

PF58581.ST25.txt
SEQUENCE LISTING

<110> CropDesign N.V.

<120> Plants having increased seed yield and a method for making the same

<130> PF58581

<150> EP 06124785.4

<151> 2006-11-24

<150> US 60/868,381

<151> 2006-12-04

<150> EP 06125156.7

<151> 2006-11-30

<150> US 60/883,166

<151> 2007-01-03

<150> EP 06126018.8

<151> 2006-12-13

<150> US 60/883,170

<151> 2007-01-03

<160> 241

<170> PatentIn version 3.3

<210> 1

<211> 945

<212> DNA

<213> Arabidopsis thaliana

<400> 1

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cgcaaaccaa	caactgagat	taaagatttc	cagatcgtgg	tctctgcttc	cgacaaagaa	180
ccaaacaaga	agagtcagaa	tcagaaccag	cttggtccta	agagaagctc	taacaaagac	240
agacacacta	aagtcgaagg	tagaggtcga	cgaattcgga	tgcctgctct	ttgtgctgct	300
aggatttttc	aattgactag	agaattgggt	cataaatctg	atggtgaaac	tatccagtgg	360
ctgcttcaac	aagctgagcc	atcgattatt	gcagctactg	gttcaggaac	tataccggcc	420
tctgctttag	cttcttcagc	tgcaacctct	aaccatcatc	aagggtgggtc	tcttactgct	480
gggtttaatga	tcagtcatga	cttagatggg	gggtctagta	gtagtggtag	accattaaat	540
tgggggattg	gtggcggtga	aggagtttct	aggtaagtt	taccaactgg	gttatggcca	600
aatgtagctg	ggtttggttc	tgggtgtgcca	accactgggt	taatgagtga	aggagctggg	660
tatagaattg	ggtttcctgg	ttttgatttt	cctggtgttg	gtcatatgag	ttttgcatct	720
attttggggtg	ggaatcataa	tcagatgcct	ggacttgagt	taggcttgct	tcaagaaggg	780
aatgttggtg	ttttgaatcc	tcagtccttt	actcagattt	atcaacagat	gggtcaggct	840
caggtcgaag	ctcaaggtag	ggttcttcac	catatgcata	ataaccatga	agaacatcag	900
caagagagtg	gtgagaaaga	tgattctcaa	ggctcaggct	gttaa		945

<210> 2

<211> 314

<212> PRT

<213> Arabidopsis thaliana

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<400> 2

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20      25      30
Ser Ala Val Val Ser Asp Glu Asn Arg Lys Pro Thr Thr Glu Ile Lys
35      40      45
Asp Phe Gln Ile Val Val Ser Ala Ser Asp Lys Glu Pro Asn Lys Lys
50      55      60
Ser Gln Asn Gln Asn Gln Leu Gly Pro Lys Arg Ser Ser Asn Lys Asp
65      70      75      80
Arg His Thr Lys Val Glu Gly Arg Gly Arg Arg Ile Arg Met Pro Ala
85      90      95
Leu Cys Ala Ala Arg Ile Phe Gln Leu Thr Arg Glu Leu Gly His Lys
100     105     110
Ser Asp Gly Glu Thr Ile Gln Trp Leu Leu Gln Gln Ala Glu Pro Ser
115     120     125
Ile Ile Ala Ala Thr Gly Ser Gly Thr Ile Pro Ala Ser Ala Leu Ala
130     135     140
Ser Ser Ala Ala Thr Ser Asn His His Gln Gly Gly Ser Leu Thr Ala
145     150     155     160
Gly Leu Met Ile Ser His Asp Leu Asp Gly Gly Ser Ser Ser Ser Gly
165     170     175
Arg Pro Leu Asn Trp Gly Ile Gly Gly Gly Glu Gly Val Ser Arg Ser
180     185     190
Ser Leu Pro Thr Gly Leu Trp Pro Asn Val Ala Gly Phe Gly Ser Gly
195     200     205
Val Pro Thr Thr Gly Leu Met Ser Glu Gly Ala Gly Tyr Arg Ile Gly
210     215     220
Phe Pro Gly Phe Asp Phe Pro Gly Val Gly His Met Ser Phe Ala Ser
225     230     235     240
Ile Leu Gly Gly Asn His Asn Gln Met Pro Gly Leu Glu Leu Gly Leu
245     250     255
Ser Gln Glu Gly Asn Val Gly Val Leu Asn Pro Gln Ser Phe Thr Gln
260     265     270
Ile Tyr Gln Gln Met Gly Gln Ala Gln Ala Gln Ala Gln Gly Arg Val
275     280     285
Leu His His Met His His Asn His Glu Glu His Gln Gln Glu Ser Gly
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<210> 3

<211> 732

<212> DNA

<213> Arabidopsis thaliana

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ggcgaaaaga ggaagaagaa ggagaatgaa gaggaagacc aagaaattca gattctttat      180
gagaaggaga agaagaaacc aaacaaagat cgtcacctta aagttgaagg aagaggtcgt      240
agagttaggt tacctccact ctgtgcagca aggatttatc aattgactaa agaattaggt      300
cacaaatcag atggtgagac tcttgaatgg ttgcttcaac atgctgagcc atcgatactc      360
tctgctactg taaatggtat caaacccact gagtctgttg tttctcaacc tcctctcacg      420
gctgatttga tgatttgtca tagcgttgaa gaagcttcaa ggactcaaat ggaggcaaat      480
gggttgtgga gaaatgaaac aggacagacc attggagggt ttgatctgaa ttacggaatt      540
gggtttgatt tcaatggtgt tccagagatt ggttttggag ataatcaaac gcctggactt      600
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<210> 4
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<212> PRT
<213> Arabidopsis thaliana

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

<210> 5
<211> 930
<212> DNA
<213> Aquilegia formosa x Aquilegia pubescens

<400> 5
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cattcttcac aacaagagat gggaggagga ggaggagaga ataaacaaac agaaatcaga 120
gattttcaaa tctcaacagt tgttgcagat aaagatggtg gtaagaagca gttagcacca 180
aaaagaactt caaataaaga tagacatact aaggtagatg gaagaggtag aaggataagg 240
atgccagctt tatgtgcagc tagaattttt cagttaacaa gagaattggg tcataaatct 300
gatggagaaa ctatacaatg gttattacaa catgctgaac catcaataat tgccgctaca 360
ggtactggaa ctataccagc ttcagcttta gttcaatcta gtagctcagt ttcacaacag 420
gggaattctg tttcagttgg tttacaaaca aagatcagtg aattgggaca tgaaattggg 480
tccagtagta gtaggaccaa ttggaatttg gttagatccc cagtaacaac aagtttatgg 540
ccctctgtca gtggttatgt accagggttt catccttctt caggccaacc gacatcgaat 600
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cttcctggat tggaattagg attatctcaa gatgtgcata ccgggggtatt gaatcctcaa 780
gctttacagt tttatcagca gatggttcaa tcaagaggag ttgtcatgca tcaacaacag 840
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gaggatgatt ctcaagggtc aagacattaa 930

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<210> 6
 <211> 309
 <212> PRT
 <213> Aquilegia formosa x Aquilegia pubescens

<400> 6

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		20					25					30			
Glu	Asn	Lys	Gln	Thr	Glu	Ile	Arg	Asp	Phe	Gln	Ile	Ser	Thr	Val	Val
		35				40					45				
Ala	Asp	Lys	Asp	Gly	Gly	Lys	Lys	Gln	Leu	Ala	Pro	Lys	Arg	Thr	Ser
	50					55				60					
Asn	Lys	Asp	Arg	His	Thr	Lys	Val	Asp	Gly	Arg	Gly	Arg	Arg	Ile	Arg
65				70				75						80	
Met	Pro	Ala	Leu	Cys	Ala	Ala	Arg	Ile	Phe	Gln	Leu	Thr	Arg	Glu	Leu
				85				90					95		
Gly	His	Lys	Ser	Asp	Gly	Glu	Thr	Ile	Gln	Trp	Leu	Leu	Gln	His	Ala
	100						105					110			
Glu	Pro	Ser	Ile	Ile	Ala	Ala	Thr	Gly	Thr	Gly	Thr	Ile	Pro	Ala	Ser
	115						120					125			
Ala	Leu	Val	Gln	Ser	Ser	Ser	Ser	Val	Ser	Gln	Gln	Gly	Asn	Ser	Val
	130						135			140					
Ser	Val	Gly	Leu	Gln	Thr	Lys	Ile	Ser	Glu	Leu	Gly	His	Glu	Ile	Gly
145				150				155						160	
Ser	Ser	Ser	Ser	Arg	Thr	Asn	Trp	Asn	Leu	Val	Arg	Ser	Pro	Val	Thr
				165				170					175		
Thr	Ser	Leu	Trp	Pro	Ser	Val	Ser	Gly	Tyr	Val	Pro	Gly	Phe	His	Pro
		180						185					190		
Ser	Ser	Gly	Gln	Pro	Thr	Ser	Asn	Leu	Ser	Ser	Asp	Gly	Leu	Asn	Tyr
	195						200					205			
Leu	Pro	Lys	Phe	Gly	Ile	His	Gly	Phe	Glu	Met	Pro	Gly	Ser	Asn	Leu
	210					215					220				
Gly	Thr	Met	Asn	Leu	Asn	Ser	Phe	Met	Gly	Val	Gly	Asn	Asn	Gln	Gln
225				230					235					240	
Leu	Pro	Gly	Leu	Glu	Leu	Gly	Leu	Ser	Gln	Asp	Val	His	Thr	Gly	Val
			245					250					255		
Leu	Asn	Pro	Gln	Ala	Leu	Gln	Phe	Tyr	Gln	Gln	Met	Val	Gln	Ser	Arg
	260						265						270		
Gly	Val	Val	Met	His	Gln	Gln	Gln	Gln	His	Gln	Gln	Gln	Gln	Gln	Gln
	275						280					285			
Gln	Gln	Gln	Gln	Gln	Gln	Gln	Pro	His	Asp	Asp	Asp	Glu	Asp	Asp	Ser
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Gln	Gly	Ser	Arg	His											
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<210> 7
 <211> 1038
 <212> DNA
 <213> Glycine max

<400> 7

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cctgcagagg  tgaaggattt ccagatagtg gtagctgaga acaaggaaga gagcaagaaa      180
cagcagcaac  agttggcacc aaagaggagt tccaacaagg acaggcacac caaggttgaa      240
ggcaggggaa  ggaggataag gatgcctgct ctctgcgcag ccagaatctt ccagttgacc      300
aggggaattgg gtcacaaatc tgatggggaa accatccagt ggctcctcca gcaggctgag      360
ccatccatca  tagctgccac tgggactggc acaataccag catctgctct tgctgctgct      420
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aagattgatg  aattgggtgg gtcagggggg agtagtagta gggccagctg gcaaatgggt      540
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cagaaaattg  cattccctgg ctttgacttg cctacttctg ccactaacat gatgggtcac      780
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ttggagcttg  gtctttccca ggatggccat attggggtgt tgaatcaaca ggccttgaac      900
cagattttatc agcagatgaa tcaggctggt agagtgcata atcatcagca tcagcatcat      960
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<210> 8
 <211> 345
 <212> PRT
 <213> Glycine max

<400> 8

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

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Gly Gly Ala Gln His Met Pro Gly Leu Glu Leu Gly Leu Ser Gln Asp
 275 280 285
 Gly His Ile Gly Val Leu Asn Gln Gln Ala Leu Asn Gln Ile Tyr Gln
 290 295 300
 Gln Met Asn Gln Ala Gly Arg Val His His His Gln His Gln His His
 305 310 315 320
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 325 330 335
 Asp Asp Ser Gln Gly Ser Gly Gly Gln
 340 345

<210> 9
 <211> 903
 <212> DNA
 <213> Gossypium hirsutum

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 gatttccaga ttgtggttgc agataaagga gaagggaaga agcaacagtt ggccccaag 180
 agaagttcta acaaagacag gcacacccaa gttgaaggaa gaggtagaag gataaggatg 240
 cctgctttat gtgctgctag aatctttcag ttgaccaggg aattgggtca caagtctgat 300
 ggggaaacca tacagtggct gttacaacaa gctgaaccat ccataattgc cgccactggg 360
 agcggaacaa ttccagcatc agctttggct gcagctggag gctcagtttc acagccaggg 420
 gcctctctat cagcagggtt gcacccaaaag atggaagatt taggggggtc cagtataggg 480
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 aatcctcatg ctttgaacca gatttatcag cagatggagc aagctcggat gcaaccccaa 840
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<210> 10
 <211> 300
 <212> PRT
 <213> Gossypium hirsutum

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 35 40 45
 Lys Gly Glu Gly Lys Lys Gln Gln Leu Ala Pro Lys Arg Ser Ser Asn
 50 55 60
 Lys Asp Arg His Thr Lys Val Glu Gly Arg Gly Arg Arg Ile Arg Met
 65 70 75 80
 Pro Ala Leu Cys Ala Ala Arg Ile Phe Gln Leu Thr Arg Glu Leu Gly
 85 90 95
 His Lys Ser Asp Gly Glu Thr Ile Gln Trp Leu Leu Gln Gln Ala Glu
 100 105 110
 Pro Ser Ile Ile Ala Ala Thr Gly Ser Gly Thr Ile Pro Ala Ser Ala
 115 120 125
 Leu Ala Ala Ala Gly Gly Ser Val Ser Gln Pro Gly Ala Ser Leu Ser
 130 135 140
 Ala Gly Leu His Gln Lys Met Glu Asp Leu Gly Gly Ser Ser Ile Gly

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145		150		155		160
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Arg Pro His His Val Ala Thr Gly Leu Trp Pro Pro Val Ser Gly Phe						
	180		185		190	
Gly Phe Gln Ser Ser Ser Gly Pro Ser Thr Thr Asn Leu Gly Ser Asp						
	195		200		205	
Ser Ser Asn Tyr Leu Gln Lys Leu Gly Phe Pro Gly Phe Asp Leu Pro						
	210		215		220	
Ala Ser Asn Met Gly Gln Ile Ser Phe Thr Ser Ile Leu Gly Gly Ala						
225		230		235		240
Asn Gln Gln Leu Pro Gly Leu Glu Leu Gly Leu Ser Gln Asp Gly His						
	245		250		255	
Ile Gly Val Leu Asn Pro His Ala Leu Asn Gln Ile Tyr Gln Gln Met						
	260		265		270	
Glu Gln Ala Arg Met Gln Pro Gln His Gln His Gln Gln Gln						
	275		280		285	
Pro Pro Ala Lys Asp Asp Ser Gln Gly Ser Gly Gln						
	290		295		300	

<210> 11
 <211> 819
 <212> DNA
 <213> Lycopersicon esculentum

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 catacaaaag ttgaaggtag agggaggaga atacgtatgc cggcgctctg tgcagcaaga 180
 atcttccagc ttacgcgcga attgggtcat aaatctgatg gtgagacaat tcagtggctg 240
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 aattggccaa tgatctgtgg gaattttgga agacccatt tggctacagc aggaatgtgg 480
 cctgcccctg cccctgttgt cactagtttt gggtttcaat cctcatctgc tccatcaagc 540
 gcgagtttag gtagtgatag ttcaaattat tacttacaga aaattgggtt tcttgattt 600
 gatctgcctg cagctacaag tatgaatccg atgtgtttta cttcaattct tgggtggaagt 660
 aatcagcaac tgccaggatt ggaactggga ttatctcaag agggtcattt aggggttttg 720
 aaccagatat accagcaggc aagaatgcaa catccgcagc agcaacatca acaacaacaa 780
 caatctccgg aggaggattc tcaaggatca ggacattaa 819

<210> 12
 <211> 272
 <212> PRT
 <213> Lycopersicon esculentum

<400> 12
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 Ala Ala Pro Lys Arg Lys Asp Arg His Thr Lys Val Glu Gly Arg Gly
 35 40 45
 Arg Arg Ile Arg Met Pro Ala Leu Cys Ala Ala Arg Ile Phe Gln Leu
 50 55 60
 Thr Arg Glu Leu Gly His Lys Ser Asp Gly Glu Thr Ile Gln Trp Leu
 65 70 75 80
 Leu Gln Gln Ala Glu Pro Ser Ile Ile Ala Ala Thr Gly Thr Gly Thr
 85 90 95

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

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<210> 13
 <211> 966
 <212> DNA
 <213> Malus domestica

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<400> 13
atggatccca agggctcaaa gcagacacaa gacataccca gcttcttgag ccttcccca      60
caatcacaaac cacaacctga gcagcagcag caaccacaac aacaacctca acccaacaac      120
aacatgagcg acaacaaacc tgctgaaatc aaagacttcc agattgtaat cgccgacaaa      180
gatgagtcgg gaaagaagca gttggcgccc aagagaagct ccaacaaaga cagacacact      240
aaagtgcgaag gcaggggaag gaggatacgg atgccggccc tctgcgccgc cagaatcttt      300
caattgacca gagagttggg tcacaaatcc gatggggaaa caatccagtg gtcctccag      360
caggccgagc cgtcgattgt tgccaccacc gggaccgga cgattccggc gtcggctttg      420
gcggcggcag gtggctctgt ttgcgaacag gggacttctt tatcagctgg attgcacaa      480
aagatcgatg aattgggggg gtccagtggg ggtaggacca gttgggcaat ggtgggcggg      540
aatttgggga gaccccatgt ggcaggggtg ggcgggctat ggccccctgt cagtagcttt      600
gggttccagt catcatctgg tcctccatcg gccaccacaa atctgggcac tgagagttca      660
aattacctgc aaaaaattgg gtttctctggc ttgacttgc ctgtctctaa catgggtccg      720
atgagtttta cttcaatttt ggggtgggggc aatcagcagc agcagcagca gcttctctgg      780
ttggaacttg ggttgtcaca ggatggacat attggggttc tgaactctca ggctttgagc      840
cagatttacc agcagatggg gcatgttaga gtgcaccagc agccgccgca gcaccaccac      900
cagcaacacc accaccacca gcagcaaccg cttccaagg acgattctca aggatccgga      960
cagtag                                           966

```

<210> 14
 <211> 321
 <212> PRT
 <213> Malus domestica

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<400> 14
Met Asp Pro Lys Gly Ser Lys Gln Thr Gln Asp Ile Pro Ser Phe Leu
1      5      10      15
Ser Leu Pro Pro Gln Ser Gln Pro Gln Pro Glu Gln Gln Gln Gln Pro
      20      25      30
Gln Gln Gln Pro Gln Pro Asn Asn Asn Met Ser Asp Asn Lys Pro Ala
      35      40      45

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

<210> 15
<211> 855
<212> DNA
<213> Medicago truncatula

<400> 15
atggatccca aaaactcaaa gcaacaatca caactctcaa acatgggaga gaacaaagaa 60
tcagagacaa aaaatcttca aattgtgtta tctgaaacaa caacaaaaga tgaaacaaag 120
aaacaactag caccaaaaag aacatcaaac aaagacagac acacaaaagt tgaaggaaga 180
ggaagaagaa taaggatgcc agctttatgt gcagcaagaa tctttcagct aacaagagag 240
ttaggtcata aatcagatgg tgaaacaatt caatggcttt tacaacaatc tgaaccatca 300
atcatagctg caacaggaac aggaacaata ccagcttcag ctttagcttc ttctggtaat 360
actttgacac cacaaggttc atctttgtct tctggtttac agttgaatga taggaatact 420
tgggctcaga cccatcaagc ccatcaggcc catcagggcc atcatgtagg ttctacaagt 480
ttatggccac atcatcatgt tgggtggattt ggatttcatac aatcatcatc atctgggtgtt 540
ttagtagcta ctactgttgg tgaaaataat agtggaattt attttcagaa aattgggttt 600
tctggatttg atatgccaac aggaacaaat ttgggagtgg gagggatgag ttttacttca 660
attttggggg gtgcaaatca gcagatgcct ggtttggaat tagggttgtc acaagatgga 720
catattggtg tgttgaatca acaagcttta actcagattt atcagcagat tgggtcaaaaat 780
caaactaggg ttcagcacca gaatcagcag aataataata ctactaagga tgattctcac 840
agttcagaac agtag 855

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<210> 16
 <211> 284
 <212> PRT
 <213> Medicago truncatula

<400> 16
 Met Asp Pro Lys Asn Ser Lys Gln Gln Ser Gln Leu Ser Asn Met Gly
 1 5 10 15
 Glu Asn Lys Glu Ser Glu Thr Lys Asn Leu Gln Ile Val Leu Ser Glu
 20 25 30
 Thr Thr Thr Lys Asp Glu Thr Lys Lys Gln Leu Ala Pro Lys Arg Thr
 35 40 45
 Ser Asn Lys Asp Arg His Thr Lys Val Glu Gly Arg Gly Arg Arg Ile
 50 55 60
 Arg Met Pro Ala Leu Cys Ala Ala Arg Ile Phe Gln Leu Thr Arg Glu
 65 70 75 80
 Leu Gly His Lys Ser Asp Gly Glu Thr Ile Gln Trp Leu Leu Gln Gln
 85 90 95
 Ser Glu Pro Ser Ile Ile Ala Ala Thr Gly Thr Gly Thr Ile Pro Ala
 100 105 110
 Ser Ala Leu Ala Ser Ser Gly Asn Thr Leu Thr Pro Gln Gly Ser Ser
 115 120 125
 Leu Ser Ser Gly Leu Gln Leu Asn Asp Arg Asn Thr Trp Ala Gln Thr
 130 135 140
 His Gln Ala His Gln Ala His Gln Gly His His Val Ser Ser Thr Ser
 145 150 155 160
 Leu Trp Pro His His His Val Gly Gly Phe Gly Phe His Gln Ser Ser
 165 170 175
 Ser Ser Gly Gly Leu Val Ala Thr Thr Val Gly Glu Asn Asn Ser Gly
 180 185 190
 Asn Tyr Phe Gln Lys Ile Gly Phe Ser Gly Phe Asp Met Pro Thr Gly
 195 200 205
 Thr Asn Leu Gly Val Gly Gly Met Ser Phe Thr Ser Ile Leu Gly Gly
 210 215 220
 Ala Asn Gln Gln Met Pro Gly Leu Glu Leu Gly Leu Ser Gln Asp Gly
 225 230 235 240
 His Ile Gly Val Leu Asn Gln Gln Ala Leu Thr Gln Ile Tyr Gln Gln
 245 250 255
 Ile Gly Gln Asn Gln Thr Arg Val Gln His Gln Asn Gln Gln Asn Asn
 260 265 270
 Asn Thr Thr Lys Asp Asp Ser His Ser Ser Glu Gln
 275 280

<210> 17
 <211> 888
 <212> DNA
 <213> Nicotiana benthamiana

<400> 17
 atgggatccca agcagccgcc agcgcagtct aacgcstatca acattaacaa caatattatg 60
 gttgagtaca ataagcctgt tcatgatcaa ataaaagatg atgaaaccaa gaagcggcag 120
 caattgggttc ctaaaagaaa agataggcac acaaaagtgt aaggcagagg gaggaggata 180
 cgtatgcctg ctctttgcgc tgctaggatt ttccaactca cccgcgaatt aggtcataaa 240
 tctgatggag agacaatcca gtggctgctg cagcaagccg agccctccat atttgcggcc 300
 accgggacag ggaccatccc tgctcggct ttagctgtag cagccgctgg cccctctgtt 360
 tcccaacaga ggacctctgt atctgctggg ttgcataaaa aaatggatga attgggagcg 420
 aatatagtcg ggtccgctag tatatgtagt agtagtagta ctagtagggc cagttggcca 480
 atgatgattg ggaatttttg aagaccccat ttggccacag caggaatatg gcccggaact 540
 actcctgttg tcaatagttt cgcgttacag acagcactga ctcttgatc aagcaccaat 600

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ttgggtagtg aaagttccaa ttattaccta caaaagattg gctttcctgg atttgatctg 660
cctgcagcca ccaatatgag ttttacttca attctagggt ccagtaataa ccagcaattg 720
ccagggttgg agcttggtt atctcaagac aggggtcata taggggtttt aaactctcaa 780
ggcttgagcc agatatacca ggctagaatt cataatcaac agcagcacca gcaaaatcag 840
catgagcatc tatctcccga ggatgattct cacggatcag gacactaa 888

```

<210> 18
 <211> 295
 <212> PRT
 <213> *Nicotiana benthamiana*

<400> 18

Met	Asp	Pro	Lys	Gln	Pro	Pro	Ala	Gln	Ser	Asn	Ala	Ile	Asn	Ile	Asn
1				5					10					15	
Asn	Asn	Ile	Met	Val	Glu	Tyr	Asn	Lys	Pro	Val	His	Asp	Gln	Ile	Lys
		20						25					30		
Asp	Asp	Glu	Thr	Lys	Lys	Arg	Gln	Gln	Leu	Val	Pro	Lys	Arg	Lys	Asp
		35					40					45			
Arg	His	Thr	Lys	Val	Glu	Gly	Arg	Gly	Arg	Arg	Ile	Arg	Met	Pro	Ala
		50				55					60				
Leu	Cys	Ala	Ala	Arg	Ile	Phe	Gln	Leu	Thr	Arg	Glu	Leu	Gly	His	Lys
65					70					75					80
Ser	Asp	Gly	Glu	Thr	Ile	Gln	Trp	Leu	Leu	Gln	Gln	Ala	Glu	Pro	Ser
				85					90					95	
Ile	Phe	Ala	Ala	Thr	Gly	Thr	Gly	Thr	Ile	Pro	Ala	Ser	Ala	Leu	Ala
			100					105					110		
Val	Ala	Ala	Ala	Gly	Pro	Ser	Val	Ser	Gln	Gln	Arg	Thr	Ser	Val	Ser
			115				120					125			
Ala	Gly	Leu	His	Lys	Lys	Met	Asp	Glu	Leu	Gly	Ala	Asn	Ile	Val	Gly
		130					135				140				
Ser	Ala	Ser	Ile	Cys	Ser	Ser	Ser	Ser	Thr	Ser	Arg	Ala	Ser	Trp	Pro
145					150					155					160
Met	Met	Ile	Gly	Asn	Phe	Gly	Arg	Pro	His	Leu	Ala	Thr	Ala	Gly	Ile
				165					170					175	
Trp	Pro	Gly	Pro	Thr	Pro	Val	Val	Asn	Ser	Phe	Ala	Leu	Gln	Thr	Ala
			180					185					190		
Leu	Thr	Pro	Gly	Ser	Ser	Thr	Asn	Leu	Gly	Ser	Glu	Ser	Ser	Asn	Tyr
		195					200					205			
Tyr	Leu	Gln	Lys	Ile	Gly	Phe	Pro	Gly	Phe	Asp	Leu	Pro	Ala	Ala	Thr
	210					215					220				
Asn	Met	Ser	Phe	Thr	Ser	Ile	Leu	Gly	Ser	Ser	Asn	Asn	Gln	Gln	Leu
225					230					235					240
Pro	Gly	Leu	Glu	Leu	Gly	Leu	Ser	Gln	Asp	Arg	Gly	His	Ile	Gly	Val
				245					250					255	
Leu	Asn	Ser	Gln	Gly	Leu	Ser	Gln	Ile	Tyr	Gln	Ala	Arg	Ile	His	Asn
			260					265					270		
Gln	Gln	Gln	His	Gln	Gln	Asn	Gln	His	Glu	His	Leu	Ser	Pro	Glu	Asp
			275				280					285			
Asp	Ser	His	Gly	Ser	Gly	His									
		290				295									

<210> 19
 <211> 894
 <212> DNA
 <213> *Ocimum basilicum*

<400> 19

atggatccga	agagctcgaa	gcagccgcag	gaggtttcga	atcacagcaa	caccaacagc	60
ttaggcgaaa	acaaagcagc	ggaaatcaag	gattttcaga	ttgtagttgc	ggagaaggat	120

PF58581.ST25.txt

```

gattcgaaga agctagccct agctccgaag cgaagctcca acaaggaccg ccacaccaag 180
gtggaaggcc gcggccggcg aattcggatg ccggcgctct gcgcccgcag aatcttccaa 240
ttgacccgag aattagggca caaatccgat ggcgagacca tccagtggct cctccagcaa 300
gccgagccgt cgatcatcgc cgccacgggg agcggcacca tccccgcctc cgccctcgcc 360
gcagccgccc gctcgatttc tcagcaaggt agctcgattt cgtctggact ccatcagaaa 420
atcgaggatt taggcgcttc tatgggtggt ggtgggggca ggaatccctg gcctatgatt 480
ggtgggaatc tgagtagacc acatgtgggc gcaagcacag gattatggcc tcccactgga 540
ttcggcttcc agacggcgtc gtcttcttcc tcgtctggtc cgtcaatcgc ggcggagaat 600
cctaattatc tccagaaaat ggggtttgct ggatttgagc tgcccgggaa tatcgggcag 660
atgagtttca cctccatctt aagcggcggc gggcagcagc tgcccggatt ggagctcggc 720
ctttcacaag atggaaatat tggggttttg aatccgcaag cttttgggca gatttatcag 780
cagattaatc cggcggcgcg tgtggttaac gcacatcaaa atcaccacca acaacaccac 840
catcagcagc cattgtcgtc gaaagatgat gattctcaag aatcaggaca gtag 894

```

<210> 20

<211> 297

<212> PRT

<213> Ocimum basilicum

<400> 20

```

Met Asp Pro Lys Ser Ser Lys Gln Pro Gln Glu Val Ser Asn His Ser
1      5      10      15
Asn Thr Asn Ser Leu Gly Glu Asn Lys Ala Ala Glu Ile Lys Asp Phe
20     25     30
Gln Ile Val Val Ala Glu Lys Asp Asp Ser Lys Lys Leu Ala Leu Ala
35     40     45
Pro Lys Arg Ser Ser Asn Lys Asp Arg His Thr Lys Val Glu Gly Arg
50     55     60
Gly Arg Arg Ile Arg Met Pro Ala Leu Cys Ala Ala Arg Ile Phe Gln
65     70     75     80
Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly Glu Thr Ile Gln Trp
85     90     95
Leu Leu Gln Gln Ala Glu Pro Ser Ile Ile Ala Ala Thr Gly Ser Gly
100    105    110
Thr Ile Pro Ala Ser Ala Leu Ala Ala Ala Ala Gly Ser Ile Ser Gln
115    120    125
Gln Gly Ser Ser Ile Ser Ser Gly Leu His Gln Lys Ile Glu Asp Leu
130    135    140
Gly Ala Ser Met Gly Gly Gly Gly Gly Arg Asn Pro Trp Pro Met Ile
145    150    155    160
Gly Gly Asn Leu Ser Arg Pro His Val Gly Ala Ser Thr Gly Leu Trp
165    170    175
Pro Pro Thr Gly Phe Gly Phe Gln Thr Ala Ser Ser Ser Ser Ser
180    185    190
Gly Pro Ser Ile Ala Ala Glu Asn Pro Asn Tyr Leu Gln Lys Met Gly
195    200    205
Phe Ala Gly Phe Glu Leu Pro Gly Asn Ile Gly Gln Met Ser Phe Thr
210    215    220
Ser Ile Leu Ser Gly Gly Gly Gln Gln Leu Pro Gly Leu Glu Leu Gly
225    230    235    240
Leu Ser Gln Asp Gly Asn Ile Gly Val Leu Asn Pro Gln Ala Phe Gly
245    250    255
Gln Ile Tyr Gln Gln Ile Asn Pro Ala Ala Arg Val Val Asn Ala His
260    265    270
Gln Asn His His Gln Gln His His His Gln Gln Pro Leu Ser Ser Lys
275    280    285
Asp Asp Asp Ser Gln Glu Ser Gly Gln
290    295

```

PF58581.ST25.txt

<210> 21
<211> 954
<212> DNA
<213> Oryza sativa

<400> 21
atggaccca aattccccc accccaccg ctaaacaaa cggagccac caccaccacc 60
accaaccagc agcatcacca cgatgagcag cagcagcagc atcgctcca gattcaagtt 120
catcctcagc agcaggagca gcaggatgga ggtggaggag gaggaagga tcagcagcag 180
cagcagcaga tgcagggtgt ggttgccggc gcggcgggg agaggaggat gcaggggcta 240
gggccgaagc ggagctcgaa caaggaccgc cacaccaagg tggacgggcg gggcgggcgg 300
atccggatgc cggcgctgtg cgccgcccgc atcttccagc tcacgcggga gctcggccac 360
aagtccgacg gcgagaccgt ccagtggctg ctccagcagg cggagccggc catcgtcgcc 420
gccacgggga cggggaccat cccggcgctc gcgtcgcct ccgtcgcccc ctccctccct 480
tcccccaact ccgccctctc caggtcgcac caccaccacc accacatgtg ggcggcagcg 540
ccgcccacgg cgtccgccgg gttcgccggg gcagggttct ccggcgccga ctccgggggtg 600
atcgcgggga tcatgcagcg gatggggatc cccgccggga tcgagctcca gggcggggga 660
gcgggggggt tgggggggtg ggggtggcgg gcgggtggcc acatcggtt cgcgcccag 720
ttcgccagcc acgcggcggc ggccggcgcc atgccggggc tagagctagg gctctcgag 780
gacggccaca tcggcggtgt cgccgcgag tcgctcagcc agttctacca ccaggtcggc 840
gccgcgggtc agctgcagca ccagcaccag catcaccatc agcagcagca gcagcagcag 900
gacggggagg acaaccgcga cgacggcgag tccgatgagg agtcggggca gtag 954

<210> 22
<211> 317
<212> PRT
<213> Oryza sativa

<400> 22
Met Asp Pro Lys Phe Pro Pro Pro Pro Pro Leu Asn Lys Thr Glu Pro
1 5 10 15
Thr Thr Thr Thr Thr Asn Gln Gln His His His Asp Glu Gln Gln Gln
20 25 30
Gln His Arg Leu Gln Ile Gln Val His Pro Gln Gln Gln Glu Gln Gln
35 40 45
Asp Gly Gly Gly Gly Gly Gly Lys Asp Gln Gln Gln Gln Gln Gln Met
50 55 60
Gln Val Val Val Ala Ala Ala Gly Glu Arg Arg Met Gln Gly Leu
65 70 75 80
Gly Pro Lys Arg Ser Ser Asn Lys Asp Arg His Thr Lys Val Asp Gly
85 90 95
Arg Gly Arg Arg Ile Arg Met Pro Ala Leu Cys Ala Ala Arg Ile Phe
100 105 110
Gln Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly Glu Thr Val Gln
115 120 125
Trp Leu Leu Gln Gln Ala Glu Pro Ala Ile Val Ala Ala Thr Gly Thr
130 135 140
Gly Thr Ile Pro Ala Ser Ala Leu Ala Ser Val Ala Pro Ser Leu Pro
145 150 155 160
Ser Pro Asn Ser Ala Leu Ser Arg Ser His His His His His Met
165 170 175
Trp Ala Ala Ala Pro Pro Thr Ala Ser Ala Gly Phe Ala Gly Ala Gly
180 185 190
Phe Ser Gly Ala Asp Ser Gly Val Ile Gly Gly Ile Met Gln Arg Met
195 200 205
Gly Ile Pro Ala Gly Ile Glu Leu Gln Gly Gly Gly Ala Gly Gly Leu
210 215 220
Gly Gly Gly Gly Gly Gly Gly Gly Gly His Ile Gly Phe Ala Pro Met
225 230 235 240

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```

Phe Ala Ser His Ala Ala Ala Ala Ala Met Pro Gly Leu Glu Leu
                245                250                255
Gly Leu Ser Gln Asp Gly His Ile Gly Val Leu Ala Ala Gln Ser Leu
                260                265                270
Ser Gln Phe Tyr His Gln Val Gly Ala Ala Gly Gln Leu Gln His Gln
                275                280                285
His Gln His His His Gln Gln Gln Gln Gln Gln Asp Gly Glu Asp
                290                295                300
Asn Arg Asp Asp Gly Glu Ser Asp Glu Glu Ser Gly Gln
305                310                315

```

<210> 23
 <211> 963
 <212> DNA
 <213> Populus tremuloides

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<400> 23
atggatccca agggctctaa ctcaaaaaaac ccacatgagt taccacttt cttgaccac 60
accacacctt ctctcctca tcctcctcca caacctcatc ttcaacaacc acaacaactc 120
catagccaaa accaacaaca acccaacatg ggagacaaca aaccagcaga aatcaaagac 180
tttcagattg tagtagctga caaagaagag caaaagaaac agttagcacc aaagagaagc 240
tcaaacaag acagacacac aaaagttgaa ggtagaggta gaaggataag gatgccagct 300
ctttgtgcag cgagaatctt tcaattgaca agagaattgg gtcacaaatc tgatggagag 360
acaatacagt ggcttctaca acaagctgaa ccatctataa ttgcagcaac tgggactggt 420
actatacctg catcagcttt agcagctgct ggcggtgcaa tttcacaaca aggagcttct 480
ctttctgctg gtttgcacaa aaagattgat gatttaggtg ggtccagtag tagtagggcc 540
agttgggcaa tgtaggtg caatttaggg agaccccatc atgttactac tgcaggatta 600
tggcccccag ttggagggtt tgggttccag tcatcatcta attccactgg tccatcaaca 660
acaaatatag ggactgaagc tgctgctgct ggtggttcta gttatttgca aaaactcggg 720
tttccagggt ttgacttgcc gggtaacaac atggggccta tgagttttac ttcaatttta 780
ggtgggggta cccagcagtt accaggattg gaacttgggt tgtcacagga cgggcatatt 840
gggggtttga gtccacaagc tttgaatcag atttatcagc agatggggca tgctagagtg 900
caccagcagc agcatcagca acaaaatcct tctaaagatg attcacaagg atcaggccag 960
tga

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<210> 24
 <211> 320
 <212> PRT
 <213> Populus tremuloides

```

<400> 24
Met Asp Pro Lys Gly Ser Asn Ser Lys Asn Pro His Glu Leu Pro Thr
1          5          10          15
Phe Leu Thr His Thr His Pro Ser Pro Pro His Pro Pro Pro Gln Pro
          20          25          30
His Leu Gln Gln Pro Gln Gln Leu His Ser Gln Asn Gln Gln Gln Pro
          35          40          45
Asn Met Gly Asp Asn Lys Pro Ala Glu Ile Lys Asp Phe Gln Ile Val
50          55          60
Val Ala Asp Lys Glu Glu Gln Lys Lys Gln Leu Ala Pro Lys Arg Ser
65          70          75          80
Ser Asn Lys Asp Arg His Thr Lys Val Glu Gly Arg Gly Arg Arg Ile
          85          90          95
Arg Met Pro Ala Leu Cys Ala Ala Arg Ile Phe Gln Leu Thr Arg Glu
          100          105          110
Leu Gly His Lys Ser Asp Gly Glu Thr Ile Gln Trp Leu Leu Gln Gln
          115          120          125
Ala Glu Pro Ser Ile Ile Ala Ala Thr Gly Thr Gly Thr Ile Pro Ala
          130          135          140

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PF58581.ST25.txt

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

<210> 25
<211> 933
<212> DNA
<213> Saccharum officinarum

<220>
<221> misc_feature
<222> (699)..(701)
<223> n is a, c, g, or t

<400> 25
atggacccca agttcccccac acccccaccg ctaaacaataa cggagcccac caccgcgacg 60
accaccacca ccacctcgac cgcgcagcag ctggatccta aggactacca gcagcagcag 120
ccggcgcagc accacctgca aatccaaatc caccagccgc cgcagcagga cgggggcggc 180
ggagggaagg agcaacagca gcagctgcag gtggtggcgc agcccgggga gcggaggcag 240
cagccgctcg cgcccaagcg gagctccaac aaggaccgcc acaccaaggt cgatggcagg 300
ggccgcccga tccgatgcc cgcgctgtgc gccgcgcgga tcttcagct cacgcgggag 360
ctcggccaca agtccgacgg cgagaccgtg cagtggctgc tgcagcaggc cgagccggcc 420
atcgctgcgc ccaccggcac gggcaccata ccggcgctcg cgctcgcatc cgctcgcccc 480
tcgctcccggt cgccacctc cgggctcgcc aggcgcacc accaccacca tccgcaccac 540
atgtggggcg cttccgcccgc gtccgcgggt ttctcctcgc cctccttcct caattccgcc 600
gccgcaggca cgggagacgc cgctggtatc ggcgcatca tgcagcggat ggggatcccc 660
gcgggcctcg agctgccggg agggggcgcc gctggggcnn ncggctttgc gccatgttc 720
gctgaacacc ccgcggccat tccggggctc gagcttgccc tctcgagga cggccacatc 780
gggttgctcg ccgcgcagtc gatcaccag ttctaccacc aggtgggtgc tgccggcggc 840
agcggccaga tgcagaccc tcacggccac cagcaggagg acggggagga cgaccgcgag 900
gacggcgagt ccgatgatga gtctgggcag tag 933

<210> 26
<211> 310
<212> PRT
<213> Saccharum officinarum

<220>
<221> UNSURE
<222> (234)..(234)

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<223> Xaa can be any naturally occurring amino acid

<400> 26

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Met Asp Pro Lys Phe Pro Thr Pro Pro Pro Leu Asn Lys Thr Glu Pro
1      5      10      15
Thr Thr Ala Thr Thr Thr Thr Thr Ser Thr Ala Gln Gln Leu Asp
20      25      30
Pro Lys Asp Tyr Gln Gln Gln Gln Pro Ala Gln His His Leu Gln Ile
35      40      45
Gln Ile His Gln Pro Pro Gln Gln Asp Gly Gly Gly Gly Gly Lys Glu
50      55      60
Gln Gln Gln Gln Leu Gln Val Val Ala Gln Pro Gly Glu Arg Arg Gln
65      70      75      80
Gln Pro Leu Ala Pro Lys Arg Ser Ser Asn Lys Asp Arg His Thr Lys
85      90      95
Val Asp Gly Arg Gly Arg Arg Ile Arg Met Pro Ala Leu Cys Ala Ala
100     105     110
Arg Ile Phe Gln Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly Glu
115     120     125
Thr Val Gln Trp Leu Leu Gln Gln Ala Glu Pro Ala Ile Val Ala Ala
130     135     140
Thr Gly Thr Gly Thr Ile Pro Ala Ser Ala Leu Ala Ser Val Ala Pro
145     150     155     160
Ser Leu Pro Ser Pro Thr Ser Gly Leu Ala Arg Pro His His His His
165     170     175
His Pro His His Met Trp Ala Pro Ser Ala Ala Ser Ala Gly Phe Ser
180     185     190
Ser Pro Ser Phe Leu Asn Ser Ala Ala Gly Thr Gly Asp Ala Ala
195     200     205
Gly Ile Gly Gly Ile Met Gln Arg Met Gly Ile Pro Ala Gly Leu Glu
210     215     220
Leu Pro Gly Gly Gly Ala Ala Gly Ala Xaa Gly Phe Ala Pro Met Phe
225     230     235     240
Ala Glu His Pro Ala Ala Ile Pro Gly Leu Glu Leu Ala Leu Ser Gln
245     250     255
Asp Gly His Ile Gly Leu Leu Ala Ala Gln Ser Ile Thr Gln Phe Tyr
260     265     270
His Gln Val Gly Ala Ala Gly Gly Ser Gly Gln Met Gln His Pro His
275     280     285
Gly His Gln Gln Glu Asp Gly Glu Asp Asp Arg Glu Asp Gly Glu Ser
290     295     300
Asp Asp Glu Ser Gly Gln
305     310

```

<210> 27

<211> 846

<212> DNA

<213> Solanum tuberosum

<400> 27

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atggatccca agcagcctaa caacaaaaat attaagccta ctcatgatca gataaaagac      60
ttgcagattt tgaaaaatga tgaaccaag aaacagcagc aggtggctgc tcctaaaaga      120
aaagataggc ataccaaagt tgaaggtaga gggaggagga tacgtatgcc tgctctatgt      180
gcagcaagaa tctttcaact tacgcgcgaa ttgggtcata aatctgatgg tgagacaatt      240
cagtggctgc tgcagcaagc cgagccttcg attattgctg ctactggcac agggacaatt      300
cctgcatcgg ctttagctgc agcagcatct gtttctcaac aggggatctc tgtatcagct      360
ggtttaatga ttgaatcggg ggcgaatatc gcggggtcag gtagcagtag aagtagtaat      420
agtaggacca attggccaat gatctgtggg aattttggaa gacccattt ggctacagta      480
ggaatatggc ctgcccctgc ccctgttgct actagttttg ggtttcagtc ctcatctgct      540

```


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```
ccatcaagcg ccagtttaga cagtgaagt tcaaactatt acttacagaa aattggggttt 600
cctggatttg atctgcctgc agctacaaat atgaatccta tgagttttac ttcaattctt 660
ggtggaagta accagcaact gccaggattg gagcttgat tatctcaaga gggtcattta 720
ggggttttga accagatata ccagcaggaa agaatgcaac atccgcagca gcaacaacaa 780
gatcagcatc agcatcagca tcaacaacaa tctccggagg atgattctca aggatcagga 840
cattaa 846
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<210> 28
 <211> 281
 <212> PRT
 <213> Solanum tuberosum

<400> 28
 Met Asp Pro Lys Gln Pro Asn Asn Lys Asn Ile Lys Pro Thr His Asp
 1 5 10 15
 Gln Ile Lys Asp Leu Gln Ile Leu Lys Asn Asp Glu Thr Lys Lys Gln
 20 25 30
 Gln Gln Val Ala Ala Pro Lys Arg Lys Asp Arg His Thr Lys Val Glu
 35 40 45
 Gly Arg Gly Arg Arg Ile Arg Met Pro Ala Leu Cys Ala Ala Arg Ile
 50 55 60
 Phe Gln Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly Glu Thr Ile
 65 70 75 80
 Gln Trp Leu Leu Gln Gln Ala Glu Pro Ser Ile Ile Ala Ala Thr Gly
 85 90 95
 Thr Gly Thr Ile Pro Ala Ser Ala Leu Ala Ala Ala Ala Ser Val Ser
 100 105 110
 Gln Gln Gly Ile Ser Val Ser Ala Gly Leu Met Ile Glu Ser Gly Ala
 115 120 125
 Asn Ile Ala Gly Ser Gly Ser Ser Arg Ser Ser Asn Ser Arg Thr Asn
 130 135 140
 Trp Pro Met Ile Cys Gly Asn Phe Gly Arg Pro His Leu Ala Thr Val
 145 150 155 160
 Gly Ile Trp Pro Ala Pro Ala Pro Val Val Thr Ser Phe Gly Phe Gln
 165 170 175
 Ser Ser Ser Ala Pro Ser Ser Ala Ser Leu Asp Ser Glu Ser Ser Asn
 180 185 190
 Tyr Tyr Leu Gln Lys Ile Gly Phe Pro Gly Phe Asp Leu Pro Ala Ala
 195 200 205
 Thr Asn Met Asn Pro Met Ser Phe Thr Ser Ile Leu Gly Gly Ser Asn
 210 215 220
 Gln Gln Leu Pro Gly Leu Glu Leu Gly Leu Ser Gln Glu Gly His Leu
 225 230 235 240
 Gly Val Leu Asn Gln Ile Tyr Gln Gln Glu Arg Met Gln His Pro Gln
 245 250 255
 Gln Gln Gln Gln Asp Gln His Gln His Gln His Gln Gln Gln Ser Pro
 260 265 270
 Glu Asp Asp Ser Gln Gly Ser Gly His
 275 280

