glu Glu Gly Ala Glu Ile Val Arg Gly Arg Thr Ala Trp Arg
385 390 395 400

Pro Lys Tyr Arg Ser Asn Phe Gly Ile Met Gly Gln Ile Pro Val Glu
405 410 415

Ser Ala

<210> 118
<211> 1248
<212> DNA
<213> Malus domestica

<400> 118
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ggtggtttgc aggtaaaggc aaatgctcaa gcccttcaa agataaatgg aactagtgtt 180
ggtttgcaa ctgtggaaag tgggaagcat ggggatgaca tttcatcccc tccggcacgg 240
actttcatta accaattacc tgattggagt gtgctccttg ctgctattac cacaatcttc 300

ttggctgcag agaagcaatg gacaatgctt gattggaaac ccaagcgacc tgacatgctc	360
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tcaattagat catatgaaat aggtgctgat cgtacggctt caatagagac gttaatgaat	480
catttacagg aaacagcact taatcatgtt aagactgctg gacttctggg agatgggttt	540
ggttcaactc cagagatgac tgtaagaaac ctgatatggg ttgtaacgaa gatgcaggtt	600
gtggtagacc gctatcctac ttggggtgac gttgttcaag ttgacacttg ggtagtgcc	660
tctgggaaga atggaatgcg tcgtgattgg attatccagg atttgaaaac tgggtcaaatt	720
ctaacaagag cctccagtgt gtgggtgatg atgaataaag tgacgaggag attatcaaag	780
atgcctgatg cagttcgcgg tgaaatagag tcctttttta tgaattctcc tcctgttgtg	840
gaggaagatg gcaggaaact gccgaaactt gatgacaaaa cagcggacgt tgttctctct	900
ggtttgactc ctagatggag tgatttagat gtcaaccagc atgttaataa cgtgaagtac	960
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gtctcaggtg ctgatatcgg caacctggga agtaatggca cgggtggagtg ccagcacatg	1140
cttcgacttg aggatggggc tgagattgtg aggggaagga ctgagtggag gcccaaatat	1200
gccaacaatc ttgggattgt gggtcattctt ccagcagaaa gcgcatag	1248

<210> 119
 <211> 415
 <212> PRT
 <213> Malus domestica

<400> 119

Met	Val	Ala	Thr	Ala	Ala	Thr	Ala	Ser	Phe	Phe	Pro	Val	Ser	Ser	Pro
1				5					10					15	

Asn	Ser	Asp	Ser	Ser	Ala	Lys	Asn	Ala	Lys	Leu	Gly	Ser	Ala	Asn	Leu
			20					25					30		

Gly	Leu	Lys	Ser	Lys	Ser	Ala	Ser	Gly	Gly	Leu	Gln	Val	Lys	Ala	Asn
		35						40				45			

Ala	Gln	Ala	Pro	Ser	Lys	Ile	Asn	Gly	Thr	Ser	Val	Gly	Leu	Ala	Thr
	50					55					60				

Val	Glu	Ser	Gly	Lys	His	Gly	Asp	Asp	Ile	Ser	Ser	Pro	Pro	Ala	Arg
65					70					75					80

Thr Phe Ile Asn Gln Leu Pro Asp Trp Ser Val Leu Leu Ala Ala Ile
85 90 95

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

Lys Pro Lys Arg Pro Asp Met Leu Ile Asp Pro Phe Gly Leu Gly Arg
115 120 125

Ile Val Gln Asp Gly Leu Val Phe Arg Gln Asn Phe Ser Ile Arg Ser
130 135 140

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

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

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

Trp Val Val Thr Lys Met Gln Val Val Val Asp Arg Tyr Pro Thr Trp
195 200 205

Gly Asp Val Val Gln Val Asp Thr Trp Val Ser Ala Ser Gly Lys Asn
210 215 220

Gly Met Arg Arg Asp Trp Ile Ile Gln Asp Leu Lys Thr Gly Gln Ile
225 230 235 240

Leu Thr Arg Ala Ser Ser Val Trp Val Met Met Asn Lys Val Thr Arg
245 250 255

Arg Leu Ser Lys Met Pro Asp Ala Val Arg Gly Glu Ile Glu Ser Phe
260 265 270

Phe Met Asn Ser Pro Pro Val Val Glu Glu Asp Gly Arg Lys Leu Pro
275 280 285

Lys Leu Asp Asp Lys Thr Ala Asp Val Val Leu Ser Gly Leu Thr Pro
290 295 300

Arg Trp Ser Asp Leu Asp Val Asn Gln His Val Asn Asn Val Lys Tyr
305 310 315 320

Ile Gly Trp Ile Leu Glu Gly Ala Pro Leu Pro Ile Leu Glu Ser His

325

330

335

Glu Leu Ser Ser Leu Thr Leu Glu Tyr Arg Arg Glu Cys Gly Arg Asp
 340 345 350

Ser Val Leu Gln Ser Leu Thr Ala Val Ser Gly Ala Asp Ile Gly Asn
 355 360 365

Leu Gly Ser Asn Gly Thr Val Glu Cys Gln His Met Leu Arg Leu Glu
 370 375 380

Asp Gly Ala Glu Ile Val Arg Gly Arg Thr Glu Trp Arg Pro Lys Tyr
 385 390 395 400

Ala Asn Asn Leu Gly Ile Val Gly His Leu Pro Ala Glu Ser Ala
 405 410 415

<210> 120

<211> 1284

<212> DNA

<213> Oryza sativa

<400> 120

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atcgctcgca agcctaattc gtctccaggg gccatgcaag tcaaggcgca ggcgcaagcc	180
cttcctaagg ttaatggaac caagggttaac ctgaagacta caagcccaga caaggaggat	240
ataataccgt aactgctcc gaagacattc tataaccaat tgccagactg gagcatgctt	300
cttgcaactg tcacgaccat tttcctggca gctgagaagc agtggactct gcttgactgg	360
aagccgaaga agcctgacat gctggctgac acattcggtt ttggtaggat catccaagac	420
gggctggtgt ttaggcaaaa cttcttgatt cggctctacg agattggtgc tgatcgtaca	480
gcttctattg agacattaat gaatcattta caggaaacag ctctgaacca tgtgaaaact	540
gctggtctct taggtgatgg ttttggtgct acgccggaga tgagcaaacg gaacttaata	600
tgggttgaca gcaaaattca gcttcttggt gagcgatacc catcatgggg agatatgggc	660
caagttgaca catgggtagc tgctgctggc aaaaatggca tgcgtcgaga ttggcatggt	720
cgggactaca actctggtca aacaatcttg agggctacaa gtgtttgggt gatgatgaat	780
aagaacacta gaagactttc aaaaatgccg gatgaagtta gagctgaaat aggcccggtat	840
ttcaatggcc gttctgctat atcagaggag cagggtgaaa agttgcctaa gccagggacc	900
acatttgatg gcgctgctac caacaattc acaagaaaag ggcttactcc gaagtggagt	960

gaccttgatg tcaaccagca tgtgaacaat gtgaagtata ttggttggat acttgagagt 1020
gctccaattt cgatactgga gaagcacgag cttgcaagca tgaccttgga ttacaggaag 1080
gagtgtggcc gtgacagtgt gcttcagtcg cttaccgctg tttcaggtga atgcgatgat 1140
ggcaacacag aatcctccat ccagtgtgac catctgcttc agctggagtc cggagcagac 1200
attgtgaagg ctcacacaga gtggcgaccg aagcgagctc agggcgaggg gaacatgggc 1260
tttttcccag ctgagagtgc atga 1284

<210> 121
<211> 427
<212> PRT
<213> *Oryza sativa*

<400> 121

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

Ser Pro Ala Ala Ser Ala Arg Ser Ser Lys Asn Thr Thr Gly Glu Leu
20 25 30

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

Pro Gly Ala Met Gln Val Lys Ala Gln Ala Gln Ala Leu Pro Lys Val
50 55 60

Asn Gly Thr Lys Val Asn Leu Lys Thr Thr Ser Pro Asp Lys Glu Asp
65 70 75 80

Ile Ile Pro Tyr Thr Ala Pro Lys Thr Phe Tyr Asn Gln Leu Pro Asp
85 90 95

Trp Ser Met Leu Leu Ala Ala Val Thr Thr Ile Phe Leu Ala Ala Glu
100 105 110

Lys Gln Trp Thr Leu Leu Asp Trp Lys Pro Lys Lys Pro Asp Met Leu
115 120 125

Ala Asp Thr Phe Gly Phe Gly Arg Ile Ile Gln Asp Gly Leu Val Phe
130 135 140

Arg Gln Asn Phe Leu Ile Arg Ser Tyr Glu Ile Gly Ala Asp Arg Thr
145 150 155 160

Ala Ser Ile Glu Thr Leu Met Asn His Leu Gln Glu Thr Ala Leu Asn

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

Gly Asn Met Gly Phe Phe Pro Ala Glu Ser Ala
420 425

<210> 122
<211> 1326
<212> DNA
<213> Picea glauca

<400> 122
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aacaagatct cgtcatctgc ttcatacagg aagcccacaa tgccagttag ctctcctgag 120
cgtgttgatg ttaagtccaa acccactgca tacaagggac tccaagtcaa tggaaattcc 180
cacggagcta ctaataagat aaatggcact aaggtgaacg gaacagcagt ggatagcatg 240
aagcataacg ttggcctgaa ggaagcatcc gaggaagaaa gcactgctaa gagcaggatc 300
aatcagctcc cagattggag tatgcttctc gcaactattg ctaccattat tctggcagcc 360
gaaaagcagt ggaccaatth tgattggaag ccaaggaaaa cagacgtgtt tggtgacgtt 420
ttcaggctgg gcaggtttgt ggaagacagt ctggttttcc ggcagaactt cgccataaga 480
tcttatgaaa ttggtgcaga caaaacggct tctattgaaa ccttgatgaa ccatcttcag 540
gaaactgccc ttaatcatgt ttggctttct gggctagctg gggatggatt cggtgctact 600
cttgagatga gccggagaaa tctcctatgg gttgtggctc gcattgcaaat tcaagttgaa 660
cgatatccct catgggggtga tgttggtggag atagatacat ggggtggggc atcaggtaaa 720
aatggcatgc ggcgtgattg gcttggttca gattcgaaga cgaatgccat ccttacacga 780
gctactagta cctgggtaat gatgaataga aagacaagaa aactgtccaa aattcctgat 840
gctgtcaaag cagagataca gccttatttc acagaaagaa atgtctttgt ggcagaagac 900
accagaaagt tgcataagct ggaggatgac actgccagc acatctgttc ggatttaaca 960
ccgcggtgga gtgatttgga tgtgaatcag catgtcaata atgttaaata tattggttgg 1020
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gagtacagac gtgaatgtgg accgacgcat gtactccaat cattgacaag tccacaggct 1140
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tggaaccct tgctgcatt gcagtttgca cacttgcttc gattgcaaga tgacagatcg 1260
gaaattctga gggcaaggct agagtggagg tcaaaggcaa agaacaacct tcacgacctt 1320
gcttga 1326

<210> 123
<211> 441

<212> PRT
<213> Picea glauca

<400> 123

Met Val Ala Ala Ala Thr Met Leu Met Phe Ser Ser Ser Ser Gln
1 5 10 15

Cys Asn Thr Gln Asn Lys Ile Ser Ser Ser Ala Ser Ser Gly Lys Pro
20 25 30

Thr Met Pro Val Ser Ser Pro Glu Arg Val Asp Val Lys Ser Lys Pro
35 40 45

Thr Ala Tyr Lys Gly Leu Gln Val Asn Gly Asn Ser His Gly Ala Thr
50 55 60

Asn Lys Ile Asn Gly Thr Lys Val Asn Gly Thr Ala Val Asp Ser Met
65 70 75 80

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

Lys Ser Arg Ile Asn Gln Leu Pro Asp Trp Ser Met Leu Leu Ala Thr
100 105 110

Ile Ala Thr Ile Ile Leu Ala Ala Glu Lys Gln Trp Thr Asn Phe Asp
115 120 125

Trp Lys Pro Arg Lys Thr Asp Val Phe Gly Asp Val Phe Arg Leu Gly
130 135 140

Arg Phe Val Glu Asp Ser Leu Val Phe Arg Gln Asn Phe Ala Ile Arg
145 150 155 160

Ser Tyr Glu Ile Gly Ala Asp Lys Thr Ala Ser Ile Glu Thr Leu Met
165 170 175

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

Ala Gly Asp Gly Phe Gly Ala Thr Leu Glu Met Ser Arg Arg Asn Leu
195 200 205

Leu Trp Val Val Ala Arg Met Gln Ile Gln Val Glu Arg Tyr Pro Ser
210 215 220

Trp Gly Asp Val Val Glu Ile Asp Thr Trp Val Gly Pro Ser Gly Lys
225 230 235 240

Asn Gly Met Arg Arg Asp Trp Leu Val Arg Asp Ser Lys Thr Asn Ala
245 250 255

Ile Leu Thr Arg Ala Thr Ser Thr Trp Val Met Met Asn Arg Lys Thr
260 265 270

Arg Lys Leu Ser Lys Ile Pro Asp Ala Val Lys Ala Glu Ile Gln Pro
275 280 285

Tyr Phe Thr Glu Arg Asn Val Phe Val Ala Glu Asp Thr Arg Lys Leu
290 295 300

His Lys Leu Glu Asp Asp Thr Ala Gln Tyr Ile Cys Ser Asp Leu Thr
305 310 315 320

Pro Arg Trp Ser Asp Leu Asp Val Asn Gln His Val Asn Asn Val Lys
325 330 335

Tyr Ile Gly Trp Ile Leu Glu Ser Leu Pro Ile Ser Val Leu Glu Gly
340 345 350

Asn Glu Leu Ala Asn Ile Thr Leu Glu Tyr Arg Arg Glu Cys Gly Pro
355 360 365

Thr His Val Leu Gln Ser Leu Thr Ser Pro Gln Ala Gly Glu Val Ile
370 375 380

Ala Ala Ser Ala Ala Pro Phe Ser Gln Arg Asn Asp Pro Pro Asp Thr
385 390 395 400

Trp Lys Pro Leu Pro Ala Leu Gln Phe Ala His Leu Leu Arg Leu Gln
405 410 415

Asp Asp Arg Ser Glu Ile Leu Arg Ala Arg Ser Glu Trp Arg Ser Lys
420 425 430

Ala Lys Asn Asn Leu His Asp Leu Ala
435 440

<210> 124
<211> 1266
<212> DNA
<213> Populus tomentosiformis

<400> 124
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tcctctggag ctttgcaggt taaggcaaata gcccaagctc ctccgaagat aaatggctct 180
ccagttggct tgacagcatc agtggaact gcgaagaagg aggatgttgt ctcacaccg 240
gcaccccgga ctttatcaa ccaattacct gattggagca tgcttcttgc tgcaattaca 300
accatgtttt tggcagcaga gaagcagtg atgatgcttg attggaaacc aaagcgagct 360
gacatgctta ttgatccctt tggatttga agaattgtcc aagatggtct tgtcttcagc 420
cagaatttct caattaggtc atatgaaatt ggtgcagatc gtactgcgtc tatagagacg 480
ttgatgaacc atttacaaga aacagcactt aatcatgtta agactgctgg gcttcttga 540
gatggatttg gttcaacccc agagatgtcc aaaaggaacc tgatatgggt ggtaactcga 600
atgcagattc tagtcgatcg ttatcctaca tggggatgat ttgtccatgt ggatacttgg 660
gtgagtgcac caggaaagaa tggatgcgc cgtgattggc ttgtccgtga tgctaaaact 720
ggtgaaactc ttacaagagc ctccagttt tgggtgatga tgaataaagt gacaaggagg 780
ttatctaaaa ttctgaaga tgttcgaggt gaaatagagc cttattttct gaattctgat 840
cctgttgtga atgaggacag cacaaaactg ccaaaacttg acgacaagac ggcggactat 900
atccgcaaag gcctaactcc tagatggaat gatttagatg tcaaccagca tgttaacaat 960
gtgaaataca taggctggat ctttagagc gtcctcccc caatcctgga gagtcagag 1020
cttgctgcca ttactttgga gtacaggagg gagtgtggca gggacagcgt gctgcagtcc 1080
ttgactgctg tatctggcgc tggcattgga aatttgggcg gtcctggtaa agttgagtgt 1140
caacatttgc tgcgacatga ggatggtgct gagatcgtga ggggaaggac cgagtggagg 1200
cccaacatg ccaacaattt tggcatgatg ggtggtcaga tgccagctga tgagagcgg 1260
gcttaa 1266

<210> 125
<211> 421
<212> PRT
<213> *Populus tomentosiformis*

<400> 125
Met Val Ala Thr Ala Ala Thr Ser Ser Phe Phe Pro Val Pro Ser Pro
1 5 10 15
Pro Gly Asp Ala Lys Ser Ser Lys Val Gly Ser Gly Ser Ala Ser Leu
20 25 30

