

PF5908220081125_F_60259_PCT_Sequence_Listing.txt
SEQUENCE LISTING

<110> BASF Plant Science GmbH

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

<130> PF60259

<160> 275

<170> PatentIn version 3.5

<210> 1

<211> 1842

<212> DNA

<213> Oryza sativa

<400> 1

atggcggagg agccacagcc agaggccgcg cccgccgchg tggcggcgac gaccgaggtg	60
gcggtggcgg agaaggcgcc cgtggaggcg gagaaggaga agaaggtgga ggaggagacg	120
ccggcgggtg aggccgaggc gaaggaggag aagaaggatg aggcggcggc ggcggcggcg	180
gcgggaggtg atgaggccgg ggcgatagag gggaccggat cgttcaagga ggagagcaac	240
ctggtggcgg acttgccctga cccggagaag aaggcgctcg atgagttcaa gcagctgac	300
gccgccgccc tcgccgctg tgagttcaat ctgcctcccc ctccgccgcc tccaaggcg	360
aaggttgaag ccgccgttga ggagaccaag gcggaggaga ccaaggccga ggaggaaccc	420
aaggctgagg agccggccaa ggaggaggag cccaaggccg aggtggcggc ggcggcggcg	480
gcgccgccgg aggcaggaac cgaggagccg aaggcggagg cgtcgtccga agaggccaag	540
accgaggagc cgaaggccga ggcggcggcc gacgagccgg ccaaggagga gtccaaagct	600
gaggcggcgc cggctgagga agccaagccg gccgagccgg agccggagga gaagaccgtc	660
gtggtcaccg aggaagaggc ggccaccaag acggtggaag cgatcgagga aaccgtcgtg	720
cccgtgctg ctgcgctgc tgccgccgcc acggaggaa cgcggcgcc ggaaccggag	780
gtgcaggcgg cggcggcgcc tgagcccgtg ttgatctggg gcgtgcccct ggtaggcgac	840
gacgagcgca ccgacacggt gtcctcaag ttctgcgcg cgcgcgagtt caaggtgaag	900
gaggccatgg cgatgctcag gtcggccgtg ctgtggcgca agcgcttcgg catcgagtcc	960
ctcctcgacg ccgacctgc cctgccggag ctgcacagcg tgggtgttcta ccgcggcgcc	1020
gaccgcgagg gccacccgt gtgctacaac gtctacggcg aattccagga caaggacctg	1080
tacgagaagg cattcggcga cgaggagaag cgggagcgct tcctcaagtg gcgcatccag	1140
ctgctggagc gcggcatcct gtcgcagctc gacttctcgc ccagtggcat ctgctccatg	1200
gttcaggta cagacctcaa gaactcgcca cctatgctcg gcaagcaccg cgccgtcacc	1260
cgccaggccg ttgctctgct ccaggacaac taccgagat tcacgcca gaaggtgttc	1320
atcaatgtgc catggtggta tctcgtgcc aacaaaatga tgagcccgtt cctcacgcag	1380
cgtaccaaga gcaagttcat ttttgccagc ccagccaaat cagctgagac cctcttcaga	1440
tatatcgcac cagagcaagt ccctgtccaa ttcggaggtc tcttcaagga agatgatcct	1500

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

gagttcacca cctcagacgc cgttaccgag ctcactatca aaccttcac	1560
ggtgagattc ctgtcactga gaattccacg attggatggg agctccgggt gcttgatgg	1620
gaggtgagct acggagcaga gttcactcct gatgccgagg gtggatacac agtcacgtg	1680
cagaaaacga ggaaggtgcc tgcaaatgag gaaccaatca tgaaaggcag cttcaaggtt	1740
ggcgagccag gaaagattgt gctaacgatc aacaaccctg catcaaagaa gaagaagctc	1800
ctctacagat ccaaggtcaa gagcaccagt gagtccgttt ga	1842

<210> 2
 <211> 613
 <212> PRT
 <213> Oryza sativa

<400> 2

Met	Ala	Glu	Glu	Pro	Gln	Pro	Glu	Ala	Ala	Pro	Ala	Ala	Val	Ala	Ala
1				5				10						15	

Thr	Thr	Glu	Val	Ala	Val	Ala	Glu	Lys	Ala	Pro	Val	Glu	Ala	Glu	Lys
			20					25					30		

Glu	Lys	Lys	Val	Glu	Glu	Glu	Thr	Pro	Ala	Val	Glu	Ala	Glu	Ala	Lys
		35					40					45			

Glu	Glu	Lys	Lys	Asp	Glu	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Gly	Gly	Asp
	50					55						60			

Glu	Ala	Gly	Ala	Ile	Glu	Gly	Thr	Gly	Ser	Phe	Lys	Glu	Glu	Ser	Asn
65					70					75					80

Leu	Val	Ala	Asp	Leu	Pro	Asp	Pro	Glu	Lys	Lys	Ala	Leu	Asp	Glu	Phe
				85					90					95	

Lys	Gln	Leu	Ile	Ala	Ala	Ala	Leu	Ala	Ala	Cys	Glu	Phe	Asn	Leu	Pro
			100					105					110		

Pro	Pro	Pro	Pro	Pro	Pro	Lys	Ala	Lys	Val	Glu	Ala	Ala	Val	Glu	Glu
							120					125			

Thr	Lys	Ala	Glu	Glu	Thr	Lys	Ala	Glu	Glu	Glu	Pro	Lys	Ala	Glu	Glu
	130					135					140				

Pro	Ala	Lys	Glu	Glu	Glu	Pro	Lys	Ala	Glu	Val	Ala	Ala	Ala	Ala	Ala
145					150					155					160

Ala	Pro	Pro	Glu	Ala	Gly	Thr	Glu	Glu	Pro	Lys	Ala	Glu	Ala	Ser	Ser
				165					170					175	

Glu	Glu	Ala	Lys	Thr	Glu	Glu	Pro	Lys	Ala	Glu	Ala	Ala	Ala	Asp	Glu
			180					185					190		

Pro	Ala	Lys	Glu	Glu	Ser	Lys	Ala	Glu	Ala	Ala	Pro	Ala	Glu	Glu	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

195

200

205

Lys Pro Ala Glu Pro Glu Pro Glu Glu Lys Thr Val Val Val Thr Glu
210 215 220

Glu Glu Ala Ala Thr Lys Thr Val Glu Ala Ile Glu Glu Thr Val Val
225 230 235 240

Pro Ala Ala Ala Ala Pro Ala Ala Ala Ala Thr Glu Glu Ala Ala Ala
245 250 255

Pro Glu Pro Glu Val Gln Ala Ala Ala Ala Pro Glu Pro Val Leu Ile
260 265 270

Trp Gly Val Pro Leu Val Gly Asp Asp Glu Arg Thr Asp Thr Val Leu
275 280 285

Leu Lys Phe Leu Arg Ala Arg Glu Phe Lys Val Lys Glu Ala Met Ala
290 295 300

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

Leu Leu Asp Ala Asp Leu Ala Leu Pro Glu Leu Asp Ser Val Val Phe
325 330 335

Tyr Arg Gly Ala Asp Arg Glu Gly His Pro Val Cys Tyr Asn Val Tyr
340 345 350

Gly Glu Phe Gln Asp Lys Asp Leu Tyr Glu Lys Ala Phe Gly Asp Glu
355 360 365

Glu Lys Arg Glu Arg Phe Leu Lys Trp Arg Ile Gln Leu Leu Glu Arg
370 375 380

Gly Ile Leu Ser Gln Leu Asp Phe Ser Pro Ser Gly Ile Cys Ser Met
385 390 395 400

Val Gln Val Thr Asp Leu Lys Asn Ser Pro Pro Met Leu Gly Lys His
405 410 415

Arg Ala Val Thr Arg Gln Ala Val Ala Leu Leu Gln Asp Asn Tyr Pro
420 425 430

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

Ala Ala Asn Lys Met Met Ser Pro Phe Leu Thr Gln Arg Thr Lys Ser
450 455 460

Lys Phe Ile Phe Ala Ser Pro Ala Lys Ser Ala Glu Thr Leu Phe Arg
465 470 475 480

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Tyr Ile Ala Pro Glu Gln Val Pro Val Gln Phe Gly Gly Leu Phe Lys
485 490 495

Glu Asp Asp Pro Glu Phe Thr Thr Ser Asp Ala Val Thr Glu Leu Thr
500 505 510

Ile Lys Pro Ser Ser Lys Glu Thr Val Glu Ile Pro Val Thr Glu Asn
515 520 525

Ser Thr Ile Gly Trp Glu Leu Arg Val Leu Gly Trp Glu Val Ser Tyr
530 535 540

Gly Ala Glu Phe Thr Pro Asp Ala Glu Gly Gly Tyr Thr Val Ile Val
545 550 555 560

Gln Lys Thr Arg Lys Val Pro Ala Asn Glu Glu Pro Ile Met Lys Gly
565 570 575

Ser Phe Lys Val Gly Glu Pro Gly Lys Ile Val Leu Thr Ile Asn Asn
580 585 590

Pro Ala Ser Lys Lys Lys Lys Leu Leu Tyr Arg Ser Lys Val Lys Ser
595 600 605

Thr Ser Glu Ser Val
610

<210> 3
<211> 1308
<212> DNA
<213> Oryza sativa

<400> 3
atgtctccga cgcaccccc atccccgcg cccgccgcgg tggcggcagc gcccaagccg 60
ccgccgtcgg ggacgggggc gaagcgcagc ctgatgtcgt cgctgatgga ggccaccgcg 120
ctgctcaggt cgtcgtcgtt caaggaggac tcgtacgtgg cgtccgcgct cccggcgctcc 180
gacctccgcg cgctcgccga cctcagggcg ctgctgtcca cgcacccgga cccaatctcc 240
atctggggcg tgccgtcaa cccggcgccg cccagggcg gggagggggc cccggccccc 300
gccgccgccg ccgacgagcg cgccgacgtc gtgctgtca agttcctccg cgcgcgggac 360
ttccggtcc gcgacgcga cgccatgtg ctccgctgcg ccgctggcg ggccgagttc 420
cgcgccgacg ccgtgctgga cgaggacctc gggttcaagg acctggaggg ggtcgtcgcc 480
tacatgcacg gctgggaccg ggagggccac ccggtctgct acaacgccta cggcgtcttc 540
aaggacaggg acatgtacga ccgctcttc ggcgacggcg agcgctcgc ccgcttcctc 600
cgctggcgcg tccaggtcat ggagcgggc gtccgcgcgc tccacctccg ccccgggcgc 660
gtcaacgcca tcatccaggt caccgacctc aaggacatgc ccaagcgca gctccgcgcc 720
gcgtccaacc agatcctctc cctcttcag gacaactacc ctgagatggt cgcgcgcaag 780

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

gtgttcatca acgtgccctg gtactttctcg gtgctgttct ccatgatctc gccgttcctc      840
acggagcgca ccaagagcaa gttcgtcatc gcgcgcgagg gcaacgtcgc cgagacgctc      900
ttcaagttca tccggccgga gctggtgccg gtgcagtacg gcgggctgag ccgcgccggc      960
gacctggaga acggcccgcc gaagccggcg tccgagttca ccatcaaggg cggcgagaag     1020
gtcttcctag agatcgacgg catcgaggcc ggcgcgacga taacgtggga cctggtggtg     1080
ggcgggtggg agctggagta cggcgcggag tacgtgccgg cggcggagga cagctacacg     1140
ctgtgctgag agcggacgag gaaggtgccg gccgccgccg acgagccggt gcacaacgcc     1200
ttcacggcga gggaggccgg caagatggtg ctctccatcg acaactccgg ctcccggaag     1260
cggaaggtcg ccgcctaccg gtacttcgtg cgcaagccgt cggcgtag                   1308

```

```

<210> 4
<211> 435
<212> PRT
<213> Oryza sativa
<400> 4

```

```

Met Ser Pro Thr Ala Thr Pro Ser Pro Ala Pro Ala Ala Val Ala Ala
1          5          10         15

```

```

Ala Pro Lys Pro Pro Pro Ser Gly Thr Gly Ala Lys Arg Ser Leu Met
          20          25         30

```

```

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

```

```

Glu Asp Ser Tyr Val Ala Ser Ala Leu Pro Ala Ser Asp Leu Arg Ala
          50          55         60

```

```

Leu Ala Asp Leu Arg Ala Leu Leu Ser Thr His Pro Asp Pro Ile Ser
          65          70         75         80

```

```

Ile Trp Gly Val Pro Leu Asn Pro Ala Pro Pro Gln Gly Gly Glu Gly
          85          90         95

```

```

Ala Pro Ala Pro Ala Ala Ala Ala Asp Glu Arg Ala Asp Val Val Leu
          100         105        110

```

```

Leu Lys Phe Leu Arg Ala Arg Asp Phe Arg Val Arg Asp Ala His Ala
          115        120        125

```

```

Met Leu Leu Arg Cys Ala Ala Trp Arg Ala Glu Phe Arg Ala Asp Ala
          130        135        140

```

```

Val Leu Asp Glu Asp Leu Gly Phe Lys Asp Leu Glu Gly Val Val Ala
          145        150        155        160

```

```

Tyr Met His Gly Trp Asp Arg Glu Gly His Pro Val Cys Tyr Asn Ala
          165        170        175

```

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

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

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

<210> 5
 <211> 1758
 <212> DNA
 <213> Oryza sativa

<400> 5
 atggctgagg aggcgaagca agagaccccc gccgccgccg aggtggtggt ggtggagaag 60
 gccgacgagg tggtagcggt ggagaaggcc gtggagggtg aggcggagga gaagaagttg 120
 gcggagcagg aggaggagga ggagaagaag gcggaggagg cggaggaggc cgctgggggc 180
 gatgaggcgg cggtgatcga ggggacgggg tcgttcaagg aggagagcaa cctcgtctcc 240
 gagctccccg acccgagcg cacggcgctc gccagctca aggagctcgt cgccgcccg 300
 cttgccgccg gcgagtttga cttcccccg ccgccgccgc ctccaccggc caaggcggag 360
 gagccggcca aggaggagga acccaaggcc gccgaggccc ccgccgccga ggagcccaag 420
 gccgaggccg aggtgaggc tgaggccgcc gccacggagg agcccaagac cgaggagccc 480
 aagaccgagg agcccgcaa ggaggaggag cccaaggcgg cggcggcggc tgcggccgag 540
 gagcccaagg cggaggcggc ggaggaggag gccaagccgg ccgagccgga aacggaggag 600
 aagaccgtcg tggtcaccga ggatgaaggc accagcaaga cggtaggagg catcgaggag 660
 accgtcgtcg tcgcccccc ggccgcggcc gcggaagccg aggtgcggc gccgaaggag 720
 gagctgatat ggggctgtcc gctgaccggc gacgacgagc gcacggacac cgtctgtctc 780
 aagttcctcc gcgccagga gttcaagggt aaggaggcca tggcgatgct caaggcggcg 840
 gtgctgtggc gcaagcgctt cggcatcgac gccgtcctgg ccgccgacct cggcctgccg 900
 gagctcgaga acgtggtgtt ctaccgcggc gccgaccgag agggccaccc cgtctgtctac 960
 aacgtctacg gcgagttcca ggacaaggac ctctacgaga aggccttcgg cgacgaggag 1020
 aagcgggagc gattcctcaa gtggcgcac cagctcctcg agcgcggcat cctcgaccag 1080
 ctgacttct cccccagcg catctgtctc atggtgcagg tcaccgacct caagaactcg 1140
 ccgcccattg tcggcaagca ccgcaccgtc acccgccagg cgctcgccct gctccaggac 1200
 aactaccccg agttcatcg caagaagatt ttcattcaac tgccatggtg gtacattgag 1260
 gctaacaaaa tggtagtcc gttcctcaca caacgcacca agagcaagat catcttttgc 1320
 accgcagcca agtctgcaga gacccttttc agatacattg ctctgagca agtccctgtc 1380
 caattcggag gcctctacaa agaggatgac accgagttct ccacctcaga tgctgtcaca 1440
 gagcttccga tcaaaccttc atccaaagaa actgttgaga ttctgtctac tgagaactcc 1500
 acggttggtg gggagcttcg ggtgcttggg tgggagggtg gctacggtgc agagttcacc 1560
 cctgatgcag aggggtggcta cactgtcatt gtgcagaaga caaggaaggt gcccgccaat 1620
 gaagagccga tcatgaaggg cagcttcaag gttggcgagc ctggcaagat cgtcctcaca 1680
 gtcgacaacg cagcatccaa gaagaagaag cagcttcttt accgattcaa ggtcaagagc 1740
 tcctctgaat ctgcctaa 1758

<210> 6

<211> 585
<212> PRT
<213> Oryza sativa

<400> 6

```

Met Ala Glu Glu Ala Lys Gln Glu Thr Pro Ala Ala Ala Glu Val Val
 1          5          10          15

Val Val Glu Lys Ala Asp Glu Val Val Ala Val Glu Lys Ala Val Glu
 20          25          30

Val Glu Ala Glu Glu Lys Lys Leu Ala Glu Gln Glu Glu Glu Glu Glu
 35          40          45

Lys Lys Ala Glu Glu Ala Glu Glu Ala Ala Gly Gly Asp Glu Ala Ala
 50          55          60

Val Ile Glu Gly Thr Gly Ser Phe Lys Glu Glu Ser Asn Leu Val Ser
 65          70          75          80

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

Val Ala Ala Ala Leu Ala Ala Gly Glu Phe Asp Leu Pro Pro Pro Pro
100          105          110

Pro Pro Pro Pro Ala Lys Ala Glu Glu Pro Ala Lys Glu Glu Glu Pro
115          120          125

Lys Ala Ala Glu Ala Pro Ala Ala Glu Glu Pro Lys Ala Glu Ala Glu
130          135          140

Ala Glu Ala Glu Ala Ala Ala Thr Glu Glu Pro Lys Thr Glu Glu Pro
145          150          155          160

Lys Thr Glu Glu Pro Ala Lys Glu Glu Glu Pro Lys Ala Ala Ala Ala
165          170          175

Ala Ala Ala Glu Glu Pro Lys Ala Glu Ala Ala Ala Glu Glu Ala Lys
180          185          190

Pro Ala Glu Pro Glu Thr Glu Glu Lys Thr Val Val Val Thr Glu Asp
195          200          205

Glu Gly Thr Ser Lys Thr Val Glu Ala Ile Glu Glu Thr Val Val Val
210          215          220

Ala Ala Pro Ala Ala Ala Ala Glu Ala Glu Ala Ala Ala Pro Lys Glu
225          230          235          240

Glu Leu Ile Trp Gly Val Pro Leu Thr Gly Asp Asp Glu Arg Thr Asp
245          250          255

```

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Thr Val Leu Leu Lys Phe Leu Arg Ala Arg Glu Phe Lys Val Lys Glu
260 265 270

Ala Met Ala Met Leu Lys Ala Ala Val Leu Trp Arg Lys Arg Phe Gly
275 280 285

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

Val Val Phe Tyr Arg Gly Ala Asp Arg Glu Gly His Pro Val Cys Tyr
305 310 315 320

Asn Val Tyr Gly Glu Phe Gln Asp Lys Asp Leu Tyr Glu Lys Ala Phe
325 330 335

Gly Asp Glu Glu Lys Arg Glu Arg Phe Leu Lys Trp Arg Ile Gln Leu
340 345 350

Leu Glu Arg Gly Ile Leu Asp Gln Leu Asp Phe Ser Pro Ser Gly Ile
355 360 365

Cys Ser Met Val Gln Val Thr Asp Leu Lys Asn Ser Pro Pro Met Leu
370 375 380

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

Asn Tyr Pro Glu Phe Ile Ala Lys Lys Ile Phe Ile Asn Val Pro Trp
405 410 415

Trp Tyr Ile Ala Ala Asn Lys Met Val Ser Pro Phe Leu Thr Gln Arg
420 425 430

Thr Lys Ser Lys Ile Ile Phe Cys Thr Ala Ala Lys Ser Ala Glu Thr
435 440 445

Leu Phe Arg Tyr Ile Ala Pro Glu Gln Val Pro Val Gln Phe Gly Gly
450 455 460

Leu Tyr Lys Glu Asp Asp Thr Glu Phe Ser Thr Ser Asp Ala Val Thr
465 470 475 480

Glu Leu Pro Ile Lys Pro Ser Ser Lys Glu Thr Val Glu Ile Pro Ala
485 490 495

Thr Glu Asn Ser Thr Val Val Trp Glu Leu Arg Val Leu Gly Trp Glu
500 505 510

Val Ser Tyr Gly Ala Glu Phe Thr Pro Asp Ala Glu Gly Gly Tyr Thr
515 520 525

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Val Ile Val Gln Lys Thr Arg Lys Val Pro Ala Asn Glu Glu Pro Ile
530 535 540

Met Lys Gly Ser Phe Lys Val Gly Glu Pro Gly Lys Ile Val Leu Thr
545 550 555 560

Val Asp Asn Ala Ala Ser Lys Lys Lys Lys Gln Leu Leu Tyr Arg Phe
565 570 575

Lys Val Lys Ser Ser Ser Glu Ser Ala
580 585

<210> 7
<211> 1554
<212> DNA
<213> Oryza sativa

<400> 7
atggcggtgg aggtcgtgtc tgaggggtgcg gcggccgccg cggcggaggt ggcggcgccg 60
gagacgaagg aggtgaccgc gaaggcggcg gcggatgagg cggtgacgct ggctgccgtc 120
gtgtccaaga acgcgtcgtt cagggaggag agcaacttcc tggatgatct caaggacggc 180
gagaggaagg cgttggctga gctccgtgcc aaggttgagg aggccatcgt cgacggcaag 240
ctgttcgatg acggcaagggt ggaggccaag aagaaggccg cggcggcgga ggaggagaag 300
gcggtggagg aggccgccgg tgagaagaaa gatggcgagg agaagaaaga ggaggaggag 360
ccggtgacgg aggagaagaa ggaagaggag caaggcgagg aggaggagga gcccaagaaa 420
gaggaagccg acgagggcga gaaggaggag aagccggcgg aggaggaggc ggcggcggtt 480
gtggacaagg acatcgctct gtggggcgctg ccgctgctgc cgagcaaggg cgacgacgcc 540
accgacgtcg tcctcctcaa gttcctccgc gcgcgcgact tcaaggccgg cgccgccttc 600
gacatgctcc gcaagacgct ccactggcgc agggagtgga agggcttcgc cgccggcacc 660
gacgacgacg acgacggcga ggcgctcccg gcggagctcg ccgacgcgtg ctacctcgac 720
ggcgcggaca gggagggcca cccggtgtgc tacaacgcgc tcggcggtgtt cgccgacgac 780
gccgtgtaca agaaggcgct cggcacggag gaaggcaagg cgaggttcct ccggtggagg 840
gtgcgcgcca tggagagcca cgtggccaag ctcgacctca ggcccggcgg cgtcgcgtcg 900
ctgctgcagg tgacggacct caagaactcg ccggggccgg ccaagaagga cctccgcgtc 960
gccatgaagc aggtgctcga cctcttcag gacaactacc ctgagctcgt cgcaagaaac 1020
attctgatca atgtgccgtt ctggtactac gcgttcagca ccctcttcta cccgttcatt 1080
acgcagagga ccaagagcaa gttcgtcatt gctcggccct ccaaggtcac cgagaccctc 1140
ctcaagtaca ttcccattga agccattcca gtgaagtacg gtggtctgaa gcgcgacgac 1200
gacaccgagt tctcggcaga ggacagtga gtcacagagc tcgttgtaa ggcaagctcc 1260
accgaaacca tcgagatcga agccacagag ggtgacacta cgctgacatg ggacctgacc 1320
gtgctgggat gggagggtga ctacaaggag gagttcgtgc cgagcgagga gggctcgtac 1380
accgtcatcg tcaagaaggg gaagaagatg gggtcgtcgg aggcggcggt ccgcaactcg 1440

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

ttccgcgccg gcgagccggg gaaggtggtc ctcaccgtcg agaacctgac gcacaggaag 1500
aagaaggtgc tgttcaggca caaggccaag agcgcctgtg ccaaggagtg ctga 1554

<210> 8
<211> 517
<212> PRT
<213> Oryza sativa

<400> 8

Met Ala Val Glu Val Val Ser Glu Gly Ala Ala Ala Ala Ala Ala Glu
1 5 10 15

Val Ala Ala Pro Glu Thr Lys Glu Val Thr Ala Lys Ala Ala Ala Asp
20 25 30

Glu Ala Val Thr Leu Ala Ala Val Val Ser Lys Asn Ala Ser Phe Arg
35 40 45

Glu Glu Ser Asn Phe Leu Asp Asp Leu Lys Asp Gly Glu Arg Lys Ala
50 55 60

Leu Ala Glu Leu Arg Ala Lys Val Glu Glu Ala Ile Val Asp Gly Lys
65 70 75 80

Leu Phe Asp Asp Gly Lys Val Glu Ala Lys Lys Lys Ala Ala Ala Ala
85 90 95

Glu Glu Glu Lys Ala Val Glu Glu Ala Ala Gly Glu Lys Lys Asp Gly
100 105 110

Glu Glu Lys Lys Glu Glu Glu Glu Pro Val Thr Glu Glu Lys Lys Glu
115 120 125

Glu Glu Gln Gly Glu Glu Glu Glu Glu Pro Lys Lys Glu Glu Ala Asp
130 135 140

Glu Gly Glu Lys Glu Glu Lys Pro Ala Glu Glu Glu Ala Ala Ala Val
145 150 155 160

Val Asp Lys Asp Ile Ala Leu Trp Gly Val Pro Leu Leu Pro Ser Lys
165 170 175

Gly Asp Asp Ala Thr Asp Val Val Leu Leu Lys Phe Leu Arg Ala Arg
180 185 190

Asp Phe Lys Ala Gly Ala Ala Phe Asp Met Leu Arg Lys Thr Leu His
195 200 205

Trp Arg Arg Glu Trp Lys Gly Phe Ala Ala Gly Thr Asp Asp Asp Asp
210 215 220

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Asp Gly Glu Ala Leu Pro Ala Glu Leu Ala Asp Ala Cys Tyr Leu Asp
225 230 235 240

Gly Ala Asp Arg Glu Gly His Pro Val Cys Tyr Asn Ala Leu Gly Val
245 250 255

Phe Ala Asp Asp Ala Val Tyr Lys Lys Ala Leu Gly Thr Glu Glu Gly
260 265 270

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

Ala Lys Leu Asp Leu Arg Pro Gly Gly Val Ala Ser Leu Leu Gln Val
290 295 300

Thr Asp Leu Lys Asn Ser Pro Gly Pro Ala Lys Lys Asp Leu Arg Val
305 310 315 320

Ala Met Lys Gln Val Leu Asp Leu Phe Gln Asp Asn Tyr Pro Glu Leu
325 330 335

Val Ala Arg Asn Ile Leu Ile Asn Val Pro Phe Trp Tyr Tyr Ala Phe
340 345 350

Ser Thr Leu Phe Tyr Pro Phe Met Thr Gln Arg Thr Lys Ser Lys Phe
355 360 365

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

Pro Ile Glu Ala Ile Pro Val Lys Tyr Gly Gly Leu Lys Arg Asp Asp
385 390 395 400

Asp Thr Glu Phe Ser Ala Glu Asp Ser Glu Val Thr Glu Leu Val Val
405 410 415

Lys Ala Ser Ser Thr Glu Thr Ile Glu Ile Glu Ala Thr Glu Gly Asp
420 425 430

Thr Thr Leu Thr Trp Asp Leu Thr Val Leu Gly Trp Glu Val Asn Tyr
435 440 445

Lys Glu Glu Phe Val Pro Ser Glu Glu Gly Ser Tyr Thr Val Ile Val
450 455 460

Lys Lys Gly Lys Lys Met Gly Ser Ser Glu Ala Ala Val Arg Asn Ser
465 470 475 480

Phe Arg Ala Gly Glu Pro Gly Lys Val Val Leu Thr Val Glu Asn Leu
485 490 495

Thr His Arg Lys Lys Lys Val Leu Phe Arg His Lys Ala Lys Ser Ala
Seite 12

Cys Ala Lys Glu Cys
515

<210> 9
<211> 1058
<212> DNA
<213> Brassica napus

<400> 9
gcgacgtcgt tttactgaag ttcctacgcg ctagggactt caaggtgaaa gattcgctgg 60
caatgctcaa gaacacagtc aagtggagaa gggagttcaa gatcgacgag ttggtcgatg 120
aagactttgt ggatgatctt gacaaggctg tgttcatgca cggacacgac cgtgaaggcc 180
acccgggtgtg ttacaatgtc tacggcgagt tccagaacaa ggagctttac aacaagacgt 240
tctccgatga ggagaagagg aagcatttct tgaggacgag gattcagttc ttggagagga 300
gtataaggaa gctagacttc agctccggtg gtgtttccac cttttttcag attaatgata 360
tgaagaactc tccgggggtg ggaagaaaag agcttagatc ggcgaccaag caagccgtgc 420
agttgcttca ggacaattac cctgagtttg tcttcaaaca ggccttcac aatgttcctt 480
ggtggtacct tgtgttttac actgtgattg gtccgttcat gacaccaaga tcaaagagca 540
agttggtgtt tgctgggtccg tcaagatcag ccgaaactct tttcaaatac atatcgcccg 600
aacaagtccc ggtacaatac ggaggattga gtgtagatcc ttgtgactgc aatccagact 660
tctctttgga tgatccagcc tcagagggtc ttgttaagcc tggaacaaag caaactgttg 720
agatcataat ctatgagaaa tgtgagattg tgtgggagat aagggttaatt ggatgggaag 780
tgagctacaa ggcagagttt gtgcctgaag agaaagatgc ttatacggtg gttgtacaga 840
aaccgaggaa gatgaaacca ttcgatgaac cgggtgttaac ccagagcttc aaagtgaatg 900
agcttggtcaa ggttttactc actgtagaca acccaacctc taagaagaag aagctcgttt 960
acaggttcaa tgtcaaacca ctctgaagtg agatgtcttc tttgtgtttt tgtatatgtg 1020
agtgttttgt atatcatatc atatcatttt gtatttgt 1058

<210> 10
<211> 307
<212> PRT
<213> Brassica napus

<400> 10

Met Leu Lys Asn Thr Val Lys Trp Arg Arg Glu Phe Lys Ile Asp Glu
1 5 10 15

Leu Val Asp Glu Asp Phe Val Asp Asp Leu Asp Lys Val Val Phe Met
20 25 30

His Gly His Asp Arg Glu Gly His Pro Val Cys Tyr Asn Val Tyr Gly
35 40 45

Glu Phe Gln Asn Lys Glu Leu Tyr Asn Lys Thr Phe Ser Asp Glu Glu
50 55 60

Lys Arg Lys His Phe Leu Arg Thr Arg Ile Gln Phe Leu Glu Arg Ser
65 70 75 80

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

Ile Asn Asp Met Lys Asn Ser Pro Gly Leu Gly Lys Lys Glu Leu Arg
100 105 110

Ser Ala Thr Lys Gln Ala Val Gln Leu Leu Gln Asp Asn Tyr Pro Glu
115 120 125

Phe Val Phe Lys Gln Ala Phe Ile Asn Val Pro Trp Trp Tyr Leu Val
130 135 140

Phe Tyr Thr Val Ile Gly Pro Phe Met Thr Pro Arg Ser Lys Ser Lys
145 150 155 160

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

Ile Ser Pro Glu Gln Val Pro Val Gln Tyr Gly Gly Leu Ser Val Asp
180 185 190

Pro Cys Asp Cys Asn Pro Asp Phe Ser Leu Asp Asp Pro Ala Ser Glu
195 200 205

Val Ile Val Lys Pro Gly Thr Lys Gln Thr Val Glu Ile Ile Ile Tyr
210 215 220

Glu Lys Cys Glu Ile Val Trp Glu Ile Arg Val Ile Gly Trp Glu Val
225 230 235 240

Ser Tyr Lys Ala Glu Phe Val Pro Glu Glu Lys Asp Ala Tyr Thr Val
245 250 255

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

Thr Gln Ser Phe Lys Val Asn Glu Leu Gly Lys Val Leu Leu Thr Val
275 280 285

Asp Asn Pro Thr Ser Lys Lys Lys Lys Leu Val Tyr Arg Phe Asn Val
290 295 300

Lys Pro Leu
305

<211> 1092

<212> DNA

<213> Helianthus annuus

<400> 11

```

tccccgctcg acgatttcgt atgatcttga gaaagttgtg attaatcatg gctttgataa      60
agaaggacac ccagattaat ataatgtgta tggtagagttt cagaacaaag agttgtataa      120
taaaatgttt agtgataatg aaggaagatt gaggttttta aggtggagaa ttcagtatct      180
tgaaaggagt ataaggaagt tggatttttag gcctggtggg gtgaatacta tttttcagat      240
tagtgatttg aagaactcgc ctggaccggc gaaacgggag cttcggttag ccaccaggca      300
agctctgcag attctgcagg ataactaccc tgaatttgtg gcaaaacagg ttttcatcaa      360
tgcccccttg tggatttttag ctttctatac aatgattagt ccattcatga ctcaaaggac      420
taaaagcaag tttgtattcg ctagcacggc caagacaccc gaaacccttt tcaaatacgt      480
gaatccggag cacgtaccaa ttcagtacgg cgggttaagc gtagattact gcgattgcaa      540
tcccgaattc acaattgatg atccggcttc agtggtcacc gttaaaccag ctaccaagca      600
gaccgtggag attatagtaa acgagaaatg cttatttgtg tgggagctac gtgtagtcgg      660
ttgggaggtg agctatagtg ctgaatatgt gccgaacaac gaaagccatt acacgataat      720
catacaaaag gctagaaaga tgactccaac cgatgaacca gtgatcagtc acagtttcaa      780
gatcagtgag cttggtaaga tacttctaac cgtcgacaac cgcacctcca agaagaaaac      840
actgctctat aggttcaagg tgaacccgct ttccgaatag aataacgtac atcaaggatc      900
gacagacaga cagtcatatg atcgcgcgag tttattatatt atttatgttt ttatttgttt      960
ctttttggta gttgttatga gtttgggtcc atggtgttgt gtttgggttc aaaaggcttg      1020
tggtttttgt attaatgtct tttggctttc aaaaaatcgg ttgctgaaat ttgactgac      1080
gagttctatt tt                                     1092

```

<210> 12

<211> 251

<212> PRT

<213> Helianthus annuus

<400> 12

```

Met Phe Ser Asp Asn Glu Gly Arg Leu Arg Phe Leu Arg Trp Arg Ile
1           5           10           15

```

```

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

```

```

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

```

```

Ala Lys Arg Glu Leu Arg Leu Ala Thr Arg Gln Ala Leu Gln Ile Leu
          50           55           60

```

```

Gln Asp Asn Tyr Pro Glu Phe Val Ala Lys Gln Val Phe Ile Asn Ala
65           70           75           80

```

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Pro Trp Trp Tyr Leu Ala Phe Tyr Thr Met Ile Ser Pro Phe Met Thr
85 90 95

Gln Arg Thr Lys Ser Lys Phe Val Phe Ala Ser Thr Ala Lys Thr Pro
100 105 110

Glu Thr Leu Phe Lys Tyr Val Asn Pro Glu His Val Pro Ile Gln Tyr
115 120 125

Gly Gly Leu Ser Val Asp Tyr Cys Asp Cys Asn Pro Glu Phe Thr Ile
130 135 140

Asp Asp Pro Ala Ser Val Val Thr Val Lys Pro Ala Thr Lys Gln Thr
145 150 155 160

Val Glu Ile Ile Val Asn Glu Lys Cys Leu Phe Val Trp Glu Leu Arg
165 170 175

Val Val Gly Trp Glu Val Ser Tyr Ser Ala Glu Tyr Val Pro Asn Asn
180 185 190

Glu Ser His Tyr Thr Ile Ile Ile Gln Lys Ala Arg Lys Met Thr Pro
195 200 205

Thr Asp Glu Pro Val Ile Ser His Ser Phe Lys Ile Ser Glu Leu Gly
210 215 220

Lys Ile Leu Leu Thr Val Asp Asn Pro Thr Ser Lys Lys Lys Thr Leu
225 230 235 240

Leu Tyr Arg Phe Lys Val Asn Pro Leu Ser Glu
245 250

<210> 13
<211> 1409
<212> DNA
<213> Zea mays

<400> 13
cggccgcgct cccggcgtcc gagctccgcg cgctcgccga cctcaaggcg ctgctcgcca 60
cccacccgga ccccatctcc atctggggcg tcccgctgaa ccctcgctcc cctcccgccg 120
cggcggacga cgccgccccg gtcgacgagc gcgccgacgt ggtgctcctc aagttcctcc 180
gcgcgcggga cttccgcgtc cgcgacgccc acgccatggt gctccgctgc gccgcctggc 240
gcgccgagtt cggcgccgac gccgtgctgg acgaggagct gggcttcaag gacctggagg 300
gcatcgtcgc ctacatgcac ggctgggacc gcgacggcca ccccgctctgc tacaacgcct 360
acggcgtctt caaagacagg gacatgtacg agcgcgtctt cggcgacggc gaccgcctcg 420
cgcgcttcct ccgctggcgc gtccagggtca tggagcgtgg cgtgcgcgcg ctcaccctga 480
ggcccggggg cgtcaacgcc atcatacagg tcaccgacct caaggacatg ccaaagcggg 540

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

agctcagagc cgccagcaac cagatcctct ccctcttcca ggacaactac ccggagatgg      600
tagcgcgga ggtgttcatt aacgtgccgt ggtacttctc cgtgctcttc tccatgatct      660
cgcccttcct cacggagcgc accaagagca agttcgtcac cgcgcgcgag ggcaacgtcg      720
ccgagacact ctacaagttc atccggccgg agctggtgcc tgtgcagtac ggcgggctga      780
gccgcaccgg tgacctcgag aacggaccac cgaagccggc gtccgagttc accatcaagg      840
gtggcgagaa ggtcttcctg gagatcgacg gtatcgaggc cgggtgcaacg ataacgtggg      900
atctggtcgt cgggggctgg gacctcgagt acggagccga gtacgtgccg gcggccgagg      960
acagctacac gctctgctg gagaaagacg ggatggtctc ggccaccgcc gaggagcccc      1020
tgacaatgc cttcacggct aggaagccg gcaagatggt gctgtccata gacaattctg      1080
gttcccggaa gcgcaagggt gccgcctaca ggtacttcgt gcgcaagtcg tcggcgtagg      1140
catgctgatg tcttgtggtg gtcgtcgcg ccggcacctt gccggcaggt agccgcgagg      1200
gggagggttaa cgtggaacaa ctggtgaagt gtttacttgg gcttgtggga tttggtgggg      1260
agaggtcaag ttaggctggt taattattag tgctataacg acatgcatgt attatgcat      1320
atgtagaata taatgtactc cgtaagagct gttgcacttt tgtcatcacc actgttataa      1380
agctaatagat gagttaagtt ttttgggct                                     1409

```

<210> 14
 <211> 307
 <212> PRT
 <213> Zea mays

<400> 14

Met Val Leu Arg Cys Ala Ala Trp Arg Ala Glu Phe Gly Ala Asp Ala
 1 5 10 15

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

Tyr Met His Gly Trp Asp Arg Asp Gly His Pro Val Cys Tyr Asn Ala
 35 40 45

Tyr Gly Val Phe Lys Asp Arg Asp Met Tyr Glu Arg Val Phe Gly Asp
 50 55 60

Gly Asp Arg Leu Ala Arg Phe Leu Arg Trp Arg Val Gln Val Met Glu
 65 70 75 80

Arg Gly Val Arg Ala Leu Thr Leu Arg Pro Gly Gly Val Asn Ala Ile
 85 90 95

Ile Gln Val Thr Asp Leu Lys Asp Met Pro Lys Arg Glu Leu Arg Ala
 100 105 110

Ala Ser Asn Gln Ile Leu Ser Leu Phe Gln Asp Asn Tyr Pro Glu Met
 115 120 125

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Val Ala Arg Lys Val Phe Ile Asn Val Pro Trp Tyr Phe Ser Val Leu
130 135 140

Phe Ser Met Ile Ser Pro Phe Leu Thr Glu Arg Thr Lys Ser Lys Phe
145 150 155 160

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

Arg Pro Glu Leu Val Pro Val Gln Tyr Gly Gly Leu Ser Arg Thr Gly
180 185 190

Asp Leu Glu Asn Gly Pro Pro Lys Pro Ala Ser Glu Phe Thr Ile Lys
195 200 205

Gly Gly Glu Lys Val Phe Leu Glu Ile Asp Gly Ile Glu Ala Gly Ala
210 215 220

Thr Ile Thr Trp Asp Leu Val Val Gly Gly Trp Asp Leu Glu Tyr Gly
225 230 235 240

Ala Glu Tyr Val Pro Ala Ala Glu Asp Ser Tyr Thr Leu Cys Val Glu
245 250 255

Lys Thr Arg Met Val Ser Ala Thr Ala Glu Glu Pro Val His Asn Ala
260 265 270

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

Gly Ser Arg Lys Arg Lys Val Ala Ala Tyr Arg Tyr Phe Val Arg Lys
290 295 300

Ser Ser Ala
305

<210> 15
<211> 1160
<212> DNA
<213> Glycine max

<400> 15
accatgctga agaacacgat ccagtggagg aaggagtttg ggatggagga gctgatggaa 60
gagaagctcg gggatgagtt ggagaagggt gtgttcatgc acggctttga caaggagggt 120
caccctgtgt gttacaacat atatgaggag ttccagaaca aggagttgta caagaagact 180
ttttctgatg aggagaagag ggagaagttc ctgaggtgga gaattcagtt cctggagaag 240
agtataagga agcttgattt caaccctggt ggcataatgca ccattgttca tgtaaatgac 300
ctcaagaact ctctggact tgccaagtgg gaacttagac aagccaccaa acatgcccta 360
caattgcttc aagacaatta ccctgaattt gttgccaaac aggtttttat taatgtgcct 420

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

tggtggtacc tggcagtga taggatgata agcccttttc ttactcagag gactaaaagc      480
aagtttgtct ttgctgggcc ttccaaatca acggaaccc ttttgagata catagctccg      540
gagcagcttc ccgtgaagta cgggtggacta agcaaagatg gggagttcgg aaatatcgat      600
gctgtcacag aaatcacagt gaggccggca gcaaaacata cagtggaatt ttcagttact      660
gagaactgct tactctcttg ggagcttaga gtaataggat gggaagtaag ttatggcgca      720
gaatttgtgc caagctcaga aggaagctac acagtaattg tccagaaggc taggaaggtt      780
gcttcatcag aagaaccagt tctttgcaac agttttaagg ttggtgaacc tgggaaagtt      840
gttctcacca ttgacaacac aagctctaag aagaagaagc tcttgtatcg cttgaagacc      900
aagccttccc cttctgacta aaatcatcat tgttatgtgt atgtgcaagt gggaagggga      960
agaacagtgc cagaattggt tgcttacatt cctgcatcaa cttctaccaa gacaccagtg     1020
cttcaaagat taactttcca gctgttcata tatgaatata aagtttttgt ttttaatttt     1080
ttggcctttt tgttttgatg attattatgt gttcaaccat attatataat tatatatacc     1140
tctttctgtg tttttcttgc                                     1160

```

<210> 16
 <211> 305
 <212> PRT
 <213> Glycine max

<400> 16

Met Leu Lys Asn Thr Ile Gln Trp Arg Lys Glu Phe Gly Met Glu Glu
 1 5 10 15

Leu Met Glu Glu Lys Leu Gly Asp Glu Leu Glu Lys Val Val Phe Met
 20 25 30

His Gly Phe Asp Lys Glu Gly His Pro Val Cys Tyr Asn Ile Tyr Glu
 35 40 45

Glu Phe Gln Asn Lys Glu Leu Tyr Lys Lys Thr Phe Ser Asp Glu Glu
 50 55 60

Lys Arg Glu Lys Phe Leu Arg Trp Arg Ile Gln Phe Leu Glu Lys Ser
 65 70 75 80

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

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

Gln Ala Thr Lys His Ala Leu Gln Leu Leu Gln Asp Asn Tyr Pro Glu
 115 120 125

Phe Val Ala Lys Gln Val Phe Ile Asn Val Pro Trp Trp Tyr Leu Ala
 130 135 140

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Val Asn Arg Met Ile Ser Pro Phe Leu Thr Gln Arg Thr Lys Ser Lys
145 150 155 160

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

Ile Ala Pro Glu Gln Leu Pro Val Lys Tyr Gly Gly Leu Ser Lys Asp
180 185 190

Gly Glu Phe Gly Asn Ile Asp Ala Val Thr Glu Ile Thr Val Arg Pro
195 200 205

Ala Ala Lys His Thr Val Glu Phe Ser Val Thr Glu Asn Cys Leu Leu
210 215 220

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

Phe Val Pro Ser Ser Glu Gly Ser Tyr Thr Val Ile Val Gln Lys Ala
245 250 255

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

Val Gly Glu Pro Gly Lys Val Val Leu Thr Ile Asp Asn Thr Ser Ser
275 280 285

Lys Lys Lys Lys Leu Leu Tyr Arg Leu Lys Thr Lys Pro Ser Pro Ser
290 295 300

Asp
305

<210> 17
<211> 2212
<212> DNA
<213> Triticum aestivum

<400> 17
ccacgcgtcc gctctcccc tctccctcct gctctatctt tctcaccgca aaagcttgaa 60
acaccccgcg gagatggcag aggagccgca gccacaggcc gccgccgccc ccgccgccgc 120
ggccacggag gtggtcgtcg ccgagaaggc gccggcggag gtggagaaga aggccgagga 180
gcccgcggcg gaggcggagg ccgaggagac ggccgccgtt gccgacgacg ggggcgccgt 240
cgaggccacc ggctctttca aggaggagag caacctcgtc gccgacctgc ctgacccgga 300
gaagaaggcg ctcgacgagt tcaaggagct gatcgtcgcc gcgctcgccg ccggtgagtt 360
caatctgccc cctccccgc cgccgccgaa ggccaagact gaggccgccg cagaggagac 420
caagacggag gcgccggcca aggaggaggc caagaccgag gagccggcca aggcggaaga 480
accagccaag gaggagccca aggctgaaga gccggccaag gccgaggcgg cagcggcgga 540

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

gccagcagcc gaggagccca aggccgtggt cgctgccgag gcagcagccg aggagccggc      600
caaggaggaa cccaaggccg aggaggccaa gccggccgag ccaaagaagg aggaggaagc      660
agtcgtggtc gccgaggagg gcaccaagac ggcggaaccg gtcgaggagg ccgccgccgc      720
cgccaccacc acagagcagg cagcggcgcc ggaaccggag gcggaggcag ccgcgcccga      780
gccggtgttc atctggggcg tgccgctggt gggcgacgac gagcgcacgg acgcggtgct      840
gctcaagttc ctgcgcgcgc gggagttcaa ggtgaaggag gcgatggcga tgctccggtc      900
cgccgtgctc tggcggaagc gtttcggcat cgagtcgctc ctggaggcgg acctggcctt      960
cccggagctg gagaaggtgg tgttctaccg cggcgccgac cgggagggcc acccgtctg     1020
ctacaacgtg tacggcgagt tccaggacaa ggaggtgtac gagaaggcgt tcggcgacga     1080
ggagaagcgg gagcggttcc tcaagtggcg catccagctg ctggagcgcg gcatcctgtc     1140
gcagctggac ttcgcgcccc gcggcatctg ctccatggtg caggtcaccg acctcaagaa     1200
ctcgccgccc atgctcggca agcaccgcgc cgtcaccgcg caggccgtcg ccctgctcca     1260
ggacaactac cccgagttca tcgccaagaa ggtgttcata aacgtgccat ggtggtatct     1320
cgctgccaac aaaatgatga gccctttcct caccagcgcc accaagagca agttcgtggt     1380
cgccagccag gccaagtcac ccgagaccct cttcagatac atcgcgccgg agcaagtccc     1440
cgtccaattc ggaggcctct tcaaggaaga tgaccctgat ttcaccacct ccgactctgt     1500
caccgagctc accatcaaag cttcatccaa agaaaccatt gagatccctg tcaccgagaa     1560
ctcaacgatt gtatgggagc tccgggtgct cggctgggag gtcagccacg gcgcggagtt     1620
cacccccgac gctgaggggc cgtacaccgt catcgtgcag aagacaagga aggtccccgc     1680
gaatgaggag cccatcatga agggcagctt caaggccggc gaggccggca agatcgtgct     1740
cacggtcagc aacgccgcgt cgaagaagaa gaagctcctc tacagatcca aggtgaagtg     1800
cagcaccggc gagtccgttg aggccgacat tccatgacca ccattggagt cagtccctga     1860
tgatgataga agaagaagaa gaagaagaag ataaaccgcc tttttggttt ttgttctttg     1920
attccattgg ttttgtgggt tttggttcgc attcccgcat ttgtttaatt attaaaatta     1980
aaaacccaaa gtgagcttga ttttgtgacg gtacagtagt tgggagagga aggttggtat     2040
ggatgggatg atataatggc atcgtgatgg ttgttgaggg tagggcaaga ggagaaaaat     2100
ggatgataca atctgctgct gctctgtaaa tttgtctgta cattgttgca atcgctggct     2160
ggatcctcat ggacatgtta tatttagaag tacctgctgc catcaaaaaa ac           2212

```

<210> 18
 <211> 587
 <212> PRT
 <213> Triticum aestivum

<400> 18

Met Ala Glu Glu Pro Gln Pro Gln Ala Ala Ala Ala Pro Ala Ala Ala
 1 5 10 15

Ala Thr Glu Val Val Val Ala Glu Lys Ala Pro Ala Glu Val Glu Lys
20 25 30

Lys Ala Glu Glu Pro Ala Ala Glu Ala Glu Ala Glu Thr Ala Ala
35 40 45

Val Ala Asp Asp Gly Gly Ala Val Glu Ala Thr Gly Ser Phe Lys Glu
50 55 60

Glu Ser Asn Leu Val Ala Asp Leu Pro Asp Pro Glu Lys Lys Ala Leu
65 70 75 80

Asp Glu Phe Lys Glu Leu Ile Val Ala Ala Leu Ala Ala Gly Glu Phe
85 90 95

Asn Leu Pro Pro Pro Pro Pro Pro Pro Lys Ala Lys Thr Glu Ala Ala
100 105 110

Ala Glu Glu Thr Lys Thr Glu Ala Pro Ala Lys Glu Glu Ala Lys Thr
115 120 125

Glu Glu Pro Ala Lys Ala Glu Glu Pro Ala Lys Glu Glu Pro Lys Ala
130 135 140

Glu Glu Pro Ala Lys Ala Glu Ala Ala Ala Ala Glu Pro Ala Ala Glu
145 150 155 160

Glu Pro Lys Ala Val Val Ala Ala Glu Ala Ala Ala Glu Glu Pro Ala
165 170 175

Lys Glu Glu Pro Lys Ala Glu Glu Ala Lys Pro Ala Glu Pro Lys Lys
180 185 190

Glu Glu Glu Ala Val Val Val Ala Glu Glu Gly Thr Lys Thr Ala Glu
195 200 205

Pro Val Glu Glu Ala Ala Ala Ala Ala Thr Thr Thr Glu Gln Ala Ala
210 215 220

Ala Pro Glu Pro Glu Ala Glu Ala Ala Ala Pro Glu Pro Val Phe Ile
225 230 235 240

Trp Gly Val Pro Leu Val Gly Asp Asp Glu Arg Thr Asp Ala Val Leu
245 250 255

Leu Lys Phe Leu Arg Ala Arg Glu Phe Lys Val Lys Glu Ala Met Ala
260 265 270

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

Leu Leu Glu Ala Asp Leu Ala Phe Pro Glu Leu Glu Lys Val Val Phe
Seite 22

290

295

300

Tyr Arg Gly Ala Asp Arg Glu Gly His Pro Val Cys Tyr Asn Val Tyr
305 310 315 320

Gly Glu Phe Gln Asp Lys Glu Val Tyr Glu Lys Ala Phe Gly Asp Glu
325 330 335

Glu Lys Arg Glu Arg Phe Leu Lys Trp Arg Ile Gln Leu Leu Glu Arg
340 345 350

Gly Ile Leu Ser Gln Leu Asp Phe Ala Pro Ser Gly Ile Cys Ser Met
355 360 365

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

Arg Ala Val Thr Arg Gln Ala Val Ala Leu Leu Gln Asp Asn Tyr Pro
385 390 395 400

Glu Phe Ile Ala Lys Lys Val Phe Ile Asn Val Pro Trp Trp Tyr Leu
405 410 415

Ala Ala Asn Lys Met Met Ser Pro Phe Leu Thr Gln Arg Thr Lys Ser
420 425 430

Lys Phe Val Phe Ala Ser Gln Ala Lys Ser Pro Glu Thr Leu Phe Arg
435 440 445

Tyr Ile Ala Pro Glu Gln Val Pro Val Gln Phe Gly Gly Leu Phe Lys
450 455 460

Glu Asp Asp Pro Asp Phe Thr Thr Ser Asp Ser Val Thr Glu Leu Thr
465 470 475 480

Ile Lys Ala Ser Ser Lys Glu Thr Ile Glu Ile Pro Val Thr Glu Asn
485 490 495

Ser Thr Ile Val Trp Glu Leu Arg Val Leu Gly Trp Glu Val Ser His
500 505 510

Gly Ala Glu Phe Thr Pro Asp Ala Glu Gly Ala Tyr Thr Val Ile Val
515 520 525

Gln Lys Thr Arg Lys Val Pro Ala Asn Glu Glu Pro Ile Met Lys Gly
530 535 540

Ser Phe Lys Ala Gly Glu Ala Gly Lys Ile Val Leu Thr Val Ser Asn
545 550 555 560

Ala Ala Ser Lys Lys Lys Lys Leu Leu Tyr Arg Ser Lys Val Lys Cys
565 570 575

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Ser Thr Gly Glu Ser Val Glu Ala Asp Ile Pro
580 585