<210> 29
 <211> 978
 <212> DNA
 <213> Sorghum bicolor

<400> 29
 atggacccca agttccccac acccccaccg ctaaacaacaa cggagcccac caccgcgacg 60
 accaccacca cctcgaccgc gcagcagcag cagcagcagc tggatcctaa ggactaccag 120
 cagccggcgc agcagcacca cctgcaaata caaatccacc agccgccgcc gcagcagcag 180

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```

cagcagcagg acggaggcaa ggagcagcag ctgcaggtgg tggcgagcc cggggagcgg 240
aggcagcagg cgctcgcgcc caagcggagc tccaacaagg accgccacac caaggtcgac 300
ggcagggggcc gccgatccg gatgcccgcg ctgtgcgccc cgggatctt ccagctcacg 360
cgggaactcg gccacaagtc cgacggcgag accgtgcagt ggctgctgca gcaggccgag 420
ccggccatcg tcgcccgcac cggcaccggc accataccgg cgtccgcgct cgcacccgctc 480
gcgcccctgc tcccgtcgcc caccctccggg ctgcgcaggc cgcaccacca ccaccaccg 540
caccacatgt gggcgccgct cgccgcgtcc gcgggtttct cctcgccctc cttcctcaat 600
tccgcccgcg cgggcacggg agacgccgct ggtatcgggc gactcatgca gcggatgggg 660
atccccgcgg gtctcgagct gccgggaggc ggcgccgctg gaggcaccct cggcgctggc 720
ggccacatcg gctttgcgcc catgttcgct ggacacgccg cggccatgcc ggggctcgag 780
ctcggcctct cgcaggacgg ccacatcggc gtgctcgag cgcagtcgat cagccagttc 840
taccaccaag tgggtgctgc tggcggcagc ggccagatgc agcaccgcga cggccaccag 900
catcaccatc atcagcagca ggaggacggg gaggacgacc gcgaggacgg cgagtccgat 960
gacgagtctg ggcagtag 978

```

<210> 30
 <211> 325
 <212> PRT
 <213> Sorghum bicolor

<400> 30

Met	Asp	Pro	Lys	Phe	Pro	Thr	Pro	Pro	Pro	Leu	Asn	Lys	Thr	Glu	Pro
1				5					10					15	
Thr	Thr	Ala	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Ala	Gln	Gln	Gln	Gln	Gln
			20					25					30		
Gln	Leu	Asp	Pro	Lys	Asp	Tyr	Gln	Gln	Pro	Ala	Gln	Gln	His	His	Leu
		35				40						45			
Gln	Ile	Gln	Ile	His	Gln	Pro	Pro	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Asp
	50				55					60					
Gly	Gly	Lys	Glu	Gln	Gln	Leu	Gln	Val	Val	Ala	Gln	Pro	Gly	Glu	Arg
65					70					75					80
Arg	Gln	Gln	Ala	Leu	Ala	Pro	Lys	Arg	Ser	Ser	Asn	Lys	Asp	Arg	His
				85					90					95	
Thr	Lys	Val	Asp	Gly	Arg	Gly	Arg	Arg	Ile	Arg	Met	Pro	Ala	Leu	Cys
			100					105					110		
Ala	Ala	Arg	Ile	Phe	Gln	Leu	Thr	Arg	Glu	Leu	Gly	His	Lys	Ser	Asp
		115					120					125			
Gly	Glu	Thr	Val	Gln	Trp	Leu	Leu	Gln	Gln	Ala	Glu	Pro	Ala	Ile	Val
	130					135				140					
Ala	Ala	Thr	Gly	Thr	Gly	Thr	Ile	Pro	Ala	Ser	Ala	Leu	Ala	Ser	Val
145					150					155					160
Ala	Pro	Ser	Leu	Pro	Ser	Pro	Thr	Ser	Gly	Leu	Ala	Arg	Pro	His	His
			165					170						175	
His	His	His	Pro	His	His	Met	Trp	Ala	Pro	Ser	Ala	Ala	Ser	Ala	Gly
		180					185						190		
Phe	Ser	Ser	Pro	Ser	Phe	Leu	Asn	Ser	Ala	Ala	Ala	Gly	Thr	Gly	Asp
	195					200						205			
Ala	Ala	Gly	Ile	Gly	Gly	Leu	Met	Gln	Arg	Met	Gly	Ile	Pro	Ala	Gly
	210					215				220					
Leu	Glu	Leu	Pro	Gly	Gly	Gly	Ala	Ala	Gly	Gly	Thr	Leu	Gly	Ala	Gly
225					230					235					240
Gly	His	Ile	Gly	Phe	Ala	Pro	Met	Phe	Ala	Gly	His	Ala	Ala	Ala	Met
			245					250						255	
Pro	Gly	Leu	Glu	Leu	Gly	Leu	Ser	Gln	Asp	Gly	His	Ile	Gly	Val	Leu
		260						265					270		
Ala	Ala	Gln	Ser	Ile	Ser	Gln	Phe	Tyr	His	Gln	Val	Gly	Ala	Ala	Gly
	275					280						285			
Gly	Ser	Gly	Gln	Met	Gln	His	Pro	His	Gly	His	Gln	His	His	His	His
	290					295					300				

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Gln Gln Gln Glu Asp Gly Glu Asp Asp Arg Glu Asp Gly Glu Ser Asp
 305 310 315 320
 Asp Glu Ser Gly Gln
 325

<210> 31
 <211> 891
 <212> DNA
 <213> Vitis vinifera

<400> 31
 atggatccca agggctcaaa gcagccgcag gaggtaccaa acttcttgag cctacctcag 60
 ccaaacatgg gagagaacaa gccagctgaa gtgaaggact ttcagattgt gattgcagat 120
 aaggaagagg gtaagaagca gttggccccc aagaggagct caaacaagga caggcacacc 180
 aaggttgaag gcagagggag gagaataagg atgccggctc tttgtgcagc cagaatTTTT 240
 cagttgacta ggggaattggg tcacaaatct gacggggaaa ccatacagtg gttgttgagc 300
 cagcccgagc cgtccataat agcggccact ggtactggga caataccggc gtcggcttta 360
 gcggcggcag gaggtctgtg gtcgcaacag ggaacttcta tatcagcagg attgcatcaa 420
 aagattgatg aattgggggg gtccagtatt gggtcaggga gtagtaggac cagttgggca 480
 atggtaggtg caaatTTTggg gagaccccat gtggccacag ggctatggcc cccagtcagt 540
 ggttttgggt ttcagtcatc atctggacca tcaaccacca atttggggaa tgaaagttcc 600
 aattatctgc aaaaaattgc cttccctggg tttgacttgc ctgcaacaaa tctgggtcct 660
 atgagtttta cttcaatttt ggggtgggagt aaccagcagc ttcttggttt ggagctgggc 720
 ctatcacagg atggtcatat tggggTTTTg aactcacaag ccttaagcca gatttaccag 780
 cagatggggc aggccagggt gcaccagcaa cagcagcatc aacatcagca tcagcatcag 840
 catcaacagc aacctcctgc taaggatgat tctcaagggt cagggcagta g 891

<210> 32
 <211> 296
 <212> PRT
 <213> Vitis vinifera

<400> 32
 Met Asp Pro Lys Gly Ser Lys Gln Pro Gln Glu Val Pro Asn Phe Leu
 1 5 10 15
 Ser Leu Pro Gln Pro Asn Met Gly Glu Asn Lys Pro Ala Glu Val Lys
 20 25 30
 Asp Phe Gln Ile Val Ile Ala Asp Lys Glu Glu Gly Lys Lys Gln Leu
 35 40 45
 Ala Pro Lys Arg Ser Ser Asn Lys Asp Arg His Thr Lys Val Glu Gly
 50 55 60
 Arg Gly Arg Arg Ile Arg Met Pro Ala Leu Cys Ala Ala Arg Ile Phe
 65 70 75 80
 Gln Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly Glu Thr Ile Gln
 85 90 95
 Trp Leu Leu Gln Gln Ala Glu Pro Ser Ile Ile Ala Ala Thr Gly Thr
 100 105 110
 Gly Thr Ile Pro Ala Ser Ala Leu Ala Ala Gly Gly Ser Val Ser
 115 120 125
 Gln Gln Gly Thr Ser Ile Ser Ala Gly Leu His Gln Lys Ile Asp Glu
 130 135 140
 Leu Gly Gly Ser Ser Ile Gly Ser Gly Ser Ser Arg Thr Ser Trp Ala
 145 150 155 160
 Met Val Gly Ala Asn Leu Gly Arg Pro His Val Ala Thr Gly Leu Trp
 165 170 175
 Pro Pro Val Ser Gly Phe Gly Phe Gln Ser Ser Ser Gly Pro Ser Thr
 180 185 190
 Thr Asn Leu Gly Asn Glu Ser Ser Asn Tyr Leu Gln Lys Ile Ala Phe
 195 200 205

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```

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

```

<210> 33
 <211> 975
 <212> DNA
 <213> Zea mays

```

<400> 33
atggagcccca agttccccac acccctagcg ctaaacaataa cggagcccac caccgcgacg      60
accaccacca cctcgaccgc gcagcatcat cagctggatc ctaaggacta ccagcagcag      120
acggcgcagc accaggagca gcagcagcac caccatcacc cccacctgca aatccaaatc      180
caccagccgc cgccgccgcc gcaggacggg ggcggcggag tgaaggagca gcagcagctg      240
ctgcaggtgg tggcgcagcc cggggatcgg aggcagcagg cgctcgcccc caagcggagc      300
tccaacaagg accgccacac caaggtcgac ggcaggggcc gccgatccg gatgcgggcg      360
ctctgcgccg cgcggtatct ccagctcacg cgggagctcg gccacaagtc cgacgggcgag      420
actgtgcagt ggctgctgca gcaggccgag ccggccatcg tcgccgccac cggcacgggc      480
accataccgg cgtccgcgct cgctccgctc gcgccctcgc tcccgctcgc tacctccggg      540
ctcgccaggc cgcaccacca ccaccgcac cacatgtggg cgccgtccgc cggcttctcc      600
tcgccctcct tctgaattc cgcgggcgcg ggcgacggca ccggtatcgg cggcatcatg      660
cagcgggatg gggccccgcg gggcctggag ctgccgggag gcggcgccgc cggcggccac      720
atcggctttg cgcccatgtt cgctggacac gccgcggcca tgccggggct cgagctcggc      780
ctctcgcagg acggtcacat cggcgtgctc gccgcgcagt cgatcagcca gttctaccac      840
caggtgggtg ccgctgccgg cggcagtggc cagatgcagc accgcacgg gcaccagcat      900
caccatcatc agcagcagga ggacggggag gacgaccgcg aggacggcga gtctgatgac      960
gagtctgggc agtag

```

<210> 34
 <211> 324
 <212> PRT
 <213> Zea mays

```

<400> 34
Met Asp Pro Lys Phe Pro Thr Pro Leu Ala Leu Asn Lys Thr Glu Pro
1      5      10      15
Thr Thr Ala Thr Thr Thr Thr Thr Ser Thr Ala Gln His His Gln Leu
      20      25      30
Asp Pro Lys Asp Tyr Gln Gln Gln Thr Ala Gln His Gln Glu Gln Gln
      35      40      45
Gln His His His His Pro His Leu Gln Ile Gln Ile His Gln Pro Pro
      50      55      60
Pro Pro Pro Gln Asp Gly Gly Gly Gly Val Lys Glu Gln Gln Gln Leu
65      70      75      80
Leu Gln Val Val Ala Gln Pro Gly Asp Arg Arg Gln Gln Ala Leu Ala
      85      90      95
Pro Lys Arg Ser Ser Asn Lys Asp Arg His Thr Lys Val Asp Gly Arg
      100      105      110
Gly Arg Arg Ile Arg Met Pro Ala Leu Cys Ala Ala Arg Ile Phe Gln
      115      120      125

```

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```

Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly Glu Thr Val Gln Trp
130 135 140
Leu Leu Gln Gln Ala Glu Pro Ala Ile Val Ala Ala Thr Gly Thr Gly
145 150 155 160
Thr Ile Pro Ala Ser Ala Leu Ala Ser Val Ala Pro Ser Leu Pro Ser
165 170 175
Pro Thr Ser Gly Leu Ala Arg Pro His His His His Pro His His Met
180 185 190
Trp Ala Pro Ser Ala Gly Phe Ser Ser Pro Ser Phe Leu Asn Ser Ala
195 200 205
Gly Ala Gly Asp Gly Thr Gly Ile Gly Gly Ile Met Gln Arg Met Gly
210 215 220
Val Pro Ala Gly Leu Glu Leu Pro Gly Gly Gly Ala Ala Gly Gly His
225 230 235 240
Ile Gly Phe Ala Pro Met Phe Ala Gly His Ala Ala Ala Met Pro Gly
245 250 255
Leu Glu Leu Gly Leu Ser Gln Asp Gly His Ile Gly Val Leu Ala Ala
260 265 270
Gln Ser Ile Ser Gln Phe Tyr His Gln Val Gly Ala Ala Gly Gly
275 280 285
Ser Gly Gln Met Gln His Pro His Gly His Gln His His His His Gln
290 295 300
Gln Gln Glu Asp Gly Glu Asp Asp Arg Glu Asp Gly Glu Ser Asp Asp
305 310 315 320
Glu Ser Gly Gln

```

<210> 35
 <211> 948
 <212> DNA
 <213> Zea mays

```

<400> 35
atggacccca agttccccc accccaccg ctaaaca aaa cggagcccac caccgcgacg 60
accaccacca cctcgaccgc gcagcagcag cagcagcagc tggatcctaa ggactaccag 120
cagcagcagc agcagccggc gcagcacctg caaatccaaa tccaccagtc gcagcaggac 180
ggagggcgggc gagggaaagg gcagcagcag ctgcaggtgg tggcgagcc cggggagagg 240
aggcagcagg cgctcgcgcc caagcggagc tccaacaagg accgacacac caaggtcgac 300
ggcagggggcc ggcggatccg gatgcccgcg ctctgcgcgc cgcgatctt ccagctcacg 360
cgggaaactcg gccacaagtc cgacggcgag accgtccagt ggctgctgca gcaggccgag 420
ccggccatcg tcgcccgcac cggcacgggc accataccgg cgtccgcgct cgctccgctc 480
gcgcccctgc tcccgtcgcc caccctccgg ctgcgcaggc cgcaccacca catgtgggcg 540
ccgtccgcgc gcttctctc gccctcttc ctgaaactctg ccgcccggg caccggcgat 600
gccgcccggta tcatgcagcg gatggggatc cccgcccggc tcgagctgcc gggagcctcc 660
gccgcccggag ccaccctcg cgccggcggc cacatcggtt ttgcgccc atgtcgctgga 720
cacgcccgcg ccatgccggg gctcgagctc gggctatcgc aggacggcca catcggcgtg 780
ctcgcccgcg agtcgatcag ccagttctac caccaggtgg gtgctgccgc cggcggcggc 840
ggccagatgc atcacgcgca cgggcaccat catcaccatc accagcagca ggaggacggg 900
gaggacgacc gcgaggacgg cgagtccgat gacgagtctg ggcagtag 948

```

<210> 36
 <211> 315
 <212> PRT
 <213> Zea mays

```

<400> 36
Met Asp Pro Lys Phe Pro Pro Pro Pro Pro Leu Asn Lys Thr Glu Pro
1 5 10 15
Thr Thr Ala Thr Thr Thr Thr Thr Ser Thr Ala Gln Gln Gln Gln Gln

```

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	20		25		30										
Gln	Leu	Asp	Pro	Lys	Asp	Tyr	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Ala	Gln
	35		40		45										
His	Leu	Gln	Ile	Gln	Ile	His	Gln	Ser	Gln	Gln	Asp	Gly	Gly	Gly	Gly
	50		55		60										
Gly	Lys	Glu	Gln	Gln	Gln	Leu	Gln	Val	Val	Ala	Gln	Pro	Gly	Glu	Arg
65			70		75										80
Arg	Gln	Gln	Ala	Leu	Ala	Pro	Lys	Arg	Ser	Ser	Asn	Lys	Asp	Arg	His
			85		90										
Thr	Lys	Val	Asp	Gly	Arg	Gly	Arg	Arg	Ile	Arg	Met	Pro	Ala	Leu	Cys
	100		105		110										
Ala	Ala	Arg	Ile	Phe	Gln	Leu	Thr	Arg	Glu	Leu	Gly	His	Lys	Ser	Asp
	115		120		125										
Gly	Glu	Thr	Val	Gln	Trp	Leu	Leu	Gln	Gln	Ala	Glu	Pro	Ala	Ile	Val
130			135		140										
Ala	Ala	Thr	Gly	Thr	Gly	Thr	Ile	Pro	Ala	Ser	Ala	Leu	Ala	Ser	Val
145			150		155										
Ala	Pro	Ser	Leu	Pro	Ser	Pro	Thr	Ser	Gly	Leu	Ala	Arg	Pro	His	His
			165		170										
His	Met	Trp	Ala	Pro	Ser	Ala	Gly	Phe	Ser	Ser	Pro	Ser	Phe	Leu	Asn
	180		185		190										
Ser	Ala	Ala	Ala	Gly	Thr	Gly	Asp	Ala	Ala	Gly	Ile	Met	Gln	Arg	Met
	195		200		205										
Gly	Ile	Pro	Ala	Gly	Phe	Glu	Leu	Pro	Gly	Ala	Ser	Ala	Ala	Gly	Ala
210			215		220										
Thr	Leu	Gly	Ala	Gly	Gly	His	Ile	Gly	Phe	Ala	Pro	Met	Phe	Ala	Gly
225			230		235										
His	Ala	Ala	Ala	Met	Pro	Gly	Leu	Glu	Leu	Gly	Leu	Ser	Gln	Asp	Gly
			245		250										
His	Ile	Gly	Val	Leu	Ala	Ala	Gln	Ser	Ile	Ser	Gln	Phe	Tyr	His	Gln
	260		265		270										
Val	Gly	Ala	Ala	Ala	Gly	Gly	Gly	Gly	Gln	Met	His	His	Ala	His	Gly
	275		280		285										
His	His	His	His	His	His	Gln	Gln	Gln	Glu	Asp	Gly	Glu	Asp	Asp	Arg
	290		295		300										
Glu	Asp	Gly	Glu	Ser	Asp	Asp	Glu	Ser	Gly	Gln					
305			310		315										

<210> 37
 <211> 648
 <212> DNA
 <213> Allium cepa

<400> 37
 atggatccaa aagaatccca acccaactcg gatcgtcaat tgatgaccca aaccgaatcc 60
 attcaagacc cgcaaaaaag agcccttctt gcccaaaaac ggacctccaa caaagaccgc 120
 cacaccaaag ttgacggccg cggccggagg attcgcgatgc ccgctctctg cgccgccaga 180
 atcttccagc tgaccgaga actcggccat aaatccgacg gcgagaccgt tcagtggctt 240
 ctgcatcatg cagaacctgc catcatcgcc gctaccgggt cgggtaccat acccgcatcc 300
 gctttagctt cttctcaggc gatgccgaac tctaagcccg acaacagttg ggctgttg 360
 ttatggggag gttttaattc cggatttatg aattccaata atagcagtaa caacaacaat 420
 aataatggag tcggccctag ctcgagcaat ttagggtttg tggggatgga gatgacaggg 480
 atgagtgggc acatgagctt tacttcaatg ctgggagggc agcctgggcc acaaatgccc 540
 gggcttcagt tagggctgtc tcaagatggg catattgggg ttttgaatac acaagggttg 600
 aaccattttt atcaacagat gggtcataat gttagggttg gaaatggg 648

<210> 38
 <211> 216
 <212> PRT

PF58581.ST25.txt

<213> Allium cepa

<400> 38

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

```

<210> 39

<211> 731

<212> DNA

<213> Brachypodium distachyon

<400> 39

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atggacccca agtttctctcc tccccaccg ctaaacaaaa cggagcccac caccggcgtg      60
acgaccacca ccaccacgac ctcccagcag cagctggatc acgagcagta tcaccagccg      120
cagcagcacc tgcaaatcca agtgcaccag cagcagcagg aggaagatgg cgcgggggga      180
aaggagcagc agcagcaggt ggtggcggcg gcgggggcgg gggagaggag ggtgcagggg      240
ctggggccga agcggagctc caacaaggac cggcacacca aggtggacgg gcgggggcgg      300
cggatccgga tgccggcgct gtgcgcggcg cggatcttcc agctgacggg ggagctgggg      360
cacaagtcgg acggggagac ggtccagtgg ctgctgcagc aggcggagcc ggccatcgtc      420
gccgccacag ggtccggcac cataccggcg tccgcgctcg cctccgtcgc gccctcgctg      480
ccttcgcccc cctccgcgct cgccaggccg caccaccacc accacctctg ggggcctctg      540
gcggcggggg tctccccggc cgggttcatg aactcgccc cagccggcgc tgactctggg      600
ggcggcctcg gcgggcttat gcagaggata gggcttccc cgggatgga gctccctggc      660
ggcggtggtg gggggcacat cgggttcgcg ccatgttcg ccagccacgc ggcggcggcg      720
gcggccatgc c

```

<210> 40

<211> 243

<212> PRT

<213> Brachypodium distachyon

<400> 40

```

Met Asp Pro Lys Phe Pro Pro Pro Pro Pro Leu Asn Lys Thr Glu Pro

```

PF58581.ST25.txt

```

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

```

<210> 41
 <211> 768
 <212> DNA
 <213> Brassica oleracea

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<400> 41
atggatccca agaaccctaaa tccacaccaa gtaccaaact tcttgatacc accaccacaa 60
ccgagagatg cttccgatga caacaaagaa gtaaatgatt ttcagatcgt ggctcgcttcc 120
gacaaagaac cgaacagtaa cggtaagaag cagcttgccc ccaagagaag ctcaaacaaa 180
gacagacaca ccaaagtga aggtcgcggt cggagaatca ggatgcctgc tctctgcgcg 240
gcaaggattt ttcaactgac cagagaattg ggtcacaaat cagacggtga aacaatccag 300
tggctgcttc aacaagccga accgtcgctt atcgagacca ccggttcagg aactgtaccg 360
gcctctgctt tagcctcagc tgcttctgct gtagtctcta accaaggcgg gtctctcact 420
gctggtttga tgatcagtca tcatgactta gactgtggtg gtgggtctag tagtggtaga 480
ccaagttggg gagaaggagg aggagaagta tggccaaatg gagctgggta cagaattggg 540
tttcccggat ttgattttcc tgggtggagct atgagttttg cttccatttt tgggtgctagt 600
ggtggtggta atggtaatca gatgcttgga cttgagttag ggttgtctca ggtagggaat 660
gttgggggtc tgaatcaaca gatttatcaa cagatggctc aagctcaggc tcaggctcag 720
ggtagggttc ttcaccatac tcttcatcat aatccaggac atgaagag 768

```

<210> 42
 <211> 256
 <212> PRT
 <213> Brassica oleracea

```

<400> 42
Met Asp Pro Lys Asn Pro Asn Pro His Gln Val Pro Asn Phe Leu Ile

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PF58581.ST25.txt

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

<210> 43
 <211> 723
 <212> DNA
 <213> Brassica rapa

<400> 43
 agaagctcaa acaaagacag acacatcaaa gtggaaggca ggggtcggag aatcaggatg 60
 cctgctctct gcgccgctag gatcttccag ttgactagag aattgggtca caaatccgac 120
 ggcgagacaa tccagtggct gcttcagcag gctgagccgt cgattatcgc agccaccggt 180
 tcaggaacta taccggcctc tgcttttagcc tcagccgctg ctgctgtatc gagccaccat 240
 cttcaggggtg gtgggtctct cactgctggt ttgatgatca gtcattgagtt ggatgggtggg 300
 tctagtagtg ggagacaaa ttgggggtgtt ggcgggggag atggaggggtc taggtcgagt 360
 ttaccaactg ggctgtggcc aaatgtagct gggtttggag ctgggggtgca gaccatgagt 420
 gatggaggtg gttacaggat tgggtttcct gggtttgatt atcctgggtg agctatgagt 480
 tttgcgtcca ttcttggttg tggtagtaac aatcagatgc ctggacttga gttaggggtg 540
 gctcaggaag ggaatgttg tgtcttgaat cctcagtctt ttgcacagat ttatcagcag 600
 cagatgagtc aggcctcaagc tcagggtagg gttcttcacc atactcttca gcataaccga 660
 tcacatgagg agcatcagca agagagtggg gagaaagatg attctcaagg gtcagggcgt 720
 taa 723

<210> 44
 <211> 240
 <212> PRT
 <213> Brassica rapa

<400> 44
 Arg Ser Ser Asn Lys Asp Arg His Ile Lys Val Glu Gly Arg Gly Arg

PF58581.ST25.txt

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

<210> 45
 <211> 696
 <212> DNA
 <213> Coffea canephora

<220>
 <221> misc_feature
 <222> (561)..(561)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (622)..(622)
 <223> n is a, c, g, or t

<400> 45	
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ttacagcagg ctgaaccatc cattatagcc gccacgggga cggggaccat accggcctcc	120
gctctagccg ctgcggccgc tggagcaggg ggctctgttt ccatgtcagc tgggctgcat	180
cctccaaaga tcagtgtgta attgggtgca caccaccccc cacacatgga tattgccggg	240
tcaggtcaag gagcgggtag caccgggtgct agtaggacca attggccaat ggtcggcggg	300
agtttgttac gagccccca tatgggaatg cccactacaa ctgcagggat atggccccct	360
acttctgctt ctggtgctgt cagtgggttc gggttcagt catcatctc ccctgctcca	420
gcagccacca gtttgggcac tgaaagtta aattacctac acaagcttg gtttctggt	480
tttgacttgc cagctgcaac taacaacttg ggtcctatga gtttcacctc catcgtggg	540
gctgctactg accagcagca ncaccttct ggattggagc tggggctatc acaagatggt	600
catgttgggg ttttgaaccc tncaaccttg agccagattt atcagcatat ggggcaggct	660
cgagcgcacc agcacaacac agcacgagac cacagc	696

PF58581.ST25.txt

<210> 46
 <211> 232
 <212> PRT
 <213> Coffea canephora

<220>
 <221> UNSURE
 <222> (187)..(187)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> UNSURE
 <222> (208)..(208)
 <223> Xaa can be any naturally occurring amino acid

<400> 46
 Ile Phe Gln Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly Glu Thr
 1 5 10 15
 Ile Gln Trp Leu Leu Gln Gln Ala Glu Pro Ser Ile Ile Ala Ala Thr
 20 25 30
 Gly Thr Gly Thr Ile Pro Ala Ser Ala Leu Ala Ala Ala Ala Ala Gly
 35 40 45
 Ala Gly Gly Ser Val Ser Met Ser Ala Gly Leu His Pro Pro Lys Ile
 50 55 60
 Ser Ala Glu Leu Gly Ala His His Pro Pro His Met Asp Ile Ala Gly
 65 70 75 80
 Ser Gly Gln Gly Ala Gly Ser Thr Gly Ala Ser Arg Thr Asn Trp Pro
 85 90 95
 Met Val Gly Gly Ser Leu Leu Arg Ala Pro His Met Gly Met Pro Thr
 100 105 110
 Thr Thr Ala Gly Ile Trp Pro Pro Thr Ser Ala Ser Gly Ala Val Ser
 115 120 125
 Gly Phe Gly Phe Gln Ser Ser Ser Ser Pro Ala Pro Ala Ala Thr Ser
 130 135 140
 Leu Gly Thr Glu Ser Ser Asn Tyr Leu His Lys Leu Gly Phe Pro Gly
 145 150 155 160
 Phe Asp Leu Pro Ala Ala Thr Asn Asn Leu Gly Pro Met Ser Phe Thr
 165 170 175
 Ser Ile Val Gly Ala Ala Thr Asp Gln Gln Xaa His Leu Pro Gly Leu
 180 185 190
 Glu Leu Gly Leu Ser Gln Asp Gly His Val Gly Val Leu Asn Pro Xaa
 195 200 205
 Thr Leu Ser Gln Ile Tyr Gln His Met Gly Gln Ala Arg Ala His Gln
 210 215 220
 His Asn Thr Ala Arg Asp His Ser
 225 230

<210> 47
 <211> 993
 <212> DNA
 <213> Helianthus annuus & petiolaris

<400> 47
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 tcaagttcaa ctttcttagc ccacccaaac cccaccacaa cagacaacat gggagatcac 120
 aacaacaata acatcaaac caacaacctc aacaaacttt ctgaaatcaa agatttccag 180
 attacagttt ctgacaaaca agagtctgct accaagaaac aacagtttagc ccccaaaaga 240
 acctccaata aagacaggca caccaagggt gaaggaagag gtaggaggat aaggatgcct 300
 gctttatgtg ctgcaagaat ctttcagctc actagagagt taggtaacaa atctgatggt 360

PF58581.ST25.txt

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gaaactattc aatggctgct acagcaagct gaggcctcca ttatagccgc caccggaacc 420
gggacaatcc cggcttctgt gttagccgcc actggggcgg cttcacacgg ggtctcgatt 480
tcggttggct tgcaacaaaa gattgatgaa ttaagcggga gtaataataa cagtaatagt 540
aatattaata ctggtgtcaa ctgtaggacc agttggccaa tggttggtcc agctttgggt 600
gtgggtagac ccactaccca tatggctacg cctacggcta tctggcccgc tgctggattc 660
gggttccagt cctcttcttc gtcccaggt ccatcgggca acaatttggg cgtcgaaagt 720
tcgaattact tgcaaaagat ggcgttttcc gggtttgatt tgcccgggtc taatatgggt 780
cagatgagtt tttcttcgat tttgggtaat cataatcata atcataatca tcatcagcag 840
cagcttcctg ggctggagct tggactgtcc caggatggtc atttaggggt tttgaatcaa 900
caggctttga atcagatata ccaaattggac cagaccagaa tgcaacaaca gcagacttca 960
aatgataatt ctcaagggtc agaggggcag tag 993

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<210> 48
 <211> 329
 <212> PRT
 <213> Helianthus annuus & petiolaris

<400> 48

Ser	Ala	Gly	Gly	Pro	Lys	Gly	Ser	Asn	Leu	His	His	Pro	Gln	Gln	Gln
1				5					10					15	
Pro	His	Glu	Ala	Ser	Ser	Ser	Thr	Phe	Leu	Ala	His	Pro	Asn	Pro	Thr
			20					25					30		
Thr	Thr	Asp	Asn	Met	Gly	Asp	His	Asn	Asn	Asn	Asn	Ile	Asn	Thr	Asn
			35				40					45			
Asn	Leu	Asn	Lys	Leu	Ser	Glu	Ile	Lys	Asp	Phe	Gln	Ile	Thr	Val	Ser
			50			55					60				
Asp	Lys	Gln	Glu	Ser	Ala	Thr	Lys	Lys	Gln	Gln	Leu	Ala	Pro	Lys	Arg
65					70					75					80
Thr	Ser	Asn	Lys	Asp	Arg	His	Thr	Lys	Val	Glu	Gly	Arg	Gly	Arg	Arg
				85					90					95	
Ile	Arg	Met	Pro	Ala	Leu	Cys	Ala	Ala	Arg	Ile	Phe	Gln	Leu	Thr	Arg
			100					105					110		
Glu	Leu	Gly	Asn	Lys	Ser	Asp	Gly	Glu	Thr	Ile	Gln	Trp	Leu	Leu	Gln
		115					120					125			
Gln	Ala	Glu	Pro	Ser	Ile	Ile	Ala	Ala	Thr	Gly	Thr	Gly	Thr	Ile	Pro
			130				135					140			
Ala	Ser	Val	Leu	Ala	Ala	Thr	Gly	Ala	Ala	Ser	His	Gly	Val	Ser	Ile
145					150					155					160
Ser	Val	Gly	Leu	Gln	Gln	Lys	Ile	Asp	Glu	Leu	Ser	Gly	Ser	Asn	Asn
			165						170					175	
Asn	Ser	Asn	Ser	Asn	Ile	Asn	Thr	Gly	Val	Asn	Cys	Arg	Thr	Ser	Trp
			180					185					190		
Pro	Met	Val	Gly	Pro	Ala	Leu	Gly	Val	Gly	Arg	Pro	Thr	Thr	His	Met
		195					200					205			
Ala	Thr	Pro	Thr	Ala	Ile	Trp	Pro	Ala	Ala	Gly	Phe	Gly	Phe	Gln	Ser
		210				215					220				
Ser	Ser	Ser	Ser	Pro	Gly	Pro	Ser	Gly	Asn	Asn	Leu	Gly	Val	Glu	Ser
225					230					235					240
Ser	Asn	Tyr	Leu	Gln	Lys	Met	Ala	Phe	Ser	Gly	Phe	Asp	Leu	Pro	Gly
			245						250					255	
Ser	Asn	Met	Gly	Gln	Met	Ser	Phe	Ser	Ser	Ile	Leu	Gly	Asn	His	Asn
		260						265					270		
His	Asn	His	Asn	His	His	Gln	Gln	Gln	Leu	Pro	Gly	Leu	Glu	Leu	Gly
		275					280					285			
Leu	Ser	Gln	Asp	Gly	His	Leu	Gly	Val	Leu	Asn	Gln	Gln	Ala	Leu	Asn
		290				295					300				
Gln	Ile	Tyr	Gln	Met	Asp	Thr	Arg	Met	Gln	Gln	Gln	Gln	Thr	Ser	Asn
305					310					315					320
Asp	Asn	Ser	Gln	Gly	Ser	Glu	Gly	Gln							

325

<210> 49
 <211> 345
 <212> DNA
 <213> Hordeum vulgare

<400> 49
 atcggcgggc tcatgcagcg gatcggcctc cccgccggga tcgagctgcc gggcgggggc 60
 gcgggggggca tgggcgggca catcgggttc gcgccatgt tcgccagcca cgcgcgggcc 120
 gcaataccgg ggctggagct cggcctgtcg caggagggcc acatcggggt gctcagccag 180
 ttctaccacc aggtcggcgg cgccggggcc agcgggcagc tgcagcacc gcaccctcat 240
 cagcaccacc accacgaaca gcaccacat caccagcagc agcagcagga ggaggacggg 300
 gaggaggagc gcgaggacgg cgactccgag gaggagtccg gccag 345

<210> 50
 <211> 115
 <212> PRT
 <213> Hordeum vulgare

<400> 50
 Ile Gly Gly Leu Met Gln Arg Ile Gly Leu Pro Ala Gly Ile Glu Leu
 1 5 10 15
 Pro Gly Gly Gly Ala Gly Gly Met Gly Gly His Ile Gly Phe Ala Pro
 20 25 30
 Met Phe Ala Ser His Ala Ala Ala Ile Pro Gly Leu Glu Leu Gly
 35 40 45
 Leu Ser Gln Glu Gly His Ile Gly Val Leu Ser Gln Phe Tyr His Gln
 50 55 60
 Val Gly Gly Ala Gly Ala Ser Gly Gln Leu Gln His Pro His Pro His
 65 70 75 80
 Gln His His His His Glu Gln His His His His Gln Gln Gln Gln
 85 90 95
 Glu Glu Asp Gly Glu Glu Glu Arg Glu Asp Gly Asp Ser Glu Glu Glu
 100 105 110
 Ser Gly Gln
 115

<210> 51
 <211> 521
 <212> DNA
 <213> Linum usitatissimum

<400> 51
 atcatcatca cccatctatt ctcttgtcta tctctctccc cctgcagctc ttcttatctt 60
 gtgcttatgg aacaacaaca acaacaacca aaggtcccaa accaccttga tgatccacac 120
 caaaacagca acaaccctct ttcggcaatg aaagacgttc aaatcacatc acttggtcca 180
 aacagcagta caaagaagca gcagagttaa ggtccgaaga ggagttcgaa caaggacagg 240
 cacaagaaag tggacggaag agggagaagg atcaggatgc cagctttatg cgccgctagc 300
 atcttccagc tgactcgaga attgggtcac aaatccgacg gcgagacat ccagtggtct 360
 ctgaaccaat ctgagccgtc catcattgca gccaccggca ccgggacaat tccggcctct 420
 gctcttgccg ctgcagggtc ctctgtttct aattcggaga tgcaggggag ctctgtttct 480
 ttctctgctg ggaacaattg ggcagccttg atgaatgcca a 521

<210> 52
 <211> 173
 <212> PRT
 <213> Linum usitatissimum

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<400> 52

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

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<210> 53

<211> 441

<212> DNA

<213> Lotus corniculatus

<400> 53

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atggatccca agggctcaaa gcagcagaac caggaggttg ttccaaactt ccttcaacaa      60
caacaacaag ggaacaacaa caacaacatg ggagagaaca aaccatccga ggttaaggat      120
ttccagattg tgattgctga gaaagatgag agcaagaagc agttggcacc aaagaggacc      180
tccaacaagg acagacacac aaaagttgaa ggcaggggaa ggaggataag gatgccagct      240
ctgtgtgcag caagaatctt ccagttgacc agagaattag gtcacaaatc tgatggtgaa      300
accatccagt ggcttctgca gcaggctgag ccatcaatca tagcagccac tggaactgga      360
acaatcccag catctgcttt agcttctgct gctggttaact ctgtttcaca acagggggacc      420
tctttatctg ctggtttgca c                                     441

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<210> 54

<211> 147

<212> PRT

<213> Lotus corniculatus

<400> 54

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Met Asp Pro Lys Gly Ser Lys Gln Gln Asn Gln Glu Val Val Pro Asn
1      5      10      15
Phe Leu Gln Gln Gln Gln Gly Asn Asn Asn Asn Asn Met Gly Glu
20      25      30
Asn Lys Pro Ser Glu Val Lys Asp Phe Gln Ile Val Ile Ala Glu Lys
35      40      45
Asp Glu Ser Lys Lys Gln Leu Ala Pro Lys Arg Thr Ser Asn Lys Asp
50      55      60
Arg His Thr Lys Val Glu Gly Arg Gly Arg Arg Ile Arg Met Pro Ala
65      70      75      80
Leu Cys Ala Ala Arg Ile Phe Gln Leu Thr Arg Glu Leu Gly His Lys
85      90      95
Ser Asp Gly Glu Thr Ile Gln Trp Leu Leu Gln Gln Ala Glu Pro Ser
100     105     110

```

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Ile Ile Ala Ala Thr Gly Thr Gly Thr Ile Pro Ala Ser Ala Leu Ala
 115 120 125
 Ser Ala Ala Gly Asn Ser Val Ser Gln Gln Gly Thr Ser Leu Ser Ala
 130 135 140
 Gly Leu His
 145

<210> 55
 <211> 668
 <212> DNA
 <213> Petunia hybrida

<400> 55
 gcggcgtcta aatatggatc cccgggctgc aggaatcggc acgagagaga aagtagcaag 60
 aaacaattag ctccaaaaag aagttcaaac aaagataggc ataaaaaagt agatggtaga 120
 ggtagaagaa ttcgtatgcc agctttatgt gctgcaagaa ttttccaatt gactcgtgaa 180
 ttgggtcata aaactgatgg tgaaacaatt caatggctgt tacaacaagc tgagccttca 240
 attattgctg ctactgggac tgggtactatt cctgcttcag ttcttgcagc tgctacttcc 300
 tctgtttctg aacaggggaa ctctgtttct gctacttctt tacattcaag aattgatgat 360
 tatggtttgt ttagagctaa ttgggctaatt ttaagtagac cccagatgcc tgtttctggt 420
 tcttggccta gttttggatc aggatttgtg caaaattcaa gtaatttgag tactcaaatg 480
 ttgagttctg ttccaagatt tggctttgag ttactcaaa attcattggg atttaatcag 540
 aatcaaaatg ttcttggttt agaacttgga ttatctcaag agggtcgaat tgggaacttg 600
 aattttcaat ctttacaaca gttttatcag caaatagcta cacaaagtgg agatgctgct 660
 gctcgagg 668

<210> 56
 <211> 222
 <212> PRT
 <213> Petunia hybrida

<400> 56
 Ala Ala Ser Lys Tyr Gly Ser Pro Gly Cys Arg Asn Arg His Glu Arg
 1 5 10 15
 Glu Ser Ser Lys Lys Gln Leu Ala Pro Lys Arg Ser Ser Asn Lys Asp
 20 25 30
 Arg His Lys Lys Val Asp Gly Arg Gly Arg Arg Ile Arg Met Pro Ala
 35 40 45
 Leu Cys Ala Ala Arg Ile Phe Gln Leu Thr Arg Glu Leu Gly His Lys
 50 55 60
 Thr Asp Gly Glu Thr Ile Gln Trp Leu Leu Gln Gln Ala Glu Pro Ser
 65 70 75 80
 Ile Ile Ala Ala Thr Gly Thr Gly Thr Ile Pro Ala Ser Val Leu Ala
 85 90 95
 Ala Ala Thr Ser Ser Val Ser Glu Gln Gly Asn Ser Val Ser Ala Thr
 100 105 110
 Ser Leu His Ser Arg Ile Asp Asp Tyr Gly Leu Phe Arg Ala Asn Trp
 115 120 125
 Ala Asn Leu Ser Arg Pro Gln Met Pro Val Ser Gly Ser Trp Pro Ser
 130 135 140
 Phe Gly Ser Gly Phe Val Gln Asn Ser Ser Asn Leu Ser Thr Gln Met
 145 150 155 160
 Leu Ser Ser Val Pro Arg Phe Gly Phe Glu Phe Thr Gln Asn Ser Leu
 165 170 175
 Gly Phe Asn Gln Asn Gln Asn Val Pro Gly Leu Glu Leu Gly Leu Ser
 180 185 190
 Gln Glu Gly Arg Ile Gly Asn Leu Asn Phe Gln Ser Leu Gln Gln Phe
 195 200 205
 Tyr Gln Gln Ile Ala Thr Gln Ser Gly Asp Ala Ala Ala Arg

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210

215

220

<210> 57
 <211> 294
 <212> DNA
 <213> *Prunus persica*

<400> 57
 gagttcaaat tacatgcaaa agatggcttt cctggctttg acttgctgt ctccaacatg 60
 ggtcctatga gtttcacctc aattttgggt ggtgggagta accaacagct tcctggcttg 120
 gagcttgggt tgtctcagga tggatcatatt ggggttttga actcacaagc cttgagccag 180
 atttaccagc agatggggca tgctagagta caccagcacc agcaccagca ccagcaccag 240
 caccagcacc agcaaccccc tgctaaggat gactctcaag gctcaggaca gtag 294

<210> 58
 <211> 97
 <212> PRT
 <213> *Prunus persica*

<400> 58
 Glu Phe Lys Leu His Ala Lys Asp Gly Phe Pro Gly Phe Asp Leu Pro
 1 5 10 15
 Val Ser Asn Met Gly Pro Met Ser Phe Thr Ser Ile Leu Gly Gly Gly
 20 25 30
 Ser Asn Gln Gln Leu Pro Gly Leu Glu Leu Gly Leu Ser Gln Asp Gly
 35 40 45
 His Ile Gly Val Leu Asn Ser Gln Ala Leu Ser Gln Ile Tyr Gln Gln
 50 55 60
 Met Gly His Ala Arg Val His Gln His Gln His Gln His Gln His Gln
 65 70 75 80
 His Gln His Gln Gln Pro Pro Ala Lys Asp Asp Ser Gln Gly Ser Gly
 85 90 95
 Gln

<210> 59
 <211> 936
 <212> DNA
 <213> *Ricinus communis*

<400> 59
 aaccacatg aattaccta cttcttgact caccctctc aaccagccct acagcaacaa 60
 caacaaccac aacaagaaca acaacatcaa aaccagaaac aacagacaaa catgggagag 120
 aataaaccag cagaaatcaa agatttccag attgttattg cagataaaga agagcagaag 180
 aaacagttag caccaaaaag aagctcaaac aaagacagac atacgaaagt tgaaggaaga 240
 gggaggagga taaggatgcc agcactttgt gcagcaagaa tctttcaatt gacaagagaa 300
 ttgggtcata aatctgatgg ggaaacaata cagtgggtat tacaacaagc tgaaccatct 360
 ataattgctg caactgggac aggaacgata ccagcatcag ctttggtagc tgctggtgga 420
 tcagtttcac agcaaggac ttctctatca gctggattac accaaaagat tgatgattta 480
 ggtgggtcca gtagtattac tagtagtaat agtaggacaa gttgggcaat ggtaggtggc 540
 aatttaggga gaccccatca tgtggcaaca acagggttat ggccccagc ttggtggttt 600
 ggattccagt catcatctac tactactggt ccagtaacat caaatttggg aaatgaaagt 660
 tctagttatt tgcaaaaaat tgggtttcct gggtttgatt tgccaggga taatatggga 720
 cctatgagtt ttacatcaat cttgggtggg actagcaacc agcagatacc tggtttggag 780
 cttgggttgt cacaagatgg tcatattggg gttttgaatt cacaagcttt tagtcagatt 840
 tatcagcaga tggggcaggc cagagtgcag caccagcacc agcaccagca ccagcaaaaat 900
 cctgctaagg atgattctca agggtcagga cagtaa 936

<210> 60

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<211> 311
<212> PRT
<213> Ricinus communis

<400> 60

```

Asn Pro His Glu Leu Pro Asn Phe Leu Thr His Pro Pro Gln Pro Ala
1      5      10      15
Leu Gln Gln Gln Gln Gln Pro Gln Gln Glu Gln Gln His Gln Asn Gln
20      25      30
Lys Gln Gln Thr Asn Met Gly Glu Asn Lys Pro Ala Glu Ile Lys Asp
35      40      45
Phe Gln Ile Val Ile Ala Asp Lys Glu Glu Gln Lys Lys Gln Leu Ala
50      55      60
Pro Lys Arg Ser Ser Asn Lys Asp Arg His Thr Lys Val Glu Gly Arg
65      70      75      80
Gly Arg Arg Ile Arg Met Pro Ala Leu Cys Ala Ala Arg Ile Phe Gln
85      90      95
Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly Glu Thr Ile Gln Trp
100     105     110
Leu Leu Gln Gln Ala Glu Pro Ser Ile Ile Ala Ala Thr Gly Thr Gly
115     120     125
Thr Ile Pro Ala Ser Ala Leu Val Ala Ala Gly Gly Ser Val Ser Gln
130     135     140
Gln Gly Thr Ser Leu Ser Ala Gly Leu His Gln Lys Ile Asp Asp Leu
145     150     155     160
Gly Gly Ser Ser Ser Ile Thr Ser Ser Asn Ser Arg Thr Ser Trp Ala
165     170     175
Met Val Gly Gly Asn Leu Gly Arg Pro His His Val Ala Thr Thr Gly
180     185     190
Leu Trp Pro Pro Val Gly Gly Phe Gly Phe Gln Ser Ser Ser Thr Thr
195     200     205
Thr Gly Pro Val Thr Ser Asn Leu Gly Asn Glu Ser Ser Ser Tyr Leu
210     215     220
Gln Lys Ile Gly Phe Pro Gly Phe Asp Leu Pro Gly Asn Asn Met Gly
225     230     235     240
Pro Met Ser Phe Thr Ser Ile Leu Gly Gly Thr Ser Asn Gln Gln Ile
245     250     255
Pro Gly Leu Glu Leu Gly Leu Ser Gln Asp Gly His Ile Gly Val Leu
260     265     270
Asn Ser Gln Ala Phe Ser Gln Ile Tyr Gln Gln Met Gly Gln Ala Arg
275     280     285
Val Gln His Gln His Gln His Gln Gln Asn Pro Ala Lys Asp
290     295     300
Asp Ser Gln Gly Ser Gly Gln
305     310