Gly Gly Ile Lys Ser Lys Ser Ala Ser Ser Gly Ala Leu Gln Val Lys
35 40 45

Ala Asn Ala Gln Ala Pro Pro Lys Ile Asn Gly Ser Pro Val Gly Leu
50 55 60

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

Ala Pro Arg Thr Phe Ile Asn Gln Leu Pro Asp Trp Ser Met Leu Leu
85 90 95

Ala Ala Ile Thr Thr Met Phe Leu Ala Ala Glu Lys Gln Trp Met Met
100 105 110

Leu Asp Trp Lys Pro Lys Arg Ala Asp Met Leu Ile Asp Pro Phe Gly
115 120 125

Ile Gly Arg Ile Val Gln Asp Gly Leu Val Phe Ser Gln Asn Phe Ser
130 135 140

Ile Arg Ser Tyr Glu Ile Gly Ala Asp Arg Thr Ala Ser Ile Glu Thr
145 150 155 160

Leu Met Asn His Leu Gln Glu Thr Ala Leu Asn His Val Lys Thr Ala
165 170 175

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

Asn Leu Ile Trp Val Val Thr Arg Met Gln Ile Leu Val Asp Arg Tyr
195 200 205

Pro Thr Trp Gly Asp Val Val His Val Asp Thr Trp Val Ser Ala Ser
210 215 220

Gly Lys Asn Gly Met Arg Arg Asp Trp Leu Val Arg Asp Ala Lys Thr
225 230 235 240

Gly Glu Thr Leu Thr Arg Ala Ser Ser Leu Trp Val Met Met Asn Lys
245 250 255

Val Thr Arg Arg Leu Ser Lys Ile Pro Glu Asp Val Arg Gly Glu Ile
260 265 270

Glu Pro Tyr Phe Leu Asn Ser Asp Pro Val Val Asn Glu Asp Ser Thr

275

280

285

Lys Leu Pro Lys Leu Asp Asp Lys Thr Ala Asp Tyr Ile Arg Lys Gly
 290 295 300

Leu Thr Pro Arg Trp Asn Asp Leu Asp Val Asn Gln His Val Asn Asn
 305 310 315 320

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

Glu Ser His Glu Leu Ala Ala Ile Thr Leu Glu Tyr Arg Arg Glu Cys
 340 345 350

Gly Arg Asp Ser Val Leu Gln Ser Leu Thr Ala Val Ser Gly Ala Gly
 355 360 365

Ile Gly Asn Leu Gly Gly Pro Gly Lys Val Glu Cys Gln His Leu Leu
 370 375 380

Arg His Glu Asp Gly Ala Glu Ile Val Arg Gly Arg Thr Glu Trp Arg
 385 390 395 400

Pro Lys His Ala Asn Asn Phe Gly Met Met Gly Gly Gln Met Pro Ala
 405 410 415

Asp Glu Ser Gly Ala
 420

<210> 126

<211> 1260

<212> DNA

<213> Ricinus communis

<400> 126

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gatgctaatt tcgataaggc acctgcaagc ttaggtggaa tcaaattaaa atctacctct 120

tgctctcggg gtttacaggt taaggcaaat gcgcaagccc ctccaagat aaatggatcc 180

tcggtaggat tcacaacatc tgtggaaact gtgaagaatg acggtgacat gccattacca 240

ccacccccta ggacttttat caaccaatta cctgattgga gcatgcttct tgctgctatt 300

acaactatct ttttggctgc tgaaaagcag tggatgatgc ttgactggaa accaaggcgg 360

cctgacatgc ttatcgaccc gtttgggtata ggtagaattg ttcaggatgg tcttattttt 420

cgccagaact tctccataag atcatatgaa attggtgctg atcgtacagc atccatagag 480

acattaatga atcatttaca agaaacggcc ctcaatcatg ttaagactgc tggacttctt 540
 ggggatggat ttgggttcaac cccagagatg agcaaaagga acctcatatg ggtgggttact 600
 cggatgcagg ttctgggtga tcgttaccca acatggggtg atgttggttca agtagatact 660
 tgggtgagta aatcaggaaa gaatggcatg cggcgtgatt ggtgcgtccg tgatagtaga 720
 actggtgaaa ctttaacgag agcatccagc gtgtgggtga tgatgaataa actgactagg 780
 aggttatcta aaattcccga agaagttcga ggagaaatag agccttattt tctgaattct 840
 gatcctattg tggatgagga tagcagaaaa ctgccaaagc ttgatgatag caatgcggac 900
 tatgtccgca aaggtctaac tcctagatgg agtgatctag atatcaacca acatgttaac 960
 aatgtgaaat acattggctg gattcttgag agtgctccac tgccaatact ggagagtcac 1020
 gaactctctg ccattactct ggagtatagg agggagtgcg ggagggacag tgtactgcag 1080
 tctctgactg ctgtatccg taatgggtatt ggaaatttgg gaaatgctgg tgatattgag 1140
 tgccagcact tgcttcgact tgaggatggg gctgagatag tgaggggaag gaccgagtgg 1200
 aggccaaagt acagcagcaa ctttggtatt atgggtcaga ttccagtcga aagtgttaa 1260

<210> 127
 <211> 419
 <212> PRT
 <213> Ricinus communis

<400> 127

Met Val Ala Thr Ala Ala Ala Ala Thr Ser Ser Phe Phe Pro Val Pro
 1 5 10 15

Ser Gln Ser Ala Asp Ala Asn Phe Asp Lys Ala Pro Ala Ser Leu Gly
 20 25 30

Gly Ile Lys Leu Lys Ser Thr Ser Cys Ser Arg Gly Leu Gln Val Lys
 35 40 45

Ala Asn Ala Gln Ala Pro Pro Lys Ile Asn Gly Ser Ser Val Gly Phe
 50 55 60

Thr Thr Ser Val Glu Thr Val Lys Asn Asp Gly Asp Met Pro Leu Pro
 65 70 75 80

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

Leu Ala Ala Ile Thr Thr Ile Phe Leu Ala Ala Glu Lys Gln Trp Met
 100 105 110

Met Leu Asp Trp Lys Pro Arg Arg Pro Asp Met Leu Ile Asp Pro Phe
115 120 125

Gly Ile Gly Arg Ile Val Gln Asp Gly Leu Ile Phe Arg Gln Asn Phe
130 135 140

Ser Ile Arg Ser Tyr Glu Ile Gly Ala Asp Arg Thr Ala Ser Ile Glu
145 150 155 160

Thr Leu Met Asn His Leu Gln Glu Thr Ala Leu Asn His Val Lys Thr
165 170 175

Ala Gly Leu Leu Gly Asp Gly Phe Gly Ser Thr Pro Glu Met Ser Lys
180 185 190

Arg Asn Leu Ile Trp Val Val Thr Arg Met Gln Val Leu Val Asp Arg
195 200 205

Tyr Pro Thr Trp Gly Asp Val Val Gln Val Asp Thr Trp Val Ser Lys
210 215 220

Ser Gly Lys Asn Gly Met Arg Arg Asp Trp Cys Val Arg Asp Ser Arg
225 230 235 240

Thr Gly Glu Thr Leu Thr Arg Ala Ser Ser Val Trp Val Met Met Asn
245 250 255

Lys Leu Thr Arg Arg Leu Ser Lys Ile Pro Glu Glu Val Arg Gly Glu
260 265 270

Ile Glu Pro Tyr Phe Leu Asn Ser Asp Pro Ile Val Asp Glu Asp Ser
275 280 285

Arg Lys Leu Pro Lys Leu Asp Asp Ser Asn Ala Asp Tyr Val Arg Lys
290 295 300

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

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

Leu Glu Ser His Glu Leu Ser Ala Ile Thr Leu Glu Tyr Arg Arg Glu
340 345 350

Cys Gly Arg Asp Ser Val Leu Gln Ser Leu Thr Ala Val Ser Gly Asn
 355 360 365

Gly Ile Gly Asn Leu Gly Asn Ala Gly Asp Ile Glu Cys Gln His Leu
 370 375 380

Leu Arg Leu Glu Asp Gly Ala Glu Ile Val Arg Gly Arg Thr Glu Trp
 385 390 395 400

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

Glu Ser Ala

<210> 128
 <211> 1263
 <212> DNA
 <213> Solanum tuberosum

<400> 128
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 ggagctaaat cgtctggaaa tttaggagga agtcttcctg gaagtataga tacacggggg 120
 cttaatgtta agaagccttc ttttgggagc ctacaagcta aggccaatgc acaagcacca 180
 cctaaggtga atggaacaaa ggtaggcggt atggatggct tcaaaaatga cgatgaggtg 240
 atttcttcac atcacccaag gactttttatc aaccagttac ctgattggag catgctcctc 300
 gccgccatca cgacaatttt tttagctgct gagaagcaat ggatgatgct tgattggaag 360
 cctaagcgtc ctgatatgct cgctgatcca tttggattag gaaaaattgt gcaggatggc 420
 tttgttttcc gtcaaaattt cagcatcagg tcttatgaaa taggggctga taggactgcg 480
 tctatagaaa caatgatgaa tcattttacag gaaactgctc ttaaccatgt caagagtgct 540
 ggactcatgc atggtggggt cggatcaact ccagagatgt ccaagagaaa tttgatctgg 600
 gtcgttacta aaatgcaggt tgtggtggac cgttatccta cttgggggtga tgttgttcaa 660
 gtagacactt gggtagctgc atcggggaaa aatgggatgc gcagagattg gctcctccgc 720
 gatagtaata caggggatat attgatgaga gcttcagacc aatgggttat gatgaataag 780
 gagacgagga gattatctaa aataccagat gaggctcggg ctgaaattga aggttatattt 840
 gttgattcac ctctgtttat tgatgaggac agcaggaagt taccaaaact tgatgagaca 900
 acagcagact aactcgaac tggtttaact ccaagatgga gtgatttaga tgtaaccag 960
 catgttaata atgtcaagta cattggctgg attcttgaga gtgcacccat gcaaatacta 1020
 gagggttgtg agcttgctgc catgactttg gagtaccgca gggagtgcag aagggacagt 1080

gtgcttcagt ctcttacctc tgtacttgac aaaggagtcg gtgacttcac cgactttggg 1140
aatgttgagt gtcaacacgt ccttcgactt gaaaatggcg gagaggttgt taagggacga 1200
actgagtgga ggccgaaact tgtcaatgga attgggaccc taggcggatt cgacttcgcc 1260
tga 1263

<210> 129
<211> 420
<212> PRT
<213> Solanum tuberosum

<400> 129

Met Met Ala Thr Ala Ala Thr Cys Ala Phe Phe Pro Ala Ala Asn Pro
1 5 10 15

Pro Pro Asp Ser Gly Ala Lys Ser Ser Gly Asn Leu Gly Gly Ser Leu
20 25 30

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

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

Gly Thr Lys Val Gly Val Met Asp Gly Phe Lys Asn Asp Asp Glu Val
65 70 75 80

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

Ser Met Leu Leu Ala Ala Ile Thr Thr Ile Phe Leu Ala Ala Glu Lys
100 105 110

Gln Trp Met Met Leu Asp Trp Lys Pro Lys Arg Pro Asp Met Leu Ala
115 120 125

Asp Pro Phe Gly Leu Gly Lys Ile Val Gln Asp Gly Phe Val Phe Arg
130 135 140

Gln Asn Phe Ser Ile Arg Ser Tyr Glu Ile Gly Ala Asp Arg Thr Ala
145 150 155 160

Ser Ile Glu Thr Met Met Asn His Leu Gln Glu Thr Ala Leu Asn His
165 170 175

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

Met Ser Lys Arg Asn Leu Ile Trp Val Val Thr Lys Met Gln Val Val
195 200 205

Val Asp Arg Tyr Pro Thr Trp Gly Asp Val Val Gln Val Asp Thr Trp
210 215 220

Val Ala Ala Ser Gly Lys Asn Gly Met Arg Arg Asp Trp Leu Leu Arg
225 230 235 240

Asp Ser Asn Thr Gly Asp Ile Leu Met Arg Ala Ser Ser Gln Trp Val
245 250 255

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

Arg Ala Glu Ile Glu Gly Tyr Phe Val Asp Ser Pro Pro Val Ile Asp
275 280 285

Glu Asp Ser Arg Lys Leu Pro Lys Leu Asp Glu Thr Thr Ala Asp Tyr
290 295 300

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

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

Met Gln Ile Leu Glu Gly Cys Glu Leu Ala Ala Met Thr Leu Glu Tyr
340 345 350

Arg Arg Glu Cys Arg Arg Asp Ser Val Leu Gln Ser Leu Thr Ser Val
355 360 365

Leu Asp Lys Gly Val Gly Asp Phe Thr Asp Phe Gly Asn Val Glu Cys
370 375 380

Gln His Val Leu Arg Leu Glu Asn Gly Gly Glu Val Val Lys Gly Arg
385 390 395 400

Thr Glu Trp Arg Pro Lys Leu Val Asn Gly Ile Gly Thr Leu Gly Gly
405 410 415

Phe Asp Phe Ala

<210> 130
 <211> 1254
 <212> DNA
 <213> *Tagetes erecta*

<400> 130
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 aagtcaaagt caacgtcttc taatggtttg caagttaaga cgaatgcaca agctcctgcg 180
 aaggtgaatg ggaccagggg aggtgttatg gatggactga aaattgatga cagttcatca 240
 tcgggtgccc caagaacatt tattaaccaa ctgcctgatt ggagcatgct tcttgctgct 300
 attactacta ttttcttggc tgctgaaaag caatggatga tgctggattg gaagactaaa 360
 cgtccggaca tgcttgctga tcttgatcct tttggtttcg ggcgaattgt tgaggatgga 420
 tttgtatttc gtcaaaactt ttcaattaga tcatatgaaa taggggcgga tcgaactgcg 480
 tcggttgaaa cgttgatgaa tcatttgcag gaaacggccc ttaatcatgt aaaaaatgct 540
 ggactcctcg gtgatggctt tggctcaaca cctgaaatgt ctaaaaggaa tctgttcttg 600
 gtggtaacta agatgcaagt gctagtagac cgttatccaa cttgggggtga cgtgggtcaa 660
 gtagatactt gggtagctgc ttctgggaaa aatggcatgc gtcgtgattg gttgattcgt 720
 gattgcaaaa cgggtcagat actaacaaga gcctcaagta attgggttat gatgaataaa 780
 gttacaagga gggttatcaa aatgcccgat gaagttcggg ctgaaattga gccgtatttt 840
 gttgacacgc ctctgtggtt tgatgatgat gatagaaaat taccaaaact tgatgagaac 900
 actgctgacc atgttcgtaa tggtttaact ccaaagtgga gtgatttgga tgtcaatcag 960
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 gagaactatg agcttgcaag cctcaccctt gagtaccgcc gtgagtgtat gaaagacagc 1080
 gtgctgcagt cactcacttc cttgctggcg ggtggtgaga aggcggattc tgatgatgtg 1140
 gactgtcaac acctgcttcg actagaaggt ggcggtgaga ttgtgaaggg aaggacaaaa 1200
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<210> 131
 <211> 417
 <212> PRT
 <213> *Tagetes erecta*

<400> 131

Met Val Ala Thr Ala Ala Thr Ala Ser Leu Phe Pro Val Ser Ser Pro
 1 5 10 15

Gln Pro Asp Ser Gly Ala Lys Asn Ser Gly Asn His Lys Gly Gly Leu
20 25 30

Gly Ser Val Asp Leu Arg Gly Ile Lys Ser Lys Ser Thr Ser Ser Asn
35 40 45

Gly Leu Gln Val Lys Thr Asn Ala Gln Ala Pro Ala Lys Val Asn Gly
50 55 60

Thr Arg Val Gly Val Met Asp Gly Leu Lys Ile Asp Asp Ser Ser Ser
65 70 75 80

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

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

Met Met Leu Asp Trp Lys Thr Lys Arg Pro Asp Met Leu Ala Asp Leu
115 120 125

Asp Pro Phe Gly Phe Gly Arg Ile Val Glu Asp Gly Phe Val Phe Arg
130 135 140

Gln Asn Phe Ser Ile Arg Ser Tyr Glu Ile Gly Ala Asp Arg Thr Ala
145 150 155 160

Ser Val Glu Thr Leu Met Asn His Leu Gln Glu Thr Ala Leu Asn His
165 170 175

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

Met Ser Lys Arg Asn Leu Phe Trp Val Val Thr Lys Met Gln Val Leu
195 200 205

Val Asp Arg Tyr Pro Thr Trp Gly Asp Val Val Gln Val Asp Thr Trp
210 215 220

Val Ala Ala Ser Gly Lys Asn Gly Met Arg Arg Asp Trp Leu Ile Arg
225 230 235 240

Asp Cys Lys Thr Gly Gln Ile Leu Thr Arg Ala Ser Ser Asn Trp Val
245 250 255

Met Met Asn Lys Val Thr Arg Arg Leu Ser Lys Met Pro Asp Glu Val
 260 265 270

Arg Ala Glu Ile Glu Pro Tyr Phe Val Asp Thr Pro Pro Val Val Asp
 275 280 285

Asp Asp Asp Arg Lys Leu Pro Lys Leu Asp Glu Asn Thr Ala Asp His
 290 295 300

Val Arg Asn Gly Leu Thr Pro Lys Trp Ser Asp Leu Asp Val Asn Gln
 305 310 315 320

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

Gln His Val Val Glu Asn Tyr Glu Leu Ala Ser Leu Thr Leu Glu Tyr
 340 345 350

Arg Arg Glu Cys Met Lys Asp Ser Val Leu Gln Ser Leu Thr Ser Leu
 355 360 365

Leu Ala Gly Gly Glu Lys Ala Asp Ser Asp Asp Val Asp Cys Gln His
 370 375 380

Leu Leu Arg Leu Glu Gly Gly Gly Glu Ile Val Lys Gly Arg Thr Lys
 385 390 395 400

Trp Arg Pro Lys Tyr Val Lys Gln Ile Gln Glu His Gln Ser Phe Pro
 405 410 415

Tyr

<210> 132
 <211> 1266
 <212> DNA
 <213> Vitis vinifera

<400> 132
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 agaaatgctc cttcaggcag tttgcaagtt aaggcaaagt cccaagcccc tcctaagata 180
 aatggtacca cagtttggtta tacctcctcg gcggaaggcg tgaagattga ggatgacatg 240
 tcgtcgctc cacctaggac tttcatcaac caattgccag actggagcat gcttcttctg 300

gctattacaa ccatcttctt ggcagctgag aagcagtgga tgatgcttga ctggaaacca	360
aggaggtctg acatgctaata cgacccattt ggcttaggga aaattgtcca agatgggtctt	420
gttttcaggc aaaacttctc gattagatca tatgaaatag gtgctgatcg aaccgcatcc	480
atagaaacgt tgatgaatca ttacaggaa actgcactta accatgttag gactgctggt	540
cttctgggtg atgggttttg ttcaacgcca gagatgagca taaggaacct aatatgggtg	600
gtcactcgaa tgcaggttgt ggtagatcgg taccctactt ggggtgatgt tgttcaagtg	660
gatacttggg tatgtgcatc tgggaagaat ggcattgcgc gtgattggat aatccgtgat	720
tgcaaaactg gggaaactct aaccagagcc tccagtgtgt ggggtgatgat gaataagcag	780
accaggagat tatcaaaaat tccagatgca gttcgagctg aaatagagcc ttattttatg	840
gattctgctc ctattgtgga tgaggatggc agaaaactgc ccaaacttga tgacagcact	900
gcggattata tccgcacagg actaactcct agatggagtg atttagatgt caatcagcat	960
gttaacaatg ttaagtacat cggttggatc cttgagagtg ctccactgcc aatcttggag	1020
agtcacgagc tttcttccat gactctggag tacaggaggg agtgtggaag ggacagtgtg	1080
ctgcagtccc tctactgctgt ctgcggaact ggtgttggtg atttgctgga ttgtggaaat	1140
gttgagtgcc agcaccttct tcgacttgag gaaggagctg agattgttaa gggaaggact	1200
gagtggaggc caaagtatgc ccacagcatg gggggtgtgg gccagatccc agcagaaagt	1260
gcttga	1266