<210> 19
<211> 1393
<212> DNA
<213> Triticum aestivum

<400> 19
gggccggaat ttccgggtcg acccaccctg ccgggaggag cccaaggccg aggaggccat 60
cgaggagacc gccgtccccg ccgcgggccga gccggaggcg gcgcccgcg cagagcccaa 120
ggaggagctg atctggggcg tgccgctggt gggcgggcag gagcgacagg acacggtgct 180
cctcaagttc ctccgcgcgc gcgagttcaa ggtgaaggag gccatggcga tgctcaaggc 240
ggcggtgctg tggcgcaaga gcttcggcat cgacgcgctc ctggggcgccg acctcggcgt 300
gccggagctg gagaacgtcg tcttctaccg cggcgccgac cgcgagggcc acccgtctg 360
ctacaacgtc tacagcgagt tccaggacaa ggacctctac gagaaggcct tcggcgacga 420
cgagaagcgg gagcgcttcc tcaggtggcg catccagctc ctcgagcgcg gcatccggga 480
gcagctcgac ttctcgcca gcggcatctg ctccatggtg caggtcaccg acctcaagaa 540
ctcgccgccc atgctcggca agcaccgcgc cgtcaccgc caggcgctcg cgctgctcca 600
ggacaactac cctgaattca tcgccaagaa ggtgttcac aatgtgccat ggtggtatct 660
tgcggaac aagatgatga gccattcct cacacagcg accaagagca aattcacgtt 720
ttgcagcca gccaaagacc cagagaccct attcagatac atcgcgccg agcagggtccc 780
tgtccaattc ggcgccctct acaaagagga tgatactgaa ttctccactt ctgatggcgt 840
gaccgagctc actgtcaaac cttcttccaa agaaactgtt gagattcctg ctactgagaa 900
ctccacggtc gtgtgggagc tccgtgtgct tggatgggag gtgagctacg gcgtggagtt 960
caccgggac gccgagggcg gctacacggt catcgtgcag aagactcgga aggtgcccgc 1020
caacgaggag ccaatcatga agggtagctt caaagcgagc gagcctggca aggtggtgct 1080
catcgtcaac aaccgacgt cgaagaagaa gaagctgctg tgccgattca aggtgaagag 1140
ctccaccgaa tcctccgcct gatgaggttc cagctgctga tacaaccgcc aaccaggtcc 1200
ataccaccgc caccatttga acatgtcgca tgatagggga gagcaaataa gattttagta 1260
gatggccgtt ttcgtgtcgg gttctttgat ttgttggtt gctgtttttt gggggtcgga 1320
tttgtatgtg tgtttactcg gaaccaaagt gggcttggtc tatgaatgag ataggtactc 1380
ctggctggga tcc 1393

<210> 20
<211> 312
<212> PRT
<213> Triticum aestivum

<400> 20

Met Ala Met Leu Lys Ala Ala Val Leu Trp Arg Lys Ser Phe Gly Ile
Seite 24

1

5

10

15

Asp Ala Leu Leu Gly Ala Asp Leu Gly Val Pro Glu Leu Glu Asn Val
20 25 30

Val Phe Tyr Arg Gly Ala Asp Arg Glu Gly His Pro Val Cys Tyr Asn
35 40 45

Val Tyr Ser Glu Phe Gln Asp Lys Asp Leu Tyr Glu Lys Ala Phe Gly
50 55 60

Asp Asp Glu Lys Arg Glu Arg Phe Leu Arg Trp Arg Ile Gln Leu Leu
65 70 75 80

Glu Arg Gly Ile Arg Glu Gln Leu Asp Phe Ser Pro Ser Gly Ile Cys
85 90 95

Ser Met Val Gln Val Thr Asp Leu Lys Asn Ser Pro Pro Met Leu Gly
100 105 110

Lys His Arg Ala Val Thr Arg Gln Ala Leu Ala Leu Leu Gln Asp Asn
115 120 125

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

Tyr Leu Ala Ala Asn Lys Met Met Ser Pro Phe Leu Thr Gln Arg Thr
145 150 155 160

Lys Ser Lys Phe Thr Phe Cys Ser Pro Ala Lys Thr Ala Glu Thr Leu
165 170 175

Phe Arg Tyr Ile Ala Pro Glu Gln Val Pro Val Gln Phe Gly Gly Leu
180 185 190

Tyr Lys Glu Asp Asp Thr Glu Phe Ser Thr Ser Asp Gly Val Thr Glu
195 200 205

Leu Thr Val Lys Pro Ser Ser Lys Glu Thr Val Glu Ile Pro Ala Thr
210 215 220

Glu Asn Ser Thr Val Val Trp Glu Leu Arg Val Leu Gly Trp Glu Val
225 230 235 240

Ser Tyr Gly Val Glu Phe Thr Pro Asp Ala Glu Gly Gly Tyr Thr Val
245 250 255

Ile Val Gln Lys Thr Arg Lys Val Pro Ala Asn Glu Glu Pro Ile Met
260 265 270

Lys Gly Ser Phe Lys Ala Ser Glu Pro Gly Lys Val Val Leu Ile Val
275 280 285

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Asn Asn Pro Thr Ser Lys Lys Lys Lys Leu Leu Cys Arg Phe Lys Val
 290 295 300

Lys Ser Ser Thr Glu Ser Ser Ala
 305 310

<210> 21
 <211> 2018
 <212> DNA
 <213> Glycine max

<220>
 <221> misc_feature
 <222> (1862)..(1862)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (1878)..(1878)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (1889)..(1889)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (1922)..(1922)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (1929)..(1930)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (1936)..(1936)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (1962)..(1962)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (1971)..(1972)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (2006)..(2006)
 <223> n is a, c, g, or t

<400> 21
 gaagcaactc ttgtcttccc tttcaacttc aactcaaccc tcaatcaaac tcattctgtc 60
 ttttcttcta tttttatttc tatccaatca tccatggccg aggaacccca aaaaccagcc 120
 tccgctgaag aagtggctgc tgttcctgcg gagaaccac catctgaagc cgaagctgaa 180
 aacatcgaag cagagaaggc ccagagtggg gtagaagaca agatttccca gtcggtttcg 240

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

ttcaaggagg agaccaacgt ggttggcgac ctccccgagg cgagaagaa agcccttgat	300
gagctcaaga agcttgttca agaagcgctc aacaaccatg agctaactgc tccaagcca	360
gaaccggaga agaagaaacc agcagcagag aagaaggagg aagttgaagt gacagaaggg	420
aagaaggaag ctgaagtcac agaagagaag aaggaagtgg aagtgacgga agagaagaag	480
gaaattgaag taacagaaga gaagaaggaa gctgaagtca tagaagagaa gaaggaagtg	540
gaagtgacgg aagagaagaa ggaaattgaa gtaacagaag agaagaagga agcagaagtg	600
aaagaagaga agaaggaagg ggaagtgacg gaagagaaga aggaagttga agtgacggaa	660
gagaagaagg aagcgggaagt gatagtagaa gagaagaagg aagttgaagt gacggaagag	720
aagaaggaag tggaagtgac cgaaggaaag aaagaagtgg aagtgatcga agagaagaag	780
gaaacagaag tgacagaaga aaagaaagaa gtggaagtga aagtgaggga agagaagaag	840
gaaagtgaag tgaaagaaga agaaaaaggt cgggaggttg ttccagagga agttgagata	900
tggggaattc ccctgctggg ggacgagagg agcgatgtga ttctgctaaa gtttcttagg	960
gcaagggatt tcaaggtgaa ggaggccttg aacatgataa gaaacacggt gcgatggaga	1020
aaggaatttg gaatagaggg tctagtggag gaagatcttg gaagtgattg ggagaagggtg	1080
gtgttcaagg atggatacga caaagaaggg caccgggtgt actacaacgt ctttggggag	1140
tttgaggaca aggagttgta cagcaagacg tttttggacg aggaaaagag gaacaagttc	1200
ataaggtgga ggattcagtc gttggagaag agcgttagaa gccttgactt ctctccgaat	1260
gggatatcga caatagttca ggtgaacgac cttaagaact ctccccgact gggcaagagg	1320
gaactgaggc aggccacaa tcaggccctt caactgcttc aggacaacta ccctgagttc	1380
gttgccaagc agatattcat caatgtcccc tgggtggtacc ttgccttttc taggatgatc	1440
agtcccttct tcacacagag gaccaagagt aaatttgttt ttgctggccc ttccaaatct	1500
gctgataccc ttttcagata tatagctccg gagctggtcc cggttcaata cgggtggtctt	1560
agcagagagg ctgaacagga attcacctct gcttaccctg ttacggagtt tactattaaa	1620
cccgctacca aacattctgt tgagttccct gtttctgaga aaagccatct tgtttgggaa	1680
atccgagtgg tgggttggga tgtcagctat ggagctgaat ttgtgcccag cgctgaggat	1740
ggatacactg tcatagtaca caagagcagg aaaattgctc ccgctgatga gaccgttctt	1800
accaacgggt tcagaattgg tgaacctggc aagattgtac tcaccataga caaccaaaaca	1860
tncaagaaga agaaactnct ctacaggtnc cagaccaaac ccattgcaga gtaagcttga	1920
tnaggatgnn tactgntact gtatattcat cattacaacc ancacaacat nngtggttgg	1980
gcgagggact tattctttca tacgngtct tcttttct	2018

<210> 22
 <211> 606
 <212> PRT
 <213> Glycine max

<220>

<221> UNSURE
<222> (590)..(590)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> UNSURE
<222> (599)..(599)
<223> Xaa can be any naturally occurring amino acid

<400> 22

Met Ala Glu Glu Pro Gln Lys Pro Ala Ser Ala Glu Glu Val Val Ala
1 5 10 15

Val Pro Ala Glu Asn Pro Pro Ser Glu Ala Glu Ala Glu Asn Ile Glu
20 25 30

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

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

Lys Lys Ala Leu Asp Glu Leu Lys Lys Leu Val Gln Glu Ala Leu Asn
65 70 75 80

Asn His Glu Leu Thr Ala Pro Lys Pro Glu Pro Glu Lys Lys Lys Pro
85 90 95

Ala Ala Glu Lys Lys Glu Glu Val Glu Val Thr Glu Gly Lys Lys Glu
100 105 110

Ala Glu Val Ile Glu Glu Lys Lys Glu Val Glu Val Thr Glu Glu Lys
115 120 125

Lys Glu Ile Glu Val Thr Glu Glu Lys Lys Glu Ala Glu Val Ile Glu
130 135 140

Glu Lys Lys Glu Val Glu Val Thr Glu Glu Lys Lys Glu Ile Glu Val
145 150 155 160

Thr Glu Glu Lys Lys Glu Ala Glu Val Lys Glu Glu Lys Lys Glu Gly
165 170 175

Glu Val Thr Glu Glu Lys Lys Glu Val Glu Val Thr Glu Glu Lys Lys
180 185 190

Glu Ala Glu Val Ile Val Glu Glu Lys Lys Glu Val Glu Val Thr Glu
195 200 205

Glu Lys Lys Glu Val Glu Val Thr Glu Gly Lys Lys Glu Val Glu Val
210 215 220

Ile Glu Glu Lys Lys Glu Thr Glu Val Thr Glu Glu Lys Lys Glu Val
225 230 235 240

Glu Val Glu Val Arg₂₄₅ Glu Glu Lys Lys Glu₂₅₀ Ser Glu Val Lys Glu₂₅₅ Glu
 Glu Lys Gly Arg₂₆₀ Glu Val Val Pro Glu₂₆₅ Glu Val Glu Ile Trp₂₇₀ Gly Ile
 Pro Leu Leu₂₇₅ Gly Asp Glu Arg Ser₂₈₀ Asp Val Ile Leu Leu₂₈₅ Lys Phe Leu
 Arg Ala₂₉₀ Arg Asp Phe Lys Val₂₉₅ Lys Glu Ala Leu Asn₃₀₀ Met Ile Arg Asn
 Thr Val Arg Trp Arg Lys₃₁₀ Glu Phe Gly Ile Glu₃₁₅ Gly Leu Val Glu₃₂₀ Glu
 Asp Leu Gly Ser Asp₃₂₅ Trp Glu Lys Val Val₃₃₀ Phe Lys Asp Gly Tyr₃₃₅ Asp
 Lys Glu Gly His₃₄₀ Pro Val Tyr Tyr Asn₃₄₅ Val Phe Gly Glu Phe₃₅₀ Glu Asp
 Lys Glu Leu₃₅₅ Tyr Ser Lys Thr Phe₃₆₀ Leu Asp Glu Glu Lys₃₆₅ Arg Asn Lys
 Phe Ile₃₇₀ Arg Trp Arg Ile Gln₃₇₅ Ser Leu Glu Lys Ser₃₈₀ Val Arg Ser Leu
 Asp₃₈₅ Phe Ser Pro Asn Gly₃₉₀ Ile Ser Thr Ile Val₃₉₅ Gln Val Asn Asp Leu₄₀₀
 Lys Asn Ser Pro Gly₄₀₅ Leu Gly Lys Arg Glu₄₁₀ Leu Arg Gln Ala Thr₄₁₅ Asn
 Gln Ala Leu Gln₄₂₀ Leu Leu Gln Asp Asn₄₂₅ Tyr Pro Glu Phe Val₄₃₀ Ala Lys
 Gln Ile Phe₄₃₅ Ile Asn Val Pro Trp₄₄₀ Trp Tyr Leu Ala Phe₄₄₅ Ser Arg Met
 Ile Ser₄₅₀ Pro Phe Phe Thr Gln₄₅₅ Arg Thr Lys Ser Lys₄₆₀ Phe Val Phe Ala
 Gly₄₆₅ Pro Ser Lys Ser Ala₄₇₀ Asp Thr Leu Phe Arg₄₇₅ Tyr Ile Ala Pro Glu₄₈₀
 Leu Val Pro Val Gln₄₈₅ Tyr Gly Gly Leu Ser₄₉₀ Arg Glu Ala Glu Gln₄₉₅ Glu
 Phe Thr Ser Ala₅₀₀ Tyr Pro Val Thr Glu₅₀₅ Phe Thr Ile Lys Pro₅₁₀ Ala Thr

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Lys His Ser Val Glu Phe Pro Val Ser Glu Lys Ser His Leu Val Trp
515 520 525

Glu Ile Arg Val Val Gly Trp Asp Val Ser Tyr Gly Ala Glu Phe Val
530 535 540

Pro Ser Ala Glu Asp Gly Tyr Thr Val Ile Val His Lys Ser Arg Lys
545 550 555 560

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

Glu Pro Gly Lys Ile Val Leu Thr Ile Asp Asn Gln Thr Xaa Lys Lys
580 585 590

Lys Lys Leu Leu Tyr Arg Xaa Gln Thr Lys Pro Ile Ala Glu
595 600 605

<210> 23
<211> 1642
<212> DNA
<213> Glycine max

<400> 23
gaaatgaaag ctaaggaaag gaagggtaaa ggagcgtaaa actggaggag tttgtgtctt 60
gttttcttgt ggcggggcat aggattccga ataaatgcat gtttcaactt tcctttttct 120
tctctcagtc tctctagcta gctttcttct ccactctctc aaatggccca aaatgattcc 180
aacctactc cgctccgga accccatgta gcggcggaac ccattactga ggatttggtc 240
caagacaaag aagaagagga tgatagtagt aagattgtta ttccagtccc agagagcgag 300
tccttgtcat tgaaggagga tagcaatagg gtttctgatt ccgagaaaaa tgccattgat 360
gagctgaaga agctcctgaa agaggaatta gaggacgagg aggtttccat ctggggcgctc 420
cctctcttta aggatgacag gactgacgtc attctcctca agtttctcag agctcgtgag 480
ctcaaagtga aggacgccct tgtcatgttt caaaacactc tccgatggag gaaggacttc 540
aacatcgacg cccttctgga tgaagatctg ggcgaccact tggagaaggt tgtcttcatg 600
cacggacacg gcagagaggg ccatcccgtc tgttacaacg tctacggcga gttccagaac 660
aaggacctct accacaaggc cttctcctct caggataatc gaaacaagtt tctccgatgg 720
cgtattcagt tgttggagcg cagtattcgg cacctcgact tcactccttc ctccggcatc 780
aacaccattt tccaagtcaa tgacctcaaa aactcccctg gccctgctaa acgtgagctt 840
cgccttgcca ccaaacaagc tttgcagttg cttcaggaca actatcccga atttgttgcc 900
aaacaggttt ttatcaacgt cccatggtgg tatcttgctt tctataccat gatcaatccc 960
ttcttgactt cgaggaccaa aagcaaattt gtctttgctg gaccatccaa gtcccccgat 1020
actcttttca agtatatttc tcctgagcaa gtgcccgttc agtatggtgg cctcagtgta 1080
gatttctgtg actgcaaccc cgatttcact atgtctgatc ctgtcaccga aattcctata 1140

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

aagcctacca ctaagcaaac tgtggaaatt gctatttatg agaagtgcac tattgtttgg      1200
gagctgcgcg tgggtgggctg ggaggttagc tacaatgctg aattcaagcc tgatgttgaa      1260
gatgcatata cggttatcat acagaaggcc acaaagatgt cccccaccga tgaaccagtt      1320
gtttccaata gctttaaagt tgttgaactg ggaaaattgt tgctcaccat agacaatcct      1380
accttgaaaa aaaagaggct tctttacagg ttcaagatca aaccctactc tgattgagag      1440
aaaataacct ctgggtgggtg ttttgggtac atgaaggaaa ttgaacttga agagtaagaa      1500
atatgcatgt catcatttgt tcggtccatt tttcatctat agttttggtc gtgagttggt      1560
tgcagattgt ctttctctgt ctttgttggg tgggtgggggtg tttgaacact ttattgctag      1620
tctaaattgt tctttaattt tc                                             1642

```

<210> 24
 <211> 424
 <212> PRT
 <213> Glycine max

<400> 24

Met Ala Gln Asn Asp Ser Asn Pro Thr Pro Pro Pro Glu Pro His Val
 1 5 10 15

Ala Ala Glu Pro Ile Thr Glu Asp Leu Val Gln Asp Lys Glu Glu Glu
 20 25 30

Asp Asp Ser Ser Lys Ile Val Ile Pro Val Pro Glu Ser Glu Ser Leu
 35 40 45

Ser Leu Lys Glu Asp Ser Asn Arg Val Ser Asp Ser Glu Lys Asn Ala
 50 55 60

Ile Asp Glu Leu Lys Lys Leu Leu Lys Glu Glu Leu Glu Asp Glu Glu
 65 70 75 80

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

Ile Leu Leu Lys Phe Leu Arg Ala Arg Glu Leu Lys Val Lys Asp Ala
 100 105 110

Leu Val Met Phe Gln Asn Thr Leu Arg Trp Arg Lys Asp Phe Asn Ile
 115 120 125

Asp Ala Leu Leu Asp Glu Asp Leu Gly Asp His Leu Glu Lys Val Val
 130 135 140

Phe Met His Gly His Gly Arg Glu Gly His Pro Val Cys Tyr Asn Val
 145 150 155 160

Tyr Gly Glu Phe Gln Asn Lys Asp Leu Tyr His Lys Ala Phe Ser Ser
 165 170 175

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Gln Asp Asn Arg Asn Lys Phe Leu Arg Trp Arg Ile Gln Leu Leu Glu
180 185 190

Arg Ser Ile Arg His Leu Asp Phe Thr Pro Ser Ser Gly Ile Asn Thr
195 200 205

Ile Phe Gln Val Asn Asp Leu Lys Asn Ser Pro Gly Pro Ala Lys Arg
210 215 220

Glu Leu Arg Leu Ala Thr Lys Gln Ala Leu Gln Leu Leu Gln Asp Asn
225 230 235 240

Tyr Pro Glu Phe Val Ala Lys Gln Val Phe Ile Asn Val Pro Trp Trp
245 250 255

Tyr Leu Ala Phe Tyr Thr Met Ile Asn Pro Phe Leu Thr Ser Arg Thr
260 265 270

Lys Ser Lys Phe Val Phe Ala Gly Pro Ser Lys Ser Pro Asp Thr Leu
275 280 285

Phe Lys Tyr Ile Ser Pro Glu Gln Val Pro Val Gln Tyr Gly Gly Leu
290 295 300

Ser Val Asp Phe Cys Asp Cys Asn Pro Asp Phe Thr Met Ser Asp Pro
305 310 315 320

Val Thr Glu Ile Pro Ile Lys Pro Thr Thr Lys Gln Thr Val Glu Ile
325 330 335

Ala Ile Tyr Glu Lys Cys Ile Ile Val Trp Glu Leu Arg Val Val Gly
340 345 350

Trp Glu Val Ser Tyr Asn Ala Glu Phe Lys Pro Asp Val Glu Asp Ala
355 360 365

Tyr Thr Val Ile Ile Gln Lys Ala Thr Lys Met Ser Pro Thr Asp Glu
370 375 380

Pro Val Val Ser Asn Ser Phe Lys Val Val Glu Leu Gly Lys Leu Leu
385 390 395 400

Leu Thr Ile Asp Asn Pro Thr Leu Lys Lys Lys Arg Leu Leu Tyr Arg
405 410 415

Phe Lys Ile Lys Pro Tyr Ser Asp
420

<210> 25
<211> 2353
<212> DNA
<213> Zea mays

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

<400> 25
tccgccccgc cctgtcgctt tcccttccac acgcgccgtt cgctttgatc gaccaggcag      60
gcatggccga cgagacgaag caagaagccg ccgccccggc ggccgaggtg gtcgtgacgg      120
aggaggagaa gaaggcagaa gagaccgccc cggcggcgga ggaaaaggcc gtggaggcgg      180
ctgtagagaa ggccgcggag gcgagggcgg gggccgagga aaaggccgcg gaagcggact      240
cggaggagga gaagaaggcg gaggaggccg aggaggccgc cgcgggcgat gaggcggccg      300
tgatcgatgg cactgggtcg ttcaaggagg agagtaacct ggtgtccgag ctccccgacc      360
ctgagcgcac agcgtcgcg cagctcaagg agctcgtcgc caccgcgctc gctaacgggg      420
agttcaacct gccgccgccg cctgccaaagg aggaggccaa gaaggaggag ccggcaaagg      480
aagaagctcc ggcggaacag gaggacgagc ccaaggcaga ggaggcggct gcccaagagc      540
ccgtcaagga ggaggccaag cctgaggagc ccaaaacgga ggcgccggcg gaagcagcgc      600
ccgaggaggt taaggacgag acaccgtgc cggaagagac caagactgag gctcccgcgc      660
cggaggagcc caaggccgag gaggcctgca aggaggagct caaggcagag gcggcgacgg      720
aagcggtcgc cgaggagacc aaaccagctg agccgggtgcc ggaggaggag gagaagacgg      780
tcgttggtgc cgaggaggag gccacaaaaa cggcgggaagc catcgaggag acggtcgccg      840
tcgccgtcgc cgccgccgcg tccgaggagc ccgaggcggg cgagccgaag gaggagctga      900
tctggggcgt gccgctggcg ggcgacgacg agcgcacgga cacgggtgctg ctcaagttcc      960
tccgcgcgcg cgagttcaag gtgaaggagg cgatggcgat gctcaagtcg gcgggtgctgt     1020
ggcgcaagcg gttcggcatc gacgagctcc tcctggacgc cgacctcggc ctgcgggagc     1080
tgaggggcgt ggtgtttctac cgcggcgccg accgcgaggg ccaccgggtc tgctacaacg     1140
tgtacggcga gttccaggac aaggagctgt acgagagggc cttcggcgac gaggagaagc     1200
gggagcgtt cctcaagtgg cgcattccagc tcctggagcg cggcatccgg gaggcagctcg     1260
acttctcgcc cagcggcatc tgctccatgg tgcaggtcac cgacctcaag aactcgccgc     1320
ccatgctcgg caagcaccgc gccgtcacgc gccaggctct cgccctgcta caggacaact     1380
acccggagtt cgtggccaag aaggtgttca tcaacgtgcc gtggtggtac ctggcggcaa     1440
acaaggtgat gagccattc ctgactcagc gcaccaagag caagatcgtc ttctgcagcc     1500
ctggcaagtc ggcgagacc ctcttcagat acatcgcccc ggagcaagtc cccgtccagt     1560
tcggcggcct gtacaaggag gacgacacgg agttctccac ctccgacgcc gtcaccgagc     1620
tcaccgtgaa accgtcctcc aaggagaccg tcgagatccc agccaccgag aactccaccg     1680
tggtgtggga gtcgcgctg ctgggggtggg aggtgagcta cggcgccgag ttcacccccg     1740
acgcggaggg cggctacacc gtcattcgtc agaagacgcg gaagggtccc gccacgagg     1800
agcccatcat gaagggcagc ttcaaggcca cgagagcccg caagctggtg ctgggcgtga     1860
acaacccggc gtccaggaag aagaagctgc tgtgccggtt caaggtgagg agcgccgccg     1920
cctgatgagg gtcgttggtc tgggtcccag caggtagcgc ctgccagctg cttgaccacc     1980
agcccgacat gtataattcg atcgatcgcc aaccagggtc ataccgccac catttgaatg     2040

```

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

aacatgctgc attgcattac atgataggag agagagagag agagagagag gacaataaag 2100
 agtttctgct tcctagctag gcccgttccg tgtcctggtc gttctttgat tatttggttg 2160
 cttgctgttc ttttttttcc ttgggggggag ggtcgcgttt gtatgtgttt attacttgaa 2220
 tgaaaacaaa agtgagcttg ttaatgaaaa aaaaaaaaaa aaatgttgag gtcaccgtgg 2280
 tccgtggtgg ggtgggggaa gaagaacagt aacagttgct gcccggcctg tacatttctt 2340
 tcaaaaaaaaa aaa 2353

<210> 26
 <211> 620
 <212> PRT
 <213> Zea mays

<400> 26

Met Ala Asp Glu Thr Lys Gln Glu Ala Ala Ala Pro Ala Ala Glu Val
 1 5 10 15

Val Val Thr Glu Glu Glu Lys Lys Ala Glu Glu Thr Ala Pro Val Ala
 20 25 30

Glu Glu Lys Ala Val Glu Ala Ala Val Glu Lys Ala Ala Glu Ala Glu
 35 40 45

Ala Gly Ala Glu Glu Lys Ala Ala Glu Ala Asp Ser Glu Glu Glu Lys
 50 55 60

Lys Ala Glu Glu Ala Glu Glu Ala Ala Ala Gly Asp Glu Ala Ala Val
 65 70 75 80

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

Leu Pro Asp Pro Glu Arg Thr Ala Leu Ala Gln Leu Lys Glu Leu Val
 100 105 110

Ala Thr Ala Leu Ala Asn Gly Glu Phe Asn Leu Pro Pro Pro Pro Ala
 115 120 125

Lys Glu Glu Ala Lys Lys Glu Glu Pro Ala Lys Glu Glu Ala Pro Ala
 130 135 140

Asp Lys Glu Asp Glu Pro Lys Ala Glu Glu Ala Ala Ala Gln Glu Pro
 145 150 155 160

Val Lys Glu Glu Ala Lys Pro Glu Glu Pro Lys Thr Glu Ala Pro Ala
 165 170 175

Glu Ala Ala Pro Glu Glu Val Lys Asp Glu Thr Pro Val Pro Glu Glu
 180 185 190

Thr Lys Thr Glu Ala Pro Ala Pro Glu Glu Pro Lys Ala Glu Glu Pro
195 200 205

Ala Lys Glu Glu Leu Lys Ala Glu Ala Ala Thr Glu Ala Val Ala Glu
210 215 220

Glu Thr Lys Pro Ala Glu Pro Val Pro Glu Glu Glu Glu Lys Thr Val
225 230 235 240

Val Val Ala Glu Glu Glu Ala Thr Lys Thr Val Glu Ala Ile Glu Glu
245 250 255

Thr Val Ala Val Ala Val Ala Ala Ala Ser Glu Glu Pro Glu Ala
260 265 270

Gly Glu Pro Lys Glu Glu Leu Ile Trp Gly Val Pro Leu Ala Gly Asp
275 280 285

Asp Glu Arg Thr Asp Thr Val Leu Leu Lys Phe Leu Arg Ala Arg Glu
290 295 300

Phe Lys Val Lys Glu Ala Met Ala Met Leu Lys Ser Ala Val Leu Trp
305 310 315 320

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

Leu Arg Glu Leu Glu Gly Val Val Phe Tyr Arg Gly Ala Asp Arg Glu
340 345 350

Gly His Pro Val Cys Tyr Asn Val Tyr Gly Glu Phe Gln Asp Lys Glu
355 360 365

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

Lys Trp Arg Ile Gln Leu Leu Glu Arg Gly Ile Arg Glu Gln Leu Asp
385 390 395 400

Phe Ser Pro Ser Gly Ile Cys Ser Met Val Gln Val Thr Asp Leu Lys
405 410 415

Asn Ser Pro Pro Met Leu Gly Lys His Arg Ala Val Thr Arg Gln Ala
420 425 430

Leu Ala Leu Leu Gln Asp Asn Tyr Pro Glu Phe Val Ala Lys Lys Val
435 440 445

Phe Ile Asn Val Pro Trp Trp Tyr Leu Ala Ala Asn Lys Val Met Ser
450 455 460

Pro Phe Leu Thr Gln Arg Thr Lys Ser Lys Ile Val Phe Cys Ser Pro

465 470 475 480
 Gly Lys Ser Ala Glu Thr Leu Phe Arg Tyr Ile Ala Pro Glu Gln Val
 485 490 495
 Pro Val Gln Phe Gly Gly Leu Tyr Lys Glu Asp Asp Thr Glu Phe Ser
 500 505 510
 Thr Ser Asp Ala Val Thr Glu Leu Thr Val Lys Pro Ser Ser Lys Glu
 515 520 525
 Thr Val Glu Ile Pro Ala Thr Glu Asn Ser Thr Val Val Trp Glu Leu
 530 535 540
 Arg Val Leu Gly Trp Glu Val Ser Tyr Gly Ala Glu Phe Thr Pro Asp
 545 550 555 560
 Ala Glu Gly Gly Tyr Thr Val Ile Val Gln Lys Thr Arg Lys Val Pro
 565 570 575
 Ala His Glu Glu Pro Ile Met Lys Gly Ser Phe Lys Ala Thr Glu Pro
 580 585 590
 Gly Lys Leu Val Leu Gly Val Asn Asn Pro Ala Ser Arg Lys Lys Lys
 595 600 605
 Leu Leu Cys Arg Phe Lys Val Arg Ser Ala Ala Ala
 610 615 620

<210> 27
 <211> 2151
 <212> DNA
 <213> Zea mays

<400> 27
 caacaatctc tctccctca ctccctctct gcagcgcgca gctttcaaag cgttgggaga 60
 gatggcagag gagacgcaac cagaggccgc agccgccgcc ggcgccgccg cggccgaggt 120
 agtcgtgacc gaagctgcgc cggcggaggc ggaggtgcct gtggcggcgg aagctgaagc 180
 cgaggccaag gatgagaaga aaggtgacga ggcggagctc accgccgatg acgcgggggt 240
 ggggaccggc tcgttcaagg aggaaagcaa cctggtggaa gacctgcccg acccgagaa 300
 gaaggcgctc gacgagttca agcagctgat cgctgccgcc ctgccgccg gtgagttcaa 360
 cctgcctccc ccgccccgc cgccgaaggc caaggagacg aaggtggagg aagccaaggc 420
 cgaggagccc gccaaagaag agcccgcggc cgaggcggag gctacggcgg aggagccaa 480
 ggcccaggtg gctgcggatg ccccggttga ggaggtcaag acggaggtgc cgccggccga 540
 ggaggccaag gctgagacac tggctgagga agccaagcct tccgagcccg agccgcagga 600
 gaagaccgtc gtggtcactg aggaggagac tgccaccaag acggtggaag caatcgagga 660
 aaccgtcgtg tccgcccccg ccgcatccc ggaggaagca gcggcgccag aggcgggtgt 720

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

cgaggctcag gcgaccgcgc ctgaacccgt gctgatttgg ggcgtgccgc tggtcggcga	780
cgacgagcgc acggacacgg ttctgctcaa gttcctgcgt gcgcgggagt tcaaggtgaa	840
ggatgccatg gcgatgctca agtccgcggt gctgtggcgc aagcgcttcg gcatcacctc	900
gctcctcgac gccgacctcg gcctgacgga gctggagaac gtggtgttct accgcggcac	960
ggaccgcgaa ggccaccccc tgtgctacaa cgtctacggt gagttccagg acaaggatct	1020
ctacgagaag gccttcggcg acgatgagaa gaggagcgc ttcctcaagt ggcgcatcca	1080
gctgctggag cgcggcattc tgtcgaagct ggacttctcg cccagcggca tctgctccat	1140
ggttcagggt accgacctca agaactcgcc gcctatgctc ggcaagcacc gcgccgtcac	1200
ccgccaggct gtcacgtgc tccaggacaa ctaccccgag ttcattgcca agaagggtgt	1260
catcaatgtg ccgtggtggt atctagccgc caacaagatg atgagcccgt tcctcacaca	1320
gcgcaccaag agcaagttcg tctttgctag cccagccaaa tcagcagcga ctctattcag	1380
atacatcgca ccggaacaag ttctgtcca atttggaggc ctcttcaagg aggatgatcc	1440
tgagttcacc acctctgaca ctgtctccga gctcactatc aaaccatcct caaaagaaac	1500
cgttgagatc cctgtcaccg agaactccac aattgtatgg gaactccggg tgctgagttg	1560
ggaagtgagc tatggcgccg agttcacccc cgacgcggag ggtgggtaca ccgtcattgt	1620
acagaagaca aggaaggtgc ctgctaacga ggaaccgatc atgaagggaa gcttcaaggc	1680
aggcgagcct ggcaaacttg tgctaactgt gaacaaccct gcatccaaga agaagacgct	1740
cctttacaga tcgaaggtga agagcaccag cgagtgagtg tgaggtcacg ccgctagctg	1800
cctggggccct acagttaaaa cgatctacag catgatagaa gagagaagga accttttgg	1860
ttggttcgtt aatttactgg gttttttttt tgggttcgca ttctacattt tgtttggttg	1920
aaaccaaagt gagcttgttt ttgtgacagt agatgggaga agtataatgg cattgtgtga	1980
tggatggttg ttgatgaggg caggaggac gaaaatgtgg gggaatgaaa ggttgagaa	2040
tgtctgttcc tctgtagatg tgttctgtac attgcatctc ttggattctc attgatatgt	2100
taaaatttag gagtacttgg tcacatcatt attcaatcca tgttactctg c	2151

<210> 28
 <211> 571
 <212> PRT
 <213> Zea mays

<400> 28

Met Ala Glu Glu Thr Gln Pro Glu Ala Ala Ala Ala Ala Pro Ala
 1 5 10 15

Ala Ala Glu Val Val Val Thr Glu Ala Ala Pro Ala Glu Ala Glu Val
 20 25 30

Pro Val Ala Ala Glu Ala Glu Ala Glu Ala Lys Asp Glu Lys Lys Gly
 35 40 45

Asp Glu Ala Glu Leu Thr Ala Asp Asp Ala Gly Val Gly Thr Gly Ser
 Seite 37

50

55

60

Phe Lys Glu Glu Ser Asn Leu Val Glu Asp Leu Pro Asp Pro Glu Lys
65 70 75 80

Lys Ala Leu Asp Glu Phe Lys Gln Leu Ile Ala Ala Ala Leu Ala Ala
85 90 95

Gly Glu Phe Asn Leu Pro Pro Pro Pro Pro Pro Lys Ala Lys Glu
100 105 110

Thr Lys Val Glu Glu Ala Lys Ala Glu Glu Pro Ala Lys Glu Glu Pro
115 120 125

Ala Ala Glu Ala Glu Ala Thr Ala Glu Glu Pro Lys Ala Gln Val Ala
130 135 140

Ala Asp Ala Pro Val Glu Glu Val Lys Thr Glu Val Pro Pro Ala Glu
145 150 155 160

Glu Ala Lys Ala Glu Thr Leu Ala Glu Glu Ala Lys Pro Ser Glu Pro
165 170 175

Glu Pro Gln Glu Lys Thr Val Val Val Thr Glu Glu Glu Thr Ala Thr
180 185 190

Lys Thr Val Glu Ala Ile Glu Glu Thr Val Val Ser Ala Pro Ala Ala
195 200 205

Ile Pro Glu Glu Ala Ala Ala Pro Glu Ala Val Val Glu Ala Gln Ala
210 215 220

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

Asp Glu Arg Thr Asp Thr Val Leu Leu Lys Phe Leu Arg Ala Arg Glu
245 250 255

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

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

Thr Glu Leu Glu Asn Val Val Phe Tyr Arg Gly Thr Asp Arg Glu Gly
290 295 300

His Pro Val Cys Tyr Asn Val Tyr Gly Glu Phe Gln Asp Lys Asp Leu
305 310 315 320

Tyr Glu Lys Ala Phe Gly Asp Asp Glu Lys Arg Glu Arg Phe Leu Lys
325 330 335

Trp Arg Ile Gln Leu Leu Glu Arg Gly Ile Leu Ser Lys Leu Asp Phe
340 345 350

Ser Pro Ser Gly Ile Cys Ser Met Val Gln Val Thr Asp Leu Lys Asn
355 360 365

Ser Pro Pro Met Leu Gly Lys His Arg Ala Val Thr Arg Gln Ala Val
370 375 380

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

Ile Asn Val Pro Trp Trp Tyr Leu Ala Ala Asn Lys Met Met Ser Pro
405 410 415

Phe Leu Thr Gln Arg Thr Lys Ser Lys Phe Val Phe Ala Ser Pro Ala
420 425 430

Lys Ser Ala Ala Thr Leu Phe Arg Tyr Ile Ala Pro Glu Gln Val Pro
435 440 445

Val Gln Phe Gly Gly Leu Phe Lys Glu Asp Asp Pro Glu Phe Thr Thr
450 455 460

Ser Asp Thr Val Ser Glu Leu Thr Ile Lys Pro Ser Ser Lys Glu Thr
465 470 475 480

Val Glu Ile Pro Val Thr Glu Asn Ser Thr Ile Val Trp Glu Leu Arg
485 490 495

Val Leu Ser Trp Glu Val Ser Tyr Gly Ala Glu Phe Thr Pro Asp Ala
500 505 510

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

Asn Glu Glu Pro Ile Met Lys Gly Ser Phe Lys Ala Gly Glu Pro Gly
530 535 540

Lys Leu Val Leu Thr Val Asn Asn Pro Ala Ser Lys Lys Lys Thr Leu
545 550 555 560

Leu Tyr Arg Ser Lys Val Lys Ser Thr Ser Glu
565 570

<210> 29
<211> 682
<212> DNA
<213> Saccharum officinarum

<220>

```

<221> misc_feature
<222> (674)..(674)
<223> n is a, c, g, or t

<400> 29
cggacgcgtg ggcaaaacgg tggaagccat cgaggagacc gctgtcgcct ccgccgtggc      60
cgaacctgag gcggaggccg cgccggcgcc ggcggccgag ccgaaggagg agctgatctg      120
gggCGtgccg ctggtgggCG acgacgagcg cacggacacg gtgctgctca agttcctccg      180
cgcgcgcgag ttcaaggtga aggaggccct ggcgatgctc aagtcggcgg tgctgtggcg      240
caagcgcttc ggcacgacg agctcctggg cgccgacctc ggcctgccgg agctggagaa      300
cgtggtgttc taccgCGcg cgcaccgca gggccacccc gtctgctaca acgtctacgg      360
cgagttccag gacaaggagc tctacgagaa ggccttcggc gacgaggaga agcgggagcg      420
cttcctcaag tggcgcatcc agctcctcga gcgCGgcatc agggagcagc tcgacttctc      480
gcccagtggc atctgctcca tgggtcaggt caccgacctc aagaactcgc cgcccatgct      540
cggcaagcac cgCGccgtca caccgaggc tctCGccctg ctccaggaca actacccga      600
gttcgtggcc caagaggtgt ttatcaatgt gccatggtgg tacctCGcg cgaaacaagt      660
gatgagccca ttcnctgact ca                                             682

```

```

<210> 30
<211> 156
<212> PRT
<213> Saccharum officinarum

```

```

<220>
<221> UNSURE
<222> (154)..(154)
<223> Xaa can be any naturally occurring amino acid

```

```

<400> 30
Met Leu Lys Ser Ala Val Leu Trp Arg Lys Arg Phe Gly Ile Asp Glu
1          5          10          15

Leu Leu Gly Ala Asp Leu Gly Leu Pro Glu Leu Glu Asn Val Val Phe
20          25          30

Tyr Arg Gly Ala Asp Arg Glu Gly His Pro Val Cys Tyr Asn Val Tyr
35          40          45

Gly Glu Phe Gln Asp Lys Glu Leu Tyr Glu Lys Ala Phe Gly Asp Glu
50          55          60

Glu Lys Arg Glu Arg Phe Leu Lys Trp Arg Ile Gln Leu Leu Glu Arg
65          70          75          80

Gly Ile Arg Glu Gln Leu Asp Phe Ser Pro Ser Gly Ile Cys Ser Met
85          90          95

Val Gln Val Thr Asp Leu Lys Asn Ser Pro Pro Met Leu Gly Lys His
100         105         110

```

Arg Ala Val Thr Arg Gln Ala Leu Ala Leu Leu Gln Asp Asn Tyr Pro
115 120 125

Glu Phe Val Ala Gln Glu Val Phe Ile Asn Val Pro Trp Trp Tyr Leu
130 135 140

Ala Ala Lys Gln Val Met Ser Pro Phe Xaa Asp Ser
145 150 155

<210> 31
<211> 837
<212> DNA
<213> Saccharum officinarum

<220>
<221> misc_feature
<222> (563)..(563)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (588)..(588)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (755)..(755)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (760)..(761)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (771)..(773)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (807)..(807)
<223> n is a, c, g, or t

<400> 31
cctggagcag cgtgacagga caactacccc gagttcattg ccaagaaggt gttcatcaat 60
gtgccgtggt ggtatctcgc tgccaacaag atgatgagcc cgttcctcac acagcgcacc 120
aagagcaagt tcgtttttgc tagcccagcc aagtcagcag agactctatt cagatacatc 180
gcagcggagc aagttcctgt ccaatttgga ggcctcttca aggaggacga ccctgagttc 240
accacctccg acactgtcgc tgagctcact atcaaaccat cgtcaaaaga aaccattgag 300
atccctgtca cggagaactc cacaattgta tgggaactcc ggggtgctcg ttgggaggtg 360
agctatggtg ctgagttcac ccctgacgct gaggggtgggt acactgtcat tgtacagaaa 420
acaaggaagg tgcccgctaa cgaggaaccg atcatgaagg gaagcttcaa ggtacgcgag 480
cccggcaaac ttgtgctaac tgtgaacaac tcggcatcca agaagaagaa gtccttcac 540

agatcaaagg tgaagagcac cancgagtga gtgtgagggt gctgctanct gcctgggtcc 600
 tacagttaaa cgatctacca cagttaatct cagcatgata gaagagagga aaaacctttt 660
 ggtttggttc gttaatttat tgggttttgc ttgttttgggt gcacattcta cattttggtt 720
 ggttaaacaa aagtgagctt gtttttgggt gattnaaatn natttccact nnnaaaaaaaa 780
 aaaaaataa atttaagggg gggccgnttt aaaaaggggg ggccgttcct ataggaa 837

<210> 32
 <211> 159
 <212> PRT
 <213> Saccharum officinarum

<220>
 <221> UNSURE
 <222> (158)..(158)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> UNSURE
 <222> (158)..(158)

<400> 32

Met Met Ser Pro Phe Leu Thr Gln Arg Thr Lys Ser Lys Phe Val Phe
 1 5 10 15

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

Glu Gln Val Pro Val Gln Phe Gly Gly Leu Phe Lys Glu Asp Asp Pro
 35 40 45

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

Ser Lys Glu Thr Ile Glu Ile Pro Val Thr Glu Asn Ser Thr Ile Val
 65 70 75 80

Trp Glu Leu Arg Val Leu Gly Trp Glu Val Ser Tyr Gly Ala Glu Phe
 85 90 95

Thr Pro Asp Ala Glu Gly Gly Tyr Thr Val Ile Val Gln Lys Thr Arg
 100 105 110

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

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

Lys Lys Lys Leu Leu His Arg Ser Lys Val Lys Ser Thr Xaa Glu
 145 150 155

<210> 33

<211> 1143
 <212> DNA
 <213> Saccharum officinarum

<220>
 <221> misc_feature
 <222> (1033)..(1033)
 <223> n is a, c, g, or t

<400> 33
 gcctgagccc gtgctgatct ggggcgtgcc gctggtgggc gacgacgagc gcacggacac 60
 ggttctgctt aagttcctgc gagcgcggga gttcaagggtg aaggaggcca ttgcgatgct 120
 caagtccgcg gtgctgtggc gcaagcgctt cggcatcacc tcgctcctcg acgccgacct 180
 cggcctgccg gagctggaga acgtggtgtt ctaccgcggc gccgaccgcg agggccaccc 240
 cgtgtgctac aacgtctacg gcgagttcca ggacaaggat ctctacgaga aggccttcgg 300
 cgacgatgag aagcggggagc gcttcctcaa gtggcgcac cagctgctgg agcgcggcat 360
 cctgtcgaag ctggactttt cggccagcgg catctgctcc atggtccagg ttaccgacct 420
 caagaactcg ccgcccattgc tcggcaagca ccgcaccgtc acccgccagg ctgtcacgct 480
 gctccaggac aactaccccc agttcattgc caagaagggtg ttcattcaat gtgccgtggt 540
 ggtatctcgc tgccaacaag atgatgagcc cgttcctcac acagcgcacc aagagcaagt 600
 tcgtttttgc tagcccagcc aagtcagcag agactctatt cagatacatc gcagcggagc 660
 aagttcctgt ccaatttgga ggcctcttca aggaggacga ccctgagttc accacctccg 720
 aactgtcgc tgagctcact atcaaaccat cgtcaaaaga aaccattgag atccctgtca 780
 cggagaactc cacaattgta tgggaactcc ggggtgctcg ttgggagggtg agctatgggtg 840
 ctgagttcac ccctgacgct gaggggtgggt aactgtcat tgtacagaat acaaggaagg 900
 tgcccgtcaa cgaggaaccg atcatgaagg gaagcttcaa ggtaggcgag cccggcaaac 960
 ttgtgctaac tgtgaacaag ctagcatcca ataagaagaa gtccttcac agatcaaagg 1020
 tgaagagcac cancgagtga gtgtgaagtt gctgctagct ggctgggtcc tacagttcaa 1080
 cgatctacca cagtttatct cagcatgata gaagaaagga aaaacctttt ggcttgggtc 1140
 cgt 1143

<210> 34
 <211> 244
 <212> PRT
 <213> Saccharum officinarum

<220>
 <221> UNSURE
 <222> (243)..(243)
 <223> Xaa can be any naturally occurring amino acid

<400> 34

Met Arg Ser Gly Ser Ala Ser Ser Ser Gly Ala Ser Ser Cys Trp Ser
 1 5 10 15

Ala Ala Ser Cys Arg Ser Trp Thr Phe Arg Pro Ala Ala Ser Ala Pro
20 25 30

Trp Ser Arg Leu Pro Thr Ser Arg Thr Arg Arg Pro Cys Ser Ala Ser
35 40 45

Thr Ala Pro Ser Pro Ala Arg Leu Ser Arg Cys Ser Arg Thr Thr Thr
50 55 60

Pro Ser Ser Leu Pro Arg Arg Cys Ser Phe Asn Val Pro Trp Trp Tyr
65 70 75 80

Leu Ala Ala Asn Lys Met Met Ser Pro Phe Leu Thr Gln Arg Thr Lys
85 90 95

Ser Lys Phe Val Phe Ala Ser Pro Ala Lys Ser Ala Glu Thr Leu Phe
100 105 110

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

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

Thr Ile Lys Pro Ser Ser Lys Glu Thr Ile Glu Ile Pro Val Thr Glu
145 150 155 160

Asn Ser Thr Ile Val Trp Glu Leu Arg Val Leu Gly Trp Glu Val Ser
165 170 175

Tyr Gly Ala Glu Phe Thr Pro Asp Ala Glu Gly Gly Tyr Thr Val Ile
180 185 190

Val Gln Asn Thr Arg Lys Val Pro Ala Asn Glu Glu Pro Ile Met Lys
195 200 205

Gly Ser Phe Lys Val Gly Glu Pro Gly Lys Leu Val Leu Thr Val Asn
210 215 220

Lys Leu Ala Ser Asn Lys Lys Lys Leu Leu His Arg Ser Lys Val Lys
225 230 235 240

Ser Thr Xaa Glu

<210> 35
<211> 1404
<212> DNA
<213> Saccharum officinarum

<220>
<221> misc_feature
<222> (565)..(565)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (577)..(577)

<223> n is a, c, g, or t

<400> 35

```

ctctctcttg ctctctctct cgccaccgcc gccgtgaaat ccgcacgcgt gctgcgtcct      60
gccgagttgt gagctgtgat tgtgagttag cgccatggcc gtggaggctg tgtctggaaa      120
tggcgccgag gcggtggcgc cggcgccggc gaaggaggtg aacgccaagg aggcggttgc      180
ggtgtccaag aacgcgtcgt tcagggagga gagcaacttc ctggacgata tcaaggagag      240
cgagcgtaag gcgctcgccg agctccgcga caaggtagag gcggccatcg tggagggcaa      300
gctgttcgac gacggcggca agccggaggc gaaggagaag gagcaggcca agaagaaggc      360
tgagaagacc gtggagaaga aagaggagga gcccgaggcc gaagagaagg gagaggagga      420
cggcaagaag gaggccgacg ccgaggagga gaaaaaggaa ggcgaggagg aaggggagaa      480
gaaggacgac gaggaggggtg gaggagaaga caccaaggac gaggccaaga aagatgaagc      540
cggcgagaag gcggcggcga aggangagaa agaggangag aagccggcgg agacggcggc      600
cgtcgtcgtc gtcgacaagg acatcgcgct gtggggcggt cctctgctcc cgagcaaggg      660
agacgaggcc acggacgtgg tgctcctcaa gttcctccgc gcgcgcgact tcaaggccgg      720
cgccgcgttc gagatgctcc gccgcacgct ccgctggcgc aggggctgga ccggcttcag      780
cgttgacgcc gacgacgacg acgccgacct ccccgaggag ctgcggggcg cgtgctacct      840
cgacggcgcg gaccgggagg gccacccggg gtgctacaac gcgccggggc tgttcgcgga      900
cgacgccgtg tacaagaagg cgctgggcac cgaggaaggc aaggccaggt tcctccggtg      960
gcgggtccgc gccatggagc gccacgtggc cgagctggac ctgaggcccg gcggcgccgc      1020
gtcgtgctg caggtgaccg acctgaagaa ctgcggggc ccggccaaga aggacctccg      1080
cgtcgccgtc aagcaggtgc tcgacctgtt ccaggacaac taccgagc tcgtcgcaag      1140
aaacatctta atcaacgtgc cgttctggta ctacgcgttc agcgccctgt tctaccggtt      1200
cctgacgcag aggaccaaga gcaagttcgt cgttgctcgc ccgtccaagg tcaccgagac      1260
cctcctcaag tacattccga ttgaggccat ccccgtagaag tacggcgggc tgaaacgcga      1320
cggcgacacc gagttcttcg cggacgacag cgaagtcaca gaaggcaccg tcaaggaaaag      1380
ctccacgcag accatcgaga tcga                                         1404

```

<210> 36

<211> 436

<212> PRT

<213> Saccharum officinarum

<220>

<221> UNSURE

<222> (157)..(157)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> UNSURE

<222> (161)..(161)

<223> Xaa can be any naturally occurring amino acid

<400> 36

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

Ala Pro Ala Lys Glu Val Asn Ala Lys Glu Ala Val Ala Val Ser Lys
 20 25 30

Asn Ala Ser Phe Arg Glu Glu Ser Asn Phe Leu Asp Asp Leu Lys Glu
 35 40 45

Ser Glu Arg Lys Ala Leu Ala Glu Leu Arg Asp Lys Val Glu Ala Ala
 50 55 60

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

Glu Lys Glu Gln Ala Lys Lys Lys Ala Glu Lys Thr Val Glu Lys Lys
 85 90 95

Glu Glu Glu Pro Glu Ala Glu Glu Lys Gly Glu Glu Asp Gly Lys Lys
 100 105 110

Glu Ala Asp Ala Glu Glu Glu Lys Lys Glu Gly Glu Glu Glu Gly Glu
 115 120 125

Lys Lys Asp Asp Glu Glu Gly Gly Gly Glu Asp Thr Lys Asp Glu Ala
 130 135 140

Lys Lys Asp Glu Ala Gly Glu Lys Ala Ala Ala Lys Xaa Glu Lys Glu
 145 150 155 160

Xaa Glu Lys Pro Ala Glu Thr Ala Ala Val Val Val Val Asp Lys Asp
 165 170 175

Ile Ala Leu Trp Gly Val Pro Leu Leu Pro Ser Lys Gly Asp Glu Ala
 180 185 190

Thr Asp Val Val Leu Leu Lys Phe Leu Arg Ala Arg Asp Phe Lys Ala
 195 200 205

Gly Ala Ala Phe Glu Met Leu Arg Arg Thr Leu Arg Trp Arg Arg Gly
 210 215 220

Trp Thr Gly Phe Ser Val Asp Ala Asp Asp Asp Ala Asp Leu Pro
 225 230 235 240

Glu Glu Leu Ala Gly Ala Cys Tyr Leu Asp Gly Ala Asp Arg Glu Gly
 245 250 255

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

His Pro Val Cys Tyr Asn Ala Pro Gly Val Phe Ala Asp Asp Ala Val
260 265 270

Tyr Lys Lys Ala Leu Gly Thr Glu Glu Gly Lys Ala Arg Phe Leu Arg
275 280 285

Trp Arg Val Arg Ala Met Glu Arg His Val Ala Glu Leu Asp Leu Arg
290 295 300

Pro Gly Gly Ala Ala Ser Leu Leu Gln Val Thr Asp Leu Lys Asn Ser
305 310 315 320

Pro Gly Pro Ala Lys Lys Asp Leu Arg Val Ala Val Lys Gln Val Leu
325 330 335

Asp Leu Phe Gln Asp Asn Tyr Pro Glu Leu Val Ala Arg Asn Ile Leu
340 345 350

Ile Asn Val Pro Phe Trp Tyr Tyr Ala Phe Ser Ala Leu Phe Tyr Pro
355 360 365

Phe Leu Thr Gln Arg Thr Lys Ser Lys Phe Val Val Ala Arg Pro Ser
370 375 380

Lys Val Thr Glu Thr Leu Leu Lys Tyr Ile Pro Ile Glu Ala Ile Pro
385 390 395 400

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

Asp Asp Ser Glu Val Thr Glu Gly Thr Val Lys Glu Ser Ser Thr Gln
420 425 430

Thr Ile Glu Ile
435

<210> 37
<211> 1658
<212> DNA
<213> Triticum aestivum

<400> 37
ccacgcgtcc gctctcccc tctccctcct gctctatctt tctcaccgca aaagcttgaa 60
acaccccgcg gagatggcag aggagccgca gccacaggcc gccgccgccc ccgccgccgc 120
ggccacggag gtggtcgtcg ccgagaaggc gccggcggag gtggagaaga aggccgagga 180
gcccgcggcg gaggcggagg ccgaggagac ggccgccgtt gccgacgacg ggggcgccgt 240
cgaggccacc ggctctttca aggaggagag caacctcgtc gccgacctgc ctgacccgga 300
gaagaaggcg ctcgacgagt tcaaggagct gatcgtcgcc gcgctcgccg ccggtgagtt 360
caatctgccc cctccccgc cgcgcgcgaa ggccaagact gaggccgccg cagaggagac 420