```

<210> 61
<211> 231
<212> DNA
<213> Salvia miltiorrhiza

<400> 61

```

agttttcacct caattttgag cggcggcgct cagcagctgc ccggattgga gcttggccta      60
tcacaagatg gaaatattgg cgtgctcaat cctcaagcat tcgggcagtt ttatcagcag      120
atggcacccg cggcgcgtgt tgcccaccac catcagcagc aacaccacca ccaccatcag      180
cagcagcctt tgtcgcccaa ggatgatgat tctcaagaat caggacagta g      231

```

<210> 62
<211> 76

PF58581.ST25.txt

<212> PRT

<213> *Salvia miltiorrhiza*

<400> 62

```

Ser Phe Thr Ser Ile Leu Ser Gly Gly Ala Gln Gln Leu Pro Gly Leu
1      5      10      15
Glu Leu Gly Leu Ser Gln Asp Gly Asn Ile Gly Val Leu Asn Pro Gln
20      25      30
Ala Phe Gly Gln Phe Tyr Gln Gln Met Ala Pro Ala Ala Arg Val Ala
35      40      45
His His His Gln Gln Gln His His His His His Gln Gln Gln Pro Leu
50      55      60
Ser Pro Lys Asp Asp Asp Ser Gln Glu Ser Gly Gln
65      70      75

```

<210> 63

<211> 598

<212> DNA

<213> *Zinnia elegans*

<400> 63

```

cacacaaagg ttaaaggaag aggtagaaga attaggatgc cagctttatg tgctgcaaga      60
atctttcaac tcactaggga gttaggtaac aaatctgatg gggaaacaat ccagtggctg      120
ctacagcagg ccgagccatc tatcatagca gccactggca ccgggactat cccggcttcc      180
gtgttagcca ccaccggagc ggcttcacac ggagtctcga tttcggtagg attgcaacat      240
aagattgatg tattaggtag tgggaatagt aacactagta ttagtaatag taacagtaat      300
agtaatatct gtggcaacaa ctgtaggacc agttggccta tgggtagacc cacaacccat      360
atggccacgc ctactacagg tatatggccc gcaatgggat acgggtcttc ggtccctcg      420
ggcaacaatt taggggttga aagctcgaat tacctgcaaa agatggcggt ttccgggttt      480
gaattgcctg ggtctaatat gggtcagatg agtttttcgt cgattttagg taatcataat      540
catgatcatc atcagcagca gcagcttcct gggttggaac ttgggttgtc ccaagatg      598

```

<210> 64

<211> 199

<212> PRT

<213> *Zinnia elegans*

<400> 64

```

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

```

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```

                165                170                175
Gly Asn His Asn His Asp His His Gln Gln Gln Gln Leu Pro Gly Leu
                180                185                190
Glu Leu Gly Leu Ser Gln Asp
                195

```

```

<210> 65
<211> 13
<212> PRT
<213> Artificial sequence

```

```

<220>
<223> consensus C-terminal motif 1

```

```

<220>
<221> VARIANT
<222> (6)..(6)
<223> /replace="Arg" /replace="Ala"

```

```

<220>
<221> UNSURE
<222> (10)..(10)
<223> Xaa can be a stretch of 1 to 5 naturally occurring amino acids

```

```

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

```

```

<400> 65
Pro Gly Leu Glu Leu Gly Leu Ser Gln Xaa Gly Val Leu
1                5                10

```

```

<210> 66
<211> 69
<212> PRT
<213> Artificial sequence

```

```

<220>
<223> Conserved TCP domain of SEQ ID NO : 02

```

```

<400> 66
Lys Asp Arg His Thr Lys Val Glu Gly Arg Gly Arg Arg Ile Arg Met
1                5                10                15
Pro Ala Leu Cys Ala Ala Arg Ile Phe Gln Leu Thr Arg Glu Leu Gly
                20                25                30
His Lys Ser Asp Gly Glu Thr Ile Gln Trp Leu Leu Gln Gln Ala Glu
                35                40                45
Pro Ser Ile Ile Ala Ala Thr Gly Ser Gly Thr Ile Pro Ala Ser Ala
                50                55                60
Leu Ala Ser Ser Ala
65

```

```

<210> 67
<211> 2193
<212> DNA
<213> Oryza sativa

```

```

<400> 67

```

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```

aatccgaaaa gtttctgcac cgttttcacc ccctaactaa caatataggg aacgtgtgct      60
aaatataaaa tgagacctta tatatgtagc gctgataact agaactatgc aagaaaaaact      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 attatttatc 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 tattgggcac acaggcaaca      840
acagagtggc tgcccacaga acaaccacaca aaaaacgatg atctaacgga ggacagcaag      900
tccgcaacaa ccttttaaca gcaggctttg cggccaggag agaggaggag agggcaagaa      960
aaccaagcat cctctcctc ccactataaa attcctcccc ccttttcccc tctctatata     1020
ggaggcatcc aagccaagaa gagggagagc accaaggaca cgcgactagc agaagccgag     1080
cgaccgcctt cttcgatcca tatcttccgg tcgagttcct ggtcgatctc ttccctcctc     1140
cacctcctcc tcacagggtg tgtgcccttc ggtgttctt ggatttattg ttctagggtg     1200
tgtagtacgg gcgttgatgt taggaaaggg gatctgtatc tgtgatgatt cctgttcttg     1260
gatttgggat agaggggttc ttgatgttgc atgttatcgg ttcggtttga ttagtagtat     1320
ggttttcaat cgtctggaga gctctatgga aatgaaatgg tttagggtac ggaatcttgc     1380
gattttgtga gtaccttttg tttgaggtaa aatcagagca ccggtgattt tgcttggtgt     1440
aataaaagta cggttgtttg gtctcgtatt ctggtagtga tgcttctcga tttgacgaag     1500
ctatcctttg tttattccct attgaacaaa aataatccaa ctttgaagac ggtcccgttg     1560
atgagattga atgattgatt cttaagcctg tccaaaattt cgcagctggc ttgttttagat     1620
acagtagtcc ccatacagaa attcatggaa acagttataa tcctcaggaa caggggattc     1680
cctgttcttc cgatttgctt tagtcccaga attttttttc ccaaatatct taaaaagtca     1740
ctttctgggt cagttcaatg aattgattgc tacaaaataa gcttttatag cgttatccta     1800
gctgtagttc agttaatagg taatacccct atagtttagt caggagaaga acttatccga     1860
tttctgatct ccatttttaa ttatatgaaa tgaactgtag cataagcagt attcatttgg     1920
attatttttt ttattagctc tcacctcttc attattctga gctgaaagtc tggcatgaac     1980
tgtcctcaat tttgttttca aattcacatc gattatctat gcattatcct cttgtatcta     2040
cctgtagaag tttctttttg gttattcctt gactgcttga ttacagaaag aaatttatga     2100
agctgtaatc gggatagtta tactgcttgt tcttatgatt catttccttt gtgcagttct     2160
tgggtgtagt tgccactttc accagcaaaag ttc                                     2193

```

<210> 68
 <211> 53
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: prm01501

<400> 68
 ggggacaagt ttgtacaaaa aagcaggctt cacaatggat cccaagaacc taa 53

<210> 69
 <211> 48
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: prm01502

<400> 69
 ggggaccact ttgtacaaga aagctggggt tttaacgacc tgagcctt 48

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<210> 70
 <211> 924
 <212> DNA
 <213> Cichorium endivia

<400> 70
 cgggggggtc cagagttcaa gcaacaacat cctcaacagc agccatatga ggtttcaagc 60
 ttcttaagca tcccgcaacc caccagcaac aacatgggag ataacgacaa cagcaagcct 120
 tctgaaatca aagatttaca gattgtaatt cccgacaagg aaaccagcaa gaagcaacaa 180
 caattagcac ccaaacgcac atccaacaaa gacaggcata caaaggttga aggccgaggt 240
 cgcaggatta ggatgccgc tctctgtgct gcaagaatct ttcagctgac tcgagaatta 300
 ggtcataaat ccgatgggga aacaatccag tggctcctac agcaggccga gccttccatt 360
 atcgccgccca ccggaactgg aactatcccg gcttcgggtg tagccacagc cggcgaggtt 420
 tcacatggggg ttctgacttc ggcggggatta caacagaaac ttgacgaatt agttgggtgtg 480
 ggaaataacta gtgacagctg taggaccagt tggccgattg ttgggtccggg ggtgggtaga 540
 cccgcaaccc acatggccac tccttttaggt atgtggccaa ccacaaccgg atttgggttt 600
 cagtcgcctc cgtcgtcctc tgggtccatca tcggccaaca atttgggcat cgaaagctcc 660
 aattacttgc aaaagattgc attttctggg tttgatctgc ccggttctaa tctgggcccg 720
 atgagttttt cttcgatttt gggtaatcat catcaacagc aacttcccgg gttggagctg 780
 ggactgtcac aagatgggtca cataggggtc ttgaatcaac aagcgctgaa ccagatttac 840
 cagatgggtc aggccagaat gcaccatcaa caacaacaac atcaaacttc taaggatgat 900
 tctcaagggtt cagggggaca atag 924

<210> 71
 <211> 307
 <212> PRT
 <213> Cichorium endivia

<400> 71
 Arg Gly Asp Pro Glu Phe Lys Gln Gln His Pro Gln Gln Gln Pro Tyr
 1 5 10 15
 Glu Val Ser Ser Phe Leu Ser Ile Pro Gln Pro Thr Ser Asn Asn Met
 20 25 30
 Gly Asp Asn Asp Asn Ser Lys Pro Ser Glu Ile Lys Asp Leu Gln Ile
 35 40 45
 Val Ile Pro Asp Lys Glu Thr Ser Lys Lys Gln Gln Gln Leu Ala Pro
 50 55 60
 Lys Arg Thr Ser Asn Lys Asp Arg His Thr Lys Val Glu Gly Arg Gly
 65 70 75 80
 Arg Arg Ile Arg Met Pro Ala Leu Cys Ala Ala Arg Ile Phe Gln Leu
 85 90 95
 Thr Arg Glu Leu Gly His Lys Ser Asp Gly Glu Thr Ile Gln Trp Leu
 100 105 110
 Leu Gln Gln Ala Glu Pro Ser Ile Ile Ala Ala Thr Gly Thr Gly Thr
 115 120 125
 Ile Pro Ala Ser Val Leu Ala Thr Ala Gly Ala Val Ser His Gly Val
 130 135 140
 Ser Thr Ser Ala Gly Leu Gln Gln Lys Leu Asp Glu Leu Val Gly Val
 145 150 155 160
 Gly Asn Thr Ser Asp Ser Cys Arg Thr Ser Trp Pro Ile Val Gly Pro
 165 170 175
 Gly Val Gly Arg Pro Ala Thr His Met Ala Thr Pro Leu Gly Met Trp
 180 185 190
 Pro Thr Thr Thr Gly Phe Gly Phe Gln Ser Pro Pro Ser Ser Ser Gly
 195 200 205
 Pro Ser Ser Ala Asn Asn Leu Gly Ile Glu Ser Ser Asn Tyr Leu Gln
 210 215 220
 Lys Ile Ala Phe Ser Gly Phe Asp Leu Pro Gly Ser Asn Leu Gly Pro

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```

225          230          235          240
Met Ser Phe Ser Ser Ile Leu Gly Asn His His Gln Gln Gln Leu Pro
          245          250          255
Gly Leu Glu Leu Gly Leu Ser Gln Asp Gly His Ile Gly Val Leu Asn
          260          265          270
Gln Gln Ala Leu Asn Gln Ile Tyr Gln Met Gly Gln Ala Arg Met His
          275          280          285
His Gln Gln Gln Gln His Gln Thr Ser Lys Asp Asp Ser Gln Gly Ser
          290          295          300
Gly Gly Gln
305

```

<210> 72
 <211> 585
 <212> DNA
 <213> Fragaria vesca

```

<400> 72
accaccggca cccgggacgat cccggcgctcg gctctagcgg cggcaggagg gtctgtatcg      60
cagcagggga gttcaatatc agctggccttg tatcaaaaga cagatgattt aggggtccagt      120
ggaggtagga ccagttgggc tatggtggga gggaatttag ggaggcccca tgtggctgca      180
gcaactgggc tatggccccc tgctgggttt ggtttttctt cacagtcac ttcatctggt      240
ccatctacta caaatctggg agggactgag agcagctcca attacctcca aaagattggc      300
cttctctggg ttgacttgcc agtcaccaac atgggaccta tgagcttcac ttcaattctg      360
ggtgggggaa gtcaacagct gcctgggttg gaacttgggt tgtctcaaga tggccatctt      420
ggggttttga attctcaggc ttaccagatt taccagcaga tgggccatgc tagagtgcac      480
caccatcaac agcagcaaca gcaacaccac cagcagcagc accaacacca gcaacagcag      540
caagctccgt cttctaagga tgattctcaa ggctcaggac agtag      585

```

<210> 73
 <211> 194
 <212> PRT
 <213> Fragaria vesca

```

<400> 73
Thr Thr Gly Thr Gly Thr Ile Pro Ala Ser Ala Leu Ala Ala Ala Gly
1          5          10          15
Gly Ser Val Ser Gln Gln Gly Ser Ser Ile Ser Ala Gly Leu Tyr Gln
          20          25          30
Lys Thr Asp Asp Leu Gly Ser Ser Gly Gly Arg Thr Ser Trp Ala Met
          35          40          45
Val Gly Gly Asn Leu Gly Arg Pro His Val Ala Ala Ala Thr Gly Leu
          50          55          60
Trp Pro Pro Ala Gly Phe Gly Phe Ser Ser Gln Ser Ser Ser Ser Gly
65          70          75          80
Pro Ser Thr Thr Asn Leu Gly Gly Thr Glu Ser Ser Ser Asn Tyr Leu
          85          90          95
Gln Lys Ile Gly Leu Pro Gly Phe Asp Leu Pro Val Thr Asn Met Gly
          100          105          110
Pro Met Ser Phe Thr Ser Ile Leu Gly Gly Gly Ser Gln Gln Leu Pro
          115          120          125
Gly Leu Glu Leu Gly Leu Ser Gln Asp Gly His Leu Gly Val Leu Asn
          130          135          140
Ser Gln Ala Tyr Gln Ile Tyr Gln Gln Met Gly His Ala Arg Val His
145          150          155          160
His His Gln Gln Gln Gln Gln Gln His His Gln Gln Gln His Gln His
          165          170          175
Gln Gln Gln Gln Gln Ala Pro Ser Ser Lys Asp Asp Ser Gln Gly Ser
          180          185          190

```

Gly Gln

<210> 74
 <211> 818
 <212> DNA
 <213> Juglans hindsii x Juglans regia

<400> 74
 ccaagggctc aacaacagca aagcagccac aacaagtacc aaacttcttg agcctccac 60
 aaccacaaca acaacctaac atgggtgaga acaagcctgc tgaaatcaaa gacttccaga 120
 ttgtgattgc tgacaaagaa gagggcaaga agcagttggc cccaagaga agctcaaaca 180
 aagaccggca caccaaagt gaaggcaggg gaaggagaat aaggatgcca gctctttgtg 240
 cagcgaggat ttttcaattg accagagaat tgggccacaa atctgatgga gaaaccatac 300
 agtggctggt acagcaggct gagccatcga taatagcagc cactgggact ggaaccatac 360
 cggttcagc ttttagcagc gcagggggtt ctgtatcaca gcagggggcc tctctatcag 420
 ctggattgca caaaagatt gatgatttgg ggggtccag tatcgggtta gggagtagga 480
 ccagttgggc aatggtaggt ggaatttag ggagaccca tgtggccaca gggctatggc 540
 cccgggtcag tgggtttggg tttcagtcac catctggtcc atcgactgcg aatttgggaa 600
 gtgagagtgc aaattacctg caaaagattg gcttccttgg ctttgacttg ccagccaccc 660
 ctatgagttt cacctcaata ttgggtggga ataatcagca gctaccggga ttggagctcg 720
 gcttatccca agatggtcat atcggggttt tgaaccaca agccttgagt cagatttatc 780
 aacagatggg gcaggctaga gtgcagcagc aacagcaa 818

<210> 75
 <211> 272
 <212> PRT
 <213> Juglans hindsii x Juglans regia

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

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225		230		235		240
Leu Ser Gln Asp Gly His Ile Gly Val Leu Asn Pro Gln Ala Leu Ser						
	245		250		255	
Gln Ile Tyr Gln Gln Met Gly Gln Ala Arg Val Gln Gln Gln Gln Gln						
	260		265		270	

<210> 76
 <211> 474
 <212> DNA
 <213> Panax ginseng

<400> 76
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 ccaatgggtg gtgggaattt gggaagaccc catatggcca cagcaggatt atggcccgct 120
 gctgcagtcg gtggctatgg gtttcagtc tcatcatctg gtccatcgac aaccaatttg 180
 ggacatgaaa gttcaaatta cttgcaaaaa attgggtttt ctgggtttga cttgccagcc 240
 accaatttgg gtcctatgag ttttgccctca attttgggtg caagtaatca gcagctccct 300
 ggtttggagc ttggcctctc acaagatgga catattgggg ttttgtgcc tcaagccttg 360
 acccagattt accagcagat gggaaatgat agaatgcacc agcaacagca acaacagcac 420
 cggaatcacc agcaggcatc tcccaaggat gaatctcaag ggtcaggaga gtag 474

<210> 77
 <211> 157
 <212> PRT
 <213> Panax ginseng

<400> 77
 Ser Ala Gly Leu Tyr Gln Lys Ile Asp Glu Leu Gly Gly Ser Ser Ser
 1 5 10 15
 Arg Ser Ser Trp Pro Met Val Gly Gly Asn Leu Gly Arg Pro His Met
 20 25 30
 Ala Thr Ala Gly Leu Trp Pro Ala Ala Val Gly Gly Tyr Gly Phe
 35 40 45
 Gln Ser Ser Ser Ser Gly Pro Ser Thr Thr Asn Leu Gly His Glu Ser
 50 55 60
 Ser Asn Tyr Leu Gln Lys Ile Gly Phe Ser Gly Phe Asp Leu Pro Ala
 65 70 75 80
 Thr Asn Leu Gly Pro Met Ser Phe Ala Ser Ile Leu Gly Ala Ser Asn
 85 90 95
 Gln Gln Leu Pro Gly Leu Glu Leu Gly Leu Ser Gln Asp Gly His Ile
 100 105 110
 Gly Val Leu Cys Pro Gln Ala Leu Thr Gln Ile Tyr Gln Gln Met Gly
 115 120 125
 Asn Asp Arg Met His Gln Gln Gln Gln Gln His Arg Asn His Gln
 130 135 140
 Gln Ala Ser Pro Lys Asp Glu Ser Gln Gly Ser Gly Glu
 145 150 155

<210> 78
 <211> 582
 <212> DNA
 <213> Poncirus trifoliata

<400> 78
 gaaccatcta tcatcgctgc tacaggaact gggactattc cagcctctat gcttgcagct 60
 gcaggggcct ctgtttctga acaggggaac tctgtttcag caggcttgca tacaaaaata 120
 gaaggggttg gaccaggtgt tgggtccatt aatagggcca actggacaat gatgagtgca 180
 aattttggaa ggtctcaa tccaagtgga gtttggccaa atataaatgg aactgggtct 240
 gggtttattc aaaattctgg ccagttgact tcaaattttg gaagtgaaaa tttgagtgca 300

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aatccaaaat	ttgggttcca	cgggattgaa	tttccaaata	tgaatatggg	tttgatgagt	360
ttctcctcta	tggttagcgg	tgctagccat	caaattcctg	gcttgagagct	tggtctctca	420
caggatgcgc	atgtgggggt	gatgaattct	caagctataa	gccagttcta	tcaacagatg	480
gggcatcaca	gaagcgcttc	aggatccttg	aatcagcagc	atcagcatca	gcaacaaatt	540
tctgataagg	atgattctca	gggatcagga	tcaaagcagt	ag		582

<210> 79
 <211> 193
 <212> PRT
 <213> Poncirus trifoliata

<400> 79
 Glu Pro Ser Ile Ile Ala Ala Thr Gly Thr Gly Thr Ile Pro Ala Ser
 1 5 10 15
 Met Leu Ala Ala Gly Ala Ser Val Ser Glu Gln Gly Asn Ser Val
 20 25 30
 Ser Ala Gly Leu His Thr Lys Ile Glu Gly Leu Gly Pro Gly Val Gly
 35 40 45
 Ser Ile Asn Arg Ala Asn Trp Thr Met Met Ser Ala Asn Phe Gly Arg
 50 55 60
 Ser Gln Ile Pro Ser Gly Val Trp Pro Asn Ile Asn Gly Thr Gly Ser
 65 70 75 80
 Gly Phe Ile Gln Asn Ser Gly Gln Leu Thr Ser Asn Phe Gly Ser Glu
 85 90 95
 Asn Leu Ser Ala Asn Pro Lys Phe Gly Phe His Gly Ile Glu Phe Pro
 100 105 110
 Asn Met Asn Met Gly Leu Met Ser Phe Ser Ser Met Leu Ser Gly Ala
 115 120 125
 Ser His Gln Ile Pro Gly Leu Glu Leu Gly Leu Ser Gln Asp Ala His
 130 135 140
 Val Gly Val Met Asn Ser Gln Ala Ile Ser Gln Phe Tyr Gln Gln Met
 145 150 155 160
 Gly His His Arg Ser Ala Ser Gly Ser Leu Asn Gln Gln His Gln His
 165 170 175
 Gln Gln Gln Ile Ser Asp Lys Asp Asp Ser Gln Gly Ser Gly Ser Lys
 180 185 190
 Gln

<210> 80
 <211> 933
 <212> DNA
 <213> Chlamydomonas reinhardtii

<400> 80
 atgcgctcag ccgttctaca acgcgggccag gcgcggcgag tgtcttgccg gggtcggggcg 60
 gatggttcgg gcgtggattc gctgccctcg accagcgcca gcagcagcgc acgccctctc 120
 attgatcgcc gtcagctcct gaccgggtgct gctgcgtcgg tcataacctt cggttggtgc 180
 ccttgccccc tgtgcaagcc tggggaggga aaggccgcag cttggaacta tggcgaagtt 240
 gcgggtccgc caacctggaa ggggtgtgtgt gcgacgggca agcgccagtc gcccatcaac 300
 atcccgttga acacatcggc gccgaaggtc gacgcggaga tgggcgaatt cgatttcgcc 360
 tacggcagct tcgagaagtg cgacgtgctg aacacgggac acagcaccat gcaggtgaac 420
 ttccccgctg gcaacctggc gttcattggc aacatggagc tggagctgct gcagttccac 480
 ttccacgcgc cctcggagca cgccatggat ggccgccgtt acgccatgga ggcgcacatc 540
 gtgcacaaga ataaaagcac cggcaaccta gctgtgctgg gcattatgct ggagcccggc 600
 ggcctgatca agaaccggc gctgtccact gctctggagg tggcgcccga ggtgcccctg 660
 gccagaagc cctcgcccaa ggcatcaac cccgtcatgc tgctgcccga gaagagcaag 720
 gccgggacac ggccgttcgt gcaactacct ggctcgctta ccacgcccc gtgttcggag 780
 ggggtggact ggtttgtgtt catgcagccc atcaaggtgc ccgacagcca gatcctggac 840

PF58581.ST25.txt

ttcatgcgct tcgtgggcga caacaagaca tacgccacca acacgcggcc actgcagctg 900
ctcaacagcc gcctggtcga atacgagctg tga 933

<210> 81
<211> 310
<212> PRT
<213> Chlamydomonas reinhardtii

<400> 81
Met Arg Ser Ala Val Leu Gln Arg Gly Gln Ala Arg Arg Val Ser Cys
1 5 10 15
Arg Val Arg Ala Asp Gly Ser Gly Val Asp Ser Leu Pro Ser Thr Ser
20 25 30
Ala Ser Ser Ser Ala Arg Pro Leu Ile Asp Arg Arg Gln Leu Leu Thr
35 40 45
Gly Ala Ala Ala Ser Val Ile Thr Phe Val Gly Cys Pro Cys Pro Leu
50 55 60
Cys Lys Pro Gly Glu Ala Lys Ala Ala Ala Trp Asn Tyr Gly Glu Val
65 70 75 80
Ala Gly Pro Pro Thr Trp Lys Gly Val Cys Ala Thr Gly Lys Arg Gln
85 90 95
Ser Pro Ile Asn Ile Pro Leu Asn Thr Ser Ala Pro Lys Val Asp Ala
100 105 110
Glu Met Gly Glu Phe Asp Phe Ala Tyr Gly Ser Phe Glu Lys Cys Asp
115 120 125
Val Leu Asn Thr Gly His Ser Thr Met Gln Val Asn Phe Pro Ala Gly
130 135 140
Asn Leu Ala Phe Ile Gly Asn Met Glu Leu Glu Leu Leu Gln Phe His
145 150 155 160
Phe His Ala Pro Ser Glu His Ala Met Asp Gly Arg Arg Tyr Ala Met
165 170 175
Glu Ala His Leu Val His Lys Asn Lys Ser Thr Gly Asn Leu Ala Val
180 185 190
Leu Gly Ile Met Leu Glu Pro Gly Gly Leu Ile Lys Asn Pro Ala Leu
195 200 205
Ser Thr Ala Leu Glu Val Ala Pro Glu Val Pro Leu Ala Lys Lys Pro
210 215 220
Ser Pro Lys Gly Ile Asn Pro Val Met Leu Leu Pro Lys Lys Ser Lys
225 230 235 240
Ala Gly Thr Arg Pro Phe Val His Tyr Pro Gly Ser Leu Thr Thr Pro
245 250 255
Pro Cys Ser Glu Gly Val Asp Trp Phe Val Phe Met Gln Pro Ile Lys
260 265 270
Val Pro Asp Ser Gln Ile Leu Asp Phe Met Arg Phe Val Gly Asp Asn
275 280 285
Lys Thr Tyr Ala Thr Asn Thr Arg Pro Leu Gln Leu Leu Asn Ser Arg
290 295 300
Leu Val Glu Tyr Glu Leu
305 310

<210> 82
<211> 1383
<212> DNA
<213> Chlamydomonas reinhardtii

<400> 82
ctttttaga cccacttgct agtgggcact gccctagaa gcggcttctt gaccagagaa 60
gatgcgctca gccgttctac aacgcggcca ggcgcggcga gtgtcttgcc gggttcgggc 120
ggatggttcg ggcgtggatt cgctgccctc gaccagcgcc agcagcagcg cacgccctct 180

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cattgatcgc cgtcagctcc tgaccggtgc tgctgcgtcg gtcataacct tcgttggctg 240
cccttgcccc ctgtgcaagc ctggggaggc aaaggccgca gcttggaact atggcggaagt 300
tgcgggtccg ccaacctgga aggggtgtgtg tgcgacgggc aagcgccagt cgcccatcaa 360
catcccgttg aacacatcgg cgccgaaggt cgacgcggag atgggcgaat tcgatttcgc 420
ctacggcagc ttcgagaagt gcgacgtgct gaacacggga cacggcacca tgcaggtgaa 480
cttccccgct ggcaacctgg cgttcattgg caacatggag ctggagctgc tgcagttcca 540
cttcacgcg ccctcgagc acgccatgga tggccgccgt tacgccatgg aggcgcattct 600
ggtgcacaag aataaaagca ccggcaacct agctgtgctg ggcattatgc tggagcccgg 660
cggcctgata aagaaccgg cgctgtccac tgctctggag gtggcgcccg aggtgcccct 720
ggccaagaag ccctcgccca agggcatcaa ccccgatcgt ctgctgcccc agaagagcaa 780
ggccgggaca cggcgttcg tgcactaccc tggctcgctt accacgcccc cgtgttcgga 840
gggggtggac tggtttgtgt tcatgcagcc catcaagggt cccgacagcc agatcctgga 900
cttcatgcgc ttcgtgggcg acaacaagac atacgccacc aacacgcggc cactgcagct 960
gctcaacagc cgctgtgctg aatacgagct gtgagcggac acgagtgtgc tagggtcagt 1020
gagcagcgtg tgaacatgaa gattacaagt ttgtgacag agagcgggag gagtgcccat 1080
gcatcgcata gtaacagccc gcgaagtacg acttaacatg acataaaaagt gcaatgcgca 1140
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ggggaggcat cgccttgac gcacttgccg tatgtaggcg tgctggtgaa tgaggtatgg 1260
ggcgagagac ccgcgaacta aacttaagta gattacccat gtatccttta tttggcttgc 1320
gtgccctctc aattggggca ccgatgcagg ggctggaagg ccccggtgaa cacatgacac 1380
tca 1383

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<210> 83
<211> 310
<212> PRT
<213> Chlamydomonas reinhardtii

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<400> 83
Met Arg Ser Ala Val Leu Gln Arg Gly Gln Ala Arg Arg Val Ser Cys
1      5      10      15
Arg Val Arg Ala Asp Gly Ser Gly Val Asp Ser Leu Pro Ser Thr Ser
20     25     30
Ala Ser Ser Ser Ala Arg Pro Leu Ile Asp Arg Arg Gln Leu Leu Thr
35     40     45
Gly Ala Ala Ala Ser Val Ile Thr Phe Val Gly Cys Pro Cys Pro Leu
50     55     60
Cys Lys Pro Gly Glu Ala Lys Ala Ala Ala Trp Asn Tyr Gly Glu Val
65     70     75     80
Ala Gly Pro Pro Thr Trp Lys Gly Val Cys Ala Thr Gly Lys Arg Gln
85     90     95
Ser Pro Ile Asn Ile Pro Leu Asn Thr Ser Ala Pro Lys Val Asp Ala
100    105    110
Glu Met Gly Glu Phe Asp Phe Ala Tyr Gly Ser Phe Glu Lys Cys Asp
115    120    125
Val Leu Asn Thr Gly His Gly Thr Met Gln Val Asn Phe Pro Ala Gly
130    135    140
Asn Leu Ala Phe Ile Gly Asn Met Glu Leu Glu Leu Leu Gln Phe His
145    150    155    160
Phe His Ala Pro Ser Glu His Ala Met Asp Gly Arg Arg Tyr Ala Met
165    170    175
Glu Ala His Leu Val His Lys Asn Lys Ser Thr Gly Asn Leu Ala Val
180    185    190
Leu Gly Ile Met Leu Glu Pro Gly Gly Leu Ile Lys Asn Pro Ala Leu
195    200    205
Ser Thr Ala Leu Glu Val Ala Pro Glu Val Pro Leu Ala Lys Lys Pro
210    215    220
Ser Pro Lys Gly Ile Asn Pro Val Met Leu Leu Pro Lys Lys Ser Lys
225    230    235    240
Ala Gly Thr Arg Pro Phe Val His Tyr Pro Gly Ser Leu Thr Thr Pro

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				245						250					255				
Pro	Cys	Ser	Glu	Gly	Val	Asp	Trp	Phe	Val	Phe	Met	Gln	Pro	Ile	Lys				
			260					265					270						
Val	Pro	Asp	Ser	Gln	Ile	Leu	Asp	Phe	Met	Arg	Phe	Val	Gly	Asp	Asn				
		275					280					285							
Lys	Thr	Tyr	Ala	Thr	Asn	Thr	Arg	Pro	Leu	Gln	Leu	Leu	Asn	Ser	Arg				
	290					295					300								
Leu	Val	Glu	Tyr	Glu	Leu														
305					310														

<210> 84
 <211> 1244
 <212> DNA
 <213> Arabidopsis thaliana

<400> 84
 caaaattcat gtgtagttc ttcttcttta caaaattgag tttaaactgt tttattacta 60
 atccaaatga ggaatcactt tgcactatta atagaaaata atacacaacc aaacatctaa 120
 aagatactat aatagtagag atcaaagacc tgagcaaaaa ctgaaagaaa aaaaaaaaaa 180
 aaaaaaaga cttctcctca aaaatggcgt ttacactagg tggaagagct cgctcgtctag 240
 tctctgcaac atcagttcat caaaatgggt gcttacacaa actgcaacaa attggatcgg 300
 atcgggtttca gcttggtgaa gcaaaagcaa taagattact acccaggtga taagataaag 360
 tttggtcttt atagtctttt aaaaaaaaaa gtgaatcaaa gaataaagac agagattact 420
 ctgttttttt gtatcatagg agaacaaaca tggttcaaga attaggaatc agggaagaat 480
 ttatggatct aaacagagaa acagagacaa gttatgattt tctggatgaa atgagacaca 540
 gatttctgaa attcaagaga caaaagtatc taccggagat agaaaagttt aaagcttttg 600
 ccatagctca atcaccaaag gtaatggtga taggatgtgc agattcaagg gtatgtccat 660
 cttatgtact aggatttcaa cctggtgaag cttttactat ccgaaatgtc gccaatctcg 720
 ttaccccggt tcagaatgga ccaacagaaa ccaactcggc tcttgagttt gcggtcacca 780
 ctcttcaggt tgagaacatt atagttagtg gtcatagcaa ttgtggagga attgcagcac 840
 ttatgagtca tcaaaaccac caagggcaac actctagttt agtagaaagg tgggttatga 900
 atgggaaagc cgctaagtta agaacacaat tagcttcatc acatttatcc tttgatgaac 960
 aatgcagaaa ctgtgagaag gaatctataa aggattctgt gatgaatttg ataacttatt 1020
 catggataag agatagagta aagagaggtg aagtcaagat tcatggatgt tattacaatt 1080
 tgtcagattg tagtcttgag aagtggagat taagttcaga caagactaac tatggattct 1140
 atatttcaga cagagagata tggagttgag taaatattga acaatcctca gttctaatat 1200
 tcagatgtat ctttgtacat acgaaatgat atttacacaa ttgg 1244

<210> 85
 <211> 286
 <212> PRT
 <213> Arabidopsis thaliana

<400> 85
 Met Ala Phe Thr Leu Gly Gly Arg Ala Arg Arg Leu Val Ser Ala Thr
 1 5 10 15
 Ser Val His Gln Asn Gly Cys Leu His Lys Leu Gln Gln Ile Gly Ser
 20 25 30
 Asp Arg Phe Gln Leu Gly Glu Ala Lys Ala Ile Arg Leu Leu Pro Arg
 35 40 45
 Arg Thr Asn Met Val Gln Glu Leu Gly Ile Arg Glu Glu Phe Met Asp
 50 55 60
 Leu Asn Arg Glu Thr Glu Thr Ser Tyr Asp Phe Leu Asp Glu Met Arg
 65 70 75 80
 His Arg Phe Leu Lys Phe Lys Arg Gln Lys Tyr Leu Pro Glu Ile Glu
 85 90 95
 Lys Phe Lys Ala Leu Ala Ile Ala Gln Ser Pro Lys Val Met Val Ile
 100 105 110
 Gly Cys Ala Asp Ser Arg Val Cys Pro Ser Tyr Val Leu Gly Phe Gln

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115	120	125
Pro Gly Glu Ala Phe Thr Ile Arg Asn Val Ala Asn Leu Val Thr Pro		
130	135	140
Val Gln Asn Gly Pro Thr Glu Thr Asn Ser Ala Leu Glu Phe Ala Val		
145	150	155
Thr Thr Leu Gln Val Glu Asn Ile Ile Val Met Gly His Ser Asn Cys		
165	170	175
Gly Gly Ile Ala Ala Leu Met Ser His Gln Asn His Gln Gly Gln His		
180	185	190
Ser Arg Trp Val Met Asn Gly Lys Ala Ala Lys Leu Arg Thr Gln Leu		
195	200	205
Ala Ser Ser His Leu Ser Phe Asp Glu Gln Cys Arg Asn Cys Glu Lys		
210	215	220
Glu Ser Ile Lys Asp Ser Val Met Asn Leu Ile Thr Tyr Ser Trp Ile		
225	230	235
Arg Asp Arg Val Lys Arg Gly Glu Val Lys Ile His Gly Cys Tyr Tyr		
245	250	255
Asn Leu Ser Asp Cys Ser Leu Glu Lys Trp Arg Leu Ser Ser Asp Lys		
260	265	270
Thr Asn Tyr Gly Phe Tyr Ile Ser Asp Arg Glu Ile Trp Ser		
275	280	285

<210> 86
 <211> 801
 <212> DNA
 <213> Medicago truncatula

<400> 86
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 gaggaactta atggggtggc cacagcaaaa attgagcagc ttatagttga attacagggg 120
 tgtcatccaa atccaattga acctgctgat cagagaatca ttgatggttt tacgtacttc 180
 aagctcaaca atttcaacaa gaaccgga ctgtatgatc gacttgctaa aggccagtct 240
 cccaagttaa tggatattgc ttgttccgac tctcgagtga gtccctctgt tatcctgaac 300
 tttcaacctg gtgaagcttt catggttcga aacattgcta acatgggtccc tccatttaac 360
 cagttaagat acagtggagt tgggtgcaacc cttgagtatg ctattacagc tctaaagggtg 420
 gagaacatct tggttattgg acatagtcgc tgcggcggaa tctcaaggct tatgaatcat 480
 ccagaggatg gttctgctcc atatgacttc atagatgatt gggtgaaaat tggtttatct 540
 tccaaagtca aggttttgaa agaacatgaa cgctgtgatt tcaaagaaca atgcaaattc 600
 tgtgaaatgg aatcagtga taactcatta gtgaacctga agacatatcc atatgttgat 660
 agagaaataa ggaacaagaa cttagctctg ttgggagggt actatgattt tgtgagtggg 720
 gaattcaagc tttggaagta taagaatcat gtcactgaac ctgttaccat ccctctaaaa 780
 ggccttgaca tgaccatcta a 801

<210> 87
 <211> 266
 <212> PRT
 <213> Medicago truncatula

<400> 87
 Met Ala Asn Gln Ser Ser Glu Leu Ala Ile Glu Gln Leu Lys Lys Leu
 1 5 10 15
 Leu Arg Glu Lys Glu Glu Leu Asn Gly Val Ala Thr Ala Lys Ile Glu
 20 25 30
 Gln Leu Ile Val Glu Leu Gln Gly Cys His Pro Asn Pro Ile Glu Pro
 35 40 45
 Ala Asp Gln Arg Ile Ile Asp Gly Phe Thr Tyr Phe Lys Leu Asn Asn
 50 55 60
 Phe Asn Lys Asn Pro Glu Leu Tyr Asp Arg Leu Ala Lys Gly Gln Ser
 65 70 75 80

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```

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

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<210> 88
 <211> 774
 <212> DNA
 <213> Medicago truncatula

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<400> 88
atggcaaatc aatcatctga gctagccatt gaacaactga agaagcttct cagagagaaa      60
gaggaactta atgaggtggc cactgcaaaa attgaggaaa ttatagttga gttgcaggga      120
tgtcatccac aaccaattga tcctgctgag cagagaatca ttgatgggtt tacttacttc      180
aagctcaaca atttcgacaa ggaccggaaa ttgtatgata gacttgctaa aggacaatcc      240
cccaagttaa tggatatttc ttgttctgac tctagagtga gtccctctat taccctgaac      300
tttcaacctg gagaagcttt catgggtccga aacattgcta acatgggtccc tccatttaat      360
cagttaagat acagtggagt tgggtgaacc cttgagtatg ctattacagc tctaaagggtg      420
gagaacatct tggttatttg acatagtcgc tgcggcggta tatcaaggct tatgagtcac      480
ccagaggatg gttctgctcc atagacttc atagatgatt ggggtgaaaat tggtttacct      540
tctaaagtca aggtcctgaa agaacataaa ttctgtgatt tcgagcaaca atgtgaattt      600
tgtgaaatgg aatcagtga taactcatta gtgaaccttc agacatatcc atatgttgat      660
gcagaaataa ggaacaagaa cttagcacta ttggggggtt actatgactt tgtgagtgga      720
gaattcaagt tttggaagta taagactcat attactgaac ccattacaat ctga      774

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<210> 89
 <211> 257
 <212> PRT
 <213> Medicago truncatula

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<400> 89
Met Ala Asn Gln Ser Ser Glu Leu Ala Ile Glu Gln Leu Lys Lys Leu
1      5      10
Leu Arg Glu Lys Glu Glu Leu Asn Glu Val Ala Thr Ala Lys Ile Glu
      20      25      30
Glu Ile Ile Val Glu Leu Gln Gly Cys His Pro Gln Pro Ile Asp Pro
      35      40      45
Ala Glu Gln Arg Ile Ile Asp Gly Phe Thr Tyr Phe Lys Leu Asn Asn
      50      55      60

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PF58581.ST25.txt

```

Phe Asp Lys Asp Arg Lys Leu Tyr Asp Arg Leu Ala Lys Gly Gln Ser
65          70          75          80
Pro Lys Phe Met Val Phe Ala Cys Ser Asp Ser Arg Val Ser Pro Ser
          85          90          95
Ile Ile Leu Asn Phe Gln Pro Gly Glu Ala Phe Met Val Arg Asn Ile
          100         105         110
Ala Asn Met Val Pro Pro Phe Asn Gln Leu Arg Tyr Ser Gly Val Gly
          115         120         125
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Val Ile Gly His Ser Arg Cys Gly Gly Ile Ser Arg Leu Met Ser His
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          165         170         175
Ile Gly Leu Pro Ser Lys Val Lys Val Leu Lys Glu His Lys Phe Cys
          180         185         190
Asp Phe Glu Gln Gln Cys Glu Phe Cys Glu Met Glu Ser Val Asn Asn
          195         200         205
Ser Leu Val Asn Leu Gln Thr Tyr Pro Tyr Val Asp Ala Glu Ile Arg
          210         215         220
Asn Lys Asn Leu Ala Leu Leu Gly Gly Tyr Tyr Asp Phe Val Ser Gly
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 <211> 1100
 <212> DNA
 <213> Arabidopsis thaliana

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gttgacggcg gagctaaagg agcttgactc aagcaattca gacgcaattg aacgaatcaa      240
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 <212> PRT
 <213> Arabidopsis thaliana

<400> 91

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Glu	Glu	His	Lys	Asp	Leu	Ser	Tyr	Asp	Asp	Gln	Cys	Asn	Lys	Cys	Glu
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 <213> Oryza sativa

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cgctcagcgt ttccctgcgt gtgggaggat ctgacgggag ggactttccg tgtaccacaa	360
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 <212> PRT
 <213> Oryza sativa

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Tyr	Asn	Phe	Ile	Asp	Cys	Thr	Phe	Glu	Lys	Trp	Lys	Leu	Val	Tyr	Arg
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<212> DNA
<213> Oryza sativa

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<212> PRT
<213> Oryza sativa

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50 55 60
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Tyr	Phe	Arg	Tyr	Ala	Gly	Ser	Leu	Thr	Ala	Pro	Pro	Cys	Thr	Glu	Asp
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Val	Tyr	Arg	Tyr	Glu	Ala	Thr	Ala	Met	Asp	Asp	Ser	Gly	Asp	Gly	Thr	
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 <213> Dunaliella salina

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 <211> 555
 <212> PRT
 <213> Dunaliella salina

<400> 99
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 35 40 45
 His Gly Ile Asp Trp Arg Asp Glu Gly Leu Asp Asn Cys Ala Gly Ser
 50 55 60
 Met Gln Ser Pro Ile Asn Ile Asp Met Ala Thr Leu Asn Arg Gly Glu
 65 70 75 80
 Glu Arg Ser Asp Val Ser Gly Leu Tyr Leu Asn Gly Leu Ala Ser Pro
 85 90 95
 Ala Tyr Asp Val Ala Ala Asp Val Thr Val Asn Ala Glu Gln Asp Met
 100 105 110
 Lys Ile Thr Phe Lys Asp Val Ala Gln Asn Asn Met Pro Ala Ile Lys
 115 120 125
 Ile Asp Gly Ser Asp Met Leu Phe Lys Pro Val Gln Leu His Phe His

130					135					140					
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Ala	His	Leu	Val	Met 165	Gly	Asp	Ala	Ser	Gly 170	Asn	Thr	Asn	Gln	Leu	Ala 175
Val	Leu	Gly	Ile 180	Met	Tyr	Gln	Tyr	Gly 185	Glu	Gln	Pro	Asp	Asp	Phe	Val
Arg	Arg	Leu 195	Gln	Thr	Lys	Thr	Ile 200	Asp	Glu	Ile	Ala 205	Thr	Asn	Gly	Ala
Gly	Tyr 210	Gly	Glu	Thr	Val	Asn 215	Val	Thr	Asp	Leu	Ser 220	Val	Asn	Ile	Met
Lys 225	Asp	Val	Leu	Pro	Pro 230	Thr	His	His	Asn 235	Tyr	Val	Gly	Tyr	Asp	Gly 240
Ser	Leu	Thr	Thr	Pro 245	Pro	Cys	Asp	Glu	Arg 250	Val	Lys	Trp	His	Val	Phe 255
Thr	Glu	Pro	Arg 260	Thr	Ile	Thr	Thr	Gly 265	Gln	Leu	Glu	Lys	Phe	Leu	Met
Ile	Thr 275	Lys	Arg	Gly	His	Thr	Asp 280	Ala	Ile	Val	Thr	Asn 285	Asn	Arg	Ile
Val 290	Gln	Pro	Ile	Gly	Arg 295	Pro	Leu	Tyr	His	Tyr	Lys 300	Pro	Thr	Pro	Ala
Ser 305	Tyr	Asn	Tyr	Ala 310	Arg	Lys	Gly	Ile	Asp 315	Trp	Arg	Glu	Ala	Gly	Leu 320
Asp	Asn	Cys	Ala 325	Gly	Asp	Arg	Gln	Ser	Pro 330	Ile	Asn	Ile	Asp	Thr	Thr 335
Asp	Leu	Gln	Pro 340	Gly	Ala	Val	Ser	Gly 345	Ile	Ser	Leu	Asn 350	Gly	Leu	Glu
Ser	Gln 355	Ser	Phe	Thr	Phe	Thr	Asp 360	Ala	Tyr	Val	Asn 365	Leu	Glu	Gln	Asp
Met 370	Lys	Val	Ser	Phe 375	Thr	Ala	Pro	Thr	Asn 380	Asn	Leu	Pro	Thr	Val	Asn
Ile 385	Asp	Gly	Asn	Asp 390	Glu	Ser	Phe	Arg	Pro 395	Ile	Gln	Leu	His	Phe	His 400
His	Phe	Ser	Ser 405	Glu	His	Thr	Val	Asp	Gly 410	Met	Ile	Tyr	Pro	Leu	Glu 415
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Val	Ile 435	Ala	Ile	Phe	Tyr	Gln	Tyr 440	Gly	Ser	Glu	Ala 445	Asp	Asp	Phe	Leu
Thr 450	Arg	Leu	His	Thr 455	Glu	Ala	Ile	Ser	Ala 460	Gln	Gln	Gly	Asn	Ala	Asn
Trp 465	Gly	Asp	Asn	Asn 470	Val	Pro	Ile	Asn	Leu 475	Pro	Ile	Thr	Phe	Ala	Thr 480
Asp	Leu	Met	Pro 485	Ser	Ser	Thr	Glu	His	Trp 490	Ala	Tyr	Glu	Gly	Ser	Leu 495
Thr	Thr	Pro	Pro 500	Cys	Asp	Glu	Arg	Val 505	Arg	Trp	Ile	Val 510	Met	Lys	Glu
Pro	Arg	Thr 515	Thr	Thr	Ala	Glu	Gln 520	Met	Glu	Thr	Phe 525	Lys	Thr	Ala	Thr
Val	Asn 530	Ala	His	Tyr	Ala 535	Ala	Glu	Ile	Val 540	Asn	Asn	Arg	Ala	Ile	Gln
Glu 545	Arg	Asn	Ser	Arg 550	Pro	Ile	Ser	Ser	Ile 555	Pro					