<210> 133
 <211> 421
 <212> PRT
 <213> Vitis vinifera

<400> 133

Met	Val	Ala	Thr	Ala	Ala	Thr	Ser	Ala	Phe	Phe	Ala	Val	Ala	Ser	Pro
1				5					10					15	

Ser	Ser	Asp	Pro	Asp	Ala	Lys	Pro	Ser	Thr	Lys	Pro	Gly	Val	Gly	Ser
			20					25					30		

Ala	Ile	Leu	Arg	Gly	Ile	Lys	Ser	Arg	Asn	Ala	Pro	Ser	Gly	Ser	Leu
		35					40					45			

Gln	Val	Lys	Ala	Asn	Ala	Gln	Ala	Pro	Pro	Lys	Ile	Asn	Gly	Thr	Thr
	50					55					60				

Val	Gly	Tyr	Thr	Ser	Ser	Ala	Glu	Gly	Val	Lys	Ile	Glu	Asp	Asp	Met
65					70					75					80

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

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

Pro Ile Leu Glu Ser His Glu Leu Ser Ser Met Thr Leu Glu Tyr Arg
340 345 350

Arg Glu Cys Gly Arg Asp Ser Val Leu Gln Ser Leu Thr Ala Val Cys
355 360 365

Gly Thr Gly Val Gly Asn Leu Leu Asp Cys Gly Asn Val Glu Cys Gln
370 375 380

His Leu Leu Arg Leu Glu Glu Gly Ala Glu Ile Val Lys Gly Arg Thr
385 390 395 400

Glu Trp Arg Pro Lys Tyr Ala His Ser Met Gly Gly Val Gly Gln Ile
405 410 415

Pro Ala Glu Ser Ala
420

<210> 134
<211> 1281
<212> DNA
<213> Zea mays

<400> 134
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tccgcgaaga acttggtcgg tgaagtaccg gatagtttga gcgtccgtgg tattgtcgca 120
aagcctaata ccaattctgg gaacatgcaa gtgaaggctc aagcacaac ccttcccaag 180
gttaatggca ccaagggtta cctcaagaat gcaagctcag acacagagga ggcgataccc 240
tacactgctc ccaagacatt ctacaaccaa ctgccagatt ggagcatgct tcttgcggtc 300
gtcactacca tcttcctggc agcagagaag cagtggacac tgcttgactg gaagccgaag 360
aaacccgaca tgcttggtga tacatttggt ttggtggga tcatccagga tgggatggtg 420
tttaggcaaa acttcattat tcggtcctat gagattggtg ccgatcgtac tgcttctata 480
gagacattaa tgaatcactt acaggaaaca gctcttaacc atgtgaagac agctggcctt 540
cttgagatg gttttggcgc cagccagag atgagcaaac gaaacttgat ccacgaggtc 600
agcaaaattc agcttcttgt tgagaagtac cccttggtgg aagacacggt tcaagtggac 660
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aagtctggat gtacgatctt gagagctaca agtggttggg tgatgatgaa taagaacact 780
agaaggtttt caaaaatgcc ggacgaagta agggctgaga taggcccgtg tttcaacgcc 840

cgcgagcca taacagatga gcagagcgag aaactggcta agccagggag cactgctggt 900
 ggcgatgcta tgaagcagtt catgagaaag gggctcactc ctaggtgggtg gggtgacctt 960
 gatgtcaacc agcacgtgaa taacgtcaag tacatcggtt ggattcttga gagtgtccg 1020
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 ggacgcgaca gcgtgctgca gtcgctcacc accgtcgcggt gtgaatgcgt agacggcgac 1140
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 aaggcgacaca cggagtggcg cccgaagcgg gcgcatggtg aggggacccc catggggggt 1260
 ttcccggcgg agagcgcggtg a 1281

<210> 135
 <211> 426
 <212> PRT
 <213> Zea mays

<400> 135

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

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

Met Gln Val Lys Ala Gln Ala Gln Thr Leu Pro Lys Val Asn Gly Thr
 50 55 60

Lys Val Asn Leu Lys Asn Ala Ser Ser Asp Thr Glu Glu Ala Ile Pro
 65 70 75 80

Tyr Thr Ala Pro Lys Thr Phe Tyr Asn Gln Leu Pro Asp Trp Ser Met
 85 90 95

Leu Leu Ala Ala Val Thr Thr Ile Phe Leu Ala Ala Glu Lys Gln Trp
 100 105 110

Thr Leu Leu Asp Trp Lys Pro Lys Lys Pro Asp Met Leu Val Asp Thr
 115 120 125

Phe Gly Phe Gly Gly Ile Ile Gln Asp Gly Met Val Phe Arg Gln Asn
 130 135 140

Phe Ile Ile Arg Ser Tyr Glu Ile Gly Ala Asp Arg Thr Ala Ser Ile
145 150 155 160

Glu Thr Leu Met Asn His Leu Gln Glu Thr Ala Leu Asn His Val Lys
165 170 175

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

Lys Arg Asn Leu Ile His Glu Val Ser Lys Ile Gln Leu Leu Val Glu
195 200 205

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

Ala Ala Gly Lys Asn Gly Met Arg Arg Asp Trp His Val Leu Asp Cys
225 230 235 240

Lys Ser Gly Cys Thr Ile Leu Arg Ala Thr Ser Val Trp Val Met Met
245 250 255

Asn Lys Asn Thr Arg Arg Phe Ser Lys Met Pro Asp Glu Val Arg Ala
260 265 270

Glu Ile Gly Pro Tyr Phe Asn Ala Arg Ala Ala Ile Thr Asp Glu Gln
275 280 285

Ser Glu Lys Leu Ala Lys Pro Gly Ser Thr Ala Gly Gly Asp Ala Met
290 295 300

Lys Gln Phe Met Arg Lys Gly Leu Thr Pro Arg Trp Trp Gly Asp Leu
305 310 315 320

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

Glu Ser Ala Pro Ile Ala Ile Leu Glu Lys His Glu Leu Ala Ser Met
340 345 350

Thr Leu Asp Tyr Arg Lys Glu Cys Gly Arg Asp Ser Val Leu Gln Ser
355 360 365

Leu Thr Thr Val Ala Gly Glu Cys Val Asp Gly Asp Thr Asp Ser Thr
370 375 380

Ile Gln Cys Asp His Leu Leu Gln Leu Glu Thr Gly Ala Asp Ile Val

385

390

395

400

Lys Ala His Thr Glu Trp Arg Pro Lys Arg Ala His Gly Glu Gly Thr
 405 410 415

Pro Met Gly Gly Phe Pro Ala Glu Ser Ala
 420 425

<210> 136

<211> 1257

<212> DNA

<213> Zea mays

<400> 136

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aagaacggcc ttggggagcg ccagagagag ctggacgtcc gcggcggtgc ggcgaagccg    120
ggagcctcgt ctagtgccgt gagggcgagc aagacgcgcg ccacgcgtgc ggtccccaag    180
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cagaacttct ccattagggt ctatgagatt ggggcagata ggacggcatc tatagagacg    480
ctgatgaacc atttgcagga aacggcactc aatcatgtga agaccgctgg gctgctaggt    540
gatggatttg gctccacacc agagatgagt aaacgaaact tgttctgggt ggtttagccaa    600
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ggccacacaa tactgaaggc gacaagtaaa tgggttatga tgaacaaact cactaggaag    780
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gctattgttg atgaagacaa ccgcaagctt ccaaaactgc cagaggggtca aagcacttct    900
gcagctaaat atgtgaggac aggcctgact cctcgttggg ctgatcttga tataaaccag    960
catgtcaata atgttaaata cattgcgtgg attcttgaga gtgcaccgat tactatTTTT    1020
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ttgcactgtg agcatgtgct gagccttgaa tcaggccga ccatagtga ggcccggacc    1200
atgtggaggc ctaagggaac caaggcccaa gaaacagcgg ttccatcttc attctga    1257

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<210> 137

<211> 418
<212> PRT
<213> Zea mays

<400> 137

Met Ala Ala Ser Ile Ala Ala Ser Ser Phe Phe Pro Gly Ser Pro Ala
1 5 10 15

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

Val Arg Gly Val Ala Ala Lys Pro Gly Ala Ser Ser Ser Ala Val Arg
35 40 45

Ala Ser Lys Thr Arg Ala His Ala Ala Val Pro Lys Met Asn Gly Gly
50 55 60

Gly Lys Ser Ala Val Ala Asp Gly Glu His Glu Thr Val Pro Ser Ser
65 70 75 80

Val Pro Lys Thr Phe Tyr Asn Gln Leu Pro Asp Trp Ser Met Leu Leu
85 90 95

Ala Ala Ile Thr Thr Ile Phe Leu Ala Ala Glu Lys Gln Trp Thr Met
100 105 110

Leu Asp Trp Lys Pro Arg Arg Pro Asp Met Leu Thr Asp Thr Phe Gly
115 120 125

Phe Gly Arg Ile Ile His Asp Gly Leu Met Phe Arg Gln Asn Phe Ser
130 135 140

Ile Arg Ser Tyr Glu Ile Gly Ala Asp Arg Thr Ala Ser Ile Glu Thr
145 150 155 160

Leu Met Asn His Leu Gln Glu Thr Ala Leu Asn His Val Lys Thr Ala
165 170 175

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

Asn Leu Phe Trp Val Val Ser Gln Met Gln Ala Ile Ile Glu Arg Tyr
195 200 205

Pro Cys Trp Gly Asp Thr Val Glu Val Asp Thr Trp Val Ser Ala Asn
210 215 220

Gly Lys Asn Gly Met Arg Arg Asp Trp His Ile Arg Asp Ser Met Thr
225 230 235 240

Gly His Thr Ile Leu Lys Ala Thr Ser Lys Trp Val Met Met Asn Lys
245 250 255

Leu Thr Arg Lys Leu Ala Arg Ile Pro Asp Glu Val Arg Thr Glu Ile
260 265 270

Glu Pro Tyr Phe Val Gly Arg Ser Ala Ile Val Asp Glu Asp Asn Arg
275 280 285

Lys Leu Pro Lys Leu Pro Glu Gly Gln Ser Thr Ser Ala Ala Lys Tyr
290 295 300

Val Arg Thr Gly Leu Thr Pro Arg Trp Ala Asp Leu Asp Ile Asn Gln
305 310 315 320

His Val Asn Asn Val Lys Tyr Ile Ala Trp Ile Leu Glu Ser Ala Pro
325 330 335

Ile Thr Ile Phe Glu Asn His Glu Leu Ala Ser Ile Val Leu Asp Tyr
340 345 350

Lys Arg Glu Cys Val Arg Asp Ser Val Leu Gln Ser His Thr Ser Val
355 360 365

His Glu Asp Cys Asn Ile Glu Ser Gly Glu Thr Thr Leu His Cys Glu
370 375 380

His Val Leu Ser Leu Glu Ser Gly Pro Thr Ile Val Lys Ala Arg Thr
385 390 395 400

Met Trp Arg Pro Lys Gly Thr Lys Ala Gln Glu Thr Ala Val Pro Ser
405 410 415

Ser Phe

<210> 138
<211> 1257
<212> DNA
<213> Populus trichocarpa

<400> 138
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tcctctgggg ctttgcaagt taacacaaat gccaagctc ctccaaagat aaatggccct    180
ccagttggct tgacagcatc agtggaaact ctgaagaatg aggatggtgt gtcgtcaccg    240
gcacctcgga cgttcatcaa ccaattacct gattggagca tgcttcttgc tgcaattaca    300
accatgtttt tggcagcaga gaagcagtgg atgatgcttg attggaaacc aaagcgacct    360
gatatgctta ttgaccctt tggatattggg agaattgtcc aagatgggtct tgtcttccgc    420
cagaatttct caattaggtc atatgaaatt ggtgcagatc gtacagcatc tatagagacg    480
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gatggatttg gtgcaacccc agagatgtcc aaaaggaacc tgatatgggt ggtaactcgt    600
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cctgttgtga atgaggacag cagaaaactt caaaaaattg atgacaatac agcggactat    900
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gtgaagtaca taggctggat ccttgagagc gtcctccac caatcatgga gagtcatgag   1020
cttgctgcca ttactttgga gtacaggagg gagtgtggca gggacagcgt gctgcagtcc   1080
ttgactgctg tatctgacac tggcattgga aatttaggca gccctggtga agttgagttc   1140
caacacttgc tccggtttga ggagggtgct gagattgtga ggggaaggac tgagtggaga   1200
cccaaacatg ccgacaattt tggtatcatg ggtcagatcc cagctgtgag cgcttaa    1257

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<210> 139
<211> 418
<212> PRT
<213> Populus trichocarpa

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<400> 139
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Met Val Ala Ala Ala Ala Ala Ser Ser Phe Phe Pro Val Pro Ser Pro
1           5           10          15

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Ser Gly Asp Ala Lys Ala Ser Lys Phe Gly Ser Val Ser Ala Ser Leu
20           25           30

```