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

caagacggag gcgccggcca aggaggaggc caagaccgag gagccggcca aggcggaaga	480
accagccaag gaggagccca aggctgaaga gccggccaag gccgaggcgg cagcggcgga	540
gccagcagcc gaggagccca aggccgtggt cgctgccgag gcagcagccg aggagccggc	600
caaggaggaa cccaaggccg aggaggccaa gccggccgag ccaaagaagg aggaggaagc	660
agtcgtggtc gccgaggagg gcaccaagac ggcggaaccg gtcgaggagg ccgccgccgc	720
cgccaccacc acagagcagg cagcggcgcc ggaaccggag gcggaggcag ccgcgcccga	780
gccggtgttc atctggggcg tgccgctggt gggcgacgac gagcgcacgg acgcggtgct	840
gctcaagtgc ctgcgcgcgc gggagttcaa ggtgaaggag gcgatggcga tgctccggtc	900
cgccgtgctg tggcggaagc gcttcggcat cgagtcgctc ctggaggccg acctggcctt	960
cccggagctg gagaaggtag tgttctaccg cggcgccgac cgggagggcc acccggtgtg	1020
ctacaacgtg tacggcgagt tccaggacaa ggaggtgtac gagaaggcgt tcggcgacga	1080
ggagaagcgg gagcggttcc tcaagtggcg catccagctg ctggagcgcg gcatacctgtc	1140
gcagctggac ttcgcgccca gcggcatctg ctccatggtg caggtcaccg acctcaagaa	1200
ctcgccgccc atgctcggca agcaccgcgc cgtaaccgcg caggccgctg ccctgctcca	1260
ggacaactac cccgagttca tcgccaagaa ggtgttcata aacgtgccat ggtggtatct	1320
cgctgccaac aaaatgatga gccctttcct caccagcgc accaagagca agttcgtggt	1380
cgccagccag gccaagtcac ccgagaccct cttcagatac attgcgccgg agcaagttcc	1440
cgtccaattt ggaggcctct tcaaggaaga tgaccctgat ttcaccacct ccgactctgt	1500
caccgagctc accatcaaag cttcatccaa agaaaccatt gagatccctg tcaccgagaa	1560
ctcaacgatt gtatgggagc tccgggtgct cggctgggag gtcagccacg gcgcggagtt	1620
caccccgac gccgaggggg cgtacaccgt catcgtgc	1658

<210> 38
 <211> 528
 <212> PRT
 <213> Triticum aestivum

<400> 38

Met Ala Glu Glu Pro Gln Pro Gln Ala Ala Ala Ala Pro Ala Ala Ala
 1 5 10 15

Ala Thr Glu Val Val Val Ala Glu Lys Ala Pro Ala Glu Val Glu Lys
 20 25 30

Lys Ala Glu Glu Pro Ala Ala Glu Ala Glu Ala Glu Glu Thr Ala Ala
 35 40 45

Val Ala Asp Asp Gly Gly Ala Val Glu Ala Thr Gly Ser Phe Lys Glu
 50 55 60

Glu Ser Asn Leu Val Ala Asp Leu Pro Asp Pro Glu Lys Lys Ala Leu
 65 70 75 80

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Asp Glu Phe Lys Glu Leu Ile Val Ala Ala Leu Ala Ala Gly Glu Phe
85 90 95

Asn Leu Pro Pro Pro Pro Pro Pro Lys Ala Lys Thr Glu Ala Ala
100 105 110

Ala Glu Glu Thr Lys Thr Glu Ala Pro Ala Lys Glu Glu Ala Lys Thr
115 120 125

Glu Glu Pro Ala Lys Ala Glu Glu Pro Ala Lys Glu Glu Pro Lys Ala
130 135 140

Glu Glu Pro Ala Lys Ala Glu Ala Ala Ala Ala Glu Pro Ala Ala Glu
145 150 155 160

Glu Pro Lys Ala Val Val Ala Ala Glu Ala Ala Ala Glu Glu Pro Ala
165 170 175

Lys Glu Glu Pro Lys Ala Glu Glu Ala Lys Pro Ala Glu Pro Lys Lys
180 185 190

Glu Glu Glu Ala Val Val Val Ala Glu Glu Gly Thr Lys Thr Ala Glu
195 200 205

Pro Val Glu Glu Ala Ala Ala Ala Ala Thr Thr Thr Glu Gln Ala Ala
210 215 220

Ala Pro Glu Pro Glu Ala Glu Ala Ala Ala Pro Glu Pro Val Phe Ile
225 230 235 240

Trp Gly Val Pro Leu Val Gly Asp Asp Glu Arg Thr Asp Ala Val Leu
245 250 255

Leu Lys Phe Leu Arg Ala Arg Glu Phe Lys Val Lys Glu Ala Met Ala
260 265 270

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

Leu Leu Glu Ala Asp Leu Ala Phe Pro Glu Leu Glu Lys Val Val Phe
290 295 300

Tyr Arg Gly Ala Asp Arg Glu Gly His Pro Val Cys Tyr Asn Val Tyr
305 310 315 320

Gly Glu Phe Gln Asp Lys Glu Val Tyr Glu Lys Ala Phe Gly Asp Glu
325 330 335

Glu Lys Arg Glu Arg Phe Leu Lys Trp Arg Ile Gln Leu Leu Glu Arg
340 345 350

Gly Ile Leu Ser Gln Leu Asp Phe Ala Pro Ser Gly Ile Cys Ser Met
355 360 365

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

Arg Ala Val Thr Arg Gln Ala Val Ala Leu Leu Gln Asp Asn Tyr Pro
385 390 395 400

Glu Phe Ile Ala Lys Lys Val Phe Ile Asn Val Pro Trp Trp Tyr Leu
405 410 415

Ala Ala Asn Lys Met Met Ser Pro Phe Leu Thr Gln Arg Thr Lys Ser
420 425 430

Lys Phe Val Phe Ala Ser Gln Ala Lys Ser Pro Glu Thr Leu Phe Arg
435 440 445

Tyr Ile Ala Pro Glu Gln Val Pro Val Gln Phe Gly Gly Leu Phe Lys
450 455 460

Glu Asp Asp Pro Asp Phe Thr Thr Ser Asp Ser Val Thr Glu Leu Thr
465 470 475 480

Ile Lys Ala Ser Ser Lys Glu Thr Ile Glu Ile Pro Val Thr Glu Asn
485 490 495

Ser Thr Ile Val Trp Glu Leu Arg Val Leu Gly Trp Glu Val Ser His
500 505 510

Gly Ala Glu Phe Thr Pro Asp Ala Glu Gly Ala Tyr Thr Val Ile Val
515 520 525

<210> 39
<211> 1722
<212> DNA
<213> Arabidopsis thaliana

<400> 39
atggctcaag aggaagtaca gaaatcggct gatgtcgctg ctgctccggt ggtgaaggag 60
aaacctatta ccgataagga gggtactatt cctacccttg tggcagagaa agaggaagtt 120
gctgctcctg tctctgatga gaaggcgggt ccagagaagg aggtgactcc ggagaaggaa 180
gccccagcgg cggaagcgga gaaatctgtt tcggtgaagg aggaagagac ggttgttgta 240
gctgagaagg ttgttgtttt aactgctgag gaagttcaga agaaggcact tgaggagttt 300
aaggagcttg taaggagggc tttgaacaaa cgtgaattca ctgctccggt gacgccgggt 360
aaggaagaga aaacagagga gaagaaaaca gaggaggaaa ctaaagagga agagaaaaca 420
gaggagaaga aagaagagac aacgactgag gttaagggtg aagaagagaa accggcgggt 480
ccagcggcgg aggaggagaa atcatcagag gctgctccgg ttgagaccaa atctgaggag 540
aaacctgaag agaaagcaga ggtaacaacc gagaaagcat ccagtgccga agaagatgga 600

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

accaagaccg tggaagcaat cgaagaatct atcgtctctg tttcaccacc tgaatccgcc      660
gtagcacctg tcgtggtaga gactgtcgcc gttgctgagg cagagccagt ggagccggaa      720
gaagtctcga tctggggagt tccactactc caagacgaga gatctgacgt gatcctcacg      780
aaattcctcc gtgcaagaga ctttaagggtc aaagaagctt taaccatgct taaaaacacc      840
gtccagtggc gtaaagaaaa caaaatcgac gaactcggtg aatccggaga agaagtgagt      900
gagttcgaga agatggtggt tgctcacggt gttgacaaag aaggacacgt cgtgatctac      960
agttcttacg gtgagtttca gaacaaggag cttttctccg acaaggagaa gcttaacaag     1020
ttcctcagct ggaggattca gctacaagag aagtgtgtga gagctattga tttcagcaac     1080
cctgaagcga agtcttcggt tgtgttcgtc agcgacttca ggaacgctcc aggacttggt     1140
aaaagagcct tgtggcaatt catcagacgc gctgttaaag aattcgagga caattatcct     1200
gaattcgccg ctaaagagct attcatcaat gtcccatggt ggtacattcc atactacaaa     1260
acattcggat ctatcatcac atccccaagg actaggagca agatggtcct tgctgggtcca     1320
tccaaatctg ccgatactat tttcaaatac atagctcctg aacaagttcc cgttaaatac     1380
ggtggactta gcaaagatac tcctttgacc gaagaaacca taacggaagc catcgttaaa     1440
ccggcagcaa actacactat tgaattgcct gcttctgagg cttgcacgct ttcattggag     1500
cttagggttt tgggtgctga tgtgagctac ggagctcagt ttgagccaac caccgaagga     1560
agctatgctg tgatcgtctc taagacacgg aagattggat caaccgatga accggtgata     1620
accgattctt ttaagggtggg tgaaccggga aagattgtga tcacaatcga caaccagact     1680
tccaagaaga agaaagtgct ctacaggttc aaaactcaat aa                        1722

```

<210> 40
 <211> 573
 <212> PRT
 <213> Arabidopsis thaliana
 <400> 40

Met Ala Gln Glu Glu Val Gln Lys Ser Ala Asp Val Ala Ala Ala Pro
 1 5 10 15

Val Val Lys Glu Lys Pro Ile Thr Asp Lys Glu Val Thr Ile Pro Thr
 20 25 30

Pro Val Ala Glu Lys Glu Glu Val Ala Ala Pro Val Ser Asp Glu Lys
 35 40 45

Ala Val Pro Glu Lys Glu Val Thr Pro Glu Lys Glu Ala Pro Ala Ala
 50 55 60

Glu Ala Glu Lys Ser Val Ser Val Lys Glu Glu Glu Thr Val Val Val
 65 70 75 80

Ala Glu Lys Val Val Val Leu Thr Ala Glu Glu Val Gln Lys Lys Ala
 85 90 95

Leu Glu Glu Phe Lys Glu Leu Val Arg Glu Ala Leu Asn Lys Arg Glu
 100 105 110
 Phe Thr Ala Pro Val Thr Pro Val Lys Glu Glu Lys Thr Glu Glu Lys
 115 120 125
 Lys Thr Glu Glu Glu Thr Lys Glu Glu Glu Lys Thr Glu Glu Lys Lys
 130 135 140
 Glu Glu Thr Thr Thr Glu Val Lys Val Glu Glu Glu Lys Pro Ala Val
 145 150 155 160
 Pro Ala Ala Glu Glu Glu Lys Ser Ser Glu Ala Ala Pro Val Glu Thr
 165 170 175
 Lys Ser Glu Glu Lys Pro Glu Glu Lys Ala Glu Val Thr Thr Glu Lys
 180 185 190
 Ala Ser Ser Ala Glu Glu Asp Gly Thr Lys Thr Val Glu Ala Ile Glu
 195 200 205
 Glu Ser Ile Val Ser Val Ser Pro Pro Glu Ser Ala Val Ala Pro Val
 210 215 220
 Val Val Glu Thr Val Ala Val Ala Glu Ala Glu Pro Val Glu Pro Glu
 225 230 235 240
 Glu Val Ser Ile Trp Gly Val Pro Leu Leu Gln Asp Glu Arg Ser Asp
 245 250 255
 Val Ile Leu Thr Lys Phe Leu Arg Ala Arg Asp Phe Lys Val Lys Glu
 260 265 270
 Ala Leu Thr Met Leu Lys Asn Thr Val Gln Trp Arg Lys Glu Asn Lys
 275 280 285
 Ile Asp Glu Leu Val Glu Ser Gly Glu Glu Val Ser Glu Phe Glu Lys
 290 295 300
 Met Val Phe Ala His Gly Val Asp Lys Glu Gly His Val Val Ile Tyr
 305 310 315 320
 Ser Ser Tyr Gly Glu Phe Gln Asn Lys Glu Leu Phe Ser Asp Lys Glu
 325 330 335
 Lys Leu Asn Lys Phe Leu Ser Trp Arg Ile Gln Leu Gln Glu Lys Cys
 340 345 350
 Val Arg Ala Ile Asp Phe Ser Asn Pro Glu Ala Lys Ser Ser Phe Val
 355 360 365

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Phe Val Ser Asp Phe Arg Asn Ala Pro Gly Leu Gly Lys Arg Ala Leu
370 375 380

Trp Gln Phe Ile Arg Arg Ala Val Lys Gln Phe Glu Asp Asn Tyr Pro
385 390 395 400

Glu Phe Ala Ala Lys Glu Leu Phe Ile Asn Val Pro Trp Trp Tyr Ile
405 410 415

Pro Tyr Tyr Lys Thr Phe Gly Ser Ile Ile Thr Ser Pro Arg Thr Arg
420 425 430

Ser Lys Met Val Leu Ala Gly Pro Ser Lys Ser Ala Asp Thr Ile Phe
435 440 445

Lys Tyr Ile Ala Pro Glu Gln Val Pro Val Lys Tyr Gly Gly Leu Ser
450 455 460

Lys Asp Thr Pro Leu Thr Glu Glu Thr Ile Thr Glu Ala Ile Val Lys
465 470 475 480

Pro Ala Ala Asn Tyr Thr Ile Glu Leu Pro Ala Ser Glu Ala Cys Thr
485 490 495

Leu Ser Trp Glu Leu Arg Val Leu Gly Ala Asp Val Ser Tyr Gly Ala
500 505 510

Gln Phe Glu Pro Thr Thr Glu Gly Ser Tyr Ala Val Ile Val Ser Lys
515 520 525

Thr Arg Lys Ile Gly Ser Thr Asp Glu Pro Val Ile Thr Asp Ser Phe
530 535 540

Lys Val Gly Glu Pro Gly Lys Ile Val Ile Thr Ile Asp Asn Gln Thr
545 550 555 560

Ser Lys Lys Lys Lys Val Leu Tyr Arg Phe Lys Thr Gln
565 570

<210> 41
<211> 1473
<212> DNA
<213> Arabidopsis thaliana

<400> 41
atggctgaag aacctactac taccactctc gttacaccgg aaaagctacc ttctccgagc 60
ctcacgcctt ctgaagtatc tgaatctact caagatgccc taccgacaga gacagaaact 120
ctggagaaaag tgactgagac taatccaccg gaaactgcag ataccaccac caagccagaa 180
gaagaaaccg cggcagagca tcatccaccg acagtgcagg aaacagaaac tgcatcgacg 240
gagaaacaag aggttaaaga cgaagcatcg cagaaagaag tagctgaaga gaaaaagagt 300

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

atgattccac agaatcttgg ttcattcaaa gaagaaagca gcaaactttc tgatctatct	360
aattccgaga agaaatcact cgatgaacta aaacatctag ttcgagaagc tctagacaat	420
caccaattca ccaacacacc agaagaagtc aagatttggg ggattccatt acttgaagac	480
gatagaagcg acgtcgtttt gttaaaattc ctaagagcta gggagttcaa ggtgaaagat	540
tcgtttgcta tgctcaagaa cacaatcaag tggagaaagg agttcaagat cgatgaattg	600
gtcgaggaag atcttgtgga tgatcttgac aaggttgtgt ttatgcatgg acatgaccga	660
gaaggtcacc ctgtttgtta caatgtctat ggtgagtttc agaacaagga gctttataat	720
aagacgtttt ctgatgagga aaagaggaaa catttcttga ggactaggat tcagttcttg	780
gagaggagta taaggaagct agattttagc tctggtgggg tttctactat ttttcaggtt	840
aatgatatga agaattctcc ggggttaggg aagaaagagc ttagatcagc tactaagcaa	900
gctgttgagt tgcttcagga caattaccct gagtttgtct tcaaacaggc ttttatcaat	960
gttccttggg ggtaccttgt gttttatact gtgattggtc cgttcatgac accaagatca	1020
aagagcaagc ttgtgtttgc tggtccttcg cgttcagctg aaaccctatt caaatacata	1080
tcacccgagc aagttccagt acaatatggg ggattgagtg ttgatccttg cgactgcaat	1140
ccagactttt cgttggaaga ttcagcctct gagatcactg ttaagcccgg aacaaaacaa	1200
actgttgaga tcataatcta tgagaaatgt gaacttgtgt gggagataag ggtaactgga	1260
tgggaagtga gctacaaggc tgaatttgtg ccggaagaga aagatgctta cacggtggtt	1320
atacaaaaac cgaggaagat gagaccatcc gatgaaccgg tgtaacccta tagcttcaaa	1380
gtgaatgagc ttggcaaggt tttactcaca gtagacaacc caacctctaa gaagaagaag	1440
ctcgtttaca ggttcaatgt caaacctctc taa	1473

<210> 42
 <211> 490
 <212> PRT
 <213> Arabdidopsis thaliana
 <400> 42

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

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

Ala Leu Pro Thr Glu Thr Glu Thr Leu Glu Lys Val Thr Glu Thr Asn
 35 40 45

Pro Pro Glu Thr Ala Asp Thr Thr Thr Lys Pro Glu Glu Glu Thr Ala
 50 55 60

Ala Glu His His Pro Pro Thr Val Thr Glu Thr Glu Thr Ala Ser Thr
 65 70 75 80

Glu Lys Gln Glu Val Lys Asp Glu Ala Ser Gln Lys Glu Val Ala Glu
 Seite 54

Glu Lys Lys Ser Met Ile Pro Gln Asn Leu Gly Ser Phe Lys Glu Glu
100 105 110

Ser Ser Lys Leu Ser Asp Leu Ser Asn Ser Glu Lys Lys Ser Leu Asp
115 120 125

Glu Leu Lys His Leu Val Arg Glu Ala Leu Asp Asn His Gln Phe Thr
130 135 140

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

Asp Arg Ser Asp Val Val Leu Leu Lys Phe Leu Arg Ala Arg Glu Phe
165 170 175

Lys Val Lys Asp Ser Phe Ala Met Leu Lys Asn Thr Ile Lys Trp Arg
180 185 190

Lys Glu Phe Lys Ile Asp Glu Leu Val Glu Glu Asp Leu Val Asp Asp
195 200 205

Leu Asp Lys Val Val Phe Met His Gly His Asp Arg Glu Gly His Pro
210 215 220

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

Lys Thr Phe Ser Asp Glu Glu Lys Arg Lys His Phe Leu Arg Thr Arg
245 250 255

Ile Gln Phe Leu Glu Arg Ser Ile Arg Lys Leu Asp Phe Ser Ser Gly
260 265 270

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

Leu Gly Lys Lys Glu Leu Arg Ser Ala Thr Lys Gln Ala Val Glu Leu
290 295 300

Leu Gln Asp Asn Tyr Pro Glu Phe Val Phe Lys Gln Ala Phe Ile Asn
305 310 315 320

Val Pro Trp Trp Tyr Leu Val Phe Tyr Thr Val Ile Gly Pro Phe Met
325 330 335

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

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

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Tyr Gly Gly Leu Ser Val Asp Pro Cys Asp Cys Asn Pro Asp Phe Ser
370 375 380

Leu Glu Asp Ser Ala Ser Glu Ile Thr Val Lys Pro Gly Thr Lys Gln
385 390 395 400

Thr Val Glu Ile Ile Ile Tyr Glu Lys Cys Glu Leu Val Trp Glu Ile
405 410 415

Arg Val Thr Gly Trp Glu Val Ser Tyr Lys Ala Glu Phe Val Pro Glu
420 425 430

Glu Lys Asp Ala Tyr Thr Val Val Ile Gln Lys Pro Arg Lys Met Arg
435 440 445

Pro Ser Asp Glu Pro Val Leu Thr His Ser Phe Lys Val Asn Glu Leu
450 455 460

Gly Lys Val Leu Leu Thr Val Asp Asn Pro Thr Ser Lys Lys Lys Lys
465 470 475 480

Leu Val Tyr Arg Phe Asn Val Lys Pro Leu
485 490

<210> 43
<211> 2052
<212> DNA
<213> Arabidopsis thaliana

<400> 43
atggctcaag aagagataca gaaacctact gcctctgttc cagtggttaa ggaggaaact 60
cctgccccgg ttaaggaggt tgaggtgccg gttactacgg agaaagctgt ggctgcgcct 120
gctccggaag ctacggagga gaaagttgtg tctgaggtgg cgggtgcctga aacagaggtg 180
acggcgggtga aagaggagga ggttgcgacg ggaaaggaga tcttgcaatc ggagtcgttt 240
aaggaggaag gctatttggc ttctgaatta caggaagctg agaagaatgc tttggctgag 300
ttaaaggagt tggttaggga ggctttgaac aagcgtgaat tcaccgcgcc accgccacca 360
ccagctccgg taaaggaaga gaaagttgag gagaagaaaa cagaggaaac agaggaaaag 420
aaggaagaag ttaaaacaga ggaaaaatct cttgaggctg aaaccaaaga agaggagaaa 480
tctgctgctc cggccaccgt agagaccaag aaagaagaga tcttggccgc tccggctccg 540
atcgtcgcag agaccaagaa ggaagagaca ccagttgctc ctgctccggt agagactaaa 600
ccggctgctc cggtcgttgc agagacaaag aaggaagaaa tattaccagc tgctccggtc 660
accacagaga ccaaggtgga agagaaagtc gttccagtag aaaccacacc ggctgctcca 720
gtcaccacag agaccaagga agaagagaaa gccgctccgg tcaccacaga gaccaaggag 780
gaagagaaaag cagctccggg agagaccaag aaagaagaga aagcaaccgc ctctactcag 840
gtcaagaggg cctcaaaatt tattaaagat atatttgtct cagtcaccac tagcgagaag 900

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

aagaaggaag aagagaaacc agcagtagta acaatcgaga aggctttcgc agctgatcaa      960
gaagaagaaa caaaaaccgt tgaagcagtc gaagaatcaa tcgtctccat cactcttcca      1020
gagacagctg catacgtaga gccagaagaa gtctcaatct ggggaatccc acttctagag      1080
gacgaaagat ccgacgtgat cctcctcaaa ttcctccgtg cacgtgactt caagggtcaaa      1140
gaagccttca cgatgctgaa aaacaccgtc caatggcgca aagagaacaa gatcgacgac      1200
ctagtctcag aagatcttga aggaagcgag tttgagaagt tgggtgttcac tcacggtgtc      1260
gacaaacaag gacatgtcgt gatctatagc tcgtacggtg agtttcagaa caaggagatt      1320
ttctcagata aagagaagct tagcaagttt ctcaaattga ggattcagtt ccaagagaag      1380
tgtgtgaggt ctcttgactt tagccctgag gctaagtcac cgttcgtgtt cgtttagtgac      1440
ttcaggaacg ctcttgactt tggtcagaga gcattgtggc agttcattaa acgcgccggt      1500
aagcaattcg aagataacta tccagagttt gtcgctaaag agctgttcat taatgtccca      1560
tgggtgtaca ttccttacta caaaacattc ggaagtatca ttacatcgcc aaggacaagg      1620
agcaagatgg tcctttctgg tccatccaaa tccgctgaga ccattttcaa atacgtagct      1680
cctgaagtag tcccggttaa gtatggtgga ctcagcaaag atagtccatt caccgttgaa      1740
gatggagtca ccgaggccgt agttaaatcg acatctaaat ataccattga tttgcctgct      1800
acagaggggt ccacgctctc atgggagctt agggtttttg gtgcggtgac gagctacgga      1860
gctcaatttg agccaagcaa tgaggcaagc tacaccgtga ttgtctctaa gaaccggaag      1920
gtcggtttaa ctgatgaacc ggtgataacc gattctttca aggcaagtga ggcgggaaag      1980
gtcgtgatca cgattgacaa ccaaaccctt aagaagaaga aggtgctcta cagggtccaa      2040
acccaagcat aa                                                                2052

```

```

<210> 44
<211> 683
<212> PRT
<213> Arabdidopsis thaliana
<400> 44

```

```

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

Lys Glu Glu Thr Pro Ala Pro Val Lys Glu Val Glu Val Pro Val Thr
20          25          30

Thr Glu Lys Ala Val Ala Ala Pro Ala Pro Glu Ala Thr Glu Glu Lys
35          40          45

Val Val Ser Glu Val Ala Val Pro Glu Thr Glu Val Thr Ala Val Lys
50          55          60

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

```

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

355

360

365

Leu Lys Phe Leu Arg Ala Arg Asp Phe Lys Val Lys Glu Ala Phe Thr
 370 375 380

Met Leu Lys Asn Thr Val Gln Trp Arg Lys Glu Asn Lys Ile Asp Asp
 385 390 395 400

Leu Val Ser Glu Asp Leu Glu Gly Ser Glu Phe Glu Lys Leu Val Phe
 405 410 415

Thr His Gly Val Asp Lys Gln Gly His Val Val Ile Tyr Ser Ser Tyr
 420 425 430

Gly Glu Phe Gln Asn Lys Glu Ile Phe Ser Asp Lys Glu Lys Leu Ser
 435 440 445

Lys Phe Leu Lys Trp Arg Ile Gln Phe Gln Glu Lys Cys Val Arg Ser
 450 455 460

Leu Asp Phe Ser Pro Glu Ala Lys Ser Ser Phe Val Phe Val Ser Asp
 465 470 475 480

Phe Arg Asn Ala Pro Gly Leu Gly Gln Arg Ala Leu Trp Gln Phe Ile
 485 490 495

Lys Arg Ala Val Lys Gln Phe Glu Asp Asn Tyr Pro Glu Phe Val Ala
 500 505 510

Lys Glu Leu Phe Ile Asn Val Pro Trp Trp Tyr Ile Pro Tyr Tyr Lys
 515 520 525

Thr Phe Gly Ser Ile Ile Thr Ser Pro Arg Thr Arg Ser Lys Met Val
 530 535 540

Leu Ser Gly Pro Ser Lys Ser Ala Glu Thr Ile Phe Lys Tyr Val Ala
 545 550 555 560

Pro Glu Val Val Pro Val Lys Tyr Gly Gly Leu Ser Lys Asp Ser Pro
 565 570 575

Phe Thr Val Glu Asp Gly Val Thr Glu Ala Val Val Lys Ser Thr Ser
 580 585 590

Lys Tyr Thr Ile Asp Leu Pro Ala Thr Glu Gly Ser Thr Leu Ser Trp
 595 600 605

Glu Leu Arg Val Leu Gly Ala Asp Val Ser Tyr Gly Ala Gln Phe Glu
 610 615 620

Pro Ser Asn Glu Ala Ser Tyr Thr Val Ile Val Ser Lys Asn Arg Lys
 625 630 635 640

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Val Gly Leu Thr Asp Glu Pro Val Ile Thr Asp Ser Phe Lys Ala Ser
645 650 655

Glu Ala Gly Lys Val Val Ile Thr Ile Asp Asn Gln Thr Phe Lys Lys
660 665 670

Lys Lys Val Leu Tyr Arg Ser Lys Thr Gln Ala
675 680

<210> 45
<211> 1230
<212> DNA
<213> Arabdidopsis thaliana

<400> 45
atggatgctt cattgtctcc attcgatcac caaaaaactc aaaacacaga gccaaagaaa 60
agcttcatta cctcactaat cactctccgt tcaaacaaca tcaaagaaga cacatacttc 120
gtctcagaac tcaaaccac ggagcaaaaa tcacttcaag aactcaaaga aaagctctca 180
gcttcaccc ccaaagcttc ttcaatgtgg ggagtctcac tcctcggtgg agacgacaaa 240
gctgacgtaa tcctcctcaa gttcctcaga gcaagagatt tcaaagtagc agactctttg 300
agaatgcttg agaagtgttt ggagtggaga gaagagttca aagcagagaa attgacagaa 360
gaagatctgg gttttaaaga tttggaaggt aaagttgctt acatgagagg ctacgacaaa 420
gaaggacacc cagtttgta caatgcttat ggtgtgttta aagagaaaga gatgtatgag 480
agagtgtttg gtgatgaaga gaagcttaac aagtttctga gatggagagt tcagggttttg 540
gagagaggtg ttaaaatgct tcattttaaa cctggtggtg ttaattccat tattcaagtt 600
acagatctta aagatatgcc taagagagag cttagagttg cttctaataca gatcctctct 660
ctttttcaag ataattaccc tgaattgggt gctactaaga tattcataaa cgtgccttgg 720
tacttcagtg tgatctactc aatgttcagc ccattcctga ctcagagAAC aaagagcaag 780
tttgtgatgt ccaaagaagg caatgcagca gaaacactct acaagttcat taggccagaa 840
gatattccgg tgcaatacgg tggctcttagc cgtcctactg attcgcaaaa cggaccgcca 900
aaaccggcgt ctgaattctc catcaagggt ggtgagaaag ttaacattca gattgaaggc 960
attgaggggtg gagcaaccat aacatgggat atagtagttg gaggatggga tttagagtac 1020
agtgcagagt ttgttccaaa cgctgaagag agttacgcga tcgttgctga gaaaccgaag 1080
aagatgaaag ctacagatga agctgtttgc aactctttca ctacagtaga agctgggaag 1140
ctcattctct ctgttgacaa tactctctct cgcaagaaga aagttgctgc ttaccgttac 1200
actgtccgga aatctactac aaccgtctaa 1230

<210> 46
<211> 409
<212> PRT
<213> Arabdidopsis thaliana

<400> 46

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Met Asp Ala Ser Leu Ser Pro Phe Asp His Gln Lys Thr Gln Asn Thr
1 5 10 15

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

Asn Ile Lys Glu Asp Thr Tyr Phe Val Ser Glu Leu Lys Pro Thr Glu
35 40 45

Gln Lys Ser Leu Gln Glu Leu Lys Glu Lys Leu Ser Ala Ser Ser Ser
50 55 60

Lys Ala Ser Ser Met Trp Gly Val Ser Leu Leu Gly Gly Asp Asp Lys
65 70 75 80

Ala Asp Val Ile Leu Leu Lys Phe Leu Arg Ala Arg Asp Phe Lys Val
85 90 95

Ala Asp Ser Leu Arg Met Leu Glu Lys Cys Leu Glu Trp Arg Glu Glu
100 105 110

Phe Lys Ala Glu Lys Leu Thr Glu Glu Asp Leu Gly Phe Lys Asp Leu
115 120 125

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

Val Cys Tyr Asn Ala Tyr Gly Val Phe Lys Glu Lys Glu Met Tyr Glu
145 150 155 160

Arg Val Phe Gly Asp Glu Glu Lys Leu Asn Lys Phe Leu Arg Trp Arg
165 170 175

Val Gln Val Leu Glu Arg Gly Val Lys Met Leu His Phe Lys Pro Gly
180 185 190

Gly Val Asn Ser Ile Ile Gln Val Thr Asp Leu Lys Asp Met Pro Lys
195 200 205

Arg Glu Leu Arg Val Ala Ser Asn Gln Ile Leu Ser Leu Phe Gln Asp
210 215 220

Asn Tyr Pro Glu Leu Val Ala Thr Lys Ile Phe Ile Asn Val Pro Trp
225 230 235 240

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

Thr Lys Ser Lys Phe Val Met Ser Lys Glu Gly Asn Ala Ala Glu Thr
260 265 270

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Leu Tyr Lys Phe Ile Arg Pro Glu Asp Ile Pro Val Gln Tyr Gly Gly
275 280 285

Leu Ser Arg Pro Thr Asp Ser Gln Asn Gly Pro Pro Lys Pro Ala Ser
290 295 300

Glu Phe Ser Ile Lys Gly Gly Glu Lys Val Asn Ile Gln Ile Glu Gly
305 310 315 320

Ile Glu Gly Gly Ala Thr Ile Thr Trp Asp Ile Val Val Gly Gly Trp
325 330 335

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

Ala Ile Val Val Glu Lys Pro Lys Lys Met Lys Ala Thr Asp Glu Ala
355 360 365

Val Cys Asn Ser Phe Thr Thr Val Glu Ala Gly Lys Leu Ile Leu Ser
370 375 380

Val Asp Asn Thr Leu Ser Arg Lys Lys Lys Val Ala Ala Tyr Arg Tyr
385 390 395 400

Thr Val Arg Lys Ser Thr Thr Thr Val
405

<210> 47
<211> 1623
<212> DNA
<213> Arabdidopsis thaliana

<400> 47
atgactgctg aagttaaggt tgaggagaaa caggtggagt cagaggttgt tattgctcct 60
gctgttggtc ctgaggagac tactgttaag gctgttggtg aagagactaa ggttgaagaa 120
gatgagagca agcctgaggg tgtggagaag agtgcttcct tcaaagaaga gaggatgttc 180
tttgctgatt tgaagaatc tgagaaaaag gactgagtg atctcaagtc taagcttgag 240
gaagctattg ttgacaacac tctcttaaag acgaagaaga aggagagctc tcctatgaag 300
gagaagaagg aagaggttgt gaaacctgaa gctgaggttg agaagaagaa ggaagaagca 360
gcagaggaga aggttgaaga agagaagaaa tctgaggctg ttgttaccga agaagcaccg 420
aaagctgaga ctgttgaggc tggtgttaca gaggagataa tccccaagga agaagtgact 480
actgttggtg agaaggtaga agaagaaacc aaggaagaag agaagaaaac cgaggatggt 540
gttactgaag aagtgaagc tgagactatt gaggtggagg atgaagatga gtcggtggat 600
aaggatatcg agctttgggg agtgccattg cttccaagca aaggagctga aagcacggat 660
gttatcctct tgaagttctt gagagcaaga gactttaaag tcaacgaagc ctttgagatg 720
ctgaagaaaa ccctcaaag gagaaagcaa aacaagattg attcgatcct tggagaggag 780
tttggggagg atcttgccac tgcagcttac atgaacggtg tggaccgcga gtcccacca 840

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

gtttgttaca atgtccacag cgaggagctt taccagacga ttgggtcgga gaagaacaga      900
gagaagttct tgagatggag gtttcagctg atggagaagg gaatccagaa gcttaatctt      960
aaaccaggag gtgttacttc tcttctccag atccacgatc tcaaaaacgc tcctggagtg     1020
tcaagaacag agatttgggt cggaatcaag aaagtaatcg agactttgca ggacaactat     1080
ccggaattcg tgtccagaaa catattcatc aacgttccat tctggttcta cgccatgaga     1140
gctgtcctct cgccattctt aactcaacga accaagagca agtttgttgt ggctcgtccc     1200
gctaagggtca gagagactct tctcaagtac attccagctg atgagctccc agttcagtac     1260
ggtggggttca aaacagtaga cgataccgaa ttctccaacg aaactgtctc tgaagttggt     1320
gttaagcctg gatcatctga aaccatcgaa atcccagctc ctgagactga aggtacattg     1380
gtatgggaca tagcgggtttt gggatgggaa gtgaattaca aggaagagtt tgtgccaaca     1440
gaagaaggag cttacacggt aatagtccaa aagggtgaaga agatgggagc aaatgaagga     1500
ccaatcagga acagtttcaa gaacagtcag gctggtaaga ttgttcttac cgttgacaat     1560
gtctctggca agaagaagaa agttctgtac aggtacagaa ccaagactga atcctcttcc     1620
tga                                                                    1623

```

```

<210> 48
<211> 540
<212> PRT
<213> Arabdidopsis thaliana

```

<400> 48

```

Met Thr Ala Glu Val Lys Val Glu Glu Lys Gln Val Glu Ser Glu Val
1          5          10          15

```

```

Val Ile Ala Pro Ala Val Val Pro Glu Glu Thr Thr Val Lys Ala Val
          20          25          30

```

```

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

```

```

Glu Lys Ser Ala Ser Phe Lys Glu Glu Ser Asp Phe Phe Ala Asp Leu
          50          55          60

```

```

Lys Glu Ser Glu Lys Lys Ala Leu Ser Asp Leu Lys Ser Lys Leu Glu
          65          70          75          80

```

```

Glu Ala Ile Val Asp Asn Thr Leu Leu Lys Thr Lys Lys Lys Glu Ser
          85          90          95

```

```

Ser Pro Met Lys Glu Lys Lys Glu Glu Val Val Lys Pro Glu Ala Glu
          100          105          110

```