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<400> 100

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gatcatagtc tcaatggcga gaactgggag ggcaaggacg gcgcggggcaa cccctgggtc    180
tgcaagactg gccgcaagca gtcgcccata aacgtgcccc agtaccatgt cctggacggg    240
aagggttcca agattgccac cggcctgcag acccagtggg cgtaccctga cctgatgtcc    300
aacggcagct cggttcaagt catcaacaac ggccacacca tccaggtgca gtggacctac    360
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gtcaccggca tcctgttcca gctcgacaac ggccccgata acgagctgct tgagcccacg    660
cgcgagggca ccttcacca cctgcccggc ggaccacca tcaagctggg tgagctgctg    720
cccagcgacc gcgactacgt cacctacgag ggagcctca ccaccccgcc ctgcagcgag    780
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gacgccggcc atcatcacca ccaccaccgc cgctgctgc acaaccacgc gcacctggag    960
gaggtgctcg ccgccacctc cgagcccaag cactacttcc gccgcgtgat ggaggagacc   1020
gagaaccccc atgcttacac ctgcacgacc gttgcctttg gccagaactt ccgcaacgcc   1080
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<210> 101

<211> 380

<212> PRT

<213> Chlamydomonas reinhardtii

<400> 101

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

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Gly Ser Leu Thr Thr Pro Pro Cys Ser Glu Gly Leu Leu Trp His Val
260 265 270
Met Thr Gln Pro Gln Arg Ile Ser Phe Gly Gln Trp Asn Arg Tyr Arg
275 280 285
Leu Ala Val Gly Glu Lys Glu Cys Asn Ser Thr Glu Thr Asp Ala Ala
290 295 300
His Ala Asp Ala Gly His His His His His Arg Arg Leu Leu His
305 310 315 320
Asn His Ala His Leu Glu Glu Val Pro Ala Ala Thr Ser Glu Pro Lys
325 330 335
His Tyr Phe Arg Arg Val Met Glu Glu Thr Glu Asn Pro Asp Ala Tyr
340 345 350
Thr Cys Thr Thr Val Ala Phe Gly Gln Asn Phe Arg Asn Ala Gln Tyr
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Ala Asn Gly Arg Thr Ile Lys Leu Ala Arg Tyr Glu
370 375 380

<210> 102
<211> 1134
<212> DNA
<213> Chlamydomonas reinhardtii

<400> 102
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gaccatggcc tcaacggcga gaactgggag ggcaaggacg gcgcaggcaa cgcctggggtt 180
tgcaagactg gccgcaagca gtgcgccatc aacgtgcccc agtaccaggt cctggacggg 240
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aacggcacct cgggtccaagt catcaacaac ggccacacca tccaggtgca gtggacttac 360
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gccgagtcgg cgaacccgga tgcctacacc tgcaaggccg ttgcctttgg ccagaacttc 1080
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<210> 103
<211> 377
<212> PRT
<213> Chlamydomonas reinhardtii

<400> 103
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20 25 30
Ala Thr Val Ser Gly Asp His Trp Asp His Gly Leu Asn Gly Glu Asn
35 40 45
Trp Glu Gly Lys Asp Gly Ala Gly Asn Ala Trp Val Cys Lys Thr Gly
50 55 60
Arg Lys Gln Ser Pro Ile Asn Val Pro Gln Tyr Gln Val Leu Asp Gly
65 70 75 80

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Lys Gly Ser Lys Ile Ala Asn Gly Leu Gln Thr Gln Trp Ser Tyr Pro
85 90 95
Asp Leu Met Ser Asn Gly Thr Ser Val Gln Val Ile Asn Asn Gly His
100 105 110
Thr Ile Gln Val Gln Trp Thr Tyr Asn Tyr Ala Gly His Ala Thr Ile
115 120 125
Ala Ile Pro Ala Met His Asn Gln Thr Asn Arg Ile Val Asp Val Leu
130 135 140
Glu Met Arg Pro Asn Asp Ala Ala Asp Arg Val Thr Ala Val Pro Thr
145 150 155 160
Gln Phe His Phe His Ser Thr Ser Glu His Leu Leu Ala Gly Lys Ile
165 170 175
Tyr Pro Leu Glu Leu His Ile Val His Gln Val Thr Glu Lys Leu Glu
180 185 190
Ala Cys Lys Gly Gly Cys Phe Ser Val Thr Gly Ile Leu Phe Gln Leu
195 200 205
Asp Asn Gly Pro Asp Asn Glu Leu Leu Glu Pro Ile Phe Ala Asn Met
210 215 220
Pro Ser Arg Glu Gly Thr Phe Ser Asn Leu Pro Ala Gly Thr Thr Ile
225 230 235 240
Lys Leu Gly Glu Leu Leu Pro Ser Asp Arg Asp Tyr Val Thr Tyr Glu
245 250 255
Gly Ser Leu Thr Thr Pro Pro Cys Ser Glu Gly Leu Leu Trp His Val
260 265 270
Met Thr Gln Pro Gln Arg Ile Ser Phe Gly Gln Trp Asn Arg Tyr Arg
275 280 285
Leu Ala Val Gly Leu Lys Glu Cys Asn Ser Thr Glu Thr Ala Ala Asp
290 295 300
Ala Gly His His His His Arg Arg Leu Leu His Asn His Ala His
305 310 315 320
Leu Glu Glu Val Pro Ala Ala Thr Ser Glu Pro Lys His Tyr Phe Arg
325 330 335
Arg Val Met Leu Ala Glu Ser Ala Asn Pro Asp Ala Tyr Thr Cys Lys
340 345 350
Ala Val Ala Phe Gly Gln Asn Phe Arg Asn Pro Gln Tyr Ala Asn Gly
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Arg Thr Ile Lys Leu Ala Arg Tyr His
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<210> 104

<211> 810

<212> DNA

<213> Physcomitrella patens

<400> 104

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gactacagcg	gtgggtcgca	tgggccaggt	ggctggggtg	acctgaaggc	cgagtggggg	180
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gaccgcagtc	tggggaagct	ggatgccaag	taccggaaga	gagttcatgc	cactctttac	300
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PF58581.ST25.txt

<210> 105
 <211> 269
 <212> PRT
 <213> Physcomitrella patens

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 35 40 45
 Pro Gly Gly Trp Gly Asp Leu Lys Ala Glu Trp Gly Val Cys Lys Ser
 50 55 60
 Gly Ser Arg Gln Ser Pro Ile Ala Ile Thr Ala Leu Asp Leu Val Thr
 65 70 75 80
 Asp Arg Ser Leu Gly Lys Leu Asp Ala Lys Tyr Arg Lys Arg Val His
 85 90 95
 Ala Thr Leu Tyr Asn Ser Gly His Gly Ala Glu Val Ser Met Pro Ala
 100 105 110
 Gly Ser Gly Arg Leu Arg Ile Gly Gly Glu Thr Tyr Arg Pro Val Gln
 115 120 125
 Phe His Ile His Met Pro Ser Glu His Thr Ile Met Asn Gln Ser Phe
 130 135 140
 Pro Leu Glu Leu His Leu Val His Lys Ser Asp Asp Gly Lys Leu Ala
 145 150 155 160
 Val Ile Gly Phe Leu Phe Glu Glu Gly Gly Glu Ser Glu Phe Leu Ala
 165 170 175
 Gln Phe Ala His Glu Val Pro Ser Ser Asn Ser Pro Gly Val Lys Val
 180 185 190
 Asp Leu Gly His Ile Lys Met Met Lys Pro Glu Arg Asn Tyr Gly Thr
 195 200 205
 Tyr Met Gly Ser Leu Thr Thr Pro Pro Cys Ala Glu Gly Val Thr Trp
 210 215 220
 Ile Leu Ser Leu Phe Asn Phe Gln Thr Ala Ser Ala Glu Gln Leu Ala
 225 230 235 240
 Lys Leu Arg Ala Ser Val Pro Lys Gly His Asn Asn Arg Pro Thr Phe
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 <211> 1519
 <212> DNA
 <213> Arabidopsis thaliana

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PF58581.ST25.txt

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<210> 107

<211> 259

<212> PRT

<213> Arabidopsis thaliana

<400> 107

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

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<210> 108

<211> 1770

PF58581.ST25.txt

<212> DNA

<213> *Dunaliella salina*

<400> 108

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tacaactatg agaaagtggg ctttgattgg acgggggggg tctgcgtcaa taccgggacc  240
agcaagcaga gcccaatcaa cattgagact gacagcctgg ctgaggaatc agagaggctg  300
gggaccgcgg atgacacttc acgcctggcc ttgaagggcc tactgtcttc atcctaccag  360
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gatgaagact tgcctcaact tactattggg ggggtgtgcc acaccttcaa gcctgtgcaa  480
atccactttc accactttgc cagcgagcac gctattgacg gccagcttta tcctcttgag  540
gccacatagg tgatggcatc ccagaatgac ggctctgacc agcttgctgt cattggcatc  600
atgtacaagt acggggaaga agatcctttc ctcaaaaggc tgcaagaaac tgcacagagc  660
aatggcgaa gctgccgaaa aaatgtggag ctgaactcgt tttccatcaa tgtggccagg  720
gatttgctgc ctgagtcaga cctgacctac tatggatatg atggtagctt gactaccccc  780
ggttgtgatg agcagtgtaa gtggcatgtg ttcaaggagg caaggactgt ctcagtggcg  840
cagctcaagg tgttttcaga ggtcacgctg gctgcccacc ctgaagctac ggttaccaac  900
aaccgtgtca ttcagccgct caatggcagg aaggtctacg agtacaaggg tgaacccaac  960
gacaagtaca actatgtcca gcatggcttt gactggcgcg ataatggctt ggatagctgt 1020
gctggcgacg tccagagccc tattgacatc gtgaccagca ctttgcaagc tggatcttct 1080
cggagtgatg tttctagtgt caacctgaat gacttgaaca ccgacgcgtt cacgctgacc 1140
ggcaacactg tgaatattgg gcaaggcatg caaatcaatt ttggtgacct ccctgcgggt 1200
gacctgcccg tcatcagaat tgggtactag gacgtcactt tcaggcccct ccaggtgcac 1260
tggcacttct ttttgagtga gcacactgtg gatggagtgc actaccccct ggaagctcat 1320
attgttatga aggacaatga caaccttggg gattctgccg gccagcttgc tgtcatcggt 1380
attatgtaca agtacggcga tgcagacccc ttctattactg atatgcagaa gaggtgtgca 1440
gataaaattg catcaggtgc catcacctat ggacaatcag gagtgtctct gaacaatcct 1500
gatgatccct tcaatgtcaa catcaagaat aatttcctgc cctctgagct tggatatgct 1560
ggctacgatg gcagcctgac caccctcctt tgctctgaga ttgtgaagtg gcatgtgttc 1620
ctggagccta ggactgtttc agtggagcag atggaggtct ttgcagatgt gactctgaac 1680
tctaataccag gtgcgaccgt gacaaccaac cgaatgatcc agccactgga gggtaggact 1740
gtgtacggat ataacggtgc tgctgcttaa                1770

```

<210> 109

<211> 589

<212> PRT

<213> *Dunaliella salina*

<400> 109

```

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

```

PF58581.ST25.txt

```

Pro Gln Leu Thr Ile Gly Gly Val Val His Thr Phe Lys Pro Val Gln
145          150          155          160
Ile His Phe His His Phe Ala Ser Glu His Ala Ile Asp Gly Gln Leu
          165          170          175
Tyr Pro Leu Glu Ala His Met Val Met Ala Ser Gln Asn Asp Gly Ser
          180          185          190
Asp Gln Leu Ala Val Ile Gly Ile Met Tyr Lys Tyr Gly Glu Glu Asp
          195          200          205
Pro Phe Leu Lys Arg Leu Gln Glu Thr Ala Gln Ser Asn Gly Glu Ala
          210          215          220
Gly Asp Lys Asn Val Glu Leu Asn Ser Phe Ser Ile Asn Val Ala Arg
225          230          235          240
Asp Leu Leu Pro Glu Ser Asp Leu Thr Tyr Tyr Gly Tyr Asp Gly Ser
          245          250          255
Leu Thr Thr Pro Gly Cys Asp Glu Arg Val Lys Trp His Val Phe Lys
          260          265          270
Glu Ala Arg Thr Val Ser Val Ala Gln Leu Lys Val Phe Ser Glu Val
          275          280          285
Thr Leu Ala Ala His Pro Glu Ala Thr Val Thr Asn Asn Arg Val Ile
          290          295          300
Gln Pro Leu Asn Gly Arg Lys Val Tyr Glu Tyr Lys Gly Glu Pro Asn
305          310          315          320
Asp Lys Tyr Asn Tyr Val Gln His Gly Phe Asp Trp Arg Asp Asn Gly
          325          330          335
Leu Asp Ser Cys Ala Gly Asp Val Gln Ser Pro Ile Asp Ile Val Thr
          340          345          350
Ser Thr Leu Gln Ala Gly Ser Ser Arg Ser Asp Val Ser Ser Val Asn
          355          360          365
Leu Met Thr Leu Asn Thr Asp Ala Phe Thr Leu Thr Gly Asn Thr Val
          370          375          380
Asn Ile Gly Gln Gly Met Gln Ile Asn Phe Gly Asp Pro Pro Ala Gly
385          390          395          400
Asp Leu Pro Val Ile Arg Ile Gly Thr Arg Asp Val Thr Phe Arg Pro
          405          410          415
Leu Gln Val His Trp His Phe Phe Leu Ser Glu His Thr Val Asp Gly
          420          425          430
Val His Tyr Pro Leu Glu Ala His Ile Val Met Lys Asp Asn Asp Asn
          435          440          445
Leu Gly Asp Ser Ala Gly Gln Leu Ala Val Ile Gly Ile Met Tyr Lys
          450          455          460
Tyr Gly Asp Ala Asp Pro Phe Ile Thr Asp Met Gln Lys Arg Val Ser
465          470          475          480
Asp Lys Ile Ala Ser Gly Ala Ile Thr Tyr Gly Gln Ser Gly Val Ser
          485          490          495
Leu Asn Asn Pro Asp Asp Pro Phe Asn Val Asn Ile Lys Asn Asn Phe
          500          505          510
Leu Pro Ser Glu Leu Gly Tyr Ala Gly Tyr Asp Gly Ser Leu Thr Thr
          515          520          525
Pro Pro Cys Ser Glu Ile Val Lys Trp His Val Phe Leu Glu Pro Arg
          530          535          540
Thr Val Ser Val Glu Gln Met Glu Val Phe Ala Asp Val Thr Leu Asn
545          550          555          560
Ser Asn Pro Gly Ala Thr Val Thr Thr Asn Arg Met Ile Gln Pro Leu
          565          570          575
Glu Gly Arg Thr Val Tyr Gly Tyr Asn Gly Ala Ala Ala
          580          585

```

<210> 110

<211> 693

PF58581.ST25.txt

<212> DNA

<213> Arabidopsis thaliana

<400> 110

```

atgaagatta tgatgatgat taagctctgc ttcttctcca tgtccctcat ctgcattgca    60
cctgcagatg ctcagacaga aggagtagtg tttggatata aaggcaaaaa tggaccaaac    120
caatggggac acttaaaccg tcacttcacc acatgcgcgg tcggtaaatt gcaatctcca    180
attgatattc aaaggaggca aatattttac aaccacaaat tgaattcaat acaccgtgaa    240
tactacttca caaacgcaac actagtgaac cacgtctgta atgttgccat gttcttcggg    300
gagggagcag gagatgtgat aatagaaaac aagaactata ccttactgca aatgcattgg    360
cacactcctt ctgaacatca cctccatgga gtccaatatg cagctgagct gcacatggta    420
caccaagcaa aagatggaag ctttgctgtg gtggcaagtc tcttcaaaat cggcactgaa    480
gagcctttcc tctctcagat gaaggagaaa ttggtgaagc taaaggaaga gagactcaaa    540
gggaaccaca cagcacaagt ggaagtagga agaatcgaca caagacacat tgaacgtaag    600
actcgaaagt actacagata cattgggttc ctactactc ctccttgctc cgagaacgtt    660
tcttggaaca tccttggaac ggtaatcttt taa                                693

```

<210> 111

<211> 284

<212> PRT

<213> Arabidopsis thaliana

<400> 111

```

Met Lys Ile Met Met Met Ile Lys Leu Cys Phe Phe Ser Met Ser Leu
1      5      10      15
Ile Cys Ile Ala Pro Ala Asp Ala Gln Thr Glu Gly Val Val Phe Gly
20      25      30
Tyr Lys Gly Lys Asn Gly Pro Asn Gln Trp Gly His Leu Asn Pro His
35      40      45
Phe Thr Thr Cys Ala Val Gly Lys Leu Gln Ser Pro Ile Asp Ile Gln
50      55      60
Arg Arg Gln Ile Phe Tyr Asn His Lys Leu Asn Ser Ile His Arg Glu
65      70      75      80
Tyr Tyr Phe Thr Asn Ala Thr Leu Val Asn His Val Cys Asn Val Ala
85      90      95
Met Phe Phe Gly Glu Gly Ala Gly Asp Val Ile Ile Glu Asn Lys Asn
100     105     110
Tyr Thr Leu Leu Gln Met His Trp His Thr Pro Ser Glu His His Leu
115     120     125
His Gly Val Gln Tyr Ala Ala Glu Leu His Met Val His Gln Ala Lys
130     135     140
Asp Gly Ser Phe Ala Val Val Ala Ser Leu Phe Lys Ile Gly Thr Glu
145     150     155     160
Glu Pro Phe Leu Ser Gln Met Lys Glu Lys Leu Val Lys Leu Lys Glu
165     170     175
Glu Arg Leu Lys Gly Asn His Thr Ala Gln Val Glu Val Gly Arg Ile
180     185     190
Asp Thr Arg His Ile Glu Arg Lys Thr Arg Lys Tyr Tyr Arg Tyr Ile
195     200     205
Gly Ser Leu Thr Thr Pro Pro Cys Ser Glu Asn Val Ser Trp Thr Ile
210     215     220
Leu Gly Lys Val Arg Ser Met Ser Lys Glu Gln Val Glu Leu Leu Arg
225     230     235     240
Ser Pro Leu Asp Thr Ser Phe Lys Asn Asn Ser Arg Pro Cys Gln Pro
245     250     255
Leu Asn Gly Arg Arg Val Glu Met Phe His Asp His Glu Arg Val Asp
260     265     270
Lys Lys Glu Thr Gly Asn Lys Lys Lys Lys Pro Asn
275     280

```

PF58581.ST25.txt

<210> 112
<211> 1053
<212> DNA
<213> Arabidopsis thaliana

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<400> 112
atgaagatat catcactagg atgggtctta gtccttatct tcatctctat taccattggt      60
tcgagtgcac cagcacctaa acctcctaaa cctaagcctg caccagcacc tacacctcct      120
aaacctaaag ccacaccagc acctacacct cctaaaccta agcccaaacc agcacctaca      180
cctcctaaac ctaagcctgc accagcacct acacctccta aacctaaagg cgcaccagca      240
cctacacctc ctaaacctaa gcccaaacca gcacctacac ctctaatcc taagcccaca      300
ccagcaccta cacctcctaa acctaaagcct gcaccagcac cagcaccaac accagcacccg      360
aaacctaaac ctgcacctaa accagcacca ggtggagaag ttgaggacga aaccgagttt      420
agctacgaga cgaaaggaaa caaggggcca gcgaaatggg gaacactaga tgcagagtgg      480
aaaatgtgtg gaataggcaa aatgcaatct cctattgatc ttctgggaaa aaatgtggta      540
gttagtaata aatttgatt gtttcgtagc cagtatctgc cttctaatac caccattaag      600
aacagaggtc atgatatcat gttgaaattc aaaggaggaa ataaaggtat tgggtgtcact      660
atccgtggta ctagatatca acttcaacaa cttcattggc actctccttc cgaacataca      720
atcaatggca aaaggtttgc gctagaggaa cacttggttc atgagagcaa agataaacgc      780
tacgtgtgtg tcgcattctt atacaatctc ggagcatctg acccttttct cttttcgttg      840
gaaaaacaat tgaagaagat aactgataca catgcgtccg aggaacatat tcgcactgtg      900
tcaagtaaac aagtgaagct tctccgtgtg gctgtacacg atgcttcaga ttcaaagtgc      960
aggccgcttc aagcagtaa taagcgcaag gtatatatat acaaaccaa gggttaagtta     1020
atgaagaaat actgtaatat aagttcttac tag                                     1053
```

<210> 113
<211> 350
<212> PRT
<213> Arabidopsis thaliana

```
<400> 113
Met Lys Ile Ser Ser Leu Gly Trp Val Leu Val Leu Ile Phe Ile Ser
1      5      10      15
Ile Thr Ile Val Ser Ser Ala Pro Ala Pro Lys Pro Pro Lys Pro Lys
20     25     30
Pro Ala Pro Ala Pro Thr Pro Pro Lys Pro Lys Pro Thr Pro Ala Pro
35     40     45
Thr Pro Pro Lys Pro Lys Pro Lys Pro Ala Pro Thr Pro Pro Lys Pro
50     55     60
Lys Pro Ala Pro Ala Pro Thr Pro Pro Lys Pro Lys Pro Ala Pro Ala
65     70     75     80
Pro Thr Pro Pro Lys Pro Lys Pro Lys Pro Ala Pro Thr Pro Pro Asn
85     90     95
Pro Lys Pro Thr Pro Ala Pro Thr Pro Pro Lys Pro Lys Pro Ala Pro
100    105    110
Ala Pro Ala Pro Thr Pro Ala Pro Lys Pro Lys Pro Ala Pro Lys Pro
115    120    125
Ala Pro Gly Gly Glu Val Glu Asp Glu Thr Glu Phe Ser Tyr Glu Thr
130    135    140
Lys Gly Asn Lys Gly Pro Ala Lys Trp Gly Thr Leu Asp Ala Glu Trp
145    150    155    160
Lys Met Cys Gly Ile Gly Lys Met Gln Ser Pro Ile Asp Leu Arg Asp
165    170    175
Lys Asn Val Val Val Ser Asn Lys Phe Gly Leu Leu Arg Ser Gln Tyr
180    185    190
Leu Pro Ser Asn Thr Thr Ile Lys Asn Arg Gly His Asp Ile Met Leu
195    200    205
Lys Phe Lys Gly Gly Asn Lys Gly Ile Gly Val Thr Ile Arg Gly Thr
```

PF58581.ST25.txt

210	215	220
Arg Tyr Gln Leu Gln Gln Leu His Trp His Ser Pro Ser Glu His Thr		
225	230	235
Ile Asn Gly Lys Arg Phe Ala Leu Glu Glu His Leu Val His Glu Ser		240
	245	250
Lys Asp Lys Arg Tyr Ala Val Val Ala Phe Leu Tyr Asn Leu Gly Ala		255
	260	265
Ser Asp Pro Phe Leu Phe Ser Leu Glu Lys Gln Leu Lys Lys Ile Thr		270
	275	280
Asp Thr His Ala Ser Glu Glu His Ile Arg Thr Val Ser Ser Lys Gln		285
	290	295
Val Lys Leu Leu Arg Val Ala Val His Asp Ala Ser Asp Ser Asn Ala		300
305	310	315
Arg Pro Leu Gln Ala Val Asn Lys Arg Lys Val Tyr Leu Tyr Lys Pro		320
	325	330
Lys Val Lys Leu Met Lys Lys Tyr Cys Asn Ile Ser Ser Tyr		335
	340	345
		350

<210> 114
 <211> 834
 <212> DNA
 <213> Arabidopsis thaliana

<400> 114
 atgaaaacca ttatcctttt tgtaacattt cttgctcttt cttcttcatt tctagccgat 60
 gagacagaga ctgaatttca ttacaaaccc ggtgagatag ccgatccctc gaaatggagc 120
 agtatcaagg ctgaatggaa aatttgcggg acagggaaga ggcaatcgcc aatcaatctt 180
 actccaaaaa tagctcgcat tggttcacaat tctacagaga ttcttcagac atattacaaa 240
 cctgtagagg ctattcttaa gaaccgtgga ttcgacatga aggttaagtg ggaagacgat 300
 gcagggaaga tcgtgatcaa tgataccgac tataaattgg ttcaaagcca ctggcacgca 360
 ccttcagagc attttctcga tggacagagg ttggcaatgg aacttcacat ggtacacaaa 420
 agtgtagaag ggcacttggc agtgattgga gttctcttca gagaaggaga accaaatgct 480
 ttcatcttgc ggatcatgga caagatccat aagatcgagc acgtacaaga tggagagggtc 540
 agcatcgga agatagatcc aagagaattt ggatgggagc ttacaaagtt ttatgaatac 600
 agaggttctc tcacgactcc tccttgacag gaagatgtca tgtggaccat catcaacaag 660
 gtggggactg tttcacgtga gcaaattgat gtattgacag atgctcgtcg cgggtggttat 720
 gagaagaacg cgagaccagc tcaacctctg aacggacgctc tgggtttattt aaacgagcag 780
 tccagtccaa gtccaactcc acgggctaaga ataccacgag ttggtccggt ctaa 834

<210> 115
 <211> 277
 <212> PRT
 <213> Arabidopsis thaliana

<400> 115
 Met Lys Thr Ile Ile Leu Phe Val Thr Phe Leu Ala Leu Ser Ser Ser
 1 5 10 15
 Ser Leu Ala Asp Glu Thr Glu Thr Glu Phe His Tyr Lys Pro Gly Glu
 20 25 30
 Ile Ala Asp Pro Ser Lys Trp Ser Ser Ile Lys Ala Glu Trp Lys Ile
 35 40 45
 Cys Gly Thr Gly Lys Arg Gln Ser Pro Ile Asn Leu Thr Pro Lys Ile
 50 55 60
 Ala Arg Ile Val His Asn Ser Thr Glu Ile Leu Gln Thr Tyr Tyr Lys
 65 70 75 80
 Pro Val Glu Ala Ile Leu Lys Asn Arg Gly Phe Asp Met Lys Val Lys
 85 90 95
 Trp Glu Asp Asp Ala Gly Lys Ile Val Ile Asn Asp Thr Asp Tyr Lys
 100 105 110

PF58581.ST25.txt

```

Leu Val Gln Ser His Trp His Ala Pro Ser Glu His Phe Leu Asp Gly
      115                      120                      125
Gln Arg Leu Ala Met Glu Leu His Met Val His Lys Ser Val Glu Gly
      130                      135                      140
His Leu Ala Val Ile Gly Val Leu Phe Arg Glu Gly Glu Pro Asn Ala
145                      150                      155                      160
Phe Ile Ser Arg Ile Met Asp Lys Ile His Lys Ile Ala Asp Val Gln
      165                      170                      175
Asp Gly Glu Val Ser Ile Gly Lys Ile Asp Pro Arg Glu Phe Gly Trp
      180                      185                      190
Asp Leu Thr Lys Phe Tyr Glu Tyr Arg Gly Ser Leu Thr Thr Pro Pro
      195                      200                      205
Cys Thr Glu Asp Val Met Trp Thr Ile Ile Asn Lys Val Gly Thr Val
      210                      215                      220
Ser Arg Glu Gln Ile Asp Val Leu Thr Asp Ala Arg Arg Gly Gly Tyr
225                      230                      235                      240
Glu Lys Asn Ala Arg Pro Ala Gln Pro Leu Asn Gly Arg Leu Val Tyr
      245                      250                      255
Leu Asn Glu Gln Ser Ser Pro Ser Pro Thr Pro Arg Leu Arg Ile Pro
      260                      265                      270
Arg Val Gly Pro Val
      275

```

<210> 116

<211> 825

<212> DNA

<213> Nicotiana langsdorffii x Nicotiana sanderae

<400> 116

```

atgaggatgg cagcaataac caaaatgttg ttcatttcgt ttcttttcct ttcaagtgta      60
tttcttgcaa ggtccggaga agttgatgat gagagtgaat ttagttacga tgaaaaaagt      120
gagaatggac cagctaattg gggcaatatt cgtccagatt ggaaagaatg tagtggcaaa      180
ttgcagtcct ctattgatat ttttgacttg agggctgaag tagtttcaaa cttgagaata      240
cttcaaaagg actacaaacc atcgaatgcc actctcttga acagagggtca tgatataatg      300
ttgagattgg atgatggagg atacttgaag ataaatgaaa ctcaatatca actcaagcaa      360
ttgcattggc acacaccttc tgaacacact atcaatggag aaagggttaa tttggaggct      420
catttggtac atgaaagtaa taatggaaag tttgttgtca ttggaatagt ctacgagatc      480
ggattatggc ctgatccctt cttatctatg atagagaacg atttgaaagt tcctgctaata      540
aaaaaaggta tagagagagg cattggaatt attgatccaa atcaaataaa attggatggc      600
aaaaaatatt ttaggtatat tggtcactt acaacacctc cttgcaccga aggtgttgct      660
tgataattg atagaaagg taaaactgta accagaagac aaataaaaact actccaagaa      720
gctgttcacg atggatttga aaccaacgct agaccaactc aaccagaaaa cgaacgttat      780
atcaactcaa cataccattc ctttggtatt gaaaagcagc agtga      825

```

<210> 117

<211> 274

<212> PRT

<213> Nicotiana langsdorffii x Nicotiana sanderae

<400> 117

```

Met Arg Met Ala Ala Ile Thr Lys Met Leu Phe Ile Ser Phe Leu Phe
1      5      10      15
Leu Ser Ser Val Phe Leu Ala Arg Ser Gly Glu Val Asp Asp Glu Ser
      20      25      30
Glu Phe Ser Tyr Asp Glu Lys Ser Glu Asn Gly Pro Ala Asn Trp Gly
      35      40      45
Asn Ile Arg Pro Asp Trp Lys Glu Cys Ser Gly Lys Leu Gln Ser Pro
      50      55      60
Ile Asp Ile Phe Asp Leu Arg Ala Glu Val Val Ser Asn Leu Arg Ile

```

PF58581.ST25.txt

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

<210> 118
 <211> 993
 <212> DNA
 <213> Flaveria bidentis

<400> 118
 atgtcggcgc cctctgcttt cgccatgaat ggcgccttcgt tcgtcaacgc ttcgtcgcgtg 60
 aagaaagcgt ctacttcagc tagatctggg gtgtgtgccc ccagatttac gtgcaattcg 120
 tcgtcgcgtc cgtcttcgtc tgcaactcct ccgagtctca ttcgtaacga gcctgttttc 180
 gctgctcccg cgcccatcat cacaccgaat tggaccgaag acggaaatga atcatacgaa 240
 gaagccattg acgcgctcaa gaaaacgctc attgaaaagg gtgagttaga accagttgcc 300
 gctacaagaa tcgaccaa atcacagctcaa gccgcagcac ccgacaccaa agctccattt 360
 gaccctgttg agaggatcaa atccgggttc gtgaagttca agacagagaa attcgtcaca 420
 aacccagcct tgtacgatga gcttgctaaa ggccaaagcc caaagttcat ggtgtttgca 480
 tgctcagact cgcgtgtttg ccggtcacac gttcttgatt tccagcccgg tgaggcgttt 540
 gttgttcgta acgttgccaa catgggtccct ccctttgaca agaccaaata ttctggagta 600
 ggagctgctg ttgagtatgc agttttgcat ctaaaggtag aagaaatctt tgtaattggg 660
 catagccgtt gtggaggaat caaggggtctc atgactttcc cagacgaagg acctcactca 720
 accgatttca tcgaagattg ggtgaaagtg tgtctccccg cgaagtcaaa agtggttagca 780
 gaacacaacg gcacacatct tgatgatcaa tgtgtactat gtgaaaagga agctgtgaac 840
 gtgtcgcctt gaaacctgtt gacataccca tttgtaaagg atggattgag gaacaagaca 900
 ctcgcgctca aggggtgtca ctatgacttt gttaacggga cctttgagct gtgggcactt 960
 gactttgggc tttcgtctcc tacctctgta tga 993

<210> 119
 <211> 330
 <212> PRT
 <213> Flaveria bidentis

<400> 119
 Met Ser Ala Ala Ser Ala Phe Ala Met Asn Ala Pro Ser Phe Val Asn

PF58581.ST25.txt

1	5	10	15
Ala Ser Ser Leu Lys Lys Ala Ser Thr Ser Ala Arg Ser Gly Val Leu			
	20	25	30
Ser Ala Arg Phe Thr Cys Asn Ser Ser Ser Ser Ser Ser Ser Ala			
	35	40	45
Thr Pro Pro Ser Leu Ile Arg Asn Glu Pro Val Phe Ala Ala Pro Ala			
	50	55	60
Pro Ile Ile Thr Pro Asn Trp Thr Glu Asp Gly Asn Glu Ser Tyr Glu			
65	70	75	80
Glu Ala Ile Asp Ala Leu Lys Lys Thr Leu Ile Glu Lys Gly Glu Leu			
	85	90	95
Glu Pro Val Ala Ala Thr Arg Ile Asp Gln Ile Thr Ala Gln Ala Ala			
	100	105	110
Ala Pro Asp Thr Lys Ala Pro Phe Asp Pro Val Glu Arg Ile Lys Ser			
	115	120	125
Gly Phe Val Lys Phe Lys Thr Glu Lys Phe Val Thr Asn Pro Ala Leu			
	130	135	140
Tyr Asp Glu Leu Ala Lys Gly Gln Ser Pro Lys Phe Met Val Phe Ala			
145	150	155	160
Cys Ser Asp Ser Arg Val Cys Pro Ser His Val Leu Asp Phe Gln Pro			
	165	170	175
Gly Glu Ala Phe Val Val Arg Asn Val Ala Asn Met Val Pro Pro Phe			
	180	185	190
Asp Lys Thr Lys Tyr Ser Gly Val Gly Ala Ala Val Glu Tyr Ala Val			
	195	200	205
Leu His Leu Lys Val Gln Glu Ile Phe Val Ile Gly His Ser Arg Cys			
	210	215	220
Gly Gly Ile Lys Gly Leu Met Thr Phe Pro Asp Glu Gly Pro His Ser			
225	230	235	240
Thr Asp Phe Ile Glu Asp Trp Val Lys Val Cys Leu Pro Ala Lys Ser			
	245	250	255
Lys Val Val Ala Glu His Asn Gly Thr His Leu Asp Asp Gln Cys Val			
	260	265	270
Leu Cys Glu Lys Glu Ala Val Asn Val Ser Leu Gly Asn Leu Leu Thr			
	275	280	285
Tyr Pro Phe Val Arg Asp Gly Leu Arg Asn Lys Thr Leu Ala Leu Lys			
	290	295	300
Gly Gly His Tyr Asp Phe Val Asn Gly Thr Phe Glu Leu Trp Ala Leu			
305	310	315	320
Asp Phe Gly Leu Ser Ser Pro Thr Ser Val			
	325	330	

<210> 120

<211> 975

<212> DNA

<213> Hordeum vulgare

<400> 120

atgtcgttgc	agattggg	gacagagagg	gcccggtccc	cggtctttgt	ctttgcacac	60
aagcggcaac	tgctccatgg	acggtgtagt	accatcgaca	atgcaaattg	cagcacctgc	120
agcatgaaaa	tcaatagcac	ttgtacattg	acggccctgc	cgattgccgc	actgcctggg	180
ccacgtacta	cctcacacta	ctcgaccgcc	gcggtactac	ggtgctacgc	aaccgtcgcg	240
ccccgtgccc	gctcctccac	catcgccgcc	agcctcgcca	ccccgcgcgc	ctcctcctcc	300
gcctccttcc	gccccaaagt	catcaggacc	acccccgtcc	aggccgcgcc	cgtcgcacct	360
gcattgatgg	acggcgccgt	ggagcgcttc	aagaccgggt	tcgagaagtt	caagaccgag	420
gtctacgaca	agaagcccga	tttcttcgag	ccgtccaagg	ccggccaggc	gcccgaagtac	480
atgggtgttcg	cgtgcgccga	ctcgcggtgtg	tgcccgtcgg	tcaccctggg	cottgagccc	540
ggtgaggcct	tcaccatccg	caacatcgcc	aacatgggtcc	cggcctactg	caagaacaag	600
tacgcccgtg	ttggatcggc	catcgaatac	gccgtctgcg	cgctcaaggt	tgagggtcatc	660

PF58581.ST25.txt

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gtgggtgattg gccacagccg ctgcggtgga atcaaggctc tgctctcgct caaggatggc 720
gcagacgact ccttccactt cggttgaggac tgggtcagga tcgggttccc ggccaagaag 780
aaggtgcaga ctgagtgcgc ctccatgcct ttcgatgacc agtgcaccgt cctggagaag 840
gaggccgtca acgtgtccct ccagaacctc ttgacctacc cgttcgtcaa ggagggtgtg 900
accaacggaa ccctcaagct cgtcggcggc cactacgact tcgtctccgg caagttcgaa 960
acatgggagc agtaa 975
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<210> 121
 <211> 324
 <212> PRT
 <213> Hordeum vulgare

<400> 121
 Met Ser Leu Gln Ile Gly Arg Thr Glu Arg Ala Arg Ser Pro Val Phe
 1 5 10 15
 Val Phe Ala His Lys Arg Gln Leu Leu His Gly Arg Cys Ser Thr Ile
 20 25 30
 Asp Asn Ala Asn Cys Ser Thr Cys Ser Met Lys Ile Asn Ser Thr Cys
 35 40 45
 Thr Leu Thr Ala Leu Pro Ile Ala Ala Leu Pro Gly Pro Arg Thr Thr
 50 55 60
 Ser His Tyr Ser Thr Ala Ala Ala Asn Trp Cys Tyr Ala Thr Val Ala
 65 70 75 80
 Pro Arg Ala Arg Ser Ser Thr Ile Ala Ala Ser Leu Gly Thr Pro Ala
 85 90 95
 Pro Ser Ser Ser Ala Ser Phe Arg Pro Lys Leu Ile Arg Thr Thr Pro
 100 105 110
 Val Gln Ala Ala Pro Val Ala Pro Ala Leu Met Asp Ala Val Glu
 115 120 125
 Arg Leu Lys Thr Gly Phe Glu Lys Phe Lys Thr Glu Val Tyr Asp Lys
 130 135 140
 Lys Pro Asp Phe Phe Glu Pro Leu Lys Ala Gly Gln Ala Pro Lys Tyr
 145 150 155 160
 Met Val Phe Ala Cys Ala Asp Ser Arg Val Cys Pro Ser Val Thr Leu
 165 170 175
 Gly Leu Glu Pro Gly Glu Ala Phe Thr Ile Arg Asn Ile Ala Asn Met
 180 185 190
 Val Pro Ala Tyr Cys Lys Asn Lys Tyr Ala Gly Val Gly Ser Ala Ile
 195 200 205
 Glu Tyr Ala Val Cys Ala Leu Lys Val Glu Val Ile Val Val Ile Gly
 210 215 220
 His Ser Arg Cys Gly Gly Ile Lys Ala Leu Leu Ser Leu Lys Asp Gly
 225 230 235 240
 Ala Asp Asp Ser Phe His Phe Val Glu Asp Trp Val Arg Ile Gly Phe
 245 250 255
 Pro Ala Lys Lys Lys Val Gln Thr Glu Cys Ala Ser Met Pro Phe Asp
 260 265 270
 Asp Gln Cys Thr Val Leu Glu Lys Glu Ala Val Asn Val Ser Leu Gln
 275 280 285
 Asn Leu Leu Thr Tyr Pro Phe Val Lys Glu Gly Val Thr Asn Gly Thr
 290 295 300
 Leu Lys Leu Val Gly Gly His Tyr Asp Phe Val Ser Gly Lys Phe Glu
 305 310 315 320
 Thr Trp Glu Gln