```

Gly Gly Ile Lys Thr Lys Ser Ala Ser Ser Gly Ala Leu Gln Val Asn
35           40           45

```

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Thr Asn Ala Gln Ala Pro Pro Lys Ile Asn Gly Pro Pro Val Gly Leu

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50

55

60

Thr Ala Ser Val Glu Thr Leu Lys Asn Glu Asp Val Val Ser Ser Pro
65 70 75 80

Ala Pro Arg Thr Phe Ile Asn Gln Leu Pro Asp Trp Ser Met Leu Leu
85 90 95

Ala Ala Ile Thr Thr Met Phe Leu Ala Ala Glu Lys Gln Trp Met Met
100 105 110

Leu Asp Trp Lys Pro Lys Arg Pro Asp Met Leu Ile Asp Pro Phe Gly
115 120 125

Ile Gly Arg Ile Val Gln Asp Gly Leu Val Phe Arg Gln Asn Phe Ser
130 135 140

Ile Arg Ser Tyr Glu Ile Gly Ala Asp Arg Thr Ala Ser Ile Glu Thr
145 150 155 160

Leu Met Asn His Leu Gln Glu Thr Ala Leu Asn His Val Lys Thr Ala
165 170 175

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

Asn Leu Ile Trp Val Val Thr Arg Met Gln Ile Leu Val Asp Arg Tyr
195 200 205

Pro Thr Trp Gly Asp Val Val Gln Val Asp Thr Trp Val Ser Ala Ser
210 215 220

Gly Lys Asn Gly Met Arg Arg Asp Trp Leu Leu Arg Asp Ala Lys Thr
225 230 235 240

Gly Glu Thr Leu Thr Arg Ala Ser Ser Val Trp Val Met Met Asn Lys
245 250 255

Val Thr Arg Arg Leu Ser Lys Ile Pro Glu Glu Val Arg Gly Glu Ile
260 265 270

Glu Pro His Phe Leu Thr Ser Asp Pro Val Val Asn Glu Asp Ser Arg
275 280 285

Lys Leu Pro Lys Ile Asp Asp Asn Thr Ala Asp Tyr Ile Cys Glu Ser
290 295 300

Leu Thr Pro Arg Trp Asn Asp Leu Asp Val Asn Gln His Val Asn Asn
305 310 315 320

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

Glu Ser His Glu Leu Ala Ala Ile Thr Leu Glu Tyr Arg Arg Glu Cys
340 345 350

Gly Arg Asp Ser Val Leu Gln Ser Leu Thr Ala Val Ser Asp Thr Gly
355 360 365

Ile Gly Asn Leu Gly Ser Pro Gly Glu Val Glu Phe Gln His Leu Leu
370 375 380

Arg Phe Glu Glu Gly Ala Glu Ile Val Arg Gly Arg Thr Glu Trp Arg
385 390 395 400

Pro Lys His Ala Asp Asn Phe Gly Ile Met Gly Gln Ile Pro Ala Val
405 410 415

Ser Ala

<210> 140
<211> 266
<212> PRT
<213> Artificial sequence

<220>
<223> IPR002864 Acyl-ACP thioesterase family comprised in SEQ ID NO: 2

<400> 140

Gly Leu Val Phe Arg Gln Asn Phe Ser Ile Arg Ser Tyr Glu Ile Gly
1 5 10 15

Ala Asp Arg Ser Ala Ser Ile Glu Thr Val Met Asn His Leu Gln Glu
20 25 30

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

Gly Ser Thr Pro Glu Met Phe Lys Lys Asn Leu Ile Trp Val Val Thr
50 55 60

Arg Met Gln Val Val Val Asp Lys Tyr Pro Thr Trp Gly Asp Val Val

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

<210> 141
 <211> 24
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> TMpred predicted transmembrane helix

 <400> 141

Thr Phe Ile Asn Gln Leu Pro Asp Trp Ser Met Leu Leu Ala Ala Ile
 1 5 10 15

Thr Thr Ile Phe Leu Ala Ala Glu
 20

<210> 142
 <211> 52
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: Prm 08145

<400> 142
 ggggacaagt ttgtacaaaa aagcaggctt aaacaatggg gccacctct gc 52

<210> 143
 <211> 50
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: Prm 08146

<400> 143
 ggggaccact ttgtacaaga aagctggggt ttttcttacg gtgcagttcc 50

<210> 144
 <211> 2194
 <212> DNA
 <213> Oryza sativa

<400> 144
 aatccgaaaa gtttctgcac cgttttcacc ccctaactaa caatataggg aacgtgtgct 60
 aaatataaaa tgagacctta tatatgtagc gctgataact agaactatgc aagaaaaact 120
 catccaccta ctttagtggc aatcgggcta aataaaaaag agtcgctaca ctagtttcgt 180
 tttccttagt aattaagtgg gaaaatgaaa tcattattgc ttagaatata cgttcacatc 240
 tctgtcatga agttaaatta ttcgaggtag ccataattgt catcaaactc ttcttgaata 300
 aaaaaatctt tctagctgaa ctcaatgggt aaagagagag atttttttta aaaaaataga 360
 atgaagatat tctgaacgta ttggcaaaga tttaaacata taattatata attttatagt 420
 ttgtgcattc gtcatatcgc acatcattaa ggacatgtct tactccatcc caatttttat 480
 ttagtaatta aagacaattg acttattttt attatttata ttttttcgat tagatgcaag 540
 gtacttacgc acacactttg tgctcatgtg catgtgtgag tgcacctcct caatacacgt 600
 tcaactagca acacatctct aatatcactc gcctatttaa tacatttagg tagcaatata 660
 tgaattcaag cactccacca tcaccagacc acttttaata atatctaaaa taaaaaaat 720

aattttacag aatagcatga aaagtatgaa acgaactatt taggtttttc acatacaaaa	780
aaaaaaagaa ttttgctcgt gcgcgagcgc caatctccca tattggggcac acaggcaaca	840
acagagtggc tgcccacaga acaaccacaca aaaaacgatg atctaacgga ggacagcaag	900
tccgcaacaa cttttaaca gcaggctttg cggccaggag agaggaggag aggcaaagaa	960
aaccaagcat cctccttctc ccatctataa attcctcccc ctttttcccc tctctatata	1020
ggaggcatcc aagccaagaa gagggagagc accaaggaca cgcgactagc agaagccgag	1080
cgaccgcctt ctcgatccat atcttccggt cgagttcttg gtcgatctct tccctcctcc	1140
acctcctcct cacaggggat gtgcctccct tcggttgttc ttggatttat tgttctaggt	1200
tgtgtagtac gggcgttgat gttaggaaaag gggatctgta tctgtgatga ttctgtttct	1260
tggatttggg atagaggggt tcttgatggt gcatgttatc ggttcgggtt gatttagtagt	1320
atggttttca atcgtctgga gagctctatg gaaatgaaat ggtttaggga tcggaatctt	1380
gcgattttgt gagtaccttt tgtttgaggt aaaatcagag caccgggtgat tttgcttggt	1440
gtaataaagt acggttggtt ggtcctcgat tctggtagtg atgcttctcg atttgacgaa	1500
gctatccttt gtttattccc tattgaacaa aaataatcca actttgaaga cggccccgtt	1560
gatgagattg aatgattgat tcttaagcct gtccaaaatt tcgcagctgg cttgtttaga	1620
tacagtagtc cccatcacga aattcatgga aacagttata atcctcagga acaggggatt	1680
ccctgttctt ccgatttgct ttagtcccag aatttttttt cccaaatata ttaaaaagtc	1740
actttctggt tcagttcaat gaattgattg ctacaaataa tgcttttata gcgttatcct	1800
agctgtagtt cagttaatag gtaatacccc tatagtttag tcaggagaag aacttatccg	1860
atttctgata tccattttta attatatgaa atgaactgta gcataagcag tattcatttg	1920
gattattttt tttattagct ctcacccctt cattattctg agctgaaagt ctggcatgaa	1980
ctgtcctcaa ttttgttttc aaattcacat cgattatcta tgcattatcc tcttgtatct	2040
acctgtagaa gtttcttttt ggttattcct tgactgcttg attacagaaa gaaatttatg	2100
aagctgtaat cgggatatgt atactgcttg ttcttatgat tcatttcctt tgtgcagttc	2160
ttggtgtagc ttgccacttt caccagcaaa gttc	2194

<210> 145
 <211> 1275
 <212> DNA
 <213> Arabidopsis thaliana

<400> 145	
atggatcctg aaggtttcac gagtggctta ttccggtgga acccaacgag agcattgggt	60
caagcaccac ctccggttcc acctccgctg cagcaacagc cgggtgacacc gcagacgggt	120

gcttttggga tgcgacttgg tggtttagag ggactattcg gtccgtacgg tatacgtttc 180
tacacggcgg cgaagatagc ggagttaggt tttacggcga gcacgcttgt gggatatgaag 240
gacgaggagc ttgaagagat gatgaatagt ctctctcata tctttcgttg ggagcttctt 300
gttgggtgaac ggtacggtat caaagctgcc gttagagctg aacggagacg attgcaagaa 360
gaggaggaag aggaatcttc tagacgccgt catttgctac tctccgccgc tggtgattcc 420
ggtactcatc acgctcttga tgctctctcc caagaagatg attggacagg gttatctgag 480
gaaccggtgc agcaacaaga ccagactgat gcggcgggga ataacggcgg aggaggaagt 540
ggttactggg acgcaggtca aggaaagatg aagaagcaac agcagcagag acggagaaag 600
aaaccaatgc tgacgtcagt ggaaaccgac gaagacgtca acgaaggtga ggatgacgac 660
gggatggata acggcaacgg aggtagtggg ttggggacag agagacagag ggagcatccg 720
tttatcgtaa cggagcctgg ggaagtggca cgtggcaaaa agaacggctt agattatctg 780
ttccacttgt acgaacaatg ccgtgagttc cttcttcagg tccagacaat tgctaaagac 840
cgtggcgaaa aatgccccac caaggtgacg aaccaagtat tcaggtacgc gaagaaatca 900
ggagcgagtt acataaacia gcctaaaatg cgacactacg ttcactgtta cgctctccac 960
tgcctagacg aagaagcttc aaatactctc agaagagcgt ttaaagaacg cggtgagaac 1020
gttggctcat ggcgtcaggc ttgttacaag ccacttgtga acatcgcttg tcgtcatggc 1080
tgggatatag acgccgtctt taacgctcat cctcgtctct ctatttggtg tgttccaaca 1140
aagctgcgtc agctttgccca tttggagcgg aacaatgcgg ttgctgcggc tgcggcttta 1200
gttggcggta ttagctgtac cggatcgtcg acgtctggac gtggtggatg cggcggcgac 1260
gacttgcggt tctag 1275

<210> 146
<211> 424
<212> PRT
<213> Arabidopsis thaliana

<400> 146

Met Asp Pro Glu Gly Phe Thr Ser Gly Leu Phe Arg Trp Asn Pro Thr
1 5 10 15

Arg Ala Leu Val Gln Ala Pro Pro Pro Val Pro Pro Pro Leu Gln Gln
20 25 30

Gln Pro Val Thr Pro Gln Thr Ala Ala Phe Gly Met Arg Leu Gly Gly
35 40 45

Leu Glu Gly Leu Phe Gly Pro Tyr Gly Ile Arg Phe Tyr Thr Ala Ala
50 55 60

Lys Ile Ala Glu Leu Gly Phe Thr Ala Ser Thr Leu Val Gly Met Lys
65 70 75 80

Asp Glu Glu Leu Glu Glu Met Met Asn Ser Leu Ser His Ile Phe Arg
85 90 95

Trp Glu Leu Leu Val Gly Glu Arg Tyr Gly Ile Lys Ala Ala Val Arg
100 105 110

Ala Glu Arg Arg Arg Leu Gln Glu Glu Glu Glu Glu Glu Ser Ser Arg
115 120 125

Arg Arg His Leu Leu Leu Ser Ala Ala Gly Asp Ser Gly Thr His His
130 135 140

Ala Leu Asp Ala Leu Ser Gln Glu Asp Asp Trp Thr Gly Leu Ser Glu
145 150 155 160

Glu Pro Val Gln Gln Gln Asp Gln Thr Asp Ala Ala Gly Asn Asn Gly
165 170 175

Gly Gly Gly Ser Gly Tyr Trp Asp Ala Gly Gln Gly Lys Met Lys Lys
180 185 190

Gln Gln Gln Gln Arg Arg Arg Lys Lys Pro Met Leu Thr Ser Val Glu
195 200 205

Thr Asp Glu Asp Val Asn Glu Gly Glu Asp Asp Asp Gly Met Asp Asn
210 215 220

Gly Asn Gly Gly Ser Gly Leu Gly Thr Glu Arg Gln Arg Glu His Pro
225 230 235 240

Phe Ile Val Thr Glu Pro Gly Glu Val Ala Arg Gly Lys Lys Asn Gly
245 250 255

Leu Asp Tyr Leu Phe His Leu Tyr Glu Gln Cys Arg Glu Phe Leu Leu
260 265 270

Gln Val Gln Thr Ile Ala Lys Asp Arg Gly Glu Lys Cys Pro Thr Lys
275 280 285

Val Thr Asn Gln Val Phe Arg Tyr Ala Lys Lys Ser Gly Ala Ser Tyr

290

295

300

Ile Asn Lys Pro Lys Met Arg His Tyr Val His Cys Tyr Ala Leu His
 305 310 315 320

Cys Leu Asp Glu Glu Ala Ser Asn Ala Leu Arg Arg Ala Phe Lys Glu
 325 330 335

Arg Gly Glu Asn Val Gly Ser Trp Arg Gln Ala Cys Tyr Lys Pro Leu
 340 345 350

Val Asn Ile Ala Cys Arg His Gly Trp Asp Ile Asp Ala Val Phe Asn
 355 360 365

Ala His Pro Arg Leu Ser Ile Trp Tyr Val Pro Thr Lys Leu Arg Gln
 370 375 380

Leu Cys His Leu Glu Arg Asn Asn Ala Val Ala Ala Ala Ala Leu
 385 390 395 400

Val Gly Gly Ile Ser Cys Thr Gly Ser Ser Thr Ser Gly Arg Gly Gly
 405 410 415

Cys Gly Gly Asp Asp Leu Arg Phe
 420

<210> 147
 <211> 55
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: prm4841

<400> 147
 ggggacaagt ttgtacaaaa aagcaggctt aaacaatgga tcctgaaggt ttcac 55

<210> 148
 <211> 50
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: prm4842

<400> 148
 ggggaccact ttgtacaaga aagctgggta accaaactag aaacgcaagt 50

<210> 149
 <211> 2194

<212> DNA

<213> *Oryza sativa*

<400> 149

aatccgaaaa	gtttctgcac	cgttttcacc	ccctaactaa	caatataggg	aacgtgtgct	60
aaatataaaa	tgagacctta	tatatgtagc	gctgataact	agaactatgc	aagaaaaact	120
catccaccta	ctttagtggc	aatcgggcta	aataaaaaag	agtcgctaca	ctagtttcgt	180
tttccttagt	aattaagtgg	gaaaatgaaa	tcattattgc	ttagaatata	cgttcacatc	240
tctgtcatga	agttaaatta	ttcgaggtag	ccataattgt	catcaaactc	ttcttgaata	300
aaaaaatctt	tctagctgaa	ctcaatgggt	aaagagagag	atTTTTTTTt	aaaaaataga	360
atgaagatat	tctgaacgta	ttggcaaaga	tttaaacata	taattatata	atTTTtatagt	420
ttgtgcattc	gtcatatcgc	acatcattaa	ggacatgtct	tactccatcc	caatTTTTt	480
ttagtaatta	aagacaattg	acttattttt	attattttatc	tttttttcgat	tagatgcaag	540
gtacttacgc	acacactttg	tgctcatgtg	catgtgtgag	tgcacctcct	caatacacgt	600
tcaactagca	acacatctct	aatatcactc	gcctatttaa	tacatttagg	tagcaatatc	660
tgaattcaag	cactccacca	tcaccagacc	acttttaata	atatctaaaa	tacaaaaaat	720
aattttacag	aatagcatga	aaagtatgaa	acgaactatt	taggtttttc	acatacaaaa	780
aaaaaaagaa	ttttgctcgt	gcgcgagcgc	caatctccca	tattgggcac	acaggcaaca	840
acagagtggc	tgcccacaga	acaaccaca	aaaaacgatg	atctaacgga	ggacagcaag	900
tccgcaacaa	ccttttaaca	gcaggctttg	cggccaggag	agaggaggag	aggcaaagaa	960
aaccaagcat	cctccttctc	ccatctataa	attcctcccc	ccttttcccc	tctctatata	1020
ggaggcatcc	aagccaagaa	gagggagagc	accaaggaca	cgcgactagc	agaagccgag	1080
cgaccgcctt	ctcgatccat	atcttccggt	cgagttcttg	gtcgatctct	tccctcctcc	1140
acctcctcct	cacagggtat	gtgcctccct	tcggttggtc	ttggatttat	tgttctaggt	1200
tgtgtagtac	gggcgttgat	gttaggaaag	gggatctgta	tctgtgatga	ttcctgttct	1260
tggatttggg	atagaggggt	tcttgatggt	gcatgttatc	ggttcgggtt	gattagtagt	1320
atggttttca	atcgtctgga	gagctctatg	gaaatgaaat	ggtttaggga	tcggaatctt	1380
gcgattttgt	gagtaccttt	tgtttgaggt	aaaatcagag	caccggtgat	tttgcttggt	1440
gtaataaaagt	acggttggtt	ggtcctcgat	tctggtagtg	atgcttctcg	atTTgacgaa	1500
gctatccttt	gtttattccc	tattgaacaa	aaataatcca	actttgaaga	cgggtcccgtt	1560
gatgagattg	aatgattgat	tcttaagcct	gtccaaaatt	tcgcagctgg	cttggtttaga	1620
tacagtagtc	cccatcacga	aattcatgga	aacagttata	atcctcagga	acaggggatt	1680