```

Val Glu Lys Lys Lys Glu Glu Ala Ala Glu Glu Lys Val Glu Glu Glu
          115          120          125

```

Lys Lys Ser Glu Ala Val Val Thr Glu Glu Ala Pro Lys Ala Glu Thr
130 135 140

Val Glu Ala Val Val Thr Glu Glu Ile Ile Pro Lys Glu Glu Val Thr
145 150 155 160

Thr Val Val Glu Lys Val Glu Glu Glu Thr Lys Glu Glu Glu Lys Lys
165 170 175

Thr Glu Asp Val Val Thr Glu Glu Val Lys Ala Glu Thr Ile Glu Val
180 185 190

Glu Asp Glu Asp Glu Ser Val Asp Lys Asp Ile Glu Leu Trp Gly Val
195 200 205

Pro Leu Leu Pro Ser Lys Gly Ala Glu Ser Thr Asp Val Ile Leu Leu
210 215 220

Lys Phe Leu Arg Ala Arg Asp Phe Lys Val Asn Glu Ala Phe Glu Met
225 230 235 240

Leu Lys Lys Thr Leu Lys Trp Arg Lys Gln Asn Lys Ile Asp Ser Ile
245 250 255

Leu Gly Glu Glu Phe Gly Glu Asp Leu Ala Thr Ala Ala Tyr Met Asn
260 265 270

Gly Val Asp Arg Glu Ser His Pro Val Cys Tyr Asn Val His Ser Glu
275 280 285

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

Arg Trp Arg Phe Gln Leu Met Glu Lys Gly Ile Gln Lys Leu Asn Leu
305 310 315 320

Lys Pro Gly Gly Val Thr Ser Leu Leu Gln Ile His Asp Leu Lys Asn
325 330 335

Ala Pro Gly Val Ser Arg Thr Glu Ile Trp Val Gly Ile Lys Lys Val
340 345 350

Ile Glu Thr Leu Gln Asp Asn Tyr Pro Glu Phe Val Ser Arg Asn Ile
355 360 365

Phe Ile Asn Val Pro Phe Trp Phe Tyr Ala Met Arg Ala Val Leu Ser
370 375 380

Pro Phe Leu Thr Gln Arg Thr Lys Ser Lys Phe Val Val Ala Arg Pro
385 390 395 400

Ala Lys Val Arg Glu Thr Leu Leu Lys Tyr Ile Pro Ala Asp Glu Leu

Pro Val Gln Tyr Gly Gly Phe Lys Thr Val Asp Asp Thr Glu Phe Ser
420 425 430

Asn Glu Thr Val Ser Glu Val Val Val Lys Pro Gly Ser Ser Glu Thr
435 440 445

Ile Glu Ile Pro Ala Pro Glu Thr Glu Gly Thr Leu Val Trp Asp Ile
450 455 460

Ala Val Leu Gly Trp Glu Val Asn Tyr Lys Glu Glu Phe Val Pro Thr
465 470 475 480

Glu Glu Gly Ala Tyr Thr Val Ile Val Gln Lys Val Lys Lys Met Gly
485 490 495

Ala Asn Glu Gly Pro Ile Arg Asn Ser Phe Lys Asn Ser Gln Ala Gly
500 505 510

Lys Ile Val Leu Thr Val Asp Asn Val Ser Gly Lys Lys Lys Lys Val
515 520 525

Leu Tyr Arg Tyr Arg Thr Lys Thr Glu Ser Ser Ser
530 535 540

<210> 49
<211> 2007
<212> DNA
<213> Arabidopsis thaliana

<400> 49
atgtctcaag attctgcaac tactactccg ccgccacctt taacctccga cgtttcaatg 60
ccttccggtg aagaagatga gccaaagcat gtaacatcgg aagaagaggc accggtgact 120
tcggagacaa atctgaagct acctttgatg ccggagctag aggagtcaaa tcatacggcg 180
gaggttggtt cagagaaggt gacgccggag acgatgactt tggagtcaga aggtctcaac 240
cacgcggcgg aggattcaga gcagacacat gaagtgacgc cggagacaga gactgcgaag 300
ctagagggtt tcaaccacac ggcggaggat tcagagcaga cacatgaagt gacgccggag 360
aaagagactg tgaaatcaga gtttctcaac cacgtggcgg aggattcaga gcagacacat 420
gaagtgacgc cggagacaga gactgtgaag tcagagggtt tcaaccatgc ggcggaggat 480
tcagagcagc cacgtggagt gacaccgacg ccggagacag aaacatcgga ggcagacacg 540
tcattgcttg taacttccga gacagaagag cctaaccatg cggcggagga ttattcagag 600
acagagccat cacagaaact aatgttgagg cagaggagaa agtacatgga agtagaagat 660
tggaacagagc cagaactacc agatgaagcg gtgttagaag ctgcagcgtc agtccctgag 720
ccaaagcaac cagagcctca gacaccacca ccaccacat ctactactac ttccactggt 780
gcatctagat ctttagccga aatgatgaac agagaagaag cagaagtaga agagaaacaa 840

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

aagattcaga ttcctcgtag tctcgggttca ttcaaagaag aaacaaacaa aatctccgat	900
ctttcagaaa cagagttaaa cgcacttcaa gagcttcgtc accttcttca agtatcacia	960
gattcaagca aaacctctat atgggggtgtg ccacttctca aagacgacag aaccgacgtc	1020
gttttggtta agtttctaag agcaagagac tttaaacctc aagaagctta ctcaatgcta	1080
aacaagacac tccaatggag aatcgacttc aacatcgaag agcttctaga cgaaaacctc	1140
ggtgacgatt tagacaaagt tgtgttcatg caaggacaag acaaggagaa tcatcctgtc	1200
tgttacaatg tctacggtga gtttcagaac aaagatcttt atcagaaaac gttttcagat	1260
gaagagaaga gagaacggtt cttgagatgg aggattcagt ttcttgaaaa gagtatcagg	1320
aatcttgatt ttgtagctgg tgggtgttcc acgatatgtc aagtaaata tcttaagaat	1380
tctccaggac ctggttaagac tgagcttagg ttagctacta agcaagctct tcatcttctt	1440
caagacaatt accctgagtt tgtctctaaa cagatattca tcaatgttcc atggtggtac	1500
cttgcgttct atagaattat tagtcctttt atgtcacaaa ggtcaaagag caaactagtt	1560
ttcgcagggtc cttcaagatc tgcagaaacc cttctcaagt acatatcacc cgaacatgtc	1620
ccggttcagt atggtggact aagtgtggat aattgagagt gtaactcgga tttcacacac	1680
gatgatatcg ctaccgagat tactgttaaa ccaactacta aacaaaccgt cgagattatt	1740
gtttacgaga aatgtacaat cgtgtgggag ataagagtag tgggatggga ggtttcgtat	1800
ggagcggagt ttgtgccgga gaacaaagaa gggataacag tgatcattca gaaaccgagg	1860
aagatgactg cgaaaaatga actggtggtg tctcatagct tcaaagttgg agaagttggc	1920
aggattttgc taactgttga taaccgcact tcgaccaaga aaatgcttat ctacaggttc	1980
aaggtttaagc ctttagcttg tgagtaa	2007

<210> 50
 <211> 668
 <212> PRT
 <213> Arabidopsis thaliana
 <400> 50

Met Ser Gln Asp Ser Ala Thr Thr Thr Pro Pro Pro Pro Leu Thr Ser
 1 5 10 15

Asp Val Ser Met Pro Ser Gly Glu Glu Asp Glu Pro Lys His Val Thr
 20 25 30

Ser Glu Glu Glu Ala Pro Val Thr Ser Glu Thr Asn Leu Lys Leu Pro
 35 40 45

Leu Met Pro Glu Leu Glu Glu Ser Asn His Thr Ala Glu Val Val Ser
 50 55 60

Glu Lys Val Thr Pro Glu Thr Met Thr Leu Glu Ser Glu Gly Leu Asn
 65 70 75 80

His Ala Ala Glu Asp Ser Glu Gln Thr His Glu Val Thr Pro Glu Thr
 Seite 66

Glu Thr Ala Lys₁₀₀ Leu Glu Val Leu Asn₁₀₅ His Thr Ala Glu Asp₁₁₀ Ser Glu
Gln Thr His₁₁₅ Glu Val Thr Pro Glu₁₂₀ Lys Glu Thr Val Lys₁₂₅ Ser Glu Phe
Leu Asn₁₃₀ His Val Ala Glu Asp₁₃₅ Ser Glu Gln Thr His₁₄₀ Glu Val Thr Pro
Glu Thr Glu Thr Val Lys₁₅₀ Ser Glu Val Leu Asn₁₅₅ His Ala Ala Glu Asp₁₆₀
Ser Glu Gln Pro Arg₁₆₅ Gly Val Thr Pro Thr₁₇₀ Pro Glu Thr Glu Thr Ser
Glu Ala Asp Thr₁₈₀ Ser Leu Leu Val Thr₁₈₅ Ser Glu Thr Glu Glu₁₉₀ Pro Asn
His Ala Ala₁₉₅ Glu Asp Tyr Ser Glu₂₀₀ Thr Glu Pro Ser Gln₂₀₅ Lys Leu Met
Leu Glu₂₁₀ Gln Arg Arg Lys Tyr₂₁₅ Met Glu Val Glu Asp₂₂₀ Trp Thr Glu Pro
Glu Leu Pro Asp Glu Ala₂₃₀ Val Leu Glu Ala Ala₂₃₅ Ala Ser Val Pro Glu₂₄₀
Pro Lys Gln Pro Glu₂₄₅ Pro Gln Thr Pro Pro₂₅₀ Pro Pro Pro Ser Thr₂₅₅ Thr
Thr Ser Thr Val₂₆₀ Ala Ser Arg Ser Leu₂₆₅ Ala Glu Met Met Asn₂₇₀ Arg Glu
Glu Ala Glu Val Glu Glu Lys Gln₂₈₀ Lys Ile Gln Ile Pro₂₈₅ Arg Ser Leu
Gly Ser₂₉₀ Phe Lys Glu Glu Thr Asn₂₉₅ Lys Ile Ser Asp₃₀₀ Leu Ser Glu Thr
Glu Leu Asn Ala Leu Gln₃₁₀ Glu Leu Arg His Leu₃₁₅ Leu Gln Val Ser Gln₃₂₀
Asp Ser Ser Lys Thr₃₂₅ Ser Ile Trp Gly Val₃₃₀ Pro Leu Leu Lys Asp₃₃₅ Asp
Arg Thr Asp Val₃₄₀ Val Leu Leu Lys Phe₃₄₅ Leu Arg Ala Arg Asp₃₅₀ Phe Lys
Pro Gln Glu Ala Tyr Ser Met Leu₃₆₀ Asn Lys Thr Leu Gln₃₆₅ Trp Arg Ile

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Asp Phe Asn Ile Glu Glu Leu Leu Asp Glu Asn Leu Gly Asp Asp Leu
 370 375 380
 Asp Lys Val Val Phe Met Gln Gly Gln Asp Lys Glu Asn His Pro Val
 385 390 395 400
 Cys Tyr Asn Val Tyr Gly Glu Phe Gln Asn Lys Asp Leu Tyr Gln Lys
 405 410 415
 Thr Phe Ser Asp Glu Glu Lys Arg Glu Arg Phe Leu Arg Trp Arg Ile
 420 425 430
 Gln Phe Leu Glu Lys Ser Ile Arg Asn Leu Asp Phe Val Ala Gly Gly
 435 440 445
 Val Ser Thr Ile Cys Gln Val Asn Asp Leu Lys Asn Ser Pro Gly Pro
 450 455 460
 Gly Lys Thr Glu Leu Arg Leu Ala Thr Lys Gln Ala Leu His Leu Leu
 465 470 475 480
 Gln Asp Asn Tyr Pro Glu Phe Val Ser Lys Gln Ile Phe Ile Asn Val
 485 490 495
 Pro Trp Trp Tyr Leu Ala Phe Tyr Arg Ile Ile Ser Pro Phe Met Ser
 500 505 510
 Gln Arg Ser Lys Ser Lys Leu Val Phe Ala Gly Pro Ser Arg Ser Ala
 515 520 525
 Glu Thr Leu Leu Lys Tyr Ile Ser Pro Glu His Val Pro Val Gln Tyr
 530 535 540
 Gly Gly Leu Ser Val Asp Asn Cys Glu Cys Asn Ser Asp Phe Thr His
 545 550 555 560
 Asp Asp Ile Ala Thr Glu Ile Thr Val Lys Pro Thr Thr Lys Gln Thr
 565 570 575
 Val Glu Ile Ile Val Tyr Glu Lys Cys Thr Ile Val Trp Glu Ile Arg
 580 585 590
 Val Val Gly Trp Glu Val Ser Tyr Gly Ala Glu Phe Val Pro Glu Asn
 595 600 605
 Lys Glu Gly Tyr Thr Val Ile Ile Gln Lys Pro Arg Lys Met Thr Ala
 610 615 620
 Lys Asn Glu Leu Val Val Ser His Ser Phe Lys Val Gly Glu Val Gly
 625 630 635 640

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Arg Ile Leu Leu Thr Val Asp Asn Pro Thr Ser Thr Lys Lys Met Leu
645 650 655

Ile Tyr Arg Phe Lys Val Lys Pro Leu Ala Cys Glu
660 665

<210> 51
<211> 1542
<212> DNA
<213> Populus trichocarpa

<400> 51
gactcagtac taacatctga atctgatgtt agtactgaga ttaaaccacc agcagagact 60
caggaatcaa aagttgaaga aaccccagaa aaagaatcac aagaagtggc aaaagaagag 120
caaaaggctg caccttcacc agaggagatc actatatggg ggatccctct tctgaaagat 180
gatagaagtg atgtggttct cttgaagttc ttgagggcaa gggattttta ggtaagcgat 240
gcatttgtaa tgatcaagaa cacaattcaa tggaggagag actttaaaat tgatgagctt 300
gttgatgaag atctaggtga tgatttggag aaagtttgtt ttatgcatgg ttatgacagg 360
gaagggcatc ctgtgtgtta taatgtgtat ggggagtttc aaaataaaga gttgtatcag 420
aagacattct ctgatgagga gaaaagattg aagtttttga ggtggcggat tcagttcttg 480
gagaggagta ttaggaagct tgattttagt cctagtggta tttccaccgt cttccagggt 540
aatgatctca agaactctcc aggacccgga aagagagagc ttaggttggc tactaaacag 600
gctctcctat tgcttcagga caattaccct gagtttgtgg ccaaacaggt gttcatcaat 660
gtcccttggt ggtatcttgc attttataca atgatcagtc cttttatgac acaaagaacc 720
aaaagcaaat ttgtattcgc aggcccatca aaatctgctg agacactttt caaatatgta 780
tctcctgagc aagttcctat tcagtatggg ggcttgagcg tggatttctg cgactgcaac 840
cccgaattta cttttgctga tcctgctact gagataactg taaaaccagc aaccaagcaa 900
actgtggaaa ttataattta tgagaaatgt ttcattgttt gggagttgag agttgttgga 960
tgggaggtga gttatagtgc tgaattcgtg ccgatttcta aagatgcata cacaattata 1020
atgacaaaac ccacaaaaat gaccccaacc aatgagccag tgggtgtctaa cagcttcaaa 1080
gttggtgagc tgggaaaaat attgctcaca gttgacaact ctacctcaa gaagaagaaa 1140
cttctctaca ggttcaagat aaacccttc tcagattgag gaactctttg tatttaatgt 1200
ttccatctca gatagtgtg gaaattgaat taattttatg tactctgggt gagccttttg 1260
tctctcgtct ttttctcta ccgaatagca catggtttgc attcgggtgt ttttttgcca 1320
atcatcttgg ggaaaacaaa cagatgtgtg ggcataatgga ggggggtgtg gttgtgaaac 1380
ttatatatac ataaatgtgc ctttctattg aggcgttttg cgatgcgctt tctcgtttat 1440
ctggatgtca atatttcagt accatttacc tttatgtaat ctcaaaactc ttatgttatt 1500
gcgacatcga atacttcaat ttgacatcat ctttaaagtt ga 1542

<210> 52

<211> 309

<212> PRT

<213> Populus trichocarpa

<400> 52

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

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Ile Met Thr Lys Pro Thr Lys Met Thr Pro Thr Asn Glu Pro Val Val
260 265 270

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

Asp Asn Ser Thr Ser Lys Lys Lys Lys Leu Leu Tyr Arg Phe Lys Ile
290 295 300

Asn Pro Phe Ser Asp
305

<210> 53
<211> 1080
<212> DNA
<213> Populus trichocarpa

<400> 53
gggaggattc aattcctgga aaaaagtatc aggacattgg atttcagtcc cgggtggaatt 60
tccacaattg ttcagggttaa tgacttgaaa aattctcctg gaccagctaa gagagagctt 120
agacaagcta ctagacaggc acttcaattg cttcaagaca actatccaga atttgtggcc 180
aaacagatct tcatcaatgt tccctggtgg tacctaacag taaatagaat gataagtcca 240
tttttaaccc agaggaccag aagcaagttt gtctttgttg gtccttccaa atctgccgaa 300
acccttatca ggtacatagc cgctgagcaa ataccagtga agtacggagg actaagcaaa 360
gatggtgaat ttggctcagc tgatgttggt actgagatta ccgtgaagcc agcagcaaag 420
cacactgtag aattcccagt tactgagaca tgccttttaa catgggaagt gagagttgcg 480
ggatgggatg tgagctatag tgcagaattt gtaccaagtg ctgaagatag ctacacagtg 540
atcatccaaa aggctagaaa ggttgctgca actgaagaac cagtggtttg caacagtttc 600
aaaattggtg aacctggtaa agttgttctc accattgaca actccacatc caagaagaag 660
aagaagctcc tctatcgctt gaaaaccaag cccgcttctt ctgattaatt aagggactat 720
atatattgaa acaacaatag aagattttgc ttacattctt gctgctgctg ctgctgccaa 780
ttttatcaac atgatcatat cacagcttga aggtgttctg agggcttga tcatggagaa 840
gataaagaaa tcttgaagat gtttatttat atgtttatatt ataattgaat tttgttttgg 900
tgtggaatgg attaaggatg ttgtgcaatt gaaggctaga agcatgtatg gggataggga 960
agaagctcca ttactagtgc caagaatttt ctttgtaaatt tctttatggc tttctttctc 1020
tttccctgta agtatctttt ggacatatta tgatattaat gaagacagta tctttcctat 1080

<210> 54
<211> 159
<212> PRT
<213> Populus trichocarpa

<400> 54

Met Ile Ser Pro Phe Leu Thr Gln Arg Thr Arg Ser Lys Phe Val Phe
1 5 10 15

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Val Gly Pro Ser Lys Ser Ala Glu Thr Leu Ile Arg Tyr Ile Ala Ala
20 25 30

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

Gly Ser Ala Asp Val Val Thr Glu Ile Thr Val Lys Pro Ala Ala Lys
50 55 60

His Thr Val Glu Phe Pro Val Thr Glu Thr Cys Leu Leu Thr Trp Glu
65 70 75 80

Val Arg Val Ala Gly Trp Asp Val Ser Tyr Ser Ala Glu Phe Val Pro
85 90 95

Ser Ala Glu Asp Ser Tyr Thr Val Ile Ile Gln Lys Ala Arg Lys Val
100 105 110

Ala Ala Thr Glu Glu Pro Val Val Cys Asn Ser Phe Lys Ile Gly Glu
115 120 125

Pro Gly Lys Val Val Leu Thr Ile Asp Asn Ser Thr Ser Lys Lys Lys
130 135 140

Lys Lys Leu Leu Tyr Arg Leu Lys Thr Lys Pro Ala Ser Ser Asp
145 150 155

<210> 55
<211> 911
<212> DNA
<213> Populus trichocarpa

<400> 55
atgtgttcat caatgttcca tgggtgtacc taacattcaa taagatgatc agccctttcc 60
tgacacacag gacaaagagc aagtttgttt ttgctggccc atccaagtct gctgaaacac 120
ttttcaaata catagctcct gaagaagtgc cagttcaata tgggtggacta agcaaggatg 180
gcgaattcac aggtgccgat accgtcacag atgttactat taagccaaca tcaaagcaca 240
ctgttgagtt cccagtgtct gaggcattgtg ttctcgtttg ggagcttcga gtttttggtt 300
gggatgtgag ctatggagct gaattcgtgc ctagcgctga ggatgggttac accgttatcg 360
tatcaaagac caggaagatt atctcatccg atgatcctgt gatctcagac acattcaaaa 420
ttggtgaacc tggcaagggt gtgcttacca ttgataacca aacctctaag aagaagaagc 480
tcctctatag gtcaaagacc aaacccttt ctgaatgagc ttcaagaatc aatgccttcg 540
tggggttttg aacttcatt aatttagaag acatggatgg cataacaagg ggtccttggt 600
catgatgcat gaacacgagg tgtggagttt tgttctgttt aaatttaata tattttttgt 660
tttataaagt ctgggttttg gctgggattt gttgtttggt gtttaattgg atacaatgta 720
ctggtgaaga cagtctggga ttatcatgga ttgacagaca catttgaggt ttaagtgtga 780

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

agaatatgaa aatgtgtttg ccaaagttga aagactatcc ttttttgttc ttggtactct 840
 tacctgtaaa atttgtgtaa atgtgatggg gttctacttc ttccttctta attaatacat 900
 gtatttttta c 911

<210> 56
 <211> 157
 <212> PRT
 <213> Populus trichocarpa
 <400> 56

Met Ile Ser Pro Phe Leu Thr His Arg Thr Lys Ser Lys Phe Val Phe
 1 5 10 15

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

Glu Glu Val Pro Val Gln Tyr Gly Gly Leu Ser Lys Asp Gly Glu Phe
 35 40 45

Thr Gly Ala Asp Thr Val Thr Asp Val Thr Ile Lys Pro Thr Ser Lys
 50 55 60

His Thr Val Glu Phe Pro Val Ser Glu Ala Cys Val Leu Val Trp Glu
 65 70 75 80

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

Ser Ala Glu Asp Gly Tyr Thr Val Ile Val Ser Lys Thr Arg Lys Ile
 100 105 110

Ile Ser Ser Asp Asp Pro Val Ile Ser Asp Thr Phe Lys Ile Gly Glu
 115 120 125

Pro Gly Lys Val Val Leu Thr Ile Asp Asn Gln Thr Ser Lys Lys Lys
 130 135 140

Lys Leu Leu Tyr Arg Ser Lys Thr Lys Pro Leu Ser Glu
 145 150 155

<210> 57
 <211> 840
 <212> DNA
 <213> Populus trichocarpa

<400> 57
 actagtttaa ttaaattaat ccccccccc gtggtattgc ttctttgctt caaatcagtg 60
 atctcaagaa ttctccttc ccatcaaaga aagagctcag gactgccatg agcaaagctg 120
 tcaccctttt gcaggacaat tatccagaat ttgttgcaaa aaatatattc ataaatgttc 180
 cattttggta ttatgctttc aacgccctgc tatctccttt cttggctcaa agaaccaaga 240

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

gcaaatttgt cgttgttcgc cctgccaaga ccaccgagac attgctcaag tatgttcagg	300
ccgaggaaat ccctgtccaa tatggtggct tcaagaggga gaatgatttc gagttctcca	360
gcgaagatgg tgaagtttca gaacttgtaa tcaaagctgg atcaactgaa accattgaga	420
tccctgcagc agaggttgga gccacattgc tttgggacct gacagttgtg ggatgggaag	480
tgaattacaa ggaggaattt gtgccaagtg atgaagcttc ctacaccatc atcatccaaa	540
agggcaagaa aatgagctca aatgaagagc caactcgcaa cactttcagg aacaatgaac	600
ctggaaaggt agttctgacc attcagaatt ggtcaagcaa gaagaagagg gtcctatacc	660
gatacaagac caagaagaat gcttcctatt gagacaagac tccattcttt tatattatca	720
gtcttttatt tgccgtgaca attcttttct agatagaaaa cattgattct tttcaggatt	780
gatatctata tctatatctg atcgtgtgat ttgatttggt atttctgggg ttcctttttc	840

<210> 58
 <211> 194
 <212> PRT
 <213> Populus trichocarpa

<400> 58

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

Ala Lys Asn Ile Phe Ile Asn Val Pro Phe Trp Tyr Tyr Ala Phe Asn
 20 25 30

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

Val Val Arg Pro Ala Lys Thr Thr Glu Thr Leu Leu Lys Tyr Val Gln
 50 55 60

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

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

Ala Gly Ser Thr Glu Thr Ile Glu Ile Pro Ala Ala Glu Val Gly Ala
 100 105 110

Thr Leu Leu Trp Asp Leu Thr Val Val Gly Trp Glu Val Asn Tyr Lys
 115 120 125

Glu Glu Phe Val Pro Ser Asp Glu Ala Ser Tyr Thr Ile Ile Ile Gln
 130 135 140

Lys Gly Lys Lys Met Ser Ser Asn Glu Glu Pro Thr Arg Asn Thr Phe
 145 150 155 160

Arg Asn Asn Glu Pro Gly Lys Val Val Leu Thr Ile Gln Asn Trp Ser

Ser Lys Lys Lys Arg Val Leu Tyr Arg Tyr Lys Thr Lys Lys Asn Ala
180 185 190

Ser Tyr

<210> 59
<211> 1564
<212> DNA
<213> Lycopersicum esculentum

<400> 59
ggagaaagta actccaccgg aaactgaagc aactccggcg ccggcagcag agacaccatc 60
tgagccatcg gagacagaga aggtggaggc agtcgaggaa atcaaggaaa ccattgtttga 120
agtaccggct gcggttgctg tgatggcctc cacggaggag ccaccggctg cagaggcaga 180
ggaaccgaaa acagagcaaa ccccaccagc agcaccagaa gaagtatcca tatggggaat 240
acccctttta gcagatgaga gaagtgatgt aatccttctc aagtttctgc gagcgagaga 300
tttcaaggtg aaagaagctt tcacatgtt gaaaagtgtt gtcgcatgga gaaaagaatt 360
caagattgat gaactcttgg atgagaaaga attaggacaa ggacttgaaa aagttgttta 420
caatcacgga gtagacaaag aaggtcaccc tgtatgttac aatgcatttg gtgagttcca 480
agacaaagaa ttgtacaaa acacttttgc tgatgacaaa gagaaactca ccaaattcct 540
cagatggaga attcaattca tggagaaatc catcaggaat cttgatttta gccctgatgg 600
tatcaacact tttgttcaag ttcttgatct gaagaattca cctggactct tcttttacia 660
gaaagaactt cgccaagcca ccaatcgtgc ctttctatta ctccaggata attaccctga 720
atgtgttgcc aagcaggtgt tcatcaatgt tccatggtgg taccagctt actacaggat 780
gattaatgca tctttcacta caaggaccaa gagcaagttt gtttttgctg gtccttcaag 840
atctgctgat actctattca aatacatagc acctgaacaa gtaccagcac aatatggtgg 900
acttagcaag gaggggtgaag aggaattcac cactgctgaa ccagccactg aggaaatcat 960
taagccagct tctaaacaca ccattgaatt cccagttact gagaaaagca cattggtttg 1020
ggaagcaaga gtgacagggt gggatgtatc atatggagct gaatttgctg ctagtgctga 1080
aggtggctac accattctca tagagaaatc aagaaaagtt ggggcaaag aatcagtgat 1140
cagcactagc tacaaggcaa gtgaagcagg caaagtggta atcacaattg acaaccaaac 1200
ttctaaaaag aagaaacttg tttacaggct caagaacaag atctcagatt gctgagccgc 1260
cttttcttgt ttcatagatt tttcttttgg ttgatatcaa ctagtactat tattttgagc 1320
tttttggggg tatttattta tattttattg gggttatttt ttgagctatt ttgctgttgg 1380
attgtttttt ttattatatg ggggaatattt attatattac aaaggggttg agatgtggag 1440
tacaagttat tgatacatct tcttctgaaa tattttgtgt aaatctaag ctgcctctca 1500
ttttccttac atttttttgg tgatgtgaag cttaacgtta gttaatccta tacttatgtt 1560

tcct

<210> 60
 <211> 370
 <212> PRT
 <213> Lycopersicum esculentum

<400> 60

Met Ala Ser Thr Glu Glu Pro Pro Ala Ala Glu Ala Glu Glu Pro Lys
 1 5 10 15

Thr Glu Gln Thr Pro Pro Ala Ala Pro Glu Glu Val Ser Ile Trp Gly
 20 25 30

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

Leu Arg Ala Arg Asp Phe Lys Val Lys Glu Ala Phe Thr Met Leu Lys
 50 55 60

Ser Val Val Ala Trp Arg Lys Glu Phe Lys Ile Asp Glu Leu Leu Asp
 65 70 75 80

Glu Lys Glu Leu Gly Gln Gly Leu Glu Lys Val Val Tyr Asn His Gly
 85 90 95

Val Asp Lys Glu Gly His Pro Val Cys Tyr Asn Ala Phe Gly Glu Phe
 100 105 110

Gln Asp Lys Glu Leu Tyr Gln Asn Thr Phe Ala Asp Asp Lys Glu Lys
 115 120 125

Leu Thr Lys Phe Leu Arg Trp Arg Ile Gln Phe Met Glu Lys Ser Ile
 130 135 140

Arg Asn Leu Asp Phe Ser Pro Asp Gly Ile Asn Thr Phe Val Gln Val
 145 150 155 160

Leu Asp Leu Lys Asn Ser Pro Gly Leu Phe Phe Tyr Lys Lys Glu Leu
 165 170 175

Arg Gln Ala Thr Asn Arg Ala Leu Leu Leu Leu Gln Asp Asn Tyr Pro
 180 185 190

Glu Phe Val Ala Lys Gln Val Phe Ile Asn Val Pro Trp Trp Tyr Pro
 195 200 205

Ala Tyr Tyr Arg Met Ile Asn Ala Ser Phe Thr Thr Arg Thr Lys Ser
 210 215 220

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

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Tyr Ile Ala Pro Glu Gln Val Pro Ala Gln Tyr Gly Gly Leu Ser Lys
245 250 255

Glu Gly Glu Glu Glu Phe Thr Thr Ala Glu Pro Ala Thr Glu Glu Ile
260 265 270

Ile Lys Pro Ala Ser Lys His Thr Ile Glu Phe Pro Val Thr Glu Lys
275 280 285

Ser Thr Leu Val Trp Glu Ala Arg Val Thr Gly Trp Asp Val Ser Tyr
290 295 300

Gly Ala Glu Phe Val Pro Ser Ala Glu Gly Gly Tyr Thr Ile Leu Ile
305 310 315 320

Glu Lys Ser Arg Lys Val Gly Ala Asn Glu Ser Val Ile Ser Thr Ser
325 330 335

Tyr Lys Ala Ser Glu Ala Gly Lys Val Val Ile Thr Ile Asp Asn Gln
340 345 350

Thr Ser Lys Lys Lys Lys Leu Val Tyr Arg Ser Lys Asn Lys Ile Ser
355 360 365

Asp Cys
370

<210> 61
<211> 2297
<212> DNA
<213> Medicago truncatula

<400> 61
ttatacataa aacacatcaa cccaagccca attgtctcca actccaactc caaacccatc 60
atctcactct ctctatatta gtcttttctc aatacccaaa tatcactttt tcttaacctt 120
aaccttaacc ctaatatcat ctctactttt tttcatatca aatggctgct gaacctcaaa 180
aacctgctga agaagttgcc acaaccacct ctgaaactgt tgttgagaaa gaacaacagg 240
ctgatggagt tgtagctgct gctgttaccg ctgccgctgt taccgctgcc accactgata 300
aggaagctgt tgctgatcct cctcctgctg ttgctgatga ggctgagaag ccggcggaag 360
ttgtggctga taaggtggcg gatgaaactg ttgttgatga aagcaagggt tctcaatcgg 420
tttcttttaa ggaagaaact aacgtgggtt ctgaacttcc tgacgttcag aaaaaagcac 480
ttgatgaact taaacaactt attcaagaag cgcttaacaa acatgaattc accgctcctc 540
caccgctcc agtcaaagca cctgaacctg aagtagctgt aaaagaagag aaaaagcctg 600
aagaagatga aaagaaaacc gaagaggtgg tagaagagaa gaaagatgaa gcagtagttg 660
aggagaagaa ggttgatgaa gaaaaagggt caacctctga ggaacctaaa gttgaaactg 720
ctgaacctga aaaggaggag aagaaagtgg aggaaacggt tgtagaagtt gttgagaaaa 780

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

tagctgcaag taccgaagaa gacgggtgcga aaacagttga ggctattcag gaaagtatatag	840
tatctgttcc agttactgaa ggtgaacaac ctgttgctga gcctgttgct gaagtggagg	900
ttactcctat tgtaccagaa gaagttgaaa tatggggaat tccattacta gctgatgaaa	960
gaagtgatgt gattcttctc aagttcttga gagctagggg ttttaagggtg aaggaggctt	1020
tcactatgat caaacaacc gtgctttggc gaaaggaatt cggagtcgaa gcacttcttc	1080
aagaagatct tggaactgac tgggacaaag ttgttttcac tgatgggtact gacaaagaag	1140
gtcaccctgt ttattacaat gtttttggtg agtttgagga taaggatttg tatcaaaaaa	1200
cattctctga tgaagagaag agaaccaagt tcgttcgttg gtggattcag tctttggaga	1260
aaagtgttag gaaactcgac tttgctccat ctggtatctc tactcttggt cagattaatg	1320
atcttaaaaa ttctcctgga cttcttggtg agaaagagct tagacaatct attaagcaga	1380
ctcttcagtt gcttcaggat aactatcctg aatttggtgc caaacagatt ttcataatg	1440
ttccttggtg gtaccttgcc ttctctagga tgatcagtc tttcctgaca caaaggacta	1500
agagcaaatt tgtatttgct ggctcctcca aatctgctga aacccttttc aaatatatag	1560
ctcctgagca agtgccagtt aaatatggag gactgagcag agacggtgaa caggaattca	1620
ccactgctga ccctgctaca gaggttacta tcaaaccagc aactaaacat gctgttgagt	1680
tcccagtttc tgagaaaagc actttggttt gggaagtaag agttgtggat tggaatgtga	1740
gctatggagc agaatttggt cctagtgtg aagatggata cactgtgata atccagaaga	1800
acaggaaaat tgctgcagct gatgaaacag taattagcaa caccttcaaa gttggtgaac	1860
ctggaaaagt tgtactcacc attgataacc aaacatccaa gaaaaagaag ctgctttaca	1920
ggtccaagac catacccatc tctgagtaaa aggaaaaatg tttaaattca ttatatggtc	1980
aataacatta ttgtgaaggt tattgggtgg gttacttata ttcttttata ggaatatttt	2040
cttcatttgg tttgtaaatt attttgtttc aagtatgggg ttgggaaatt ttatttacag	2100
ttattatcac ttatcaatat tcttaaatta atgtggtatt ttgttctttt gtgttggaat	2160
tggtatgaaac ctttgctgga tgaagaacac aattgggttc ttttgtaaaa caaagttta	2220
ttgtttttgt tatctgtgga ctctgtgatt gaaggattta tttgagtaat ttttttattc	2280
caattagtct agtggcc	2297

<210> 62
 <211> 595
 <212> PRT
 <213> Medicago truncatula

<400> 62

Met Ala Ala Glu Pro Gln Lys Pro Ala Glu Glu Val Ala Thr Thr Thr
 1 5 10 15

Ser Glu Thr Val Val Glu Lys Glu Gln Gln Ala Asp Gly Val Val Ala
 20 25 30

Ala Ala Val Thr Ala Ala Ala Val Thr Ala Ala Thr Thr Asp Lys Glu
 Seite 78

35

40

45

Ala Val Ala Asp Pro Pro Pro Ala Val Ala Asp Glu Ala Glu Lys Pro
 50 55 60

Ala Glu Val Val Ala Asp Lys Val Ala Asp Glu Thr Val Val Asp Glu
 65 70 75 80

Ser Lys Val Ser Gln Ser Val Ser Phe Lys Glu Glu Thr Asn Val Val
 85 90 95

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

Leu Ile Gln Glu Ala Leu Asn Lys His Glu Phe Thr Ala Pro Pro Pro
 115 120 125

Ala Pro Val Lys Ala Pro Glu Pro Glu Val Ala Val Lys Glu Glu Lys
 130 135 140

Lys Pro Glu Glu Asp Glu Lys Lys Thr Glu Glu Val Val Glu Glu Lys
 145 150 155 160

Lys Asp Glu Ala Val Val Glu Glu Lys Lys Val Asp Glu Glu Lys Gly
 165 170 175

Ser Thr Ser Glu Glu Pro Lys Val Glu Thr Ala Glu Pro Glu Lys Glu
 180 185 190

Glu Lys Lys Val Glu Glu Thr Val Val Glu Val Val Glu Lys Ile Ala
 195 200 205

Ala Ser Thr Glu Glu Asp Gly Ala Lys Thr Val Glu Ala Ile Gln Glu
 210 215 220

Ser Ile Val Ser Val Pro Val Thr Glu Gly Glu Gln Pro Val Ala Glu
 225 230 235 240

Pro Val Ala Glu Val Glu Val Thr Pro Ile Val Pro Glu Glu Val Glu
 245 250 255

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

Leu Lys Phe Leu Arg Ala Arg Asp Phe Lys Val Lys Glu Ala Phe Thr
 275 280 285

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

Leu Leu Gln Glu Asp Leu Gly Thr Asp Trp Asp Lys Val Val Phe Thr
 305 310 315 320

Asp Gly Thr Asp Lys₃₂₅ Glu Gly His Pro Val₃₃₀ Tyr Tyr Asn Val Phe Gly
 Glu Phe Glu Asp₃₄₀ Lys Asp Leu Tyr Gln₃₄₅ Lys Thr Phe Ser Asp₃₅₀ Glu Glu
 Lys Arg Thr₃₅₅ Lys Phe Val Arg Trp₃₆₀ Trp Ile Gln Ser Leu₃₆₅ Glu Lys Ser
 Val Arg₃₇₀ Lys Leu Asp Phe Ala₃₇₅ Pro Ser Gly Ile Ser₃₈₀ Thr Leu Val Gln
 Ile₃₈₅ Asn Asp Leu Lys Asn₃₉₀ Ser Pro Gly Leu Leu₃₉₅ Gly Lys Lys Glu Leu₄₀₀
 Arg Gln Ser Ile Lys₄₀₅ Gln Thr Leu Gln Leu₄₁₀ Leu Gln Asp Asn Tyr₄₁₅ Pro
 Glu Phe Val Ala₄₂₀ Lys Gln Ile Phe Ile₄₂₅ Asn Val Pro Trp Trp₄₃₀ Tyr Leu
 Ala Phe Ser₄₃₅ Arg Met Ile Ser Pro₄₄₀ Phe Leu Thr Gln Arg₄₄₅ Thr Lys Ser
 Lys Phe Val Phe Ala Gly Ser₄₅₅ Ser Lys Ser Ala Glu₄₆₀ Thr Leu Phe Lys
 Tyr₄₆₅ Ile Ala Pro Glu Gln₄₇₀ Val Pro Val Lys Tyr₄₇₅ Gly Gly Leu Ser Arg₄₈₀
 Asp Gly Glu Gln Glu₄₈₅ Phe Thr Thr Ala Asp₄₉₀ Pro Ala Thr Glu Val₄₉₅ Thr
 Ile Lys Pro Ala₅₀₀ Thr Lys His Ala Val₅₀₅ Glu Phe Pro Val Ser₅₁₀ Glu Lys
 Ser Thr Leu₅₁₅ Val Trp Glu Val Arg₅₂₀ Val Val Asp Trp Asn₅₂₅ Val Ser Tyr
 Gly Ala₅₃₀ Glu Phe Val Pro Ser₅₃₅ Ala Glu Asp Gly Tyr₅₄₀ Thr Val Ile Ile
 Gln₅₄₅ Lys Asn Arg Lys Ile₅₅₀ Ala Ala Ala Asp Glu₅₅₅ Thr Val Ile Ser Asn₅₆₀
 Thr Phe Lys Val Gly₅₆₅ Glu Pro Gly Lys Val₅₇₀ Val Leu Thr Ile Asp₅₇₅ Asn
 Gln Thr Ser Lys₅₈₀ Lys Lys Lys Leu Leu₅₈₅ Tyr Arg Ser Lys Thr₅₉₀ Ile Pro

Ile Ser Glu
595

<210> 63
<211> 1510
<212> DNA
<213> Beta vulgaris

<220>
<221> misc_feature
<222> (2)..(3)
<223> n is a, c, g, or t

```

<400> 63
tnncccgggc tgcaggaatt cggcacgagc tcatttctct acatcaaaaa cacaacaaag      60
agatcaccca tggcggaaga aacccataag ccagaatcaa cgggtggctga agtgggtggtt      120
ccagtagccg agaaaccagc tgagaagcca gctgagaagg cagttctacc acctgaagct      180
gagaaactag ctgcagctga atcagctgaa gccgagaagc cagctgattc agccgaggct      240
aagatagctc aacaagtctc attcaaagag gagactaatg ttgcaagtga gctacctgag      300
ctacatagaa aggctctcga ggacttgaag aaacttattc aagaagccct cgagaagcac      360
gagttctctt ctctcctcc tccgcctccg cctgctccag ctaaagttga ggagaaggcg      420
gaagagaaga aagaggaaca acctccatcc accacctcca ccaccaccac caccaccacc      480
gcggtttcag atgaggttgc tgttgctcct ccatccgaag aggccccgaa aactgacgag      540
gcctctccga aagtggagga ggagcctgca aaaatagttg agcaaccacc tacaacaccg      600
gcagaagaac ctgaaccagc aaaaacacct gaggttggtt ttgctgaaga ggagaaaact      660
ggtgaggata ttaaagaaac tatagtagtc gaggttgcca caactacagc agcaccagta      720
ctaacagaac cagaatctgt tgaggagaca caaaagaag ctgaagttgt agtggaagaa      780
tcaccaaagg agccagaaga agtatcaata tggggaattc cacttcttgc tgatgaaaga      840
agtgatgtaa ttctattgaa attcttaaga gcaagagatt atagagtga agatgctttc      900
actatgatta gaaatactgc tcgttgagga aaagaatttg aggttgattc tttacttgat      960
gaagatcttg gaaatgatta tgagaaagtt gtttttacac atggagttga taaacaaggt     1020
cgtcctgttt gttataatgt gtttgagag tttcaaaata aggaacttta tcagaatact     1080
ttctctgatg cagaaaaaag gaaaaagttc ttgagatggt tgattcaatt cttgaaaaa     1140
actattagaa ctcttgattt tagtcctgaa ggaattaatt cttttgttct tgттаатgat     1200
ttgaagaatt ctctgggta tggtaagaga gatctttaca aagttattga caagtttctt     1260
gagattctcc aggataatta cccagaattt gctgctaaac agttgtgcat caatgtttca     1320
tggtggtctt ggcatacaac tggatctatt tgactgtatt tacaccaagg agcaagagca     1380
agtttggtt tgcaagccca tctaaaactg ctgagaccct tttcaagtac atagctcctg     1440
agcaggtgcc tgttcaattt ggtgggcaca gcaagtttgg cgagcatgag tttcccctg     1500
ctgatactgt                                     1510

```

<210> 64
 <211> 427
 <212> PRT
 <213> Beta vulgaris

<400> 64

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

Val Pro Val Ala Glu Lys Pro Ala Glu Lys Pro Ala Glu Lys Ala Val
 20 25 30

Leu Pro Pro Glu Ala Glu Lys Leu Ala Ala Ala Glu Ser Ala Glu Ala
 35 40 45

Glu Lys Pro Ala Asp Ser Ala Glu Ala Lys Ile Ala Gln Gln Val Ser
 50 55 60

Phe Lys Glu Glu Thr Asn Val Ala Ser Glu Leu Pro Glu Leu His Arg
 65 70 75 80

Lys Ala Leu Glu Asp Leu Lys Lys Leu Ile Gln Glu Ala Leu Glu Lys
 85 90 95

His Glu Phe Ser Ser Pro Pro Pro Pro Pro Pro Pro Ala Pro Ala Lys
 100 105 110

Val Glu Glu Lys Ala Glu Glu Lys Lys Glu Glu Gln Pro Pro Ser Thr
 115 120 125

Thr Ser Thr Thr Thr Thr Thr Thr Thr Ala Val Ser Asp Glu Val Ala
 130 135 140

Val Ala Pro Pro Ser Glu Glu Ala Pro Lys Thr Asp Glu Ala Ser Pro
 145 150 155 160

Lys Val Glu Glu Glu Pro Ala Lys Ile Val Glu Gln Pro Pro Thr Thr
 165 170 175

Pro Ala Glu Glu Pro Glu Pro Ala Lys Thr Pro Glu Val Val Val Ala
 180 185 190

Glu Glu Glu Lys Thr Gly Glu Asp Ile Lys Glu Thr Ile Val Val Glu
 195 200 205

Val Ala Thr Thr Thr Ala Ala Pro Val Leu Thr Glu Pro Glu Ser Val
 210 215 220

Glu Glu Thr Pro Lys Glu Ala Glu Val Val Val Glu Glu Ser Pro Lys
 225 230 235 240

Glu Pro Glu Glu Val Ser Ile Trp Gly Ile Pro Leu Leu Ala Asp Glu
 Seite 82

Arg Ser Asp Val Ile Leu Leu Lys Phe Leu Arg Ala Arg Asp Tyr Arg
260 265 270

Val Lys Asp Ala Phe Thr Met Ile Arg Asn Thr Ala Arg Trp Arg Lys
275 280 285

Glu Phe Glu Val Asp Ser Leu Leu Asp Glu Asp Leu Gly Asn Asp Tyr
290 295 300

Glu Lys Val Val Phe Thr His Gly Val Asp Lys Gln Gly Arg Pro Val
305 310 315 320

Cys Tyr Asn Val Phe Gly Glu Phe Gln Asn Lys Glu Leu Tyr Gln Asn
325 330 335

Thr Phe Ser Asp Ala Glu Lys Arg Lys Lys Phe Leu Arg Trp Leu Ile
340 345 350

Gln Phe Leu Glu Lys Thr Ile Arg Thr Leu Asp Phe Ser Pro Glu Gly
355 360 365

Ile Asn Ser Phe Val Leu Val Asn Asp Leu Lys Asn Ser Pro Gly Tyr
370 375 380

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

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

Ser Trp Trp Ser Trp His Thr Thr Gly Ser Ile
420 425

<210> 65
<211> 552
<212> DNA
<213> Chlamydomonas reinhardtii

<400> 65
gtcgtgctac tcaagttctt gcgcgcacgg cagtggaacg tggcggccgc agttaacatg 60
cttgtcaact gtctgcggtg gcggcgcgac ttcgacgtgg ccggcctcgg cctggagacc 120
ttcccgccgc agctggcggc ggcggggcag ctcaccggac acgaccgggc cggcaaccga 180
gtcacctaca actactacgg cacgggtgtg gacttgaacg cggatgatggg cagcccgggc 240
gggtgtggcca ccttcgtgcg gtggcgggtg cggctgatgg agcaggcgat tgcgcagctg 300
gacttcgagc gcggcgtgga gcacgtcacg cagatccacg actacgccgg cgcctccatg 360
ttccgcatgg acgcgggcat caagtccgcc agccgcgaga tcatacgact gttccaggac 420
aactatcccg aactgctgtc cgccaagctg ttcctcaacg tgccgcgggt catggagtgc 480

ctgttcggcg tggtcagcgg cctggcggac gccgccaccc gcgccaagtt caccatggcc 540
tcgccccgcc gc 552

<210> 66
<211> 184
<212> PRT
<213> Chlamydomonas reinhardtii
<400> 66

Val Val Leu Leu Lys Phe Leu Arg Ala Arg Gln Trp Asn Val Ala Ala
1 5 10 15

Ala Val Asn Met Leu Val Asn Cys Leu Arg Trp Arg Arg Asp Phe Asp
20 25 30

Val Ala Gly Leu Gly Leu Glu Thr Phe Pro Pro Gln Leu Ala Ala Ala
35 40 45

Gly Gln Leu Thr Gly His Asp Arg Ala Gly Asn Pro Val Thr Tyr Asn
50 55 60

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

Gly Val Ala Thr Phe Val Arg Trp Arg Val Arg Leu Met Glu Gln Ala
85 90 95

Ile Ala Gln Leu Asp Phe Glu Arg Gly Val Glu His Val Thr Gln Ile
100 105 110

His Asp Tyr Ala Gly Ala Ser Met Phe Arg Met Asp Ala Gly Ile Lys
115 120 125

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

Leu Leu Ser Ala Lys Leu Phe Leu Asn Val Pro Arg Val Met Glu Phe
145 150 155 160

Leu Phe Gly Val Phe Ser Gly Leu Ala Asp Ala Ala Thr Arg Ala Lys
165 170 175

Phe Thr Met Ala Ser Pro Ala Arg
180

<210> 67
<211> 1335
<212> DNA
<213> Dictyostelium discoideum
<400> 67

atgagtggat ttattaaaga tttatctcaa cctcaaagtg aagcttttaa tcaattttaa 60

gaatatttaa ataaaaaaga aacaattgtg caaattaaat cagatattaa aaataaatta 120

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

ccaacaacta caacaactac aacaactact aatacagaaa cagaagaatc atcatcatca      180
tcaccacccat catcaaaaga agaagaaaaa cacttaaaaaa tttggaatat taatttagaa      240
aatgattcaa aagagcgtga tattatttta ttaaaatfff tacgtgctag agaattttaa      300
attgaaaatt caaaacaaat gttaattgat tgtttaatff ggagaaaaca aaatcaagta      360
gatgattatg aaaagatagt taatgaagca tttccagact attataaaaa cattggtacc      420
atfffcaaga ctgataaaga gggtagacca gtaatgatca atcattacca tgcaattaat      480
ccagatgtta ffffcaaaga tgggtgtggac caatffgttc gttggaaagt ccaacaaatg      540
gaaatcgcca ttagggatac actcatccca tgcgaatggg aaattgaaga fffaatagtc      600
attcacgact ataaagattg ctcattctff agaatggatc cacgtataaa acaagcatct      660
aatcaaacca fffcaaccct tcaaaataac taccagaat ffftagctcg taaattctff      720
attaacatcc catggffaaf ggagaagttg fffcaatff tcacagtatt cacatcagag      780
cgtacaaaaa gcaaatfcac aatffgttct ggaaattatc gggaaaaact fffaaaatat      840
attgaagcag attcaatcgc fccaaaatta fctggfftcg aagataacca atcaccaatt      900
ffaaatatta aaatcaaacc fcaaaaatca cattcaatfc aattaggtaa acttgatgct      960
gataaaacta ffgaatggga atffftgtaca aatgagattg atffctgaaat tgggtgctaaa     1020
atfftaattg aaccaaataa ccaaccaaca actfftaatg atatffftata ffftaataaf     1080
aatagtaata ataataataa taataataaf tcaccaacac caagtaatag taattatcca     1140
ffcaattgtt fffffftaat tgaaccaaga gaatffaata gtggffcaaf fcaaatfgaa     1200
gatgattctt attatactff agffffftaat aatcattffaa ataaacaatg tgatffatff     1260
tatcgtataa ctataaaatc aaaaacaact cattctffcaa ctacaactfc aacaatcgaa     1320
actfftaggaa attaa                                           1335

```

<210> 68
 <211> 444
 <212> PRT
 <213> Dictyostelium discoideum

<400> 68

Met Ser Gly Phe Ile Lys Asp Leu Ser Gln Pro Gln Ser Glu Ala Leu
 1 5 10 15

Asn Gln Phe Lys Glu Tyr Leu Asn Lys Lys Glu Thr Ile Val Gln Ile
 20 25 30

Lys Ser Asp Ile Lys Asn Lys Leu Pro Thr Thr Thr Thr Thr Thr Thr
 35 40 45

Thr Thr Asn Thr Glu Thr Glu Glu Ser Ser Ser Ser Ser Ser Pro Ser
 50 55 60

Ser Lys Glu Glu Glu Lys His Leu Lys Ile Trp Asn Ile Asn Leu Glu
 65 70 75 80

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

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

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Asn Asp Ile Leu Tyr Phe Asn Asn Asn Ser Asn Asn Asn Asn Asn
355 360 365

Asn Asn Ser Pro Thr Pro Ser Asn Ser Asn Tyr Pro Phe Asn Cys Phe
370 375 380

Leu Ser Ile Glu Pro Arg Glu Phe Asn Ser Gly Ser Ile Gln Ile Glu
385 390 395 400

Asp Asp Ser Tyr Tyr Thr Leu Val Phe Asn Asn His Leu Asn Lys Gln
405 410 415

Cys Asp Leu Phe Tyr Arg Ile Thr Ile Lys Ser Lys Thr Thr His Ser
420 425 430

Ser Thr Thr Thr Ser Thr Ile Glu Thr Leu Gly Asn
435 440

<210> 69
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> motif 1

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

<400> 69

Leu Leu Lys Phe Leu Arg Ala Arg
1 5

<210> 70
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> motif 2

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

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

<400> 70

Leu Gln Asp Asn Tyr Pro Glu Phe
1 5

<210> 71
 <211> 169
 <212> PRT
 <213> Artificial sequence

<220>
 <223> SEC domain

<400> 71

Leu Pro Glu Leu Asp Ser Val Val Phe Tyr Arg Gly Ala Asp Arg Glu
 1 5 10 15

Gly His Pro Val Cys Tyr Asn Val Tyr Gly Glu Phe Gln Asp Lys Asp
 20 25 30

Leu Tyr Glu Lys Ala Phe Gly Asp Glu Glu Lys Arg Glu Arg Phe Leu
 35 40 45

Lys Trp Arg Ile Gln Leu Leu Glu Arg Gly Ile Leu Ser Gln Leu Asp
 50 55 60

Phe Ser Pro Ser Gly Ile Cys Ser Met Val Gln Val Thr Asp Leu Lys
 65 70 75 80

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

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

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

Pro Phe Leu Thr Gln Arg Thr Lys Ser Lys Phe Ile Phe Ala Ser Pro
 130 135 140

Ala Lys Ser Ala Glu Thr Leu Phe Arg Tyr Ile Ala Pro Glu Gln Val
 145 150 155 160

Pro Val Gln Phe Gly Gly Leu Phe Lys
 165

<210> 72
 <211> 102
 <212> PRT
 <213> Artificial sequence

<220>
 <223> GOLD domain

<400> 72

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

Val Glu Ile Pro Val Thr Glu Asn Ser Thr Ile Gly Trp Glu Leu Arg
20 25 30

Val Leu Gly Trp Glu Val Ser Tyr Gly Ala Glu Phe Thr Pro Asp Ala
35 40 45

Glu Gly Gly Tyr Thr Val Ile Val Gln Lys Thr Arg Lys Val Pro Ala
50 55 60

Asn Glu Glu Pro Ile Met Lys Gly Ser Phe Lys Val Gly Glu Pro Gly
65 70 75 80

Lys Ile Val Leu Thr Ile Asn Asn Pro Ala Ser Lys Lys Lys Lys Leu
85 90 95

Leu Tyr Arg Ser Lys Val
100

<210> 73
<211> 51
<212> DNA
<213> Artificial sequence

<220>
<223> primer 1

<400> 73
ggggacaagt ttgtacaaaa aagcaggctt aaacaatggc ggaggagcca c 51

<210> 74
<211> 50
<212> DNA
<213> Artificial sequence

<220>
<223> primer 2

<400> 74
ggggaccact ttgtacaaga aagctgggtg tggatgaatct ggtgatcagg 50

<210> 75
<211> 2194
<212> DNA
<213> Oryza sativa

<400> 75
aatccgaaaa gtttctgcac cgttttcacc ccctaactaa caatataggg aacgtgtgct 60
aaatataaaa tgagacctta tatatgtagc gctgataact agaactatgc aagaaaaact 120
catccaccta ctttagtggc aatcgggcta aataaaaaag agtcgctaca ctagtttcgt 180
tttccttagt aattaagtgg gaaaatgaaa tcattattgc ttagaatata cgttcacatc 240
tctgtcatga agttaaatta ttcgaggtag ccataattgt catcaaactc ttcttgaata 300
aaaaaatctt tctagctgaa ctcaatgggt aaagagagag atttttttta aaaaaataga 360
atgaagatat tctgaacgta ttggcaaaga tttaaacata taattatata attttatagt 420
ttgtgcattc gtcatatcgc acatcattaa ggacatgtct tactccatcc caatttttat 480

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

ttagtaatta aagacaattg acttattttt attattttatc ttttttcgat tagatgcaag	540
gtacttacgc acacactttg tgctcatgtg catgtgtgag tgcacctcct caatacacgt	600
tcaactagca acacatctct aatatcactc gcctattttaa tacatttagg tagcaatatc	660
tgaattcaag cactccacca tcaccagacc actttttaata atatctaaaa taaaaaaat	720
aattttacag aatagcatga aaagtatgaa acgaactatt taggtttttc acatacaaaa	780
aaaaaaagaa ttttgctcgt gcgcgagcgc caatctccca tattgggcac acaggcaaca	840
acagagtggc tgcccacaga acaaccaca aaaaacgatg atctaacgga ggacagcaag	900
tccgcaacaa ctttttaaca gcaggctttg cggccaggag agaggaggag aggcaaagaa	960
aaccaagcat cctccttctc ccatctataa attcctcccc ctttttcccc tctctatata	1020
ggaggcatcc aagccaagaa gaggggagagc accaaggaca cgcgactagc agaagccgag	1080
cgaccgcctt ctcgatccat atcttccggt cgagttcttg gtcgatctct tccctcctcc	1140
acctcctcct cacagggtat gtgcctccct tcggttggtt ttggatttat tgttctaggt	1200
tgtgtagtac gggcgttgat gttaggaaag gggatctgta tctgtgatga ttcctgttct	1260
tggatttggg atagaggggt tcttgatggt gcatgttatc ggttcgggtt gattagtagt	1320
atggttttca atcgtctgga gagctctatg gaaatgaaat ggtttaggga tcggaatcct	1380
gcgattttgt gagtacctt tgtttgaggt aaaatcagag caccggtgat tttgcttggt	1440
gtaataaagt acggttggtt ggtcctcgat tctggtagtg atgcttctcg atttgacgaa	1500
gctatccttt gtttattccc tattgaacaa aaataatcca actttgaaga cgggtcccgtt	1560
gatgagattg aatgattgat tcttaagcct gtccaaaatt tcgcagctgg cttgtttaga	1620
tacagtagtc cccatcacga aattcatgga aacagttata atcctcagga acaggggatt	1680
ccctgttctt ccgatttgct ttagtcccag aatttttttt cccaaatatc ttaaaaagtc	1740
actttctggt tcagttcaat gaattgattg ctacaaataa tgcttttata gcgttatcct	1800
agctgtagtt cagttaatag gtaatacccc tatagtttag tcaggagaag aacttatccg	1860
atttctgatc tccattttta attatatgaa atgaactgta gcataagcag tattcatttg	1920
gattattttt tttattagct ctcacccctt cattattctg agctgaaagt ctggcatgaa	1980
ctgtcctcaa ttttgttttc aaattcacat cgattatcta tgcattatcc tcttgatatc	2040
acctgtagaa gtttcttttt ggttattcct tgactgcttg attacagaaa gaaatttatg	2100
aagctgtaat cgggatagtt atactgcttg ttcttatgat tcatttcctt tgtgcagttc	2160
ttggtgtagc ttgccacttt caccagcaaa gttc	2194

<210> 76
 <211> 1182
 <212> DNA
 <213> Arabidopsis thaliana

<400> 76	
atggcggaga tacagtcaaa tggaagggca tatgagtcatt tattggaaaa ggttctttca	60
atgaacattc tttcttctga ctattttaaa gagctctatg gtttaaagac ttatcatgag	120

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

gtaattgatg aaatctacaa ccaagttaat catgtggagc cgtggatggg tgggaattgc      180
cgtggtcctt caacagcgta ttgtcttctc tacaaattct ttaccatgaa acttacagtg      240
aagcagatgc atggactggt aaagcacaca gattctcctt atattagagc ggttggattc      300
ctatatttaa gatatgttgc agatgcaaag acgttgtgga catggtatga accatacatt      360
aaagatgatg aggagttttc accaggacca aatggacgga tgacgacaat ggggtgtttat      420
gtacgtgatt tgctgcttgg actgtactac tttgatactt tgtttcctcg tatacctggt      480
cctgtcatgc gccagattgt atcaaacctt gagaagatga atttaccac taaaccttct      540
ggttcaaccg gagacatgac ccgtggctca gaagacactg cccgtcgtcc accatcagta      600
aaagcatccc tctctgcttc atttggtcag cgtgcacctc atcgtgcttc caccagaggc      660
tcttctcctg ttcgccgtcc tccaccgact ggttatgaca gaaatggagg cgatgaagta      720
caacagcggg cccacgtag aagccagagc cgagactatt attctgacag agactcagat      780
agacaacggg aaagagagag ggagaaagac cgcgaaagag agagggggag ggatagatac      840
agagaaaggg aaagggatta tggtaatgat aggagatcaa ggcgtgacta tgatagtaga      900
agcaggcgca atgattatga ggacgacaga agtagacatg accggagaag caggagcaga      960
agcagaagta ggagcaggag tgtgcagatt gagcgtgaac cgactcctaa aagagatagt     1020
agcaacaaag agaaatcggc ggtgacagtg aacagcaatc tcgcaaagct aaaagatttg     1080
tatggagacg caagtagtca gaaaagggat gaaggatttg gaacaaggaa agattcaagt     1140
tcagaagaag tgataaagct tggtggttcc tcttgagggt ga                        1182

```

<210> 77
 <211> 393
 <212> PRT
 <213> Arabidopsis thaliana

<400> 77

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

Lys Val Leu Ser Met Asn Ile Leu Ser Ser Asp Tyr Phe Lys Glu Leu
 20 25 30

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

Val Asn His Val Glu Pro Trp Met Gly Gly Asn Cys Arg Gly Pro Ser
 50 55 60

Thr Ala Tyr Cys Leu Leu Tyr Lys Phe Phe Thr Met Lys Leu Thr Val
 65 70 75 80

Lys Gln Met His Gly Leu Leu Lys His Thr Asp Ser Pro Tyr Ile Arg
 85 90 95

Ala Val Gly Phe Leu Tyr Leu Arg Tyr Val Ala Asp Ala Lys Thr Leu
100 105 110

Trp Thr Trp Tyr Glu Pro Tyr Ile Lys Asp Asp Glu Glu Phe Ser Pro
115 120 125

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

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

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

Thr Lys Pro Ser Gly Ser Thr Gly Asp Met Thr Arg Gly Ser Glu Asp
180 185 190

Thr Ala Arg Arg Pro Pro Ser Val Lys Ala Ser Leu Ser Ala Ser Phe
195 200 205

Gly Gln Arg Ala Pro His Arg Ala Ser Thr Arg Gly Ser Ser Pro Val
210 215 220

Arg Arg Pro Pro Pro Thr Gly Tyr Asp Arg Asn Gly Gly Asp Glu Val
225 230 235 240

Gln Gln Arg Ser Pro Arg Arg Ser Gln Ser Arg Asp Tyr Tyr Ser Asp
245 250 255

Arg Asp Ser Asp Arg Gln Arg Glu Arg Glu Arg Glu Lys Asp Arg Glu
260 265 270

Arg Glu Arg Gly Arg Asp Arg Tyr Arg Glu Arg Glu Arg Asp Tyr Gly
275 280 285

Asn Asp Arg Arg Ser Arg Arg Asp Tyr Asp Ser Arg Ser Arg Arg Asn
290 295 300

Asp Tyr Glu Asp Asp Arg Ser Arg His Asp Arg Arg Ser Arg Ser Arg
305 310 315 320

Ser Arg Ser Arg Ser Arg Ser Val Gln Ile Glu Arg Glu Pro Thr Pro
325 330 335

Lys Arg Asp Ser Ser Asn Lys Glu Lys Ser Ala Val Thr Val Asn Ser
340 345 350

Asn Leu Ala Lys Leu Lys Asp Leu Tyr Gly Asp Ala Ser Ser Gln Lys
355 360 365

Arg Asp Glu Gly Phe Gly Thr Arg Lys Asp Ser Ser Ser Glu Glu Val
Seite 92

370

375

380

Ile Lys Leu Gly Gly Ser Ser Trp Arg
385 390

<210> 78
<211> 1182
<212> DNA
<213> Arabidopsis thaliana

```

<400> 78
atggcggaga tacagtcaaa tggaagggca tatgagtcac tattggaaaa gggtctttca      60
atgaacattc tttcttctga ctattttaaa gagctctatg gtttaaagac ttatcatgag      120
gtaattgatg aaatctacaa ccaagttaat catgtggagc cgtggatggg tgggaattgc      180
cgtggtcctt caacagcgta ttgtcttctc tacaaattct ttaccatgaa acttacagtg      240
aagcagatgc atggactgtt aaagcacaca gattctcctt atattagagc gggtggattc      300
ctatatttaa gatatgttgc agatgcaaag acgttgtgga catggtatga accatacatt      360
aaagatgatg aggagttttc accaggatca aatggacgga tgacgacaat ggggtgtttat      420
gtacgtgatt tgctgcttgg actgtactac tttgatactt tgtttcctcg tatacctggt      480
cctgtcatgc gccagattgt atcaaacctt gagaagatga atttaccac taaaccttct      540
ggttcaaccg gagacatgac ccgtggctca gaagacactg cccgtcgtcc accatcagta      600
aaagcatccc tctctgtttc atttggtcag cgtgcacctc atcgtgcttc caccagaggg      660
tcttctcctg ttcgccgtcc tccaccgact ggttatgaca gaaatggagg cgatgaagta      720
caacagcggg cccacgtag aagccagagc cgagactatt attctgacag agactcagat      780
agacaacggg aaagagagag ggagaaagac cgcgaaagag agagggggag ggatagatac      840
agagaaaggg aaagggatta tggtaatgat aggagatcaa ggcgtgacta tgatagtaga      900
agcaggcgca atgattatga ggacgacaga agtagacatg accggagaag caggagcaga      960
agcagaagta ggagcaggag tgtgcagatt gagcgtgaac cgactcctaa aagagatagt     1020
agcaacaaag agaaatcggc ggtgacagtg aacagcaatc tcgcaaagct aaaagatttg     1080
tatggagacg caagtagtca gaaaagggat gaaggatttg gaacaaggaa agattcaagt     1140
tcagaagaag tgataaagct tgggtggttc tcttgagagt ga                        1182
    
```

<210> 79
<211> 393
<212> PRT
<213> Arabidopsis thaliana

<400> 79

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

Lys Val Leu Ser Met Asn Ile Leu Ser Ser Asp Tyr Phe Lys Glu Leu
20 25 30

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

Val Asn His Val Glu Pro Trp Met Gly Gly Asn Cys Arg Gly Pro Ser
50 55 60

Thr Ala Tyr Cys Leu Leu Tyr Lys Phe Phe Thr Met Lys Leu Thr Val
65 70 75 80

Lys Gln Met His Gly Leu Leu Lys His Thr Asp Ser Pro Tyr Ile Arg
85 90 95

Ala Val Gly Phe Leu Tyr Leu Arg Tyr Val Ala Asp Ala Lys Thr Leu
100 105 110

Trp Thr Trp Tyr Glu Pro Tyr Ile Lys Asp Asp Glu Glu Phe Ser Pro
115 120 125

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

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

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

Thr Lys Pro Ser Gly Ser Thr Gly Asp Met Thr Arg Gly Ser Glu Asp
180 185 190

Thr Ala Arg Arg Pro Pro Ser Val Lys Ala Ser Leu Ser Val Ser Phe
195 200 205

Gly Gln Arg Ala Pro His Arg Ala Ser Thr Arg Gly Ser Ser Pro Val
210 215 220

Arg Arg Pro Pro Pro Thr Gly Tyr Asp Arg Asn Gly Gly Asp Glu Val
225 230 235 240

Gln Gln Arg Ser Pro Arg Arg Ser Gln Ser Arg Asp Tyr Tyr Ser Asp
245 250 255

Arg Asp Ser Asp Arg Gln Arg Glu Arg Glu Arg Glu Lys Asp Arg Glu
260 265 270

Arg Glu Arg Gly Arg Asp Arg Tyr Arg Glu Arg Glu Arg Asp Tyr Gly
275 280 285

Asn Asp Arg Arg Ser Arg Arg Asp Tyr Asp Ser Arg Ser Arg Arg Asn
290 295 300

Asp Tyr Glu Asp Asp Arg Ser Arg His Asp Arg Arg Ser Arg Ser Arg
Seite 94

<400>	80						
atggcggaga	tacagtcaaa	tggaagggca	tatgagtc	tattggaaaa	ggttctttca		60
atgaacattc	tttcttctga	ctatttttaa	gagctctatg	gtttaaagac	ttatcatgag		120
gtaattgatg	aaatctacaa	ccaagttaat	catgtggagc	cgtggatggg	tgggaattgc		180
cgtggtcctt	caacagcgta	ttgtcttctc	tacaaattct	ttaccatgaa	acttacagtg		240
aagcagatgc	atggactgtt	aaagcacaca	gattctcctt	atattagagc	ggttggattc		300
ctatatttta	gatatgttgc	agatgcaaag	acgttgtgga	catggtatga	accatacatt		360
aaagatgatg	aggagttttc	accaggatca	aatggacgga	tgacgacaat	gggtgtttat		420
tactactttg	atactttgtt	tcctcgtata	cctgttcctg	tcatgcgcca	gattgtatca		480
aaccttgaga	agatgaattt	accaactaaa	ccttctgggt	caaccggaga	catgaccctg		540
ggctcagaag	acactgcccc	tcgtccacca	tcagtaaaag	catccctctc	tgtttcattt		600
ggtcagcgtg	cacctcatcg	tgcttccacc	agaggctctt	ctcctgttcg	ccgtcctcca		660
ccgactgggt	atgacagaaa	tggaaggcga	gaagtacaac	agcgggtccc	acgtagaagc		720
cagagccgag	actattattc	tgacagagac	tcagatagac	aacgggaaaag	agagagggag		780
aaagaccgcg	aaagagagag	ggggagggat	agatacagag	aaagggaaaag	ggattatggt		840
aatgatagga	gatcaaggcg	tgactatgat	agtagaagca	ggcgcaatga	ttatgaggac		900
gacagaagta	gacatgaccg	gagaagcagg	agcagaagca	gaagtaggag	caggagtgtg		960
cagattgagc	gtgaaccgac	tcctaaaaga	gatagtagca	acaagagaaa	atcggcgggtg		1020
acagtgaaca	gcaatctcgc	aaagctaaaa	gatttgtatg	gagacgcaag	tagtcagaaa		1080
agggatgaag	gatttggaac	aaggaaagat	tcaagttcag	aagaagtgat	aaagcttggt		1140
ggttcctctt	ggaggtga						1158

<210> 81
 <211> 385
 <212> PRT
 <213> Arabidopsis thaliana

<400> 81

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

Lys Val Leu Ser Met Asn Ile Leu Ser Ser Asp Tyr Phe Lys Glu Leu
 20 25 30

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

Val Asn His Val Glu Pro Trp Met Gly Gly Asn Cys Arg Gly Pro Ser
 50 55 60

Thr Ala Tyr Cys Leu Leu Tyr Lys Phe Phe Thr Met Lys Leu Thr Val
 65 70 75 80

Lys Gln Met His Gly Leu Leu Lys His Thr Asp Ser Pro Tyr Ile Arg
 85 90 95

Ala Val Gly Phe Leu Tyr Leu Arg Tyr Val Ala Asp Ala Lys Thr Leu
 100 105 110

Trp Thr Trp Tyr Glu Pro Tyr Ile Lys Asp Asp Glu Glu Phe Ser Pro
 115 120 125

Gly Ser Asn Gly Arg Met Thr Thr Met Gly Val Tyr Tyr Tyr Phe Asp
 130 135 140

Thr Leu Phe Pro Arg Ile Pro Val Pro Val Met Arg Gln Ile Val Ser
 145 150 155 160

Asn Leu Glu Lys Met Asn Leu Pro Thr Lys Pro Ser Gly Ser Thr Gly
 165 170 175

Asp Met Thr Arg Gly Ser Glu Asp Thr Ala Arg Arg Pro Pro Ser Val
 180 185 190

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

Ser Thr Arg Gly Ser Ser Pro Val Arg Arg Pro Pro Pro Thr Gly Tyr
 210 215 220

Asp Arg Asn Gly Gly Asp Glu Val Gln Gln Arg Ser Pro Arg Arg Ser
 225 230 235 240

Gln Ser Arg Asp Tyr Tyr Ser Asp Arg Asp Ser Asp Arg Gln Arg Glu
 Seite 96

Arg Glu Arg Glu Lys Asp Arg Glu Arg Glu Arg Gly Arg Asp Arg Tyr
260 265 270

Arg Glu Arg Glu Arg Asp Tyr Gly Asn Asp Arg Arg Ser Arg Arg Asp
275 280 285

Tyr Asp Ser Arg Ser Arg Arg Asn Asp Tyr Glu Asp Asp Arg Ser Arg
290 295 300

His Asp Arg Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Val
305 310 315 320

Gln Ile Glu Arg Glu Pro Thr Pro Lys Arg Asp Ser Ser Asn Lys Glu
325 330 335

Lys Ser Ala Val Thr Val Asn Ser Asn Leu Ala Lys Leu Lys Asp Leu
340 345 350

Tyr Gly Asp Ala Ser Ser Gln Lys Arg Asp Glu Gly Phe Gly Thr Arg
355 360 365

Lys Asp Ser Ser Ser Glu Glu Val Ile Lys Leu Gly Gly Ser Ser Trp
370 375 380

Arg
385

<210> 82
<211> 680
<212> DNA
<213> Arabidopsis thaliana

<400> 82
caaaccttga gaagatgaat ttaccaacta aaccttcttg ttcaaccgga gacatgaccc 60
gtggctcaga agacactgcc cgtcgtccac catcagtaaa agcatctctc tctgtttcat 120
ttggtcagcg tgcacctcat cgtgcttcca ccagaggctc ttctcctggt cgccgtcctc 180
caccgactgg ttatgacaga aatggaggcg atgaagtaca acagcgggtcc ccacgtagaa 240
gccagagccg agactattat tctgacagag actcagatag acaacgggaa agagagaggg 300
agaaagaccg cgaaagagag aggggggaggg atagatacag agaaagggag agggattatg 360
gtaatgatag gagatcaagg cgcgactatg atagtagaag caggcgcaat gattatgagg 420
acgacagaag tagacatgac cggagaagca ggagcagaag cagaagtagg agcaggagtg 480
tgcagattga gcgtgaaccg actcctaaaa gagatagtag caacaaagag aaatcggcgg 540
tgacagtga cagcaatctc gcaaagctaa aagatttgta tggagacgca agtagtcaga 600
aaagggatga aggatttgga acaaggaaag attcaagttc agaagaagtg ataaagcttg 660
gtggttcctc ttggaggtga 680

<210> 83
 <211> 225
 <212> PRT
 <213> Arabidopsis thaliana

<400> 83

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

Asp Met Thr Arg Gly Ser Glu Asp Thr Ala Arg Arg Pro Pro Ser Val
 20 25 30

Lys Ala Ser Leu Ser Val Ser Phe Gly Gln Arg Ala Pro His Arg Ala
 35 40 45

Ser Thr Arg Gly Ser Ser Pro Val Arg Arg Pro Pro Pro Thr Gly Tyr
 50 55 60

Asp Arg Asn Gly Gly Asp Glu Val Gln Gln Arg Ser Pro Arg Arg Ser
 65 70 75 80

Gln Ser Arg Asp Tyr Tyr Ser Asp Arg Asp Ser Asp Arg Gln Arg Glu
 85 90 95

Arg Glu Arg Glu Lys Asp Arg Glu Arg Glu Arg Gly Arg Asp Arg Tyr
 100 105 110

Arg Glu Arg Glu Arg Asp Tyr Gly Asn Asp Arg Arg Ser Arg Arg Asp
 115 120 125

Tyr Asp Ser Arg Ser Arg Arg Asn Asp Tyr Glu Asp Asp Arg Ser Arg
 130 135 140

His Asp Arg Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Val
 145 150 155 160

Gln Ile Glu Arg Glu Pro Thr Pro Lys Arg Asp Ser Ser Asn Lys Glu
 165 170 175

Lys Ser Ala Val Thr Val Asn Ser Asn Leu Ala Lys Leu Lys Asp Leu
 180 185 190

Tyr Gly Asp Ala Ser Ser Gln Lys Arg Asp Glu Gly Phe Gly Thr Arg
 195 200 205

Lys Asp Ser Ser Ser Glu Glu Val Ile Lys Leu Gly Gly Ser Ser Trp
 210 215 220

Arg
 225

<210> 84

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

<211> 1068

<212> DNA

<213> Arabidopsis thaliana

<400> 84