<210> 122
 <211> 804
 <212> DNA

PF58581.ST25.txt

<213> Chlamydomonas reinhardtii

<400> 122

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atgtcgtcgc ggaatgtcgc taccgctctg cgcatgttcg cgaccctcgg tccgagccag      60
gctggcgagg cctcggccat gatgggcacc ggctcggcgc tgctcgcgca gcgcgcggcc      120
gccctgggcg gcgcctcggc tgtaacaag ggctgcagct gccgctgcgg ccgcgtggcg      180
tgcattggcg cgtgcatgcc gatgcgccac ctccacgccc accccaaccc gccctcggac      240
cccgaccagg ccctggagta ccttcgcgag ggcaacaagc gcttcgtgaa caacaagccg      300
cacgactcgc accccacgcg caacctggac cgcgtcaagg ccaccgccgc gggccagaag      360
cccttcgcgc ccttcctgtc ctgcgccgac tcgcgcgtgc ctgtcgagat catcttcgac      420
cagggtctcg gtgacgtggt cgtgacgcgc gtggccggca acatcgtgac caacgagatc      480
acggcgctgc tggagttcgg cacggccgtc ctgggctcca aggtgctcat ggtgctgggc      540
cacagcgctt gcggcgccgt ggccggccacc atgaacggcg ccgccgtgcc tggcgatcac      600
tcctctctct actacagcat cagcccggcc tgcaagaagg ctacggctgg cgacgttgac      660
ggtgccattg ccgagaacgt caaggtccag atggagcagc tcaaggtgtc gcccggtgctg      720
caggggctcg tgaaggagg caagctcaag atcgtgggcg gcgtgtacga cctggccacc      780
ggcaaggtga ccgagatcgc ctaa

```

<210> 123

<211> 267

<212> PRT

<213> Chlamydomonas reinhardtii

<400> 123

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

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<210> 124
 <211> 846
 <212> DNA
 <213> Oryza sativa

<400> 124
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 agctgggtgct tcgccactgt caccgccgcgc tcccgcgccca cagtcgtcgc cagcctcgcc 120
 tccccatcac cgtcctcctc ctctctctcc tccaacagca gcaacctccc ggcccccttc 180
 cgcccccgcc tcatccgcaa caccgccgtc ttcgccgccc ccgtcgcccc cgccgcgatg 240
 gacgccgcgc tcgaccgcct caaggatggg ttcgccaagt tcaagaccga gttctatgac 300
 aagaagccgg agctcttcga gccgctcaag gccggccagg caccgaagta catggtgttc 360
 tcgtgcgcgc actctcgcgt gtgcccgctc gtgaccatgg gcctggagcc cggcgaggcc 420
 ttcaccgtcc gcaacatcgc caacatggtc ccagcttact gcaagatcaa gcacgctggc 480
 gtcgggtcgg ccatcgagta cgcggtctgc gccctcaagg tcgaactcat cgtggtgatt 540
 ggccacagcc gctgcggtgg aatcaaggcc ctctctcac tcaaggatgg agcaccagac 600
 tccttccact tcgtcgagga ctgggtcagg accggtttcc ccgccaagaa gaaggttcag 660
 accgagcacg cctcgtgcc ttctgatgac caatgcgcca tcttgagaa ggaggccgtg 720
 aaccaatccc tggagaacct caagacctac ccgttcgtca aggaggggat cgccaacggc 780
 accctcaagc tcgtcggcgc ccactacgac ttctgtctcc gcaacttga cttatgggag 840
 ccctaa 846

<210> 125
 <211> 273
 <212> PRT
 <213> Oryza sativa

<400> 125
 Met Ser Thr Ala Ala Ala Ala Ala Ala Gln Ser Trp Cys Phe Ala
 1 5 10 15
 Thr Val Thr Pro Arg Ser Arg Ala Thr Val Val Ala Ser Leu Ala Ser
 20 25 30
 Pro Ser Pro Ser Ser Ser Ser Ser Ser Ser Ser Asn Ser Ser Asn Leu
 35 40 45
 Pro Ala Pro Phe Arg Pro Arg Leu Ile Arg Asn Thr Pro Val Phe Ala
 50 55 60
 Ala Pro Val Ala Pro Ala Ala Met Asp Ala Ala Val Asp Arg Leu Lys
 65 70 75 80
 Asp Gly Phe Ala Lys Phe Lys Thr Glu Phe Tyr Asp Lys Lys Pro Glu
 85 90 95
 Leu Phe Glu Pro Leu Lys Ala Gly Gln Ala Pro Lys Tyr Met Val Phe
 100 105 110
 Ser Cys Ala Asp Ser Arg Val Cys Pro Ser Val Thr Met Gly Leu Glu
 115 120 125
 Pro Gly Glu Ala Phe Thr Val Arg Asn Ile Ala Asn Met Val Pro Ala
 130 135 140
 Tyr Cys Lys Ile Lys His Ala Gly Val Gly Ser Ala Ile Glu Tyr Ala
 145 150 155 160
 Val Cys Ala Leu Lys Val Glu Leu Ile Val Val Ile Gly His Ser Arg
 165 170 175
 Cys Gly Gly Ile Lys Ala Leu Leu Ser Leu Lys Asp Gly Ala Pro Asp
 180 185 190
 Ser Phe His Phe Val Glu Asp Trp Val Arg Thr Gly Phe Pro Ala Lys
 195 200 205
 Lys Lys Val Gln Thr Glu His Ala Ser Leu Pro Phe Asp Asp Gln Cys
 210 215 220
 Ala Ile Leu Glu Lys Glu Ala Val Asn Gln Ser Leu Glu Asn Leu Lys
 225 230 235 240
 Thr Tyr Pro Phe Val Lys Glu Gly Ile Ala Asn Gly Thr Leu Lys Leu

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				245						250					255				
Val	Gly	Gly	His	Tyr	Asp	Phe	Val	Ser	Gly	Asn	Leu	Asp	Leu	Trp	Glu				
			260					265					270						
Pro																			

<210> 126
 <211> 993
 <212> DNA
 <213> Arabidopsis thaliana

<400> 126
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 caatctgctt caaaagccac aaaacagtat aaatatcctt ctcttcgtcc ctctcatcgc 120
 ctgtctctcc tcttcctctt cccgttccat ttatccgcaa acggagcttg ttttcgggtgc 180
 acctgcttca gccacttcaa acttgaactg agaaggatgg gaaacgaatc atatgaagac 240
 gccatcgaag ctctcaagaa gcttctcatt gagaaggatg atctgaagga tgtagctgcg 300
 gccaaagtgga agaagatcac ggcggagctt caggcagcct cgtcatcgga cagcaaattct 360
 tttgatcccg tcgaacgaat taaggaaggc ttcgtcacct tcaagaagga gaaatacgag 420
 accaatcctg ctttgtatgg tgagctcgcc aaagggtcaaa gcccaaagta catggtgttt 480
 gcttggtcgg actcacgagt gtgcccacac cacgtactag acttccatcc tggagatgcc 540
 ttcgtggttc gtaatatcgc caatatggtt cctccttttg acaagggtcaa atatgcagga 600
 gttggagccg ccattgaata cgctgtcttg caccttaagg tggaaaacat tgtggtgata 660
 gggcacagtg catgtggtgg catcaagggg cttatgtcat ttcctcttga cggaacaac 720
 tctactgact tcatagagga ttgggtcaaa atctgtttac cagcaaagtc aaaagttttg 780
 gcagaaagtg aaagttcagc atttgaagac caatgtggcc gatgcgaaag ggcagtgaat 840
 gtgtcactag caaacctatt gacatatcca tttgtgagag aaggagttgt gaaaggaaca 900
 cttgctttga agggaggcta ctatgacttt gttaatggct cctttgagct ttgggagctc 960
 cagtttgga tttccccgt tcattctata tga 993

<210> 127
 <211> 347
 <212> PRT
 <213> Arabidopsis thaliana

<400> 127
 Met Ser Thr Ala Pro Leu Ser Gly Phe Phe Leu Thr Ser Leu Ser Pro
 1 5 10 15
 Ser Gln Ser Ser Leu Gln Lys Leu Ser Leu Arg Thr Ser Ser Thr Val
 20 25 30
 Ala Cys Leu Pro Pro Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser
 35 40 45
 Ser Ser Arg Ser Val Pro Thr Leu Ile Arg Asn Glu Pro Val Phe Ala
 50 55 60
 Ala Pro Ala Pro Ile Ile Ala Pro Tyr Trp Ser Glu Glu Met Gly Thr
 65 70 75 80
 Glu Ala Tyr Asp Glu Ala Ile Glu Ala Leu Lys Lys Leu Leu Ile Glu
 85 90 95
 Lys Glu Glu Leu Lys Thr Val Ala Ala Lys Val Glu Gln Ile Thr
 100 105 110
 Ala Ala Leu Gln Thr Gly Thr Ser Ser Asp Lys Lys Ala Phe Asp Pro
 115 120 125
 Val Glu Thr Ile Lys Gln Gly Phe Ile Lys Phe Lys Lys Glu Lys Tyr
 130 135 140
 Glu Thr Asn Pro Ala Leu Tyr Gly Glu Leu Ala Lys Gly Gln Ser Pro
 145 150 155 160
 Lys Tyr Met Val Phe Ala Cys Ser Asp Ser Arg Val Cys Pro Ser His
 165 170 175
 Val Leu Asp Phe Gln Pro Gly Asp Ala Phe Val Val Arg Asn Ile Ala

PF58581.ST25.txt

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

<210> 128
 <211> 990
 <212> DNA
 <213> Flaveria pringlei

<400> 128

atgtcgaccg	cctctgcttt	cgccattaat	gcgccttcgt	tcgtcaacgc	ttcgtcgctg	60
aagaagtcgt	cttcttcagc	cagatctggt	gtgttgtccg	ccagatttac	gtgcaattcg	120
tcgtcgctctt	cttcgtctgc	tactcctccg	agtctcattc	gtaacgagcc	tgttttcgct	180
gtcccggtctc	ctatcatcac	accgaattgg	accgaagatg	gaaatgaatc	atacgaggaa	240
gccattgaag	cactcaagaa	aatgtctcatt	gaaaagggtg	agttagaacc	agttgccgct	300
gcaagaatcg	accaaatac	agctcaagcc	gcagcaccgc	acaccaaagc	tccatttgac	360
cctgttgaga	ggatcaaatac	cggcttcgtg	aagttaaga	cagagaaatt	cgtcacaaac	420
ccggtcttgt	acgatgagct	tgctaaaggc	caaagcccaa	agttcatggt	gtttgcatgc	480
tcagactcgc	gtgtttgccc	atcacacggt	cttgatttcc	agcccgggtg	ggcgtttggt	540
gtccgtaacg	ttgccaacat	ggtccctccc	tttgacaaga	ccaaatattc	tggagtagga	600
gctgctgttg	agtatgcagt	tttgcatcta	aaggtaacaag	aaatatttgt	aattgggcat	660
agccgttgtg	gagggatcaa	gggtctcatg	actttcccag	acgaaggacc	tactcaacc	720
gatttcatcg	aagattgggt	gaaagtatgt	ctccccgcga	agtcaaaagt	ggtagcagaa	780
cacaacggca	cacatcttga	tgatcaatgt	gtactatgtg	aaaaggaagc	tgtgaacgtg	840
tcgcttgga	acctgttgac	ataccattt	gtaagggatg	gattgaggaa	caatacactc	900
gcgctcaagg	gtggtcacta	tgactttgtt	aacgggacct	ttgagctgtg	ggcacttgac	960
tttggccttt	cgtctcctac	ctctgtatga				990

<210> 129
 <211> 329
 <212> PRT
 <213> Flaveria pringlei

<400> 129

Met Ser Thr Ala Ser Ala Phe Ala Ile Asn Ala Pro Ser Phe Val Asn	
1	15
Ala Ser Ser Leu Lys Lys Ser Ser Ser Ser Ala Arg Ser Gly Val Leu	
20	30
Ser Ala Arg Phe Thr Cys Asn Ser Ser Ser Ser Ser Ser Ala Thr	
35	45
Pro Pro Ser Leu Ile Arg Asn Glu Pro Val Phe Ala Ala Pro Ala Pro	

PF58581.ST25.txt

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

<210> 130
 <211> 993
 <212> DNA
 <213> Flaveria linearis

<400> 130
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 aagaagtcgt cgacttcttc agccagatct ggtgtgttgt ccgccagatt tacgtgcaat 120
 tcgtcgctgt cttcttcgtc tgcaactcct ccgagtctca ttcgtaacga gcctgttttc 180
 gctgccccgg cgcccatcat aacaccgaat tggaccgaag acggaaatga atcatacgag 240
 gaagccattg acgcactcaa gaaaatgctc attgaaaagg gtgagttaga acccgttgcc 300
 gctgcaagaa tcgaccaa atcacagctcaa gccgcagcac ccgacaccaa agctccattc 360
 gaccctgttg agaggatcaa atccggcttc gtgaagttca agacagagaa attcgtaaca 420
 aacccagccc tgtacgatga gcttgctaaa ggccaaagcc caaagttcat ggtgtttgca 480
 tgctcagact cgcgtgtttg cccatcacac gttcttgatt tccagcccgg tgaggcggtt 540
 gttgtccgta acgttgccaa catggtccct ccctttgaca agaccaaata ttctggagta 600
 ggagctgctg ttgagtatgc agttttgcat cttaaaggtag aagaaatatt tgtaattggg 660
 catagccggt gcggagggat caagggtctc atgactttcc cagacgaagg acctcactca 720
 actgatttca tcgaagattg ggtgaaagta tgcctccccg caaagtcaaa agtggtagca 780
 gaacacaacg gcacacatct tgatgatcaa tgtgtacaat gtgaaaagga agctgtgaac 840
 gtgtcgcttg gaaacctgtt gacataccca tttgtaaagg atggtttgag gaacaataca 900
 ctcgcgctca aggggtgtca ctatgatttt gttaacggga cctttgagct gtgggcactt 960
 gactttgggc tttcgtctcc tacctctgta tga 993

PF58581.ST25.txt

<210> 131
 <211> 330
 <212> PRT
 <213> Flaveria linearis

<400> 131
 Met Ser Thr Ala Ser Ala Phe Ala Ile Asn Ala Pro Ser Phe Val Asn
 1 5 10 15
 Ala Ser Ser Leu Lys Lys Ser Ser Thr Ser Ser Ala Arg Ser Gly Val
 20 25 30
 Leu Ser Ala Arg Phe Thr Cys Asn Ser Ser Ser Ser Ser Ser Ala
 35 40 45
 Thr Pro Pro Ser Leu Ile Arg Asn Glu Pro Val Phe Ala Ala Pro Ala
 50 55 60
 Pro Ile Ile Thr Pro Asn Trp Thr Glu Asp Gly Asn Glu Ser Tyr Glu
 65 70 75 80
 Glu Ala Ile Asp Ala Leu Lys Lys Met Leu Ile Glu Lys Gly Glu Leu
 85 90 95
 Glu Pro Val Ala Ala Ala Arg Ile Asp Gln Ile Thr Ala Gln Ala Ala
 100 105 110
 Ala Pro Asp Thr Lys Ala Pro Phe Asp Pro Val Glu Arg Ile Lys Ser
 115 120 125
 Gly Phe Val Lys Phe Lys Thr Glu Lys Phe Val Thr Asn Pro Ala Leu
 130 135 140
 Tyr Asp Glu Leu Ala Lys Gly Gln Ser Pro Lys Phe Met Val Phe Ala
 145 150 155 160
 Cys Ser Asp Ser Arg Val Cys Pro Ser His Val Leu Asp Phe Gln Pro
 165 170 175
 Gly Glu Ala Phe Val Val Arg Asn Val Ala Asn Met Val Pro Pro Phe
 180 185 190
 Asp Lys Thr Lys Tyr Ser Gly Val Gly Ala Ala Val Glu Tyr Ala Val
 195 200 205
 Leu His Leu Lys Val Gln Glu Ile Phe Val Ile Gly His Ser Arg Cys
 210 215 220
 Gly Gly Ile Lys Gly Leu Met Thr Phe Pro Asp Glu Gly Pro His Ser
 225 230 235 240
 Thr Asp Phe Ile Glu Asp Trp Val Lys Val Cys Leu Pro Ala Lys Ser
 245 250 255
 Lys Val Val Ala Glu His Asn Gly Thr His Leu Asp Asp Gln Cys Val
 260 265 270
 Gln Cys Glu Lys Glu Ala Val Asn Val Ser Leu Gly Asn Leu Leu Thr
 275 280 285
 Tyr Pro Phe Val Arg Asp Gly Leu Arg Asn Asn Thr Leu Ala Leu Lys
 290 295 300
 Gly Gly His Tyr Asp Phe Val Asn Gly Thr Phe Glu Leu Trp Ala Leu
 305 310 315 320
 Asp Phe Gly Leu Ser Ser Pro Thr Ser Val
 325 330

<210> 132
 <211> 993
 <212> DNA
 <213> Flaveria brownii

<400> 132
 atgtcgaccg cctctgcttt cgccactaac gtgccttcgt tcgtcaacgc ttcacgctg 60
 aagaagtcgt ccacttcttc agccagatct ggtgtgttgt ccgccaaatt tacgtgcaat 120
 tcgtcgtcgt cttcttcgtc tgcaactcct ccgagtctca ttcgtaacga gcctgttttc 180

PF58581.ST25.txt

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gctgctccgg cgcccatcat cacaccgaat tggaccgaag acggaaatga atcatacgag 240
gaagccattg acgcactcaa gaaaatgctc attgaaaagg gtgagttaga accagttgcg 300
gctgcaagaa tcgaccaa atcacgtcaa gccgcggcac ccgacaccaa agctccattc 360
gaccctgttg agaggatcaa atccgggttc gtgaagttca agactgagaa attcgtaaca 420
aaccagccc tgtacgatga gcttgctaaa ggccaaagcc caaagttcat ggtgtttgca 480
tgctcagact cgcgtgtttg cccatcacac gttcttgatt tccagcccgg tgaggcgttt 540
gttgctcgta acgttgccaa catggtcctt ccctttgaca agaccaaata ttctggagta 600
ggagctgctg ttgagtatgc agttttgcat ctgaaggtag aagaaatatt tgtaattggg 660
catagccgtt gcggagggat caaggggtctc atgactttcc cagacgaagg acctcactca 720
accgatttca tcgaagattg ggtgaaagta tgctccccg cgaagtcaaa agtggtagca 780
gaacacaacg gcacacatct tgatgatcaa tgtgtactat gtgaaaagga agctgtgaac 840
gtgtcgcttg gaaacctgtt gacataccca tttgtaaggg atggtttgag gaacaatata 900
ctcgcgctca aggggtgtca ctatgatttt gttaacggga cctttgagct gtgggcactt 960
gactttgggc tttcgtctcc tacctctgta tga 993

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<210> 133

<211> 330

<212> PRT

<213> *Flaveria brownii*

<400> 133

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Met Ser Thr Ala Ser Ala Phe Ala Thr Asn Val Pro Ser Phe Val Asn
1      5      10      15
Ala Ser Ser Leu Lys Lys Ser Ser Thr Ser Ser Ala Arg Ser Gly Val
20     25     30
Leu Ser Ala Lys Phe Thr Cys Asn Ser Ser Ser Ser Ser Ser Ala
35     40     45
Thr Pro Pro Ser Leu Ile Arg Asn Glu Pro Val Phe Ala Ala Pro Ala
50     55     60
Pro Ile Ile Thr Pro Asn Trp Thr Glu Asp Gly Asn Glu Ser Tyr Glu
65     70     75     80
Glu Ala Ile Asp Ala Leu Lys Lys Met Leu Ile Glu Lys Gly Glu Leu
85     90     95
Glu Pro Val Ala Ala Ala Arg Ile Asp Gln Ile Thr Ala Gln Ala Ala
100    105    110
Ala Pro Asp Thr Lys Ala Pro Phe Asp Pro Val Glu Arg Ile Lys Ser
115    120    125
Gly Phe Val Lys Phe Lys Thr Glu Lys Phe Val Thr Asn Pro Ala Leu
130    135    140
Tyr Asp Glu Leu Ala Lys Gly Gln Ser Pro Lys Phe Met Val Phe Ala
145    150    155    160
Cys Ser Asp Ser Arg Val Cys Pro Ser His Val Leu Asp Phe Gln Pro
165    170    175
Gly Glu Ala Phe Val Val Arg Asn Val Ala Asn Met Val Pro Pro Phe
180    185    190
Asp Lys Thr Lys Tyr Ser Gly Val Gly Ala Ala Val Glu Tyr Ala Val
195    200    205
Leu His Leu Lys Val Gln Glu Ile Phe Val Ile Gly His Ser Arg Cys
210    215    220
Gly Gly Ile Lys Gly Leu Met Thr Phe Pro Asp Glu Gly Pro His Ser
225    230    235    240
Thr Asp Phe Ile Glu Asp Trp Val Lys Val Cys Leu Pro Ala Lys Ser
245    250    255
Lys Val Val Ala Glu His Asn Gly Thr His Leu Asp Asp Gln Cys Val
260    265    270
Leu Cys Glu Lys Glu Ala Val Asn Val Ser Leu Gly Asn Leu Leu Thr
275    280    285
Tyr Pro Phe Val Arg Asp Gly Leu Arg Asn Asn Thr Leu Ala Leu Lys
290    295    300

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Gly Gly His Tyr Asp Phe Val Asn Gly Thr Phe Glu Leu Trp Ala Leu
 305 310 315 320
 Asp Phe Gly Leu Ser Ser Pro Thr Ser Val
 325 330

<210> 134
 <211> 969
 <212> DNA
 <213> Nicotiana paniculata

<400> 134
 atgtcaactg cttccattaa cagttgcctt actatctccc cagctcaagc ttcccttaag 60
 aaaccaattc gtcctgttgc ttttgctagg cttagcaaca cctcttcttc ttcttcttcc 120
 gttcccagtc tcatcagaaa cgagcccgtc ttcgccgccc caactcccat catcaacccc 180
 attttgagag aagaaatggc aaaggaatcc tatgagcagg ccattgctgc actcgagaaa 240
 ctccctcagcg aaaaaggaga acttggacca attgctgcag caagagttga ccagattaca 300
 gctgaattgc aatcatcaga tggcagcaaa ccattcgacc ctggtgagca catgaaagct 360
 ggctttattc acttcaaaac tgagaaatac gagaagaacc cagccttata tggggaacta 420
 tcaaaaggcc agagcccca gttcatggtc tttgcctgct ctgactctcg agtgtgcca 480
 tcacatgttc tgaacttcca acctggtgag gctttcgtgg tccgaaacat cgccaacatg 540
 gtccccgctt atgacaagac cagatactct ggtgtcggag cagctatcga atacgctgtt 600
 ctccacctta aggtagagaa cattgttgtc attggccaca gcgcatgtgg aggtatcaaa 660
 ggtctcatgt ctctatctgc agatggttct gaatcaactg cctttattga ggattgggtg 720
 aaaattgggt tacctgccaa ggccaagggt gaggtgaac acgcggataa atgttttgca 780
 gatcaatgca cagcttgtga gaaggaagct gtgaatgtgt cacttggaat tttgctgacc 840
 tatccatttg tgagagaagg tttggtgaag aaaacactag cattgaaggg aggtcactat 900
 gattttgtga atggaggatt tgagctgtgg ggacttgagt tcggtctttc tccttctctt 960
 tccgtatga 969

<210> 135
 <211> 322
 <212> PRT
 <213> Nicotiana paniculata

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

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```

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

```

<210> 136
 <211> 966
 <212> DNA
 <213> Nicotiana tabacum

<400> 136

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atgtcaactg cttccattaa cagttgcctt actatctccc ctgctcaagc ttcccttaag      60
aaaccaactc gtcctgttgc ttttgcaagg cttagcaact cttcttcttc tacttctggt      120
cccagttctc tcagaaacga gcccgctctc gccgccccta ctcccatcat caaccctatt      180
ttgagagaag aaatggcaaa ggaatcctat gagcaggcca ttgctgcact cgagaaactc      240
ctcagcgaaa aaggagaact tggaccaatt gctgcagcaa gagttgacca gattacagct      300
gaattgcaat catcagatgg cagcaaacca ttcgaccctg ttgagcacat gaaagctggc      360
tttattcact tcaaaactga gaaatacgag aagaaccag ccttatatgg ggaactatca      420
aaaggccaga gccccaagtt catggtcttt gctgctctg actctcgagt gtgcccatca      480
catgtcctga acttccaacc tgggtgaggct ttcgtggtcc gaaacatcgc caacatgggtc      540
cctgcttatg acaagaccag atactccgga gtcggagcag ctatcgaata cgctgttctt      600
caccttaagg tagagaacat tgttgtcatt ggccatagcg catgtggagg tatcaaaggt      660
ctcatgtctt tacctgcaga tggttctgaa tcaactgcct tcattgagga ttgggtgaaa      720
attgggtttac ctgccaaggc gaaggtgcag ggtgaacacg tggataaatg ttttgcatat      780
caatgcacag cttgtgagaa ggaagctgtg aatgtgtcac ttggaaattt gctgacctat      840
ccatttgtga gagaaggttt ggtgaagaaa aactagcat tgaaggagg tcatatgat      900
ttcgtgaatg gaggatttga gctgtgggga cttgagttcg gtctttctcc ttctctttcc      960
gtatga

```

<210> 137
 <211> 321
 <212> PRT
 <213> Nicotiana tabacum

<400> 137

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Met Ser Thr Ala Ser Ile Asn Ser Cys Leu Thr Ile Ser Pro Ala Gln
1      5      10      15
Ala Ser Leu Lys Lys Pro Thr Arg Pro Val Ala Phe Ala Arg Leu Ser
      20      25      30
Asn Ser Ser Ser Thr Ser Val Pro Ser Leu Ile Arg Asn Glu Pro
      35      40      45
Val Phe Ala Ala Pro Thr Pro Ile Ile Asn Pro Ile Leu Arg Glu Glu
      50      55      60
Met Ala Lys Glu Ser Tyr Glu Gln Ala Ile Ala Ala Leu Glu Lys Leu
      65      70      75      80

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

<210> 138
<211> 963
<212> DNA
<213> Populus tremula x Populus tremuloides

<400> 138
atgtcgactg cttcgattaa cagctggtgt ctcacctctg tctctgcctc taagaaatca 60
ctaccgcgat tacgtccttc agtcttttgc agcctcaact cctctgtttc tctcctacc 120
cttatcagaa accagcctgt ttctgcagcc cctgctccta ttctctatcc acggagagggc 180
gaagaaatgg gaaacgacta caacgaggcc attgaatctc tcaagaaact cctcagtgc 240
aaggaagagc tgaaaactgt agcagctgcg aaagtggagc agataacagc tgaattacaa 300
accgtctcat cttctgaccc caaggcattc gatcctgttg agaagattaa atccggattc 360
attcacttca agaaggagaa atatgacaag aatccgggac tgtactccga gcttgccaaa 420
ggccaaagcc ccaagtttat ggtgtttgca tgctcggatt cccgggtttg cccgtcccat 480
gtgcttgatt tccaaccagg ggaagctttt gtggtccgca atgttgcgaa tatggtccc 540
ccatacgata agactaagta cgctggagtt ggggcagcga tagagtacgc agttttgcat 600
ctgaagggtg aatacattgt ggtcatcgga cacagcgctt gtggtggaat taagggcctc 660
atgtccttcc cgtatgatgg aacaacatca actgatttca tagaagactg ggtcaaagtc 720
tgctacaatg ccaagaccaa gatttttagc gaacatgcc actcacctt cccagacatg 780
tgtacacaat gtgaaaagga ggcagtgaac gtgtccatcg gacacttgct cacctaccgg 840
tttgtgagag atggcttggt gaacaaaact ctaggactga aggggtggta ttatgatttt 900
gtcaaaggca gttttgagct ctgggggctt gagtacagcc tctccccctc tctctccgta 960
tga

<210> 139
<211> 320

PF58581.ST25.txt

<212> PRT

<213> Populus tremula x Populus tremuloides

<400> 139

```

Met Ser Thr Ala Ser Ile Asn Ser Trp Cys Leu Thr Ser Val Ser Ala
1      5      10      15
Ser Lys Lys Ser Leu Pro Ala Leu Arg Pro Ser Val Phe Ala Ser Leu
20      25      30
Asn Ser Ser Val Ser Pro Pro Thr Leu Ile Arg Asn Gln Pro Val Phe
35      40      45
Ala Ala Pro Ala Pro Ile Leu Tyr Pro Arg Arg Gly Glu Glu Met Gly
50      55      60
Asn Asp Tyr Asn Glu Ala Ile Glu Ser Leu Lys Lys Leu Leu Ser Asp
65      70      75      80
Lys Glu Glu Leu Lys Thr Val Ala Ala Ala Lys Val Glu Gln Ile Thr
85      90      95
Ala Glu Leu Gln Thr Val Ser Ser Ser Asp Pro Lys Ala Phe Asp Pro
100     105     110
Val Glu Lys Ile Lys Ser Gly Phe Ile His Phe Lys Lys Glu Lys Tyr
115     120     125
Asp Lys Asn Pro Gly Leu Tyr Ser Glu Leu Ala Lys Gly Gln Ser Pro
130     135     140
Lys Phe Met Val Phe Ala Cys Ser Asp Ser Arg Val Cys Pro Ser His
145     150     155     160
Val Leu Asp Phe Gln Pro Gly Glu Ala Phe Val Val Arg Asn Val Ala
165     170     175
Asn Met Val Pro Pro Tyr Asp Lys Thr Lys Tyr Ala Gly Val Gly Ala
180     185     190
Ala Ile Glu Tyr Ala Val Leu His Leu Lys Val Glu Tyr Ile Val Val
195     200     205
Ile Gly His Ser Ala Cys Gly Gly Ile Lys Gly Leu Met Ser Phe Pro
210     215     220
Tyr Asp Gly Thr Thr Ser Thr Asp Phe Ile Glu Asp Trp Val Lys Val
225     230     235     240
Cys Tyr Asn Ala Lys Thr Lys Ile Leu Ala Glu His Ala Asn Ser Pro
245     250     255
Phe Pro Asp Met Cys Thr Gln Cys Glu Lys Glu Ala Val Asn Val Ser
260     265     270
Ile Gly His Leu Leu Thr Tyr Pro Phe Val Arg Asp Gly Leu Val Asn
275     280     285
Lys Thr Leu Gly Leu Lys Gly Tyr Tyr Asp Phe Val Lys Gly Ser
290     295     300
Phe Glu Leu Trp Gly Leu Glu Tyr Ser Leu Ser Pro Ser Leu Ser Val
305     310     315     320

```

<210> 140

<211> 963

<212> DNA

<213> Populus tremula x Populus tremuloides

<400> 140

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atgtcgactg cttcgattaa cagctggtgt ctcacctctg tctctccctc taagaaatca      60
ctacccgcac tacgtccttc agtcttttgc agcctcaact cctctgtttc tcctcctacc      120
cttatcagaa accagcctgt ttctgcagcc cctgtctcta ttctctatcc acggagaggg      180
gaagaaatgg gaaacgacta caacgaggcc attgaatctc tcaagaaact cctcagtgat      240
aaggaggagc tgaaaactgt agcagctgcg aaagtggagc agataacagc tgaattacaa      300
accgtctcat cttctgaccc caaggcattc gatcctgttg agaagattaa atccggattc      360
attcacttca agaaggagaa atatgacaag aatccgggac tgtactccga gcttgccaaa      420
ggccaaagcc ccaagtttat ggtgtttgca tgctcggatt cccgggtttg cccgtcccat      480

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gtgcttgatt tccaaccggg ggaagctttt gtgtgccgca atgttgcgaa tatgggcccg 540
ccatacgata agactaagta cgctggagtt ggggcagcga tagagtacgc agttttgcat 600
ctgaagggtgg aatacattgt ggatcatcga cacagcgctt gtggtggaat taagggcctc 660
atgtccttcc cgtatgatgg aacaacatca actgatttca tagaagactg ggtcaaagtc 720
tgctacaatg ccaagaccaa gatttttagca gaacatgcc aactcacctt cccagacatg 780
tgtacacaat gtgaaaagga ggcagtgaac gtgtccctcg gacacttgct cacctaccg 840
tttgtgagag atggcttggg gaacaaaact ctaggcctta aggggtggta ttatgatttt 900
gtcaaaggaa gttttgagct ctggggcctt gagtacagcc tctctccctc tctctccgta 960
tga

```

<210> 141
 <211> 320
 <212> PRT
 <213> Populus tremula

<400> 141

Met	Ser	Thr	Ala	Ser	Ile	Asn	Ser	Trp	Cys	Leu	Thr	Ser	Val	Ser	Pro
1				5					10				15		
Ser	Lys	Lys	Ser	Leu	Pro	Ala	Leu	Arg	Pro	Ser	Val	Phe	Ala	Ser	Leu
			20					25				30			
Asn	Ser	Ser	Val	Ser	Pro	Pro	Thr	Leu	Ile	Arg	Asn	Gln	Pro	Val	Phe
		35					40					45			
Ala	Ala	Pro	Ala	Pro	Ile	Leu	Tyr	Pro	Arg	Arg	Gly	Glu	Glu	Met	Gly
	50					55					60				
Asn	Asp	Tyr	Asn	Glu	Ala	Ile	Glu	Ser	Leu	Lys	Lys	Leu	Leu	Ser	Asp
65				70					75					80	
Lys	Glu	Glu	Leu	Lys	Thr	Val	Ala	Ala	Ala	Lys	Val	Glu	Gln	Ile	Thr
			85					90						95	
Ala	Glu	Leu	Gln	Thr	Val	Ser	Ser	Ser	Asp	Pro	Lys	Ala	Phe	Asp	Pro
		100						105					110		
Val	Glu	Lys	Ile	Lys	Ser	Gly	Phe	Ile	His	Phe	Lys	Lys	Glu	Lys	Tyr
		115					120					125			
Asp	Lys	Asn	Pro	Gly	Leu	Tyr	Ser	Glu	Leu	Ala	Lys	Gly	Gln	Ser	Pro
	130					135					140				
Lys	Phe	Met	Val	Phe	Ala	Cys	Ser	Asp	Ser	Arg	Val	Cys	Pro	Ser	His
145				150						155				160	
Val	Leu	Asp	Phe	Gln	Pro	Gly	Glu	Ala	Phe	Val	Val	Arg	Asn	Val	Ala
			165					170					175		
Asn	Met	Val	Pro	Pro	Tyr	Asp	Lys	Thr	Lys	Tyr	Ala	Gly	Val	Gly	Ala
		180					185						190		
Ala	Ile	Glu	Tyr	Ala	Val	Leu	His	Leu	Lys	Val	Glu	Tyr	Ile	Val	Val
		195					200					205			
Ile	Gly	His	Ser	Ala	Cys	Gly	Gly	Ile	Lys	Gly	Leu	Met	Ser	Phe	Pro
	210					215					220				
Tyr	Asp	Gly	Thr	Thr	Ser	Thr	Asp	Phe	Ile	Glu	Asp	Trp	Val	Lys	Val
225					230					235				240	
Cys	Tyr	Asn	Ala	Lys	Thr	Lys	Ile	Leu	Ala	Glu	His	Ala	Asn	Ser	Pro
			245						250				255		
Phe	Pro	Asp	Met	Cys	Thr	Gln	Cys	Glu	Lys	Glu	Ala	Val	Asn	Val	Ser
		260						265					270		
Leu	Gly	His	Leu	Leu	Thr	Tyr	Pro	Phe	Val	Arg	Asp	Gly	Leu	Val	Asn
		275					280					285			
Lys	Thr	Leu	Gly	Leu	Lys	Gly	Tyr	Tyr	Asp	Phe	Val	Lys	Gly	Ser	
	290					295				300					
Phe	Glu	Leu	Trp	Gly	Leu	Glu	Tyr	Ser	Leu	Ser	Pro	Ser	Leu	Ser	Val
305					310					315					320

<210> 142
 <211> 777

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<212> DNA

<213> Arabidopsis thaliana

<400> 142

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atgtcgacag agtcgtacga agacgccatt aaaagactcg gagagcttct cagtaagaaa      60
tcggatctcg ggaacgtggc agccgcaaag atcaagaagt taacggatga gttagaggaa      120
cttgattcca acaagttaga tgccgtagaa cgaatcaaat ccggatttct ccatttcaag      180
actaataatt atgagaagaa tcctactttg tacaattcac ttgccaagag ccagaccccc      240
aagtttttgg tgtttgcttg tgccgattca cgagttagtc catctcacat cttgaatttc      300
caacttgggg aagccttcat cgttagaaac attgcaaaca tggtgccacc ttatgacaag      360
acaagcact ctaatgttgg tgccggccctt gaatatccaa ttacagtcct caacgtggag      420
aacattcttg ttattggaca cagctgttgt ggtggaataa agggactcat ggccattgaa      480
gataatacag ctcccactaa gaccgagttc atagaaaact ggatccagat ctgtgcaccg      540
gccagaaca ggatcaagca ggattgtaaa gacctaagct ttgaagatca gtgcaccaac      600
tgtgagaagg aagccgtgaa cgtgtccttg gggaatcttt tgtcttacct attcgtgaga      660
gaaagagtgg tgaagaacaa gcttgccata agaggagctc actatgattt cgtaaaagga      720
acgtttgatc tttgggaact tgacttcaag actaccctcg cctttgcctt gtcttaa      777

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<210> 143

<211> 258

<212> PRT

<213> Arabidopsis thaliana

<400> 143

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

```

PF58581.ST25.txt

<210> 144
<211> 960
<212> DNA
<213> Spinacia oleracea

<400> 144
atgtctacta ttaacggctg cctcacctct atctctcctt cccgtactca attgaaaaat 60
acctccactt taaggccaac tttcattgct aacagcaggg ttaacccttc ttcttctggt 120
cctccttccc ttattagaaa ccagcccgtt ttccgcccgc ccgccctat catcacccct 180
actttgaaag aagatatggc atacgaagaa gccatcgctg cccttaagaa gcttctaagc 240
gagaagggag aacttgaaaa tgaagccgca tcaaaggtgg cacagataac atctgagtta 300
gccgacgggtg gcacaccatc cgccagttac ccggttcaga gaattaagga aggggtttatc 360
aaattcaaga aggagaaata cgagaaaaat ccagcattgt atggtgagct ttctaagggc 420
caagctccca agtttatggt gtttgcggtg tcagactccc gtgtgtgtcc ctgcgacgta 480
ctagattttcc agcccgggtga ggctttcatg gttcgcaaca tcgccaacat ggtgccagtg 540
tttgacaagg acaaatacgc tggagtcgga gcagccattg aatacgcagt gttgcacctt 600
aaggtggaga acattgtcgt gattggacac agtgcttggt gtggaatcaa ggggcttatg 660
tctttcccag atgcaggacc aaccacaact gattttattg aggattgggt caaaatctgc 720
ttgcctgcca agcacaaggt gttagccgag catggtaatg caactttcgc tgaacaatgc 780
accattgtgt aaaaggaagc tgtgaatgta tctctcggaa acttggtgac ttaccattt 840
gtaagagatg gtttggtgaa gaagactcta gctttgcagg gtggttacta cgattttgtc 900
aatggatcat tcgagctatg gggactcgaa tacggcctct ctcttccca atctgtatga 960

<210> 145
<211> 319
<212> PRT
<213> Spinacia oleracea

<400> 145
Met Ser Thr Ile Asn Gly Cys Leu Thr Ser Ile Ser Pro Ser Arg Thr
1 5 10 15
Gln Leu Lys Asn Thr Ser Thr Leu Arg Pro Thr Phe Ile Ala Asn Ser
20 25 30
Arg Val Asn Pro Ser Ser Ser Val Pro Pro Ser Leu Ile Arg Asn Gln
35 40 45
Pro Val Phe Ala Ala Pro Ala Pro Ile Ile Thr Pro Thr Leu Lys Glu
50 55 60
Asp Met Ala Tyr Glu Glu Ala Ile Ala Ala Leu Lys Lys Leu Leu Ser
65 70 75 80
Glu Lys Gly Glu Leu Glu Asn Glu Ala Ala Ser Lys Val Ala Gln Ile
85 90 95
Thr Ser Glu Leu Ala Asp Gly Gly Thr Pro Ser Ala Ser Tyr Pro Val
100 105 110
Gln Arg Ile Lys Glu Gly Phe Ile Lys Phe Lys Lys Glu Lys Tyr Glu
115 120 125
Lys Asn Pro Ala Leu Tyr Gly Glu Leu Ser Lys Gly Gln Ala Pro Lys
130 135 140
Phe Met Val Phe Ala Cys Ser Asp Ser Arg Val Cys Pro Ser His Val
145 150 155 160
Leu Asp Phe Gln Pro Gly Glu Ala Phe Met Val Arg Asn Ile Ala Asn
165 170 175
Met Val Pro Val Phe Asp Lys Asp Lys Tyr Ala Gly Val Gly Ala Ala
180 185 190
Ile Glu Tyr Ala Val Leu His Leu Lys Val Glu Asn Ile Val Val Ile
195 200 205
Gly His Ser Ala Cys Gly Gly Ile Lys Gly Leu Met Ser Phe Pro Asp
210 215 220
Ala Gly Pro Thr Thr Thr Asp Phe Ile Glu Asp Trp Val Lys Ile Cys
225 230 235 240

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```

Leu Pro Ala Lys His Lys Val Leu Ala Glu His Gly Asn Ala Thr Phe
                245                250                255
Ala Glu Gln Cys Thr His Cys Glu Lys Glu Ala Val Asn Val Ser Leu
                260                265                270
Gly Asn Leu Leu Thr Tyr Pro Phe Val Arg Asp Gly Leu Val Lys Lys
                275                280                285
Thr Leu Ala Leu Gln Gly Gly Tyr Tyr Asp Phe Val Asn Gly Ser Phe
                290                295                300
Glu Leu Trp Gly Leu Glu Tyr Gly Leu Ser Pro Ser Gln Ser Val
305                310                315

```

<210> 146
 <211> 987
 <212> DNA
 <213> Pisum sativum

```

<400> 146
atgtctacct cttcaataaa cggtcttagt ctttcttctt tgtcccctgc caaaacttct 60
accaaaagaa ctacattgag accctttggt tctgcatctc ttaacacttc ttcttcatct 120
tcttcctcga ctttcccttc tcttattcaa gacaagccgg ttttcgcttc ttcttctcct 180
atcatcaccc cagttttgag agaagaaatg ggaaagggct atgatgaagc tattgaagaa 240
ctccaaaagt tgttgaggga gaagactgaa ctgaaagcca cagctgctga gaaggttgag 300
caaatcacag ctgagctagg aacaacatca tcatctgatg gcattccaaa atctgaagcc 360
tctgaaagga tcaaaactgg tttccttcac ttcaagaaag agaaatatga caagaatcca 420
gctttgtatg gtgaacttgc caaaggccaa agccctccgt ttatggtgtt tgcattgttca 480
gactcaagag tctgcccata tcatgtgcta gatttccagc caggtgaagc ctttgtgggtc 540
agaaatgttg ctaacttggg tccaccatat gaccaggcaa aatatgccgg aactggtgct 600
gcaattgagt acgcagttct gcattctcaag gtttccaaca ttgttgtcat tggacacagt 660
gcttgtgggt gtattaaggg acttttgtcc ttccatttg atggaaccta ctccactgat 720
ttcattgagg agtgggtcaa aattgggtta cctgcaaagg cgaaggtgaa agcacaacat 780
ggagatgcac cttttgcaga gctatgcaca cactgtgaga aggaagctgt gaatgcttcc 840
cttggaacc ttctcaccta cccatttgtg agagagggat tgggtgaacaa gacattggca 900
ctcaaaggag gatactatga ctttgtgaaa ggatcctttg agctttgggg acttgaattt 960
ggcctttcgt ccactttctc cgtatga 987

```

<210> 147
 <211> 328
 <212> PRT
 <213> Pisum sativum

```

<400> 147
Met Ser Thr Ser Ser Ile Asn Gly Phe Ser Leu Ser Ser Leu Ser Pro
1          5          10          15
Ala Lys Thr Ser Thr Lys Arg Thr Thr Leu Arg Pro Phe Val Ser Ala
20        25        30
Ser Leu Asn Thr Ser Ser Ser Ser Ser Ser Ser Thr Phe Pro Ser Leu
35        40        45
Ile Gln Asp Lys Pro Val Phe Ala Ser Ser Ser Pro Ile Ile Thr Pro
50        55        60
Val Leu Arg Glu Glu Met Gly Lys Gly Tyr Asp Glu Ala Ile Glu Glu
65        70        75        80
Leu Gln Lys Leu Leu Arg Glu Lys Thr Glu Leu Lys Ala Thr Ala Ala
85        90        95
Glu Lys Val Glu Gln Ile Thr Ala Gln Leu Gly Thr Thr Ser Ser Ser
100       105       110
Asp Gly Ile Pro Lys Ser Glu Ala Ser Glu Arg Ile Lys Thr Gly Phe
115       120       125
Leu His Phe Lys Lys Glu Lys Tyr Asp Lys Asn Pro Ala Leu Tyr Gly
130       135       140

```

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

<210> 148
 <211> 996
 <212> DNA
 <213> Medicago truncatula

<400> 148
 atgtctacct cttccataaaa cggtcttagt ctctcttctt tgtcccctac aaaaacttct 60
 attaaaaaag ttacattgag acctattgtt tctgcatctc ttaactcttc ttcttcttcc 120
 tcttccactt ctaacttccc ttctcttatt caagacaagc ctgtttttgc ttcattcttct 180
 tctcctatca tcaccccgagt tttgagagaa gaaatgggaa agggctatga tgaagctatt 240
 gaagaactcc aaaaattgtt gagggagaag actgaattga aagccacagc agctgaaaag 300
 gttgagcaaa ttacagctca gctaggaaca acagcatcag ctgatggtgt tccaacatct 360
 gatcaagcct cagagaggat caaaactggt ttccttcaact tcaagaaaga gaaatatgac 420
 acaaaaccag ctttgtatgg tgaacttgcc aaaggccaag ccccccggtt tatggtgttt 480
 gcatgctcag actcaagagt ctgcccatct catgtgctag acttccagcc aggagaagct 540
 tttgtggtca gaaatgttgc taacatgggt ccaccatatg accaggcaaa atatgctgga 600
 actggatctg caattgagta tgcgttcttg catctcaagg tttccaacat tgtggtcatt 660
 ggacacagtg cttgtggtgg tattaagggg cttttgtctt ttccatttga tggagcctac 720
 tccactgatt tcattgagga gtgggtcaaa attggtttac ctgcaaaggc aaagggtgaag 780
 gcaaagcatg gagatgcacc ttttgagag ctatgcacac actgtgagaa ggaagctgtg 840
 aatgtttctc ttggaaacct tctaacctac ccatttgtga gagagggatt ggtgaacaaa 900
 acattggcac taaaaggagg atactatgac tttgtgaaag gatcttttga gctttgggga 960
 cttgaatttg gcctttcttc aactttctcc gtatga 996

<210> 149
 <211> 331
 <212> PRT
 <213> Medicago truncatula

<400> 149
 Met Ser Thr Ser Ser Ile Asn Gly Phe Ser Leu Ser Ser Leu Ser Pro
 1 5 10 15
 Thr Lys Thr Ser Ile Lys Lys Val Thr Leu Arg Pro Ile Val Ser Ala
 20 25 30

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```

Ser Leu Asn Ser Ser Ser Ser Ser Ser Ser Thr Ser Asn Phe Pro Ser
   35                               40                               45
Leu Ile Gln Asp Lys Pro Val Phe Ala Ser Ser Ser Ser Pro Ile Ile
   50                               55                               60
Thr Pro Val Leu Arg Glu Glu Met Gly Lys Gly Tyr Asp Glu Ala Ile
   65                               70                               75                               80
Glu Glu Leu Gln Lys Leu Leu Arg Glu Lys Thr Glu Leu Lys Ala Thr
   85                               90                               95
Ala Ala Glu Lys Val Glu Gln Ile Thr Ala Gln Leu Gly Thr Thr Ala
  100                               105                               110
Ser Ala Asp Gly Val Pro Thr Ser Asp Gln Ala Ser Glu Arg Ile Lys
  115                               120                               125
Thr Gly Phe Leu His Phe Lys Lys Glu Lys Tyr Asp Thr Lys Pro Ala
  130                               135                               140
Leu Tyr Gly Glu Leu Ala Lys Gly Gln Ala Pro Pro Phe Met Val Phe
  145                               150                               155                               160
Ala Cys Ser Asp Ser Arg Val Cys Pro Ser His Val Leu Asp Phe Gln
  165                               170                               175
Pro Gly Glu Ala Phe Val Val Arg Asn Val Ala Asn Met Val Pro Pro
  180                               185                               190
Tyr Asp Gln Ala Lys Tyr Ala Gly Thr Gly Ser Ala Ile Glu Tyr Ala
  195                               200                               205
Val Leu His Leu Lys Val Ser Asn Ile Val Val Ile Gly His Ser Ala
  210                               215                               220
Cys Gly Gly Ile Lys Gly Leu Leu Ser Phe Pro Phe Asp Gly Ala Tyr
  225                               230                               235                               240
Ser Thr Asp Phe Ile Glu Glu Trp Val Lys Ile Gly Leu Pro Ala Lys
  245                               250                               255
Ala Lys Val Lys Ala Lys His Gly Asp Ala Pro Phe Gly Glu Leu Cys
  260                               265                               270
Thr His Cys Glu Lys Glu Ala Val Asn Val Ser Leu Gly Asn Leu Leu
  275                               280                               285
Thr Tyr Pro Phe Val Arg Glu Gly Leu Val Asn Lys Thr Leu Ala Leu
  290                               295                               300
Lys Gly Gly Tyr Tyr Asp Phe Val Lys Gly Ser Phe Glu Leu Trp Gly
  305                               310                               315                               320
Leu Glu Phe Gly Leu Ser Ser Thr Phe Ser Val
  325                               330

```

<210> 150

<211> 471

<212> DNA

<213> Medicago truncatula

<400> 150

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atggtatttg cttgctctga ctctagagtg agtccctcta ttatcctgaa ctttcaacat      60
ggagaagctt tcatgggtccg aaacattgct aacatgggtcc ctacatttaa tcaggtggag      120
aacatcttgg ttattggaca tagtcgctgc ggtggaatct caaggcttat gccttcaga      180
ggatggctgc tccataatga ttgggtgaaa attggtttat ctttcaaagt caaggttctg      240
aaagaacatg aatgctgtga tttcaaagaa caatgcaaat tttgtgaaat ggaatcagtg      300
aataattcat tagtgaaacct gaagacatat ctatatgttg atagagaagt aaggaacaag      360
aacttagcac tattgggagg ttactatgat tttgtgaatg gagaattcaa gctctggaag      420
tataagaccc atgtcactaa acccattaca atcccctcta aaagaccttg a      471

```

<210> 151

<211> 156

<212> PRT

<213> Medicago truncatula

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<400> 151

```

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

```

<210> 152

<211> 828

<212> DNA

<213> Arabidopsis thaliana

<400> 152

```

atggtgaact actcatcaat cagttgcatc ttctttgtgg ctctgttttag tattttcaca      60
attgttttcga tttcagatgc tgcttcaagt cacggagaag ttgaggacga acgcgagttt    120
aactacaaga agaacgatga gaaggggcca gagagatggg gagaacttaa accggaatgg    180
gaaatgtgtg gaaaaggaga gatgcaatct cccatagatc ttatgaacga gagagttaac    240
attgtttctc atcttgggaag gcttaataga gactataatc cttcaaatgc aactcttaag    300
aacagaggcc atgacatcat gttaaaattt gaagatggag caggaactat taagatcaat    360
ggttttgaat atgaacttca acagcttcac tggcactctc cgtctgaaca tactattaat    420
ggaagaaggt ttgcacttga gctgcatatg gttcacgaag gcaggaatag aagaatggct    480
gttgtgactg tgttgtacaa gatcggaaga gcagatactt ttatcagatc gttggagaaa    540
gaattagagg gcattgctga aatggaggag gctgagaaaa atgtaggaat gattgatccc    600
acaaaaatta agatcggaag cagaaaatat tacagataca ctggttcact taccactcct    660
ccttgcactc aaaacgttac ttggagcgtc gttagaaagg ttaggaccgt gacaagaaaa    720
caagtgaagc tcctccgctg ggcagtgcac gatgatgcta attcgaatgc gaggccggtt    780
caaccaacca acaagcgcat agtgcactta tacagaccaa tagtttaa      828