ccctgttctt	ccgatttgct	ttagtcccag	aatTTTTTTT	cccaaataatc	ttaaaaagtc	1740

actttctggt tcagttcaat gaattgattg ctacaaataa tgcttttata gcgttatcct	1800
agctgtagtt cagttaatag gtaatacccc tatagtttag tcaggagaag aacttatccg	1860
atttctgata tccattttta attatatgaa atgaactgta gcataagcag tattcatttg	1920
gattatTTTT tttattagct ctcacccctt cattattctg agctgaaagt ctggcatgaa	1980
ctgtcctcaa ttttgTTTT aaattcacat cgattatcta tgcattatcc tcttgtatct	2040
acctgtagaa gtttctTTTT ggttattcct tgactgcttg attacagaaa gaaatttatg	2100
aagctgtaat cgggatatgt atactgcttg ttcttatgat tcatttcctt tgtgcagttc	2160
ttggtgtagc ttgccacttt caccagcaaa gttc	2194

<210> 150
 <211> 1179
 <212> DNA
 <213> *Oryza sativa*

<400> 150	
ttgcagttgt gaccaagtaa gctgagcatg cccttaactt cacctagaaa aaagtatact	60
tggcttaact gctagtaaga catttcagaa ctgagactgg tgtacgcatt tcatgcaagc	120
cattaccact ttacctgaca ttttgacag agattagaaa tagtttcgta ctacctgcaa	180
gttgcaactt gaaaagtga atttgttctt tgctaataa ttggcgtgta attcttttat	240
gcgttagcgt aaaaagttga aatttgggtc aagttactgg tcagattaac cagtaactgg	300
ttaaagttga aagatggtct tttagtaatg gagggagtac tacactatcc tcagctgatt	360
taaatcttat tccgtcggtg gtgatttcgt caatctccca acttagtttt tcaatatatt	420
cataggatag agtgtgcata tgtgtgttta tagggatgag tctacgcgcc ttatgaacac	480
ctacttttgt actgtatttg tcaatgaaaa gaaaatctta ccaatgctgc gatgctgaca	540
ccaagaagag gcgatgaaaa gtgcaacgga tatcgtgcc agtcgggtgc caagtcagca	600
cagaccaat gggcctttcc tacgtgtctc ggccacagcc agtcgtttac cgcacgttca	660
catgggcacg aactcgcgtc atcttcccac gcaaaacgac agatctgccc tatctggtcc	720
cacccatcag tggcccacac ctcccatgct gcattatttg cgactcccat cccgtcctcc	780
acgcccacac accgcacacg ggtcgcgata gccacgacct aatcacacaa cgccacgtca	840
ccatatgtta cgggcagcca tgcgcagaag atcccgcgac gtcgctgtcc cccgtgtcgg	900
ttacgaaaaa atatcccacc acgtgtcgtc ttacaggac aatatctcga aggaaaaaaa	960
tcgtagcggg aaatccgagg cacgagctgc gattggctgg gaggcgtcca gcgtggtggg	1020
gggcccaccc ccttatectt agcccgtggc gtcctcgtc cctcgggtcc gtgtataaat	1080
accctccgga actcactctt gctggtcacc aacacgaagt aaaaggacac cagaaacata	1140

gtacacttga gctcactcca aactcaaaca ctcacacca

1179

<210> 151
<211> 420
<212> PRT
<213> Arabidopsis thaliana

<400> 151

Met Asp Pro Glu Gly Phe Thr Ser Gly Leu Phe Arg Trp Asn Pro Thr
1 5 10 15

Arg Ala Leu Val Gln Ala Pro Pro Pro Val Pro Pro Pro Leu Gln Gln
20 25 30

Gln Pro Val Thr Pro Gln Thr Ala Ala Phe Gly Met Arg Leu Gly Gly
35 40 45

Leu Glu Gly Leu Phe Gly Pro Tyr Gly Ile Arg Phe Tyr Thr Ala Ala
50 55 60

Lys Ile Ala Glu Leu Gly Phe Thr Ala Ser Thr Leu Val Gly Met Lys
65 70 75 80

Asp Glu Glu Leu Glu Glu Met Met Asn Ser Leu Ser His Ile Phe Arg
85 90 95

Trp Glu Leu Leu Val Gly Glu Arg Tyr Gly Ile Lys Ala Ala Val Arg
100 105 110

Ala Glu Arg Arg Arg Leu Gln Glu Glu Glu Glu Glu Ser Ser Arg
115 120 125

Arg Arg His Leu Leu Leu Ser Ala Ala Gly Asp Ser Gly Thr His His
130 135 140

Ala Leu Asp Ala Leu Ser Gln Glu Gly Leu Ser Glu Glu Pro Val Gln
145 150 155 160

Gln Gln Asp Gln Thr Asp Ala Ala Gly Asn Asn Gly Gly Gly Gly Ser
165 170 175

Gly Tyr Trp Asp Ala Gly Gln Gly Lys Met Lys Lys Gln Gln Gln Gln
180 185 190

Arg Arg Arg Lys Lys Pro Met Leu Thr Ser Val Glu Thr Asp Glu Asp
195 200 205

Val Asn Glu Gly Glu Asp Asp Asp Gly Met Asp Asn Gly Asn Gly Gly
210 215 220

Ser Gly Leu Gly Thr Glu Arg Gln Arg Glu His Pro Phe Ile Val Thr
225 230 235 240

Glu Pro Gly Glu Val Ala Arg Gly Lys Lys Asn Gly Leu Asp Tyr Leu
245 250 255

Phe His Leu Tyr Glu Gln Cys Arg Glu Phe Leu Leu Gln Val Gln Thr
260 265 270

Ile Ala Lys Asp Arg Gly Glu Lys Cys Pro Thr Lys Val Thr Asn Gln
275 280 285

Val Phe Arg Tyr Ala Lys Lys Ser Gly Ala Ser Tyr Ile Asn Lys Pro
290 295 300

Lys Met Arg His Tyr Val His Cys Tyr Ala Leu His Cys Leu Asp Glu
305 310 315 320

Glu Ala Ser Asn Ala Leu Arg Arg Ala Phe Lys Glu Arg Gly Glu Asn
325 330 335

Val Gly Ser Trp Arg Gln Ala Cys Tyr Lys Pro Leu Val Asn Ile Ala
340 345 350

Cys Arg His Gly Trp Asp Ile Asp Ala Val Phe Asn Ala His Pro Arg
355 360 365

Leu Ser Ile Trp Tyr Val Pro Thr Lys Leu Arg Gln Leu Cys His Leu
370 375 380

Glu Arg Asn Asn Ala Val Ala Ala Ala Ala Leu Val Gly Gly Ile
385 390 395 400

Ser Cys Thr Gly Ser Ser Thr Ser Gly Arg Gly Gly Cys Gly Gly Asp
405 410 415

Asp Leu Arg Phe
420

<210> 152
<211> 420
<212> PRT

<213> Brassica juncea

<400> 152

Met Asp Pro Glu Gly Phe Thr Ser Gly Leu Phe Arg Trp Asn Pro Thr
1 5 10 15

Arg Ala Leu Val Gln Ala Pro Pro Pro Val Pro Pro Pro Leu Gln Gln
20 25 30

Gln Pro Val Thr Pro Gln Thr Ala Ala Phe Gly Met Arg Leu Gly Gly
35 40 45

Leu Glu Gly Leu Phe Gly Pro Tyr Gly Ile Arg Phe Tyr Thr Ala Ala
50 55 60

Lys Ile Ala Glu Leu Gly Phe Thr Ala Ser Thr Leu Val Gly Met Lys
65 70 75 80

Asp Glu Glu Leu Glu Glu Met Met Asn Ser Leu Ser His Ile Phe Arg
85 90 95

Trp Glu Leu Leu Val Gly Glu Arg Tyr Gly Ile Lys Ala Ala Val Arg
100 105 110

Ala Glu Arg Arg Arg Leu Gln Glu Glu Glu Glu Glu Glu Ser Ser Arg
115 120 125

Arg Arg His Leu Leu Leu Ser Ala Ala Gly Asp Ser Gly Thr His His
130 135 140

Ala Leu Asp Ala Leu Ser Gln Glu Glu Leu Ser Glu Glu Pro Val Gln
145 150 155 160

Gln Gln Asp Gln Thr Asp Ala Ala Gly Asn Asn Gly Gly Gly Gly Ser
165 170 175

Gly Tyr Trp Asp Ala Gly Gln Gly Lys Met Lys Lys Gln Gln Gln Gln
180 185 190

Arg Arg Arg Lys Lys Pro Met Leu Thr Ser Val Glu Thr Asp Glu Asp
195 200 205

Val Asn Glu Gly Glu Asp Asp Asp Gly Met Asp Asn Gly Asn Gly Gly
210 215 220

Ser Gly Leu Gly Thr Glu Arg Gln Arg Glu His Pro Phe Ile Val Thr

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

<210> 153
 <211> 426
 <212> PRT
 <213> Ionopsidium acaule

<400> 153

Met	Asp	Pro	Glu	Gly	Phe	Thr	Ser	Gly	Leu	Phe	Arg	Trp	Asn	Thr	Thr
1				5					10					15	

Arg Ala Met Val Gln His Gln Pro Pro Pro Gln Val Pro Pro Pro Pro
20 25 30

Ser Gln Gln Ser Pro Val Thr Pro Gln Thr Ala Ala Phe Gly Met Arg
35 40 45

Leu Gly Gly Leu Glu Gly Leu Phe Gly Pro Tyr Gly Ile Arg Phe Tyr
50 55 60

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

Gly Met Lys Asp Glu Glu Leu Glu Asp Met Met Asn Ser Leu Ser His
85 90 95

Ile Phe Arg Trp Glu Leu Leu Val Gly Glu Arg Tyr Gly Ile Lys Ala
100 105 110

Ala Val Arg Ala Glu Arg Arg Arg Leu Gln Glu Glu Glu Glu Asp Asp
115 120 125

Ser Ser Arg Arg Arg His Leu Leu Leu Ser Ala Ala Gly Asp Ser Gly
130 135 140

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

Leu Ser Glu Glu Pro Val His Gln Asp Gln Thr Asp Ala Ala Gly Asn
165 170 175

Gly Gly Phe Gly Gly Tyr Leu Glu Ser Ser Val His Gly Lys Met Lys
180 185 190

Lys His Gln Pro Arg Arg Arg Lys Lys Pro Leu Val Leu Thr Ser Val
195 200 205

Glu Thr Asp Asp Asp Gly Asn Asp Asn Glu Asp Asp Asp Gly Met Asp
210 215 220

Asn Gly Asn Gly Gly Ile Gly Leu Gly Thr Glu Arg Gln Arg Glu His
225 230 235 240

Pro Phe Ile Val Thr Glu Pro Gly Glu Val Ala Arg Gly Lys Lys Asn
245 250 255

Gly Leu Asp Tyr Leu Phe His Leu Tyr Glu Gln Cys Arg Glu Phe Leu
260 265 270

Leu Gln Val Gln Thr Ile Ala Lys Asp Arg Gly Glu Lys Cys Pro Thr
275 280 285

Lys Val Thr Asn Gln Val Phe Arg Tyr Ala Lys Lys Ser Gly Ala Ser
290 295 300

Tyr Ile Asn Lys Pro Lys Met Arg His Tyr Val His Cys Tyr Ala Leu
305 310 315 320

His Cys Leu Asp Glu Glu Ala Ser Asn Ala Leu Arg Arg Ala Phe Lys
325 330 335

Glu Arg Gly Glu Asn Val Gly Ser Trp Arg Gln Ala Cys Tyr Lys Pro
340 345 350

Leu Val Asn Ile Ala Cys Arg His Gly Trp Asp Ile Asp Ala Val Phe
355 360 365

Asn Ala His Pro Arg Leu Ser Ile Trp Tyr Val Pro Thr Lys Leu Arg
370 375 380

Gln Leu Cys His Leu Glu Arg Asn Asn Ala Val Ala Ala Ala Ala Ala
385 390 395 400

Leu Val Gly Gly Ile Ser Cys Thr Gly Ser Ser Ala Ser Gly Arg Gly
405 410 415

Gly Cys Gly Gly Asp Glu Glu Leu Arg Tyr
420 425

<210> 154
<211> 417
<212> PRT
<213> Leavenworthia crassa

<400> 154

Met Asp Pro Glu Gly Phe Thr Ser Gly Leu Phe Arg Trp Asn Pro Thr
1 5 10 15

Arg Ala Thr Val Gln Ala Leu Pro Pro Val Pro Pro Pro Leu Gln Gln
20 25 30

Gln Pro Ala Thr Val Gln Ser Ala Ala Phe Gly Thr Arg Leu Gly Gly
35 40 45

Leu Glu Gly Leu Phe Gly Val Tyr Gly Ile Arg Phe Tyr Thr Ala Ala
50 55 60

Lys Ile Ala Glu Leu Gly Phe Thr Ala Ser Thr Leu Val Gly Met Arg
65 70 75 80

Asp Glu Glu Leu Glu Glu Met Met Asn Ser Leu Ser His Ile Phe Arg
85 90 95

Trp Glu Leu Leu Val Gly Glu Arg Tyr Gly Ile Lys Ala Ala Val Arg
100 105 110

Ala Glu Arg Arg Arg Leu Gln Glu Glu Glu Glu Glu Glu Ser Ser Arg
115 120 125

Arg Arg His Leu Leu Leu Ser Ala Ala Gly Asp Ser Gly Thr His His
130 135 140

Ala Leu Asp Ala Leu Ser Gln Glu Asp Asp Trp Thr Gly Leu Ser Glu
145 150 155 160

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

Gly Gly Tyr Trp Glu Ala Asn Lys Gly Lys Met Lys Lys Gln Gln Gln
180 185 190

Arg Arg Arg Lys Lys Pro Met Leu Thr Ser Val Glu Thr Asp Asp Asp
195 200 205

Ile Asn Glu Gly Glu Asp Glu Asp Gly Met Asp Asn Ser Asn Gly Gly
210 215 220

Leu Gly Thr Glu Arg Gln Arg Glu His Pro Phe Ile Val Thr Glu Pro
225 230 235 240

Gly Glu Val Ala Arg Gly Lys Lys Asn Gly Leu Asp Tyr Leu Phe His
245 250 255

Leu Tyr Glu Gln Cys Arg Glu Phe Leu Leu Gln Val Gln Thr Ile Ala
260 265 270

Lys Asp Arg Gly Glu Lys Cys Pro Thr Lys Val Thr Asn Gln Val Phe
275 280 285

Arg Tyr Ala Lys Lys Ser Gly Ala Ser Tyr Ile Asn Lys Pro Lys Met
290 295 300

Arg His Tyr Val His Cys Tyr Ala Leu His Cys Leu Asp Glu Glu Ala
305 310 315 320

Ser Asn Ala Leu Arg Arg Ala Phe Lys Glu Arg Gly Glu Asn Val Gly
325 330 335

Ser Trp Arg Gln Ala Cys Tyr Lys Pro Leu Val Asn Ile Ala Cys Arg
340 345 350

His Gly Trp Asp Ile Asp Ala Val Phe Asn Ser His Pro Arg Leu Ser
355 360 365

Ile Trp Tyr Val Pro Thr Lys Leu Arg Gln Leu Cys His Met Glu Arg
370 375 380

Asn Asn Glu Val Ala Ala Ala Thr Val Leu Val Gly Gly Ile Ser Cys
385 390 395 400

Thr Gly Thr Ser Ala Ser Gly His Gly Glu Cys Gly Gly Glu Leu His
405 410 415

Tyr

<210> 155
<211> 403
<212> PRT
<213> Selenia aurea

<400> 155

Met Asp Pro Glu Gly Phe Thr Ser Gly Leu Phe Arg Trp Asn Pro Thr
1 5 10 15

Arg Ala Thr Val Gln Ala Leu Ala Pro Val Pro Pro Pro Leu Gln Gln
20 25 30

Gln Pro Ala Thr Ala Gln Thr Ala Ala Phe Gly Met Arg Leu Gly Gly
35 40 45

Leu Glu Gly Leu Phe Gly Ala Tyr Gly Ile Arg Phe Tyr Thr Ala Ala
50 55 60

Lys Ile Ala Glu Leu Gly Phe Thr Ala Ser Thr Leu Val Gly Met Arg

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

Glu Asp Ala Ser Asn Ala Leu Arg Arg Ala Phe Lys Glu Arg Gly Glu
325 330 335

Asn Val Gly Ser Trp Arg Gln Ala Arg Tyr Lys Pro Leu Val Asp Ile
340 345 350

Ala Cys Arg His Gly Trp Asp Ile Asp Ala Val Phe Asn Ala His Pro
355 360 365

Arg Leu Ser Ile Trp Tyr Val Pro Thr Lys Leu Arg Gln Leu Cys His
370 375 380

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

Ile Ser Cys

<210> 156
<211> 430
<212> PRT
<213> Arabidopsis lyrata

<400> 156

Met Asp Pro Glu Gly Phe Thr Ser Gly Leu Phe Arg Trp Asn Pro Thr
1 5 10 15

Arg Ala Met Val Ala Ala Pro Pro Pro Val Pro Pro Gln Pro Gln Gln
20 25 30

Gln Pro Ala Thr Pro Gln Thr Arg Ala Phe Gly Met Arg Leu Gly Gly
35 40 45

Leu Glu Gly Leu Phe Gly Ala Tyr Gly Ile Arg Phe Tyr Thr Ala Ala
50 55 60

Lys Ile Ala Glu Leu Gly Phe Thr Ala Ser Thr Leu Val Gly Met Lys
65 70 75 80

Asp Glu Glu Leu Glu Glu Met Met Asn Ser Leu Ser His Ile Phe Arg
85 90 95

Trp Glu Leu Leu Val Gly Glu Arg Tyr Gly Ile Lys Ala Ala Val Thr
100 105 110

Ala Glu Arg Arg Arg Leu Gln Glu Glu Glu Glu Glu Glu Ser Ser Arg
115 120 125

Arg Arg His Leu Leu Leu Ser Ala Ala Gly Asp Ser Gly Thr His His
130 135 140

Ala Leu Asp Ala Leu Ser Gln Glu Asp Asp Trp Thr Gly Leu Ser Glu
145 150 155 160

Glu Leu Asp Arg Glu Pro Val Gln Gln Gln Asn Gln Thr Asp Ala Ala
165 170 175

Gly Asn Asn Gly Gly Gly Gly Ser Gly Tyr Trp Glu Ala Gly Gln Ala
180 185 190

Lys Met Lys Lys Gln Gln Gln Gln Arg Arg Arg Lys Lys Pro Met Val
195 200 205

Thr Ser Val Glu Thr Asp Asp Asp Val Asn Glu Gly Asp Asp Asp Asp
210 215 220

Gly Met Asp Asn Gly Asn Gly Gly Gly Gly Gly Gly Leu Gly Thr Glu
225 230 235 240

Arg Gln Arg Glu His Pro Phe Ile Val Thr Glu Pro Gly Glu Val Ala
245 250 255