```

atggcaaaca gaacagatcc gttggcaaag aatataagag gaacgaatcc gcagaatctg      60
gtagagaaga ttgtgcgaac gaagatttat cagcacacct tttggaagga gcagtgcctt      120
ggctctcacgg cggagacatt ggtggacaaa gctatggagc tcgaccatct aggtgggtacc      180
tttggtggta gccgcaagcc tactccgttc ctttgcctca tattgaagat gcttcaaadc      240
cagcctgaga aggaaattgt cgtggagttc ataaaaaatg atgactacaa atatgttcgt      300
attcttgggtg cgttctatct gcgtctcact gggactgatg ttgatgtcta tcgctacctc      360
gaacctctct acaatgacta ccggaaagtg agacaaaagt tatctgatgg gaagttttcg      420
ctgacacatg tggacgaagt cattgaggaa cttctaacca aggattattc ttgtgatatt      480
gcaatgccac gtttgaagaa aaggtggacg cttgaacaga atggttttatt agagccaagg      540
aaaagtgttt tggaagacga ctttgaagaa gaggaagaaa aggaggagaa tgaagggatt      600
gctgatggat ctgaagatga gatggatcag cgccgtaaga gtcctgaaag agaaagagaa      660
agagacagag acaggagacg cgacagtcac agacacaggg atcgtgatta tgacagagac      720
tatgatatgg atcgagatca tgacagagac tatgaaagag aacgtgggca tggtcgagac      780
cgggataggg agagagacag ggatcactat agagagcgag atagggacag ggaaagaggg      840
agagatagag aacgagacag aagagacagg gcaaggcgca gaagtagaag caggagtagg      900
gatcgtgaaga gacatgaaac tgatgatgtg cgggatcggg aagaacctaa gaaaaagaaa      960
gaaaagaagg agaagatgaa ggaagatgga accgatcatc caaatcctga aattgcagag     1020
atgaatagac tgagagcatc actgggaatg aaaccctca gggactga                       1068

```

<210> 85

<211> 355

<212> PRT

<213> Arabidopsis thaliana

<400> 85

```

Met Ala Asn Arg Thr Asp Pro Leu Ala Lys Asn Ile Arg Gly Thr Asn
1           5           10           15

Pro Gln Asn Leu Val Glu Lys Ile Val Arg Thr Lys Ile Tyr Gln His
          20           25           30

Thr Phe Trp Lys Glu Gln Cys Phe Gly Leu Thr Ala Glu Thr Leu Val
          35           40           45

Asp Lys Ala Met Glu Leu Asp His Leu Gly Gly Thr Phe Gly Gly Ser
          50           55           60

Arg Lys Pro Thr Pro Phe Leu Cys Leu Ile Leu Lys Met Leu Gln Ile
65           70           75           80

```

Gln Pro Glu Lys Glu Ile Val Val Glu Phe Ile Lys Asn Asp Asp Tyr
85 90 95

Lys Tyr Val Arg Ile Leu Gly Ala Phe Tyr Leu Arg Leu Thr Gly Thr
100 105 110

Asp Val Asp Val Tyr Arg Tyr Leu Glu Pro Leu Tyr Asn Asp Tyr Arg
115 120 125

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

Asp Glu Val Ile Glu Glu Leu Leu Thr Lys Asp Tyr Ser Cys Asp Ile
145 150 155 160

Ala Met Pro Arg Leu Lys Lys Arg Trp Thr Leu Glu Gln Asn Gly Leu
165 170 175

Leu Glu Pro Arg Lys Ser Val Leu Glu Asp Asp Phe Glu Glu Glu Glu
180 185 190

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

Asp Gln Arg Arg Lys Ser Pro Glu Arg Glu Arg Glu Arg Asp Arg Asp
210 215 220

Arg Arg Arg Asp Ser His Arg His Arg Asp Arg Asp Tyr Asp Arg Asp
225 230 235 240

Tyr Asp Met Asp Arg Asp His Asp Arg Asp Tyr Glu Arg Glu Arg Gly
245 250 255

His Gly Arg Asp Arg Asp Arg Glu Arg Asp Arg Asp His Tyr Arg Glu
260 265 270

Arg Asp Arg Asp Arg Glu Arg Gly Arg Asp Arg Glu Arg Asp Arg Arg
275 280 285

Asp Arg Ala Arg Arg Arg Ser Arg Ser Arg Ser Arg Asp Arg Lys Arg
290 295 300

His Glu Thr Asp Asp Val Arg Asp Arg Glu Glu Pro Lys Lys Lys Lys
305 310 315 320

Glu Lys Lys Glu Lys Met Lys Glu Asp Gly Thr Asp His Pro Asn Pro
325 330 335

Glu Ile Ala Glu Met Asn Arg Leu Arg Ala Ser Leu Gly Met Lys Pro
340 345 350

Leu Arg Asp

355

<210> 86
 <211> 1185
 <212> DNA
 <213> *Brachypodium sylvaticum*

<400> 86
 atggagatac agtcgtccgg gaggcccatc gaggtgctca tggagaaggt gctgtccatg 60
 aacatcgtct cctcggacta cttcaaggag ctctacaaga tcaagacgta ccacgaggtc 120
 atcgacgaga tctacaacca ggtcgaccac gtcgagccgt ggatgaccgg caactgccgc 180
 ggcccatcca ccgccttctg cctcctctac aagctcttca ccatgaagct caccatgaac 240
 cagatgcacg gcctgtcaa gcaccctgat tccccttaca tcagagctat tggatttctc 300
 tacctacgat acgttgcgga accaaagacg ctatggactt ggtatgagcc ctacattaaa 360
 gatgatgagg agttttcccc tgggtcgaat ggtaaaatga caactatggg cgtttatgtg 420
 cgtgatgtcc tccttgcca gtactacttc gacagtcttc ttccgcgagt gcctctccta 480
 attttgcgac aggtcagtgc ccatcttgag aagatgaagc tccaacaaa gcagtcaggg 540
 atgactgggg attcaagtcg ccttggttca gatgatactg cccggcgtcc tccttcggtg 600
 aaggcctctt tgtctgtctc ttttggtcag cgtgcgccac accgtgcgtc cacaagggac 660
 tcgtctccag ttcgaaagac attgccttct atacgggaaa gggaaaggag tcatgacggt 720
 gatcgtgcaa aatctccacc caggaagcgc cgaagtgaat gtcgggagcg taatcgtgaa 780
 actgagaggg accgttcgga tcgtgatcgt ggtagatata acgatagaga acaaggtcgg 840
 caaagccgtg acagcagaga tcgtgattac catcgttcga gctatgcaga aagagatggt 900
 gaaagacgag gccatgaaag gagggacagg aactctgacg gaaatggacg ttcgagcgcc 960
 cacagaagca ggagtaggag caggagtcca agccgtggca gaaccaacgg ggaccaccgt 1020
 cgctctagcc catttggtaa agcaccggag tcatccaact tggctaagtt gaaggatctt 1080
 tacggcgatg cgtcaaatgc aaaggaagat gcaggcgatg gtagagctcg cagggattcc 1140
 ggagctgaag aggtaatcag attgggaggt gcaagggtgga ggtga 1185

<210> 87
 <211> 394
 <212> PRT
 <213> *Brachypodium sylvaticum*

<400> 87
 Met Glu Ile Gln Ser Ser Gly Arg Pro Ile Glu Val Leu Met Glu Lys
 1 5 10 15
 Val Leu Ser Met Asn Ile Val Ser Ser Asp Tyr Phe Lys Glu Leu Tyr
 20 25 30
 Lys Ile Lys Thr Tyr His Glu Val Ile Asp Glu Ile Tyr Asn Gln Val
 35 40 45

Asp His Val Glu Pro Trp Met Thr Gly Asn Cys Arg Gly Pro Ser Thr
50 55 60

Ala Phe Cys Leu Leu Tyr Lys Leu Phe Thr Met Lys Leu Thr Met Asn
65 70 75 80

Gln Met His Gly Leu Leu Lys His Pro Asp Ser Pro Tyr Ile Arg Ala
85 90 95

Ile Gly Phe Leu Tyr Leu Arg Tyr Val Ala Glu Pro Lys Thr Leu Trp
100 105 110

Thr Trp Tyr Glu Pro Tyr Ile Lys Asp Asp Glu Glu Phe Ser Pro Gly
115 120 125

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

Leu Gly Gln Tyr Tyr Phe Asp Ser Leu Leu Pro Arg Val Pro Leu Leu
145 150 155 160

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

Lys Gln Ser Gly Met Thr Gly Asp Ser Ser Arg Leu Gly Ser Asp Asp
180 185 190

Thr Ala Arg Arg Pro Pro Ser Val Lys Ala Ser Leu Ser Val Ser Phe
195 200 205

Gly Gln Arg Ala Pro His Arg Ala Ser Thr Arg Asp Ser Ser Pro Val
210 215 220

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

Asp Arg Ala Lys Ser Pro Pro Arg Lys Arg Arg Ser Glu Ser Arg Glu
245 250 255

Arg Asn Arg Glu Thr Glu Arg Asp Arg Ser Asp Arg Asp Arg Gly Arg
260 265 270

Tyr Asn Asp Arg Glu Gln Gly Arg Gln Ser Arg Asp Ser Arg Asp Arg
275 280 285

Asp Tyr His Arg Ser Ser Tyr Ala Glu Arg Asp Val Glu Arg Arg Gly
290 295 300

His Glu Arg Arg Asp Arg Asn Ser Asp Arg Asn Gly Arg Ser Ser Ala
305 310 315 320

His Arg Ser Arg Ser Arg Ser Arg Ser Pro Ser Arg Gly Arg Thr Asn
Seite 102

Gly Asp His Arg Arg Ser Ser Pro Phe Gly Lys Ala Pro Glu Ser Ser
 340 345 350

Asn Leu Ala Lys Leu Lys Asp Leu Tyr Gly Asp Ala Ser Asn Ala Lys
 355 360 365

Glu Asp Ala Gly Asp Gly Arg Ala Arg Arg Asp Ser Gly Ala Glu Glu
 370 375 380

Val Ile Arg Leu Gly Gly Ala Arg Trp Arg
 385 390

<210> 88
 <211> 489
 <212> DNA
 <213> Brachypodium sylvaticum

<400> 88
 atggagatac agtcgtccgg gaggcccatc gaggtgctca tggagaaggt gctgtccatg 60
 aacatcgtct cctcggacta cttcaaggag ctctacaaga tcaagacgta ccacgaggtc 120
 atcgacgaga tctacaacca ggtcgaccac gtcgagccgt ggatgaccgg caactgccgc 180
 ggcccatcca ccgccttctg cctcctctac aagctcttca ccatgaagct caccatgaac 240
 cagatgcacg gcctgctcaa gcaccctgat tccccttaca tcagagctat tggatttctc 300
 tacctacgat acgttgcgga accaaagacg ctatggactt ggtatgagcc ctacattaaa 360
 gatgatgagg agttttcccc tgggtcgaat ggtaaaatga caactatggg cgtttatgtg 420
 cgtgatgtcc tccttgcca ggtatatctc ttaaagtatg ctcccacttc ttccattaaa 480
 catatttga 489

<210> 89
 <211> 162
 <212> PRT
 <213> Brachypodium sylvaticum

<400> 89
 Met Glu Ile Gln Ser Ser Gly Arg Pro Ile Glu Val Leu Met Glu Lys
 1 5 10 15

Val Leu Ser Met Asn Ile Val Ser Ser Asp Tyr Phe Lys Glu Leu Tyr
 20 25 30

Lys Ile Lys Thr Tyr His Glu Val Ile Asp Glu Ile Tyr Asn Gln Val
 35 40 45

Asp His Val Glu Pro Trp Met Thr Gly Asn Cys Arg Gly Pro Ser Thr
 50 55 60

Ala Phe Cys Leu Leu Tyr Lys Leu Phe Thr Met Lys Leu Thr Met Asn
 65 70 75 80

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Gln Met His Gly Leu Leu Lys His Pro Asp Ser Pro Tyr Ile Arg Ala
85 90 95

Ile Gly Phe Leu Tyr Leu Arg Tyr Val Ala Glu Pro Lys Thr Leu Trp
100 105 110

Thr Trp Tyr Glu Pro Tyr Ile Lys Asp Asp Glu Glu Phe Ser Pro Gly
115 120 125

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

Leu Gly Gln Val Tyr Leu Leu Lys Tyr Ala Pro Thr Ser Ser Ile Lys
145 150 155 160

His Ile

<210> 90
<211> 1116
<212> DNA
<213> Chlamydomonas reinhardtii

<400> 90
atggaaatcc atggctccaa caccaccttc aacctcgaga acgtgctgcg tcaaaacatc 60
ctgagctcgg actactacaa ggggacctgc tcggaactga gcaactgttc agacattgtg 120
gacgaaatct acgagtctgt cgatcatgtg gaaccttgga tgagcggcaa cgcgcgcggg 180
ccttccacgg ctttctgcct tctgcaccgc ctcttcacgc tcaagctctc agcaaaggag 240
gtgaaaggca tgctggacca caaggactct ccctacatcc gcgcagtggg cttcctgtac 300
ctgcgctacg tgggggaccc gaagacgctg tggagctggg tggcgccgta cgtgaaggat 360
caggagaaat tttcgccgag cgggcccgaac gagaaggagg tggccatggg cgactacgta 420
cgtgacctgc tgctctccca gtactacttc gagaccatct tcccgcgcat cccgaagccc 480
gtgcaagacc aaatcaacga cgagctgacg aagcgcagcc tggccacgac ggccaagggc 540
aatggcggcg ccggcggcg tgaccgccgc ggcatggacg actccggcaa ccgtcgaccc 600
gcctcgggtga aggcgtcgct gtcggtcgcg ttcggccagc gcgcgcccga ccgctccggt 660
gctcgcgagg agggtcgcg ccgggaccca tcgcttgcg agcgcgacgg cactgcagcg 720
gctcgcggcg gccgcggctc cgcctcgccg gagccgccac gcgaccggcg ggaggcgccg 780
gcaccgcggc gggatttcga ccgggagcgg gacgtgcgcg gaggcggtgg tggcggcgct 840
gaccgccgtg acaaccggga ctacggccgc gaccgggacc gtggtcgcga ctacgacaag 900
agccgggatt atgacaagag ccgggattac gccaaaggca gggactatga ccgggggcg 960
gactacgggc gcggcggtgg cgctggtggt ggcgggccgc gctacgatga ccgccgggac 1020
gaacggcggc gcagccggag ccggagccgc agccgggacc gcaacggcgg cggtgctcgg 1080
gacgcgcgcg atgtattcaa ggacgcccgg cggtag 1116

<210> 91
 <211> 371
 <212> PRT
 <213> Chlamydomonas reinhardtii

<400> 91

Met Glu Ile His Gly Ser Asn Thr Thr Phe Asn Leu Glu Asn Val Leu
 1 5 10 15

Arg Gln Asn Ile Leu Ser Ser Asp Tyr Tyr Lys Gly Thr Cys Ser Glu
 20 25 30

Leu Ser Asn Cys Ser Asp Ile Val Asp Glu Ile Tyr Glu Ser Val Asp
 35 40 45

His Val Glu Pro Trp Met Ser Gly Asn Ala Arg Gly Pro Ser Thr Ala
 50 55 60

Phe Cys Leu Leu His Arg Leu Phe Thr Leu Lys Leu Ser Ala Lys Glu
 65 70 75 80

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

Gly Phe Leu Tyr Leu Arg Tyr Val Gly Asp Pro Lys Thr Leu Trp Ser
 100 105 110

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

Pro Asn Glu Lys Glu Val Ala Met Gly Asp Tyr Val Arg Asp Leu Leu
 130 135 140

Leu Ser Gln Tyr Tyr Phe Glu Thr Ile Phe Pro Arg Ile Pro Lys Pro
 145 150 155 160

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

Thr Ala Lys Gly Asn Gly Gly Ala Gly Gly Ala Asp Arg Arg Gly Met
 180 185 190

Asp Asp Ser Gly Asn Arg Arg Pro Ala Ser Val Lys Ala Ser Leu Ser
 195 200 205

Val Ala Phe Gly Gln Arg Ala Pro Asn Arg Ser Gly Ala Arg Glu Glu
 210 215 220

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

Ala Arg Gly Gly Arg Gly Ser Ala Ser Pro Glu Pro Pro Arg Asp Arg
245 250 255

Arg Glu Ala Pro Ala Pro Arg Arg Asp Phe Asp Arg Glu Arg Asp Val
260 265 270

Arg Gly Gly Gly Gly Gly Gly Ala Asp Arg Arg Asp Asn Arg Asp Tyr
275 280 285

Gly Arg Asp Arg Asp Arg Gly Arg Asp Tyr Asp Lys Ser Arg Asp Tyr
290 295 300

Asp Lys Ser Arg Asp Tyr Ala Lys Gly Arg Asp Tyr Asp Arg Gly Arg
305 310 315 320

Asp Tyr Gly Arg Gly Gly Gly Ala Gly Gly Gly Gly Arg Gly Tyr Asp
325 330 335

Asp Arg Arg Asp Glu Arg Arg Arg Ser Arg Ser Arg Ser Arg Ser Arg
340 345 350

Asp Arg Asn Gly Gly Gly Ala Arg Asp Ala Arg Asp Val Phe Lys Asp
355 360 365

Ala Arg Arg
370

<210> 92
<211> 1676
<212> DNA
<213> Hordeum vulgare

<400> 92
attcggcacg aggcctcccc tttcctcgcc tccttcatcc atactccggc gatctcccag 60
ctaccgtcga atcccaaaca tcacaccctc cgccgtcgcc gaagccgata cgagttcatc 120
ctctacagag agtcgtcatc ccctctggtt tgggggtctc cgcaagccgc cctcgctctc 180
ggaagccaag gaggtcgtag ggtttgcgcg catcctccgt gtttgtgttc gctgaaatat 240
ggagatacag acttcaggaa agcccatcga tatgttgatg gagaagggtc tttgtatgaa 300
tattctttct tctgattact tcaaggagct ctacaggatg aagacctatc atgagggtcat 360
tgacgagatc tataaccaag ttgatcatgt ggagccttgg atgactggca attgcagggg 420
tccttcact gcattttgtc tcctgtacaa gttcttcaca atgaagctta ctgtgaaaca 480
gatgcatggg ttgttgaaagc atcctgactc cccgtacatt agagctatag gatttttgta 540
tcttcgatat gttgcagatc caaagatcct atggacatgg tatgagccct acttgaagga 600
tgatgaggaa ttctcccctg gatctaattg tcgcatgaca accatgggtg tatttgtgcg 660
tgatcttata cttggacagt actactttga tagtatcctt ccaagagttc ctgttccagt 720
agttcgtcaa gtaacagcca atcttgagaa gatgaagctg cctaccaagc tttctggggg 780
gactggagac agtcgccacg gatcagagga tactgcccgt cgccccctt ctgttaaagc 840

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

ttctttgtca gtttcttttg gacagcgtgc gccacaccgt gcttccacac gggattcttc      900
cccagtgcga cgaacagtca cccaagatga tcaacggaga tcattcttccc catttcgtcg      960
tagtgcaagt cgggagggggc cttacagtga ccgttcaatt cacgaccgag aaggttaaccg    1020
ttcaagccgt gaccgagata ctgaccattc aagccgtgac cgagatactg tccgttcaag    1080
ccgtgaccga gatactggcc gttcaagccg tgaccgagat actggccttt caagccgtga    1140
cagagagcgt gattatgacc gtgacagcag ggattgtgac tattacaggt tcaggcattc    1200
agaagaaaaa aggaattacc gaagcgaaca tgacaatagt agacacagac gctccagctc    1260
atgtcatagg agcagaagcc ggagtcggag caggagcagg agcaggaatg agcatcgttc    1320
cagtccattt ggggatacaa gcaaagagaa ggctgctgct gcctcgagca acctagctaa    1380
gctgaaagac ctgtacggcg acgtagctga gaagaaggat gatgggtgatg ccaggcggct    1440
tcacatgat  tcatgtgccg aagaggttat taggttggga ggccctaggt ggagataaat    1500
atgaaccgcc gactctgtca tccaggtcat gctgttactg caccgttcga tttacctgct    1560
tttgattga  cattagtga atcactcttt gtaaactctc ggtactttat gtggttcatt    1620
aatccatata ttttggacgt gcagtcaatc tatcaaattc atcaacgtaa aaaaag      1676

```

<210> 93
 <211> 365
 <212> PRT
 <213> Hordeum vulgare

<400> 93

Met Glu Ile Gln Thr Ser Gly Lys Pro Ile Asp Met Leu Met Glu Lys
 1 5 10 15

Val Leu Cys Met Asn Ile Leu Ser Ser Asp Tyr Phe Lys Glu Leu Tyr
 20 25 30

Arg Met Lys Thr Tyr His Glu Val Ile Asp Glu Ile Tyr Asn Gln Val
 35 40 45

Asp His Val Glu Pro Trp Met Thr Gly Asn Cys Arg Gly Pro Ser Thr
 50 55 60

Ala Phe Cys Leu Leu Tyr Lys Phe Phe Thr Met Lys Leu Thr Val Lys
 65 70 75 80

Gln Met His Gly Leu Leu Lys His Pro Asp Ser Pro Tyr Ile Arg Ala
 85 90 95

Ile Gly Phe Leu Tyr Leu Arg Tyr Val Ala Asp Pro Lys Ile Leu Trp
 100 105 110

Thr Trp Tyr Glu Pro Tyr Leu Lys Asp Asp Glu Glu Phe Ser Pro Gly
 115 120 125

Ser Asn Gly Arg Met Thr Thr Met Gly Val Phe Val Arg Asp Leu Ile
130 135 140

Leu Gly Gln Tyr Tyr Phe Asp Ser Ile Leu Pro Arg Val Pro Val Pro
145 150 155 160

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

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

Ala Arg Arg Pro Pro Ser Val Lys Ala Ser Leu Ser Val Ser Phe Gly
195 200 205

Gln Arg Ala Pro His Arg Ala Ser Thr Arg Asp Ser Ser Pro Val Arg
210 215 220

Arg Thr Val Thr Gln Asp Asp Gln Arg Arg Ser Ser Ser Pro Phe Arg
225 230 235 240

Arg Ser Ala Ser Arg Glu Gly Pro Tyr Ser Asp Arg Ser Ile His Asp
245 250 255

Arg Glu Gly Asn Arg Ser Ser Arg Asp Arg Asp Thr Asp His Ser Ser
260 265 270

Arg Asp Arg Asp Thr Val Arg Ser Ser Arg Asp Arg Asp Thr Gly Arg
275 280 285

Ser Ser Arg Asp Arg Asp Thr Gly Leu Ser Ser Arg Asp Arg Glu Arg
290 295 300

Asp Tyr Asp Arg Asp Ser Arg Asp Cys Asp Tyr Tyr Arg Phe Arg His
305 310 315 320

Ser Glu Glu Lys Arg Asn Tyr Arg Ser Glu His Asp Asn Ser Arg His
325 330 335

Arg Arg Ser Ser Ser Cys His Arg Ser Arg Ser Arg Ser Arg Ser Arg
340 345 350

Ser Arg Ser Arg Asn Glu His Arg Ser Ser Pro Phe Gly
355 360 365

<210> 94

<211> 1824

<212> DNA

<213> Lycopersicum esculentum

<400> 94

gagcttttgt atcccctcga tctccggttc ctctctcctt cttcttctct tcgtcgtcaa 60

ttttccattt tccctcatcg attctccggc ggaaaaccga aaaaaggtaa ttcataatct 120

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

gaacctaaac cttttccgat atcatttttta ttgttggcca cagaaggtag gaaaagataa      180
cactctgggtg tccaagtcac taagggcatg gctgagctta agacttcttg gagacctata      240
gaccagtgtgt tggagaagggt tctctgcatg aacattctat cttctgatta cttcagagac      300
cttttgcgcc tgaaaactta tcatgaagtgt attgatgaaa tctataatca agttgaccat      360
gtggaaccat ggatgactgg caactgtcgt ggtccttcaa cagccttctg ctttctctac      420
aagttcttca caatgaaact tactgtcaag caaatgcatg gcctgttaaa gcatccagat      480
tctccttaca ttagagctat tgggttcctt tatctgagat atcttggtga ttttaagaca      540
ttatgggggtt ggtatgagcc ttacctcaaa gatgatgagg aattctctcc tggatccagt      600
gggcaaatga ccacaatggg tgtatatgtg cgtgacttat ttctcgggca gtattatatt      660
gacacactac taccgccgat tcctgttcct gtcgtgcgga cagcagttgc cagtctcgaa      720
aaaatgaatc tgccgaccaa actttctggg tcgattgggg attctagtcg tggatctgag      780
gaaacttctc gccggccacc ttctgtcaaa gcttcccttt cagtgtcctt tggtcagcgg      840
gcacctcatc gtgcatcaac tagagattca tctcccatcc gaagaacaat tgcaccacca      900
tcctatgata aggatggtgc aaatggttca agacgttccc ccagcatgcg ccggagtcaa      960
agccgtgatt tatctgaccg ggaaaattct gaaagggaca ggggccggga ccgggacagg     1020
gacaggggaca gggacaggga cagggacagg gaaagaacta gggacagaga acgtgatagg     1080
gatagggata gggataggta tagggaccag gaaagagaaa gggatagggg cagggatcgg     1140
gatagagata gaaggtatga taacgaaaga gatcgtgaaa gggacagaga caggaggcat     1200
gattatgaca gagaccgggg aagggataga gacaggaggt atgactatga tcgaagggtca     1260
attgagagaa gcagaagaga ctatgacagg agcaggagcc gtagtaggag tagaagccac     1320
agccgaagct tgcattgatc aggtacaagg cttgaccagc agcgaactcc acctagggat     1380
gagagcaagg agaagaaggc tgcatttagc aatctggcca agcttaaaga tctatatggc     1440
gacttcggca ataaaaagga gaacataggt gatgacaggg ctccaaatag ggatactagt     1500
actgaggagg ttatcagact tgggtggttct acatggaggt agttgggttac atttacgttt     1560
tgtaagagtt tggatactct cactgtctca ctttctcaga agagcacatt gacagctagc     1620
cttttgttga aagggaatat gcaaactgat agctgcagag aggagatgct gtttcatgtt     1680
ttctgcagtc ggcagagctg cttgtaaact ggatttcctt tactattatt ttagacttgt     1740
gttacaatat tggatggatt tcaattgtcc ctttgtttgt taaaacatta ttactactta     1800
aagcaattga caaacttata agcc                                           1824

```

<210> 95

<211> 444

<212> PRT

<213> Lycopersicum esculentum

<400> 95

Met Ala Glu Leu Lys Thr Ser Gly Arg Pro Ile Asp Gln Leu Leu Glu
1 5 10 15

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Lys Val Leu Cys₂₀ Met Asn Ile Leu Ser₂₅ Ser Asp Tyr Phe Arg₃₀ Asp Leu
 Leu Arg Leu₃₅ Lys Thr Tyr His Glu₄₀ Val Ile Asp Glu₄₅ Ile Tyr Asn Gln
 Val Asp₅₀ His Val Glu Pro Trp₅₅ Met Thr Gly Asn Cys₆₀ Arg Gly Pro Ser
 Thr Ala Phe Cys Leu₇₀ Leu Tyr Lys Phe Phe Thr₇₅ Met Lys Leu Thr Val₈₀
 Lys Gln Met His Gly₈₅ Leu Leu Lys His Pro₉₀ Asp Ser Pro Tyr Ile₉₅ Arg
 Ala Ile Gly Phe₁₀₀ Leu Tyr Leu Arg Tyr₁₀₅ Leu Gly Asp Phe Lys₁₁₀ Thr Leu
 Trp Gly Trp₁₁₅ Tyr Glu Pro Tyr Leu₁₂₀ Lys Asp Asp Glu Glu₁₂₅ Phe Ser Pro
 Gly Ser₁₃₀ Ser Gly Gln Met Thr₁₃₅ Thr Met Gly Val Tyr₁₄₀ Val Arg Asp Leu
 Phe Leu Gly Gln Tyr Tyr₁₅₀ Phe Asp Thr Leu Leu₁₅₅ Pro Arg Ile Pro Val₁₆₀
 Pro Val Val Arg Thr₁₆₅ Ala Val Ala Ser Leu₁₇₀ Glu Lys Met Asn Leu₁₇₅ Pro
 Thr Lys Leu Ser₁₈₀ Gly Ser Ile Gly Asp₁₈₅ Ser Ser Arg Gly Ser₁₉₀ Glu Glu
 Thr Ser Arg₁₉₅ Arg Pro Pro Ser Val₂₀₀ Lys Ala Ser Leu Ser₂₀₅ Val Ser Phe
 Gly Gln Arg Ala Pro His Arg₂₁₅ Ala Ser Thr Arg Asp₂₂₀ Ser Ser Pro Ile
 Arg Arg Thr Ile Ala Pro₂₃₀ Pro Ser Tyr Asp Lys₂₃₅ Asp Gly Ala Asn Gly₂₄₀
 Ser Arg Arg Ser Pro₂₄₅ Ser Met Arg Arg Ser₂₅₀ Gln Ser Arg Asp Leu Ser₂₅₅
 Asp Arg Glu Asn₂₆₀ Ser Glu Arg Asp Arg₂₆₅ Gly Arg Asp Arg Asp₂₇₀ Arg Asp
 Arg Asp Arg₂₇₅ Asp Arg Asp Arg Asp₂₈₀ Arg Glu Arg Thr Arg₂₈₅ Asp Arg Glu

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Arg Asp Arg Asp Arg Asp Arg Asp Arg Tyr Arg Asp Gln Glu Arg Glu
290 295 300

Arg Asp Arg Gly Arg Asp Arg Asp Arg Asp Arg Tyr Asp Asn Glu
305 310 315 320

Arg Asp Arg Glu Arg Asp Arg Asp Arg Arg His Asp Tyr Asp Arg Asp
325 330 335

Arg Gly Arg Asp Arg Asp Arg Arg Tyr Asp Tyr Asp Arg Arg Ser Ile
340 345 350

Glu Arg Ser Arg Arg Asp Tyr Asp Arg Ser Arg Ser Arg Ser Arg Ser
355 360 365

Arg Ser His Ser Arg Ser Leu His Asp Gln Gly Thr Arg Leu Asp Gln
370 375 380

Gln Arg Thr Pro Pro Arg Asp Glu Ser Lys Glu Lys Lys Ala Ala Ser
385 390 395 400

Ser Asn Leu Ala Lys Leu Lys Asp Leu Tyr Gly Asp Phe Gly Asn Lys
405 410 415

Lys Glu Asn Ile Gly Asp Asp Arg Ala Pro Asn Arg Asp Thr Ser Thr
420 425 430

Glu Glu Val Ile Arg Leu Gly Gly Ser Thr Trp Arg
435 440

<210> 96
<211> 1157
<212> DNA
<213> Medicago truncatula

<400> 96
atggcaaadc gcactgatcc agcagcgaag agtattcgag gcacaaaccc tcaaaacctt 60
gttgaaaaaa ttctccgctc aaagatctat cagcacactt attggaaaga acaatgcttc 120
ggcttaacag cagaaaccct agtcgacaaa gccatggagc tcgaccacct cggcggaact 180
tacggtggca accgcaaacc cactcccttc atgtgcctcg tcatgaaaat gcttcagatt 240
caacccgaga aagaaatcgt catcgaattc atcaaaaacg atgattacaa gtatgtgagg 300
atactgggtg cattttatct gcgtcttact ggatctgata cggatgtgta ccattatctg 360
gagccgttgt ataatgatta taggaaactg cggcggaat taccggatgg acagtttgct 420
ttgacacatg ttgatgaggt tattgatgaa cttcttataa ctgattattc ctgtgatatt 480
gctatgcccc gtattaagaa aaggtggact cttgaatctc ttggtgcctt agaacctaga 540
caaagtgcac ttgaagagga ttttgaggag gaagaggaaa atgaggataa tgaacagcct 600
gctgaggagc ctgagaagga ttataatcgt gggcgaagcc ctgcaaggga aagagatagg 660

gatagaagac gtgatagtca tagacacagg gatcgtgact atgacagaga atatgataga	720
gattatgaca gagagcgagg acgtggccga gatagagatc gggacagaga tagggaaaag	780
gaaagggaca gagatagga gagggacaga gaccgatatc gtctgaggga agaaaaggat	840
tatggtcgtg agagagaagg tagggagcgc gagaggagag acagagatcg tgaccgtggt	900
aggaggagga gctactcaag gagtcgaagt agaagcaggg atcgcaagga tcatgatggt	960
ggggactaca gaaagagaca tgctcgaagt agcgtaagtc caagaagaga tggagctgag	1020
gatggtgagc caaagaagaa gaaggaaaag aaagaaaaga aggaaaagaa ggatgacggg	1080
accgaccatc cagatccaga gattgcagaa gcaaacagga tacgagcatc actggggttg	1140
aaaccactta agatgtg	1157

<210> 97
 <211> 385
 <212> PRT
 <213> Medicago truncatula

<400> 97

Met Ala Asn Arg Thr Asp Pro Ala Ala Lys Ser Ile Arg Gly Thr Asn
 1 5 10 15

Pro Gln Asn Leu Val Glu Lys Ile Leu Arg Ser Lys Ile Tyr Gln His
 20 25 30

Thr Tyr Trp Lys Glu Gln Cys Phe Gly Leu Thr Ala Glu Thr Leu Val
 35 40 45

Asp Lys Ala Met Glu Leu Asp His Leu Gly Gly Thr Tyr Gly Gly Asn
 50 55 60

Arg Lys Pro Thr Pro Phe Met Cys Leu Val Met Lys Met Leu Gln Ile
 65 70 75 80

Gln Pro Glu Lys Glu Ile Val Ile Glu Phe Ile Lys Asn Asp Asp Tyr
 85 90 95

Lys Tyr Val Arg Ile Leu Gly Ala Phe Tyr Leu Arg Leu Thr Gly Ser
 100 105 110

Asp Thr Asp Val Tyr His Tyr Leu Glu Pro Leu Tyr Asn Asp Tyr Arg
 115 120 125

Lys Leu Arg Arg Lys Leu Pro Asp Gly Gln Phe Ala Leu Thr His Val
 130 135 140

Asp Glu Val Ile Asp Glu Leu Leu Thr Thr Asp Tyr Ser Cys Asp Ile
 145 150 155 160

Ala Met Pro Arg Ile Lys Lys Arg Trp Thr Leu Glu Ser Leu Gly Ala
 165 170 175

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Leu Glu Pro Arg Gln Ser Ala Leu Glu Glu Asp Phe Glu Glu Glu Glu
180 185 190

Glu Asn Glu Asp Asn Glu Gln Pro Ala Glu Glu Pro Glu Lys Asp Tyr
195 200 205

Asn Arg Gly Arg Ser Pro Ala Arg Glu Arg Asp Arg Asp Arg Arg Arg
210 215 220

Asp Ser His Arg His Arg Asp Arg Asp Tyr Asp Arg Glu Tyr Asp Arg
225 230 235 240

Asp Tyr Asp Arg Glu Arg Gly Arg Gly Arg Asp Arg Asp Arg Asp Arg
245 250 255

Asp Arg Glu Lys Glu Arg Asp Arg Asp Arg Glu Arg Asp Arg Asp Arg
260 265 270

Tyr Arg Leu Arg Glu Glu Lys Asp Tyr Gly Arg Glu Arg Glu Gly Arg
275 280 285

Glu Arg Glu Arg Arg Asp Arg Asp Arg Asp Arg Gly Arg Arg Arg Ser
290 295 300

Tyr Ser Arg Ser Arg Ser Arg Ser Arg Asp Arg Lys Asp His Asp Gly
305 310 315 320

Gly Asp Tyr Arg Lys Arg His Ala Arg Ser Ser Val Ser Pro Arg Arg
325 330 335

Asp Gly Ala Glu Asp Gly Glu Pro Lys Lys Lys Lys Glu Lys Lys Glu
340 345 350

Lys Lys Glu Lys Lys Asp Asp Gly Thr Asp His Pro Asp Pro Glu Ile
355 360 365

Ala Glu Ala Asn Arg Ile Arg Ala Ser Leu Gly Leu Lys Pro Leu Lys
370 375 380

Met
385

<210> 98
<211> 1305
<212> DNA
<213> Oryza sativa

<400> 98
atggagatac aaacttcagg gaagccatt gatctgctga tggagaaggt tctttgtatg 60
aacattatgt cttctgatta cttcaaggag ctctacaggc tgaagaccta tcatgaggtc 120
attgatgaaa tatacaatca agttgatcat gtggagcctt ggatgactgg caattgcagg 180

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

ggccccctcca ctgcattctg tctcctctac aagttcttca ccatgaagct tactgtcaaa 240
cagatgcatg gtttgttgaa gcatcctgat tccccatata ttagagctat agggttcttg 300
tatcttcgat atgttgacaga tccgaagatc ttgtggacgt ggtatgagcc ctacttgaag 360
gatgatgagg aattctcccc tggatctaata ggtcgcata gaacatggg tgtttatgtg 420
cgtgatctta tacttggaca gtactacttc gatagtcttc ttccaagagt tcctcttcca 480
gtaattcgtc aagtgcacac caatcttgag aagatgaagt tgcccactaa gctttctggg 540
attactggag agtctaatac tcatggatca gaagatactg cccgccggcc tccttccgtg 600
aaggcttctc tgtcagtttc ctttggacag cgtgctccgc atcgtgcac cacacgggag 660
tcactctccag ttcggaggac agtcacccat gatggccatc gtaaactctc ctcacatct 720
cgccgtagcg gaagccgca ggttcctgat cgtgatcgat caagccgtga ccgttctagt 780
cgtgactatg accgttcaag ccatgaccgt gatcgtgacc attccagtcg tgactatgac 840
cgtccaagcc atgaccgtga ccgtgatcgt gaccgttcca gtcgtgacta tgaccgttca 900
agtcgtgacc gggatcatga tagagacatc agagactatc atcggcgtga tcgtgacagc 960
agggaccgtg actataggtc taggcattca tccgaaagac aagatgaccg aagggaccgt 1020
gaccgtgagg gtagcaggca cagacggtcc agctctcggc acagaagcag aagccgcagc 1080
cgagccgca gccgcagcag aagcaggagc cgcagcagaa atgaggagag atccagtcct 1140
tttggaatg caggcaaaga aaagactgct gccatctcga gcaacctagc aaagctcaag 1200
gacttgtatg gtgatgtaac tgagaagaag gacgacggtg aagcccctcg ccgtgattcg 1260
tgcgcgagg aggttatcag gttgggtggc ccgagatgga gatag 1305

```

<210> 99
 <211> 434
 <212> PRT
 <213> Oryza sativa

<400> 99

Met Glu Ile Gln Thr Ser Gly Lys Pro Ile Asp Leu Leu Met Glu Lys
 1 5 10 15

Val Leu Cys Met Asn Ile Met Ser Ser Asp Tyr Phe Lys Glu Leu Tyr
 20 25 30

Arg Leu Lys Thr Tyr His Glu Val Ile Asp Glu Ile Tyr Asn Gln Val
 35 40 45

Asp His Val Glu Pro Trp Met Thr Gly Asn Cys Arg Gly Pro Ser Thr
 50 55 60

Ala Phe Cys Leu Leu Tyr Lys Phe Phe Thr Met Lys Leu Thr Val Lys
 65 70 75 80

Gln Met His Gly Leu Leu Lys His Pro Asp Ser Pro Tyr Ile Arg Ala
 85 90 95

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Ile Gly Phe Leu Tyr Leu Arg Tyr Val Ala Asp Pro Lys Ile Leu Trp
100 105 110

Thr Trp Tyr Glu Pro Tyr Leu Lys Asp Asp Glu Glu Phe Ser Pro Gly
115 120 125

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

Leu Gly Gln Tyr Tyr Phe Asp Ser Leu Leu Pro Arg Val Pro Leu Pro
145 150 155 160

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

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

Thr Ala Arg Arg Pro Pro Ser Val Lys Ala Ser Leu Ser Val Ser Phe
195 200 205

Gly Gln Arg Ala Pro His Arg Ala Ser Thr Arg Glu Ser Ser Pro Val
210 215 220

Arg Arg Thr Val Thr His Asp Gly His Arg Lys Ser Ser Ser Pro Ser
225 230 235 240

Arg Arg Ser Gly Ser Arg Glu Val Pro Asp Arg Asp Arg Ser Ser Arg
245 250 255

Asp Arg Ser Ser Arg Asp Tyr Asp Arg Ser Ser His Asp Arg Asp Arg
260 265 270

Asp His Ser Ser Arg Asp Tyr Asp Arg Pro Ser His Asp Arg Asp Arg
275 280 285

Asp Arg Asp Arg Ser Ser Arg Asp Tyr Asp Arg Ser Ser Arg Asp Arg
290 295 300

Asp His Asp Arg Asp Ile Arg Asp Tyr His Arg Arg Asp Arg Asp Ser
305 310 315 320

Arg Asp Arg Asp Tyr Arg Ser Arg His Ser Ser Glu Arg Gln Asp Asp
325 330 335

Arg Arg Asp Arg Asp Arg Glu Gly Ser Arg His Arg Arg Ser Ser Ser
340 345 350

Arg His Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser
355 360 365

Arg Ser Arg Ser Arg Asn Glu Glu Arg Ser Ser Pro Phe Gly Asn Ala
370 375 380

Gly Lys Glu Lys Thr Ala Ala Ile Ser Ser Asn Leu Ala Lys Leu Lys
385 390 395 400

Asp Leu Tyr Gly Asp Val Thr Glu Lys Lys Asp Asp Gly Glu Ala Pro
405 410 415

Arg Arg Asp Ser Cys Ala Glu Glu Val Ile Arg Leu Gly Gly Pro Arg
420 425 430

Trp Arg

<210> 100
<211> 1179
<212> DNA
<213> Oryza sativa

<400> 100
atggcgaacc gcacggaccc cctggcgaag agcatccacg ggacgaaccc tcagaacctg 60
gtggagaaga tcgtccggtc caagatctac cagagcacct actggaagga gcagtgtttt 120
ggcctcaccg ccgagaccct cgtcgacaag gccatggagc tcgaccacac cggcggcacc 180
tacggcggca accgcaagcc caccctctc ctctgcctcg ccctcaagat gctccagatc 240
cagcccgaca aggacatcgt cgtcgagttc atcaagaacg aggattacaa gtatgtccgt 300
gttcttgggtg ctttctacct tcgcctcact gccaccgtcg ccgacgtcta ccaatacctc 360
gagccgctct acaacgacta ccgcaagatc aggcacaagc tcagtgatgg aaagtttacc 420
ctgaccacag tcgacgagtt cattgacgac ctctcacca aggactactc ctgcgatacg 480
gccctcccc gcacccagaa aagatgggtt cttgaaactt ctggaactct agaaccaaga 540
agaagtgcac ttgaagatga ttttgaggaa gaggaggaag acaaggagga tgaacaacct 600
atggatatag atgagccaaa tggctcgtgaa aagcatgac attatcgtgg aaggagccct 660
actagagatc gagacagga gaggaacat gaaagacacc acagggaccg agattacgac 720
agagatcggg attatggtag gggacgggaa agagaccgag atagagaccg tgaaagagat 780
agagacaggg atagagatcg ggatcgggat cgggatcgag accgtcatcg catacgagat 840
gaggactaca gtcgagatag ggaccgagca agagataggg atggcaggga aagagaacgc 900
tgggacagag accgtgggag gcgcaggagc cgttcaagga gcaggagcag ggatcgacga 960
gaaagagacc gagaagatgg agagtaccgt aggaggcgtg atcggggtag tgccagtcct 1020
cgagggtcatg cggaggatgg tggctcaaga gatgagccga agaagagaaa ggaaaagaaa 1080
gagaagaagg gtgaaggaaa tgcaccagat ccaaatgacc cagagattat agaaatgaac 1140
aagctccgag cctctctagg gttgaaacca ctgaagtag 1179

<210> 101
<211> 392

<212> PRT

<213> Oryza sativa

<400> 101

Met Ala Asn Arg Thr Asp Pro Leu Ala Lys Ser Ile His Gly Thr Asn
 1 5 10 15

Pro Gln Asn Leu Val Glu Lys Ile Val Arg Ser Lys Ile Tyr Gln Ser
 20 25 30

Thr Tyr Trp Lys Glu Gln Cys Phe Gly Leu Thr Ala Glu Thr Leu Val
 35 40 45

Asp Lys Ala Met Glu Leu Asp His Thr Gly Gly Thr Tyr Gly Gly Asn
 50 55 60

Arg Lys Pro Thr Pro Phe Leu Cys Leu Ala Leu Lys Met Leu Gln Ile
 65 70 75 80

Gln Pro Asp Lys Asp Ile Val Val Glu Phe Ile Lys Asn Glu Asp Tyr
 85 90 95

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

Val Ala Asp Val Tyr Gln Tyr Leu Glu Pro Leu Tyr Asn Asp Tyr Arg
 115 120 125

Lys Ile Arg His Lys Leu Ser Asp Gly Lys Phe Thr Leu Thr His Val
 130 135 140

Asp Glu Phe Ile Asp Asp Leu Leu Thr Lys Asp Tyr Ser Cys Asp Thr
 145 150 155 160

Ala Leu Pro Arg Ile Gln Lys Arg Trp Val Leu Glu Thr Ser Gly Thr
 165 170 175

Leu Glu Pro Arg Arg Ser Ala Leu Glu Asp Asp Phe Glu Glu Glu Glu
 180 185 190

Glu Asp Lys Glu Asp Glu Gln Pro Met Asp Ile Asp Glu Pro Asn Gly
 195 200 205

Arg Glu Lys His Asp His Tyr Arg Gly Arg Ser Pro Thr Arg Asp Arg
 210 215 220

Asp Arg Glu Arg Lys His Glu Arg His His Arg Asp Arg Asp Tyr Asp
 225 230 235 240

Arg Asp Arg Asp Tyr Gly Arg Gly Arg Glu Arg Asp Arg Asp Arg Asp
 245 250 255

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Arg Glu Arg Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg Asp
260 265 270

Arg Asp Arg His Arg Ile Arg Asp Glu Asp Tyr Ser Arg Asp Arg Asp
275 280 285

Arg Ala Arg Asp Arg Asp Gly Arg Glu Arg Glu Arg Trp Asp Arg Asp
290 295 300

Arg Gly Arg Arg Arg Ser Arg Ser Arg Ser Arg Ser Arg Asp Arg Arg
305 310 315 320

Glu Arg Asp Arg Glu Asp Gly Glu Tyr Arg Arg Arg Arg Asp Arg Gly
325 330 335

Ser Ala Ser Pro Arg Gly His Ala Glu Asp Gly Gly Ser Arg Asp Glu
340 345 350

Pro Lys Lys Arg Lys Glu Lys Lys Glu Lys Lys Gly Glu Gly Asn Ala
355 360 365

Pro Asp Pro Asn Asp Pro Glu Ile Ile Glu Met Asn Lys Leu Arg Ala
370 375 380

Ser Leu Gly Leu Lys Pro Leu Lys
385 390

<210> 102
<211> 915
<212> DNA
<213> *Ostreococcus tauri*

<400> 102
atgacgtact ggaaggagaa gtgcttcggc gtgagcgccg aggcggttggc cgatctcgcg 60
gtcgacctca ggtcgggtggg tgggatttac ggcgggaaca acagagcgac ggagtttttg 120
tgcctcacgc tgaagctgtt gcagatacag cctgagaagg agatcgtgtt agagtttatt 180
aagaatgagg atcacaagta cgtcaggttg ctcggcgcggt tttacctacg gttggtgggg 240
aaaccgacgg acgtgtacag atacctcgag ccgctgttga acgactatag aaaggttcgg 300
tatcgcacgc gtgatgggaa gtacgcactg acgcatgttg atgagtttgt gaacaatttg 360
ttgacgaagg atatgttttg cgacgtgacg ctcccacgcg tgccgcatcg ccagggtgta 420
gaggccgcgg gagcgcttga gccacgcgta tctgcgcttg aggaggatat cgcagatttg 480
gaggaagagc tcgagagcgc ggtggaggag gcaataggtc aacggatgaa catggatgtc 540
gacgcaggcg aggccgctgc cgcggcgctc actcgaggtg cgcgcgagga cggcgagatc 600
gttgcgtcgg gatcgaagcg ttcgcgcgag cacgatggcg ttcggtatcg agaattgtgac 660
gatagcgacg gtgacagga cgtccgaagg cgcgagcggc cgagatctag gagtcgcgac 720
cgcgtgccgg caccgccgca cgacgctcgg cccggagttt tggctagtgg cgaagagatg 780
gatcacagag agaagaagga gaagaaagag aagaaggaaa aacgagagaa gaaggagaag 840

accgagatgg accccgaaat cgcagaggcg aatgcgatca gggccaagct cgggttgaag 900
ccgcttcgtg gatga 915

<210> 103
<211> 304
<212> PRT
<213> *Ostreococcus tauri*

<400> 103

Met Thr Tyr Trp Lys Glu Lys Cys Phe Gly Val Ser Ala Glu Ala Leu
1 5 10 15

Val Asp Leu Ala Val Asp Leu Arg Ser Val Gly Gly Ile Tyr Gly Gly
20 25 30

Asn Asn Arg Ala Thr Glu Phe Leu Cys Leu Thr Leu Lys Leu Leu Gln
35 40 45

Ile Gln Pro Glu Lys Glu Ile Val Leu Glu Phe Ile Lys Asn Glu Asp
50 55 60

His Lys Tyr Val Arg Leu Leu Gly Ala Phe Tyr Leu Arg Leu Val Gly
65 70 75 80

Lys Pro Thr Asp Val Tyr Arg Tyr Leu Glu Pro Leu Leu Asn Asp Tyr
85 90 95

Arg Lys Val Arg Tyr Arg Thr Arg Asp Gly Lys Tyr Ala Leu Thr His
100 105 110

Val Asp Glu Phe Val Asn Asn Leu Leu Thr Lys Asp Met Phe Cys Asp
115 120 125

Val Thr Leu Pro Arg Val Pro His Arg Gln Val Leu Glu Ala Ala Gly
130 135 140

Ala Leu Glu Pro Arg Val Ser Ala Leu Glu Glu Asp Ile Ala Asp Leu
145 150 155 160

Glu Glu Glu Leu Glu Ser Ala Val Glu Glu Ala Ile Gly Gln Arg Met
165 170 175

Asn Met Asp Val Asp Ala Gly Glu Ala Ala Ala Ala Ala Ser Thr Arg
180 185 190

Gly Ala Arg Glu Asp Gly Glu Ile Val Ala Ser Gly Ser Lys Arg Ser
195 200 205

Arg Glu His Asp Gly Val Arg Tyr Arg Glu Cys Asp Asp Ser Asp Gly
210 215 220

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Asp Arg Tyr Val Arg Arg Arg Glu Arg Ser Arg Ser Arg Ser Arg Asp
225 230 235 240

Arg Val Pro Ala Arg Arg Asp Asp Ala Arg Pro Gly Val Leu Ala Ser
245 250 255

Gly Glu Glu Met Asp His Arg Glu Lys Lys Glu Lys Lys Glu Lys Lys
260 265 270

Glu Lys Arg Glu Lys Lys Glu Lys Thr Glu Met Asp Pro Glu Ile Ala
275 280 285

Glu Ala Asn Ala Ile Arg Ala Lys Leu Gly Leu Lys Pro Leu Arg Gly
290 295 300

<210> 104
<211> 630
<212> DNA
<213> Ostreococcus tauri

<400> 104
atgccgtcgg tgatcgaaaa ccacggacga ccgatctgga ccccgttcgg gaacggcgcg 60
gcgacgagcg ggaagtcgca cggcgtcgag gaggtgcttc gacaaaacat tgcgcactca 120
gaatactttc gaaaacttcg tcgcgcggaac gatctggggc gaccggcgta cgatttcatg 180
gcgctcgtgg atgagattta tgaattggtc gatcactgcg aaccgtggat gtgcgggaac 240
gcgcgggggg cgtcgacggg gttttgcatc ttgtttcaat tctgtgagat ggagctcagc 300
gacggcaacg tgtggcattt gttgaggcac ggagactcgc cgtttatccg agctttaggg 360
ttcctgtatg tacggtacgt gaagaacggg cgggagctct tgaagtgggtg cgaggagttc 420
ttcggagacg aggaaaagtt taaaccgtcg ccggacggga aggaggtgac gatgggcgcg 480
ttcgttcgcg acttgctgct cgagcagagg tacttcgaaa ccatacctgcc gaggattcct 540
gaggttgcca ggagagagat cataaaggtc tcggttgcgg tggtcagggc gggagccgca 600
ttgctggtgg ttctcagccg cagtctgtga 630