```

<210> 153

<211> 275

<212> PRT

<213> Arabidopsis thaliana

<400> 153

```

Met Val Asn Tyr Ser Ser Ile Ser Cys Ile Phe Phe Val Ala Leu Phe
1          5          10          15
Ser Ile Phe Thr Ile Val Ser Ile Ser Ser Ala Ala Ser Ser His Gly
20          25          30
Glu Val Glu Asp Glu Arg Glu Phe Asn Tyr Lys Lys Asn Asp Glu Lys
35          40          45
Gly Pro Glu Arg Trp Gly Glu Leu Lys Pro Glu Trp Glu Met Cys Gly
50          55          60
Lys Gly Glu Met Gln Ser Pro Ile Asp Leu Met Asn Glu Arg Val Asn
65          70          75          80

```

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

<210> 154
<211> 987
<212> DNA
<213> *Flaveria pringlei*

<400> 154
atgtatgcta cagctgccgc atttgcaccc tccttcacca cctcccgccg caaaccgtea 60
tcgtcgtcct ccaccgtatc cacttgcttt gcaaggctta gcaacagcgc tcagtcgtcg 120
tcgtcgtctg ccactccacc acccagcctc atccgtaatc agcccgtttt tgccgccccg 180
actcccatca tcaccccccac tgtgagagga gacatgggaa gtgaatcata tgatgaggca 240
attgctgcac tcaagaagct tttaagtga aaggaggagt tggcacctgt ggctgctgcc 300
aaaatcgacg aaatcacggc ccaacttcaa actctcgaca ccaaacctgc atttgacgcg 360
gtcgagagga tcaaaaccgg gtttgccaag ttcaagaccg agaaatacct gacaaatcca 420
gctttgtacg atgaactttc caaaggccag agcccaaat ttatggtttt tgcattgctc 480
gactctcgag tttgcccgtc acacgtgctg gatttccaac ccggtgaggc gtttgtggtc 540
cgtaacgtag ccaacattgt ccccccttt gataagctta aatacgctgg agtaggatcc 600
gcagtcgagt atgcagttct gcatctcaag gtggagcaga tagtcgtaat tgggcatagt 660
aaatgtggtg ggatcaaggg tctgatgact ttccccgatg agggaccgac cagcaccgac 720
ttcattgagg actgggtcag agttggtctc cctgcaaagt caaaggtgaa agcggagcat 780
ggaagtgcac cacttgatga tcaatgtgta tcctgcgaga aggaggcggg gaatgtgtct 840
cttgcaaacc tgttgactta cccgtttgtg agaaacgat tgatgaacaa aacattggcg 900
ctcaagggtg cacactatga ctttgttaac ggggcctttg agttgtgggg gcttgatttc 960
agcctttcgc ctccctacctc ggcataa 987

<210> 155
<211> 328
<212> PRT
<213> *Flaveria pringlei*

<400> 155
Met Tyr Ala Thr Ala Ala Ala Phe Ala Pro Ser Phe Thr Thr Ser Arg
1 5 10 15

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Arg Lys Pro Ser Ser Ser Ser Ser Thr Val Ser Thr Cys Phe Ala Arg
 20 25 30
 Leu Ser Asn Ser Ala Gln Ser Ser Ser Ser Ala Thr Pro Pro Pro
 35 40 45
 Ser Leu Ile Arg Asn Gln Pro Val Phe Ala Ala Pro Thr Pro Ile Ile
 50 55 60
 Thr Pro Thr Val Arg Gly Asp Met Gly Ser Glu Ser Tyr Asp Glu Ala
 65 70 75 80
 Ile Ala Ala Leu Lys Lys Leu Leu Ser Glu Lys Glu Glu Leu Ala Pro
 85 90 95
 Val Ala Ala Ala Lys Ile Asp Glu Ile Thr Ala Gln Leu Gln Thr Leu
 100 105 110
 Asp Thr Lys Pro Ala Phe Asp Ala Val Glu Arg Ile Lys Thr Gly Phe
 115 120 125
 Ala Lys Phe Lys Thr Glu Lys Tyr Leu Thr Asn Pro Ala Leu Tyr Asp
 130 135 140
 Glu Leu Ser Lys Gly Gln Ser Pro Lys Phe Met Val Phe Ala Cys Ser
 145 150 155 160
 Asp Ser Arg Val Cys Pro Ser His Val Leu Asp Phe Gln Pro Gly Glu
 165 170 175
 Ala Phe Val Val Arg Asn Val Ala Asn Ile Val Pro Pro Phe Asp Lys
 180 185 190
 Leu Lys Tyr Ala Gly Val Gly Ser Ala Val Glu Tyr Ala Val Leu His
 195 200 205
 Leu Lys Val Glu Gln Ile Val Val Ile Gly His Ser Lys Cys Gly Gly
 210 215 220
 Ile Lys Gly Leu Met Thr Phe Pro Asp Glu Gly Pro Thr Ser Thr Asp
 225 230 235 240
 Phe Ile Glu Asp Trp Val Arg Val Gly Leu Pro Ala Lys Ser Lys Val
 245 250 255
 Lys Ala Glu His Gly Ser Ala Ser Leu Asp Asp Gln Cys Val Ser Cys
 260 265 270
 Glu Lys Glu Ala Val Asn Val Ser Leu Ala Asn Leu Leu Thr Tyr Pro
 275 280 285
 Phe Val Arg Asn Gly Leu Met Asn Lys Thr Leu Ala Leu Lys Gly Ala
 290 295 300
 His Tyr Asp Phe Val Asn Gly Ala Phe Glu Leu Trp Gly Leu Asp Phe
 305 310 315 320
 Ser Leu Ser Pro Pro Thr Ser Ala
 325

<210> 156

<211> 996

<212> DNA

<213> *Flaveria linearis*

<400> 156

atgtatgcca cagctgccgc attaatgca ccctccttca ccacctctct ccgcaaaccg 60
 tcatcgctcgt cttccaccgt atccgctccc ttcgcaaggc taattaccaa caactcgctg 120
 gcgtcgctcgt cgttgtctgc cactccacca ccgagcctca tccgtaacca gcccgttttt 180
 gccgccccga ctcccatcat cccccccact gtgagaggag acatgggaag tgaatcatat 240
 gacgaggcaa ttgctgcact gaagaagctt ttaagtgaag gggaggattt ggcacctgtg 300
 gctgctgcaa aaatcgacga aatcacctcc caacttcaaa cgctcgacac caaaccgcga 360
 tttgacgcgg tcgagaggat caaaaccggc tttgccaagt tcaagaccga gaaatacttg 420
 acaaatccag ctttgtacga tgaactttcc aaaggccaga gcccaaaatt tatgggtttt 480
 gcatgctctg actctcgagt ttgcccgtca cactgtctcg atttccaacc tgggtgaggcg 540
 tttgtggtcc gtaacgtagc caacattgtc cccccctttg ataagcttaa atatgctgga 600
 gtaggatccg ctgtcgagta tgcagttttg catctcaagg tggagcagat agttgtaatt 660
 gggcatagta aatgtggtgg gatcaagggt ctgatgactt tcccggacga aggaccgaca 720

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```

agcaccgact tcattgagga ctgggtcaga gttggtctcc ctgcaaagtc aaaggtgaaa 780
gcggagcatg gaagtgcata aattgatgat caatgtgtat cctgcgagaa ggaggcgggtg 840
aatgtgtctc ttgcaaacct gttgacttac ccgtttgtga gaaacggatt gataaacaac 900
acattggcgc tcaaggggtgc acactatgac tttgttaacg ggacctttga gttgtggggg 960
cttgatttct gcctttcgcc tcctacctcg gcataa 996

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<210> 157
 <211> 331
 <212> PRT
 <213> *Flaveria linearis*

<400> 157

Met	Tyr	Ala	Thr	Ala	Ala	Ala	Leu	Ile	Ala	Pro	Ser	Phe	Thr	Thr	Ser
1			5						10					15	
Leu	Arg	Lys	Pro	Ser	Ser	Ser	Ser	Ser	Thr	Val	Ser	Ala	Pro	Phe	Ala
			20					25					30		
Arg	Leu	Ile	Thr	Asn	Asn	Ser	Leu	Ala	Ser	Ser	Ser	Leu	Ser	Ala	Thr
		35					40					45			
Pro	Pro	Pro	Ser	Leu	Ile	Arg	Asn	Gln	Pro	Val	Phe	Ala	Ala	Pro	Thr
	50					55					60				
Pro	Ile	Ile	Thr	Pro	Thr	Val	Arg	Gly	Asp	Met	Gly	Ser	Glu	Ser	Tyr
65					70					75					80
Asp	Glu	Ala	Ile	Ala	Ala	Leu	Lys	Lys	Leu	Leu	Ser	Glu	Arg	Glu	Asp
				85					90					95	
Leu	Ala	Pro	Val	Ala	Ala	Ala	Lys	Ile	Asp	Glu	Ile	Thr	Ser	Gln	Leu
			100					105					110		
Gln	Thr	Leu	Asp	Thr	Lys	Pro	Ala	Phe	Asp	Ala	Val	Glu	Arg	Ile	Lys
	115						120					125			
Thr	Gly	Phe	Ala	Lys	Phe	Lys	Thr	Glu	Lys	Tyr	Leu	Thr	Asn	Pro	Ala
	130						135				140				
Leu	Tyr	Asp	Glu	Leu	Ser	Lys	Gly	Gln	Ser	Pro	Lys	Phe	Met	Val	Phe
145					150					155					160
Ala	Cys	Ser	Asp	Ser	Arg	Val	Cys	Pro	Ser	His	Val	Leu	Asp	Phe	Gln
				165					170					175	
Pro	Gly	Glu	Ala	Phe	Val	Val	Arg	Asn	Val	Ala	Asn	Ile	Val	Pro	Pro
			180					185					190		
Phe	Asp	Lys	Leu	Lys	Tyr	Ala	Gly	Val	Gly	Ser	Ala	Val	Glu	Tyr	Ala
	195						200					205			
Val	Leu	His	Leu	Lys	Val	Glu	Gln	Ile	Val	Val	Ile	Gly	His	Ser	Lys
	210					215					220				
Cys	Gly	Gly	Ile	Lys	Gly	Leu	Met	Thr	Phe	Pro	Asp	Glu	Gly	Pro	Thr
225					230					235					240
Ser	Thr	Asp	Phe	Ile	Glu	Asp	Trp	Val	Arg	Val	Gly	Leu	Pro	Ala	Lys
			245						250					255	
Ser	Lys	Val	Lys	Ala	Glu	His	Gly	Ser	Ala	Ser	Ile	Asp	Asp	Gln	Cys
			260					265					270		
Val	Ser	Cys	Glu	Lys	Glu	Ala	Val	Asn	Val	Ser	Leu	Ala	Asn	Leu	Leu
			275				280					285			
Thr	Tyr	Pro	Phe	Val	Arg	Asn	Gly	Leu	Ile	Asn	Lys	Thr	Leu	Ala	Leu
	290					295					300				
Lys	Gly	Ala	His	Tyr	Asp	Phe	Val	Asn	Gly	Thr	Phe	Glu	Leu	Trp	Gly
305					310					315					320
Leu	Asp	Phe	Cys	Leu	Ser	Pro	Pro	Thr	Ser	Ala					
			325						330						

<210> 158
 <211> 828
 <212> DNA
 <213> *Arabidopsis thaliana*

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```
<400> 158
atgggaaccc taggcagagc attttactcg gtcggttttt ggatccgtga gactgggtcaa 60
gctcttgatc gcctcgggtg tcgccttcaa ggcaaaaatt acttccgaga acaactgtca 120
aggcacgga cactgatgaa tgtatttgat aaggctccga ttgtggacaa ggaagctttt 180
gtggcaccaa gcgcctcagt tattggggac gttcacattg gaagaggatc gtccatttgg 240
tatggatgcg tattacgagg cgatgtgaac accgtaagtg ttgggtcagg aactaatatt 300
caggacaact cacttgtgca tgtggcaaaa tcaaacttaa gcgggaaggt gcacccaacc 360
ataattggag acaatgtaac cattgggtcat agtgctgttt tacatggatg tactgttgag 420
gatgagacct ttattgggat ggggtgcgaca cttcttgatg gggtcgttgt tgaaaagcat 480
gggatgggtg ctgctgggtc acttgtagca caaaacacca gaattccttc tggagaggta 540
tggggaggaa acccagcaag gttcctcagg aagctcactg atgaggaaat tgcttttatc 600
tctcagtcag caacaaacta ctcaaacctc gcacaggctc acgctgcaga gaatgcaaag 660
ccattaaatg tgattgagtt cgagaagggt ctacgcaaga agcatgctct aaaggacgag 720
gagtatgact caatgctcgg aatagtgaga gaaactccac cagagcttaa cctccctaac 780
aacatactgc ctgataaaga aaccaagcgt ctttctaata tgaactga 828
```

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<210> 159
<211> 275
<212> PRT
<213> Arabidopsis thaliana
```

```
<400> 159
Met Gly Thr Leu Gly Arg Ala Phe Tyr Ser Val Gly Phe Trp Ile Arg
1 5 10 15
Glu Thr Gly Gln Ala Leu Asp Arg Leu Gly Cys Arg Leu Gln Gly Lys
20 25 30
Asn Tyr Phe Arg Glu Gln Leu Ser Arg His Arg Thr Leu Met Asn Val
35 40 45
Phe Asp Lys Ala Pro Ile Val Asp Lys Asp Ala Phe Val Ala Pro Ser
50 55 60
Ala Ser Val Ile Gly Asp Val His Ile Gly Arg Gly Ser Ser Ile Trp
65 70 75 80
Tyr Gly Cys Val Leu Arg Gly Asp Val Asn Thr Val Ser Val Gly Ser
85 90 95
Gly Thr Asn Ile Gln Asp Asn Ser Leu Val His Val Ala Lys Ser Asn
100 105 110
Leu Ser Gly Lys Val His Pro Thr Ile Ile Gly Asp Asn Val Thr Ile
115 120 125
Gly His Ser Ala Val Leu His Gly Cys Thr Val Glu Asp Glu Thr Phe
130 135 140
Ile Gly Met Gly Ala Thr Leu Leu Asp Gly Val Val Val Glu Lys His
145 150 155 160
Gly Met Val Ala Ala Gly Ala Leu Val Arg Gln Asn Thr Arg Ile Pro
165 170 175
Ser Gly Glu Val Trp Gly Gly Asn Pro Ala Arg Phe Leu Arg Lys Leu
180 185 190
Thr Asp Glu Glu Ile Ala Phe Ile Ser Gln Ser Ala Thr Asn Tyr Ser
195 200 205
Asn Leu Ala Gln Ala His Ala Ala Glu Asn Ala Lys Pro Leu Asn Val
210 215 220
Ile Glu Phe Glu Lys Val Leu Arg Lys Lys His Ala Leu Lys Asp Glu
225 230 235 240
Glu Tyr Asp Ser Met Leu Gly Ile Val Arg Glu Thr Pro Pro Glu Leu
245 250 255
Asn Leu Pro Asn Asn Ile Leu Pro Asp Lys Glu Thr Lys Arg Pro Ser
260 265 270
Asn Leu Asn
275
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<210> 160
 <211> 874
 <212> DNA
 <213> *Gossypium hirsutum*

<400> 160
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 gctctcgatc gcctaggctg ccgcctacaa ggcaactatt ttttccagga gcaactttct 180
 aggcatcgga ctctgatgaa cgtatttgat aaatctcctc tgggtggacaa ggatgcattt 240
 gtagccccta gcgcatctgt cattggcgat gttaggtgga gaagaggatc atctatttgg 300
 tatggatgtg ttttaagggg ggatgtcaac agcattagtg ttggatctgg aactaatata 360
 caagacaact cccttggtgca tgttgcaaag tctaatactaa gtgggaaagt gctaccaact 420
 aacattggaa acaatgttac tgtaggtcat agtgctgttt tacatggctg taccgttgag 480
 gatgaagcat ttgttggtcat gggagccaca cttcttgatg gtgtagttgt ggaaaaacat 540
 gctatggttg ctgctggagc ccttgtaaga cagaatacaa ggatccctgc tggagagggtg 600
 tggggaggga atcctgctaa attcctgagg aagctaactg aagaagagat agcgtttatt 660
 tcccagtcag ccaccaatta taccaacctt gcacaggtag atgctgctga gaatgcaaaa 720
 ccctttgatg aaattgaatt tgagaaaatt cttcgcaaga agtttgcgaa gagggatgaa 780
 gagtatgact caatgctggg tgttgctcgt gaaactccac cagaactaat tcttcagac 840
 aatgtcctac cagataaaga gcaaaagtcc tctc 874

<210> 161
 <211> 273
 <212> PRT
 <213> *Gossypium hirsutum*

<400> 161
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 20 25 30
 Tyr Phe Phe Gln Glu Gln Leu Ser Arg His Arg Thr Leu Met Asn Val
 35 40 45
 Phe Asp Lys Ser Pro Leu Val Asp Lys Asp Ala Phe Val Ala Pro Ser
 50 55 60
 Ala Ser Val Ile Gly Asp Val Gln Val Gly Arg Gly Ser Ser Ile Trp
 65 70 75 80
 Tyr Gly Cys Val Leu Arg Gly Asp Val Asn Ser Ile Ser Val Gly Ser
 85 90 95
 Gly Thr Asn Ile Gln Asp Asn Ser Leu Val His Val Ala Lys Ser Asn
 100 105 110
 Leu Ser Gly Lys Val Leu Pro Thr Asn Ile Gly Asn Asn Val Thr Val
 115 120 125
 Gly His Ser Ala Val Leu His Gly Cys Thr Val Glu Asp Glu Ala Phe
 130 135 140
 Val Gly Met Gly Ala Thr Leu Leu Asp Gly Val Val Val Glu Lys His
 145 150 155 160
 Ala Met Val Ala Ala Gly Ala Leu Val Arg Gln Asn Thr Arg Ile Pro
 165 170 175
 Ala Gly Glu Val Trp Gly Gly Asn Pro Ala Lys Phe Leu Arg Lys Leu
 180 185 190
 Thr Glu Glu Glu Ile Ala Phe Ile Ser Gln Ser Ala Thr Asn Tyr Thr
 195 200 205
 Asn Leu Ala Gln Val His Ala Ala Glu Asn Ala Lys Pro Phe Asp Glu
 210 215 220
 Ile Glu Phe Glu Lys Val Leu Arg Lys Lys Phe Ala Lys Arg Asp Glu
 225 230 235 240

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Glu Tyr Asp Ser Met Leu Gly Val Val Arg Glu Thr Pro Pro Glu Leu
 245 250 255
 Ile Leu Pro Asp Asn Val Leu Pro Asp Lys Glu Gln Lys Ser Ser Gln
 260 265 270
 Lys

<210> 162
 <211> 1217
 <212> DNA
 <213> Lycopersicon esculentum

<400> 162
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 agggctaaac cgaaagaaga agaaggagga ggtcaaacat gggaaccctc gggaaagcaa 180
 tttactccct gggatccatc gttcgagcga ccggcaaagc tcttgatcgc gtcggaaatc 240
 gcctacaagg cagctccac atagaggaac acctgtccag gcatcgact cttatgaacg 300
 tattcgataa agctccggtg gtggataagg atgtatttgt agctccaggt gcctcagtca 360
 ttggagatgt ccatgtggga cgcaattcat ctatttggta tggatgtgta ctaagaggtg 420
 atgttaacag catcagtgtc ggatctggta ccaatataca ggacaactcc cttgttcatg 480
 tggccaaatc aatatataagt caaaaggtgc tgcccaccat catagggaac aatgttactg 540
 ttggtcatag tgctgttgta catggctgca ccattgagga tgaggccttc attggtatgg 600
 gggccacact gcttgatggt gttcatgtag agaaacatgc catgggtgct gcaggagccc 660
 ttgtgaaaca gaacacaagg attccctccg gagaggtatg ggcaggcaat cccgctaagt 720
 ttctgaggaa gctaactgat gaagagatag ccttcattgc tcagtcagca accaactact 780
 gtaaccttgc tcgtgtccat gcagctgaga actccaagtc ctttgacgaa attgaatttg 840
 aaaagatgct tcgtaagaag tatgccaaac gtgatgagga atatgattct atgattggtg 900
 ttgtccgtga aacacctccc gagcttgtac ttcctgataa tctcctcccc gaaaaagctg 960
 ctaagagcat cgcccaatga gatcagtgcc caagcaactc tctctttttt tgctttccag 1020
 agattttatt tacaccgtga gcatctgtat ggagaacagt catggatatt ggctgttacc 1080
 cttccaaata atatcaaact tattggatag catcggtacg tctactgcttt gtagttaaga 1140
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 aaaaaaaaaa aaaaaaa 1217

<210> 163
 <211> 273
 <212> PRT
 <213> Lycopersicon esculentum

<400> 163
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 20 25 30
 Ser His Ile Glu Glu His Leu Ser Arg His Arg Thr Leu Met Asn Val
 35 40 45
 Phe Asp Lys Ala Pro Val Val Asp Lys Asp Val Phe Val Ala Pro Gly
 50 55 60
 Ala Ser Val Ile Gly Asp Val His Val Gly Arg Asn Ser Ser Ile Trp
 65 70 75 80
 Tyr Gly Cys Val Leu Arg Gly Asp Val Asn Ser Ile Ser Val Gly Ser
 85 90 95
 Gly Thr Asn Ile Gln Asp Asn Ser Leu Val His Val Ala Lys Ser Asn
 100 105 110
 Ile Ser Gln Lys Val Leu Pro Thr Ile Ile Gly Asn Asn Val Thr Val
 115 120 125
 Gly His Ser Ala Val Val His Gly Cys Thr Ile Glu Asp Glu Ala Phe
 130 135 140

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Ile Gly Met Gly Ala Thr Leu Leu Asp Gly Val His Val Glu Lys His
 145 150 155 160
 Ala Met Val Ala Ala Gly Ala Leu Val Lys Gln Asn Thr Arg Ile Pro
 165 170 175
 Ser Gly Glu Val Trp Ala Gly Asn Pro Ala Lys Phe Leu Arg Lys Leu
 180 185 190
 Thr Asp Glu Glu Ile Ala Phe Ile Ala Gln Ser Ala Thr Asn Tyr Cys
 195 200 205
 Asn Leu Ala Arg Val His Ala Ala Glu Asn Ser Lys Ser Phe Asp Glu
 210 215 220
 Ile Glu Phe Glu Lys Met Leu Arg Lys Lys Tyr Ala Lys Arg Asp Glu
 225 230 235 240
 Glu Tyr Asp Ser Met Ile Gly Val Val Arg Glu Thr Pro Pro Glu Leu
 245 250 255
 Val Leu Pro Asp Asn Ile Leu Pro Glu Lys Ala Ala Lys Ser Ile Ala
 260 265 270
 Gln

<210> 164
 <211> 1962
 <212> DNA
 <213> Zea mays

<400> 164
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 cgccgccccg ccaccgtcgt gggcatggac ccaccgtcg agcgcttgaa gagcgggttc 180
 cagaagttca agaccgaggt ctatgacaag aagccggagc tgttcgagcc tctcaagtcc 240
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 ccctacgaca agatcaagta cgccggcaca ggggtccgca tcgagtacgc cgtgtgcgcg 420
 ctcaagggtgc aggtcatcgt ggtcattggc cacagctgct gcggtggcat cagggcgctc 480
 ctctccctca aggacggcgc gcccgacaac ttcaccttcg tggaggactg ggtcaggatc 540
 ggcagccctg ccaagaacaa ggtgaagaaa gagcacgcgt ccgtgccgtt cgatgaccag 600
 tgctccatcc tggagaagga ggccgtgaac gtgtcgctcc agaacctcaa gagctacccc 660
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 gtcaaagggc agttcgtcac atgggagcct cccagggacg ccatcgagcg cttgacgagc 780
 ggcttccagc agttcaaggt caatgtctat gacaagaagc cggagctttt cgggcctctc 840
 aagtccggcc agggcccca gtacatggtg ttgcctgct ccgactcccg tgtgtgcccg 900
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 gaccagtgt ccatcctgga gaaggaggcc gtgaacgtgt cgctccagaa cctcaagagc 1260
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 ctcaagtccg gccaggcccc caagtacatg gtgttcgcct gctccgactc ccgtgtgtcc 1500
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 gatgaccagt ggtccattct cgagaaggag gccgtgaacg tgtccctgga gaacctcaag 1860
 acctacccct tcgtcaagga agggcttgca aatgggaccc tcaagctgat cggcgcccac 1920
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<210> 165
 <211> 653
 <212> PRT
 <213> Zea mays

<400> 165

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			20					25					30		
Gly	Ser	Ser	Gly	Thr	Pro	Arg	Leu	Arg	Arg	Pro	Ala	Thr	Val	Val	Gly
			35				40					45			
Met	Asp	Pro	Thr	Val	Glu	Arg	Leu	Lys	Ser	Gly	Phe	Gln	Lys	Phe	Lys
	50					55					60				
Thr	Glu	Val	Tyr	Asp	Lys	Lys	Pro	Glu	Leu	Phe	Glu	Pro	Leu	Lys	Ser
65					70					75					80
Gly	Gln	Ser	Pro	Arg	Tyr	Met	Val	Phe	Ala	Cys	Ser	Asp	Ser	Arg	Val
				85					90					95	
Cys	Pro	Ser	Val	Thr	Leu	Gly	Leu	Gln	Pro	Gly	Glu	Ala	Phe	Thr	Val
			100					105					110		
Arg	Asn	Ile	Ala	Ser	Met	Val	Pro	Pro	Tyr	Asp	Lys	Ile	Lys	Tyr	Ala
	115						120					125			
Gly	Thr	Gly	Ser	Ala	Ile	Glu	Tyr	Ala	Val	Cys	Ala	Leu	Lys	Val	Gln
	130					135					140				
Val	Ile	Val	Val	Ile	Gly	His	Ser	Cys	Cys	Gly	Gly	Ile	Arg	Ala	Leu
145					150					155					160
Leu	Ser	Leu	Lys	Asp	Gly	Ala	Pro	Asp	Asn	Phe	Thr	Phe	Val	Glu	Asp
				165					170					175	
Trp	Val	Arg	Ile	Gly	Ser	Pro	Ala	Lys	Asn	Lys	Val	Lys	Lys	Glu	His
			180					185						190	
Ala	Ser	Val	Pro	Phe	Asp	Asp	Gln	Cys	Ser	Ile	Leu	Glu	Lys	Glu	Ala
			195				200					205			
Val	Asn	Val	Ser	Leu	Gln	Asn	Leu	Lys	Ser	Tyr	Pro	Phe	Val	Lys	Glu
	210					215					220				
Gly	Leu	Ala	Gly	Gly	Thr	Leu	Lys	Leu	Val	Gly	Ala	His	Tyr	Ser	Phe
225					230					235					240
Val	Lys	Gly	Gln	Phe	Val	Thr	Trp	Glu	Pro	Pro	Gln	Asp	Ala	Ile	Glu
				245					250					255	
Arg	Leu	Thr	Ser	Gly	Phe	Gln	Gln	Phe	Lys	Val	Asn	Val	Tyr	Asp	Lys
			260					265					270		
Lys	Pro	Glu	Leu	Phe	Gly	Pro	Leu	Lys	Ser	Gly	Gln	Ala	Pro	Lys	Tyr
		275					280					285			
Met	Val	Phe	Ala	Cys	Ser	Asp	Ser	Arg	Val	Cys	Pro	Ser	Val	Thr	Leu
	290					295					300				
Gly	Leu	Gln	Pro	Ala	Lys	Ala	Phe	Thr	Val	Arg	Asn	Ile	Ala	Ala	Met
305					310					315					320
Val	Pro	Gly	Tyr	Asp	Lys	Thr	Lys	Tyr	Thr	Gly	Ile	Gly	Ser	Ala	Ile
				325					330					335	
Glu	Tyr	Ala	Val	Cys	Ala	Leu	Lys	Val	Glu	Val	Leu	Val	Val	Ile	Gly
			340					345					350		
His	Ser	Cys	Cys	Gly	Gly	Ile	Arg	Ala	Leu	Leu	Ser	Leu	Lys	Asp	Gly
		355					360					365			
Ala	Pro	Asp	Asn	Phe	His	Phe	Val	Glu	Asp	Trp	Val	Arg	Ile	Gly	Ser
		370				375					380				
Pro	Ala	Lys	Asn	Lys	Val	Lys	Lys	Glu	His	Ala	Ser	Val	Pro	Phe	Asp
385					390					395					400
Asp	Gln	Cys	Ser	Ile	Leu	Glu	Lys	Glu	Ala	Val	Asn	Val	Ser	Leu	Gln
				405					410					415	
Asn	Leu	Lys	Ser	Tyr	Pro	Leu	Val	Lys	Glu	Gly	Leu	Ala	Gly	Gly	Thr

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420				425				430							
Ser	Ser	Gly	Trp	Pro	His	Tyr	Asp	Phe	Val	Lys	Gly	Gln	Phe	Val	Thr
435				440				445							
Trp	Glu	Pro	Pro	Gln	Asp	Ala	Ile	Glu	Arg	Leu	Thr	Ser	Gly	Phe	Gln
450				455				460							
Gln	Phe	Lys	Val	Asn	Val	Tyr	Asp	Lys	Lys	Pro	Glu	Leu	Phe	Gly	Pro
465					470					475					480
Leu	Lys	Ser	Gly	Gln	Ala	Pro	Lys	Tyr	Met	Val	Phe	Ala	Cys	Ser	Asp
485				490				495							
Ser	Arg	Val	Ser	Pro	Ser	Val	Thr	Leu	Gly	Leu	Gln	Pro	Gly	Glu	Ala
500				505				510							
Phe	Thr	Val	Arg	Asn	Ile	Ala	Ala	Met	Val	Pro	Gly	Tyr	Asp	Lys	Thr
515				520				525							
Lys	Tyr	Thr	Gly	Ile	Gly	Ser	Ala	Ile	Glu	Tyr	Ala	Val	Cys	Ala	Leu
530				535				540							
Lys	Val	Glu	Val	Leu	Val	Val	Ile	Gly	His	Ser	Cys	Cys	Gly	Gly	Ile
545					550					555					560
Arg	Ala	Leu	Leu	Ser	Leu	Gln	Asp	Gly	Ala	Pro	Asp	Thr	Phe	His	Phe
565				570				575							
Val	Glu	Asp	Trp	Val	Lys	Ile	Ala	Phe	Ile	Ala	Lys	Met	Lys	Val	Lys
580				585				590							
Lys	Glu	His	Ala	Ser	Val	Pro	Phe	Asp	Asp	Gln	Trp	Ser	Ile	Leu	Glu
595				600				605							
Lys	Glu	Ala	Val	Asn	Val	Ser	Leu	Glu	Asn	Leu	Lys	Thr	Tyr	Pro	Phe
610				615				620							
Val	Lys	Glu	Gly	Leu	Ala	Asn	Gly	Thr	Leu	Lys	Leu	Ile	Gly	Ala	His
625					630					635					640
Tyr	Asp	Phe	Val	Ser	Gly	Glu	Phe	Leu	Thr	Trp	Lys	Lys			
645				650											

<210> 166
 <211> 1920
 <212> DNA
 <213> Zea mays

<400> 166

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gtcttcgcgc	ccccgccac	cgtctgtaaa	cgggacggcg	ggcagctgag	gagtcaaacg	180
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actccttcag	aaccagaagc	cctccaacct	ccacctctc	cctccaaggc	ttcctccaag	420
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aatgtctatg	acaagaagcc	ggagcttttc	gggcctctca	agtcgggcca	ggccccaaag	1140
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ccgggcgagg	ccttcaccgt	tcgcaacatc	gccgccatgg	tcccaggcta	cgacaagacc	1260
aagtagaccg	gcatcggttc	cgccatcgag	tacgtgtgt	gcgccctcaa	ggtaggagtc	1320
ctcgtggtca	ttggccatag	ctgctgcggt	ggcatcaggg	cgctcctctc	actccaggac	1380

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ggcgcagcct acaccttcca cttcgctcgag gactgggtta agatcggctt cattgccaaag 1440
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<210> 167
 <211> 545
 <212> PRT
 <213> Zea mays

<400> 167

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Leu	Ala	Thr	Pro	Ala	Pro	Ser	Ser	Ser	Ser	Gly	Ser	Gly	Arg	Pro	Arg
			20					25					30		
Leu	Arg	Leu	Ile	Arg	Asn	Ala	Pro	Val	Phe	Ala	Ala	Pro	Ala	Thr	Val
		35				40						45			
Cys	Lys	Arg	Asp	Gly	Gly	Gln	Leu	Arg	Ser	Gln	Thr	Arg	Glu	Ile	Glu
	50					55				60					
Arg	Glu	Arg	Lys	Gly	Gly	His	Pro	Pro	Ala	Gly	Gly	His	Lys	Arg	Gly
65					70				75					80	
Gly	Glu	Arg	Gly	Gln	Arg	Arg	Gly	Gly	Glu	Glu	Glu	Glu	Asp	Glu	Gln
				85				90					95		
Leu	Pro	Leu	Pro	Ser	Glu	Lys	Lys	Gly	Gly	Ala	Ser	Glu	Gly	Glu	Ala
			100					105					110		
Val	His	Arg	Tyr	Pro	His	Leu	Val	Thr	Pro	Ser	Glu	Pro	Glu	Ala	Leu
		115				120						125			
Gln	Pro	Pro	Pro	Pro	Pro	Ser	Lys	Ala	Ser	Ser	Lys	Gly	Met	Asp	Pro
	130					135					140				
Thr	Val	Glu	Arg	Leu	Lys	Ser	Gly	Phe	Gln	Lys	Phe	Lys	Thr	Glu	Val
145					150				155					160	
Tyr	Asp	Lys	Lys	Pro	Glu	Leu	Phe	Glu	Pro	Leu	Lys	Ser	Gly	Gln	Ser
				165				170					175		
Pro	Arg	Tyr	Met	Val	Phe	Ala	Cys	Ser	Asp	Ser	Arg	Val	Cys	Pro	Ser
		180						185					190		
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		195				200						205			
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	210					215					220				
Ser	Ala	Ile	Glu	Tyr	Ala	Val	Cys	Ala	Leu	Lys	Val	Gln	Val	Ile	Val
225					230				235					240	
Val	Ile	Gly	His	Ser	Cys	Cys	Gly	Gly	Ile	Arg	Ala	Leu	Leu	Ser	Leu
				245				250					255		
Lys	Asp	Gly	Ala	Pro	Asp	Asn	Phe	Thr	Phe	Val	Glu	Asp	Trp	Val	Arg
		260						265				270			
Ile	Gly	Ser	Pro	Ala	Lys	Asn	Lys	Val	Lys	Lys	Glu	His	Ala	Ser	Val
	275					280						285			
Pro	Phe	Asp	Asp	Gln	Cys	Ser	Ile	Leu	Glu	Lys	Glu	Ala	Val	Asn	Val
	290					295					300				
Ser	Leu	Gln	Asn	Leu	Lys	Ser	Tyr	Pro	Phe	Val	Lys	Glu	Gly	Leu	Ala
305					310				315					320	
Gly	Gly	Thr	Leu	Lys	Leu	Val	Gly	Ala	His	Ser	His	Phe	Val	Lys	Gly
			325					330					335		
Gln	Phe	Val	Thr	Trp	Glu	Pro	Pro	Gln	Asp	Ala	Ile	Glu	Arg	Leu	Thr

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340 345 350
 Ser Gly Phe Gln Gln Phe Lys Val Asn Val Tyr Asp Lys Lys Pro Glu
 355 360 365
 Leu Phe Gly Pro Leu Lys Ser Gly Gln Ala Pro Lys Tyr Met Val Phe
 370 375 380
 Ala Cys Ser Asp Ser Arg Val Cys Pro Ser Val Thr Leu Gly Leu Gln
 385 390 395 400
 Pro Gly Glu Ala Phe Thr Val Arg Asn Ile Ala Ala Met Val Pro Gly
 405 410 415
 Tyr Asp Lys Thr Lys Tyr Thr Gly Ile Gly Ser Ala Ile Glu Tyr Ala
 420 425 430
 Val Cys Ala Leu Lys Val Glu Val Leu Val Val Ile Gly His Ser Cys
 435 440 445
 Cys Gly Gly Ile Arg Ala Leu Leu Ser Leu Gln Asp Gly Ala Ala Tyr
 450 455 460
 Thr Phe His Phe Val Glu Asp Trp Val Lys Ile Gly Phe Ile Ala Lys
 465 470 475 480
 Met Lys Val Lys Lys Glu His Ala Ser Val Pro Phe Asp Asp Gln Cys
 485 490 495
 Ser Ile Leu Glu Lys Glu Ala Val Asn Val Ser Leu Glu Asn Leu Lys
 500 505 510
 Thr Tyr Pro Phe Val Lys Glu Gly Leu Ala Asn Gly Thr Leu Lys Leu
 515 520 525
 Ile Gly Ala His Tyr Asp Phe Val Ser Gly Glu Phe Leu Thr Trp Lys
 530 535 540
 Lys
 545

<210> 168
 <211> 1208
 <212> DNA
 <213> Urochloa panicoides

<400> 168
 gggcagcccg cactttaatg tcggcattgg ccatccgtgc agccccgtcc agcatcatcg 60
 ccagcgctcg caccgccgct ctctccgccc gccgcgcccc caggctcgtc ggcaacgccg 120
 ccgccgcca cgcgcgtcgtg taaaccggcc gccgcacggg gagctcgaaa gtcaaacgag 180
 agactagaga gagggggcg agaagtacta gtaggtcgaa gccggctgtg ataaaaagag 240
 gagaagatga gcggtgcct ctgcctcccc ggctacaaaa agaagaccat ggaccccgctc 300
 gagcgcttgc agagcgggtt caagcagttc aagagcgagg tctacgacaa gaagccggag 360
 ctgttcgagc cactcaagga aggccaggcc cccacgtaca tgggtgttcgc ctgctccgac 420
 tcccgttgc gcccgtcgtt gaccctcggc ctgaagcccc gcgaggcctt caccgtccgc 480
 aacatcgccg ccatggtccc accctacgac aagaatcggt acaccggcat cgggtccgac 540
 atcgagtacg ccgtctgcgc cctcaaggct aaggtcctca ccgtcatcgg ccacagccgc 600
 tgcggtggca tcaaggcgt cctctcaatg caggacggcg cagccgacaa cttccacttc 660
 gtcgaggact gggtcaggat cggcttcttc gccagaaga aggttctcac cgaccacccc 720
 atggctccct tcgacgacca gtgctccatc ttggagaagg aggccgtcaa cgtctccctg 780
 tacaacctcc tgacctacc ctgggtgaag gaaggtgtgt ccaacggctc cctcaagctg 840
 gtcggcggcc actacgactt cgtcaagggc gcgttcgtca catgggagaa ataagccacc 900
 cgatttacaa ctctacacc atcatacata tatacatacg tacatcgtct cccgatatgc 960
 accccatccg acgtgaatgg gtggagtgt cactacctat tttcgccgc tacatacggg 1020
 atcgctcgtc ttctatgtga atgtaataag caatagcatc ctctaccgct ttaatttcta 1080
 taaggccgag ctttttattt taccatatga tgcataattt gaccgccttg tggtaaaaag 1140
 acatcaccaa tatatgtata agccttcttc ataataatat ataatcatca agtgtttacc 1200
 tttttatt 1208

<210> 169
 <211> 157
 <212> PRT

<213> Urochloa panicoides

<400> 169

```

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

```

<210> 170

<211> 1034

<212> DNA

<213> Urochloa panicoides

<400> 170

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ccgcactgga atgtcggcat tggccatccg ctcagccccg tccagcatca tcgccagcgt      60
ccgcaccccc ggcacccgcc gccccgggct cgtcaggaac gccgcgcgcca ccaccgccga      120
gttgaccatg gaccccgctg agcgccttgc gagcggcttc aagcagttca agagcgaggt      180
ctatgacaag aagccggagc tgctcgagcc actcaaggaa ggccaggccc ccacgtacat      240
ggtgttcgcc tgctccgact ctcgttgctg cccgtcggtg accctcggcc tgaagcccgg      300
cgaggccctt accgtccgca acatcgccgc catggtccca ccctacgaca agaaccggta      360
caccggcatc gggtcgcgca tcgagtagcg cgtctgcgcc ctcaaggtca aggtcctcac      420
cgtcacatcg cacagccgct gcggtggcat caaggcgctc ctctccatgc aggatggcgc      480
agccgacaac ttccacttcg tcgaggattg ggtcaggatc ggcttcctcg cgaagaagaa      540
ggttctgacc gaccaccca tggtccggtt cgatgaccag tgctccatct tggagaagga      600
ggcagtcaac gtctccctct acaacctctt gacctacccc tgggtgaagg aaggcgtgtc      660
caacgggtcc ctcaagctgg tcggcggcca ctacgacttc gtcaaggggg cgttcgtcac      720
atgggagaaa taagccaccc gatttacagc tcctacacca ccgtacatac atacgtacat      780
cccgatatgt accccatccg acgtgaacgg gtggagtact tactactacc tattttcggc      840
cgctacgtac cgggtcgtcg ttctatgtga atgtaataag caatagcatt ctctaccgct      900
ttaatttcta aggccgagct ttttatatat gtaccgtatg atgcataatt tgacctcctt      960
gtgggtcaaaa gacatcagct atatatgtat aagtcttctt cataatataa tcataaagtg     1020
tttacctttt tact                                     1034

```

<210> 171

<211> 240

<212> PRT

<213> Urochloa panicoides

<400> 171

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Met Ser Ala Leu Ala Ile Arg Ser Ala Pro Ser Ser Ile Ile Ala Ser
1      5      10      15
Val Arg Thr Pro Ala His Arg Arg Pro Gly Leu Val Arg Asn Ala Ala
      20      25      30

```

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

<210> 172

<211> 795

<212> DNA

<213> Chlamydomonas reinhardtii

<400> 172

atgggatgcg gtgccagcgt gcctcagaat ggtggaggag ctcccgttac gcgggttatg 60
cccgcgccag cacaaccagt gtctgaggcg caatcggcaa tcagcttcca accatcgcg 120
agcaaccgca gcagccttga aaagatcaat tcgctcacgg atagggcatc gcctgagcag 180
gtgctgcaga acctgctgga cggcaacatg cgcttcctgg atggcgccgt cgcgcatccc 240
caccaggact tcagccgcgt gcaggccatt aaggccaagc aaaagcccct cgcggccatc 300
ctgggctgcg ccgactctcg cgtgcctgcg gaaattgtgt tcgaccaagg ctttggcgac 360
gtgttcgtgt gccgtgtcgc cggcaacatt gctacgccag aggagatcgc cagtctggag 420
tatgccgtgc ttgacctcgg agttaagggtg gtgatgggtc tcggacacac acgctgcgga 480
gccgtgaagg ctgcactttc aggcaaggcg ttccccggct tcatcgacac gctggtggac 540
cacctggacg tcgccatcag ccgcgtcaac agcatgagcg ccaaggcgca ccaggccatc 600
aaggacggcg acgtggacat gctggaccgc gtggtgaagg agaacgtcaa gtaccagggtg 660
cagcgggtgcc agcgtctcgt catcatccag gaggggttgc agaaggggaa cctgctgctg 720
gcgggcgcgg tgtacgacct ggacacgggc aaggtgcacg tcagcgtcac caaggcgggc 780
agcagcgccg agtag 795

<210> 173

<211> 264

<212> PRT

<213> Chlamydomonas reinhardtii

<400> 173

Met Gly Cys Gly Ala Ser Val Pro Gln Asn Gly Gly Gly Ala Pro Val
1 5 10 15
Thr Arg Val Met Pro Ala Pro Ala Gln Pro Val Ser Glu Ala Gln Ser
20 25 30
Ala Ile Ser Phe Gln Pro Ser Arg Ser Asn Arg Ser Ser Leu Glu Lys

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

<210> 174
 <211> 939
 <212> DNA
 <213> Chlamydomonas reinhardtii

<400> 174	
atgtcgctat tcaagtctag cctgcctgcg ggcttcctat tcccctatcg gcaccccaag	60
gccaaaggggc ttgttgaggg cacgctttat ggactgggct ccctgtttcg cggcgtgggc	120
gccgcgctgg atgagctggg ctctatgggt cagggccctc agggtagtgt caaggaccac	180
gtccagccta acctggcggt tgcaccagtg caccgcaagc cggatgtgcc cgttaacgcg	240
ggccagggtgg tgcccgctcc acccgctgct gctcgcacgc tgaaaatcaa ggaggtgggt	300
gtgcccaaca agcacagcac cgcgttcgtg gctgccaacg ccaatgtgct cgggaacggt	360
aagctggggg cgggctcatc ggtgtggtat ggcgcgtgc tgcgcgtga cgtgaacggc	420
attgaggtgg gcgccaacag caacatccag gacaacgcca tcgtgcacgt gtccaagtac	480
agcatggaag gcacggcacg gcccaccgtc atcggaaca atgtgaccat tggccacgcc	540
gccacggtgc acgctgcac cattgaggac aactgcctgg tgggcatggg cgccaccgtg	600
ctcgacggag cgacgtcaa gagcggctcc atcgtggctg ccggcgccgt ggtgccgccc	660
aacaccacca tcccctcggg ccagggtgtg gccggctgc ccgccaagtt cctgcgccac	720
ctggagccgg aggaggccag cttcatcggc aagtctgcca gctgctacgc cgagctgtcc	780
gccatccaca agttcgagca gagcaagacg tttgaggagc agtacacgga gagctgcatc	840
atcaaggacc gcgcgctct ggccgacccg tcaaactcag tgcaccagat gtgggagtag	900
gacagccaga cggcgttggt ggcccgcgcc aagaggtag	939

<210> 175
 <211> 312
 <212> PRT
 <213> Chlamydomonas reinhardtii

<400> 175

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```

Met Ser Leu Phe Lys Ser Ser Leu Pro Ala Gly Phe Leu Phe Pro Tyr
1      5      10      15
Arg His Pro Lys Ala Lys Gly Leu Val Glu Gly Thr Leu Tyr Gly Leu
20      25      30
Gly Ser Leu Phe Arg Gly Val Gly Ala Ala Leu Asp Glu Leu Gly Ser
35      40      45
Met Val Gln Gly Pro Gln Gly Ser Val Lys Asp His Val Gln Pro Asn
50      55      60
Leu Ala Phe Ala Pro Val His Arg Lys Pro Asp Val Pro Val Asn Ala
65      70      75      80
Gly Gln Val Val Pro Ala Pro Pro Ala Ala Ala Arg Thr Leu Lys Ile
85      90      95
Lys Glu Val Val Val Pro Asn Lys His Ser Thr Ala Phe Val Ala Ala
100     105     110
Asn Ala Asn Val Leu Gly Asn Val Lys Leu Gly Ala Gly Ser Ser Val
115     120     125
Trp Tyr Gly Ala Val Leu Arg Gly Asp Val Asn Gly Ile Glu Val Gly
130     135     140
Ala Asn Ser Asn Ile Gln Asp Asn Ala Ile Val His Val Ser Lys Tyr
145     150     155     160
Ser Met Asp Gly Thr Ala Arg Pro Thr Val Ile Gly Asn Asn Val Thr
165     170     175
Ile Gly His Ala Ala Thr Val His Ala Cys Thr Ile Glu Asp Asn Cys
180     185     190
Leu Val Gly Met Gly Ala Thr Val Leu Asp Gly Ala Thr Val Lys Ser
195     200     205
Gly Ser Ile Val Ala Ala Gly Ala Val Val Pro Pro Asn Thr Thr Ile
210     215     220
Pro Ser Gly Gln Val Trp Ala Gly Ser Pro Ala Lys Phe Leu Arg His
225     230     235     240
Leu Glu Pro Glu Glu Ala Ser Phe Ile Gly Lys Ser Ala Ser Cys Tyr
245     250     255
Ala Glu Leu Ser Ala Ile His Lys Phe Glu Gln Ser Lys Thr Phe Glu
260     265     270
Glu Gln Tyr Thr Glu Ser Cys Ile Ile Lys Asp Arg Ala Ala Leu Ala
275     280     285
Asp Pro Ser Asn Ser Val His Gln Met Trp Glu Tyr Asp Ser Gln Thr
290     295     300
Ala Leu Val Ala Arg Ala Lys Arg
305     310