Arg Gly Lys Lys Asn Gly Leu Asp Tyr Leu Phe His Leu Tyr Glu Gln
260 265 270

Cys Arg Glu Phe Leu Leu Gln Val Gln Thr Ile Ala Lys Asp Arg Gly
275 280 285

Glu Lys Cys Pro Thr Lys Val Thr Asn Gln Val Phe Arg Tyr Ala Lys
290 295 300

Lys Ser Gly Ala Ser Tyr Ile Asn Lys Pro Lys Met Arg His Tyr Val
305 310 315 320

His Cys Tyr Ala Leu His Cys Leu Asp Glu Asp Ala Ser Asn Ala Leu
325 330 335

Arg Arg Ala Phe Lys Glu Arg Gly Glu Asn Val Gly Ser Trp Arg Gln
340 345 350

Ala Cys Tyr Lys Pro Leu Val Asn Ile Ala Cys Arg His Gly Trp Asp

355

360

365

Ile Asp Ala Val Phe Asn Ala His Pro Arg Leu Ser Ile Trp Tyr Val
 370 375 380

Pro Thr Lys Leu Arg Gln Leu Cys His Leu Glu Arg Asn Asn Ala Val
 385 390 395 400

Ala Ala Ala Ala Ala Leu Val Gly Gly Ile Ser Cys Thr Gly Ser Ser
 405 410 415

Thr Ser Gly Arg Gly Gly Cys Gly Gly Asp Asp Leu Arg Phe
 420 425 430

<210> 157

<211> 403

<212> PRT

<213> Streptanthus glandulosus

<400> 157

Ser Gly Leu Phe Arg Trp Asn Ser Thr Arg Ala Leu Val Gln Gln Pro
 1 5 10 15

Pro Pro Val Pro Pro Pro Gln Gln Gln Pro Pro Glu Thr Pro Gln Thr
 20 25 30

Val Ala Phe Gly Met Arg Leu Gly Gly Leu Glu Gly Leu Phe Gly Ala
 35 40 45

Tyr Gly Ile Arg Phe Tyr Thr Ala Ala Lys Ile Ala Glu Leu Gly Phe
 50 55 60

Thr Ala Ser Thr Leu Val Gly Met Lys Asp Glu Glu Leu Glu Asp Met
 65 70 75 80

Met Asn Ser Leu Ser His Ile Phe Arg Trp Glu Leu Leu Val Gly Glu
 85 90 95

Arg Tyr Gly Ile Lys Ala Ala Val Arg Ala Glu Arg Arg Arg Leu Gln
 100 105 110

Glu Val Glu Glu Glu Glu Ser Ser Arg Arg Arg His Leu Leu Leu Cys
 115 120 125

Ala Ala Gly Asp Ser Gly Thr His His Ala Leu Asp Thr Leu Ser Gln
 130 135 140

Glu Asp Tyr Trp Thr Gly Leu Ser Glu Glu Pro Gly Gln Gln Gln Asp
145 150 155 160

Gln Thr Asp Ala Ala Gly Asn Asn Gly Gly Asn Gly Gly Gly Glu Gly
165 170 175

Gly Gly Tyr Trp Glu Ala Gly Gln Ala Lys Met Lys Lys Pro Gln Gln
180 185 190

Arg Arg Arg Lys Lys Ser Met Val Thr Ser Val Glu Ile Asp Asp Glu
195 200 205

Cys Asn Glu Gly Glu Asp Asp Asp Gly Met Asp Asn Cys Asn Gly Gly
210 215 220

Gly Gly Gly Leu Gly Ile Glu Arg Gln Arg Glu His Pro Phe Ile Val
225 230 235 240

Thr Glu Pro Gly Glu Val Ala Arg Gly Lys Lys Asn Gly Leu Asp Tyr
245 250 255

Leu Phe His Leu Tyr Glu Gln Cys Arg Glu Phe Leu Leu Gln Val Gln
260 265 270

Thr Ile Ala Lys Asp Arg Gly Glu Lys Cys Pro Thr Lys Gly Thr Asn
275 280 285

Gln Val Phe Arg Tyr Ala Lys Asn Ser Gly Ala Ser Tyr Ile Asn Lys
290 295 300

Pro Lys Met Arg His Tyr Val His Cys Tyr Ala Leu His Cys Leu Asp
305 310 315 320

Glu Glu Ala Ser Asn Ala Leu Arg Arg Ala Phe Lys Glu Arg Gly Glu
325 330 335

Asn Val Gly Ser Trp Arg Gln Ala Cys Tyr Lys Pro Leu Val Asn Ile
340 345 350

Ala Cys Arg His Gly Trp Asp Ile Asp Ala Val Phe Asn Ala His Pro
355 360 365

His Leu Ser Ile Trp Tyr Val Pro Thr Lys Leu Arg Gln Leu Cys His
370 375 380

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

Ile Ser Cys

<210> 158
<211> 407
<212> PRT
<213> Cochlearia officinalis

<400> 158

Met Asp Pro Glu Gly Phe Thr Asn Gly Leu Phe Arg Trp Asn Thr Thr
1 5 10 15

Arg Ala Met Ile Gln Gln Gln Gln Gln Leu Pro Pro Pro Gln Ile Thr
20 25 30

Pro Pro Pro Gln Gln Ser Pro Ala Thr Pro Gln Thr Ala Ala Phe Gly
35 40 45

Met Arg Leu Gly Gly Leu Glu Gly Leu Phe Gly Pro Tyr Gly Ile Arg
50 55 60

Phe Tyr Thr Ala Ala Lys Ile Ala Glu Leu Gly Phe Thr Ala Ser Thr
65 70 75 80

Leu Val Gly Met Lys Asp Glu Glu Leu Glu Asp Met Met Asn Ser Leu
85 90 95

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

Lys Ala Ala Val Arg Thr Glu Arg Arg Arg Leu Gln Glu Glu Glu
115 120 125

Glu Glu Ser Ser Arg Arg Arg His Phe Met Leu Ser Ala Gly Gly Asp
130 135 140

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

Thr Gly Leu Ser Glu Glu Pro Val His Gln Asp Gln Thr Asp Ala Ala
165 170 175

Gly Asn Gly Gly Phe Gly Gly Tyr Leu Glu Ser Gly His Gly Lys Met
180 185 190

Lys Lys Gln Gln Gln Gln Lys Arg Arg Lys Lys Pro Leu Val Thr Ser
195 200 205

Val Glu Thr Asp Asp Asp Gly Asn Asp Asp Asp Asp Gly Met Asp Asn
210 215 220

Gly Asn Gly Gly Ser Ser Gly Leu Gly Thr Glu Arg Gln Arg Glu His
225 230 235 240

Pro Phe Ile Val Thr Glu Pro Gly Glu Val Ala Arg Gly Lys Lys Asn
245 250 255

Gly Leu Asp Tyr Leu Phe His Leu Tyr Glu Gln Cys Arg Glu Phe Leu
260 265 270

Leu Gln Val Gln Thr Ile Ala Lys Asp Arg Gly Glu Lys Cys Pro Thr
275 280 285

Lys Val Thr Asn Gln Val Phe Arg Tyr Ala Lys Lys Ser Gly Ala Ser
290 295 300

Tyr Ile Asn Lys Pro Lys Met Arg His Tyr Val His Cys Tyr Ala Leu
305 310 315 320

His Cys Leu Asp Glu Asp Ala Ser Asn Ala Leu Arg Arg Ala Phe Lys
325 330 335

Glu Arg Gly Glu Asn Val Gly Ser Trp Arg Gln Ala Cys Tyr Lys Pro
340 345 350

Leu Val Asn Ile Ala Cys Arg His Gly Trp Asp Ile Asp Ala Val Phe
355 360 365

Asn Ala His Pro Arg Leu Ser Ile Trp Tyr Val Pro Thr Lys Leu Arg
370 375 380

Gln Leu Cys His Leu Glu Arg Asn Asn Ala Val Ala Ala Ala Ser Ala
385 390 395 400

Leu Val Gly Gly Ile Ser Cys
405

<210> 159
<211> 415
<212> PRT

<213> Brassica oleracea var. botrytis

<400> 159

Met Asp Pro Glu Gly Phe Thr Ser Gly Leu Phe Arg Trp Asn Pro Thr
1 5 10 15

Arg Val Met Val Gln Ala Pro Thr Pro Ile Pro Pro Pro Gln Gln Gln
20 25 30

Ser Pro Ala Thr Pro Gln Thr Ala Ala Phe Gly Met Arg Leu Gly Gly
35 40 45

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

Lys Ile Ala Glu Leu Gly Phe Thr Ala Ser Thr Leu Val Gly Met Lys
65 70 75 80

Asp Glu Glu Leu Glu Asp Met Met Asn Ser Leu Ser His Ile Phe Arg
85 90 95

Trp Glu Leu Leu Val Gly Glu Arg Tyr Gly Ile Lys Ala Ala Val Arg
100 105 110

Ala Glu Arg Arg Arg Leu Gln Glu Glu Glu Glu Glu Glu Ser Ser Arg
115 120 125

Arg Arg His Leu Leu Leu Ser Ala Ala Gly Asp Ser Gly Thr His Leu
130 135 140

Ala Leu Asp Ala Leu Ser Gln Glu Asp Asp Trp Thr Gly Leu Ser Gln
145 150 155 160

Glu Pro Val Gln His Gln Asp Gln Thr Asp Ala Ala Gly Ile Asn Gly
165 170 175

Gly Gly Arg Gly Gly Tyr Trp Glu Ala Gly Gln Thr Thr Ile Lys Lys
180 185 190

Gln Gln Gln Arg Arg Arg Lys Lys Arg Leu Tyr Val Ser Glu Thr Asp
195 200 205

Asp Asp Gly Asn Glu Gly Glu Asp Asp Asp Gly Met Asp Ile Val Asn
210 215 220

Gly Ser Gly Val Gly Met Glu Arg Gln Arg Glu His Pro Phe Ile Val

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

<210> 160
 <211> 389
 <212> PRT
 <213> *Idahoia scapigera*

<400> 160

Met	Asp	Pro	Asp	Gly	Phe	Ala	Asn	Gly	Leu	Phe	Arg	Trp	Lys	Pro	Thr
1				5					10					15	

Arg	Ala	Met	Val	Gln	Ser	Pro	Pro	Pro	Val	Pro	Pro	Pro	Pro	Gln	Gln
			20					25					30		

Gln Gln Thr Ala Ala Ala Glu Ala Phe Gly Met Arg Val Gly Gly Leu
35 40 45

Glu Gly Leu Phe Arg Ala Tyr Gly Ile Arg Phe Tyr Thr Ser Ala Lys
50 55 60

Ile Ala Glu Leu Gly Phe Thr Ala Ser Thr Leu Leu Asn Met Lys Asp
65 70 75 80

Glu Glu Leu Asp Glu Met Met Asn Ser Leu Ser His Ile Phe Arg Trp
85 90 95

Glu Leu Leu Val Gly Glu Arg Tyr Gly Ile Lys Ala Ala Val Arg Ala
100 105 110

Glu Arg Arg Arg Val Gln Glu Glu Glu Glu Glu Ser Ser Arg Arg
115 120 125

Arg His Leu Leu Leu Ser Ala Ala Gly Asp Ser Val Ala His His Ala
130 135 140

Leu Ser Gln Glu Asp Asp Trp Thr Ser Leu Ser Glu Glu Pro Val Gln
145 150 155 160

Gln Lys Asp Gln Thr Asp Ala Ala Gly Ser Asn Gly Gly Gly Val Tyr
165 170 175

Trp Gly Ala Gly Gln Ala Lys Met Lys Gln Lys Arg Arg Lys Lys Pro
180 185 190

Thr Val Met Met Thr Ser Val Glu Thr Asp Asp Glu Ile Asn Glu Cys
195 200 205

Glu Asp Asp Asp Arg Met Asp Asn Gly Asn Gly Gly Met Ala Ile Glu
210 215 220

Arg Gln Arg Glu His Pro Phe Ile Val Thr Glu Pro Gly Glu Val Ala
225 230 235 240

Arg Gly Lys Lys Asn Gly Leu Asp Tyr Leu Phe His Leu Tyr Glu Gln
245 250 255

Cys Arg Glu Phe Leu Leu Gln Val Gln Thr Ile Ala Lys Asp Arg Gly
260 265 270

Glu Lys Cys Pro Thr Lys Val Thr Asn Gln Val Phe Arg Tyr Ala Lys
275 280 285

Lys Ser Gly Ala Ser Tyr Ile Asn Lys Pro Lys Met Arg His Tyr Val
290 295 300

His Cys Tyr Ala Leu His Cys Leu Asp Glu Asn Ala Ser Asn Ala Leu
305 310 315 320

Arg Arg Ser Phe Lys Glu Arg Gly Glu Asn Val Gly Ser Trp Arg Gln
325 330 335

Ala Cys Tyr Lys Pro Leu Val Asp Val Ala Phe Arg His Gly Gly Asp
340 345 350

Ile Asp Ala Val Phe Asn Ala His Pro Arg Leu Ser Ile Trp Tyr Val
355 360 365

Pro Thr Lys Leu Arg Gln Leu Cys His Leu Glu Arg Asn Asn Ala Gly
370 375 380

Ser Ala Thr Ala Ala
385

<210> 161
<211> 399
<212> PRT
<213> Capsella bursa-pastoris

<400> 161

Gly Leu Phe Arg Trp Asn Pro Met Arg Ala Met Val Gln Ala Pro Pro
1 5 10 15

Pro Val Pro Pro Ser Pro Gln Gln Gln Gln Pro Ala Thr Pro Gln Thr
20 25 30

Ala Ala Phe Gly Met Arg Leu Gly Gly Leu Glu Gly Leu Phe Gly Ala
35 40 45

Tyr Gly Ile Arg Phe Tyr Thr Ala Ala Lys Ile Ala Glu Leu Gly Phe
50 55 60

Thr Ala Ser Thr Leu Val Gly Met Lys Asp Glu Glu Leu Glu Glu Met
65 70 75 80

Met Asn Ser Leu Ser His Ile Phe Arg Trp Glu Leu Leu Val Gly Glu
85 90 95

Arg Tyr Gly Ile Lys Ala Ala Val Arg Ala Glu Arg Arg Arg Leu Gln
100 105 110

Glu Glu Glu Glu Glu Ser Ser Arg Arg Arg His Leu Leu Leu Ser Ala
115 120 125

Ala Gly Asp Ser Gly Thr His His Ala Leu Asp Ala Leu Ser Gln Glu
130 135 140

Asp Asp Trp Thr Gly Leu Ser Glu Glu Pro Val Gln Gln Gln Asp Gln
145 150 155 160

Thr Asp Ala Ala Gly Asn Asn Gly Gly Gly Gly Ser Gly Tyr Trp Glu
165 170 175

Ala Gly Gln Ala Lys Met Lys Lys Pro Gln Gln Arg Arg Arg Lys Lys
180 185 190

Pro Met Val Ala Ser Val Glu Thr Asp Asp Asp Gly Asn Glu Gly Glu
195 200 205

Asp Asp Asp Gly Met Asp Asn Gly Asn Gly Gly Ser Gly Gly Met Gly
210 215 220

Thr Glu Arg Gln Arg Glu His Pro Phe Ile Val Thr Glu Pro Gly Glu
225 230 235 240

Val Ala Arg Gly Lys Lys Asn Gly Leu Asp Tyr Leu Phe His Leu Tyr
245 250 255

Glu Gln Cys Arg Glu Phe Leu Leu Gln Val Ile Gln Thr Ile Ala Lys
260 265 270

Asp Arg Gly Glu Lys Cys Pro Thr Lys Val Thr Tyr Gln Val Phe Arg
275 280 285

Tyr Ala Lys Lys Ser Gly Ala Ser Tyr Ile Asn Lys Pro Lys Met Arg
290 295 300

His Tyr Val His Cys Tyr Ala Leu His Cys Leu Asp Glu Asp Ala Ser
305 310 315 320

Asn Ala Leu Arg Arg Ser Phe Lys Glu Arg Gly Glu Asn Val Gly Ser
325 330 335

Trp Arg Gln Ala Cys Tyr Lys Pro Leu Val Asn Ile Ala Cys Arg His
340 345 350

Gly Trp Asp Ile Asp Ala Val Phe Asn Ala His Pro Arg Leu Ser Ile
355 360 365

Trp Tyr Val Pro Thr Lys Leu Arg Gln Leu Cys His Leu Glu Arg Asn
370 375 380

Asn Ala Val Ala Ala Ala Thr Ala Leu Val Gly Gly Ile Ser Cys
385 390 395

<210> 162
<211> 393
<212> PRT
<213> Barbarea vulgaris

<400> 162

Gly Leu Phe Arg Trp Asn Pro Thr Arg Ala Thr Val Gln Ala Leu Pro
1 5 10 15

Pro Val Pro Pro Pro Pro Gln Gln Gln Pro Ala Thr Thr Gln Thr Ala
20 25 30

Ala Phe Gly Met Arg Leu Gly Gly Leu Glu Gly Leu Phe Gly Ala Tyr
35 40 45

Gly Ile Arg Phe Tyr Thr Ala Ala Lys Ile Ala Glu Leu Gly Phe Thr
50 55 60

Ala Ser Thr Leu Val Gly Met Arg Asp Glu Glu Leu Glu Glu Met Met
65 70 75 80

Asn Ser Leu Ser His Ile Phe Arg Trp Glu Leu Leu Val Gly Glu Arg
85 90 95

Tyr Gly Ile Lys Ala Ala Val Arg Ala Glu Arg Arg Arg Leu Gln Glu
100 105 110

Glu Glu Glu Glu Glu Ser Ser Arg Arg Arg His Leu Leu Leu Ser Ala
115 120 125

Ala Gly Asp Ser Gly Thr His His Ala Leu Asp Ala Leu Ser Gln Glu
130 135 140

Asp Asp Trp Thr Gly Leu Ser Glu Glu Pro Val Gln Gln Gln Asp His

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

<210> 163
<211> 412
<212> PRT
<213> Petunia hybrida

<400> 163

Met Asp Pro Glu Ala Phe Ser Ala Ser Leu Phe Lys Trp Asp Pro Arg
1 5 10 15

Gly Ala Met Pro Pro Pro Asn Arg Leu Leu Glu Ala Val Ala Pro Pro
20 25 30

Gln Pro Pro Pro Pro Pro Leu Pro Pro Pro Gln Pro Leu Pro Pro Ala
35 40 45

Tyr Ser Ile Arg Thr Arg Glu Leu Gly Gly Leu Glu Glu Met Phe Gln
50 55 60

Ala Tyr Gly Ile Arg Tyr Tyr Thr Ala Ala Lys Ile Thr Glu Leu Gly
65 70 75 80

Phe Thr Val Asn Thr Leu Leu Asp Met Lys Asp Asp Glu Leu Asp Asp
85 90 95

Met Met Asn Ser Leu Ser Gln Ile Phe Arg Trp Glu Leu Leu Val Gly
100 105 110

Glu Arg Tyr Gly Ile Lys Ala Ala Ile Arg Ala Glu Arg Arg Arg Leu
115 120 125

Glu Glu Glu Glu Gly Arg Arg Arg His Ile Leu Ser Asp Gly Gly Thr
130 135 140

Asn Val Leu Asp Ala Leu Ser Gln Glu Gly Leu Ser Glu Glu Pro Val
145 150 155 160