<210> 105
<211> 209
<212> PRT
<213> Ostreococcus tauri

<400> 105
Met Pro Ser Val Ile Glu Asn His Gly Arg Pro Ile Trp Thr Pro Phe
1 5 10 15

Gly Asn Gly Ala Ala Thr Ser Gly Lys Ser His Gly Val Glu Glu Val
20 25 30

Leu Arg Gln Asn Ile Ala His Ser Glu Tyr Phe Arg Lys Leu Arg Arg
35 40 45

Ala Asp Asp Leu Gly Arg Pro Ala Tyr Asp Phe Met Ala Leu Val Asp
Seite 120

50

55

60

Glu Ile Tyr Glu Leu Val Asp His Cys Glu Pro Trp Met Cys Gly Asn
65 70 75 80

Ala Arg Gly Ala Ser Thr Gly Phe Cys Ile Leu Phe Gln Phe Cys Glu
85 90 95

Met Glu Leu Ser Asp Gly Asn Val Trp His Leu Leu Arg His Gly Asp
100 105 110

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

Asn Gly Arg Glu Leu Leu Lys Trp Cys Glu Glu Phe Phe Gly Asp Glu
130 135 140

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

Phe Val Arg Asp Leu Leu Leu Glu Gln Arg Tyr Phe Glu Thr Ile Leu
165 170 175

Pro Arg Ile Pro Glu Val Ala Arg Arg Glu Ile Ile Lys Val Ser Val
180 185 190

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

Leu

<210> 106
<211> 1409
<212> DNA
<213> Populus trichocarpa

<400> 106
ctcaggagtg cttggattgt ttagtacagt atggagatac agacaaatgg gaaaccaata 60
gattcgctgt tagagaaggt cctttgtatg aacatactat catcagatta cttcaaggag 120
ctttaccgat taaagacata ccatgaagtg atagatgaaa tatacaatca agttgaccat 180
gttgagccat ggatgactgg caactgtcgt ggtccatcta cttccttttg ctttctatac 240
aagttcttca ccatgaaact cactgtcaaa caaatgcatg gtttgctaaa gcacaaggat 300
tctccttata tcagagcggg tgggttcctc tacctgagat atgctgggga tccaaagaca 360
ctgtggaatt ggtttgaacc atatattaaa gacgatgagg aattttctcc aggaactagt 420
ggaaggaaga cgacaatggg tgtttatgtg cgtgatttgc ttctcggaca gtactacttt 480
gatacccttt tccccgatat tcctgttcct gtcatgcggc agatcacatc gaatctggag 540
aagttgaagc taccaacaaa aatctctggt tcgacagggg atggaaaccg tcatggatct 600

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

gatgatacgg cacgccggcc accatctgtg aaggcagcac tttcagtctc ttttggtcag 660
cgtgctcctc atcgtgcatc aaccagggat tcgtctcctg ttcgtcgcac aataccttcc 720
ccctcctatg acagaaccag tgatgattca cgaagtcgac tcggccagag tcgtgaatat 780
tctgataaag aatattcaga tcgggatcat gataggggta gggaaaggga ccaagaccat 840
gatcgggata gagagaggga cagggttcgg gatagggatc aggagagaga aagggaccgg 900
gatcgtgaaa gggattggga tcagagtcgg gacagagaca gggatcggga aagggataga 960
tacagaaggt atgattatga tagaagttcc aggtacactg atagggaaaag cagaagggat 1020
tctgaacaga gcagccgtga cagaagtagg cattatagag aaagtagttc ttatagaagc 1080
cgcagtcgaa gcaggagcag gagcaggagc cgaagctcgc aagctggcgc atcaccatct 1140
gatcgccatc caactcctca aagggatgga aacaaggata agacatctgc gcctagcaat 1200
ctggctaagc tcaaagatct ttatggtgat cttagtgatc agaaagggga tgctggcctg 1260
gaaaggggtc ctcggagggga taatgatggt gaagaggttt ttagactcgg tggttccact 1320
tggaggtagg tagttcaatc ttaaaacagt agcttcagtg gctgtcacat cagctgtatc 1380
aatgaggtct tcagccaggc caaatttct 1409

```

<210> 107
 <211> 432
 <212> PRT
 <213> Populus trichocarpa

<400> 107

Met Glu Ile Gln Thr Asn Gly Lys Pro Ile Asp Ser Leu Leu Glu Lys
 1 5 10 15

Val Leu Cys Met Asn Ile Leu Ser Ser Asp Tyr Phe Lys Glu Leu Tyr
 20 25 30

Arg Leu Lys Thr Tyr His Glu Val Ile Asp Glu Ile Tyr Asn Gln Val
 35 40 45

Asp His Val Glu Pro Trp Met Thr Gly Asn Cys Arg Gly Pro Ser Thr
 50 55 60

Ser Phe Cys Leu Leu Tyr Lys Phe Phe Thr Met Lys Leu Thr Val Lys
 65 70 75 80

Gln Met His Gly Leu Leu Lys His Lys Asp Ser Pro Tyr Ile Arg Ala
 85 90 95

Val Gly Phe Leu Tyr Leu Arg Tyr Ala Gly Asp Pro Lys Thr Leu Trp
 100 105 110

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

Thr Ser Gly Arg Lys Thr Thr Met Gly Val Tyr Val Arg Asp Leu Leu

130

135

140

Leu Gly Gln Tyr Tyr Phe Asp Thr Leu Phe Pro Arg Ile Pro Val Pro
145 150 155 160

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

Lys Ile Ser Gly Ser Thr Gly Asp Gly Asn Arg His Gly Ser Asp Asp
180 185 190

Thr Ala Arg Arg Pro Pro Ser Val Lys Ala Ala Leu Ser Val Ser Phe
195 200 205

Gly Gln Arg Ala Pro His Arg Ala Ser Thr Arg Asp Ser Ser Pro Val
210 215 220

Arg Arg Thr Ile Pro Ser Pro Ser Tyr Asp Arg Thr Ser Asp Asp Ser
225 230 235 240

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

Asp Arg Asp His Asp Arg Gly Arg Glu Arg Asp Gln Asp His Asp Arg
260 265 270

Asp Arg Glu Arg Asp Arg Val Arg Asp Arg Asp Gln Glu Arg Glu Arg
275 280 285

Asp Arg Asp Arg Glu Arg Asp Trp Asp Gln Ser Arg Asp Arg Asp Arg
290 295 300

Asp Arg Glu Arg Asp Arg Tyr Arg Arg Tyr Asp Tyr Asp Arg Ser Ser
305 310 315 320

Arg Tyr Thr Asp Arg Glu Ser Arg Arg Asp Ser Glu Gln Ser Ser Arg
325 330 335

Asp Arg Ser Arg His Tyr Arg Glu Ser Ser Ser Tyr Arg Ser Arg Ser
340 345 350

Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Ser Gln Ala Gly Ala Ser
355 360 365

Pro Phe Asp Arg His Pro Thr Pro Gln Arg Asp Gly Asn Lys Asp Lys
370 375 380

Thr Ser Ala Pro Ser Asn Leu Ala Lys Leu Lys Asp Leu Tyr Gly Asp
385 390 395 400

Leu Ser Asp Gln Lys Gly Asp Ala Gly Leu Glu Arg Val Pro Arg Arg
405 410 415

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Asp Asn Asp Gly Glu Glu Val Phe Arg Leu Gly Gly Ser Thr Trp Arg
420 425 430

<210> 108
<211> 1394
<212> DNA
<213> Populus trichocarpa

<400> 108
acaggagtgc ttgcatttgt ttagtacatt atggaggtac agacaaatgg gaaaccgata 60
gattcactct ttgagaaggt cttttgtatg aacattctat catcggatta cttcaaggag 120
ctttaccgat taaagacgta ccatgaagtg attgatgaaa tatacaatca agttgacaat 180
gttgagccat ggatgactgg taactgtcgt ggcccatcta cgtccttttg ctttctgtac 240
aagttcttca ccatgaagct cactgtcaaa caaatgcatg gtctgctaaa gcacaaggat 300
tctccttata tcagagcggg tgggttcctt tacctgagat atgctggtga cccaaagaca 360
ctgtggaatt ggtttgaacc atatatcaaa gatgatgagg aattttctcc tggatctagt 420
ggaaggaaga caacaatagg catatatgtg cgtgatttac ttctcggaca gtactacttt 480
gatacccttt tccccgtat tcctgttcct gtcttgccgc agatcacagc caatcttgag 540
atgatgaagc taccacaaa aatttctggt tcaacagggg atggcaaccg tcatggatct 600
gatgatactg cacgtcgacc accatctgtg aaggctgcac tttcagtctc ttttggtcag 660
cgtgctcctc atcgtgcatc aactagggac tcattctctg ttcgtcgac gctaccgcca 720
ccctcctatg acagaaccag tgatgatcca cgaagtcac gcagccagag tcgcaatat 780
tctgataaag aatattcaga cagggatcgg gatcaagata ggggtagaga gagggaccgt 840
gatagggaca gagagagga cagggttcgg gatagagatc atgatagaga aagagatcgg 900
gaccgtggca gggacagtga caggaaacag gaacgtgaga ggggtagaga ccgaaggtct 960
gattacgata ggagttccag gtacactgac agggagagca gaagggatta tgaacggagc 1020
agccgtgatg gaagtaggcg tcatagagaa agtaattata gaaccggag tcggagcagg 1080
agcagaagta gaagccaaag cttgcaagct ggcacatcac catttgatca gcatccaact 1140
cctcaaaggg atggaagcaa ggataggaca tctgcatcta gcaatctggc taagctcaaa 1200
gatctttatg gtgatcttgg tgatcagaaa ggggatgctg gcctggaaag gggtcctcgg 1260
agggacaatg atggtgaaga agtttttaga ctgggtgggt ctacttgag gtaggtagtt 1320
caatgaaagc tgtaactgtc tgatgtatca gtaaggctct cagccatgcc aaatcactgt 1380
ttgagtcaag aaaa 1394

<210> 109
<211> 427
<212> PRT
<213> Populus trichocarpa

<400> 109

Met Glu Val Gln Thr Asn Gly Lys Pro Ile Asp Ser Leu Phe Glu Lys
Seite 124

1

5

10

15

Val Leu Cys Met Asn Ile Leu Ser Ser Asp Tyr Phe Lys Glu Leu Tyr
20 25 30

Arg Leu Lys Thr Tyr His Glu Val Ile Asp Glu Ile Tyr Asn Gln Val
35 40 45

Asp Asn Val Glu Pro Trp Met Thr Gly Asn Cys Arg Gly Pro Ser Thr
50 55 60

Ser Phe Cys Leu Leu Tyr Lys Phe Phe Thr Met Lys Leu Thr Val Lys
65 70 75 80

Gln Met His Gly Leu Leu Lys His Lys Asp Ser Pro Tyr Ile Arg Ala
85 90 95

Val Gly Phe Leu Tyr Leu Arg Tyr Ala Gly Asp Pro Lys Thr Leu Trp
100 105 110

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

Ser Ser Gly Arg Lys Thr Thr Ile Gly Ile Tyr Val Arg Asp Leu Leu
130 135 140

Leu Gly Gln Tyr Tyr Phe Asp Thr Leu Phe Pro Arg Ile Pro Val Pro
145 150 155 160

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

Lys Ile Ser Gly Ser Thr Gly Asp Gly Asn Arg His Gly Ser Asp Asp
180 185 190

Thr Ala Arg Arg Pro Pro Ser Val Lys Ala Ala Leu Ser Val Ser Phe
195 200 205

Gly Gln Arg Ala Pro His Arg Ala Ser Thr Arg Asp Ser Ser Pro Val
210 215 220

Arg Arg Thr Leu Pro Pro Pro Ser Tyr Asp Arg Thr Ser Asp Asp Pro
225 230 235 240

Arg Ser His Arg Ser Gln Ser Arg Glu Tyr Ser Asp Lys Glu Tyr Ser
245 250 255

Asp Arg Asp Arg Asp Gln Asp Arg Gly Arg Glu Arg Asp Arg Asp Arg
260 265 270

Asp Arg Glu Arg Asp Arg Val Arg Asp Arg Asp His Asp Arg Glu Arg
275 280 285

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Asp Arg Asp Arg Gly Arg Asp Ser Asp Arg Lys Gln Glu Arg Glu Arg
290 295 300

Gly Arg Asp Arg Arg Ser Asp Tyr Asp Arg Ser Ser Arg Tyr Thr Asp
305 310 315 320

Arg Glu Ser Arg Arg Asp Tyr Glu Arg Ser Ser Arg Asp Gly Ser Arg
325 330 335

Arg His Arg Glu Ser Asn Tyr Arg Thr Arg Ser Arg Ser Arg Ser Arg
340 345 350

Ser Arg Ser Gln Ser Leu Gln Ala Gly Thr Ser Pro Phe Asp Gln His
355 360 365

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

Asn Leu Ala Lys Leu Lys Asp Leu Tyr Gly Asp Leu Gly Asp Gln Lys
385 390 395 400

Gly Asp Ala Gly Leu Glu Arg Gly Pro Arg Arg Asp Asn Asp Gly Glu
405 410 415

Glu Val Phe Arg Leu Gly Gly Ser Thr Trp Arg
420 425

<210> 110
<211> 1281
<212> DNA
<213> Saccharum officinarum

<220>
<221> misc_feature
<222> (1140)..(1141)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1220)..(1220)
<223> n is a, c, g, or t

<400> 110	
cgggctcctt tcctccgcct ctcgtctagt ccctctccta ccgaaccctc ccaatccaaa	60
gcgattcctc cgggccgccg ccgtcccgat cgcgccgcgc cgccggggcg gcgtctcccc	120
ggctgccctt agctcagctc gcgttcgggt ggaacagaga agagaggtgg ggggaatgga	180
gatccagtcg tctggccggc ccatcgaggg gctgatggag aaggtgctgt ccgtgaacat	240
cctctcctcg gactacttca aggagctctt caagtacaag acctaccacg aggtgggtcga	300
cgagatctac aaccaggtgg accacgtcga gccctggatg accggcaact gccgcggggc	360
ctcctccgcc ttctgcctcc tctacaagtt cttcaccatg aagctcaccg tcaagcagat	420

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```
gcacgggctg ctcaagcacc aggactcccc ctacatcaga gctattggat tcctctacct 480
gcgatatgtt gcagaaccga agacgctgtg gacttggtat gaaccctata tcaaggatga 540
cgaggagttt gcccttggat caaatggtaa aatgactaca atgggcgttt atgtgcgtga 600
tctcctcctt ggtcagtact atttcgacag tcttcttcca cgagtgcctc tcccaattct 660
ccgacaggtc actagccatc ttgagaagct gaagcttcca acaaagcagt caggaatgac 720
tggggattcc aataggcttg aatcaaataa tactgccaga aggcctcctt ccgtaaaggc 780
ttctttgtct gtctcttttg gtcagcgtgc tccacaccgt gcatacaca gggattcttc 840
cccagtccga agaacattac cttccaaaca ggacaaggaa agaagttatg atggtgacca 900
tgcaaaatcg ccaccaagga agcgcagaag tcagagctct gagcgccatc atgactcaga 960
gagggaccgt tcaaatacgt atcgtggcaa gtacaaggat agggagcatg atcgttatgc 1020
tcgtgatcac agagaccggg atcatcatcg gcagagttat tcagataggg atgacgaaag 1080
gcgaggccgt gaaaagaggg acagggattc tgaccgaaag agatattcaa gctcccgcan 1140
ngagcaggag tccagtccgt ggcagaactg acggcgacaa acatcgctcc agcccaattt 1200
gtagggcacc agaatactn cacctggcaa agctaaagga ttatcacggt gatgcaacaa 1260
acacaaagaa tgatgcttgc g 1281
```

<210> 111
 <211> 331
 <212> PRT
 <213> Saccharum officinarum

<220>
 <221> misc_feature
 <222> (322)..(322)
 <223> Xaa can be any naturally occurring amino acid
 <400> 111

Met Glu Ile Gln Ser Ser Gly Arg Pro Ile Glu Gly Leu Met Glu Lys
 1 5 10 15

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

Lys Tyr Lys Thr Tyr His Glu Val Val Asp Glu Ile Tyr Asn Gln Val
 35 40 45

Asp His Val Glu Pro Trp Met Thr Gly Asn Cys Arg Gly Pro Ser Ser
 50 55 60

Ala Phe Cys Leu Leu Tyr Lys Phe Phe Thr Met Lys Leu Thr Val Lys
 65 70 75 80

Gln Met His Gly Leu Leu Lys His Gln Asp Ser Pro Tyr Ile Arg Ala
 85 90 95

Ile Gly Phe Leu Tyr Leu Arg Tyr Val Ala Glu Pro Lys Thr Leu Trp

Thr Trp Tyr Glu Pro Tyr Ile Lys Asp Asp Glu Glu Phe Ala Pro Gly
115 120 125

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

Leu Gly Gln Tyr Tyr Phe Asp Ser Leu Leu Pro Arg Val Pro Leu Pro
145 150 155 160

Ile Leu Arg Gln Val Thr Ser His Leu Glu Lys Leu Lys Leu Pro Thr
165 170 175

Lys Gln Ser Gly Met Thr Gly Asp Ser Asn Arg Leu Glu Ser Asn Asp
180 185 190

Thr Ala Arg Arg Pro Pro Ser Val Lys Ala Ser Leu Ser Val Ser Phe
195 200 205

Gly Gln Arg Ala Pro His Arg Ala Tyr Thr Arg Asp Ser Ser Pro Val
210 215 220

Arg Arg Thr Leu Pro Ser Lys Gln Asp Lys Glu Arg Ser Tyr Asp Gly
225 230 235 240

Asp His Ala Lys Ser Pro Pro Arg Lys Arg Arg Ser Gln Ser Ser Glu
245 250 255

Arg His His Asp Ser Glu Arg Asp Arg Ser Asn Arg Asp Arg Gly Lys
260 265 270

Tyr Lys Asp Arg Glu His Asp Arg Tyr Ala Arg Asp His Arg Asp Arg
275 280 285

Asp His His Arg Gln Ser Tyr Ser Asp Arg Asp Asp Glu Arg Arg Gly
290 295 300

Arg Glu Lys Arg Asp Arg Asp Ser Asp Arg Lys Arg Tyr Ser Ser Ser
305 310 315 320

Arg Xaa Glu Gln Glu Ser Ser Pro Trp Gln Asn
325 330

<210> 112
<211> 1179
<212> DNA
<213> Saccharum officinarum

<400> 112
atggagatcc agtcatctgc ccggcccatc gaggggctga tggagaaggt gctgtccgtg 60

aacatcctct cctcggacta cttcaaggag ctcttcaagt acaagaccta ccacgaggtg 120

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

gtcgacgaga tctacaacca ggtggaccac gtcgagccct ggatgaccgg caactgccgc 180
gggccctcct ccgccttctg cctcctctac aagttcttca ccatgaagct caccgtcaag 240
cagatgcacg ggctgctcaa gcatcaggac tccccctaca tcagagctat tggattcctc 300
tacctgcgat atgttgacga accgaagacg ctgtggactt ggtatgaacc ctatatcaag 360
gatgacgagg agtttgcccc tggatcaaat ggtaaattga ctacaatggg cgtttatgtg 420
cgtgatctcc tccttgggtca gtactatttc gacagtcttc ttccacgagt gcctctccca 480
attctccgac aggtcactag ccatcttgag aagctgaagc ttccaacaaa gcagtcagga 540
atgactgggg attccaatag gcttgaatca aatgatactg ccagaaggcc tccttccgta 600
aaggcttctt tgtctgtctc ttttggtcag cgtgctccac accgtgcatc cacaagggat 660
tcttccccag tccgaagaac attaccttcc aaacaggaca aagaaagaag ttatgatggt 720
gaccatgcaa aatcgccacc aaggaagcgc agaagtcaga gctctgagcg tcatcatgac 780
tctgagaggg accgttcaga tcgtgatcgt ggcaggtaca agggtaggga gcatgatcgt 840
tatgctcgtg atcacagaga ccgggatcat catcggcaga gttattcaga tagggatgac 900
gaaaggcgag gccgtgaaaa gagggacagg gattctgacc acaatagaca ttcaagctcc 960
cgcaggagca ggagcaggag tccagtccgt ggcagaactg acggtgacaa gcatcgtctc 1020
agcccatttg gtagggcacc agaatcatcc aacctggcaa agctaaagga ttatacggg 1080
gatgcaacaa acacaaagaa tgatgctggc gatgatagag ctcacaggga ttctggaacg 1140
gaagaggtaa tccgactggg aggggcaagg tggaggtga 1179

```

<210> 113
 <211> 392
 <212> PRT
 <213> Saccharum officinarum
 <400> 113

Met Glu Ile Gln Ser Ser Ala Arg Pro Ile Glu Gly Leu Met Glu Lys
 1 5 10 15

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

Lys Tyr Lys Thr Tyr His Glu Val Val Asp Glu Ile Tyr Asn Gln Val
 35 40 45

Asp His Val Glu Pro Trp Met Thr Gly Asn Cys Arg Gly Pro Ser Ser
 50 55 60

Ala Phe Cys Leu Leu Tyr Lys Phe Phe Thr Met Lys Leu Thr Val Lys
 65 70 75 80

Gln Met His Gly Leu Leu Lys His Gln Asp Ser Pro Tyr Ile Arg Ala
 85 90 95

Ile Gly Phe Leu Tyr Leu Arg Tyr Val Ala Glu Pro Lys Thr Leu Trp

Thr Trp Tyr Glu Pro Tyr Ile Lys Asp Asp Glu Glu Phe Ala Pro Gly
115 120 125

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

Leu Gly Gln Tyr Tyr Phe Asp Ser Leu Leu Pro Arg Val Pro Leu Pro
145 150 155 160

Ile Leu Arg Gln Val Thr Ser His Leu Glu Lys Leu Lys Leu Pro Thr
165 170 175

Lys Gln Ser Gly Met Thr Gly Asp Ser Asn Arg Leu Glu Ser Asn Asp
180 185 190

Thr Ala Arg Arg Pro Pro Ser Val Lys Ala Ser Leu Ser Val Ser Phe
195 200 205

Gly Gln Arg Ala Pro His Arg Ala Ser Thr Arg Asp Ser Ser Pro Val
210 215 220

Arg Arg Thr Leu Pro Ser Lys Gln Asp Lys Glu Arg Ser Tyr Asp Gly
225 230 235 240

Asp His Ala Lys Ser Pro Pro Arg Lys Arg Arg Ser Gln Ser Ser Glu
245 250 255

Arg His His Asp Ser Glu Arg Asp Arg Ser Asp Arg Asp Arg Gly Arg
260 265 270

Tyr Lys Gly Arg Glu His Asp Arg Tyr Ala Arg Asp His Arg Asp Arg
275 280 285

Asp His His Arg Gln Ser Tyr Ser Asp Arg Asp Asp Glu Arg Arg Gly
290 295 300

Arg Glu Lys Arg Asp Arg Asp Ser Asp His Asn Arg His Ser Ser Ser
305 310 315 320

Arg Arg Ser Arg Ser Arg Ser Pro Val Arg Gly Arg Thr Asp Gly Asp
325 330 335

Lys His Arg Ser Ser Pro Phe Gly Arg Ala Pro Glu Ser Ser Asn Leu
340 345 350

Ala Lys Leu Lys Asp Leu Tyr Gly Asp Ala Thr Asn Thr Lys Asn Asp
355 360 365

Ala Gly Asp Asp Arg Ala His Arg Asp Ser Gly Thr Glu Glu Val Ile
370 375 380

Arg Leu Gly Gly Ala Arg Trp Arg
385 390

<210> 114
<211> 729
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 114
atggctgtca atgaatttca agtggagtct aacatctctc caaaacaact gaataaccag 60
tcagtgtcac ttgtttattcc tcggttgaca agagataaaa ttcataattc aatgtactat 120
aaagtaaadc taagcaacga atctttgaga ggcaatacaa tggtagagct tttgaaagtt 180
atgattggcg catttggtac cataaaaggt caaaatgggc atttacacat gatggttctc 240
ggtaggcattg agtttaaatg catcttaatg aagttaatcg aaatcagacc gaatttccag 300
cagttgaact tcttattgaa tgtaaaaaat gagaacgggt ttgactcgaa atatattatt 360
gctttgcttc tggtttatgc gcggttacag tattattatt tgaatggcaa taacaaaaac 420
gatgatgatg aaaatgattt gataaagtta tttaaagtac aattatacaa atattcacag 480
cattatttca aactaaaaag tttcccacta caagtagact gctttgctca ctcctataac 540
gaagaacttt gtataatata cattgatgaa ttagtcgatt ggtagggcac acaggaccat 600
atctggggta ttccattagg gaaatgtcaa tggaataaaa tatacaactc tgatgaagag 660
agtagttcta gcgaaagcga aagtaatggg gacagtgaag atgacaacga caccagcagc 720
gaatcatag 729

<210> 115
<211> 242
<212> PRT
<213> *Saccharomyces cerevisiae*

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

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Pro Asn Phe Gln Gln Leu Asn Phe Leu Leu Asn Val Lys Asn Glu Asn
100 105 110

Gly Phe Asp Ser Lys Tyr Ile Ile Ala Leu Leu Leu Val Tyr Ala Arg
115 120 125

Leu Gln Tyr Tyr Tyr Leu Asn Gly Asn Asn Lys Asn Asp Asp Asp Glu
130 135 140

Asn Asp Leu Ile Lys Leu Phe Lys Val Gln Leu Tyr Lys Tyr Ser Gln
145 150 155 160

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

His Ser Tyr Asn Glu Glu Leu Cys Ile Ile His Ile Asp Glu Leu Val
180 185 190

Asp Trp Leu Ala Thr Gln Asp His Ile Trp Gly Ile Pro Leu Gly Lys
195 200 205

Cys Gln Trp Asn Lys Ile Tyr Asn Ser Asp Glu Glu Ser Ser Ser Ser
210 215 220

Glu Ser Glu Ser Asn Gly Asp Ser Glu Asp Asp Asn Asp Thr Ser Ser
225 230 235 240

Glu Ser

<210> 116
<211> 1182
<212> DNA
<213> Triticum aestivum

<400> 116
atggcgaacc gcacggaccc ccgggcccgg agcatccacg gcaccaaccc tcagaacctg 60
gtggagaaga tcgtgcgggc caagatctac cagagcaact actggaagga gcagtgttct 120
ggcctcacgg cggagaccct cgtcgacaag gccatggagc tcgactacac cggcggcacc 180
cacggcggca accgcaggcc gacccccttc ctctgcctcg ctctcaagat gctccagatc 240
cagcccgaca aggaaatcgt cgtcgagttc atcaaggacg aggactacaa gtatgtccgg 300
gttcttgggg cttctacct gcgcctcact ggcaccgtcg ccgacgttta ccagtacctc 360
gagccgtctt acaacgacta ccgcaagatt aggcaaaagc tcagcgatgg aaaattcacg 420
ctgacacacg ttgacgaatt cattgacgag ctctgacca aggactatag ctgcggcact 480
gccctcccc gcattcagaa aagatggatc cttgaagctt ctggaactct agaacctaga 540
agaagtgcac ttgaagacga ttttgaggaa gaggaggaag ataaggagga tggacagcct 600
atggacgtag atgagcctaa cactcatgaa aaggaccatc ttcgtggaag aagccccacc 660

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

aaagaacgcg acaggggaaag ggagaggggac agagacagga aacacgaaag gcatcacagg	720
gaccgagatc atgacagaga tcgggatcac gacagggact atggaagagg ccgggaaaga	780
gatcgagaca gagatagagg ccgtgaaaga gatagagaga gggataggga acgagaccgt	840
caccgcatcc gagatgacga ctaccaccga gatcgagacc gggatggcag ggaaagggaa	900
cgccgggaca gagaccgtgg caggcacagg agccgctcag ggagcagaag ccgggatcgg	960
cgtgaaagag accgtgaagt gggagagctc cgtaagaggc gtggccgtgg tagtgccagt	1020
cctcctcggg ggcgtgccga ggatggtccg agggaggagc ctaagaagag aaaggaaaag	1080
aaagagaaga agggcagcgg gaacggtcca gatacctaag atccagagat tatagagatg	1140
aacaagctgc gtgcatcgat agggttggga ccactgaagt ag	1182

<210> 117
 <211> 393
 <212> PRT
 <213> Triticum aestivum

<400> 117

Met Ala Asn Arg Thr Asp Pro Arg Ala Arg Ser Ile His Gly Thr Asn
 1 5 10 15

Pro Gln Asn Leu Val Glu Lys Ile Val Arg Ala Lys Ile Tyr Gln Ser
 20 25 30

Asn Tyr Trp Lys Glu Gln Cys Phe Gly Leu Thr Ala Glu Thr Leu Val
 35 40 45

Asp Lys Ala Met Glu Leu Asp Tyr Thr Gly Gly Thr His Gly Gly Asn
 50 55 60

Arg Arg Pro Thr Pro Phe Leu Cys Leu Ala Leu Lys Met Leu Gln Ile
 65 70 75 80

Gln Pro Asp Lys Glu Ile Val Val Glu Phe Ile Lys Asp Glu Asp Tyr
 85 90 95

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

Val Ala Asp Val Tyr Gln Tyr Leu Glu Pro Leu Tyr Asn Asp Tyr Arg
 115 120 125

Lys Ile Arg Gln Lys Leu Ser Asp Gly Lys Phe Thr Leu Thr His Val
 130 135 140

Asp Glu Phe Ile Asp Glu Leu Leu Thr Lys Asp Tyr Ser Cys Gly Thr
 145 150 155 160

Ala Leu Pro Arg Ile Gln Lys Arg Trp Ile Leu Glu Ala Ser Gly Thr
 165 170 175

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Leu Glu Pro Arg Arg Ser Ala Leu Glu Asp Asp Phe Glu Glu Glu Glu
180 185 190

Glu Asp Lys Glu Asp Gly Gln Pro Met Asp Val Asp Glu Pro Asn Thr
195 200 205

His Glu Lys Asp His Leu Arg Gly Arg Ser Pro Thr Lys Glu Arg Asp
210 215 220

Arg Glu Arg Glu Arg Asp Arg Asp Arg Lys His Glu Arg His His Arg
225 230 235 240

Asp Arg Asp His Asp Arg Asp Arg Asp His Asp Arg Asp Tyr Gly Arg
245 250 255

Gly Arg Glu Arg Asp Arg Asp Arg Asp Arg Gly Arg Glu Arg Asp Arg
260 265 270

Glu Arg Asp Arg Glu Arg Asp Arg His Arg Ile Arg Asp Asp Asp Tyr
275 280 285

His Arg Asp Arg Asp Arg Asp Gly Arg Glu Arg Glu Arg Arg Asp Arg
290 295 300

Asp Arg Gly Arg His Arg Ser Arg Ser Gly Ser Arg Ser Arg Asp Arg
305 310 315 320

Arg Glu Arg Asp Arg Glu Val Gly Glu Leu Arg Lys Arg Arg Gly Arg
325 330 335

Gly Ser Ala Ser Pro Pro Arg Gly Arg Ala Glu Asp Gly Pro Arg Glu
340 345 350

Glu Pro Lys Lys Arg Lys Glu Lys Lys Glu Lys Lys Gly Ser Gly Asn
355 360 365

Gly Pro Asp Pro Asn Asp Pro Glu Ile Ile Glu Met Asn Lys Leu Arg
370 375 380

Ala Ser Ile Gly Leu Gly Pro Leu Lys
385 390

<210> 118
<211> 1119
<212> DNA
<213> Vitis vinifera

<400> 118
atggcgaacc gtacggaccc agcggcgaag agcatacgag gcacgaatcc gcaaaacttg 60
gtggagaaga ttctgaggtc gaagatttac cagaacacgt actggaagga gcagtgcttt 120
ggattgaccg cggagactct ggttgacaag gccatggagc tcgaccacct cggcggcacc 180

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

tttgggtggta accgcaagcc cagccccttc atgtgcctcg tcatgaaaat gctccagatc 240
cagccccgaga aggacatcgt cgtcgagttc ataaaaaacg aagagtacaa atatgtccga 300
atacttgggtg cattttatatt gcgtcttaca gggatagata ctgatgtgta ccaataccta 360
gagcctctat acaatgacta tcggaaattg aggagaaaat tatctgatgg aaattattct 420
ttgacacacg ttgatgaggt tatcgatgaa cttctgacaa aagattattc ctgtgacggt 480
gccttgcccc gtatcaagaa aagatggact cttgaatccc ttggtacact ggaaccaaga 540
agaagtgcct tggaagatga ttttgaggaa gaggaagaaa aagaagagga tgaccaactc 600
atggatgaat tagatgttgg ggctcatgaa aaggattatt atcgtgggcg aagccctgca 660
agggagagag atagggatag aaagcgtgac agtcacagat atagagatcg agattatgat 720
agggaaactg gaagaggacg agaaagagat cgggaaaggg aaagggacag agacagctat 780
agagacaggg agagggagag ggacagagac agggaccgct atcgtctgag agatgataaa 840
gaatatgggtc gtgacagggg gaggggaaagg gagagggaag gcagggagag ggagaggcga 900
gacaggggacc gagccattca aggagccgaa gtaggagcaa ggatcaggca tgctcgcagc 960
agcaccaaca tgccagagga tggaaccact cgagaagagc caaggaagaa gaaagaaaag 1020
aaggagaaga aggatgatgg cactgaccac ccagatccag agattgcaga agcaaacagg 1080
ttgcgggcat cccttgggct taaacccttg aaactctaa 1119

```

<210> 119
 <211> 372
 <212> PRT
 <213> Vitis vinifera

<400> 119

Met Ala Asn Arg Thr Asp Pro Ala Ala Lys Ser Ile Arg Gly Thr Asn
 1 5 10 15

Pro Gln Asn Leu Val Glu Lys Ile Leu Arg Ser Lys Ile Tyr Gln Asn
 20 25 30

Thr Tyr Trp Lys Glu Gln Cys Phe Gly Leu Thr Ala Glu Thr Leu Val
 35 40 45

Asp Lys Ala Met Glu Leu Asp His Leu Gly Gly Thr Phe Gly Gly Asn
 50 55 60

Arg Lys Pro Thr Pro Phe Met Cys Leu Val Met Lys Met Leu Gln Ile
 65 70 75 80

Gln Pro Glu Lys Asp Ile Val Val Glu Phe Ile Lys Asn Glu Glu Tyr
 85 90 95

Lys Tyr Val Arg Ile Leu Gly Ala Phe Tyr Leu Arg Leu Thr Gly Ile
 100 105 110

Asp Thr Asp Val Tyr Gln Tyr Leu Glu Pro Leu Tyr Asn Asp Tyr Arg

115

120

125

Lys Leu Arg Arg Lys Leu Ser Asp Gly Asn Tyr Ser Leu Thr His Val
 130 135 140

Asp Glu Val Ile Asp Glu Leu Leu Thr Lys Asp Tyr Ser Cys Asp Val
 145 150 155 160

Ala Leu Pro Arg Ile Lys Lys Arg Trp Thr Leu Glu Ser Leu Gly Thr
 165 170 175

Leu Glu Pro Arg Arg Ser Ala Leu Glu Asp Asp Phe Glu Glu Glu Glu
 180 185 190

Glu Lys Glu Glu Asp Asp Gln Leu Met Asp Glu Leu Asp Val Gly Ala
 195 200 205

His Glu Lys Asp Tyr Tyr Arg Gly Arg Ser Pro Ala Arg Glu Arg Asp
 210 215 220

Arg Asp Arg Lys Arg Asp Ser His Arg Tyr Arg Asp Arg Asp Tyr Asp
 225 230 235 240

Arg Glu Arg Gly Arg Gly Arg Glu Arg Asp Arg Glu Arg Glu Arg Asp
 245 250 255

Arg Asp Ser Tyr Arg Asp Arg Glu Arg Glu Arg Asp Arg Asp Arg Asp
 260 265 270

Arg Tyr Arg Leu Arg Asp Asp Lys Glu Tyr Gly Arg Asp Arg Glu Arg
 275 280 285

Glu Arg Glu Arg Glu Gly Arg Glu Arg Glu Arg Arg Asp Arg Asp Arg
 290 295 300

Ala Ile Gln Gly Ala Glu Val Gly Ala Arg Ile Arg His Ala Arg Ser
 305 310 315 320

Ser Thr Asn Met Pro Glu Asp Gly Thr Thr Arg Glu Glu Pro Arg Lys
 325 330 335

Lys Lys Glu Lys Lys Glu Lys Lys Asp Asp Gly Thr Asp His Pro Asp
 340 345 350

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

Pro Leu Lys Leu
 370

<210> 120

<211> 33

<212> PRT
<213> Artificial sequence

<220>
<223> Motif I

<400> 120

Arg Arg Pro Pro Ser Val Lys Ala Ser Leu Ser Val Ser Phe Gly Gln
1 5 10 15

Arg Ala Pro His Arg Ala Ser Thr Arg Asp Ser Ser Pro Val Arg Arg
20 25 30

Thr

<210> 121
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<223> Motif II

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

<400> 121

Ser Pro Tyr Ile Arg Ala Ile Gly Phe Leu Tyr Leu Arg Tyr
1 5 10

<210> 122
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Motif III

<400> 122

Lys Leu Lys Asp Leu Tyr Gly Asp
1 5

<210> 123
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Motif IV

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

<220>

```

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

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

<400> 123
Leu Xaa Glu Lys Val Leu
1      5

<210> 124
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Motif V

<400> 124
Leu Val Glu Lys Ile
1      5

<210> 125
<211> 55
<212> DNA
<213> Artificial sequence

<220>
<223> primer 1

<400> 125
ggggacaagt ttgtacaaaa aagcaggctt aaacaatggc ggagatacag tcaaa      55

<210> 126
<211> 48
<212> DNA
<213> Artificial sequence

<220>
<223> primer 2

<400> 126
ggggaccact ttgtacaaga aagctggggtt cacctccaag aggaacca      48

<210> 127
<211> 2194
<212> DNA
<213> Oryza sativa

<400> 127
aatccgaaaa gtttctgcac cgttttcacc ccctaactaa caatataggg aacgtgtgct      60
aaatataaaa tgagacctta tatatgtagc gctgataact agaactatgc aagaaaaact      120
catccaccta ctttagtggc aatcgggcta aataaaaaaag agtcgctaca ctagtttcgt      180
tttccttagt aattaagtgg gaaaatgaaa tcattattgc ttagaatata cgttcacatc      240
tctgtcatga agttaaatta ttcgaggtag ccataattgt catcaaactc ttcttgaata      300

```

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

aaaaaatctt tctagctgaa ctcaatgggt aaagagagag atttttttta aaaaaataga	360
atgaagatat tctgaacgta ttggcaaaga tttaaacata taattatata attttatagt	420
ttgtgcattc gtcatatcgc acatcattaa ggacatgtct tactccatcc caatttttat	480
ttagtaatta aagacaattg acttattttt attattttatc ttttttcgat tagatgcaag	540
gtacttacgc acacactttg tgctcatgtg catgtgtgag tgcacctcct caatacacgt	600
tcaactagca acacatctct aatatcactc gcctatttaa tacatttagg tagcaatatc	660
tgaattcaag cactccacca tcaccagacc actttttaata atatctaaaa taaaaaaat	720
aattttacag aatagcatga aaagtatgaa acgaactatt taggtttttc acatacaaaa	780
aaaaaaagaa ttttgctcgt gcgcgagcgc caatctccca tattgggcac acaggcaaca	840
acagagtggc tgcccacaga acaaccaca aaaaacgatg atctaacgga ggacagcaag	900
tccgcaacaa cttttaaca gcaggctttg cggccaggag agaggaggag aggcaagaa	960
aaccaagcat cctccttctc ccatctataa attcctcccc cttttcccc tctctatata	1020
ggaggcatcc aagccaagaa gaggagagc accaaggaca cgcgactagc agaagccgag	1080
cgaccgcctt ctgatccat atcttccggt cgagttcttg gtcgatctct tccctcctcc	1140
acctcctcct cacagggtat gtgcctccct tcggttggtc ttggatttat tgttctaggt	1200
tgtgtagtac gggcgttgat gttaggaaag gggatctgta tctgtgatga ttcctgttct	1260
tggatttggg atagaggggt tcttgatgtt gcatgttatc ggttcggttt gatttagtagt	1320
atggttttca atcgtctgga gagctctatg gaaatgaaat ggtttaggga tcggaatctt	1380
gcgattttgt gagtacctt tgtttgaggt aaaatcagag caccggtgat tttgcttggt	1440
gtaataaagt acggttggtt ggtcctcgat tctggtagt atgcttctcg atttgacgaa	1500
gctatcctt gtttattccc tattgaacaa aaataatcca actttgaaga cgggtcccgtt	1560
gatgagattg aatgattgat tcttaagcct gtccaaaatt tcgcagctgg cttgtttaga	1620
tacagtagtc cccatcacga aattcatgga aacagttata atcctcagga acaggggatt	1680
ccctgttctt ccgatttgct ttagtcccag aatttttttt cccaaatatc ttaaaaagtc	1740
actttctggt tcagttcaat gaattgattg ctacaaataa tgcttttata gcgttatcct	1800
agctgtagtt cagttaatag gtaatacccc tatagtttag tcaggagaag aacttatccg	1860
atttctgata tccattttta attatatgaa atgaactgta gcataagcag tattcatttg	1920
gattattttt tttattagct ctcaccctt cattattctg agctgaaagt ctggcatgaa	1980
ctgtcctcaa ttttgttttc aaattcacat cgattatcta tgcattatcc tcttgtatct	2040
acctgtagaa gtttcttttt gggtattcct tgactgcttg attacagaaa gaaatttatg	2100
aagctgtaat cgggatagtt atactgcttg ttcttatgat tcatttcctt tgtgcagttc	2160
ttggtgtagc ttgccacttt caccagcaaa gttc	2194

<210> 128
 <211> 1062
 <212> DNA
 <213> Oryza sativa

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

<400> 128
atgtctacta tctacatgag ccagctacct gctactctcc ctctaattga gggggatcag      60
gatcaggggc tctaccagc cttccataga gcaaaggacc ctccatatctt gttccctttc      120
atgatcgaca gcgccgtcga gcaccaaggg caaatctatg gagatcaggg cttgaggagg      180
cagcaggttt tgggtgaatc caatcaacag ttcaatgatc acatgatgat gggcggatca      240
gatgtcttcc tcacaccgtc tccgttccga ccaaccatcc aaagcatcgg cagcgacatg      300
atccagcgat catcttatga tccatacgat atcgagagta acaacaagca gcatgccaat      360
ggatcaacca gcaagtggat gtcgacgccg ccaatgaaga tgaggatcat aaggaagggg      420
gcggcaaccg atcctgaggg cggggcggtg agaaagccaa ggagaagagc acaagcgcac      480
caggatgaga gccagcaaca actgcagcaa gctttgggtg tcgttagagt gtgctcggac      540
tgcaacacca ccaagacccc cttgtggaga agtggtcctt gtggcccca gtccttttgc      600
aacgcgtgtg gcatcaggca aaggaaggcg cggcgggcga tggccgctgc tgccaacggc      660
ggagcggcgg tggcgccggc aaagagcgtg gccgcggcgc cggatgaaca taagccggcg      720
gcgaagaagg agaagagggc ggcggacgtc gaccggtcgc tgccgttcaa gaaacggtgc      780
aagatggtcg atcacgttgc tgctgccgtc gctgccacca agcccacggc tgctggagaa      840
gtagtggccg ccgctccgaa ggaccaagat cagtcatcgc tcgtcgggtg cgagaacgcc      900
gccgccacct ccatgccggc acagaacccg atatccaagg cggcggcgac cgccgctgcc      960
gccgccgctt ctccggcggt cttccacggc ctccctcgcg acgagatcac cgacgccgcc      1020
atgctgctca tgaccctatc ctgtggcctc gtccacagct ag                        1062

```

```

<210> 129
<211> 353
<212> PRT
<213> Oryza sativa

```

```

<400> 129
Met Ser Thr Ile Tyr Met Ser Gln Leu Pro Ala Thr Leu Pro Leu Met
1           5           10           15

Glu Gly Asp Gln Asp Gln Gly Leu Tyr Pro Ala Phe His Arg Ala Lys
20          25          30

Asp Pro Pro Ile Leu Phe Pro Phe Met Ile Asp Ser Ala Val Glu His
35          40          45

Gln Gly Gln Ile Tyr Gly Asp Gln Gly Leu Arg Arg Gln Gln Val Leu
50          55          60

Gly Glu Ser Asn Gln Gln Phe Asn Asp His Met Met Met Gly Gly Ser
65          70          75          80

Asp Val Phe Leu Thr Pro Ser Pro Phe Arg Pro Thr Ile Gln Ser Ile
85          90          95

```


PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Gly Ser Asp Met Ile Gln Arg Ser Ser Tyr Asp Pro Tyr Asp Ile Glu
100 105 110

Ser Asn Asn Lys Gln His Ala Asn Gly Ser Thr Ser Lys Trp Met Ser
115 120 125

Thr Pro Pro Met Lys Met Arg Ile Ile Arg Lys Gly Ala Ala Thr Asp
130 135 140

Pro Glu Gly Gly Ala Val Arg Lys Pro Arg Arg Arg Ala Gln Ala His
145 150 155 160

Gln Asp Glu Ser Gln Gln Gln Leu Gln Gln Ala Leu Gly Val Val Arg
165 170 175

Val Cys Ser Asp Cys Asn Thr Thr Lys Thr Pro Leu Trp Arg Ser Gly
180 185 190

Pro Cys Gly Pro Lys Ser Leu Cys Asn Ala Cys Gly Ile Arg Gln Arg
195 200 205

Lys Ala Arg Arg Ala Met Ala Ala Ala Ala Asn Gly Gly Ala Ala Val
210 215 220

Ala Pro Ala Lys Ser Val Ala Ala Ala Pro Val Asn Asn Lys Pro Ala
225 230 235 240

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

Lys Lys Arg Cys Lys Met Val Asp His Val Ala Ala Ala Val Ala Ala
260 265 270

Thr Lys Pro Thr Ala Ala Gly Glu Val Val Ala Ala Ala Pro Lys Asp
275 280 285

Gln Asp His Val Ile Val Val Gly Gly Glu Asn Ala Ala Ala Thr Ser
290 295 300

Met Pro Ala Gln Asn Pro Ile Ser Lys Ala Ala Ala Thr Ala Ala Ala
305 310 315 320

Ala Ala Ala Ser Pro Ala Phe Phe His Gly Leu Pro Arg Asp Glu Ile
325 330 335

Thr Asp Ala Ala Met Leu Leu Met Thr Leu Ser Cys Gly Leu Val His
340 345 350

Ser

```

<210> 130
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<223> Motif 1

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

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

<220>
<221> UNSURE
<222> (5)..(5)
<223> Xaa can be any naturally occurring amino acid, preferably one of
      Asn, Lys, Gly, His, Asp

<220>
<221> VARIANT
<222> (7)..(7)
<223> / replace = "Ser" / replace = "Ala"

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

<220>
<221> VARIANT
<222> (11)..(11)
<223> / replace = "Met"

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

<400> 130
Cys Ser Asp Cys Xaa Thr Thr Lys Thr Pro Leu Trp Arg Ser Gly Pro
1      5      10      15

```

```

<210> 131
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Motif 2

<220>
<221> UNSURE
<222> (13)..(13)
<223> Xaa can be any naturally occurring amino acid, preferably one of
      Gln, His, Asn, Ser, Tyr, Phe

<220>
<221> VARIANT
<222> (14)..(14)

```

<223> / replace = "Lys"

<400> 131

Gly Pro Lys Ser Leu Cys Asn Ala Cys Gly Ile Arg Xaa Arg Lys
1 5 10 15

<210> 132

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Motif 3

<220>

<221> VARIANT

<222> (1)..(1)

<223> / replace = "Ser"

<220>

<221> VARIANT

<222> (2)..(2)

<223> / replace = "Trp"

<220>

<221> UNSURE

<222> (3)..(3)

<223> Xaa can be any naturally occurring amino acid, preferably one of Met, Leu, Val, Ile, Arg

<220>

<221> VARIANT

<222> (4)..(4)

<223> / replace = "Cys"

<220>

<221> VARIANT

<222> (5)..(5)

<223> / replace = "Asn"

<220>

<221> VARIANT

<222> (6)..(6)

<223> / replace = "Leu" / replace = "Val"

<220>

<221> VARIANT

<222> (7)..(7)

<223> / replace = "Leu" / replace = "Ala"

<220>

<221> VARIANT

<222> (8)..(8)

<223> / replace = "Asp"

<220>

<221> VARIANT

<222> (9)..(9)

<223> / replace = "Arg"

<400> 132

Ala Ala Xaa Leu Leu Met Thr Leu Ser
1 5

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

<210> 133
<211> 58
<212> DNA
<213> Artificial sequence

<220>
<223> primer: prm10133

<400> 133
ggggacaagt ttgtacaaaa aagcaggctt aaacaatgtc tactatctac atgagcca      58

<210> 134
<211> 50
<212> DNA
<213> Artificial sequence

<220>
<223> primer: prm10134

<400> 134
ggggaccact ttgtacaaga aagctgggta gctagctagt tttgatcagc      50

<210> 135
<211> 2194
<212> DNA
<213> Oryza sativa

<400> 135
aatccgaaaa gtttctgcac cgttttcacc ccctaactaa caatataggg aacgtgtgct      60
aaatataaaa tgagacctta tatatgtagc gctgataact agaactatgc aagaaaaact      120
catccaccta ctttagtggc aatcgggcta aataaaaaag agtcgctaca ctagtttcgt      180
tttccttagt aattaagtgg gaaaatgaaa tcattattgc ttagaatata cgttcacatc      240
tctgtcatga agttaaatTA ttcgaggtag ccataattgt catcaaactc ttcttgaata      300
aaaaaatctt tctagctgaa ctcaatgggt aaagagagag atttttttta aaaaaataga      360
atgaagatat tctgaacgta ttggcaaaga tttaaacata taattatata attttatagt      420
ttgtgcattc gtcatatcgc acatcattaa ggacatgtct tactccatcc caatttttat      480
ttagtaatta aagacaattg acttattttt attatttatc ttttttcgat tagatgcaag      540
gtacttacgc acacactttg tgctcatgtg catgtgtgag tgcacctcct caatacacgt      600
tcaactagca acacatctct aatatcactc gcctatttaa tacatttagg tagcaatatc      660
tgaattcaag cactccacca tcaccagacc actttttaata atatctaaaa taaaaaaat      720
aattttacag aatagcatga aaagtatgaa acgaactatt taggtttttc acatacaaaa      780
aaaaaaagaa ttttgctcgt gcgcgagcgc caatctccca tattgggcac acaggcaaca      840
acagagtggc tgcccacaga acaaccaca aaaaacgatg atctaacgga ggacagcaag      900
tccgcaacaa ctttttaaca gcaggctttg cggccaggag agaggaggag aggcaaagaa      960
aaccaagcat cctccttctc ccatctataa attcctcccc ctttttcccc tctctatata      1020
ggaggcatcc aagccaagaa gagggagagc accaaggaca cgcgactagc agaagccgag      1080
cgaccgcctt ctcgatccat atcttccggg cgagttcttg gtcgatctct tccctcctcc      1140
acctcctcct cacaggggat gtgcctccct tcggttggtt ttggatttat tgttctaggt      1200

```

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

tgtgtagtac	gggcgttgat	gttaggaaaag	gggatctgta	tctgtgatga	ttcctgttct	1260
tggatttggg	atagaggggt	tcttgatggt	gcatgttatc	ggttcggttt	gattagtagt	1320
atggttttca	atcgtctgga	gagctctatg	gaaatgaaat	ggtttaggga	tcggaatcct	1380
gcgattttgt	gagtaccttt	tgtttgaggt	aaaatcagag	caccggtgat	tttgcttggt	1440
gtaataaagt	acggttgttt	ggtcctcgat	tctggtagtg	atgcttctcg	atttgacgaa	1500
gctatccttt	gtttattccc	tattgaacaa	aaataatcca	actttgaaga	cgggtcccgtt	1560
gatgagattg	aatgattgat	tcttaagcct	gtccaaaatt	tcgcagctgg	cttgttttaga	1620
tacagtagtc	cccatcacga	aattcatgga	aacagttata	atcctcagga	acaggggatt	1680
ccctgttctt	ccgatttgct	ttagtcccag	aatTTTTTTT	cccaaatac	ttaaaaagtc	1740
actttctggt	tcagttcaat	gaattgattg	ctacaaataa	tgcttttata	gcgttatcct	1800
agctgtagtt	cagttaatag	gtaatacccc	tatagtttag	tcaggagaag	aacttatccg	1860
atttctgatc	tccattttta	attatatgaa	atgaactgta	gcataagcag	tattcatttg	1920
gattatTTTT	tttatttagct	ctcaccctt	cattattctg	agctgaaagt	ctggcatgaa	1980
ctgtcctcaa	ttttgttttc	aaattcacat	cgattatcta	tgcattatcc	tcttgtatct	2040
acctgtagaa	gtttcttttt	ggttattcct	tgactgcttg	attacagaaa	gaaatttatg	2100
aagctgtaat	cgggtagatt	atactgcttg	ttcttatgat	tcatttcctt	tgtgcagttc	2160
ttggtgtagc	ttgccacttt	caccagcaaa	gttc			2194

<210> 136
 <211> 3308
 <212> DNA
 <213> Artificial sequence

<220>
 <223> expression cassette

<400> 136		
aatccgaaaa	gtttctgcac	
cgttttcacc	ccctaactaa	
caatataggg	aacgtgtgct	60
aaatataaaa	tgagacctta	
tatatgtagc	gctgataact	
agaactatgc	aagaaaaact	120
catccaccta	ctttagtggc	
aatcgggcta	aataaaaaag	
agtcgctaca	ctagtttctg	180
tttccttagt	aattaagtgg	
gaaaatgaaa	tcattattgc	
ttagaatata	cgttcacatc	240
tctgtcatga	agttaaatta	
ttcgaggtag	ccataattgt	
catcaaactc	ttcttgaata	300
aaaaaatctt	tctagctgaa	
ctcaatgggt	aaagagagag	
atTTTTTTT	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	gcctatTTT	
tacatttagg	tagcaatatc	660
tgaattcaag	cactccacca	
tcaccagacc	actTTTtaata	
atatctaaaa	tacaaaaaat	720