```

<210> 176
 <211> 1238
 <212> DNA
 <213> Oryza sativa

```

<400> 176
ggggctcatc tctctctctc tcaactcttct ccctcttctc accaccagac gccatcaaac      60
ccctacctcc cgcggcggcg gcggcggcg gcggcggcg cgagctccg acagacagag      120
gagggcgcgga gcggagagg cgaggaggga aggagggagg gaggcgacag gcatggggac      180
cctcgggcgc gcgatctaca cgggtgggaa gtggatccgc ggcacggggc aggccatgga      240
ccgcctcgga tccaccatcc agggcggcct ccgcgctcag gagcagcttt caaggcatcg      300
cacgatcatg aacatatttg agaaagagcc cagagtccac aaggatgttt ttgttgctcc      360
cagtgcagct gtgattggcg atgttgagat cggacatgga tcctcaatct ggtacggctc      420
cattttaaga ggtgatgtca acagcattca tattggatct ggatcaaata tacaagacaa      480
ttcccttgta catgttgcaa aagctaacat cagcgggaag gttctcccaa ccataattgg      540
aaacaatgtt acaatagggtc atagtgtgt tctgcacgca tgcaccgtcg aggatgaagc      600
ttttgttggt atgggtgcc ctctgcttga tggagtgtc gttgaaaagc acagcatggt      660
tggtgcagga tcgcttgta agcagaacac aaggattcct tctggagagg tctgggtcgg      720

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PF58581.ST25.txt

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taatcctgcc aagttcctaa gaaagcttac tgaagaggag atagcgttca ttgctcagtc 780
agcaacgaac tacatcaatc tggcccaagt ccatgctgcc gagaattcca agaccttcga 840
cgagatcgag ctcgagaaga tgctgaggaa aaagtatgcc cacaaagacg aggagtatga 900
ttcgatgctc ggcgtggtcc gtgagatccc gccggagctc atcctcccgg acaacatcct 960
cccaaacaag gctcagaagg ctgttgctca ctgaatgttt tgtcaagctc ccgcttgga 1020
aaagcttggt tttttgtta cgtgttttga cctggaacaa catttgacac atgtcttttg 1080
atctcattgt ctgtttttca agcccaataa gaatttgggt cgagcattgt tttaggatcg 1140
accatataca gtacctctct ttgcattaca atgaagagca gttaatttgg gtcacttttt 1200
acatctttac tgaagtagaa acgcgtctc tgtctgtg 1238

```

<210> 177
 <211> 273
 <212> PRT
 <213> *Oryza sativa*

<400> 177

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

His

<210> 178
 <211> 657
 <212> DNA
 <213> *Oryza sativa*

<400> 178

PF58581.ST25.txt

```

atggggttcga ctcgcctcct cgtactgctc gccgccgctt ccctcctcct cgccaccgcc      60
gtcccggcag ccagagcaca ggaagaaact gatcacgagg aggagtacac gtacatcagc      120
ggggacgaga aggggccgga gcaactggggc aagctgaagc cggagtgggc gcagtgcggc      180
gccggcgaga tgcagtcgcc gatcgacctc tcccacgagc ggggtcaagct ggtgcgcgac      240
ctcggctacc tcgacgactc ctaccgcgcc gccgaggcct ccatcgtcaa ccgcggccac      300
gacatcatgg tcaggttcga cggcgacgcc ggcagcgctc tcatcaacgg caccgcctac      360
tacctccgcc agctccactg gcactcccc accgagcaca gcgtcgacgg ccgcaggtag      420
gacatggagc tgcacatggt ccacgagagc gccgagaaga aggccgccgt gatcggcctc      480
ctctacgagg tcggccgccc cgaccgcttc ctccaaaaga tggagccata tctcaagatg      540
attgcggaca aggaggacag ggccgccttg cacgcagggg gtggtctgga cgattgtcaa      600
gagggttcgc accgtgtcga ggtatcagct cgaccttctc agggaagctg tgcatga      657

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<210> 179
 <211> 275
 <212> PRT
 <213> *Oryza sativa*

<400> 179

Met	Gly	Ser	Thr	Arg	Leu	Leu	Val	Leu	Leu	Ala	Ala	Ala	Ser	Leu	Leu
1				5					10					15	
Leu	Ala	Thr	Ala	Val	Pro	Ala	Ala	Arg	Ala	Gln	Glu	Glu	Thr	Asp	His
			20					25					30		
Glu	Lys	Glu	Phe	Thr	Tyr	Ile	Ser	Gly	Asp	Glu	Lys	Gly	Pro	Glu	His
			35				40					45			
Trp	Gly	Lys	Leu	Lys	Pro	Glu	Trp	Ala	Gln	Cys	Gly	Ala	Gly	Glu	Met
	50					55					60				
Gln	Ser	Pro	Ile	Asp	Leu	Ser	His	Glu	Arg	Val	Lys	Leu	Val	Arg	Asp
65					70					75				80	
Leu	Gly	Tyr	Leu	Asp	Ser	Tyr	Arg	Ala	Ala	Glu	Ala	Ser	Ile	Val	
				85				90					95		
Asn	Arg	Gly	His	Asp	Ile	Met	Val	Arg	Phe	Asp	Gly	Asp	Ala	Gly	Ser
			100					105					110		
Val	Val	Ile	Asn	Gly	Thr	Ala	Tyr	Tyr	Leu	Arg	Gln	Leu	His	Trp	His
			115				120					125			
Ser	Pro	Thr	Glu	His	Ser	Val	Asp	Gly	Arg	Arg	Tyr	Asp	Met	Glu	Leu
			130				135					140			
His	Met	Val	His	Glu	Ser	Ala	Glu	Lys	Lys	Ala	Ala	Val	Ile	Gly	Leu
145					150					155				160	
Leu	Tyr	Glu	Val	Gly	Arg	Pro	Asp	Arg	Phe	Leu	Gln	Lys	Met	Glu	Pro
				165				170						175	
Tyr	Leu	Lys	Met	Ile	Ala	Asp	Lys	Glu	Asp	Arg	Glu	Glu	Lys	Val	Gly
			180					185						190	
Met	Ile	Asp	Pro	Arg	Gly	Ala	Arg	Gly	Arg	Ala	Ser	Val	Tyr	Tyr	Arg
			195				200					205			
Tyr	Met	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Thr	Gln	Gly	Val	Val	Trp
			210			215					220				
Thr	Ile	Val	Lys	Arg	Val	Arg	Thr	Val	Ser	Arg	Tyr	Gln	Leu	Asp	Leu
225					230					235				240	
Leu	Arg	Glu	Ala	Val	His	Asp	Glu	Met	Glu	Asn	Asn	Ala	Arg	Pro	Leu
				245					250					255	
Gln	Ala	Val	Asn	Asn	Arg	Asp	Ile	Ser	Ile	Phe	Arg	Pro	Tyr	Pro	His
			260					265					270		
Lys	Arg	Tyr													
			275												

<210> 180
 <211> 822
 <212> DNA
 <213> *Dioscorea cayenensis*

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<400> 180
atgagttcat ccacccttct ccatctctct ctcctctcct ccctcctctt ctcttgccct 60
ccaaatgcaa aacctcagca agctgaggat gagtttagct acattgaagg aagtcctaata 120
ggtcctgaaa actggggaaa tcttaaaaag gagtgggaga cttgtggcaa aggcattggag 180
cagtcaccca ttcaattgcg tgataacaga gtgatattcg atcaaacttt gggggagctg 240
agaagaaatt atagagccgc tgaagcaaca ttaaggaaaca gtggacatga tgtattggtg 300
gaatttgagg gtaatgctgg ttactatccc atcaatcgag ttgcatacca actcaagcga 360
attcattttc actccccttc agagcatgaa atgaatggcg aaaggtttga ccttgaggca 420
cagctggtcc atgagagcca agaccaaag agagcagtgg tttctattct tttcagattt 480
ggacgtgctg atacattcct ctcagatctt gaagacttta tcaagcagtt tagcagtagc 540
cagaagaatg aaataaatgc aggagtgtgt gatccaaatc aattacagtt tgatgactgt 600
gcatatttta gatacatggg ctcattcaca gctccacctt gcaactgaagg tatttcatgg 660
accgtcatga ggaaggttgc aactgtttca ccaaggcaag tacttctgtt gaagcaggca 720
gtgaatgaaa atgctataaa caatgcgaga ccacttcaac caaccaatta ccgctccggt 780
ttttactttg aacagctgaa atcgaagctt ggtgtcatat aa 822

```

```

<210> 181
<211> 273
<212> PRT
<213> Dioscorea cayenensis

```

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<400> 181
Met Ser Ser Ser Thr Leu Leu His Leu Leu Leu Leu Ser Ser Leu Leu
1 5 10 15
Phe Ser Cys Leu Pro Asn Ala Lys Pro Gln Gln Ala Glu Asp Glu Phe
20 25 30
Ser Tyr Ile Glu Gly Ser Pro Asn Gly Pro Glu Asn Trp Gly Asn Leu
35 40 45
Lys Lys Glu Trp Glu Thr Cys Gly Lys Gly Met Glu Gln Ser Pro Ile
50 55 60
Gln Leu Arg Asp Asn Arg Val Ile Phe Asp Gln Thr Leu Gly Glu Leu
65 70 75 80
Arg Arg Asn Tyr Arg Ala Ala Glu Ala Thr Leu Arg Asn Ser Gly His
85 90 95
Asp Val Leu Val Glu Phe Glu Gly Asn Ala Gly Ser Leu Ser Ile Asn
100 105 110
Arg Val Ala Tyr Gln Leu Lys Arg Ile His Phe His Ser Pro Ser Glu
115 120 125
His Glu Met Asn Gly Glu Arg Phe Asp Leu Glu Ala Gln Leu Val His
130 135 140
Glu Ser Gln Asp Gln Lys Arg Ala Val Val Ser Ile Leu Phe Arg Phe
145 150 155 160
Gly Arg Ala Asp Thr Phe Leu Ser Asp Leu Glu Asp Phe Ile Lys Gln
165 170 175
Phe Ser Ser Ser Gln Lys Asn Glu Ile Asn Ala Gly Val Val Asp Pro
180 185 190
Asn Gln Leu Gln Phe Asp Asp Cys Ala Tyr Phe Arg Tyr Met Gly Ser
195 200 205
Phe Thr Ala Pro Pro Cys Thr Glu Gly Ile Ser Trp Thr Val Met Arg
210 215 220
Lys Val Ala Thr Val Ser Pro Arg Gln Val Leu Leu Lys Gln Ala
225 230 235 240
Val Asn Glu Asn Ala Ile Asn Asn Ala Arg Pro Leu Gln Pro Thr Asn
245 250 255
Tyr Arg Ser Val Phe Tyr Phe Glu Gln Leu Lys Ser Lys Leu Gly Val
260 265 270
Ile

```


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<210> 182
 <211> 807
 <212> DNA
 <213> Dioscorea batatas

<400> 182
 atgagttcat ccacccttct ccatctcctc ctctctcct ccctcctctt ctcttgctt 60
 gcaaagttag aggatgagtt tagctacatt gaaggaaatc ctaatggtcc tgaaaactgg 120
 ggaaatctta aaccggagtg ggagacttgt ggcaaaggca tggagcagtc acccattcag 180
 ttgcgtgata acagagtgat attcgatcaa actttgggga ggttgagaag aaattacaga 240
 gccgttgatg caagattaag gaacagtgga catgatgtat tgggtggaatt taagggtaat 300
 gctggttcac tatcaatcaa tcgagttgca taccaactca agcgaattca ttttcactcc 360
 ccttcagagc atgaaatgaa tggcgaaagg tttgaccttg aggcacagct ggttcatgag 420
 agccaagatc aaaagagagc agtggtttct attcttttca tatttgagcg tgctgaccca 480
 ttctctcag atcttgaaga ctttatcaag cagtttagca gtagccagaa gaatgaaata 540
 aatgcaggag ttgtggatcc aaatcaatta cagattgatg actctgcata ttatagatac 600
 atgggctcat tcacagctcc accttgact gaaggtatct catggaccgt catgaggaag 660
 gttgcaactg tttcaccaag acaagtactg ctgttgaagc aggcagtga tgaaaatgct 720
 ataaacaatg caagaccact tcaaccaacc aatttccgct ccgtttttta ctttgaacag 780
 ctgaaatcga aggtttgtgc catataa 807

<210> 183
 <211> 268
 <212> PRT
 <213> Dioscorea batatas

<400> 183
 Met Ser Ser Ser Thr Leu Leu His Leu Leu Leu Ser Ser Leu Leu
 1 5 10 15
 Phe Ser Cys Leu Ala Asn Val Glu Asp Glu Phe Ser Tyr Ile Glu Gly
 20 25 30
 Asn Pro Asn Gly Pro Glu Asn Trp Gly Asn Leu Lys Pro Glu Trp Glu
 35 40 45
 Thr Cys Gly Lys Gly Met Glu Gln Ser Pro Ile Gln Leu Arg Asp Asn
 50 55 60
 Arg Val Ile Phe Asp Gln Thr Leu Gly Arg Leu Arg Arg Asn Tyr Arg
 65 70 75 80
 Ala Val Asp Ala Arg Leu Arg Asn Ser Gly His Asp Val Leu Val Glu
 85 90 95
 Phe Lys Gly Asn Ala Gly Ser Leu Ser Ile Asn Arg Val Ala Tyr Gln
 100 105 110
 Leu Lys Arg Ile His Phe His Ser Pro Ser Glu His Glu Met Asn Gly
 115 120 125
 Glu Arg Phe Asp Leu Glu Ala Gln Leu Val His Glu Ser Gln Asp Gln
 130 135 140
 Lys Arg Ala Val Val Ser Ile Leu Phe Ile Phe Gly Arg Ala Asp Pro
 145 150 155 160
 Phe Leu Ser Asp Leu Glu Asp Phe Ile Lys Gln Phe Ser Ser Ser Gln
 165 170 175
 Lys Asn Glu Ile Asn Ala Gly Val Val Asp Pro Asn Gln Leu Gln Ile
 180 185 190
 Asp Asp Ser Ala Tyr Tyr Arg Tyr Met Gly Ser Phe Thr Ala Pro Pro
 195 200 205
 Cys Thr Glu Gly Ile Ser Trp Thr Val Met Arg Lys Val Ala Thr Val
 210 215 220
 Ser Pro Arg Gln Val Leu Leu Leu Lys Gln Ala Val Asn Glu Asn Ala
 225 230 235 240
 Ile Asn Asn Ala Arg Pro Leu Gln Pro Thr Asn Phe Arg Ser Val Phe

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	245		250		255
Tyr Phe Glu Gln Leu Lys Ser Lys Val Cys Ala Ile					
	260		265		

<210> 184
 <211> 822
 <212> DNA
 <213> Dioscorea alata

<400> 184

atgagttcat	ccaccctttt	ccatctcttc	ctcctctcct	ccctcctctt	ctcttgcttt	60
tcaaatgcaa	ggcttgatgg	cgatgatgac	tttagctaca	ttgaaggaag	tcctaattgg	120
cctgaaaact	ggggaaatct	tagaccggag	tggaagactt	gtggctatgg	catggagcag	180
tcacccatta	atgtgtgtga	tgatagagtg	atacggactc	caactttggg	gaagctgaga	240
acaagttatc	aggctgctcg	tgcaacagtg	aagaacaatg	gacatgatat	aatgggtgtac	300
tttaaaagtg	atgctggtac	acaattcatc	aatcaagtag	agtaccaact	caaacgaatt	360
catttttca	ccccatcaga	acatgcactc	agtggtgaaa	ggtatgacct	tgaggttcag	420
atggtccatg	agagccaaga	tcaaaggaga	gcagtaattg	ctattatggt	cagatttgga	480
cgttctgacc	cattcctccc	agaccttgaa	gactttatca	gccagataag	cagacgtgag	540
accaatgaag	tagatgcagg	agttgtggat	ccaaggcaat	tattacagtt	tgatgacctt	600
gcatattata	gatacatggg	ctcatacaca	gctccacctt	gcactgaaga	tattacatgg	660
accgttatta	agaagcttgg	aactgtttca	ccaaagcaag	tactgatggt	gaagcaagca	720
gtgaatgaaa	attctatgaa	caatgcaagg	ccacttcaac	cactgaaatt	tcgcaccggt	780
tttttctatc	cgcgtcagaa	atctgatcat	gttgccatat	aa		822

<210> 185
 <211> 273
 <212> PRT
 <213> Dioscorea alata

<400> 185

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

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Lys Leu Gly Thr Val Ser Pro Lys Gln Val Leu Met Leu Lys Gln Ala
 225 230 235 240
 Val Asn Glu Asn Ser Met Asn Asn Ala Arg Pro Leu Gln Pro Leu Lys
 245 250 255
 Phe Arg Thr Val Phe Phe Tyr Pro Arg Gln Lys Ser Asp His Val Ala
 260 265 270
 Ile

<210> 186
 <211> 831
 <212> DNA
 <213> Oryza sativa

<400> 186
 atgagtactt cagctcgccg cctcctcctc ctcgccggcg ccgctgccgc catcgcactc 60
 ctgctctcgg ccactgcccc ggtggccgga gccgaggacg acggctacag ctacatccct 120
 ggctcaccga gggggccgca gaactggggc agcctgaagc cggaatgggc cacctgcagc 180
 agcggcaaga tgcagtcgcc gatcaacctc ggcctcctcg acctcacctt ggctcccggc 240
 ctcggaacc tcaactacac ctaccagaac gccaacgcct ccgtcgtcaa ccgtggccac 300
 gacatcatgg tcaggtttga cggcgacgcc ggtagcctaa agataaatgg cacggcgtag 360
 cagctccggc agatgcactg gcacacgccg tcggagcaca ccatcgatgg ccggaggtac 420
 gacatggagc tgcacatggt gcacctcaac gcccagaacc aggccgccgt cattggcatc 480
 ctctacacca tcggcacccg ggacgagttt ctgcaaaagc tagagcctta tataattgag 540
 atatcaaagc aagaaggcaa agagagagtg atcattggtg gggcggatcc aaatgtagcc 600
 aagggacagg ataccgtgta ctaccgctac atgggctcct ttaccacacc accttgcaact 660
 gagggagtca tctggaccgt tgtcaggaag gtgcgcaccg tgtcactgtc ccaaatacaca 720
 cttctcaagg cagctgtgct cacgggtaac gagaacaacg cgagaccctt tcaggggcgtg 780
 aacaacaggg agattgacct gttccttctc ctccctctca tcaacaactg a 831

<210> 187
 <211> 276
 <212> PRT
 <213> Oryza sativa

<400> 187
 Met Ser Thr Ser Ala Arg Arg Leu Leu Leu Leu Ala Gly Ala Ala Ala
 1 5 10 15
 Ala Ile Ala Leu Leu Leu Ser Ala Thr Ala Pro Val Ala Gly Ala Glu
 20 25 30
 Asp Asp Gly Tyr Ser Tyr Ile Pro Gly Ser Pro Arg Gly Pro Gln Asn
 35 40 45
 Trp Gly Ser Leu Lys Pro Glu Trp Ala Thr Cys Ser Ser Gly Lys Met
 50 55 60
 Gln Ser Pro Ile Asn Leu Gly Leu Leu Asp Leu Thr Leu Ala Pro Gly
 65 70 75 80
 Leu Gly Asn Leu Asn Tyr Thr Tyr Gln Asn Ala Asn Ala Ser Val Val
 85 90 95
 Asn Arg Gly His Asp Ile Met Val Arg Phe Asp Gly Asp Ala Gly Ser
 100 105 110
 Leu Lys Ile Asn Gly Thr Ala Tyr Gln Leu Arg Gln Met His Trp His
 115 120 125
 Thr Pro Ser Glu His Thr Ile Asp Gly Arg Arg Tyr Asp Met Glu Leu
 130 135 140
 His Met Val His Leu Asn Ala Gln Asn Gln Ala Ala Val Ile Gly Ile
 145 150 155 160
 Leu Tyr Thr Ile Gly Thr Arg Asp Glu Phe Leu Gln Lys Leu Glu Pro
 165 170 175
 Tyr Ile Ile Glu Ile Ser Lys Gln Glu Gly Lys Glu Arg Val Ile Ile

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180								185				190			
Gly	Gly	Ala	Asp	Pro	Asn	Val	Ala	Lys	Gly	Gln	Asp	Thr	Val	Tyr	Tyr
195								200				205			
Arg	Tyr	Met	Gly	Ser	Phe	Thr	Thr	Pro	Pro	Cys	Thr	Glu	Gly	Val	Ile
210								215				220			
Trp	Thr	Val	Val	Arg	Lys	Val	Arg	Thr	Val	Ser	Leu	Ser	Gln	Ile	Thr
225								230				235			
Leu	Leu	Lys	Ala	Ala	Val	Leu	Thr	Gly	Asn	Glu	Asn	Asn	Ala	Arg	Pro
245								250				255			
Leu	Gln	Gly	Val	Asn	Asn	Arg	Glu	Ile	Asp	Leu	Phe	Leu	Pro	Leu	Pro
260								265				270			
Leu	Ile	Asn	Asn												
275															

<210> 188
 <211> 846
 <212> DNA
 <213> Oryza sativa

<400> 188
 atgggtgtctc tccgcgcggc catcgtctctc gtcgtcgcgc cctcgtcggg cgccgtcgcc 60
 ttctctcatg cggaagggaa cgaggggccc gacttcacct acatcgaagg cgccatggac 120
 gggccgtcga actgggggaa gctgagcccg gactacagga tgtgcggcga ggggaggtcg 180
 cagtcgccga tcgacatcaa caccaagacc gtcgtcccgc gctcggacct cgacacgctg 240
 gaccgcaact acaacgccgt gaacgccacc atcgtcaaca acggcaagga catcaccatg 300
 aagttccacg gcgaggtcgg ccaggtgatc atcgccggga agccgtacag gttccaggcg 360
 atccactggc acgcgccgtc ggagcacacc atcaacggca ggcgcttccc gctcgagctc 420
 cacctcgtcc acaagtcgga cgccgacggc ggctcgcgc tcatctccgt cctctacaag 480
 ctcggcgccc cggaactcct ctacctccag ttcaaggacc acctcgccga gctcggcgcc 540
 gacgagtgcg acttcagcaa ggaggaggcc cagtcgcgc ccgggctggg gcagatgagg 600
 tcgctgcaga agcgacggg gagctacttc cggtagcgcg gctcgtgac gacgcgcgcg 660
 tgccggcgaga acgtggtgtg gagcgtgctc gggaagggtga gggagatcag ccaggagcag 720
 ctgcacctgc tcatgtcgcc attgccgacc aaggacgcca ggccggcgca gccgctcaat 780
 ggcaggggcg tcttctacta caaccgcgcg ggcagcgccg tctccttcca ggaattcgcc 840
 aagtga 846

<210> 189
 <211> 281
 <212> PRT
 <213> Oryza sativa

<400> 189
 Met Val Ser Leu Arg Ala Ala Ile Val Leu Val Val Ala Ala Ser Ser
 1 5 10 15
 Val Ala Val Ala Phe Ser His Ala Glu Gly Asn Glu Gly Pro Asp Phe
 20 25 30
 Thr Tyr Ile Glu Gly Ala Met Asp Gly Pro Ser Asn Trp Gly Lys Leu
 35 40 45
 Ser Pro Glu Tyr Arg Met Cys Gly Glu Gly Arg Ser Gln Ser Pro Ile
 50 55 60
 Asp Ile Asn Thr Lys Thr Val Val Pro Arg Ser Asp Leu Asp Thr Leu
 65 70 75 80
 Asp Arg Asn Tyr Asn Ala Val Asn Ala Thr Ile Val Asn Asn Gly Lys
 85 90 95
 Asp Ile Thr Met Lys Phe His Gly Glu Val Gly Gln Val Ile Ile Ala
 100 105 110
 Gly Lys Pro Tyr Arg Phe Gln Ala Ile His Trp His Ala Pro Ser Glu
 115 120 125
 His Thr Ile Asn Gly Arg Arg Phe Pro Leu Glu Leu His Leu Val His

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130		135		140	
Lys Ser Asp Ala Asp Gly Gly Leu Ala Val Ile Ser Val Leu Tyr Lys					
145		150		155	160
Leu Gly Ala Pro Asp Ser Phe Tyr Leu Gln Phe Lys Asp His Leu Ala					
	165		170		175
Glu Leu Gly Ala Asp Glu Cys Asp Phe Ser Lys Glu Glu Ala His Val					
	180		185		190
Ala Ala Gly Leu Val Gln Met Arg Ser Leu Gln Lys Arg Thr Gly Ser					
	195		200		205
Tyr Phe Arg Tyr Gly Gly Ser Leu Thr Thr Pro Pro Cys Gly Glu Asn					
	210		215		220
Val Val Trp Ser Val Leu Gly Lys Val Arg Glu Ile Ser Gln Glu Gln					
225		230		235	240
Leu His Leu Leu Met Ser Pro Leu Pro Thr Lys Asp Ala Arg Pro Ala					
	245		250		255
Gln Pro Leu Asn Gly Arg Ala Val Phe Tyr Tyr Asn Pro Pro Gly Ser					
	260		265		270
Ala Val Ser Phe Gln Glu Phe Ala Lys					
	275		280		

<210> 190
 <211> 804
 <212> DNA
 <213> Arabidopsis thaliana

<400> 190
 atggatacca acgcaaaaac aattttcttc atggctatgt gtttcatcta tctatctttc 60
 cctaataattt cacacgtcca ttctgaagtc gacgacgaaa ctccatttac ttacgaacaa 120
 aaaacggaaa agggaccaga gggatggggc aaaataaatc cgcactggaa agtttgtaac 180
 accggaagat atcaatcccc gatcgatctt actaacgaaa gagtcagtct tattcatgat 240
 caagcatgga caagacaata taaaccagct cgggctgtaa ttacaaacag aggccatgac 300
 attatggtat catggaaagg agatgctggg aagatgacaa tacggaaaac ggattttta 360
 ttggtgcaat gccattggca ttcaccttct gagcataccg ttaacggaac taggtacgac 420
 ctagagcttc acatggttca cacgagtgcg cgaggcagaa ctgctggtat cggagttctt 480
 taaaaattag gcgaacctaa tgaattcctc accaagctac taaatggaat aaaagcagt 540
 ggaaataaag agataaatct agggatgatt gatccacgag agattagggt tcaaacaaga 600
 aaattctata gataattgg ctctctcact gttcctcctt gactgaagg cgtcatttgg 660
 actgtcgtca aaagggtgaa cacaatatca atggagcaaa ttacagctct taggcaagcc 720
 gttgacgatg gatttgagac aaattcaaga ccggttcaag actcaaaggg aagatcagtt 780
 tggttctatg atccaaatgt ttga 804

<210> 191
 <211> 267
 <212> PRT
 <213> Arabidopsis thaliana

<400> 191
 Met Asp Thr Asn Ala Lys Thr Ile Phe Phe Met Ala Met Cys Phe Ile
 1 5 10 15
 Tyr Leu Ser Phe Pro Asn Ile Ser His Ala His Ser Glu Val Asp Asp
 20 25 30
 Glu Thr Pro Phe Thr Tyr Glu Gln Lys Thr Glu Lys Gly Pro Glu Gly
 35 40 45
 Trp Gly Lys Ile Asn Pro His Trp Lys Val Cys Asn Thr Gly Arg Tyr
 50 55 60
 Gln Ser Pro Ile Asp Leu Thr Asn Glu Arg Val Ser Leu Ile His Asp
 65 70 75 80
 Gln Ala Trp Thr Arg Gln Tyr Lys Pro Ala Pro Ala Val Ile Thr Asn
 85 90 95

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Arg Gly His Asp Ile Met Val Ser Trp Lys Gly Asp Ala Gly Lys Met
      100      105      110
Thr Ile Arg Lys Thr Asp Phe Asn Leu Val Gln Cys His Trp His Ser
      115      120      125
Pro Ser Glu His Thr Val Asn Gly Thr Arg Tyr Asp Leu Glu Leu His
      130      135      140
Met Val His Thr Ser Ala Arg Gly Arg Thr Ala Val Ile Gly Val Leu
      145      150      155      160
Tyr Lys Leu Gly Glu Pro Asn Glu Phe Leu Thr Lys Leu Leu Asn Gly
      165      170      175
Ile Lys Ala Val Gly Asn Lys Glu Ile Asn Leu Gly Met Ile Asp Pro
      180      185      190
Arg Glu Ile Arg Phe Gln Thr Arg Lys Phe Tyr Arg Tyr Ile Gly Ser
      195      200      205
Leu Thr Val Pro Pro Cys Thr Glu Gly Val Ile Trp Thr Val Val Lys
      210      215      220
Arg Val Asn Thr Ile Ser Met Glu Gln Ile Thr Ala Leu Arg Gln Ala
      225      230      235      240
Val Asp Asp Gly Phe Glu Thr Asn Ser Arg Pro Val Gln Asp Ser Lys
      245      250      255
Gly Arg Ser Val Trp Phe Tyr Asp Pro Asn Val
      260      265

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<210> 192

<211> 792

<212> DNA

<213> Arabidopsis thaliana

<400> 192

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atgaaacaca ttttttttaa ctcgtgtata accaaaaaaa atatagagga cgaaacgcag      60
tttaactacg agaagaaagg agagaagggg ccagagaact ggggaagact aaagccagag      120
tgggcaatgt gtggaaaagg caacatgcag tctccgattg atcttacgga caaaagagtc      180
ttgattgata ataatcttgg ataccttctg agccagtatt taccttcaaa tgccaccatt      240
aagaacagag gccatgatat catgatgaaa ttggaaggag gaaatgcagg tttaggtatc      300
actattaatg gtactgaata taaacttcaa cagattcatt ggcactctcc ttccgaacac      360
acactcaatg gcaaaagggt tgttcttgag gaacacatgg ttcacagag caaagatgga      420
cgcaacgctg ttgtcgcttt cttttacaaa ttgggaaaac ctgactatth tctcctcacg      480
ttggaaagat acttgaagag gataactgat acacacgaat cccaggaatt tgctcgagatg      540
gttcatccta gaacattcgg ttttgaatca aaacactatt atagatttat cggatcactt      600
acaactccac cgtgttctga aaatgtgatt tggacgattt ccaaagagat gaggactgtg      660
acattaaaac aattgatcat gcttcgagtg actgtacacg atcaatctaa ctcaaagtgt      720
agaccgcttc agcgtaaaaa tgagcggtccg gtggcacttt acataccaac atggcatagt      780
aaactatatt aa                                     792

```

<210> 193

<211> 263

<212> PRT

<213> Arabidopsis thaliana

<400> 193

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Met Lys His Ile Phe Phe Asn Ser Cys Ile Thr Lys Lys Asn Ile Glu
1      5      10      15
Asp Glu Thr Gln Phe Asn Tyr Glu Lys Lys Gly Glu Lys Gly Pro Glu
      20      25      30
Asn Trp Gly Arg Leu Lys Pro Glu Trp Ala Met Cys Gly Lys Gly Asn
      35      40      45
Met Gln Ser Pro Ile Asp Leu Thr Asp Lys Arg Val Leu Ile Asp His
      50      55      60
Asn Leu Gly Tyr Leu Arg Ser Gln Tyr Leu Pro Ser Asn Ala Thr Ile

```

PF58581.ST25.txt

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

<210> 194
 <211> 275
 <212> PRT
 <213> Adonis aestivalis

<400>	194														
Met	Gly	Thr	Leu	Gly	Lys	Ala	Ile	Tyr	Thr	Val	Gly	Phe	Trp	Ile	Arg
1				5					10					15	
Glu	Thr	Gly	Gln	Ala	Ile	Asp	Arg	Leu	Gly	Ser	Arg	Leu	Gln	Gly	Asn
			20					25					30		
Tyr	Tyr	Phe	His	Glu	Gln	Leu	Ser	Arg	His	Arg	Thr	Leu	Met	Asn	Ile
		35					40					45			
Phe	Asp	Lys	Ala	Pro	Val	Val	Asp	Lys	Asp	Ala	Phe	Ile	Ala	Pro	Ser
	50					55				60					
Ala	Ser	Val	Ile	Gly	Asp	Val	Gln	Val	Gly	Arg	Ser	Ser	Ser	Ile	Trp
65					70					75					80
Tyr	Gly	Cys	Val	Leu	Arg	Gly	Asp	Val	Asn	Ser	Ile	Ser	Val	Gly	Ser
			85						90					95	
Gly	Thr	Asn	Ile	Gln	Asp	Asn	Ser	Leu	Val	His	Val	Ala	Lys	Ser	Asn
		100						105					110		
Leu	Ser	Gly	Lys	Val	Leu	Pro	Thr	Ile	Ile	Gly	Asn	Asn	Val	Thr	Val
		115					120					125			
Gly	His	Ser	Ala	Val	Leu	His	Gly	Cys	Thr	Val	Gln	Asp	Ser	Ala	Phe
	130					135					140				
Val	Gly	Met	Gly	Ala	Thr	Leu	Leu	Asp	Gly	Val	Val	Val	Glu	Asn	His
145					150					155					160
Ala	Met	Val	Ala	Ala	Gly	Ala	Leu	Val	Arg	Gln	Asn	Thr	Arg	Ile	Pro
				165					170					175	
Lys	Gly	Glu	Val	Trp	Gly	Gly	Asn	Pro	Ala	Lys	Phe	Leu	Arg	Lys	Leu
			180					185					190		
Thr	Glu	Glu	Glu	Ile	Ala	Phe	Ile	Ser	Gln	Ser	Ala	Thr	Asn	Tyr	Thr
		195					200					205			
Asn	Leu	Ala	Gln	Val	His	Ala	Ala	Glu	Asn	Ala	Lys	Thr	Phe	Glu	Glu

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```

      210              215              220
Ile Glu Phe Glu Lys Leu Leu Arg Lys Lys Phe Ala Arg Lys Asp Glu
225              230              235              240
Glu Tyr Asp Ser Met Leu Gly Val Val Arg Glu Thr Pro Gln Glu Leu
      245              250              255
Ile Leu Pro Asp Asn Ile Leu Ala Asp Lys Gln Ser Pro Lys Ala Val
      260              265              270
Ser Ser Ser
      275

```

<210> 195
 <211> 276
 <212> PRT
 <213> Glycine max

```

<400> 195
Met Gly Thr Leu Gly Arg Ala Ile Tyr Ser Val Gly Asn Trp Ile Arg
1      5      10      15
Gly Thr Gly Gln Ala Ile Asp Arg Leu Gly Ser Leu Leu Gln Gly Gly
      20      25      30
Tyr Tyr Val Gln Glu Gln Leu Ser Arg His Arg Thr Leu Met Asp Ile
      35      40      45
Phe Asp Lys Ala Pro Val Val Asp Glu Asp Val Phe Val Ala Pro Ser
      50      55      60
Ala Ser Val Ile Gly Asp Val Gln Leu Gly Arg Gly Ser Ser Ile Trp
65      70      75      80
Tyr Gly Val Val Leu Arg Gly Asp Val Asn Ser Ile Arg Val Gly Asn
      85      90      95
Gly Thr Asn Ile Gln Asp Asn Ser Leu Val His Val Ala Lys Ser Asn
      100     105     110
Leu Ser Gly Lys Val Leu Pro Thr Ile Ile Gly Asp Asn Val Thr Val
      115     120     125
Gly His Ser Ala Val Ile His Gly Cys Thr Val Glu Asp Glu Ala Phe
      130     135     140
Val Gly Met Gly Ala Ile Leu Leu Asp Gly Val Val Val Glu Lys Asn
145     150     155     160
Ala Met Val Ala Ala Gly Ala Leu Val Arg Gln Asn Thr Arg Ile Pro
      165     170     175
Ser Gly Glu Val Trp Ala Gly Asn Pro Ala Lys Phe Leu Arg Lys Leu
      180     185     190
Thr Asp Glu Glu Ile Ala Phe Ile Ser Gln Ser Ala Thr Asn Tyr Thr
      195     200     205
Asn Leu Ala Gln Val His Ala Ala Glu Asn Ser Lys Ser Phe Asp Glu
      210     215     220
Ile Glu Phe Glu Lys Val Leu Arg Lys Lys Phe Ala Arg Lys Asp Glu
225     230     235     240
Glu Tyr Asp Ser Met Leu Gly Val Val Arg Glu Ile Pro Pro Glu Leu
      245     250     255
Ile Leu Pro Asp Asn Val Leu Pro Asp Lys Ala Glu Lys Ala Leu Lys
      260     265     270
Lys Ser Gly Ile
      275

```

<210> 196
 <211> 276
 <212> PRT
 <213> Brassica napus

<400> 196

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```

Met Gly Thr Leu Gly Arg Val Ile Tyr Thr Val Gly Lys Trp Ile Arg
1      5      10      15
Gly Ser Gly Gln Ala Leu Asp Arg Val Gly Ser Ile Leu Gln Gly Ser
20      25      30
His Arg Leu Glu Glu His Leu Ser Arg His Arg Thr Leu Met Asn Val
35      40      45
Phe Asp Lys Ser Pro Leu Val Asp Lys Asp Val Phe Val Ala Pro Ser
50      55      60
Ala Ser Val Ile Gly Asp Val Gln Ile Gly Lys Gly Ser Ser Ile Trp
65      70      75      80
Tyr Gly Cys Val Leu Arg Gly Asp Val Asn Asn Ile Ser Val Gly Ser
85      90      95
Gly Thr Asn Ile Gln Asp Asn Ser Leu Val His Val Ala Lys Thr Asn
100     105     110
Leu Gly Gly Lys Val Leu Pro Thr Thr Ile Gly Asp Asn Val Thr Val
115     120     125
Gly His Ser Ala Val Ile His Gly Cys Thr Val Glu Asp Glu Ala Phe
130     135     140
Val Gly Met Gly Ala Thr Leu Leu Asp Gly Val Val Val Glu Lys His
145     150     155     160
Ala Met Val Ala Ala Gly Ser Leu Val Arg Glu Asn Thr Arg Ile Pro
165     170     175
Ser Gly Glu Val Trp Gly Gly Asn Pro Ala Lys Phe Met Arg Lys Leu
180     185     190
Thr Asp Glu Glu Ile Ala Tyr Ile Ser Lys Ser Ala Glu Asn Tyr Ile
195     200     205
Asn Leu Ala His Ile His Ala Ala Glu Asn Ser Lys Ser Phe Glu Glu
210     215     220
Ile Glu Val Glu Arg Ala Leu Arg Lys Lys Tyr Ala Arg Lys Asp Glu
225     230     235     240
Asp Tyr Asp Ser Met Leu Gly Ile Val Arg Glu Thr Pro Ala Glu Leu
245     250     255
Ile Leu Pro Asp Asn Val Leu Pro Glu Lys Thr Thr Thr Arg Val Pro
260     265     270
Thr Thr His Tyr
275

```

<210> 197
 <211> 273
 <212> PRT
 <213> Zea mays

```

<400> 197
Met Gly Thr Leu Gly Arg Ala Ile Phe Thr Val Gly Lys Trp Ile Arg
1      5      10      15
Gly Thr Gly Gln Ala Met Asp Arg Leu Gly Ser Thr Ile Gln Gly Gly
20      25      30
Leu Arg Val Glu Glu Gln Val Ser Arg His Arg Thr Ile Met Asn Ile
35      40      45
Phe Glu Lys Glu Pro Arg Ile His Arg Asp Val Phe Val Ala Pro Ser
50      55      60
Ala Ala Val Ile Gly Asp Val Glu Ile Gly His Gly Ser Ser Ile Trp
65      70      75      80
Tyr Gly Ser Ile Leu Arg Gly Asp Val Asn Ser Ile His Ile Gly Ser
85      90      95
Gly Thr Asn Ile Gln Asp Asn Ser Leu Val His Val Ser Lys Ala Asn
100     105     110
Ile Ser Gly Lys Val Leu Pro Thr Ile Ile Gly Ser Asn Val Thr Val
115     120     125

```

PF58581.ST25.txt

Gly His Ser Ala Val Leu His Ala Cys Thr Ile Glu Asp Glu Ala Phe
130 135 140
Val Gly Met Gly Ala Thr Leu Leu Asp Gly Val Val Val Glu Lys His
145 150 155 160
Ser Met Val Gly Ala Gly Ser Leu Val Lys Gln Asn Thr Arg Ile Pro
165 170 175
Ser Gly Glu Val Trp Val Gly Asn Pro Ala Lys Phe Leu Arg Lys Leu
180 185 190
Thr Glu Glu Glu Ile Ala Phe Ile Ala Gln Ser Ala Thr Asn Tyr Ile
195 200 205
Asn Leu Ala Gln Val His Ala Ala Glu Asn Ala Lys Ser Phe Asp Glu
210 215 220
Ile Glu Leu Glu Lys Met Leu Arg Lys Lys Tyr Ala His Lys Asp Glu
225 230 235 240
Glu Tyr Asp Ser Met Leu Gly Val Val Arg Glu Ile Pro Pro Gln Leu
245 250 255
Ile Leu Pro Asp Asn Ile Leu Pro His Asn Ala Gln Lys Ala Val Ala
260 265 270
Arg

<210> 198
<211> 274
<212> PRT
<213> Triticum aestivum

<400> 198
Met Gly Thr Leu Gly Arg Ala Ile Tyr Thr Val Gly Lys Trp Ile Arg
1 5 10 15
Gly Thr Gly Gln Ala Met Asp Arg Leu Gly Ser Thr Ile Gln Gly Gly
20 25 30
Leu Arg Thr Glu Glu Gln Val Ser Arg His Arg Thr Val Met Ser Ile
35 40 45
Phe Asp Lys Glu Pro Arg Ile Asn Lys Asp Val Phe Val Ala Pro Ser
50 55 60
Ala Ser Val Ile Gly Asp Val Glu Ile Gly His Gly Ser Ser Ile Trp
65 70 75 80
Tyr Gly Ser Val Leu Arg Gly Asp Val Asn Ser Ile Arg Ile Gly Ser
85 90 95
Gly Ser Asn Ile Gln Asp Asn Ser Leu Val His Val Ala Lys Thr Asn
100 105 110
Ile Ser Gly Lys Val Leu Pro Thr Ile Ile Gly Ser Asn Val Thr Val
115 120 125
Gly His Ser Ala Val Leu His Ala Cys Thr Ile Glu Asp Glu Ala Phe
130 135 140
Val Gly Met Gly Ala Thr Leu Leu Asp Gly Val Val Val Glu Lys His
145 150 155 160
Ser Met Val Gly Ala Gly Ser Leu Val Lys Gln Asn Thr Arg Ile Pro
165 170 175
Ser Gly Glu Val Trp Val Gly Asn Pro Ala Lys Phe Leu Arg Lys Leu
180 185 190
Thr Glu Glu Glu Ile Thr Phe Ile Ala Gln Ser Ala Ala Asn Tyr Ile
195 200 205
Asn Leu Ala His Val His Ala Thr Glu Asn Ser Lys Ser Phe Asp Glu
210 215 220
Ile Glu Leu Glu Lys Lys Leu Arg Lys Lys Phe Ala His Lys Asp Glu
225 230 235 240
Glu Tyr Asp Ser Met Leu Gly Val Val Arg Glu Ile Pro Pro Gln Leu
245 250 255

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Ile Leu Pro Asp Asn Ile Leu Pro Asp Lys Ala Pro Lys Ala Ala Val
 260 265 270
 Ala His

<210> 199
 <211> 270
 <212> PRT
 <213> Glycine max

<400> 199
 Met Gly Thr Leu Gly Arg Val Phe Tyr Ala Val Gly Phe Trp Ile Arg
 1 5 10 15
 Glu Thr Gly Gln Ala Ile Asp Arg Leu Gly Ser Arg Leu Gln Gly Asn
 20 25 30
 Tyr Leu Phe Gln Glu Gln Leu Ser Arg His Arg Pro Leu Met Asn Leu
 35 40 45
 Phe Asp Lys Ala Pro Ser Val His Arg Asp Ala Phe Val Ala Pro Ser
 50 55 60
 Ala Ser Leu Leu Gly Asp Val His Val Gly Pro Ala Ser Ser Ile Trp
 65 70 75 80
 Tyr Gly Cys Val Leu Arg Gly Asp Val Asn Ser Ile Thr Ile Gly Ser
 85 90 95
 Gly Thr Asn Ile Gln Asp Asn Ser Leu Val His Val Ala Lys Ser Asn
 100 105 110
 Leu Ser Gly Lys Val Leu Pro Thr Ile Ile Gly Asp Asn Val Thr Val
 115 120 125
 Gly His Ser Ala Val Leu Gln Gly Cys Thr Val Glu Asp Glu Ala Phe
 130 135 140
 Ile Gly Met Gly Ala Thr Leu Leu Asp Gly Val Tyr Val Glu Lys His
 145 150 155 160
 Ala Met Val Ala Ala Gly Ala Leu Val Arg Gln Asn Thr Arg Ile Pro
 165 170 175
 Tyr Gly Glu Val Trp Gly Gly Asn Pro Ala Arg Phe Leu Arg Lys Leu
 180 185 190
 Thr Glu Asp Glu Met Thr Phe Phe Ser Gln Ser Ala Leu Asn Tyr Ser
 195 200 205
 Asn Leu Ala Gln Ala His Ser Ala Glu Asn Ala Lys Gly Leu Asp Glu
 210 215 220
 Thr Glu Phe Val Lys Val Leu His Lys Lys Phe Ala Arg His Gly Asp
 225 230 235 240
 Glu Tyr His Ser Val Leu Gly Gly Val Gln Glu Thr Pro Thr Glu Leu
 245 250 255
 Lys Ser Ser Asp Asn Val Leu Leu Asp Lys Val Pro Lys Ala
 260 265 270

<210> 200
 <211> 307
 <212> PRT
 <213> Hordeum vulgare

<400> 200
 Met Ala Lys Ala Ser Tyr Ala Val Gly Phe Trp Ile Arg Glu Thr Gly
 1 5 10 15
 Gln Ala Leu Asp Arg Leu Gly Cys Arg Leu Gln Gly Asn Tyr Phe Phe
 20 25 30
 His Glu Gln Ile Ser Arg His Arg Thr Leu Met Asn Ile Phe Asp Lys
 35 40 45
 Ala Pro His Val His Lys Glu Ala Phe Val Ala Pro Ser Ala Ser Leu

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

<210> 201
 <211> 279
 <212> PRT
 <213> Zea mays

<400> 201
Met Val Ser Ser Ser Arg Ala Val Val Val Val Gly Leu Leu Val
1 5 10 15
Ala Ala Ser Ser Leu Ala Val Ala Ala Ser Asp Gly Gly Gly Pro Thr
20 25 30
Tyr Gly Tyr Thr Ala Gly Ser Pro Asp Gly Pro Glu Asn Trp Gly Lys
35 40 45
Leu Ser Pro Ala Tyr Lys Leu Cys Gly Gln Gly Lys Gln Gln Ser Pro
50 55 60
Ile Asp Ile Val Thr Lys Gln Ala Val Pro Thr Ala Thr Leu Asp Thr
65 70 75 80
Leu Asn Arg Thr Tyr Gly Ala Thr Asn Ala Thr Leu Ile Asn Asp Gly
85 90 95
His Asp Ile Thr Met Ala Leu Glu Gly Lys Val Gly Thr Val Thr Val
100 105 110
Asn Gly Lys Ala Tyr Ser Phe Glu Lys Leu His Trp His Ser Pro Ser
115 120 125
Asp His Thr Ile Asn Gly Gln Arg Phe Pro Leu Glu Leu His Leu Val
130 135 140
His Arg Ser Ala Asp Gly Ala Leu Ala Val Ile Gly Ile Leu Tyr Gln

PF58581.ST25.txt