Gln Gln Gln Glu Arg Glu Ala Ala Gly Ser Gly Gly Gly Gly Thr Ala
165 170 175

Trp Glu Val Val Ala Pro Gly Gly Gly Arg Met Arg Gln Arg Arg Arg
180 185 190

Lys Lys Val Val Val Gly Arg Glu Arg Arg Gly Ser Ser Met Glu Glu
195 200 205

Asp Glu Asp Thr Glu Glu Gly Gln Glu Asp Asn Glu Asp Tyr Asn Ile
210 215 220

Asn Asn Glu Gly Gly Gly Gly Ile Ser Glu Arg Gln Arg Glu His Pro
225 230 235 240

Phe Ile Val Thr Glu Pro Gly Glu Val Ala Arg Gly Lys Lys Asn Gly
245 250 255

Leu Asp Tyr Leu Phe His Leu Tyr Glu Gln Cys Arg Asp Phe Leu Ile
260 265 270

Gln Val Gln Asn Ile Ala Lys Glu Arg Gly Glu Lys Cys Pro Thr Lys
275 280 285

Val Thr Asn Gln Val Phe Arg Phe Ala Lys Lys Ala Gly Ala Ser Tyr
290 295 300

Ile Asn Lys Pro Lys Met Arg His Tyr Val His Cys Tyr Ala Leu His
305 310 315 320

Cys Leu Asp Glu Asp Ala Ser Asn Ala Leu Arg Arg Ala Phe Lys Glu
325 330 335

Arg Gly Glu Asn Val Gly Ala Trp Arg Gln Ala Cys Tyr Lys Pro Leu
340 345 350

Val Ala Ile Ala Ala Arg Gln Gly Trp Asp Ile Asp Ala Ile Phe Asn
355 360 365

Gly His Pro Arg Leu Ser Ile Trp Tyr Val Pro Thr Lys Leu Arg Gln
370 375 380

Leu Cys His Ser Glu Arg Ser Asn Ala Ala Ala Ala Ser Thr Ser
385 390 395 400

Val Ser Gly Gly Gly Val Asp His Leu Pro His Phe
405 410

<210> 164
<211> 396
<212> PRT
<213> Antirrhinum majus

<400> 164

Met Asp Pro Asp Ala Phe Leu Phe Lys Trp Asp His Arg Thr Ala Leu
1 5 10 15

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

Gln Val Gln Thr Ile Ala Lys Glu Arg Gly Glu Lys Cys Pro Thr Lys
260 265 270

Val Thr Asn Gln Val Phe Arg Tyr Ala Lys Lys Ala Gly Ala Asn Tyr
275 280 285

Ile Asn Lys Pro Lys Met Arg His Tyr Val His Cys Tyr Ala Leu His
290 295 300

Cys Leu Asp Glu Ala Ala Ser Asn Ala Leu Arg Arg Ala Phe Lys Glu
305 310 315 320

Arg Gly Glu Asn Val Gly Ala Trp Arg Gln Ala Cys Tyr Lys Pro Leu
325 330 335

Val Ala Ile Ala Ala Arg Gln Gly Trp Asp Ile Asp Thr Ile Phe Asn
340 345 350

Ala His Pro Arg Leu Ser Ile Trp Tyr Val Pro Thr Lys Leu Arg Gln
355 360 365

Leu Cys His Ala Glu Arg Ser Ser Ala Ala Val Ala Ala Thr Ser Ser
370 375 380

Ile Thr Gly Gly Gly Pro Ala Asp His Leu Pro Phe
385 390 395

<210> 165
<211> 413
<212> PRT
<213> Nicotiana tabacum

<400> 165

Met Asp Pro Glu Ala Phe Ser Ala Ser Leu Phe Lys Trp Asp Pro Arg
1 5 10 15

Gly Ala Met Pro Pro Pro Thr Arg Leu Leu Glu Ala Ala Val Ala Pro
20 25 30

Pro Pro Pro Pro Pro Val Leu Pro Pro Pro Gln Pro Leu Ser Ala Ala
35 40 45

Tyr Ser Ile Arg Thr Arg Glu Leu Gly Gly Leu Glu Glu Leu Phe Gln
50 55 60

Ala Tyr Gly Ile Arg Tyr Tyr Thr Ala Ala Lys Ile Ala Glu Leu Gly

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

His Cys Leu Asp Glu Glu Ala Ser Asn Ala Leu Arg Arg Ala Phe Lys
325 330 335

Glu Arg Gly Glu Asn Val Gly Ala Trp Arg Gln Ala Cys Tyr Lys Pro
340 345 350

Leu Val Ala Ile Ala Ala Arg Gln Gly Trp Asp Ile Asp Thr Ile Phe
355 360 365

Asn Ala His Pro Arg Leu Ala Ile Trp Tyr Val Pro Thr Arg Leu Arg
370 375 380

Gln Leu Cys His Ser Glu Arg Ser Asn Ala Ala Ala Ala Ala Ser Ser
385 390 395 400

Ser Val Ser Gly Gly Val Gly Asp His Leu Pro His Phe
405 410

<210> 166
<211> 416
<212> PRT
<213> Nicotiana tabacum

<400> 166

Met Asp Pro Glu Ala Phe Ser Ala Ser Leu Phe Lys Trp Asp Pro Arg
1 5 10 15

Gly Ala Met Pro Pro Pro Thr Arg Leu Leu Glu Ala Ala Val Ala Pro
20 25 30

Pro Pro Pro Pro Pro Ala Leu Pro Pro Pro Gln Pro Leu Ser Ala Ala
35 40 45

Tyr Ser Ile Lys Thr Arg Glu Leu Gly Gly Leu Glu Glu Leu Phe Gln
50 55 60

Ala Tyr Gly Ile Arg Tyr Tyr Thr Ala Ala Lys Ile Ala Glu Leu Gly
65 70 75 80

Phe Thr Val Asn Thr Leu Leu Asp Met Lys Asp Glu Glu Leu Asp Asp
85 90 95

Met Met Asn Ser Leu Ser Gln Ile Phe Arg Trp Glu Leu Leu Val Gly
100 105 110

Glu Arg Tyr Gly Ile Lys Ala Ala Ile Arg Ala Glu Arg Arg Arg Leu
115 120 125

Glu Glu Glu Glu Leu Arg Arg Arg Gly His Leu Leu Ser Asp Gly Gly
130 135 140

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

Val Gln Gln Gln Glu Arg Glu Ala Val Gly Ser Gly Gly Gly Gly Thr
165 170 175

Thr Trp Glu Val Val Ala Ala Ala Gly Gly Gly Arg Met Lys Gln Arg
180 185 190

Arg Arg Lys Lys Val Val Ala Ala Gly Arg Glu Lys Arg Gly Gly Ala
195 200 205

Ser Ala Glu Glu Asp Glu Glu Thr Glu Glu Gly Gln Glu Asp Asp Trp
210 215 220

Asn Ile Asn Asp Ala Ser Gly Gly Ile Ser Glu Arg Gln Arg Glu His
225 230 235 240

Pro Phe Ile Val Thr Glu Pro Gly Glu Val Ala Arg Gly Lys Lys Asn
245 250 255

Gly Leu Asp Tyr Leu Phe His Leu Tyr Glu Gln Cys Arg Asp Phe Leu
260 265 270

Ile Gln Val Gln Asn Ile Ala Lys Glu Arg Gly Glu Lys Cys Pro Thr
275 280 285

Lys Val Thr Asn Gln Val Phe Arg Tyr Ala Lys Lys Ala Gly Ala Ser
290 295 300

Tyr Ile Asn Lys Pro Lys Met Arg His Tyr Val His Cys Tyr Ala Leu
305 310 315 320

His Cys Leu Asp Glu Glu Ala Ser Asn Ala Leu Arg Arg Ala Phe Lys
325 330 335

Glu Arg Gly Glu Asn Val Gly Ala Trp Arg Gln Ala Cys Tyr Lys Pro
340 345 350

Leu Val Ala Ile Ala Ala Arg Gln Gly Trp Asp Ile Asp Thr Ile Phe

355

360

365

Asn Ala His Pro Arg Leu Ala Ile Trp Tyr Val Pro Thr Lys Leu Arg
 370 375 380

Gln Leu Cys His Ser Glu Arg Ser Asn Ala Ala Ala Ala Ala Ser
 385 390 395 400

Ser Ser Val Ser Gly Gly Gly Gly Gly Gly Asp His Leu Pro His Phe
 405 410 415

<210> 167

<211> 392

<212> PRT

<213> Triticum aestivum

<400> 167

Met Asp Pro Asn Asp Ala Phe Leu Ala Ala His Pro Phe Arg Trp Asp
 1 5 10 15

Leu Gly Pro Pro Ala Pro Ala Ala Val Pro Pro Pro Pro Pro Pro Pro
 20 25 30

Pro Pro Pro Pro Ala Leu Pro Pro Ala Asn Ala Pro Arg Glu Leu Glu
 35 40 45

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

Ser Glu Leu Gly Phe Thr Ala Ser Thr Leu Leu Val Met Thr Glu Arg
 65 70 75 80

Glu Leu Asp Asp Met Thr Ala Ala Leu Ala Gly Leu Phe Arg Trp Asp
 85 90 95

Leu Leu Ile Gly Glu Arg Phe Gly Leu Arg Ala Ala Leu Arg Ala Glu
 100 105 110

Arg Gly Arg Leu Met Ser Pro Gly Cys Arg His His Gly Tyr Gln Ser
 115 120 125

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

Asp Gly Ala Ala Ser Gly Gly Ile Gly Glu Glu Asp Ala Met Arg Met
 145 150 155 160

Met Ala Ser Gly Lys Lys Gln Lys Asn Gly Ser Ala Gly Arg Lys Ala
165 170 175

Lys Lys Ala Arg Arg Lys Lys Val Asn Asp Leu Arg Leu Asp Met Gln
180 185 190

Gly Asp Glu His Glu Glu Gly Gly Gly Gly Arg Ser Glu Ser Thr Glu
195 200 205

Ser Ser Ala Gly Gly Gly Val Gly Gly Glu Arg Gln Arg Glu His Pro
210 215 220

Phe Val Val Thr Glu Pro Gly Glu Val Ala Arg Ala Lys Lys Asn Gly
225 230 235 240

Leu Asp Tyr Leu Phe His Leu Tyr Glu Gln Cys Arg Leu Phe Leu Leu
245 250 255

Gln Val Gln Ser Met Ala Lys Leu His Gly Gln Lys Ser Pro Thr Lys
260 265 270

Val Thr Asn Gln Val Phe Arg Tyr Ala Ser Lys Val Gly Ala Ser Tyr
275 280 285

Ile Asn Lys Pro Lys Met Arg His Tyr Val His Cys Tyr Ala Leu His
290 295 300

Cys Leu Asp Glu Asp Ala Ser Asp Ala Leu Arg Arg Ala Tyr Lys Ala
305 310 315 320

Arg Gly Glu Asn Val Gly Ala Trp Arg Gln Ala Cys Tyr Ala Pro Leu
325 330 335

Val Asp Ile Ala Ala Arg His Gly Phe Asp Ile Asp Ala Val Phe Ala
340 345 350

Ala His Pro Arg Leu Ala Ile Trp Tyr Val Pro Thr Arg Leu Arg Gln
355 360 365

Leu Cys His Gln Ala Arg Ser Ala His Asp Thr Ala Ala Ala His Ala
370 375 380

Gly Ala Met Pro Pro Pro Met Phe
385 390

<210> 168
<211> 392
<212> PRT
<213> Triticum aestivum

<400> 168

Met Asp Pro Asn Asp Ala Phe Leu Ala Ala His Pro Phe Arg Trp Asp
1 5 10 15

Leu Gly Pro Pro Ala Pro Ala Ala Val Pro Pro Pro Pro Pro Pro Pro
20 25 30

Pro Leu Pro Pro Ala Leu Pro Pro Ala Asn Ala Pro Arg Glu Leu Glu
35 40 45

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

Ser Glu Leu Gly Phe Thr Ala Ser Thr Leu Leu Val Met Thr Glu Ser
65 70 75 80

Glu Leu Asp Asp Met Thr Ala Ala Leu Ala Gly Leu Phe Arg Trp Asp
85 90 95

Leu Leu Ile Gly Glu Arg Phe Gly Leu Arg Ala Ala Leu Arg Ala Glu
100 105 110

Arg Gly Arg Leu Met Ser Pro Gly Cys Arg His His Gly Tyr Gln Ser
115 120 125

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

Asp Gly Ala Ala Ser Gly Gly Ile Gly Glu Asp Asp Ala Met Arg Met
145 150 155 160

Met Ala Ser Gly Lys Lys Gln Lys Asn Gly Ser Ala Ala Arg Lys Ala
165 170 175

Lys Lys Ala Arg Arg Asn Lys Val Lys Glu Leu Arg Leu Asp Met Gln
180 185 190

Gly Asp Glu His Glu Asp Gly Gly Gly Gly Arg Ser Glu Ser Thr Glu
195 200 205

Ser Ser Ala Gly Gly Val Gly Gly Glu Arg Gln Arg Glu His Pro Phe
210 215 220

Val Val Thr Glu Pro Gly Glu Val Ala Arg Ala Lys Lys Asn Gly Leu
225 230 235 240

Asp Tyr Leu Phe His Leu Tyr Glu Gln Arg Arg Leu Phe Leu Leu Gln
245 250 255

Val Gln Ser Met Ala Lys Leu His Gly Gln Lys Ser Pro Thr Lys Val
260 265 270

Thr Asn Gln Val Phe Arg Tyr Ala Ser Lys Val Gly Ala Ser Tyr Ile
275 280 285

Asn Lys Pro Lys Met Arg His Tyr Val His Cys Tyr Ala Leu His Cys
290 295 300

Leu Asp Glu Asp Ala Ser Asp Ala Leu Arg Arg Ala Tyr Lys Ala Arg
305 310 315 320

Gly Glu Asn Val Gly Ala Trp Arg Gln Ala Cys Tyr Ala Pro Leu Val
325 330 335

Asp Ile Ala Ala Arg His Gly Phe Asp Ile Asp Ala Val Phe Ala Ala
340 345 350

His Pro Arg Leu Ala Ile Trp Tyr Val Pro Thr Arg Leu Arg Gln Leu
355 360 365

Cys His Gln Ala Arg Ser Ala His Asp Ala Ala Ala Ala Ala His Ala
370 375 380

Gly Ser Met Pro Pro Pro Met Phe
385 390

<210> 169
<211> 400
<212> PRT
<213> Lolium temulentum

<400> 169

Met Asp Pro His Asp Ala Phe Leu Ala Ala His Pro Phe Arg Trp Asp
1 5 10 15

Leu Gly Pro Pro Ala Pro Ala Ala Val Pro Pro Pro Pro Pro Leu Pro
20 25 30

Met Pro Gln Thr Pro Ala Leu Pro Pro Ala Asn Ser Pro Arg Glu Leu
 35 40 45

Glu Asp Leu Val Ala Gly Tyr Gly Val Arg Gly Ala Thr Val Ala Arg
 50 55 60

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

Arg Glu Leu Asp Asp Met Thr Ala Ala Leu Ala Gly Leu Phe Arg Trp
 85 90 95

Asp Leu Leu Ile Gly Glu Arg Phe Gly Leu Arg Ala Ala Leu Arg Ala
 100 105 110

Glu Arg Gly Arg Leu Met Ala Leu His Gly Gly Arg His His Gly His
 115 120 125

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

Glu Arg Asp Gly Ala Ala Ser Gly Glu Asp Asp Ala Gly Arg Met Met
 145 150 155 160

Leu Ser Gly Lys Lys Leu Lys Asn Gly Ser Val Ala Arg Lys Ala Lys
 165 170 175

Lys Ala Arg Arg Lys Lys Val Asp Gly Leu Arg Leu Asp His Met Gln
 180 185 190

Glu Asp Glu Arg Glu Asp Gly Gly Gly Arg Ser Glu Ser Thr Glu Ser
 195 200 205

Ser Ala Gly Gly Gly Gly Gly Val Gly Gly Glu Arg Gln Arg Glu His
 210 215 220

Pro Phe Val Val Thr Glu Pro Gly Glu Val Ala Arg Ala Lys Lys Asn
 225 230 235 240

Gly Leu Asp Tyr Leu Phe His Leu Tyr Glu Gln Cys Arg Leu Phe Leu
 245 250 255

Leu Gln Val Gln Ser Met Ala Lys Leu His Gly His Lys Ser Pro Thr
 260 265 270

Lys Val Thr Asn Gln Val Phe Arg Tyr Ala Ser Lys Val Gly Ala Ser

275

280

285

Tyr Ile Asn Lys Pro Lys Met Arg His Tyr Val His Cys Tyr Ala Leu
 290 295 300

His Cys Leu Asp Gln Glu Ala Ser Asp Ala Leu Arg Arg Ala Tyr Lys
 305 310 315 320

Ala Arg Gly Glu Asn Val Gly Ala Trp Arg Gln Ala Cys Tyr Ala Pro
 325 330 335

Leu Val Asp Ile Ala Ala Gly His Gly Phe Asp Val Asp Ala Val Phe
 340 345 350

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

Gln Leu Cys His Gln Ala Arg Ser Ala His Glu Ala Ala Ala Ala Asn
 370 375 380

Ala Asn Ala Asn Gly Ala Met Pro Pro Pro Pro Pro Pro Met Phe
 385 390 395 400

<210> 170
 <211> 389
 <212> PRT
 <213> Oryza sativa

<400> 170

Met Asp Pro Asn Asp Ala Phe Ser Ala Ala His Pro Phe Arg Trp Asp
 1 5 10 15

Leu Gly Pro Pro Ala Pro Ala Pro Val Pro Pro Pro Pro Pro Pro Pro
 20 25 30

Pro Pro Pro Pro Pro Ala Asn Val Pro Arg Glu Leu Glu Glu Leu Val
 35 40 45

Ala Gly Tyr Gly Val Arg Met Ser Thr Val Ala Arg Ile Ser Glu Leu
 50 55 60

Gly Phe Thr Ala Ser Thr Leu Leu Ala Met Thr Glu Arg Glu Leu Asp
 65 70 75 80

Asp Met Met Ala Ala Leu Ala Gly Leu Phe Arg Trp Asp Leu Leu Leu
 85 90 95

Gly Glu Arg Phe Gly Leu Arg Ala Ala Leu Arg Ala Glu Arg Gly Arg
100 105 110

Leu Met Ser Leu Gly Gly Arg His His Gly His Gln Ser Gly Ser Thr
115 120 125

Val Asp Gly Ala Ser Gln Glu Val Leu Ser Asp Glu His Asp Met Ala
130 135 140

Gly Ser Gly Gly Met Gly Asp Asp Asp Asn Gly Arg Arg Met Val Thr
145 150 155 160

Gly Lys Lys Gln Ala Lys Lys Gly Ser Ala Ala Arg Lys Gly Lys Lys
165 170 175