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

aattttacag	aatagcatga	aaagtatgaa	acgaactatt	taggtttttc	acatacaaaa	780
aaaaaaagaa	ttttgctcgt	gcgcgagcgc	caatctccca	tattgggcac	acaggcaaca	840
acagagtggc	tgccacaga	acaaccaca	aaaaacgatg	atctaacgga	ggacagcaag	900
tccgcaacaa	ccttttaaca	gcaggctttg	cggccaggag	agaggaggag	aggcaaagaa	960
aaccaagcat	cctcctcctc	ccatctataa	attcctcccc	ccttttcccc	tctctatata	1020
ggaggcatcc	aagccaagaa	gaggagagc	accaaggaca	cgcgactagc	agaagccgag	1080
cgaccgcctt	cttcgatcca	tatcttccgg	tcgagttctt	ggtcgatctc	ttccctcctc	1140
cacctcctcc	tcacagggtg	tgtgcccttc	ggttggttctt	ggattttattg	ttctagggttg	1200
tgtagtacgg	gcgttgatgt	taggaaaggg	gatctgtatc	tgtgatgatt	cctgttcttg	1260
gatttgggat	agaggggttc	ttgatgttgc	atgttatcgg	ttcggtttga	ttagtagtat	1320
ggttttcaat	cgtctggaga	gctctatgga	aatgaaatgg	tttaggggtac	ggaatcttgc	1380
gattttgtga	gtaccttttg	tttgaggtaa	aatcagagca	ccggtgattt	tgcttggtgt	1440
aataaaagta	cggttgtttg	gtcctcgatt	ctggtagtga	tgcttctcga	tttgacgaag	1500
ctatcctttg	tttattccct	attgaacaaa	aataatccaa	ctttgaagac	ggccccgttg	1560
atgagattga	atgattgatt	cttaagcctg	tccaaaattt	cgagctggc	ttgtttagat	1620
acagtagtcc	ccatcacgaa	attcatggaa	acagttataa	tcctcaggaa	caggggatcc	1680
cctgttcttc	cgatttgctt	tagtcccaga	atTTTTTTTc	ccaaatatct	taaaaagtca	1740
ctttctggtt	cagttcaatg	aattgattgc	tacaaataat	gcttttatag	cgttatccta	1800
gctgtagttc	agttaatagg	taatacccct	atagtttagt	caggagaaga	acttatccga	1860
tttctgatct	ccatttttaa	ttatatgaaa	tgaactgtag	cataagcagt	attcatttgg	1920
attatTTTTt	ttattagctc	tcacccttc	attattctga	gctgaaagtc	tggcatgaac	1980
tgtcctcaat	tttgttttca	aattcacatc	gattatctat	gcattatcct	cttgatatcta	2040
cctgtagaag	tttctTTTTg	gttattcctt	gactgcttga	ttacagaaag	aaatttatga	2100
agctgtaatc	gggatagtta	tactgcttgt	tcttatgatt	catttccttt	gtgcagttct	2160
tggtgtagct	tgccactttc	accagcaaag	ttcatttaaa	tcaactaggg	atatcacaag	2220
tttgtaaaaa	aaagcaggct	taaacaatgt	ctactatcta	catgagccag	ctacctgcta	2280
ctctccctct	aatggagggg	gatcaggatc	aggggctcta	cccagccttc	catagagcaa	2340
aggaccctcc	tatcttgttc	cctttcatga	tcgacagcgc	cgtcgagcac	caagggcaaa	2400
tctatggaga	tcagggcttg	aggaggcagc	aggttttggg	tgaatccaat	caacagttca	2460
atgatcacat	gatgatgggc	ggatcagatg	tcttcctcac	accgtctccg	ttccgaccaa	2520
ccatccaaag	catcggcagc	gacatgatcc	agcgatcatc	ttatgatcca	tacgatatcg	2580
agagtaaaaa	caagcagcat	gccaatggat	caaccagcaa	gtggatgtcg	acgccgcaa	2640
tgaagatgag	gatcataagg	aagggggcgg	caaccgatcc	tgagggcggg	gcggtgagaa	2700
agccaaggag	aagagcacia	gcgcaccagg	atgagagcca	gcaacaactg	cagcaagctt	2760
tgggtgtcgt	tagagtgtgc	tcggactgca	acaccaccaa	gacccccttg	tggagaagtg	2820

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

gtccttgtgg	ccccaagtcc	ctttgcaacg	cgtgtggcat	caggcaaagg	aaggcgcggc	2880
gggcgatggc	cgctgctgcc	aacggcggag	cggcggtggc	gccggcaaag	agcgtggccg	2940
cggcgccggt	gaacaataag	ccggcggcga	agaaggagaa	gagggcgggc	gacgtcgacc	3000
ggtcgctgcc	gttcaagaaa	cggtgcaaga	tggtcgatca	cgttgctgct	gccgtcgctg	3060
ccaccaagcc	cacggctgct	ggagaagtag	tggccgccgc	tccgaaggac	caagatcacg	3120
tcatcgctgt	cggtggcgag	aacgccgccg	ccacctccat	gccggcacag	aacccgatat	3180
ccaaggcggc	ggcgaccgcc	gctgccgccg	ccgcctctcc	ggcgttcttc	cacggcctcc	3240
ctcgcgacga	gatcaccgac	gccgccatgc	tgctcatgac	cctatcctgt	ggcctcgtec	3300
acagctag						3308

<210> 137
 <211> 1044
 <212> DNA
 <213> Oryza sativa

<400> 137						
atgtctacta	tctacatgag	ccagctacct	gctactctcc	ctctaattga	gggggatcag	60
gatcaggggc	tctaccagc	cttccataga	gcaaaggacc	ctcctatctt	gttccctttc	120
atgatcgaca	gcgccgtcga	gcaccaaggg	caaattctatg	gagatcaggg	cttgaggagg	180
cagcaggttt	tgggtgaatc	caatcaacag	ttcaatgatc	acatgatgat	gggcggatca	240
gatgtcttcc	tcacaccgtc	tccgttccga	ccaaccatcc	aaagcatcgg	cagtgacatg	300
atccagcgat	catcttatga	tccatacgat	atcgagagta	acaacaagca	gcatgccaat	360
ggatcaacca	gcaagtggat	gtcgacgccg	ccaatgaaga	tgaggatcat	aaggaagggg	420
gcggcaaccg	atcctgaggg	cggggcggtg	agaaagccaa	ggagaagagc	acaagcgcac	480
caggatgaga	gccagcaaca	actgcagcaa	gctttgggtg	tcgttagagt	gtgctcggac	540
tgcaacacca	ccaagacccc	cttgtggaga	agtggtcctt	gtggccccaa	gtccctttgc	600
aacgcgtgtg	gcatcaggca	aaggaaggcg	cggcgggcga	tggccgctgc	tgccaacggc	660
ggagcggcgg	tggcgccggc	aaagagcgtg	gccgcggcgc	cggtgaacaa	taagccggcg	720
gcgaagaagg	agaagagggc	ggcggacgtc	gaccggtcgc	tgccgttcaa	gaaacggtgc	780
aagatggtcg	atcacgttgc	tgctgccgtc	gctgccacca	agcccacggc	tgctggagaa	840
gtagtggccg	ccgctccgaa	ggaccaagat	cacgtcatcg	tcgtcggtgg	cgagaacgcc	900
gccgccacct	ccatgccggc	acagaacccg	atatccaagg	cggcggcggc	ctctccggcg	960
ttcttccacg	gcctccctcg	cgacgagatc	accgacgccg	ccatgctgct	catgacccta	1020
tcctgtggcc	tcgtccacag	ctag				1044

<210> 138
 <211> 347
 <212> PRT
 <213> Oryza sativa

<400> 138

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Met Ser Thr Ile Tyr Met Ser Gln Leu Pro Ala Thr Leu Pro Leu Met
1 5 10 15

Glu Gly Asp Gln Asp Gln Gly Leu Tyr Pro Ala Phe His Arg Ala Lys
20 25 30

Asp Pro Pro Ile Leu Phe Pro Phe Met Ile Asp Ser Ala Val Glu His
35 40 45

Gln Gly Gln Ile Tyr Gly Asp Gln Gly Leu Arg Arg Gln Gln Val Leu
50 55 60

Gly Glu Ser Asn Gln Gln Phe Asn Asp His Met Met Met Gly Gly Ser
65 70 75 80

Asp Val Phe Leu Thr Pro Ser Pro Phe Arg Pro Thr Ile Gln Ser Ile
85 90 95

Gly Ser Asp Met Ile Gln Arg Ser Ser Tyr Asp Pro Tyr Asp Ile Glu
100 105 110

Ser Asn Asn Lys Gln His Ala Asn Gly Ser Thr Ser Lys Trp Met Ser
115 120 125

Thr Pro Pro Met Lys Met Arg Ile Ile Arg Lys Gly Ala Ala Thr Asp
130 135 140

Pro Glu Gly Gly Ala Val Arg Lys Pro Arg Arg Arg Ala Gln Ala His
145 150 155 160

Gln Asp Glu Ser Gln Gln Gln Leu Gln Gln Ala Leu Gly Val Val Arg
165 170 175

Val Cys Ser Asp Cys Asn Thr Thr Lys Thr Pro Leu Trp Arg Ser Gly
180 185 190

Pro Cys Gly Pro Lys Ser Leu Cys Asn Ala Cys Gly Ile Arg Gln Arg
195 200 205

Lys Ala Arg Arg Ala Met Ala Ala Ala Ala Asn Gly Gly Ala Ala Val
210 215 220

Ala Pro Ala Lys Ser Val Ala Ala Ala Pro Val Asn Asn Lys Pro Ala
225 230 235 240

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

Lys Lys Arg Cys Lys Met Val Asp His Val Ala Ala Ala Val Ala Ala
260 265 270

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Thr Lys Pro Thr Ala Ala Gly Glu Val Val Ala Ala Ala Pro Lys Asp
275 280 285

Gln Asp His Val Ile Val Val Gly Gly Glu Asn Ala Ala Ala Thr Ser
290 295 300

Met Pro Ala Gln Asn Pro Ile Ser Lys Ala Ala Ala Ala Ser Pro Ala
305 310 315 320

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

Leu Met Thr Leu Ser Cys Gly Leu Val His Ser
340 345

<210> 139
<211> 1065
<212> DNA
<213> Oryza sativa

<400> 139
atgtctacta tctacatgag ccagctacct gctactctcc ctctaattgga gggggatcag 60
gatcaggggc tctaccacgc cttccataga gcaaaggacc ctcttatctt gttccctttc 120
atgatcgaca gcgccgtcga gcaccaaggg caaatctatg gagatcaggg cttgaggagg 180
cagcaggttt tgggtgaatc caatcaacag ttcaatgatc acatgatgat gggcggatca 240
gatgtcttcc tcacaccgtc tccgttccga ccaaccatcc aaagcatcgg cagcgacatg 300
atccagcgat catcttatga tccatacgat atcgagagta acaacaagca gcatgccaat 360
ggatcaacca gcaagtggat gtcgacgccg ccaatgaaga tgaggatcat aaggaagggg 420
gcggcaaccg atcctgaggg cggggcggtg agaaagccaa ggagaagagc acaagcgcac 480
caggatgaga gccagcaaca actgcagcaa gctttgggtg tcgttagagt gtgctcggac 540
tgcaacacca ccaagacccc cttgtggaga agtggtcctt gtggcccaa gtccctttgc 600
aacgcgtgtg gcatcaggca aaggaaggcg cggcggcgga tggccgctgc tgccaacggg 660
cggagcggcc ggtggcgccg gcaaagaggc gtggcccgcg cgccggtgaa caataagccg 720
gcggcgaaga aggagaagag ggcggcggac gtcgaccggt cgctgccgtt caagaaacgg 780
tgcaagatgg tcgatcacgt tgctgctgcc gtcgctgcca ccaagcccac ggctgctgga 840
gaagtagtgg ccgccgctcc gaaggaccaa gatcacgtca tcgtcgtcgg tggcgagaac 900
gccgccgcca cctccatgcc ggcacagaac ccgatatcca aggcggcggc gaccgccgct 960
gccgccgccc cctctccggc gttcttccac ggcctccctc gcgacgagat caccgacgcc 1020
gcatgctgc tcatgaccct atcctgtggc ctctgccaca gctag 1065

<210> 140
<211> 354
<212> PRT
<213> Oryza sativa

<400> 140

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Met Ser Thr Ile Tyr Met Ser Gln Leu Pro Ala Thr Leu Pro Leu Met
1 5 10 15

Glu Gly Asp Gln Asp Gln Gly Leu Tyr Pro Ala Phe His Arg Ala Lys
20 25 30

Asp Pro Pro Ile Leu Phe Pro Phe Met Ile Asp Ser Ala Val Glu His
35 40 45

Gln Gly Gln Ile Tyr Gly Asp Gln Gly Leu Arg Arg Gln Gln Val Leu
50 55 60

Gly Glu Ser Asn Gln Gln Phe Asn Asp His Met Met Met Gly Gly Ser
65 70 75 80

Asp Val Phe Leu Thr Pro Ser Pro Phe Arg Pro Thr Ile Gln Ser Ile
85 90 95

Gly Ser Asp Met Ile Gln Arg Ser Ser Tyr Asp Pro Tyr Asp Ile Glu
100 105 110

Ser Asn Asn Lys Gln His Ala Asn Gly Ser Thr Ser Lys Trp Met Ser
115 120 125

Thr Pro Pro Met Lys Met Arg Ile Ile Arg Lys Gly Ala Ala Thr Asp
130 135 140

Pro Glu Gly Gly Ala Val Arg Lys Pro Arg Arg Arg Ala Gln Ala His
145 150 155 160

Gln Asp Glu Ser Gln Gln Gln Leu Gln Gln Ala Leu Gly Val Val Arg
165 170 175

Val Cys Ser Asp Cys Asn Thr Thr Lys Thr Pro Leu Trp Arg Ser Gly
180 185 190

Pro Cys Gly Pro Lys Ser Leu Cys Asn Ala Cys Gly Ile Arg Gln Arg
195 200 205

Lys Ala Arg Arg Ala Met Ala Ala Ala Ala Asn Gly Arg Ser Gly Arg
210 215 220

Trp Arg Arg Gln Arg Gly Val Ala Ala Ala Pro Val Asn Asn Lys Pro
225 230 235 240

Ala Ala Lys Lys Glu Lys Arg Ala Ala Asp Val Asp Arg Ser Leu Pro
245 250 255

Phe Lys Lys Arg Cys Lys Met Val Asp His Val Ala Ala Ala Val Ala
260 265 270

Ala Thr Lys Pro Thr Ala Ala Gly Glu Val Val Ala Ala Ala Pro Lys
275 280 285

Asp Gln Asp His Val Ile Val Val Gly Gly Glu Asn Ala Ala Ala Thr
290 295 300

Ser Met Pro Ala Gln Asn Pro Ile Ser Lys Ala Ala Ala Thr Ala Ala
305 310 315 320

Ala Ala Ala Ala Ser Pro Ala Phe Phe His Gly Leu Pro Arg Asp Glu
325 330 335

Ile Thr Asp Ala Ala Met Leu Leu Met Thr Leu Ser Cys Gly Leu Val
340 345 350

His Ser

<210> 141
<211> 1128
<212> DNA
<213> Oryza sativa

<400> 141
atggaggggg agcaccacca tcaccaccag gatcatcacc aaggccactt ccaagccttc 60
tccctgcagc ctaaggatcc cccagtctta ttcccctttg tgatcagtag aagaagcagc 120
agcagcagcc ctagcgacag caccactcta agctatgggt cagaccatca cttgacacag 180
cagcagcagc atcagcatca agccatgctt gagcccaaaa atatgattgg aggatcatcc 240
gctggcatct ttgcgacgcc gttcccgacc gtcaagagca tccgcgacga catgatcgag 300
cggtcgcagt tcgatccata cgataccgag aagctgcagg cgagctgcgg gttagccaag 360
gtcgtcgccg gcggcaagtg gagcgcggtg ccagcggcca agatgaagat cagcaggaag 420
atgggtgagc cgtcgtccgg tgtcactggc ggggctgcga cgacgggtggc gccgaagaag 480
ccgaggagga ggccggcgca ggcgtacgag gatcacggcc atggcggcgc catgggccaa 540
gcttttggcg tgattagggt gtgctccgac tgcaacacca ccaagactcc cttgtggagg 600
agtggcccgt gcggcccaaa gtcgctttgc aacgcgtgcg gcatcaggca gaggaaggcg 660
cggcgggcca tgatggcctc cggactacca gcgtcccca acgcccggg cccaaggcg 720
gccgcacata gcggcgccgc tgcggtggcg gctgcgacgc cgaaggtgaa gaaggagaag 780
agagccgacg tcgaccggtc gtcgctgccg ttcaagaaac ggtgcaaggc cgtccaggtc 840
gaggatcatc aaacgctgcc cgccgccaca aacgcagccg ccgcagctgc catggaggag 900
acggccgagt ccgccaccgt cgccccgccc ccggcgccga cgacgagggg tgggtactctc 960
gtcgacagca tcgggctcag ctggagcaag acccatgccg ccgccaccgc ctctgcagc 1020
ttccggccgt caccggtggc tccgggcttc gcggcgccgg tgcaggacga gatcactgac 1080
gccgcatgc tgctcatgac gctgtcctgc gggcttgtcc ggagctga 1128

<210> 142
 <211> 375
 <212> PRT
 <213> Oryza sativa

<400> 142

Met Glu Gly Glu His His His His His Gln Asp His His Gln Gly His
 1 5 10 15

Phe Gln Ala Phe Ser Leu Gln Pro Lys Asp Pro Pro Val Leu Phe Pro
 20 25 30

Phe Val Ile Ser Arg Arg Ser Ser Ser Ser Ser Pro Ser Asp Ser Thr
 35 40 45

Thr Leu Ser Tyr Gly Ser Asp His His Leu Thr Gln Gln Gln Gln His
 50 55 60

Gln His Gln Ala Met Leu Glu Pro Gln Asn Met Ile Gly Gly Ser Ser
 65 70 75 80

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

Asp Met Ile Glu Arg Ser Gln Phe Asp Pro Tyr Asp Thr Glu Lys Leu
 100 105 110

Gln Ala Ser Cys Gly Leu Ala Lys Val Val Ala Gly Gly Lys Trp Ser
 115 120 125

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

Ser Ser Gly Val Thr Gly Gly Ala Ala Thr Thr Val Ala Pro Lys Lys
 145 150 155 160

Pro Arg Arg Arg Pro Ala Gln Ala Tyr Glu Asp His Gly His Gly Gly
 165 170 175

Ala Met Gly Gln Ala Phe Gly Val Ile Arg Val Cys Ser Asp Cys Asn
 180 185 190

Thr Thr Lys Thr Pro Leu Trp Arg Ser Gly Pro Cys Gly Pro Lys Ser
 195 200 205

Leu Cys Asn Ala Cys Gly Ile Arg Gln Arg Lys Ala Arg Arg Ala Met
 210 215 220

Met Ala Ser Gly Leu Pro Ala Ser Pro Asn Ala Ala Gly Pro Lys Ala
 225 230 235 240

Ala Ala His Ser Gly Ala Ala Ala Val Ala Ala Ala Gln Pro Lys Val
 245 250 255

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Lys Lys Glu Lys Arg Ala Asp Val Asp Arg Ser Ser Leu Pro Phe Lys
260 265 270

Lys Arg Cys Lys Val Val Gln Val Glu Asp His Gln Thr Leu Pro Ala
275 280 285

Ala Thr Asn Ala Ala Ala Ala Ala Met Glu Glu Thr Ala Glu Ser
290 295 300

Ala Thr Val Ala Pro Pro Pro Ala Pro Thr Thr Arg Gly Gly Thr Leu
305 310 315 320

Val Asp Ser Ile Gly Leu Ser Trp Ser Lys Thr His Ala Ala Ala Thr
325 330 335

Ala Ser Cys Ser Phe Arg Pro Ser Pro Val Ala Pro Gly Phe Ala Ala
340 345 350

Ala Val Gln Asp Glu Ile Thr Asp Ala Ala Met Leu Leu Met Thr Leu
355 360 365

Ser Cys Gly Leu Val Arg Ser
370 375

<210> 143
<211> 1119
<212> DNA
<213> Oryza sativa

<400> 143
atggaggggg agcaccacca ggatcatcac caaggccact tccaagcctt ctccctgcag 60
cctaaggatc ccccagtctt attccccctt gtgatcaata gaagaagcag cagcagcagc 120
cctagcgaca gcaccactct aagctatggt tcagaccatc acttgacaca gcagcagcag 180
catcagcatc aagccatgct tgagcccaa catatgattg gaggatcatc cgctggcatc 240
tttgcgacgc cgttcccgc cgtcaagagc atccgcgacg acatgatcga gcggctgcag 300
ttcgatccat acgataccga gaagctgcag gcgagctgcg ggtagccaa ggtcgtcgcc 360
ggcggcaagt ggagcgcggt gccagcggcc aagatgaaga tcacgaggaa gatgggtgag 420
ccgtcgtccg gtgtcactgg cggggctgcg acgacggtgg cgccgaagaa gccgaggagg 480
aggctggcgc aggcgtacga ggatcacggc catggcggcg ccatgggcca agcttttggc 540
gtgattaggg tgtgtctccga ctgcaacacc accaagactc ctttgtggag gagtggcccc 600
tgcggcccca agtcgctttg caacgcgtgc ggcatcaggc agaggaaggc gcggcgggcg 660
atgatggcct ccggactacc agcgtcccc aacgccgccg gcccgaaggc ggccgcacat 720
agcggcgccg ctgcggtggc ggctgcgcag ccgaaggtga agaaggagaa gagagccgac 780
gtcgaccggt cgtcgtgcc gttcaagaaa cggtgcaagg ccgtccaggt cgaggatcat 840
caaacgctgc ccgccccac aaacgcagcc gccgcagctg ccatggagga gacggccgag 900

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

tccgccaccg tgcggccgcc cccggcgccg acgacgaggg gttgtactct cgtcgacagc	960
atcggggtca gctggagcaa gacccatgcc gccgccaccg cctcctgcag cttccggccg	1020
tcaccggtgg ctcccggtt cgcggcgccg gtgcaggacg agatcactga cgccgccatg	1080
ctgctcatga cgctgtcctg cgggcttgtc cggagctga	1119

<210> 144
 <211> 372
 <212> PRT
 <213> Oryza sativa

<400> 144

Met Glu Gly Glu His His Gln Asp His His Gln Gly His Phe Gln Ala
 1 5 10 15

Phe Ser Leu Gln Pro Lys Asp Pro Pro Val Leu Phe Pro Phe Val Ile
 20 25 30

Asn Arg Arg Ser Ser Ser Ser Ser Pro Ser Asp Ser Thr Thr Leu Ser
 35 40 45

Tyr Gly Ser Asp His His Leu Thr Gln Gln Gln Gln His Gln His Gln
 50 55 60

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

Phe Ala Thr Pro Phe Pro Thr Val Lys Ser Ile Arg Asp Asp Met Ile
 85 90 95

Glu Arg Ser Gln Phe Asp Pro Tyr Asp Thr Glu Lys Leu Gln Ala Ser
 100 105 110

Cys Gly Leu Ala Lys Val Val Ala Gly Gly Lys Trp Ser Ala Val Pro
 115 120 125

Ala Ala Lys Met Lys Ile Thr Arg Lys Met Gly Glu Pro Ser Ser Gly
 130 135 140

Val Thr Gly Gly Ala Ala Thr Thr Val Ala Pro Lys Lys Pro Arg Arg
 145 150 155 160

Arg Leu Ala Gln Ala Tyr Glu Asp His Gly His Gly Gly Ala Met Gly
 165 170 175

Gln Ala Phe Gly Val Ile Arg Val Cys Ser Asp Cys Asn Thr Thr Lys
 180 185 190

Thr Pro Leu Trp Arg Ser Gly Pro Cys Gly Pro Lys Ser Leu Cys Asn
 195 200 205

Ala Cys Gly Ile Arg Gln Arg Lys Ala Arg Arg Ala Met Met Ala Ser
210 215 220

Gly Leu Pro Ala Ser Pro Asn Ala Ala Gly Pro Lys Ala Ala Ala His
225 230 235 240

Ser Gly Ala Ala Ala Val Ala Ala Ala Gln Pro Lys Val Lys Lys Glu
245 250 255

Lys Arg Ala Asp Val Asp Arg Ser Ser Leu Pro Phe Lys Lys Arg Cys
260 265 270

Lys Ala Val Gln Val Glu Asp His Gln Thr Leu Pro Ala Ala Thr Asn
275 280 285

Ala Ala Ala Ala Ala Ala Met Glu Glu Thr Ala Glu Ser Ala Thr Val
290 295 300

Ala Pro Pro Pro Ala Pro Thr Thr Arg Gly Cys Thr Leu Val Asp Ser
305 310 315 320

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

Ser Phe Arg Pro Ser Pro Val Ala Pro Gly Phe Ala Ala Ala Val Gln
340 345 350

Asp Glu Ile Thr Asp Ala Ala Met Leu Leu Met Thr Leu Ser Cys Gly
355 360 365

Leu Val Arg Ser
370

<210> 145
<211> 1044
<212> DNA
<213> Oryza sativa

<400> 145
atgtctacca tctacatgag tcagctctca gctgctctcc ctctcatgga gggggagcac 60
caccatcacc accaggatca tcaccaaggc cacttccaag ctttctccct gcagcctaag 120
gatccccag tcttattccc ctttgtgatc agtagaagaa gcagcagcag cagccctagc 180
gacagcacca ctctaagcta tggttcagac catcacttga cacagcagca gcagcatcag 240
catcaagcca tgcttgagcc ccaaaatatg attggaggat catccgctgg catctttgcg 300
acgccgttcc cgaccgtcaa gagcatccgc gacgacatga tcgagcggtc gcagttcgat 360
ccatacgata ccgagaagct gcaggcgagc tgcggggttag ccaaggtcgt cgccggcggc 420
aagtggagcg cggtgccagc ggccaagatg aagatcacga ggaagatggg tgagccgtcg 480
tccggtgtca ctggcggggc tgcgacgacg gtggcgccga agaagccgag gaggaggccg 540
gcgcaggcgt acgaggatca cggccatggc ggcgcatgg gccaagcttt tggcgtgatt 600

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

agggtgtgct ccgactgcaa caccaccaag actcccttgt ggaggagtgg cccgtgcggc      660
cccaagtcgc ttgcaacgc gtgcggcatc aggagagga aggcgcggcg ggcgatgatg      720
gcctccggac taccagcgtc cccaacgcc gccggcccca aggcggccgc acatagcggc      780
gccacaaacg cagccgccgc agctgccatg gaggagacgg ccgagtccgc caccgtcgcc      840
ccgcccccg cgccgacgac gaggggtggt actctcgtcg acagcatcgg gctcagctgg      900
agcaagaccc atgccgccgc caccgcctcc tgcagcttcc ggccgtcacc ggtggctccc      960
ggcttcgcgg cggcgggtgca ggacgagatc actgacgccg ccatgctgct catgacgctg    1020
tcctgcgggc ttgtccggag ctga                                           1044

```

<210> 146
 <211> 347
 <212> PRT
 <213> Oryza sativa

<400> 146

Met Ser Thr Ile Tyr Met Ser Gln Leu Ser Ala Ala Leu Pro Leu Met
 1 5 10 15

Glu Gly Glu His His His His His Gln Asp His His Gln Gly His Phe
 20 25 30

Gln Ala Phe Ser Leu Gln Pro Lys Asp Pro Pro Val Leu Phe Pro Phe
 35 40 45

Val Ile Ser Arg Arg Ser Ser Ser Ser Pro Ser Asp Ser Thr Thr
 50 55 60

Leu Ser Tyr Gly Ser Asp His His Leu Thr Gln Gln Gln Gln His Gln
 65 70 75 80

His Gln Ala Met Leu Glu Pro Gln Asn Met Ile Gly Gly Ser Ser Ala
 85 90 95

Gly Ile Phe Ala Thr Pro Phe Pro Thr Val Lys Ser Ile Arg Asp Asp
 100 105 110

Met Ile Glu Arg Ser Gln Phe Asp Pro Tyr Asp Thr Glu Lys Leu Gln
 115 120 125

Ala Ser Cys Gly Leu Ala Lys Val Val Ala Gly Gly Lys Trp Ser Ala
 130 135 140

Val Pro Ala Ala Lys Met Lys Ile Thr Arg Lys Met Gly Glu Pro Ser
 145 150 155 160

Ser Gly Val Thr Gly Gly Ala Ala Thr Thr Val Ala Pro Lys Lys Pro
 165 170 175

Arg Arg Arg Pro Ala Gln Ala Tyr Glu Asp His Gly His Gly Gly Ala
180 185 190

Met Gly Gln Ala Phe Gly Val Ile Arg Val Cys Ser Asp Cys Asn Thr
195 200 205

Thr Lys Thr Pro Leu Trp Arg Ser Gly Pro Cys Gly Pro Lys Ser Leu
210 215 220

Cys Asn Ala Cys Gly Ile Arg Gln Arg Lys Ala Arg Arg Ala Met Met
225 230 235 240

Ala Ser Gly Leu Pro Ala Ser Pro Asn Ala Ala Gly Pro Lys Ala Ala
245 250 255

Ala His Ser Gly Ala Thr Asn Ala Ala Ala Ala Ala Met Glu Glu
260 265 270

Thr Ala Glu Ser Ala Thr Val Ala Pro Pro Pro Ala Pro Thr Thr Arg
275 280 285

Gly Gly Thr Leu Val Asp Ser Ile Gly Leu Ser Trp Ser Lys Thr His
290 295 300

Ala Ala Ala Thr Ala Ser Cys Ser Phe Arg Pro Ser Pro Val Ala Pro
305 310 315 320

Gly Phe Ala Ala Ala Val Gln Asp Glu Ile Thr Asp Ala Ala Met Leu
325 330 335

Leu Met Thr Leu Ser Cys Gly Leu Val Arg Ser
340 345

<210> 147
<211> 363
<212> DNA
<213> Arabidopsis thaliana

<400> 147
atggatccaa ggaagctact atcttgttca tcctcttacg tgtcagtgag aatgaaagaa 60
gagaagggga caattaggtg ttgcagtgag tgtaagacca ccaagacacc aatgtggaga 120
ggtggaccaa ctggctctaa gtcactttgc aatgcatgtg gaattagaca cagaaaacag 180
agacgatcag agttattggg tattcatatt attcgcagcc aaaaagctt agcctccaag 240
aagataaacc tattatcatc atcacacggt ggcgtggcgg tgaagaaacg aaggagtcta 300
aaggaggaag aacaagctgc tttgtgtcta ttgttattgt cttgtagctc tgttttggcc 360
tga 363

<210> 148
<211> 120
<212> PRT
<213> Arabidopsis thaliana

<400> 148

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

<210> 149

<211> 1653

<212> DNA

<213> Arabidopsis thaliana

<400> 149

atggagcgat ctcgctcaga aacgccatcg tctcgctcac gattgaagct gtgcttcata 60
aactcgccgc catcatcgat attcacgggg tccaagatcg aagctgagga tggttctccg 120
cttgtgatcg agctcgtgga cgccaccaca aacactctag ttagtacggg accgttctcg 180
tcttctcggg tcgagctcgt gccgctgaac gctgatttca cggaagaaag ctggaccggt 240
gagggattta atcggaatat tctcacgcaa cgtgaaggga aacgtccggt gtcactgga 300
gacctaacgg tgatgcttaa aaacggtggt ggagttataa ccggagatat agctttctcg 360
gataactcga gctggactag gagtcggaag ttccggttag gtgctaagtt gaccggagat 420
ggagccgtgg aggcgagaag tgaagctttt ggatgtagag accaacgagg agaatgggtc 480
tcaaagaaaa catggaacac aattgtatca catgccatgg attgcgtttt ggacgaaaca 540
gagtgttaca ttacaatgc aaacactccg ggcgtaacac ttctcttcaa ctctgtttat 600
gagttgataa gagtgtcatt caatggcaac gatatccaaa accttgatca gccaatctta 660
gaccaattaa aggccgaagc ttatcaaaac cttaacgcga ttacagcggg taacgatagg 720
acctttgtgg gtcatccaca aaggctccta cagtgcccg c aagatcctgg atttgtcgtta 780
acatgttctg gatcgagca catcgacttt caaggaagtt tggatccatc aagctcttcg 840

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

atggctcttt gccacaaagc ttcaagctca acggtccacc ctgatgtcct gatgagtttt 900
gataactcat caaccgcgag gtttcatatc gacaaaaagt tcttaccgac tttcggaac 960
agcttcaaag taagtgaact cgatcaagta cacggaaaat cacaactgt tgtgacaaaa 1020
ggttgtatag agaataacga ggaggatgag aacgcgtttt cttatcatca ccatgatgac 1080
atgacctcaa gctggtcacc tggtagcac caagccgttg aaacgatgtt tcttaccgtg 1140
tctgagacgg aagaagctgg aatgttcgat gttcattttg caaacgttaa tttgggatct 1200
ccaagagcca ggtggtgtaa ggttaaggca gctttcaagg ttagggcagc ttttaaggaa 1260
gtccggagac acacaactgc cagaaatccg aggggaaggct tgaagctact atcttgttca 1320
tcctcttacg tgtcagttag aatgaaagaa gagaagggga caattagggtg ttgcagttag 1380
tgtaagacca ccaagacacc aatgtggaga ggtggaccaa ctggtcctaa gtcactttgc 1440
aatgcatgtg gaattagaca cagaaaacag agacgatcag agttattggg tattcatatt 1500
attcgagcc aaaaagctt agcctccaag aagataaacc tattatcatc atcacacggt 1560
ggcgtggcgg tgaagaaacg aaggagtcta aaggaggaag aacaagctgc tttgtgtcta 1620
ttgtattgt cttgtagctc tgttttggcc taa 1653

```

<210> 150
 <211> 550
 <212> PRT
 <213> Arabidopsis thaliana

<400> 150

Met Glu Arg Ser Arg Ser Glu Thr Pro Ser Ser Arg Ser Arg Leu Lys
 1 5 10 15

Leu Cys Phe Ile Asn Ser Pro Pro Ser Ser Ile Phe Thr Gly Ser Lys
 20 25 30

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

Thr Thr Asn Thr Leu Val Ser Thr Gly Pro Phe Ser Ser Ser Arg Val
 50 55 60

Glu Leu Val Pro Leu Asn Ala Asp Phe Thr Glu Glu Ser Trp Thr Val
 65 70 75 80

Glu Gly Phe Asn Arg Asn Ile Leu Thr Gln Arg Glu Gly Lys Arg Pro
 85 90 95

Leu Leu Thr Gly Asp Leu Thr Val Met Leu Lys Asn Gly Val Gly Val
 100 105 110

Ile Thr Gly Asp Ile Ala Phe Ser Asp Asn Ser Ser Trp Thr Arg Ser
 115 120 125

Arg Lys Phe Arg Leu Gly Ala Lys Leu Thr Gly Asp Gly Ala Val Glu

130

135

140

Ala Arg Ser Glu Ala Phe Gly Cys Arg Asp Gln Arg Gly Glu Trp Val
145 150 155 160

Ser Lys Lys Thr Trp Asn Thr Ile Val Ser His Ala Met Asp Cys Val
165 170 175

Leu Asp Glu Thr Glu Cys Tyr Ile Tyr Asn Ala Asn Thr Pro Gly Val
180 185 190

Thr Leu Leu Phe Asn Ser Val Tyr Glu Leu Ile Arg Val Ser Phe Asn
195 200 205

Gly Asn Asp Ile Gln Asn Leu Asp Gln Pro Ile Leu Asp Gln Leu Lys
210 215 220

Ala Glu Ala Tyr Gln Asn Leu Asn Arg Ile Thr Ala Val Asn Asp Arg
225 230 235 240

Thr Phe Val Gly His Pro Gln Arg Ser Leu Gln Cys Pro Gln Asp Pro
245 250 255

Gly Phe Val Val Thr Cys Ser Gly Ser Gln His Ile Asp Phe Gln Gly
260 265 270

Ser Leu Asp Pro Ser Ser Ser Ser Met Ala Leu Cys His Lys Ala Ser
275 280 285

Ser Ser Thr Val His Pro Asp Val Leu Met Ser Phe Asp Asn Ser Ser
290 295 300

Thr Ala Arg Phe His Ile Asp Lys Lys Phe Leu Pro Thr Phe Gly Asn
305 310 315 320

Ser Phe Lys Val Ser Glu Leu Asp Gln Val His Gly Lys Ser Gln Thr
325 330 335

Val Val Thr Lys Gly Cys Ile Glu Asn Asn Glu Glu Asp Glu Asn Ala
340 345 350

Phe Ser Tyr His His His Asp Asp Met Thr Ser Ser Trp Ser Pro Gly
355 360 365

Thr His Gln Ala Val Glu Thr Met Phe Leu Thr Val Ser Glu Thr Glu
370 375 380

Glu Ala Gly Met Phe Asp Val His Phe Ala Asn Val Asn Leu Gly Ser
385 390 395 400

Pro Arg Ala Arg Trp Cys Lys Val Lys Ala Ala Phe Lys Val Arg Ala
405 410 415

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Ala Phe Lys Glu Val Arg Arg His Thr Thr Ala Arg Asn Pro Arg Glu
420 425 430

Gly Leu Lys Leu Leu Ser Cys Ser Ser Ser Tyr Val Ser Val Arg Met
435 440 445

Lys Glu Glu Lys Gly Thr Ile Arg Cys Cys Ser Glu Cys Lys Thr Thr
450 455 460

Lys Thr Pro Met Trp Arg Gly Gly Pro Thr Gly Pro Lys Ser Leu Cys
465 470 475 480

Asn Ala Cys Gly Ile Arg His Arg Lys Gln Arg Arg Ser Glu Leu Leu
485 490 495

Gly Ile His Ile Ile Arg Ser His Lys Ser Leu Ala Ser Lys Lys Ile
500 505 510

Asn Leu Leu Ser Ser Ser His Gly Gly Val Ala Val Lys Lys Arg Arg
515 520 525

Ser Leu Lys Glu Glu Glu Gln Ala Ala Leu Cys Leu Leu Leu Leu Ser
530 535 540

Cys Ser Ser Val Leu Ala
545 550

<210> 151
<211> 363
<212> DNA
<213> Arabidopsis thaliana

<400> 151
atggatccaa ggaagctact atcttgttca tcctcttacg tgtcagtgag aatgaaagaa 60
gagaagggga caattagggtg ttgcagtgag tgtaagacca ccaagacacc aatgtggaga 120
ggtggaccaa ctggtcctaa gtcactttgc aatgcatgtg gaattagaca cagaaaacag 180
agacgatcag agttattggg tattcatatt attcgcagcc acaaaagctt agcctccaag 240
aagataaacc tattatcatc atcacacggt ggcgtggcgg tgaagaaacg aaggagtcta 300
aaggaggaag aacaagctgc tttgtgtcta ttgttattgt cttgtagctc tgttttggcc 360
gga 363

<210> 152
<211> 121
<212> PRT
<213> Arabidopsis thaliana

<400> 152
Met Asp Pro Arg Lys Leu Leu Ser Cys Ser Ser Ser Tyr Val Ser Val
1 5 10 15

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Arg Met Lys Glu Glu Lys Gly Thr Ile Arg Cys Cys Ser Glu Cys Lys
20 25 30

Thr Thr Lys Thr Pro Met Trp Arg Gly Gly Pro Thr Gly Pro Lys Ser
35 40 45

Leu Cys Asn Ala Cys Gly Ile Arg His Arg Lys Gln Arg Arg Ser Glu
50 55 60

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

Lys Ile Asn Leu Leu Ser Ser Ser His Gly Gly Val Ala Val Lys Lys
85 90 95

Arg Arg Ser Leu Lys Glu Glu Glu Gln Ala Ala Leu Cys Leu Leu Leu
100 105 110

Leu Ser Cys Ser Ser Val Leu Ala Gly
115 120

<210> 153
<211> 363
<212> DNA
<213> Arabidopsis thaliana

<400> 153
atggatccaa ggaagctact atcttgttca tcctcttacg tgtcaatgag aatgaaagaa 60
gagaagggga caattaggtg ttgcagtgag tgtaagacca ccaagacacc aatgtggaga 120
ggtggaccaa ctggtcctaa gtcactttgc aatgcatgtg gaattagaca cagaaaacag 180
agacgatcag agttattggg tattcatatt attcgcagcc acaaaagctt agcctccaag 240
aagataaacc tattatcatc atcacacggt ggcgtggcgg tgaagaaacg aaggagtcta 300
aaggaggaag aacaagctgc tttgtgtcta ttgttattgt cttgtagctc tgttttggcc 360
taa 363

<210> 154
<211> 120
<212> PRT
<213> Arabidopsis thaliana

<400> 154
Met Asp Pro Arg Lys Leu Leu Ser Cys Ser Ser Ser Tyr Val Ser Met
1 5 10 15

Arg Met Lys Glu Glu Lys Gly Thr Ile Arg Cys Cys Ser Glu Cys Lys
20 25 30

Thr Thr Lys Thr Pro Met Trp Arg Gly Gly Pro Thr Gly Pro Lys Ser
35 40 45

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Leu Cys Asn Ala Cys Gly Ile Arg His Arg Lys Gln Arg Arg Ser Glu
50 55 60

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

Lys Ile Asn Leu Leu Ser Ser Ser His Gly Gly Val Ala Val Lys Lys
85 90 95

Arg Arg Ser Leu Lys Glu Glu Glu Gln Ala Ala Leu Cys Leu Leu Leu
100 105 110

Leu Ser Cys Ser Ser Val Leu Ala
115 120

<210> 155
<211> 1197
<212> DNA
<213> Arabidopsis thaliana

<400> 155
atggattcaa attttcatta ctcgatagat cttaacgaag atcaaaacca tcacgaacaa 60
ccctttttct atcctcttgg atcctcttcc tcgcttcatt atcatcatca tcattcatcat 120
catcaagtcc cttctaattc ttcatcttct tcttcgtcca ttcatcgct ctctctttac 180
ctccctttct tgatcaactc tcaagaagat caacatgttg cctacaacaa cacttatcac 240
gctgatcatc tccatctttc tcaaccctc aaggccaaga tgtttgtggc taacggtgga 300
tcattcagcat gcatcacat ggtgccaaag aaggagacaa gactgaaact aacgataagg 360
aaaaaagatc acgaagacca accccatcct cttcatcaaa acccgacaaa acccgattca 420
gactccgaca agtggttgat gtcccaaag atgcggttga tcaagaaaac aatcaccaac 480
aataaacagc tcattgatca gactaataat aataatcata aagaaagtga tctactacct 540
ttgaatcata agactaattt cgacgaggat caccatgaag atcttaattt caagaacgtc 600
ttgaccagga agaccacggc cgcgaccacc gagaatcgct acaatacaat caacgagaac 660
ggttatagta ataacaatgg cgtgattagg gtttgttcgg attgtaacac caccaagact 720
cctctttggc gaagtggacc tcgaggtccc aagtctcttt gtaacgcatg tgggtatacgg 780
caaagaaagg caaggcgagc cgctatggcc gcggccgctg cagccggcga ccaagaggtg 840
gcggtagcgc cccgagtgc acaattaccg ctgaaaaaga agttgcaaaa taaaaaaaag 900
agatcaaacg gaggggaaaa atacaatcac tctcctcaa tgggtggcaa ggccaaaaag 960
tgcaagatca aagaggaaga ggagaaggaa atggaagcgg aaacggttgc cggagattca 1020
gagatcagca aatctacaac ttcttctaatt tcttcgattt cgtcaaacaa attttgtttc 1080
gatgatttga caataatgtt gagcaaaagc tcagcttatt aacaagtgtt cccacaagat 1140
gagaaggagg ctgctgtttt gctcatggct ctgtcgtatg gaatggttca cggttga 1197

<210> 156
<211> 398

<212> PRT

<213> Arabidopsis thaliana

<400> 156

Met Asp Ser Asn Phe His Tyr Ser Ile Asp Leu Asn Glu Asp Gln Asn
 1 5 10 15

His His Glu Gln Pro Phe Phe Tyr Pro Leu Gly Ser Ser Ser Ser Leu
 20 25 30

His His His His His His His His Gln Val Pro Ser Asn Ser Ser
 35 40 45

Ser Ser Ser Ser Ser Ile Ser Ser Leu Ser Ser Tyr Leu Pro Phe Leu
 50 55 60

Ile Asn Ser Gln Glu Asp Gln His Val Ala Tyr Asn Asn Thr Tyr His
 65 70 75 80

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

Ala Asn Gly Gly Ser Ser Ala Cys Asp His Met Val Pro Lys Lys Glu
 100 105 110

Thr Arg Leu Lys Leu Thr Ile Arg Lys Lys Asp His Glu Asp Gln Pro
 115 120 125

His Pro Leu His Gln Asn Pro Thr Lys Pro Asp Ser Asp Ser Asp Lys
 130 135 140

Trp Leu Met Ser Pro Lys Met Arg Leu Ile Lys Lys Thr Ile Thr Asn
 145 150 155 160

Asn Lys Gln Leu Ile Asp Gln Thr Asn Asn Asn His Lys Glu Ser
 165 170 175

Asp His Tyr Pro Leu Asn His Lys Thr Asn Phe Asp Glu Asp His His
 180 185 190

Glu Asp Leu Asn Phe Lys Asn Val Leu Thr Arg Lys Thr Thr Ala Ala
 195 200 205

Thr Thr Glu Asn Arg Tyr Asn Thr Ile Asn Glu Asn Gly Tyr Ser Asn
 210 215 220

Asn Asn Gly Val Ile Arg Val Cys Ser Asp Cys Asn Thr Thr Lys Thr
 225 230 235 240

Pro Leu Trp Arg Ser Gly Pro Arg Gly Pro Lys Ser Leu Cys Asn Ala
 245 250 255

Cys Gly Ile Arg Gln Arg Lys Ala Arg Arg Ala Ala Met Ala Ala Ala
260 265 270

Ala Ala Ala Gly Asp Gln Glu Val Ala Val Ala Pro Arg Val Gln Gln
275 280 285

Leu Pro Leu Lys Lys Lys Leu Gln Asn Lys Lys Lys Arg Ser Asn Gly
290 295 300

Gly Glu Lys Tyr Asn His Ser Pro Pro Met Val Ala Lys Ala Lys Lys
305 310 315 320

Cys Lys Ile Lys Glu Glu Glu Lys Glu Met Glu Ala Glu Thr Val
325 330 335

Ala Gly Asp Ser Glu Ile Ser Lys Ser Thr Thr Ser Ser Asn Ser Ser
340 345 350

Ile Ser Ser Asn Lys Phe Cys Phe Asp Asp Leu Thr Ile Met Leu Ser
355 360 365

Lys Ser Ser Ala Tyr Gln Gln Val Phe Pro Gln Asp Glu Lys Glu Ala
370 375 380

Ala Val Leu Leu Met Ala Leu Ser Tyr Gly Met Val His Gly
385 390 395

<210> 157
<211> 1197
<212> DNA
<213> Arabidopsis thaliana

<400> 157
atggattcaa attttcatta ctcgatagat cttaacgaag atcaaaacca tcacgaacaa 60
ccctttttct atcctcttgg atcctcttcc tcgcttcatt atcatcatca tcatcatcat 120
catcaagtcc cttctaattc ttcatcttct tcttcgtcca tttcatcgct ctctctttac 180
ctccctttct tgatcaactc tcaagaagat caacatgttg cctacaacaa cacttatcac 240
gctgatcatc tccatctttc tcaaccctc aaggccaaga tgtttgtggc taacggtgga 300
tcatcagcat gcgatcacat ggtgccaaag aaggagacaa gactgaaact aacgataagg 360
aaaaaagatc acgaagacca acccctcct ctcatcaaa acccgacaaa acccgattca 420
gactccgaca agtggttgat gtcccaaag atgcggttga tcaagaaaac aataaccaac 480
aataaacagc tcattgatca gactaataat aataatcata aagaaagtga tctactacct 540
ttgaatcata agactaattt cgacaggat caccatgaag atcttaattt caagaacgtc 600
ttgaccagga agaccacggc cgcgaccacc gagaatcgct acaatacaat caacgagaac 660
ggttatagta ataacaatgg cgtgattagg gtttgttcgg attgtaacac caccaagact 720
cctctttggc gaagtggacc tcgaggtccc aagtctcttt gtaacgcatg tgggtatacgg 780
caaagaaagg caaggcgagc cgctatggcc gcggccgctg cagccggcga ccaagagggtg 840

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```
gcggtagcgc cccgagtgc acaattaccg ctgaaaaaga atttgcaaaa taaaaaaaag      900
agatcaaacg gaggggaaaa atacaatcac tctcctccaa tgggtggccaa ggccaaaaag      960
tgcaagatca aagaggaaga ggagaaggaa atggaagcgg aaacggttgc cggagattca     1020
gagatcagca aatctacaac ttcttctaata tcttcgattt cgtcaaacia attttgcttc     1080
gatgatttga caataatggt gagcaaaagc tcagcttatc aacaagtgtt cccacaagat     1140
gagaaggagg ctgctgtttt gctcatggct ctgtcgtatg gaatggttca cggttga       1197
```

<210> 158
 <211> 398
 <212> PRT
 <213> Arabidopsis thaliana

<400> 158

Met Asp Ser Asn Phe His Tyr Ser Ile Asp Leu Asn Glu Asp Gln Asn
 1 5 10 15

His His Glu Gln Pro Phe Phe Tyr Pro Leu Gly Ser Ser Ser Ser Leu
 20 25 30

His His His His His His His His Gln Val Pro Ser Asn Ser Ser
 35 40 45

Ser Ser Ser Ser Ser Ile Ser Ser Leu Ser Ser Tyr Leu Pro Phe Leu
 50 55 60

Ile Asn Ser Gln Glu Asp Gln His Val Ala Tyr Asn Asn Thr Tyr His
 65 70 75 80

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

Ala Asn Gly Gly Ser Ser Ala Cys Asp His Met Val Pro Lys Lys Glu
 100 105 110

Thr Arg Leu Lys Leu Thr Ile Arg Lys Lys Asp His Glu Asp Gln Pro
 115 120 125

His Pro Leu His Gln Asn Pro Thr Lys Pro Asp Ser Asp Ser Asp Lys
 130 135 140

Trp Leu Met Ser Pro Lys Met Arg Leu Ile Lys Lys Thr Ile Thr Asn
 145 150 155 160

Asn Lys Gln Leu Ile Asp Gln Thr Asn Asn Asn Asn His Lys Glu Ser
 165 170 175

Asp His Tyr Pro Leu Asn His Lys Thr Asn Phe Asp Glu Asp His His
 180 185 190

Glu Asp Leu Asn Phe Lys Asn Val Leu Thr Arg Lys Thr Thr Ala Ala
195 200 205

Thr Thr Glu Asn Arg Tyr Asn Thr Ile Asn Glu Asn Gly Tyr Ser Asn
210 215 220

Asn Asn Gly Val Ile Arg Val Cys Ser Asp Cys Asn Thr Thr Lys Thr
225 230 235 240

Pro Leu Trp Arg Ser Gly Pro Arg Gly Pro Lys Ser Leu Cys Asn Ala
245 250 255

Cys Gly Ile Arg Gln Arg Lys Ala Arg Arg Ala Ala Met Ala Ala Ala
260 265 270

Ala Ala Ala Gly Asp Gln Glu Val Ala Val Ala Pro Arg Val Gln Gln
275 280 285

Leu Pro Leu Lys Lys Asn Leu Gln Asn Lys Lys Lys Arg Ser Asn Gly
290 295 300

Gly Glu Lys Tyr Asn His Ser Pro Pro Met Val Ala Lys Ala Lys Lys
305 310 315 320

Cys Lys Ile Lys Glu Glu Glu Glu Lys Glu Met Glu Ala Glu Thr Val
325 330 335

Ala Gly Asp Ser Glu Ile Ser Lys Ser Thr Thr Ser Ser Asn Ser Ser
340 345 350

Ile Ser Ser Asn Lys Phe Cys Phe Asp Asp Leu Thr Ile Met Leu Ser
355 360 365

Lys Ser Ser Ala Tyr Gln Gln Val Phe Pro Gln Asp Glu Lys Glu Ala
370 375 380

Ala Val Leu Leu Met Ala Leu Ser Tyr Gly Met Val His Gly
385 390 395

<210> 159

<211> 1059

<212> DNA

<213> Arabidopsis thaliana

<400> 159

atgggttcca attttcatta cacaatagat ctcaatgaag atcaaaacca tcagcctttt 60

ttcgcttctc ttggatcctc ttttcatcat catctacaac aacaacaaca acaacaacaa 120

cattttcatc accaagcttc ttctaattccc tcttctttga tgtcaccgtc tctttcctac 180

tttcctttct tgataaactc tcgccaagat caagtatatg ttgggtacaa caataacact 240

tttcatgatg ttcttgatac ccatatctcc caacctctcg agaccaagaa ctttgtatct 300

gatggtggtt catcatcaag tgatcaaagt gtgcccaaga aggagacacg actaaaattg 360

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

acgataaaga agaaagataa tcatcaagac caaaccgatc ttcctcaatc cccaataaaa      420
gacatgacag gaactaactc gctcaagtgg atatcttcga aggtgagatt aatgaagaag      480
aaaaaggcga ttattaccac cagcgacagc agcaaacaac acactaataa cgaccaatcc      540
tcaaacctaa gcaattcgga aagacagaat ggttataaca acgattgcgt gattaggatt      600
tgctccgatt gtaacacaac caagactcct ctttggagaa gtggtccgag aggtcccaag      660
tctctttgta acgcttgtgg aataaggcaa aggaaggcca ggcggggccgc tatggccacg      720
gcaaccgcaa ccgcagtctc tggcgtatcc ccaccggtca tgaagaagaa gatgcaaaac      780
aagaacaaga tatcaaatgg agtttataaa atcttatctc ctttgcccct aaaggtaaac      840
acgtgtaaga gaatgatcac actagaggag accgcattag ccgaggattt ggagaccag      900
agcaactcca cgatgttatc atcttcagac aatatctatt tcgatgatct agcattactg      960
ttgagcaaaa gttcagctta tcagcaagtt ttccctcaag atgagaagga ggctgccatt     1020
ttactaatgg ctctatcgca cggaatgggt caccgggtga                          1059