```

145          150          155          160
Leu Gly Ala Pro Asp Ser Phe Tyr Tyr Gln Leu Lys Arg Gln Leu Gly
165          170          175
Glu Met Ala Gln Asp Arg Cys Asp Phe Ala Glu Glu Glu Glu Ser Arg
180          185          190
Val Glu Ala Gly Leu Ile His Leu Arg Ser Leu Gln Lys Arg Thr Gly
195          200          205
Ser Tyr Phe Arg Tyr Thr Gly Ser Leu Thr Val Pro Pro Cys Thr Glu
210          215          220
Asn Val Val Trp Ser Val Leu Gly Lys Val Arg Gln Ile Ser Gln Asp
225          230          235          240
Gln Leu Gln Leu Leu Lys Ala Pro Leu Pro Gly Ser Asp Ala Arg Pro
245          250          255
Thr Gln Pro Leu Asn Gly Arg Thr Val Gln Phe Tyr Asn Pro Pro Asn
260          265          270
Ser Thr Ile Ser Phe Gln Ile
275

```

```

<210> 202
<211> 274
<212> PRT
<213> Brassica napus

```

```

<400> 202
Met Lys Arg Pro Ser Ile Val Arg Val Ile Phe Leu Ile Val Ile Ser
1      5      10      15
Ile Thr Thr Ala Ser Gly Ser Pro Asp His Gly Glu Val Glu Asp Glu
20     25     30
Thr Glu Phe Asn Tyr Glu Lys Gly Glu Lys Gly Pro Glu Lys Trp
35     40     45
Gly Thr Leu Lys Pro Glu Trp Lys Met Cys Gly Asn Gly Thr Met Gln
50     55     60
Ser Pro Ile Asp Leu Thr Asp Lys Arg Val Phe Ile Asp His Asn Leu
65     70     75     80
Gly Pro Leu Arg Ser His Tyr Leu Pro Ser Asn Ala Thr Ile Lys Asn
85     90     95
Arg Gly His Asp Ile Met Leu Glu Phe Glu Gly Gly Asn Ala Gly Met
100    105    110
Gly Ile Ile Ile Asn Gly Thr Val Tyr Gln Leu Gln Gln Leu His Trp
115    120    125
His Ser Pro Ser Glu His Thr Ile Asn Gly Lys Arg Phe Val Leu Glu
130    135    140
Gln His Met Leu His Gln Ser Lys Asp Gly Arg Leu Ala Val Val Ala
145    150    155    160
Phe Leu Tyr Ser Leu Gly Arg Pro Asp Ser Phe Leu Leu Ser Leu Glu
165    170    175
Arg Gln Leu Lys Arg Ile Thr Asp Ala His Gly Ser Glu Asp Phe Val
180    185    190
Ser Trp Ile Asp Pro Arg Ala Val Asn Phe Lys Thr Arg Leu Tyr Tyr
195    200    205
Arg Tyr Leu Gly Ser Leu Thr Thr Pro Pro Cys Ser Glu Asn Val Thr
210    215    220
Trp Ser Ile Ser Arg Glu Met Arg Thr Val Thr Leu Lys Gln Leu Asp
225    230    235    240
Leu Leu Arg Val Ser Val His Asp Gln Ser Asn Thr Asn Ala Arg Pro
245    250    255
Leu Gln Arg Gln Asn Gly Arg Pro Val Lys Phe Tyr Leu Pro Ala Trp
260    265    270
His Ile

```

```

<210> 203
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> motif 1

<220>
<221> VARIANT
<222> (1)..(1)
<223> / replace = "Thr"

<220>
<221> VARIANT
<222> (3)..(3)
<223> / replace = "Asn"

<220>
<221> UNSURE
<222> (4)..(4)
<223> Xaa can be any naturally occurring amino acid

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

<220>
<221> UNSURE
<222> (6)..(9)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (10)..(10)
<223> / replace = "Tyr" / replace = "Leu" / replace = "His"

<220>
<221> UNSURE
<222> (11)..(12)
<223> Xaa can be any naturally occurring amino acid

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

<220>
<221> UNSURE
<222> (14)..(14)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (15)..(15)
<223> / replace = "Gln"

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<220>
 <221> VARIANT
 <222> (16)..(16)
 <223> / replace = "Ile" / replace = "Val" / replace = "Met" / replace =
 "Phe" / replace = "Ala"

<220>
 <221> VARIANT
 <222> (17)..(17)
 <223> / replace = "Ile" / replace = "Val" / replace = "Met" / replace =
 "Phe" / replace = "Ala"

<400> 203
 Ser Glu His Xaa Leu Xaa Xaa Xaa Xaa Phe Xaa Xaa Glu Xaa His Leu
 1 5 10 15
 Leu

<210> 204
 <211> 7
 <212> PRT
 <213> Artificial sequence

<220>
 <223> motif 2

<220>
 <221> VARIANT
 <222> (1)..(1)
 <223> / replace = "Asn" / replace = "Tyr" / replace = "Met" / replace =
 "Thr" / replace = "Phe" / replace = "Ala" / replace = "Arg"

<220>
 <221> VARIANT
 <222> (2)..(2)
 <223> / replace = "Val" / replace = "Ser"

<220>
 <221> VARIANT
 <222> (4)..(4)
 <223> / replace = "Ile" / replace = "Leu" / replace = "Thr"

<220>
 <221> VARIANT
 <222> (5)..(5)
 <223> / replace = "Thr" / replace = "Gly" / replace = "Ser"

<220>
 <221> VARIANT
 <222> (6)..(6)
 <223> / replace = "Val" / replace = "Ile" / replace = "Ser" / replace =
 "Thr"

<220>
 <221> VARIANT
 <222> (7)..(7)
 <223> / replace = "Phe" / replace = "Val" / replace = "Met"

<400> 204
 Leu Ala Val Val Ala Phe Leu
 1 5

<210> 205
 <211> 16
 <212> PRT
 <213> Artificial sequence

<220>
 <223> motif 3

<220>
 <221> VARIANT
 <222> (1)..(1)
 <223> / replace = "Phe"

<220>
 <221> VARIANT
 <222> (2)..(2)
 <223> / replace = "Phe" / replace = "Val" / replace = "Gly" / replace =
 "Ala"

<220>
 <221> VARIANT
 <222> (3)..(3)
 <223> / replace = "Glu" / replace = "Gly" / replace = "Thr" / replace =
 "His"

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

<220>
 <221> UNSURE
 <222> (5)..(5)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> VARIANT
 <222> (8)..(8)
 <223> / replace = "Phe" / replace = "Tyr"

<220>
 <221> VARIANT
 <222> (10)..(10)
 <223> / replace = "Val" / replace = "Ala"

<220>
 <221> VARIANT
 <222> (14)..(14)
 <223> / replace = "Thr" / replace = "Gly" / replace = "Asp" / replace =
 "Ala"

<220>
 <221> VARIANT
 <222> (15)..(15)
 <223> / replace = "Gln"


```

<220>
<221> VARIANT
<222> (16)..(16)
<223> / replace = "Gly" / replace = "Asp" / replace = "Arg"

<400> 205
Tyr Tyr Arg Tyr Xaa Gly Ser Leu Thr Thr Pro Pro Cys Ser Glu Asn
1          5          10          15

<210> 206
<211> 1416
<212> DNA
<213> Oryza sativa

<400> 206
cccacgcgtc cgccacgcg tccgggacac cagaaacata gtacacttga gctcactcca      60
aactcaaaca ctcacaccaa tggctctcca agttcaggcc gcactcctgc cctctgctct      120
ctctgtcccc aagaagggtg acttgagcgc ggtggtgaag gagccggggt tccttagcgt      180
gagcagaagg ccaagaagcc gtcgctggtg gtgaggcgcg tggcgacgcg gcgggcccgt      240
ggcgagcccc ggcgcgggca cgtcgaaggc ggacgggaag aagacgctgc ggcagggggg      300
ggtggtgatc accggcgcgt cgtcggggct cgggctcgcg gcggcgaagg cgcttgccgg      360
agacggggaa gtggcacgtg gtgatggcgt tccgcgactt tcctgaaggc ggcgacggcg      420
gcgaaggcgg cggggatggc ggcggggagc tacaccgtca tgcacctgga cctcgccctc      480
ctcgacagcg tccgccagtt cgtggacaac ttccggcgct ccggcatgcc gctcgacgcg      540
ctgggtgtgca acgccgcaca tctaccggcc gacggcgcgg caaccgacgt tcaacgccga      600
cgggtacgag atgagcgtcg ggggtgaacca cctgggccac ttcttcctcg ccgcctcat      660
gctcgacgac ctcaagaaat ccgactaccg gtcgcggcgg ctcatcatcc tcggctccat      720
caccggcaac accaacacct tcgccggcaa cgtccctccc aaggccgggc taggcgacct      780
ccggggggctc gccggcgggc tccgcgggca gaacgggtcg gcgatgatcg acggcgcgga      840
gagcttcgac ggcgccaagg cgtacaagga cagcaagatc tgtaacatgc tgacgatgca      900
ggagttccac cggagattcc acgaggagac cgggatcacg ttcgcgctcg tgtaccggg      960
gtgcatcgcg acgacgggct tgttcgcgca gcacatcccg ctgttcggcg tgtgttccc      1020
gccgttccag cggttcgtga cgaaggggtt cgtgtcggag gcggagtccg ggaagcggct      1080
ggcgaggtg gtggcgacc cgagcctgac caagtccggc gtgtactgga gctggaacaa      1140
ggactcggcg tcgttcgaga accagctctc gcaggaggcc agcgaccggg agaaggccag      1200
gaagctctgg gacctcagcg agaagctcgt cggcctcgtc tgagtttatt atttacccat      1260
tcgtttcaac tgttaatttc ttcggggttt agggggtttc agctttcagt gagagaggcc      1320
tgtcaagtga tgtacaatta gtaatttttt ttaccgcgac aaatcatgca ataaaaccac      1380
aggcttacat tatcgatttg tccacctaaa ttaagt                                1416

<210> 207
<211> 51
<212> DNA
<213> Artificial sequence

<220>
<223> primer: prm8571

<400> 207
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<210> 214

<211> 987

<212> PRT

<213> Brassica napus

<400> 214

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20        25        30
Thr Asp Met Asp His Leu Leu Thr Leu Lys Ser Ser Met Val Gly Pro
35        40        45
Asn Gly His Gly Leu His Asp Trp Val Arg Ser Pro Ser Pro Ser Ala
50        55        60
His Cys Ser Phe Ser Gly Val Ser Cys Asp Gly Asp Ala Arg Val Ile
65        70        75        80
Ser Leu Asn Val Ser Phe Thr Pro Leu Phe Gly Thr Ile Ser Pro Glu
85        90        95

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Ile Gly Met Leu Asp Arg Leu Val Asn Leu Thr Leu Ala Ala Asn Asn
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Phe Ser Gly Met Leu Pro Leu Glu Met Lys Ser Leu Thr Ser Leu Lys
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Val Leu Asn Ile Ser Asn Asn Val Asn Leu Asn Gly Thr Phe Pro Gly
      130      135      140
Glu Ile Leu Thr Pro Met Val Asp Leu Glu Val Leu Asp Ala Tyr Asn
145      150      155      160
Asn Asn Phe Thr Gly Pro Leu Pro Pro Glu Ile Pro Gly Leu Lys Lys
      165      170      175
Leu Arg His Leu Ser Leu Gly Gly Asn Phe Leu Thr Gly Glu Ile Pro
      180      185      190
Glu Ser Tyr Gly Asp Ile Gln Ser Leu Glu Tyr Leu Gly Leu Asn Gly
      195      200      205
Ala Gly Leu Ser Gly Glu Ser Pro Ala Phe Leu Ser Arg Leu Lys Asn
      210      215      220
Leu Lys Glu Met Tyr Val Gly Tyr Phe Asn Ser Tyr Thr Gly Gly Val
225      230      235      240
Pro Pro Glu Phe Gly Glu Leu Thr Asn Leu Glu Val Leu Asp Met Ala
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Ser Cys Thr Leu Thr Gly Glu Ile Pro Thr Thr Leu Ser Asn Leu Lys
      260      265      270
His Leu His Thr Leu Phe Leu His Ile Asn Asn Leu Thr Gly Asn Ile
      275      280      285
Pro Pro Glu Leu Ser Gly Leu Ile Ser Leu Lys Ser Leu Asp Leu Ser
      290      295      300
Ile Asn Gln Leu Thr Gly Glu Ile Pro Gln Ser Phe Ile Ser Leu Trp
305      310      315      320
Asn Ile Thr Leu Val Asn Leu Phe Arg Asn Asn Leu His Gly Pro Ile
      325      330      335
Pro Glu Phe Ile Gly Asp Met Pro Asn Leu Gln Val Leu Gln Val Trp
      340      345      350
Glu Asn Asn Phe Thr Leu Glu Leu Pro Ala Asn Leu Gly Arg Asn Gly
      355      360      365
Asn Leu Lys Lys Leu Asp Val Ser Asp Asn His Leu Thr Gly Leu Ile
      370      375      380
Pro Met Asp Leu Cys Arg Gly Gly Lys Leu Glu Thr Leu Val Leu Ser
385      390      395      400
Asp Asn Phe Phe Phe Gly Ser Ile Pro Glu Lys Leu Gly Arg Cys Lys
      405      410      415
Ser Leu Asn Lys Ile Arg Ile Val Lys Asn Leu Leu Asn Gly Thr Val
      420      425      430
Pro Ala Gly Leu Phe Thr Leu Pro Leu Val Thr Ile Ile Glu Leu Thr
      435      440      445
Asp Asn Phe Phe Ser Gly Glu Leu Pro Gly Glu Met Ser Gly Asp Leu
      450      455      460
Leu Asp His Ile Tyr Leu Ser Asn Asn Trp Phe Thr Gly Leu Ile Pro
465      470      475      480
Pro Ala Ile Gly Asn Phe Lys Asn Leu Gln Asp Leu Phe Leu Asp Arg
      485      490      495
Asn Arg Phe Ser Gly Asn Ile Pro Arg Glu Val Phe Glu Leu Lys His
      500      505      510
Leu Thr Lys Ile Asn Thr Ser Ala Asn Asn Leu Thr Gly Asp Ile Pro
      515      520      525
Asp Ser Ile Ser Arg Cys Thr Ser Leu Ile Ser Val Asp Leu Ser Arg
      530      535      540
Asn Arg Ile Gly Gly Asp Ile Pro Lys Asp Ile His Asp Val Ile Asn
545      550      555      560
Leu Gly Thr Leu Asn Leu Ser Gly Asn Gln Leu Thr Gly Ser Ile Pro

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                    565                    570                    575
Ile Gly Ile Gly Lys Met Thr Ser Leu Thr Thr Leu Asp Leu Ser Phe
                    580                    585                    590
Asn Asp Leu Ser Gly Arg Val Pro Leu Gly Gly Gln Phe Leu Val Phe
                    595                    600                    605
Asn Asp Thr Ser Phe Ala Gly Asn Pro Tyr Leu Cys Leu Pro Arg His
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Val Ser Cys Leu Thr Arg Pro Gly Gln Thr Ser Asp Arg Ile His Thr
        625                    630                    635                    640
Ala Leu Phe Ser Pro Ser Arg Ile Ala Ile Thr Ile Ile Ala Ala Val
        645                    650                    655
Thr Ala Leu Ile Leu Ile Ser Val Ala Ile Arg Gln Met Asn Lys Lys
        660                    665                    670
Lys His Glu Arg Ser Leu Ser Trp Lys Leu Thr Ala Phe Gln Arg Leu
        675                    680                    685
Asp Phe Lys Ala Glu Asp Val Leu Glu Cys Leu Gln Glu Glu Asn Ile
        690                    695                    700
Ile Gly Lys Gly Gly Ala Gly Ile Val Tyr Arg Gly Ser Met Pro Asn
        705                    710                    715                    720
Asn Val Asp Val Ala Ile Lys Arg Leu Val Gly Arg Gly Thr Gly Arg
        725                    730                    735
Ser Asp His Gly Phe Thr Ala Glu Ile Gln Thr Leu Gly Arg Ile Arg
        740                    745                    750
His Arg His Ile Val Arg Leu Leu Gly Tyr Val Ala Asn Arg Asp Thr
        755                    760                    765
Asn Leu Leu Leu Tyr Glu Tyr Met Pro Asn Gly Ser Leu Gly Glu Leu
        770                    775                    780
Leu His Gly Ser Lys Gly Gly His Leu Gln Trp Glu Thr Arg His Arg
        785                    790                    795                    800
Val Ala Val Glu Ala Ala Lys Gly Leu Cys Tyr Leu His His Asp Cys
        805                    810                    815
Ser Pro Leu Ile Leu His Arg Asp Val Lys Ser Asn Asn Ile Leu Leu
        820                    825                    830
Asp Ser Asp Phe Glu Ala His Val Ala Asp Phe Gly Leu Ala Lys Phe
        835                    840                    845
Leu Leu Asp Gly Ala Ala Ser Glu Cys Met Ser Ser Ile Ala Gly Ser
        850                    855                    860
Tyr Gly Tyr Ile Ala Pro Glu Tyr Ala Tyr Thr Leu Lys Val Asp Glu
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Lys Ser Asp Val Tyr Ser Phe Gly Val Val Leu Leu Glu Leu Ile Ala
        885                    890                    895
Gly Lys Lys Pro Val Gly Glu Phe Gly Glu Gly Val Asp Ile Val Arg
        900                    905                    910
Trp Val Arg Asn Thr Glu Gly Glu Ile Pro Gln Pro Ser Asp Ala Ala
        915                    920                    925
Thr Val Val Ala Ile Val Asp Gln Arg Leu Thr Gly Tyr Pro Leu Thr
        930                    935                    940
Ser Val Ile His Val Phe Lys Ile Ala Met Met Cys Val Glu Asp Glu
        945                    950                    955                    960
Ala Thr Thr Arg Pro Thr Met Arg Glu Val Val His Met Leu Thr Asn
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<210> 215
 <211> 2925
 <212> DNA
 <213> Eucalyptus grandis

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<400> 215

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ccggcgcagcc	tcgcgaagct	gaagaacctc	cagtggctct	acctgggcta	cttcaacacg	660
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<210> 216

<211> 974

<212> PRT

<213> Eucalyptus grandis

<400> 216

Met	Ala	Ala	Thr	Ala	Ala	Lys	Pro	Pro	Cys	Lys	Pro	Ala	Ser	Tyr	Phe
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Cys	Phe	Ser	Ser	Ser	Phe	Cys	Leu	Leu	Leu	Phe	Val	Ser	Ala	Ser	Leu
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		35					40					45			
Ala	Pro	Asn	Ser	Thr	Ala	Leu	His	Asp	Trp	Val	Gly	Pro	Ser	Ser	Ser
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Ser	Ser	Ser	Ser	Ser	Ser	Pro	Pro	Pro	Phe	Pro	His	Cys	Ser	Phe	Thr
65					70					75					80
Gly	Val	Thr	Cys	Asp	Ala	Gly	Ser	Arg	Val	Val	Ser	Leu	Asn	Leu	Thr
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Asp	Val	Arg	Leu	Phe	Gly	Arg	Val	Pro	Arg	Glu	Ile	Gly	Leu	Leu	Arg
			100					105					110		
Asp	Leu	Val	Asn	Leu	Thr	Leu	Thr	Ser	Cys	Asn	Leu	Ser	Gly	Thr	Leu
		115					120					125			
Pro	Pro	Glu	Leu	Gly	Asn	Leu	Thr	Glu	Leu	Glu	Val	Leu	Asp	Val	Tyr
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Asp	Asn	Asn	Phe	Thr	Ala	Gln	Leu	Pro	Pro	Glu	Val	Val	Gly	Leu	Lys
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Lys	Leu	Lys	Trp	Leu	Asn	Leu	Ala	Gly	Asn	Tyr	Phe	Phe	Gly	Glu	Ile
				165				170						175	
Pro	Glu	Val	Tyr	Ser	Glu	Met	Glu	Ser	Leu	Glu	Tyr	Leu	Gly	Leu	Gln
			180				185						190		
Ala	Asn	Gln	Leu	Ser	Gly	Arg	Val	Pro	Ala	Ser	Leu	Ala	Lys	Leu	Lys
		195					200					205			
Asn	Leu	Gln	Trp	Leu	Tyr	Leu	Gly	Tyr	Phe	Asn	Thr	Tyr	Asp	Gly	Glu
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Ile	Pro	Ala	Glu	Phe	Gly	Ser	Met	Lys	Glu	Leu	Arg	Arg	Leu	Asp	Leu
225					230					235					240
Ala	Ser	Cys	Gly	Leu	Ser	Gly	Glu	Ile	Pro	Val	Ser	Leu	Ser	Glu	Leu
				245					250					255	
Lys	Lys	Leu	Asp	Ser	Leu	Phe	Leu	Gln	Trp	Asn	Asn	Leu	Met	Gly	Val
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Ser	Asn	Asn	Tyr	Leu	Thr	Gly	Val	Ile	Pro	Ala	Thr	Phe	Ala	Glu	Leu
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Lys	Asn	Leu	Thr	Leu	Leu	Asn	Leu	Phe	Ala	Asn	His	Leu	Glu	Gly	Gln
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				325					330					335	
Trp	Gly	Asn	Asn	Phe	Thr	Met	Met	Leu	Pro	Ala	Gly	Leu	Gly	Arg	Asn
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Gly	Arg	Leu	Leu	Tyr	Val	Asp	Val	Thr	Gln	Asn	His	Phe	Thr	Gly	Thr
		355					360					365			
Ile	Pro	Arg	Glu	Leu	Cys	Arg	Gly	Gly	Arg	Leu	Lys	Thr	Leu	Ile	Leu
	370					375					380				
Thr	Asn	Asn	Ser	Phe	Phe	Gly	Pro	Ile	Pro	Asp	Glu	Phe	Gly	Glu	Cys
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Lys	Ser	Leu	Thr	Lys	Val	Arg	Val	Gly	Lys	Asn	Phe	Leu	Asp	Gly	Thr
				405					410					415	
Ile	Pro	Arg	Gly	Ile	Phe	Asn	Leu	Pro	Gln	Ala	Thr	Ile	Ile	Glu	Leu
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Asn	Asp	Asn	Leu	Phe	Ser	Gly	Glu	Leu	Pro	Ala	Gln	Met	Ser	Gly	Glu
		435					440					445			
Asn	Leu	Val	Ile	Leu	Ser	Leu	Ser	Asn	Asn	Arg	Ile	Ser	Gly	Glu	Ile
	450					455					460				
Pro	Pro	Ala	Ile	Gly	Asn	Phe	Ser	Gly	Leu	Arg	Thr	Leu	Leu	Leu	Asp
465					470					475					480
Ala	Asn	Arg	Phe	Ser	Gly	Lys	Ile	Pro	Ser	Glu	Leu	Phe	Ser	Pro	Arg

				485				490				495			
Phe	Leu	Leu	Arg	Val	Asn	Ile	Ser	Gly	Asn	Ser	Ile	Ser	Gly	Arg	Ile
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Pro	Gly	Ser	Val	Thr	Gly	Cys	Thr	Ser	Leu	Ala	Ala	Leu	Asp	Leu	Ser
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Arg	Asn	Asn	Leu	Ala	Gly	Glu	Ile	Pro	Asn	Gly	Leu	Ser	Ser	Leu	Lys
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Val	Leu	Ala	Val	Leu	Asn	Leu	Ser	Ser	Asn	Arg	Leu	Thr	Gly	Pro	Val
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Leu	Lys	Cys	Leu	Glu	Glu	Glu	Asn	Ile	Ile	Gly	Lys	Gly	Gly	Ala	Gly
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Gln	Leu	Ala	Gly	Arg	Gly	Gly	Asn	Gly	Leu	Ser	Asp	His	Gly	Phe	Ser
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Ile Ser Gly Asn Asn Leu Thr Gly Pro Ile Pro Thr Thr Phe Thr Arg
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Cys Val Ser Leu Ala Ala Val Asp Leu Ser Arg Asn Met Leu Asp Gly
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Asn Gly Ser Leu Gly Glu Trp Leu His Gly Ala Lys Gly Gly His Leu
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Lys Trp Glu Met Arg Tyr Lys Ile Ala Val Glu Ala Ala Lys Gly Leu
785      790      795      800
Cys Tyr Leu His His Asp Cys Ser Pro Leu Ile Ile His Arg Asp Val
      805      810      815
Lys Ser Asn Asn Ile Leu Leu Asp Ala His Phe Glu Ala His Val Ala
      820      825      830
Asp Phe Gly Leu Ala Lys Phe Leu Tyr Asp Leu Gly Ser Ser Gln Ser
      835      840      845
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PF58581.ST25.txt

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Lys	Ser	Met	Lys	Gly	Glu	Lys	Ala	Lys	Asp	Asp	Ala	Leu	Lys	Asp
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Lys	Phe	Ser	Thr	Ser	Ala	Ser	Ala	His	Cys	Ser	Phe	Ser	Gly	Val
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Cys	Asp	Glu	Asp	Gln	Arg	Val	Ile	Ala	Leu	Asn	Val	Thr	Gln	Val
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Leu	Phe	Gly	His	Leu	Ser	Lys	Glu	Ile	Gly	Glu	Leu	Asn	Met	Leu
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Ser	Leu	Thr	Ile	Thr	Met	Asp	Asn	Leu	Thr	Gly	Glu	Leu	Pro	Thr
		100					105						110	Glu
Leu	Ser	Lys	Leu	Thr	Ser	Leu	Arg	Ile	Leu	Asn	Ile	Ser	His	Asn
		115					120				125			Leu
Phe	Ser	Gly	Asn	Phe	Pro	Gly	Asn	Ile	Thr	Phe	Gly	Met	Lys	Lys
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 195 200 205
 Ser Leu Ser Lys Leu Lys Met Leu Lys Glu Leu Gln Leu Gly Tyr Glu
 210 215 220
 Asn Ala Tyr Ser Gly Gly Ile Pro Pro Glu Leu Gly Ser Ile Lys Ser
 225 230 235 240
 Leu Arg Tyr Leu Glu Ile Ser Asn Ala Asn Leu Thr Gly Glu Ile Pro
 245 250 255
 Pro Ser Leu Gly Asn Leu Glu Asn Leu Asp Ser Leu Phe Leu Gln Met
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 275 280 285
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 Glu Thr Phe Ser Lys Leu Lys Asn Leu Thr Leu Ile Asn Phe Phe Gln
 305 310 315 320
 Asn Lys Leu Arg Gly Ser Ile Pro Ala Phe Ile Gly Asp Leu Pro Asn
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 Leu Glu Thr Leu Gln Val Trp Glu Asn Asn Phe Ser Phe Val Leu Pro
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 Gln Asn Leu Gly Ser Asn Gly Lys Phe Ile Tyr Phe Asp Val Thr Lys
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 Asn His Leu Thr Gly Leu Ile Pro Pro Glu Leu Cys Lys Ser Lys Lys
 370 375 380
 Leu Lys Thr Phe Ile Val Thr Asp Asn Phe Phe Arg Gly Pro Ile Pro
 385 390 395 400
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 405 410 415
 Asn Tyr Leu Asp Gly Pro Val Pro Pro Gly Ile Phe Gln Leu Pro Ser
 420 425 430
 Val Gln Ile Ile Glu Leu Gly Asn Asn Arg Phe Asn Gly Gln Leu Pro
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 Thr Glu Ile Ser Gly Asn Ser Leu Gly Asn Leu Ala Leu Ser Asn Asn
 450 455 460
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 Gln Thr Leu Leu Leu Asp Ala Asn Gln Phe Leu Gly Glu Ile Pro Ala
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 Glu Val Phe Ala Leu Pro Val Leu Thr Arg Ile Asn Ile Ser Gly Asn
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 515 520 525
 Thr Ala Val Asp Phe Ser Arg Asn Met Leu Thr Gly Glu Val Pro Lys
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 Gly Met Lys Asn Leu Lys Val Leu Ser Ile Phe Asn Val Ser His Asn
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 Ser Ile Ser Gly Lys Ile Pro Asp Glu Ile Arg Phe Met Thr Ser Leu
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 Gly Gly Gln Phe Leu Val Phe Asn Asp Arg Ser Phe Ala Gly Asn Pro
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Glu	Met	Gly	Pro	Ala	Arg	Pro	Thr	Met	Arg	Glu	Val	Val	His	Met	Leu
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 <213> Oryza sativa

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 <212> PRT
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 Asp Pro Ala Ala Thr Ser Pro Ala His Cys Thr Phe Ser Gly Val Thr
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 Cys Asp Gly Arg Ser Arg Val Val Ala Ile Asn Leu Thr Ala Leu Pro
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 Leu His Ser Gly Tyr Leu Pro Pro Glu Ile Ala Leu Leu Asp Ser Leu

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595 600 605
Ser Phe Val Gly Asn Pro Gly Leu Cys Gly Gly Pro Val Ala Asp Ala
610 615 620
Cys Pro Pro Ser Met Ala Gly Gly Gly Gly Ala Gly Ser Gln Leu
625 630 635 640
Arg Leu Arg Trp Asp Ser Lys Lys Met Leu Val Ala Leu Val Ala Ala
645 650 655
Phe Ala Ala Val Ala Val Ala Phe Leu Gly Ala Arg Lys Gly Cys Ser
660 665 670
Ala Trp Arg Ser Ala Ala Arg Arg Arg Ser Gly Ala Trp Lys Met Thr
675 680 685
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Gly Arg Ile Arg His Arg Asn Ile Val Arg Leu Leu Gly Phe Val Ser
755 760 765
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770 775 780
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785 790 795 800
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<211> 2931

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<213> Pisum sativa

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<211> 976

<212> PRT

<213> Pisum sativa

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<400> 228

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Glu Ser Met Lys Gly Glu Lys Ser Lys His Pro Asp Ser Leu Gly Asp
35      40      45
Trp Lys Phe Ser Ala Ser Gly Ser Ala His Cys Ser Phe Ser Gly Val
50      55      60
Thr Cys Asp Gln Asp Asn Arg Val Ile Thr Leu Asn Val Thr Gln Val
65      70      75      80
Pro Leu Phe Gly Arg Ile Ser Lys Glu Ile Gly Val Leu Asp Lys Leu
85      90      95
Glu Arg Leu Ile Ile Thr Met Asp Asn Leu Thr Gly Glu Leu Pro Phe
100     105     110
Glu Ile Ser Asn Leu Thr Ser Leu Lys Ile Leu Asn Ile Ser His Asn
115     120     125
Thr Phe Ser Gly Asn Phe Pro Gly Asn Ile Thr Leu Arg Met Thr Lys
130     135     140
Leu Glu Val Leu Asp Ala Tyr Asp Asn Ser Phe Thr Gly His Leu Pro
145     150     155     160
Glu Glu Ile Val Ser Leu Lys Glu Leu Thr Ile Leu Cys Leu Ala Gly
165     170     175
Asn Tyr Phe Thr Gly Thr Ile Pro Glu Ser Tyr Ser Glu Phe Gln Lys
180     185     190
Leu Glu Ile Leu Ser Ile Asn Ala Asn Ser Leu Ser Gly Lys Ile Pro
195     200     205
Lys Ser Leu Ser Lys Leu Lys Thr Leu Lys Glu Leu Arg Leu Gly Tyr
210     215     220
Asn Asn Ala Tyr Asp Gly Val Pro Pro Glu Phe Gly Ser Leu Lys
225     230     235     240
Ser Leu Arg Tyr Leu Glu Val Ser Asn Cys Asn Leu Thr Gly Glu Ile
245     250     255
Pro Pro Ser Phe Gly Asn Leu Glu Asn Leu Asp Ser Leu Phe Leu Gln
260     265     270
Met Asn Asn Leu Thr Gly Ile Ile Pro Pro Glu Leu Ser Ser Met Lys
275     280     285
Ser Leu Met Ser Leu Asp Leu Ser Asn Asn Ala Leu Ser Gly Glu Ile
290     295     300
Pro Glu Ser Phe Ser Asn Leu Lys Ser Leu Thr Leu Leu Asn Phe Phe
305     310     315     320
Gln Asn Lys Phe Arg Gly Ser Ile Pro Ala Phe Ile Gly Asp Leu Pro
325     330     335
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340     345     350
Pro Gln Asn Leu Gly Ser Asn Gly Lys Phe Ile Phe Phe Asp Val Thr
355     360     365
Lys Asn His Leu Thr Gly Leu Ile Pro Pro Asp Leu Cys Lys Ser Lys
370     375     380
Lys Leu Gln Thr Phe Ile Val Thr Asp Asn Phe Phe His Gly Pro Ile
385     390     395     400
Pro Lys Gly Ile Gly Ala Cys Lys Ser Leu Leu Lys Ile Arg Val Ala
405     410     415
Asn Asn Tyr Leu Asp Gly Pro Val Pro Gln Gly Ile Phe Gln Met Pro
420     425     430
Ser Val Thr Ile Ile Glu Leu Gly Asn Asn Arg Phe Asn Gly Gln Leu
435     440     445
Pro Ser Glu Val Ser Gly Val Asn Leu Gly Ile Leu Thr Ile Ser Asn
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Leu Thr Ala Val Asp Phe Ser Arg Asn Met Ile Thr Gly Glu Val Pro
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Arg Gly Met Lys Asn Leu Lys Val Leu Ser Ile Phe Asn Leu Ser His
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Thr Gly Gly Gln Phe Leu Val Phe Asn Asp Arg Ser Phe Phe Gly Asn
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Pro Asn Leu Cys Phe Pro His Gln Ser Ser Cys Ser Ser Tyr Thr Phe
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Pro Ser Ser Lys Ser His Ala Lys Val Lys Ala Ile Ile Thr Ala Ile
625                               630                               635                               640
Ala Leu Ala Thr Ala Val Leu Leu Val Ile Ala Thr Met His Met Met
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Arg Lys Arg Lys Leu His Met Ala Lys Ala Trp Lys Leu Thr Ala Phe
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Gln Arg Leu Asp Phe Lys Ala Glu Glu Val Val Glu Cys Leu Lys Glu
675                               680                               685
Glu Asn Ile Ile Gly Lys Gly Gly Ala Gly Ile Val Tyr Arg Gly Ser
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Ser Gly Arg Asn Asp Tyr Gly Phe Lys Ala Glu Ile Glu Thr Leu Gly
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Arg Ile Arg His Arg Asn Ile Met Arg Leu Leu Gly Tyr Val Ser Asn
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Lys Asp Thr Asn Leu Leu Leu Tyr Glu Tyr Met Pro Asn Gly Ser Leu
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Gly Glu Trp Leu His Gly Ala Lys Gly Cys His Leu Ser Trp Glu Met
770                               775                               780
Arg Tyr Lys Ile Ala Val Glu Ala Gly Lys Gly Leu Cys Tyr Leu His
785                               790                               795                               800
His Asp Cys Ser Pro Leu Ile Ile His Arg Asp Val Lys Ser Asn Asn
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Asp Lys Ala Leu Val Ser Ala Val Val Asp Pro Arg Leu Thr Gly Tyr
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Pro Met Ala Ser Val Ile Tyr Met Phe Asn Ile Ala Met Met Cys Val

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<210> 229
 <211> 2922
 <212> DNA
 <213> Populus tremuloides

<400> 229

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 <211> 973
 <212> PRT
 <213> Populus tremuloides

<400> 230
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 35 40 45
 Pro Ala Ser Pro Thr Ala His Cys Tyr Phe Ser Gly Val Thr Cys Asp
 50 55 60
 Glu Asp Ser Arg Val Val Ser Leu Asn Val Ser Phe Arg His Leu Pro
 65 70 75 80
 Gly Ser Ile Pro Pro Glu Ile Gly Leu Leu Asn Lys Leu Val Asn Leu
 85 90 95
 Thr Leu Ser Gly Asn Asn Leu Thr Gly Gly Phe Pro Val Glu Ile Ala
 100 105 110
 Met Leu Thr Ser Leu Arg Ile Leu Asn Ile Ser Asn Asn Val Ile Ala
 115 120 125
 Gly Asn Phe Pro Gly Lys Ile Thr Leu Gly Met Ala Leu Leu Glu Val
 130 135 140
 Leu Asp Val Tyr Asn Asn Asn Phe Thr Gly Ala Leu Pro Thr Glu Ile
 145 150 155 160
 Val Lys Leu Lys Asn Leu Lys His Val His Leu Gly Gly Asn Phe Phe
 165 170 175
 Ser Gly Thr Ile Pro Glu Glu Tyr Ser Glu Ile Leu Ser Leu Glu Tyr
 180 185 190
 Leu Gly Leu Asn Gly Asn Ala Leu Ser Gly Lys Val Pro Ser Ser Leu
 195 200 205
 Ser Arg Leu Lys Asn Leu Lys Ser Leu Cys Val Gly Tyr Phe Asn Arg
 210 215 220
 Tyr Glu Gly Ser Ile Pro Pro Glu Phe Gly Ser Leu Ser Asn Leu Glu
 225 230 235 240
 Leu Leu Asp Met Ala Ser Cys Asn Leu Asp Gly Glu Ile Pro Ser Ala
 245 250 255
 Leu Ser Gln Leu Thr His Leu His Ser Leu Phe Leu Gln Val Asn Asn
 260 265 270
 Leu Thr Gly His Ile Pro Pro Glu Leu Ser Gly Leu Ile Ser Leu Lys
 275 280 285
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 290 295 300
 Phe Ser Asp Leu Lys Asn Ile Glu Leu Ile Asn Leu Phe Gln Asn Lys
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 325 330 335
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 340 345 350
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 355 360 365
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 370 375 380
 Thr Leu Ile Leu Met Asn Asn Phe Phe Leu Gly Ser Leu Pro Asp Glu
 385 390 395 400

PF58581.ST25.txt

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435 440 445
Ile Ser Gly Asp Ala Leu Gly Leu Leu Ser Val Ser Asn Asn Arg Ile
450 455 460
Thr Gly Lys Ile Pro Pro Ala Ile Gly Asn Leu Lys Asn Leu Gln Thr
465 470 475 480
Leu Ser Leu Asp Thr Asn Arg Leu Ser Gly Glu Ile Pro Glu Glu Ile
485 490 495
Trp Gly Leu Lys Ser Leu Thr Lys Ile Asn Ile Arg Ala Asn Asn Ile
500 505 510
Arg Gly Glu Ile Pro Ala Ser Ile Ser His Cys Thr Ser Leu Thr Ser
515 520 525
Val Asp Phe Ser Gln Asn Ser Leu Ser Gly Glu Ile Pro Lys Lys Ile
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Thr Gly Gln Leu Pro Gly Glu Ile Gly Tyr Met Arg Ser Leu Thr Ser
565 570 575
Leu Asn Leu Ser Tyr Asn Asn Leu Phe Gly Arg Ile Pro Ser Ala Gly
580 585 590
Gln Phe Leu Ala Phe Asn Asp Ser Ser Phe Leu Gly Asn Pro Asn Leu
595 600 605
Cys Ala Ala Arg Asn Asn Thr Cys Ser Phe Gly Asp His Gly His Arg
610 615 620
Gly Gly Ser Phe Ser Thr Ser Lys Leu Ile Ile Thr Val Ile Ala Leu
625 630 635 640
Val Thr Val Leu Leu Leu Ile Val Val Thr Val Tyr Arg Leu Arg Lys
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Lys Arg Leu Gln Lys Ser Arg Ala Trp Lys Leu Thr Ala Phe Gln Arg
660 665 670
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675 680 685
Ile Ile Gly Lys Gly Gly Ala Gly Ile Val Tyr Arg Gly Ser Met Pro
690 695 700
Glu Gly Val Asp His Val Ala Ile Lys Arg Leu Val Gly Arg Gly Ser
705 710 715 720
Gly Arg Ser Asp His Gly Phe Ser Ala Glu Ile Gln Thr Leu Gly Arg
725 730 735
Ile Arg His Arg Asn Ile Val Arg Leu Leu Gly Tyr Val Ser Asn Lys
740 745 750
Asp Thr Asn Leu Leu Leu Tyr Glu Tyr Met Pro Asn Gly Ser Leu Gly
755 760 765
Glu Leu Leu His Gly Ser Lys Gly Gly His Leu Gln Trp Glu Thr Arg
770 775 780
Tyr Arg Ile Ala Val Glu Ala Ala Lys Gly Leu Cys Tyr Leu His His
785 790 795 800
Asp Cys Ser Pro Leu Ile Ile His Arg Asp Val Lys Ser Asn Asn Ile
805 810 815
Leu Leu Asp Ser Asp Phe Glu Ala His Val Ala Asp Phe Gly Leu Ala
820 825 830
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PF58581.ST25.txt

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Asp	Glu	Ser	Ser	Ala	Arg	Pro	Thr	Met	Arg	Glu	Val	Val	His	Met	Leu
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<400> 231

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<400> 232

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 Ile Arg His Arg Asn Ile Val Arg Leu Leu Gly Tyr Val Ser Asn Lys
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820 825 830
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PF58581.ST25.txt

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Gly Phe Ser Ala Glu Ile Lys Thr Leu Gly Arg Ile Arg His Arg His
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Ile Ile Arg Leu Leu Gly Tyr Ala Ser Asn Arg Asp Thr Asn Leu Leu

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690		695		700																
Leu	Tyr	Glu	Tyr	Met	Pro	Asn	Gly	Ser	Leu	Ser	Gly	Ile	Leu	His	Gly					
705					710				715						720					
Thr	Asn	Gly	Ala	Asn	Leu	Leu	Trp	Glu	Met	Arg	Phe	Arg	Ile	Ala	Val					
				725					730						735					
Glu	Ala	Ala	Lys	Gly	Leu	Cys	Tyr	Leu	His	His	Asp	Cys	Ser	Pro	Pro					
			740					745						750						
Ile	Ile	His	Arg	Asp	Val	Lys	Ser	Asn	Asn	Ile	Leu	Leu	Thr	Ser	Asp					
		755					760							765						
Tyr	Ile	Ala	Cys	Ile	Ala	Asp	Phe	Gly	Leu	Ala	Lys	Ser								
	770					775						780								

<210> 236
 <211> 4
 <212> PRT
 <213> Artificial sequence

<220>
 <223> motif 1

<220>
 <221> UNSURE
 <222> (2)..(2)
 <223> Xaa can be any naturally occurring amino acid

<400> 236
 Leu Xaa Asp Trp
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<210> 237
 <211> 11
 <212> PRT
 <213> Artificial sequence

<220>
 <223> motif 2

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

<220>
 <221> UNSURE
 <222> (4)..(4)
 <223> Xaa can be any naturally occurring amino acid

<220>
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 <222> (6)..(6)
 <223> / replace = "Thr"

<220>
 <221> VARIANT
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<400> 237
 Ala His Cys Xaa Phe Ser Gly Val Ser Cys Asp

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1                5                10

<210> 238
<211> 56
<212> DNA
<213> Artificial sequence

<220>
<223> primer: prm08591

<400> 238
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<210> 239
<211> 51
<212> DNA
<213> Artificial sequence

<220>
<223> primer: prm08592

<400> 239
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<210> 240
<211> 1243
<212> DNA
<213> Oryza sativa

<400> 240
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ttattccgga gcatgattgg gaagggagga cataaggccc atgtcgcgat tgtttggacg      180
gtccagatct ccagatcact cagcaggatc ggccgcgttc gcgtagcacc cgcggtttga      240
ttcggcttcc cgcaaggcgg cggccgggtg ccgtagccgc gtagcttccg ccggaagcga      300
gcacgcgcgc gccgcgcgac cggctctgcg tttgcaccgc cttgcacgcg atacatcggg      360
atagatagct actactctct cggtttcaca atgtaaatca ttctactatt ttccacattc      420
atattgatgt taatgaatat agacatatat atctatttag attcattaac atcaatatga      480
atgtaggaaa tgctagaatg acttacattg tgaattgtga aatggacgaa gtacctacga      540
tggtatgatg caggatcatg aaagaattaa tgcaagatcg tatctgccgc atgcaaaatc      600
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cattaatcac caaatatttc gccttctcca gcagaatata tatctctcca tcttgatcac      840
tgtacacact gacagtgtac gcataaacgc agcagccagc ttaactgtcg tctcacgcgc      900
gcacactggc cttccatctc aggetagctt tctcagccac ccacgtaca tgtcaactcg      960
gcgcgcgcac aggcacaaat tacgtacaaa acgcatgacc aaatcaaaac caccggagaa      1020
gaatcgctcc cgcgcgcggc ggcggcgcgc acgtacgaat gcacgcacgc acgccaacc      1080
ccacgacacg atcgcgcgcg acgcggcgga caccggccat ccaccgcgc cctcacctcg      1140
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aggaaaaaaaa aacaaaacac accaagccaa ataaaagcga caa      1243

<210> 241
<211> 230
<212> PRT
<213> Artificial sequence

<220>
<223> C-terminal domain of SEQ ID NO: 212

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<400> 241

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

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