Ala Arg Arg Lys Lys Val Asp Asp Leu Arg Leu Asp Met Gln Glu Asp
180 185 190

Glu Met Asp Cys Cys Asp Glu Asp Gly Gly Gly Gly Ser Glu Ser Thr
195 200 205

Glu Ser Ser Ala Gly Gly Gly Gly Gly Glu Arg Gln Arg Glu His Pro
210 215 220

Phe Val Val Thr Glu Pro Gly Glu Val Ala Arg Ala Lys Lys Asn Gly
225 230 235 240

Leu Asp Tyr Leu Phe His Leu Tyr Glu Gln Cys Arg Leu Phe Leu Leu
245 250 255

Gln Val Gln Ser Met Ala Lys Leu His Gly His Lys Ser Pro Thr Lys
260 265 270

Val Thr Asn Gln Val Phe Arg Tyr Ala Lys Lys Val Gly Ala Ser Tyr
275 280 285

Ile Asn Lys Pro Lys Met Arg His Tyr Val His Cys Tyr Ala Leu His
290 295 300

Cys Leu Asp Glu Glu Ala Ser Asp Ala Leu Arg Arg Ala Tyr Lys Ala
305 310 315 320

Arg Gly Glu Asn Val Gly Ala Trp Arg Gln Ala Cys Tyr Ala Pro Leu
325 330 335

Val Asp Ile Ser Ala Arg His Gly Phe Asp Ile Asp Ala Val Phe Ala
340 345 350

Ala His Pro Arg Leu Ala Ile Trp Tyr Val Pro Thr Arg Leu Arg Gln
355 360 365

Leu Cys His Gln Ala Arg Ser Ser His Ala Ala Ala Ala Ala Leu
370 375 380

Pro Pro Pro Leu Phe
385

<210> 171
<211> 393
<212> PRT
<213> Zea mays

<400> 171

Asp Pro Asn Asp Ala Phe Ser Ala Ala His Pro Phe Arg Trp Asp Leu
1 5 10 15

Gly Pro Pro Ala Pro Ala Ala Pro Ala Pro Pro Pro Pro Pro Pro Pro
20 25 30

Ala Pro Gln Leu Leu Pro His Ala Pro Leu Leu Ser Ala Pro Arg Glu
35 40 45

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

Arg Ile Ser Glu Leu Gly Phe Thr Ala Ser Thr Leu Leu Gly Met Thr
65 70 75 80

Glu Arg Glu Leu Asp Asp Met Met Ala Ala Leu Ala Gly Leu Phe Arg
85 90 95

Trp Asp Val Leu Leu Gly Glu Arg Phe Gly Leu Arg Ala Ala Leu Arg
100 105 110

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

Ser Thr Leu Asp Ala Ala Ser Gln Glu Val Leu Ser Asp Glu Arg Asp
130 135 140

Ala Ala Ala Ser Gly Gly Leu Ala Glu Gly Glu Ala Gly Arg Arg Met
145 150 155 160

Val Thr Thr Gly Lys Lys Lys Gly Lys Lys Gly Val Gly Ala Arg Lys
165 170 175

Gly Lys Lys Ala Arg Arg Lys Lys Glu Leu Arg Pro Leu Asp Val Leu
180 185 190

Asp Asp Glu Asn Asp Gly Asp Glu Asp Gly Gly Gly Gly Gly Ser Asp
195 200 205

Ser Thr Glu Ser Ser Ala Gly Gly Ser Gly Gly Gly Glu Arg Gln Arg
210 215 220

Glu His Pro Phe Val Val Thr Glu Pro Gly Glu Val Ala Arg Ala Lys
225 230 235 240

Lys Asn Gly Leu Asp Tyr Leu Phe His Leu Tyr Glu Gln Cys Arg Val
245 250 255

Phe Leu Leu Gln Val Gln Ser Leu Ala Lys Leu Gly Gly His Lys Ser
260 265 270

Pro Thr Lys Val Thr Asn Gln Val Phe Arg Tyr Ala Lys Lys Cys Gly
275 280 285

Ala Ser Tyr Ile Asn Lys Pro Lys Met Arg His Tyr Val His Cys Tyr
290 295 300

Ala Leu His Cys Leu Asp Glu Asp Ala Ser Asn Ala Leu Arg Arg Ala
305 310 315 320

Tyr Lys Ala Arg Gly Glu Asn Val Gly Ala Trp Arg Gln Ala Cys Tyr
325 330 335

Ala Pro Leu Val Glu Ile Ala Ala Arg His Gly Phe Asp Ile Asp Ala
340 345 350

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

Leu Arg Gln Leu Cys His Gln Ala Arg Gly Ser His Ala His Ala Ala
370 375 380

Ala Gly Leu Pro Pro Pro Pro Met Phe
385 390

<210> 172
<211> 391
<212> PRT
<213> Zea mays

<400> 172

Met Asp Pro Asn Asp Ala Phe Ser Ala Ala His Pro Phe Arg Trp Asp
1 5 10 15

Leu Gly Pro Pro Ala His Ala Ala Pro Ala Pro Ala Pro Pro Pro Pro
20 25 30

Pro Leu Ala Pro Leu Leu Leu Pro Pro His Ala Pro Arg Glu Leu Glu
35 40 45

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

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

Glu Leu Asp Asp Met Met Ala Ala Leu Ala Gly Leu Phe Arg Trp Asp
85 90 95

Val Leu Leu Gly Glu Arg Phe Gly Leu Arg Ala Ala Leu Arg Ala Glu
100 105 110

Arg Gly Arg Val Met Ser Leu Gly Ala Arg Cys Phe His Ala Gly Ser
115 120 125

Thr Leu Asp Ala Ala Ser Gln Glu Ala Leu Ser Asp Glu Arg Asp Ala
130 135 140

Ala Ala Ser Gly Gly Gly Met Ala Glu Gly Glu Ala Gly Arg Arg Met
145 150 155 160

Val Thr Thr Thr Ala Gly Lys Lys Gly Lys Lys Gly Val Val Gly Thr
165 170 175

Arg Lys Gly Lys Lys Ala Arg Arg Lys Lys Glu Leu Arg Pro Leu Asn
180 185 190

Val Leu Asp Asp Glu Asn Asp Gly Asp Glu Tyr Gly Gly Gly Ser Glu
195 200 205

Ser Thr Glu Ser Ser Ala Gly Gly Ser Gly Glu Arg Gln Arg Glu His

210

215

220

Pro Phe Val Val Thr Glu Pro Gly Glu Val Ala Arg Ala Lys Lys Asn
 225 230 235 240

Gly Leu Asp Tyr Leu Phe His Leu Tyr Glu Gln Cys Arg Val Phe Leu
 245 250 255

Leu Gln Val Gln Ser Ile Ala Lys Leu Gly Gly His Lys Ser Pro Thr
 260 265 270

Lys Val Thr Asn Gln Val Phe Arg Tyr Ala Asn Lys Cys Gly Ala Ser
 275 280 285

Tyr Ile Asn Lys Pro Lys Met Arg His Tyr Val His Cys Tyr Ala Leu
 290 295 300

His Cys Leu Asp Glu Glu Ala Ser Asn Ala Leu Arg Arg Ala Tyr Lys
 305 310 315 320

Ser Arg Gly Glu Asn Val Gly Ala Trp Arg Gln Ala Cys Tyr Ala Pro
 325 330 335

Leu Val Glu Ile Ala Ala Arg His Gly Phe Asp Ile Asp Ala Val Phe
 340 345 350

Ala Ala His Pro Arg Leu Ala Val Trp Tyr Val Pro Thr Arg Leu Arg
 355 360 365

Gln Leu Cys His Gln Ala Arg Gly Ser His Ala His Ala Ala Ala Gly
 370 375 380

Leu Pro Pro Pro Pro Met Phe
 385 390

<210> 173
 <211> 456
 <212> PRT
 <213> Ophrys tenthredinifera

<400> 173

Met Val Leu Ala Thr Ser Gln Gln His His Gln His Asn Pro His Glu
 1 5 10 15

Val Gln Gln His Leu Gln Pro His Ser Thr Ala Thr Glu Ser Ser Arg
 20 25 30

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

Ala Arg Ile Gly Asp Leu Gly Phe Thr Ala Ser Thr Leu Ala Gly Met
50 55 60

Arg Glu Glu Glu Val Asp Asp Met Met Ala Ala Leu Ser His Leu Phe
65 70 75 80

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

Arg Ala Glu Arg Arg Arg Leu Glu Ala Leu Ile Phe Ser His Val Ser
100 105 110

Gly Ala Ala Arg Leu Ser His His Gln His Gln Met Gly Tyr Leu Phe
115 120 125

Ser Ser Ala Thr Thr Gly Tyr His Leu Met Pro Asp Asp Pro Arg Lys
130 135 140

Arg His Leu Leu Leu Ser Pro Asp His His Ser Ala Leu Asp Ala Leu
145 150 155 160

Ser Gln Glu Gly Leu Ser Glu Glu Pro Val Gln Leu Glu Arg Glu Ala
165 170 175

Ala Gly Ser Gly Gly Glu Val Val Gly Arg Arg Asp Gly Lys Gly Lys
180 185 190

Asn Gln Gln Arg Gln Thr Ser Ala Lys Lys Lys Asp Ala Ser Ser Thr
195 200 205

Lys Ser Lys Lys Lys Lys Lys Lys Gly Ile Glu Glu Gly Asp Asp Glu
210 215 220

Glu Glu Glu Val Glu Val Trp Gly Arg Gly Ala Ser Ile Glu Asn Asp
225 230 235 240

Glu Asp Asp Asp Gly Asp Glu Ser Gln Ser Glu Gln Ser Ser Ala Ala
245 250 255

Glu Arg Gln Arg Glu His Pro Phe Ile Val Thr Glu Pro Gly Glu Val
260 265 270

Ala Arg Ala Lys Lys Asn Gly Leu Asp Tyr Leu Phe Asn Leu Tyr Glu
275 280 285

Gln Cys His Glu Phe Leu Asn Gln Val Gln Ser Val Ala Lys Glu Arg
290 295 300

Gly Asp Lys Cys Pro Thr Lys Val Thr Asn Leu Val Phe Arg Tyr Ala
305 310 315 320

Lys Lys Lys Val Gly Ala Ser Tyr Ile Asn Lys Pro Lys Met Arg His
325 330 335

Tyr Val His Cys Tyr Ala Leu His Val Leu Asp Glu Asp Ala Ser Asn
340 345 350

Ser Leu Arg Arg Ala Phe Lys Glu Arg Gly Glu Asn Val Gly Ala Trp
355 360 365

Arg Leu Ala Cys Tyr Lys Pro Leu Val Ala Ile Ser Ala Ser His Ser
370 375 380

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

Tyr Val Pro Thr Lys Leu Arg Gln Leu Cys His Leu Ala Arg Ser Ser
405 410 415

Thr Ser Gln Phe Pro Leu Ala Val Pro Arg Thr Thr Gly Ser Ser Asn
420 425 430

Gln Arg Val Ser Ser Thr Val His Val Val Glu Asp Ser Ala Ala Ala
435 440 445

His Ser Phe Arg Pro Pro Met Phe
450 455

<210> 174
<211> 412
<212> PRT
<213> Lycopersicon esculentum

<400> 174

Met Asp Pro Asp Ala Phe Ser Ala Ser Leu Phe Lys Trp Asp Pro Arg
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275 280 285

Val Thr Asn Gln Val Phe Arg Tyr Ala Lys Lys Ala Gly Ala Ser Tyr
290 295 300

Ile Asn Lys Pro Lys Met Arg His Tyr Val His Cys Tyr Ala Leu His
305 310 315 320

Cys Leu Asp Glu Asp Ala Ser Asn Ala Leu Arg Arg Ala Phe Lys Glu
325 330 335

Arg Gly Glu Asn Val Gly Ala Trp Arg Gln Ala Cys Tyr Lys Pro Leu
340 345 350

Val Ala Ile Ala Ala Arg Gln Gly Trp Asp Ile Asp Ala Ile Phe Asn
355 360 365

Ala His Pro Arg Leu Ala Ile Trp Tyr Val Pro Thr Lys Leu Arg Gln
370 375 380

Leu Cys His Ser Glu Arg Ser Asn Ala Ala Ala Ala Ser Ser Ser
385 390 395 400

Val Ser Gly Gly Val Ala Asp His Leu Pro His Phe
405 410

<210> 175
<211> 367
<212> PRT
<213> Carica papaya

<400> 175

Met Asp Pro Asp Gly Phe Ser Ser Ser Leu Phe Lys Trp Asp Pro Thr
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Ala Pro Thr Gln Ala Ala Tyr Gly Val Arg Pro Arg Glu Leu Gly Gly
35 40 45

Leu Glu Glu Leu Phe Gln Asp Tyr Gly Ile Arg Tyr Phe Thr Ala Ala
50 55 60

Lys Ile Ala Glu Leu Gly Phe Thr Ala Ser Thr Leu Val Asp Met Lys

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Trp	Glu	Leu	Leu	Val	Gly	Glu	Arg	Tyr	Gly	Ile	Lys	Ala	Ala	Val	Arg
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Ala	Glu	Arg	Arg	Arg	Leu	Asp	Asp	Asp	Asp	Ser	Arg	Arg	Arg	Gln	Thr
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Leu	Ser	Thr	Asp	Thr	Thr	His	Ala	Leu	Asp	Ala	Leu	Ser	Gln	Glu	Gly
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Gly	Gly	Thr	Ile	Trp	Glu	Val	Gly	Pro	Gly	Lys	Lys	Lys	Gln	Arg	Arg
			165						170					175	
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Ser	Glu	Arg	Gln	Arg	Glu	His	Pro	Phe	Ile	Val	Thr	Glu	Pro	Gly	Glu
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Arg	Gly	Glu	Lys	Cys	Pro	Thr	Lys	Val	Thr	Asn	Gln	Val	Phe	Arg	Tyr
				245					250					255	
Ala	Lys	Lys	Ala	Gly	Ala	Ser	Tyr	Ile	Asn	Lys	Pro	Lys	Met	Arg	His
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Tyr	Val	His	Cys	Tyr	Ala	Leu	His	Cys	Leu	Asp	Glu	Lys	Glu	Ser	Asn
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Ala	Leu	Arg	Thr	Ala	Phe	Lys	Glu	Arg	Gly	Glu	Asn	Val	Gly	Ser	Trp
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Arg	Gln	Ala	Cys	Tyr	Lys	Pro	Leu	Val	Ala	Ile	Ala	Ala	Arg	Gln	Gly
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Trp Asp Ile Asp Ala Ile Phe Asn Ala His Pro Arg Leu Ala Ile Trp
325 330 335

Tyr Val Pro Asn Lys Leu Arg Gln Leu Cys His Ala Glu Arg Asn Asn
340 345 350

Thr Ala Ile Ala Ser Thr Ser Ala Ala Ala His His Leu Pro Phe
355 360 365

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<213> Arabidopsis thaliana

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<212> DNA
<213> Brassica juncea

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<211> 1281
<212> DNA
<213> Ionopsidium acaule

<400> 178

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<211> 1254

<212> DNA

<213> Leavenworthia crassa

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 <212> DNA
 <213> Selenia aurea

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 <211> 1293
 <212> DNA
 <213> Arabidopsis lyrata

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 <213> Streptanthus glandulosus

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<213> Cochlearia officinalis

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<213> Brassica oleracea

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 <213> *Idahoia scapigera*

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 <213> Capsella bursa-pastoris

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 <213> *Barbarea vulgaris*

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 <212> DNA
 <213> *Antirrhinum majus* subsp. *majus floricaula*

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 <211> 1242
 <212> DNA
 <213> Nicotiana tabacum

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 <212> DNA
 <213> *Nicotiana tabacum*

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<210> 192
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 <212> DNA
 <213> Triticum aestivum

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<210> 193
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 <212> DNA
 <213> Triticum aestivum

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 <211> 1203
 <212> DNA
 <213> *Lolium temulentum*

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 <213> *Oryza sativa*

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 <213> Zea mays

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<212> DNA
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