```

<210> 160
 <211> 352
 <212> PRT
 <213> Arabidopsis thaliana

<400> 160

Met Gly Ser Asn Phe His Tyr Thr Ile Asp Leu Asn Glu Asp Gln Asn
 1 5 10 15

His Gln Pro Phe Phe Ala Ser Leu Gly Ser Ser Leu His His His Leu
 20 25 30

Gln Gln Gln Gln Gln Gln Gln Gln His Phe His His Gln Ala Ser Ser
 35 40 45

Asn Pro Ser Ser Leu Met Ser Pro Ser Leu Ser Tyr Phe Pro Phe Leu
 50 55 60

Ile Asn Ser Arg Gln Asp Gln Val Tyr Val Gly Tyr Asn Asn Asn Thr
 65 70 75 80

Phe His Asp Val Leu Asp Thr His Ile Ser Gln Pro Leu Glu Thr Lys
 85 90 95

Asn Phe Val Ser Asp Gly Gly Ser Ser Ser Ser Asp Gln Met Val Pro
 100 105 110

Lys Lys Glu Thr Arg Leu Lys Leu Thr Ile Lys Lys Lys Asp Asn His
 115 120 125

Gln Asp Gln Thr Asp Leu Pro Gln Ser Pro Ile Lys Asp Met Thr Gly
 130 135 140

Thr Asn Ser Leu Lys Trp Ile Ser Ser Lys Val Arg Leu Met Lys Lys
145 150 155 160

Lys Lys Ala Ile Ile Thr Thr Ser Asp Ser Ser Lys Gln His Thr Asn
165 170 175

Asn Asp Gln Ser Ser Asn Leu Ser Asn Ser Glu Arg Gln Asn Gly Tyr
180 185 190

Asn Asn Asp Cys Val Ile Arg Ile Cys Ser Asp Cys Asn Thr Thr Lys
195 200 205

Thr Pro Leu Trp Arg Ser Gly Pro Arg Gly Pro Lys Ser Leu Cys Asn
210 215 220

Ala Cys Gly Ile Arg Gln Arg Lys Ala Arg Arg Ala Ala Met Ala Thr
225 230 235 240

Ala Thr Ala Thr Ala Val Ser Gly Val Ser Pro Pro Val Met Lys Lys
245 250 255

Lys Met Gln Asn Lys Asn Lys Ile Ser Asn Gly Val Tyr Lys Ile Leu
260 265 270

Ser Pro Leu Pro Leu Lys Val Asn Thr Cys Lys Arg Met Ile Thr Leu
275 280 285

Glu Glu Thr Ala Leu Ala Glu Asp Leu Glu Thr Gln Ser Asn Ser Thr
290 295 300

Met Leu Ser Ser Ser Asp Asn Ile Tyr Phe Asp Asp Leu Ala Leu Leu
305 310 315 320

Leu Ser Lys Ser Ser Ala Tyr Gln Gln Val Phe Pro Gln Asp Glu Lys
325 330 335

Glu Ala Ala Ile Leu Leu Met Ala Leu Ser His Gly Met Val His Gly
340 345 350

<210> 161

<211> 636

<212> DNA

<213> Vitis vinifera

<400> 161

atggcggatg acaataagag cagccacaaa ttrtcggttt ttaagaagga agaaggagat 60

gaaggtaata aaagtactga gaaatggatg tcttcaaaga tgaggctgat gagaaaaatg 120

atgaactcgg attgcactac agcgaaaatc gagcagaagg ttgaagatca tcagcagtgg 180

gacaatatta aygagwtcaa ctcttccaac aatactagta atatcccaat tagagtctgc 240

agtgattgta acacaaccaa aaccctctt tggaggagy gtcctagagg tccaagtca 300

ctttgcaatg cctgtggaat taggcaaagg aaggcgagac gagccatggc agcagcggca 360

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

gcagcagcag cgaatggcac agccgttggg accgagatat cgcctatgaa gatgaagctg 420
 cccaacaagg aaaagaagat gcatacaagc aatgtagggc aacagaagaa gctctgcaag 480
 cccccttgtc ctctccac cgagaagaag ctttgcttcg aagatttcac ttcgagtatt 540
 tgcaagaact caggtttttag acgagtgttc cctcgggatg aagaagaagc cgcgatcctc 600
 ctaatggcct tatcttgtga ccttgtttac agttga 636

<210> 162
 <211> 211
 <212> PRT
 <213> Vitis vinifera

<220>
 <221> misc_feature
 <222> (66)..(66)
 <223> Xaa can be any naturally occurring amino acid
 <400> 162

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

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

Asp Glu Glu Glu Ala Ala Ile Leu Leu Met Ala Leu Ser Cys Asp Leu
195 200 205

Val Tyr Ser
210

<210> 163
<211> 546
<212> DNA
<213> Vitis vinifera

<400> 163
atgatctcgg atcaaactgg tgcccaaaaa ccaagcaaca ctgcactcaa ttttggagat 60
cacaagcagc aatccttgcc ttctgaaacc gattacaata gcatcaattc ctctaataatc 120
aacagcaaca acacaattag ggtttgtgca gattgtaaca caactaagac ccctctgtgg 180
aggagtggcc caagaggccc taagtctctc tgcaacgcct gcggaatcag gcaaaggaag 240
gctagacggg ccatggctgc tgctgctgca actgctaattg gcacaattct tccaaccaac 300
acagcaccca caaagaccaa ggccaagcac aaagacaaga agtcgagcaa tggatcatgtt 360
tcacactaca agaaacggtg caaactggct gcggcccat cttgtgaaac aaagaagctt 420
tgtttcgagg acttcacat aagcttgagt aagaattccg ctttccaccg agttttcctc 480
caagacgaga tcaaggaagc ggcgatcctg ctaatggctc tatcttgcg cctcgtccat 540
ggttga 546

<210> 164
<211> 181
<212> PRT
<213> Vitis vinifera

<400> 164
Met Ile Ser Asp Gln Thr Gly Ala Gln Lys Pro Ser Asn Thr Ala Leu
1 5 10 15

Asn Phe Gly Asp His Lys Gln Gln Ser Leu Pro Ser Glu Thr Asp Tyr
20 25 30

Asn Ser Ile Asn Ser Ser Asn Ile Asn Ser Asn Asn Thr Ile Arg Val
35 40 45

Cys Ala Asp Cys Asn Thr Thr Lys Thr Pro Leu Trp Arg Ser Gly Pro
50 55 60

Arg Gly Pro Lys Ser Leu Cys Asn Ala Cys Gly Ile Arg Gln Arg Lys
65 70 75 80

Ala Arg Arg Ala Met Ala Ala Ala Ala Ala Thr Ala Asn Gly Thr Ile
85 90 95

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Leu Pro Thr Asn Thr Ala Pro Thr Lys Thr Lys Ala Lys His Lys Asp
100 105 110

Lys Lys Ser Ser Asn Gly His Val Ser His Tyr Lys Lys Arg Cys Lys
115 120 125

Leu Ala Ala Ala Pro Ser Cys Glu Thr Lys Lys Leu Cys Phe Glu Asp
130 135 140

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

Gln Asp Glu Ile Lys Glu Ala Ala Ile Leu Leu Met Ala Leu Ser Cys
165 170 175

Gly Leu Val His Gly
180

<210> 165
<211> 420
<212> DNA
<213> Arabidopsis thaliana

<400> 165
atgctagatc acagtgaata ggtcttattg gttgattcag aaaccatgaa aacaagagct 60
gaagatatga tcgaacagaa caacactagt gttaacgaca agaagaagac ttgtgctgat 120
tgtggaacca gtaaaactcc tctttggcgt ggtgggtcctg ttggtccaaa gtcgtttgtgt 180
aacgcgtgtg ggatcagaaa cagaaagaag agaagaggag gaacagaaga taataagaaa 240
ttaaagaaat cgagttcttg cggcggaac cgtaaatttg gtgaatcggt aaaacagagt 300
ttgatggatt tggggataag gaagagatca acggtggaga agcaacgaca gaagcttggg 360
gaagaagaac aagccgctgt gttactcatg gctctttctt atggctctgt ttacgcttag 420

<210> 166
<211> 139
<212> PRT
<213> Arabidopsis thaliana

<400> 166
Met Leu Asp His Ser Glu Lys Val Leu Leu Val Asp Ser Glu Thr Met
1 5 10 15

Lys Thr Arg Ala Glu Asp Met Ile Glu Gln Asn Asn Thr Ser Val Asn
20 25 30

Asp Lys Lys Lys Thr Cys Ala Asp Cys Gly Thr Ser Lys Thr Pro Leu
35 40 45

Trp Arg Gly Gly Pro Val Gly Pro Lys Ser Leu Cys Asn Ala Cys Gly
50 55 60

Ile Arg Asn Arg Lys Lys Arg Arg Gly Gly Thr Glu Asp Asn Lys Lys
65 70 75 80

Leu Lys Lys Ser Ser Ser Gly Gly Gly Asn Arg Lys Phe Gly Glu Ser
85 90 95

Leu Lys Gln Ser Leu Met Asp Leu Gly Ile Arg Lys Arg Ser Thr Val
100 105 110

Glu Lys Gln Arg Gln Lys Leu Gly Glu Glu Glu Gln Ala Ala Val Leu
115 120 125

Leu Met Ala Leu Ser Tyr Gly Ser Val Tyr Ala
130 135

<210> 167
<211> 363
<212> DNA
<213> Vitis vinifera

<400> 167
atgaacaaca aaaaccaga tgctgtttcg tcggctgaga gccaggtaa cgagccgaag 60
aagacctgcg ctgattgtgg caccacaaa acccctctct ggagaggcgg tccagctggg 120
cctaagtctc tgtgcaatgc atgtggtatc agaagcagga agaagagaag agccttcctg 180
ggaagcagca accactccca taacaatggt ggcggcaacg ggaacaataa attggggggac 240
tcgctgaaga ggaggctctt cgcattggga agagaggtgt tgttgcagag atcaacactg 300
ggagaagaag agcaagcggc cgtactgtta atggctctgt cttacggcta cgtctatgct 360
taa 363

<210> 168
<211> 120
<212> PRT
<213> Vitis vinifera

<400> 168
Met Asn Asn Lys Asn Pro Asp Ala Val Ser Ser Ala Glu Ser Gln Val
1 5 10 15

Asn Glu Pro Lys Lys Thr Cys Ala Asp Cys Gly Thr Thr Lys Thr Pro
20 25 30

Leu Trp Arg Gly Gly Pro Ala Gly Pro Lys Ser Leu Cys Asn Ala Cys
35 40 45

Gly Ile Arg Ser Arg Lys Lys Arg Arg Ala Phe Leu Gly Ser Ser Asn
50 55 60

His Ser His Asn Asn Gly Gly Gly Asn Gly Asn Asn Lys Leu Gly Asp
65 70 75 80

Ser Leu Lys Arg Arg Leu Phe Ala Leu Gly Arg Glu Val Leu Leu Gln
Seite 173

Arg Ser Thr Leu Gly Glu Glu Glu Gln Ala Ala Val Leu Leu Met Ala
100 105 110

Leu Ser Tyr Gly Tyr Val Tyr Ala
115 120

<210> 169
<211> 378
<212> DNA
<213> Vitis vinifera

<400> 169
atgatggatc tgagcaaaaa ggaatcattg tctgaggaaa tgaatgagat caagaaatgt 60
tgtactgatt gcaagaccac caagacgccc ctgtggagag gtgggccagc tgggcctaag 120
tcactctgca atgcatgtgg gatcagatac aggaagagga ggagttccat ggtgggtgtg 180
aacaaaaaga aagagagaat gaacagtggg agccatgatt tgagtgaaac tttgaagcag 240
tcactcatgg ctttggggaa tgaggtgatg atgcagagggc agagatcttc agtgaagaaa 300
cagaggagga agttggggga agaagaacaa gcagctgtac tgttgatggc actctcatgt 360
ggctctgttt ttgcctag 378

<210> 170
<211> 125
<212> PRT
<213> Vitis vinifera

<400> 170

Met Met Asp Leu Ser Lys Lys Glu Ser Leu Ser Glu Glu Met Asn Glu
1 5 10 15

Ile Lys Lys Cys Cys Thr Asp Cys Lys Thr Thr Lys Thr Pro Leu Trp
20 25 30

Arg Gly Gly Pro Ala Gly Pro Lys Ser Leu Cys Asn Ala Cys Gly Ile
35 40 45

Arg Tyr Arg Lys Arg Arg Ser Ser Met Val Gly Val Asn Lys Lys Lys
50 55 60

Glu Arg Met Asn Ser Gly Ser His Asp Leu Ser Glu Thr Leu Lys Gln
65 70 75 80

Ser Leu Met Ala Leu Gly Asn Glu Val Met Met Gln Arg Gln Arg Ser
85 90 95

Ser Val Lys Lys Gln Arg Arg Lys Leu Gly Glu Glu Glu Gln Ala Ala
100 105 110

Val Leu Leu Met Ala Leu Ser Cys Gly Ser Val Phe Ala
115 120 125

<210> 171
<211> 411
<212> DNA
<213> Oryza sativa

<400> 171
atggattcct cgtcggtcga gaaggggagt gggtcgatag atccggacga ggcacacggcc 60
tccggcgagc ccaaggcgtg caccgactgc cacaccacca agactccgct ctggcgcggc 120
ggcccctccg gcccgaagtc gctatgcaac gcgtgcggga tccgggtaccg gaagaagaga 180
cgggaggcgc tggggctcga cgccggcgag ggcggcgagg agcggcagga gaagaagaag 240
agcaagaggg agagagggga ggaggtgacc atggagctcc gcatggtggg gttcgggaag 300
gaggtggtcc tgaagcagcg gcggcgatg cggcggagga gacgcctcgg cgaggaggag 360
aaggcgcca tcctcctcat ggccctctcc tccggagtca tctacgcctg a 411

<210> 172
<211> 136
<212> PRT
<213> Oryza sativa

<400> 172
Met Asp Ser Ser Ser Val Glu Lys Gly Ser Gly Ser Ile Asp Pro Asp
1 5 10 15
Glu Arg Thr Ala Ser Gly Glu Pro Lys Ala Cys Thr Asp Cys His Thr
20 25 30
Thr Lys Thr Pro Leu Trp Arg Gly Gly Pro Ser Gly Pro Lys Ser Leu
35 40 45
Cys Asn Ala Cys Gly Ile Arg Tyr Arg Lys Lys Arg Arg Glu Ala Leu
50 55 60
Gly Leu Asp Ala Gly Glu Gly Gly Ala Glu Arg Gln Glu Lys Lys Lys
65 70 75 80
Ser Lys Arg Glu Arg Gly Glu Glu Val Thr Met Glu Leu Arg Met Val
85 90 95
Gly Phe Gly Lys Glu Val Val Leu Lys Gln Arg Arg Arg Met Arg Arg
100 105 110
Arg Arg Arg Leu Gly Glu Glu Glu Lys Ala Ala Ile Leu Leu Met Ala
115 120 125
Leu Ser Ser Gly Val Ile Tyr Ala
130 135

<210> 173
<211> 429
<212> DNA

<213> Oryza sativa

<400> 173

```

atggatatgg attcttcctc ctccccggtg gacaaggtgg atcccgacga gtgcaacggc      60
tctaaggctt gcgctgactg ccacactacc aagactccgc tatggcgagg cggacccgga      120
ggaccaagt  cgctgtgcaa cgcattgcggg atccggtatc ggaagaggcg gcgggcggcg      180
ctcggcctgg actcttcctc caccgccacc gccaccgacg gagcggagca gcagaagaag      240
actaaggcca agaaggaaaa ggcacaggag gaggaggtca ccatggagct ccacacggtg      300
ggcttccgca gcaaggacgc tgctgtgttc aagcagcgcc ggcggtatgcg ccgcaggaaa      360
tgccttggcg aggaggagag ggccgccatc ctgctcatgg cactctcctc gggcgatcatc      420
tacgcctga                                     429

```

<210> 174

<211> 142

<212> PRT

<213> Oryza sativa

<400> 174

```

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

```

<210> 175

<211> 885

<212> DNA

<213> Arabidopsis thaliana

<400> 175

```

atgcagactc cgtacactac ttcaacgcag gggcaatatt gtcattcttg tggaatgttc      60
caccaccata gccaaagctg ctgctacaac aacaacaaca actccaacgc cggttcttac      120
tcgatgggtct tctccatgca aaacggtggc gttttcgagc agaacggtga ggactatcat      180
cactcttcct ccctcgttga ctgcactctc tctcttggaa ctctttctac gaggccttct      240
gaggaagatg agaaacgtag acgctctact tcattctggtg cttcttcttg catctccaac      300
ttttgggact tgattcacac caaaaacaac aactccaaaa cggcaccgta caataacgtt      360
ccttctttct ccgctaacaa gccaaagtcgc ggttggtccg gtggtggtga tggcggagga      420
ggcgggtggcg gaggtgactc tcttctcgct agacgctgtg ccaactgtga cactacttct      480
actccactat ggaggaatgg tcctagaggc cctaagtccc tatgcaacgc atgcggcatt      540
cgtttcaaga aggaagagag aagaactact gcggcttcag gaaacaccgt cgtcggagct      600
gcaccgggtc aaaccgacca gtacgggcat cacaactctg gctacaataa ttaccatgct      660
gccactaata acaacaataa taatggtact ccgtgggctc atcaccactc gacgcagagg      720
gttccgtgta attatccggc aaatgagatc aggttcatgg atgattacgg cagtggagta      780
gcaaacaacg ttgaatccga cgggtgtcac ggcggtgttc cgttcctttc ttggaggcct      840
aatgtagcgg atagggcaag tcttgtccat gactttacca gatga                        885

```

```

<210> 176
<211> 295
<212> PRT
<213> Arabidopsis thaliana
<400> 176

```

```

Met Met Gln Thr Pro Tyr Thr Thr Ser Thr Gln Gly Gln Tyr Cys His
1          5          10          15

```

```

Ser Cys Gly Met Phe His His His Ser Gln Ser Cys Cys Tyr Asn Asn
          20          25          30

```

```

Asn Asn Asn Ser Asn Ala Gly Ser Tyr Ser Met Val Phe Ser Met Gln
          35          40          45

```

```

Asn Gly Gly Val Phe Glu Gln Asn Gly Glu Asp Tyr His His Ser Ser
          50          55          60

```

```

Ser Leu Val Asp Cys Thr Leu Ser Leu Gly Thr Pro Ser Thr Arg Leu
65          70          75          80

```

```

Cys Glu Glu Asp Glu Lys Arg Arg Arg Ser Thr Ser Ser Gly Ala Ser
          85          90          95

```

```

Ser Cys Ile Ser Asn Phe Trp Asp Leu Ile His Thr Lys Asn Asn Asn
          100          105          110

```

```

Ser Lys Thr Ala Pro Tyr Asn Asn Val Pro Ser Phe Ser Ala Asn Lys
          115          120          125

```

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Pro Ser Arg Gly Cys Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
130 135 140

Gly Gly Asp Ser Leu Leu Ala Arg Arg Cys Ala Asn Cys Asp Thr Thr
145 150 155 160

Ser Thr Pro Leu Trp Arg Asn Gly Pro Arg Gly Pro Lys Ser Leu Cys
165 170 175

Asn Ala Cys Gly Ile Arg Phe Lys Lys Glu Glu Arg Arg Thr Thr Ala
180 185 190

Ala Thr Gly Asn Thr Val Val Gly Ala Ala Pro Val Gln Thr Asp Gln
195 200 205

Tyr Gly His His Asn Ser Gly Tyr Asn Asn Tyr His Ala Ala Thr Asn
210 215 220

Asn Asn Asn Asn Asn Gly Thr Pro Trp Ala His His His Ser Thr Gln
225 230 235 240

Arg Val Pro Cys Asn Tyr Pro Ala Asn Glu Ile Arg Phe Met Asp Asp
245 250 255

Tyr Gly Ser Gly Val Ala Asn Asn Val Glu Ser Asp Gly Ala His Gly
260 265 270

Gly Val Pro Phe Leu Ser Trp Arg Leu Asn Val Ala Asp Arg Ala Ser
275 280 285

Leu Val His Asp Phe Thr Arg
290 295

<210> 177
<211> 840
<212> DNA
<213> Oryza sativa

<400> 177
atgcttcacc attactacag cggcggcgcc ggccatcatc aggacgtcgc tgcagctggt 60
agccccggcg acatggcttc ctccaccttc tcgctcttct tcccgatgtc caatgggcag 120
tggtggccgc cgtcgacggt ggaggagtcc gcggcctacg acgaccacag caccgtcacc 180
acctctcctt cctcgccttc gtcgtcctcc accggctccg tcgactgcac gctctcgctc 240
ggcacgccgt cgtctcgccg cgccgagccc gtcgcgggcg cggcgccagc ggcaaaccat 300
ggggcgcccc tgccggcgca ttatccgtcg ctgtcagcgg cgaccgtgtc ctgggacgcg 360
actgccgagt cgtactattg tggccagcag gggaggccgg ccaccggcgc cgccaagtgc 420
gccgccggcg ccgggcacga cgcgctcctc gaccgccgct gcgccaactg cggcaccgcg 480
tccacgccgc tctggaggaa cggccctcgc ggaccaagt cgctgtgcaa cgcgtgcggg 540

atcaggtaca agaaggagga gcggcgcgcg gcggcgacga cgacgacggc cgacggcgcc	600
gccggatgcg gcttcatcac cgcgcagcgt ggacgcgggt cgaccgcggc caaggcggcg	660
cccgccgtga cgacgtgcgg cgaggagacg tcaccgtacg tcgtcggcgg cggcggcggc	720
ggcggcgagg tcgcggacgc ggcgtatctc gcctggcggc tcaacgtcgt cccaccggcg	780
gcgacggcga cggcgttctc ggtgtggccg gagcgagcta gcctctacca ctacaactag	840

<210> 178
 <211> 279
 <212> PRT
 <213> Oryza sativa

<400> 178

Met Leu His His Tyr Tyr Ser Gly Gly Ala Gly His His Gln Asp Val
 1 5 10 15

Ala Ala Ala Gly Ser Pro Gly Asp Met Ala Ser Ser Thr Phe Ser Leu
 20 25 30

Phe Phe Pro Met Ser Asn Gly Gln Cys Trp Pro Pro Ser Thr Val Glu
 35 40 45

Glu Ser Ala Ala Tyr Asp Asp His Ser Thr Val Thr Thr Ser Pro Ser
 50 55 60

Ser Pro Ser Ser Ser Ser Thr Gly Ser Val Asp Cys Thr Leu Ser Leu
 65 70 75 80

Gly Thr Pro Ser Ser Arg Arg Ala Glu Pro Val Ala Ala Ala Ala Pro
 85 90 95

Ala Ala Asn His Gly Ala Pro Val Pro Ala His Tyr Pro Ser Leu Ser
 100 105 110

Ala Ala Thr Val Ser Trp Asp Ala Thr Ala Glu Ser Tyr Tyr Cys Gly
 115 120 125

Gln Gln Gly Arg Pro Ala Thr Gly Ala Ala Lys Cys Ala Ala Gly Ala
 130 135 140

Gly His Asp Ala Leu Leu Asp Arg Arg Cys Ala Asn Cys Gly Thr Ala
 145 150 155 160

Ser Thr Pro Leu Trp Arg Asn Gly Pro Arg Gly Pro Lys Ser Leu Cys
 165 170 175

Asn Ala Cys Gly Ile Arg Tyr Lys Lys Glu Glu Arg Arg Ala Ala Ala
 180 185 190

Thr Thr Thr Thr Ala Asp Gly Ala Ala Gly Cys Gly Phe Ile Thr Ala
 195 200 205

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Gln Arg Gly Arg Gly Ser Thr Ala Ala Lys Ala Ala Pro Ala Val Thr
210 215 220

Thr Cys Gly Glu Glu Thr Ser Pro Tyr Val Val Gly Gly Gly Gly Gly
225 230 235 240

Gly Gly Glu Val Ala Asp Ala Ala Tyr Leu Ala Trp Arg Leu Asn Val
245 250 255

Val Pro Pro Ala Ala Thr Ala Thr Ala Phe Ser Val Trp Pro Glu Arg
260 265 270

Ala Ser Leu Tyr His Tyr Asn
275

<210> 179
<211> 56
<212> DNA
<213> Artificial sequence

<220>
<223> primer: prm10106

<400> 179
ggggacaagt ttgtacaaaa aagcaggcctt aaacaatgct tcaccattac tacagc 56

<210> 180
<211> 48
<212> DNA
<213> Artificial sequence

<220>
<223> primer: prm10107

<400> 180
ggggaccact ttgtacaaga aagctggggtc caacgctaata gctacact 48

<210> 181
<211> 1647
<212> DNA
<213> Arabidopsis thaliana

<400> 181
atgggtcgtt cgaaactagc ttctcgtcct gctgaggaag acctgaatcc aggaaaatca 60
aaaaggaaaa agatatcatt gggtcctgag aatgctgcgg catcaatttc caccggaatt 120
gaagctggga atgagaggaa acctggcctt tactgttgta actattgcga taaagatctg 180
tctggtttgg ttcgtttcaa atgtgctgtt tgtatggact ttgatctttg tgtggaatgc 240
ttttctgtcg gcgttgaact taatcgtcac aagaacagtc acccatatcg tgttatggac 300
aatttgtctt tttcgcttgt tacttctgat tggaatgccg atgaagagat actccttctt 360
gaggccattg cgacatacgg gtttggcaat tggaaagaag ttgcagacca tgttggtagt 420
aagacaacga cagaatgtat taaacacttc aattctgctt acatgcagtc accatgcttt 480
ccacttccgg acttgtccca tactattgga aagagcaaag atgagctgct tgctatgagt 540

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

aaagatagtg cagtcaaaac agaaatacct gcatttgtga ggctatctcc aaaagaagag      600
ttacctgtgt cagctgaaat caaacacgaa gcttcagggg aggtcaatga aatagatcca      660
cctttgtctg ccttagctgg agtcaagaag aaaggcaatg taccgcaggc taaggacatc      720
atcaagttgg aagctgcaaa acaacaatct gacaggagtg tcggggagaa gaaactcaga      780
cttcctggag agaaagttcc attagtaaca gagttatatg gttacaatct aaagagggaa      840
gaatttgaga tcgaacatga caacgatgct gagcaactgc ttgctgacat ggaatttaag      900
gattctgaca cagatgctga gcgtgagcag aaactgcagg ttcttcgtat ttactcgaaa      960
aggcttgatg agaggaagcg gaggaaggaa tttgttctgg aaagaaactt gttgtaccct    1020
gatcaatatg agatgagcct ttcagcagag gagagaaaaa tatataaaag ctgtaaagtg    1080
tttgcgcggt tccaatccaa agaagagcac aaggaactga ttaagaaagt cattgaagag    1140
caccaaattc tcagaagaat cgaggatctt caggaagcta gaactgctgg ttgcaggaca    1200
acttcagacg caaatagatt tatagaagag aagagaaaaga aggaagctga agaaagtatg    1260
ctgctgcggc ttaaccacgg tgcaccaggc agtatagccg gtaaaacact aaaaagtcca    1320
agagggttac ccagaaattht gcatcccttht ggthctgact cactgccaaa ggtcacacct    1380
ccaagaatat acagcggtht ggacacttgg gatgttgatg gtctccttgg agctgactta    1440
ctctcagaga ccgaaaagaa gatgtgcaat gagaccagaa tactgcctgt acactatttg    1500
aagatgttgg atatcttaac aagagaaata aagaaggggg agataaagaa aaagtctgat    1560
gcttatagct tcttcaaagt agagccgagt aaagtagaca gagtatatga tatgctggtt    1620
cataagggaa taggtgactc aacatga                                     1647

```

<210> 182
 <211> 548
 <212> PRT
 <213> Arabidopsis thaliana
 <400> 182

Met Gly Arg Ser Lys Leu Ala Ser Arg Pro Ala Glu Glu Asp Leu Asn
 1 5 10 15

Pro Gly Lys Ser Lys Arg Lys Lys Ile Ser Leu Gly Pro Glu Asn Ala
 20 25 30

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

Gly Leu Tyr Cys Cys Asn Tyr Cys Asp Lys Asp Leu Ser Gly Leu Val
 50 55 60

Arg Phe Lys Cys Ala Val Cys Met Asp Phe Asp Leu Cys Val Glu Cys
 65 70 75 80

Phe Ser Val Gly Val Glu Leu Asn Arg His Lys Asn Ser His Pro Tyr
 85 90 95

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Arg Val Met Asp 100 Asn Leu Ser Phe Ser 105 Leu Val Thr Ser Asp 110 Trp Asn

Ala Asp Glu 115 Glu Ile Leu Leu 120 Glu Ala Ile Ala Thr 125 Tyr Gly Phe

Gly Asn 130 Trp Lys Glu Val Ala 135 Asp His Val Gly Ser 140 Lys Thr Thr Thr

Glu 145 Cys Ile Lys His Phe 150 Asn Ser Ala Tyr Met 155 Gln Ser Pro Cys Phe 160

Pro Leu Pro Asp 165 Leu Ser His Thr Ile Gly 170 Lys Ser Lys Asp Glu 175 Leu

Leu Ala Met Ser 180 Lys Asp Ser Ala Val 185 Lys Thr Glu Ile Pro 190 Ala Phe

Val Arg Leu 195 Ser Pro Lys Glu Glu 200 Leu Pro Val Ser Ala 205 Glu Ile Lys

His Glu 210 Ala Ser Gly Lys Val 215 Asn Glu Ile Asp Pro 220 Pro Leu Ser Ala

Leu 225 Ala Gly Val Lys Lys 230 Lys Gly Asn Val Pro 235 Gln Ala Lys Asp Ile 240

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

Lys Lys Leu Arg 260 Leu Pro Gly Glu Lys 265 Val Pro Leu Val Thr 270 Glu Leu

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

Asp Ala 290 Glu Gln Leu Leu Ala 295 Asp Met Glu Phe Lys 300 Asp Ser Asp Thr

Asp 305 Ala Glu Arg Glu Gln Lys Leu Gln Val Leu 315 Arg Ile Tyr Ser Lys 320

Arg Leu Asp Glu 325 Arg Lys Arg Arg Lys Glu 330 Phe Val Leu Glu Arg 335 Asn

Leu Leu Tyr Pro 340 Asp Gln Tyr Glu Met 345 Ser Leu Ser Ala Glu 350 Glu Arg

Lys Ile Tyr 355 Lys Ser Cys Lys Val 360 Phe Ala Arg Phe Gln 365 Ser Lys Glu

Glu His Lys Glu Leu Ile Lys Lys Val Ile Glu Glu His Gln Ile Leu
370 375 380

Arg Arg Ile Glu Asp Leu Gln Glu Ala Arg Thr Ala Gly Cys Arg Thr
385 390 395 400

Thr Ser Asp Ala Asn Arg Phe Ile Glu Glu Lys Arg Lys Lys Glu Ala
405 410 415

Glu Glu Ser Met Leu Leu Arg Leu Asn His Gly Ala Pro Gly Ser Ile
420 425 430

Ala Gly Lys Thr Leu Lys Ser Pro Arg Gly Leu Pro Arg Asn Leu His
435 440 445

Pro Phe Gly Ser Asp Ser Leu Pro Lys Val Thr Pro Pro Arg Ile Tyr
450 455 460

Ser Gly Leu Asp Thr Trp Asp Val Asp Gly Leu Leu Gly Ala Asp Leu
465 470 475 480

Leu Ser Glu Thr Glu Lys Lys Met Cys Asn Glu Thr Arg Ile Leu Pro
485 490 495

Val His Tyr Leu Lys Met Leu Asp Ile Leu Thr Arg Glu Ile Lys Lys
500 505 510

Gly Gln Ile Lys Lys Lys Ser Asp Ala Tyr Ser Phe Phe Lys Val Glu
515 520 525

Pro Ser Lys Val Asp Arg Val Tyr Asp Met Leu Val His Lys Gly Ile
530 535 540

Gly Asp Ser Thr
545

<210> 183
<211> 1464
<212> DNA
<213> Arabidopsis thaliana

<400> 183
atgggtcgct ctcgaggga cttccaaaat ttcgaagacc ctactcagag aacgaggaaa 60
aagaaaaatg cggctaattgt ggagaacttt gagtctactt ctttggtacc aggtgctgag 120
ggaggaggga agtataactg cgattattgc cagaaagaca ttactggaaa aattaggata 180
aagtgtgctg tctgtccaga ttttgatctc tgtatagaat gtatgtctgt tggagcagag 240
atcactcctc acaaattgtga tcaccatac cgagttatgg gaaatctaac tttcccgcctt 300
atttgcctg actggagtgc ggatgatgaa atgcttctcc tggagggact tgaaatttat 360
ggcttgggaa actgggcaga ggttgaggag cacgtgggaa cgaagagtaa agaacagtgt 420
cttgagcact acagaaacat ctatttgaac tcaccatttt tcccacttcc ggatatgtca 480

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

catgtagcag ggaagaacag aaaagaactt caagccatgg ctaaaggacg cattgatgac      540
aagaaagcag agcagaacat gaaagaagag taccggttct ctcttcctaa agtcaaagtt      600
gaagacacac aaaaagagtc ttttgtagac agaagttttg gaggggaagaa acctgtttcc      660
acctcggtaa acaactcttt ggttgagctg agtaattaca accagaaaag agaagagttt      720
gacctgaat atgacaatga tgctgagcaa ctcttggcgg agatggagtt caaagagaac      780
gatactcctg aagaacatga actgaagctg cgtgtgttgc gtatctattc aaaaaggctt      840
gatgagagga aacgtagaaa agaattcata atagaaagaa acctgttgta cccaaatccc      900
tttgagaagg acctgtctca ggaggagaaa gtacaatgcc gacgtttgga cgtttttatg      960
cgttttcatt caaaagagga gcacgacgag ctactccgta atgttgtaag cgagtaccgc     1020
atggtgaaac ggctcaaaga tctcaaggaa gctcaagtgg caggggtgtcg ttcaacggct     1080
gaagcagaga ggtatctggg aaggaagagg aagagagaaa acgaagaagg gatgaacaga     1140
gggaaagaga gcggtcaatt tgggtcaaatt gcaggggaga tgggctctag accacctgtg     1200
caagcttctt caagctatgt gaatgatttg gacttgattg ggttcacgga gtcgcaactg     1260
ctgtctgaat ccgagaagcg tctctgcagc gaggtcaagt tggttccacc ggtttatcta     1320
cagatgcaac aagtgatgtc acatgagata ttcaaagga atgtaacgaa gaagtcggat     1380
gcatatagcc ttttcaagat tgatccaacc aaagtggatc gagtttatga tatgcttgtg     1440
aagaagggtg ttgctcaact ttaa                                             1464

```

```

<210> 184
<211> 487
<212> PRT
<213> Arabidopsis thaliana
<400> 184

```

Met Gly Arg Ser Arg Gly Asn Phe Gln Asn Phe Glu Asp Pro Thr Gln
1 5 10 15

Arg Thr Arg Lys Lys Lys Asn Ala Ala Asn Val Glu Asn Phe Glu Ser
20 25 30

Thr Ser Leu Val Pro Gly Ala Glu Gly Gly Gly Lys Tyr Asn Cys Asp
35 40 45

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

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

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

Thr Phe Pro Leu Ile Cys Pro Asp Trp Ser Ala Asp Asp Glu Met Leu
100 105 110

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

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

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Gly Gln Phe Gly Gln Ile Ala Gly Glu Met Gly Ser Arg Pro Pro Val
385 390 395 400

Gln Ala Ser Ser Ser Tyr Val Asn Asp Leu Asp Leu Ile Gly Phe Thr
405 410 415

Glu Ser Gln Leu Leu Ser Glu Ser Glu Lys Arg Leu Cys Ser Glu Val
420 425 430

Lys Leu Val Pro Pro Val Tyr Leu Gln Met Gln Gln Val Met Ser His
435 440 445

Glu Ile Phe Lys Gly Asn Val Thr Lys Lys Ser Asp Ala Tyr Ser Leu
450 455 460

Phe Lys Ile Asp Pro Thr Lys Val Asp Arg Val Tyr Asp Met Leu Val
465 470 475 480

Lys Lys Gly Ile Ala Gln Leu
485

<210> 185
<211> 2745
<212> DNA
<213> Dictyostelium discoideum

<400> 185
atgacttcaa caataaataa agaagaacct acaacacttg taaataaaaa aaggagaaaa 60
gaacatgttg atgatgacga tgataatgat gatgacattg aaatgcaaaa tgtatcaaat 120
gataatatta ataatacaga tgatgaaaat aataatgtaa atacaaatgg aaataataca 180
aacaaaacca acaacaacaa caacaacaac aacaacaaca acaacaataa taatgaagaa 240
gatgacgatg aagaagactt attaattacc aaaagaagga atagtagatc aacaacaatg 300
agtaataata gtagtaataa atcaacacca tctaaaaaga aaagaattaa gaaatcatat 360
gataatgata aagattttgt aggagatgat gaagaggaag atgataatga tgatgaagat 420
gatgatggtg atgttgtaat ctcaaataat aataataata ataataataa taataactaat 480
aataataata ataataataa tggtaatggt aatggtaata acaatacaaa caattcattc 540
gaagaagatg atgatgaaga ggatgatgat gaagaagatg aagaagaaga agaagaaggt 600
atgaaaatat caaaaagtaa aagacaaaca caaataatac caccaacaca aagtgaagtt 660
gatgatcttg taaataaaaag ttttaatagt gtagatgatg atgaagaaga taatgaagag 720
gatgataaaa caaaaaatac tactactact actgctacaa atactactaa tgtaccaaca 780
acaacaacaa caactacaac aacatcgaac aatactacat taccaactac taccactact 840
accaccacta ataatacaac aaaaccaa atgttaaaatag aacaacaaa aacacaacaa 900
ccaccacaac cacaaccaat aaataaacca actcaatcaa atactatcac aacaatata 960
aatacaagta caaatacaaa cacagctaca aatacaaatt caaatacagc tacagccaca 1020

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

acaacatcac	ctacctcaat	gacaaaacaa	acaaggaagt	caaccaattc	accaactaac	1080
agtaatggta	ataataataa	taataataat	aataataatt	ttatagagga	acaagtgaat	1140
gaaggattat	atcattgtga	ttattgtcaa	aaggatatta	gtgggtgttg	acgtataaga	1200
tgttcagtat	gtactgattt	cgatttatgt	ttagaatggt	ttagtgttg	tgtagagatt	1260
acaccacatc	gtaattttca	tgattatcat	gtagttgata	atatgcattt	cccaatgttt	1320
actgatgatt	gggggtgctga	tgaagaatta	ttacttttag	aagcaattga	attatatggt	1380
ttaggtaatt	ggaatgaagt	ttcagagaat	gtaggcgcac	attcaaaatc	acctttagaa	1440
tgtaaagcac	attatttcgc	tcattattta	aatagttcaa	cttcaccttt	accagataca	1500
tcaaagggtt	taactacaaa	tgaaaatggt	cactttaaaa	gagcaaaaac	aactgtaaat	1560
ggtaattatt	ataatgatta	tattattgat	aatagtgacg	atgatgataa	taataataat	1620
aataataatt	ataacgataa	tagtaataat	acaacaccaa	caaagtcatt	caatagtgtt	1680
aataaaaagta	aaaaattaaa	tcatagaaat	agtcattggtg	aagaaggacc	aagtggacca	1740
gtaacagatt	cagttggata	tatgaagaat	agaggacatt	ttgaagtaga	atatgataat	1800
gaagcagagt	tggttgtaaa	ggatttaaca	tttgaacctg	acgatagtca	agcagataga	1860
gatattaaat	tgaatgtatt	agaatcctat	gatcaaagat	tggatgaacg	tattagaaga	1920
aggaatttca	ttgttgagaa	aggtttatta	gattatagaa	aagtagagag	aaaacgatac	1980
aaagatgata	aagagatatt	aaattcattg	aaatgtttcc	ttcaaacagt	taccaaagaa	2040
gagcatgaat	caatgataaa	tggattaata	aatgaaaaga	atataaagaa	tagaattcta	2100
caattacaag	agtatcgtga	aaatggtatt	aaaacattgg	cagatggtca	aaattttgat	2160
gaagataaaa	gaaaacgtga	agttgataaa	tctatgaaac	gttccaaatc	tgaattggca	2220
tcatatagtt	taaatagtgg	attaagttca	tacaatccaa	atcataatcc	atttggtcat	2280
cattatttag	gtggtagtag	tagtggatta	agtggtggta	gtggtggagg	tggtgggtgt	2340
ggtggtgata	catcatttaa	aactcaaaaa	caattaacta	aagaaaaaga	agatatttat	2400
ttaggatttg	gtgagaatag	gaaacatcat	tcaagtaaat	tgaaaaagaa	tgctaaaatg	2460
gaattggaag	gtttaccaa	tgctgatgca	ctctcattaa	aagagaaaca	aatttgatca	2520
actcataaac	ttttaccaca	acaataccta	attgtcaaac	aagcattaat	ctctgaatct	2580
ttaaaaactc	aagggtgtaat	taaattatca	accgctttta	aactaattaa	attaaatcaa	2640
gttaaaattc	atagactttt	agaattcttt	gaaagaaatc	attggttaaa	atttaatat	2700
gattgtgaaa	ctaacacttc	taatactact	tcaaattata	aataa		2745

<210> 186

<211> 914

<212> PRT

<213> Dictyostelium discoideum

<400> 186

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

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

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

Pro Asn Val Lys Ile Glu Gln Pro Lys Thr Gln Gln Pro Pro Gln Pro
290 295 300

Gln Pro Ile Asn Lys Pro Thr Gln Ser Asn Thr Ile Thr Thr Asn Thr
305 310 315 320

Asn Thr Ser Thr Asn Thr Asn Thr Ala Thr Asn Thr Asn Ser Asn Thr
325 330 335

Ala Thr Ala Thr Thr Thr Ser Pro Thr Ser Met Thr Lys Gln Thr Arg
340 345 350

Lys Ser Thr Asn Ser Pro Thr Asn Ser Asn Gly Asn Asn Asn Asn
355 360 365

Asn Asn Asn Asn Asn Phe Ile Glu Glu Gln Val Asn Glu Gly Leu Tyr
370 375 380

His Cys Asp Tyr Cys Gln Lys Asp Ile Ser Gly Val Val Arg Ile Arg
385 390 395 400

Cys Ser Val Cys Thr Asp Phe Asp Leu Cys Leu Glu Cys Phe Ser Val
405 410 415

Gly Val Glu Ile Thr Pro His Arg Asn Phe His Asp Tyr His Val Val
420 425 430

Asp Asn Met His Phe Pro Met Phe Thr Asp Asp Trp Gly Ala Asp Glu
435 440 445

Glu Leu Leu Leu Leu Glu Ala Ile Glu Leu Tyr Gly Leu Gly Asn Trp
450 455 460

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

Cys Lys Ala His Tyr Phe Ala His Tyr Leu Asn Ser Ser Thr Ser Pro
485 490 495

Leu Pro Asp Thr Ser Lys Val Leu Thr Thr Asn Glu Asn Val His Phe
500 505 510

Lys Arg Ala Lys Thr Thr Val Asn Gly Asn Tyr Tyr Asn Asp Tyr Ile
515 520 525

Ile Asp Asn Ser Asp Asp Asp Asn Asn Asn Asn Asn Asn Asn Tyr
530 535 540

Asn Asp Asn Ser Asn Asn Thr Thr Pro Thr Lys Ser Phe Asn Ser Val
545 550 555 560

Asn Lys Ser Lys Lys Leu Asn His Arg Asn Ser His Gly Glu Glu Gly
Seite 189

Pro Ser Gly Pro Val Thr Asp Ser Val Gly Tyr Met Lys Asn Arg Gly
580 585 590

His Phe Glu Val Glu Tyr Asp Asn Glu Ala Glu Leu Val Val Lys Asp
595 600 605

Leu Thr Phe Glu Pro Asp Asp Ser Gln Ala Asp Arg Asp Ile Lys Leu
610 615 620

Asn Val Leu Glu Ser Tyr Asp Gln Arg Leu Asp Glu Arg Ile Arg Arg
625 630 635 640

Arg Asn Phe Ile Val Glu Lys Gly Leu Leu Asp Tyr Arg Lys Val Glu
645 650 655

Arg Lys Arg Tyr Lys Asp Asp Lys Glu Ile Leu Asn Ser Leu Lys Cys
660 665 670

Phe Leu Gln Thr Val Thr Lys Glu Glu His Glu Ser Met Ile Asn Gly
675 680 685

Leu Ile Asn Glu Lys Asn Ile Lys Asn Arg Ile Leu Gln Leu Gln Glu
690 695 700

Tyr Arg Glu Asn Gly Ile Lys Thr Leu Ala Asp Gly Gln Asn Phe Asp
705 710 715 720

Glu Asp Lys Arg Lys Arg Glu Val Asp Lys Ser Met Lys Arg Ser Lys
725 730 735

Ser Glu Leu Ala Ser Tyr Ser Leu Asn Ser Gly Leu Ser Ser Tyr Asn
740 745 750

Pro Asn His Asn Pro Phe Gly His His Tyr Leu Gly Gly Ser Ser Ser
755 760 765

Gly Leu Ser Gly Gly Ser Gly Gly Gly Gly Gly Gly Gly Asp Pro
770 775 780

Ser Phe Lys Thr Gln Lys Gln Leu Thr Lys Glu Lys Glu Asp Ile Tyr
785 790 795 800

Leu Gly Ile Gly Glu Asn Arg Lys His His Ser Ser Lys Leu Lys Lys
805 810 815

Asn Ala Lys Met Glu Leu Glu Gly Leu Pro Asn Ala Asp Ala Leu Ser
820 825 830

Leu Lys Glu Lys Gln Ile Cys Thr Thr His Lys Leu Leu Pro Gln Gln
835 840 845

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Tyr Leu Ile Val Lys Gln Ala Leu Ile Ser Glu Ser Leu Lys Thr Gln
850 855 860

Gly Val Ile Lys Leu Ser Thr Ala Phe Lys Leu Ile Lys Leu Asn Gln
865 870 875 880

Val Lys Ile His Arg Leu Leu Glu Phe Phe Glu Arg Asn His Trp Leu
885 890 895

Lys Phe Asn Ile Asp Cys Glu Thr Asn Thr Ser Asn Thr Thr Ser Asn
900 905 910

Tyr Lys

<210> 187
<211> 1683
<212> DNA
<213> Lycopersicum esculentum

<400> 187
atgggtcgtt ctcgggctgt tcatcaatcc actgatgatg atccaagcca gaggtctaag 60
agaaaaaggg cagtgccaaa tgtggagagt tttgatactg cagctactgg ccaaataattg 120
actgaaggga aaaaggcttt gtaccattgc aattattgca ataaagacat atctggaagg 180
attcggatta aatgtgttgt gtgttctgac tttgatcttt gtgtggaatg cttttctgtt 240
ggagcagaag tgcagcctca caaaagcaat catctgtata gggttatgga taacctgtca 300
tttcctctca tatgtgctga ctggaatgct gatgaggaaa tggtacttct agagggtttg 360
gaaatgtacg gattggcaaa ctgggctgaa gttgccgaac atgttggaac gaagagtaaa 420
cagcagtgtg ttgaccacta taagtccacc tatattagtt ctccttgttt tccgcttccg 480
gacatgtccc atgttatggg aaagaacaga gaggaacttc ttgcatggc caaggatcaa 540
ggatatgcag ctcccggggg agttaatgtt aaagaagagt ctccattctc tgcaggaatc 600
aagatggaag atcaaagga agaaaattca actggacttg cctcagttgg aggttctgct 660
tctggtacat tagcaggagc tggaaagagg acatctagct tacttcatag taaggagaat 720
catgatagca tcaaagtgga aggttgtcct gcagacagga gtgtcggaga gaaaaagcct 780
aggtcatcag tggacgaggg gccttccatg acagaattaa gtggttataa ttccaagaga 840
gaggagtttg aaattgaata cgataatgat gctgagcaga tgggtggctga tatggaattt 900
aaagagacag ataccaatgc tgagcgtgaa ctgaaacttc gggatttgcg tatatacaat 960
aaaaggcttg atgagaggaa acgtaggaag gatTTTTttt tggaaaggaa actacttcat 1020
cctgatcctt ttgagaaaga cctcaccctg gaggagaagg acatatgccg tcgttacagg 1080
gtgttcatgc gttttagtct taaagaggag catgaggatt tccttaggag cataatcgag 1140
gagcaccgaa tagttaaacg aatacgagat cttcaggatg cccgaattgc tggttgccga 1200
actttagctg aggcagaaag atatgttgaa caaaagagag cgcggaatc tgaagaaaat 1260

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

atacgtagac tgaaggagaa caccagagt ggcccaagtg gaaaatattt gcaaagagca      1320
ggtcacttta aagtggagca tgacagcagc cccagaggag ttggtagggg ccctgaaatg      1380
atggattgtt gcaatgactt atcatcaacc accgcaccac atggtgttgg aagtgtgtga      1440
gacatttggg atgtcagtgg gttttcagga gctgagttgc tctcagaagc tgaaaaaaag      1500
ctttgtgatg agatgagaat cctgccggct cattatctaa acatgtcgca aaccatgtcc      1560
atggggatct ttaatggcaa catcaccaag aaatctgatg cgcattgtct attcaatgtt      1620
gatccgaata agattgacaa agtgtatgag atgcttgtca aaaagggcct ggctcaagca      1680
taa                                                                    1683

```

<210> 188
 <211> 560
 <212> PRT
 <213> Lycopersicum esculentum

<400> 188

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

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

Thr Ala Ala Thr Gly Gln Ile Leu Thr Glu Gly Lys Lys Ala Leu Tyr
35 40 45

His Cys Asn Tyr Cys Asn Lys Asp Ile Ser Gly Arg Ile Arg Ile Lys
50 55 60

Cys Val Val Cys Ser Asp Phe Asp Leu Cys Val Glu Cys Phe Ser Val
65 70 75 80

Gly Ala Glu Val Gln Pro His Lys Ser Asn His Leu Tyr Arg Val Met
85 90 95

Asp Asn Leu Ser Phe Pro Leu Ile Cys Ala Asp Trp Asn Ala Asp Glu
100 105 110

Glu Met Leu Leu Leu Glu Gly Leu Glu Met Tyr Gly Leu Ala Asn Trp
115 120 125

Ala Glu Val Ala Glu His Val Gly Thr Lys Ser Lys Gln Gln Cys Ile
130 135 140

Asp His Tyr Lys Ser Thr Tyr Ile Ser Ser Pro Cys Phe Pro Leu Pro
145 150 155 160

Asp Met Ser His Val Met Gly Lys Asn Arg Glu Glu Leu Leu Ala Met
165 170 175

Ala Lys Asp Gln Gly Tyr Ala Ala Pro Gly Gly Val Asn Val Lys Glu
180 185 190

Glu Ser Pro Phe Ser Ala Gly Ile Lys Met Glu Asp Gln Arg Glu Glu
195 200 205

Asn Ser Thr Gly Leu Ala Ser Val Gly Gly Ser Ala Ser Gly Thr Leu
210 215 220

Ala Gly Ala Gly Lys Arg Thr Ser Ser Leu Leu His Ser Lys Glu Asn
225 230 235 240

His Asp Ser Ile Lys Val Glu Gly Cys Pro Ala Asp Arg Ser Val Gly
245 250 255

Glu Lys Lys Pro Arg Ser Ser Val Asp Glu Gly Pro Ser Met Thr Glu
260 265 270

Leu Ser Gly Tyr Asn Ser Lys Arg Glu Glu Phe Glu Ile Glu Tyr Asp
275 280 285

Asn Asp Ala Glu Gln Met Val Ala Asp Met Glu Phe Lys Glu Thr Asp
290 295 300

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

Lys Arg Leu Asp Glu Arg Lys Arg Arg Lys Asp Phe Ile Leu Glu Arg
325 330 335

Lys Leu Leu His Pro Asp Pro Phe Glu Lys Asp Leu Thr Pro Glu Glu
340 345 350

Lys Asp Ile Cys Arg Arg Tyr Arg Val Phe Met Arg Phe Ser Ser Lys
355 360 365

Glu Glu His Glu Asp Phe Leu Arg Ser Ile Ile Glu Glu His Arg Ile
370 375 380

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

Thr Leu Ala Glu Ala Glu Arg Tyr Val Glu Gln Lys Arg Ala Arg Glu
405 410 415

Ser Glu Glu Asn Ile Arg Arg Leu Lys Glu Asn Thr Gln Ser Gly Pro
420 425 430

Ser Gly Lys Tyr Leu Gln Arg Ala Gly His Phe Lys Val Glu His Asp
435 440 445

Ser Ser Pro Arg Gly Val Gly Arg Gly Pro Glu Met Met Asp Cys Cys

450

455

460

Asn Asp Leu Ser Ser Thr Thr Ala Pro His Gly Val Gly Ser Ala Val
465 470 475 480

Asp Ile Trp Asp Val Ser Gly Phe Ser Gly Ala Glu Leu Leu Ser Glu
485 490 495

Ala Glu Lys Lys Leu Cys Asp Glu Met Arg Ile Leu Pro Ala His Tyr
500 505 510

Leu Asn Met Ser Gln Thr Met Ser Met Gly Ile Phe Asn Gly Asn Ile
515 520 525

Thr Lys Lys Ser Asp Ala His Gly Leu Phe Asn Val Asp Pro Asn Lys
530 535 540

Ile Asp Lys Val Tyr Glu Met Leu Val Lys Lys Gly Leu Ala Gln Ala
545 550 555 560

<210> 189

<211> 1632

<212> DNA

<213> Lycopersicum esculentum

<400> 189

atgggtcgct ctcgtgggaa ttttcaagct gatgaagatc ccagccaaag atcaaggagg	60
aaaaagaatg cctcaagtgt agacaattta gaatctgcga ccactgggtca aggacagct	120
gatggcaaaa gggccttgta tcaactgcaat tattgcaaca aagacattag cgggagaact	180
cgtataaaat gtgctgtatg ttacgatttt gacctatgta tagagtgctt ctctgttggt	240
gctgaggtgc atccccacaa aagccatcac cactataggg ttatggatat cttagctttc	300
ccgcttattt gccagactg gaatgctgat gaagagatgt tgctccttga gggaattgag	360
atgtatggca tgggtaattg ggctgaagta ggtgagcatg tcggaacaaa gacaaaagaa	420
gcctgcattg accatttttaa ggatgcgtac ttaaagtcac cttactttcc tctaccagat	480
atgactcacg tcatggggaa aaacagaatg gaactccttg ccatggctaa agggaatttc	540
actgataaga aaggactctc ttcaattggg gatgttgctc ctaaagatga atcgttctct	600
ccgtctcgaa tcaaagttga agacactcat aaaattgggtc cttcaggacg tttaacttct	660
gtatccaatg cgggaatcac aggcataaaa aagccatcca gcaaaacgct aatcaaagat	720
caaatgaac ctgttaaatt tgaagataat tcaggcagaa attttgagg caagaaaccg	780
aatctttga aggatgatgg atcctcattg atgaaattaa gtggatatat tccaagagg	840
caagaatttg atcctgaata tgataatgat gcggagcaac tattggctga tatggaattc	900
aaggaaactg aaactgaaga ggagcgcgaa cttaaactgc gtgttctgcg tatctattcc	960
aagaggcttg atgaaagaaa acgccgcaag gtttttattc tagagaggaa ttactccag	1020
ccaagtgaat ttgagaagaa tttgtcacca gaagagaaag gtatatgccg atgttatgat	1080

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```
gccattatgc gctttctctc gaaggaggag catgaagaat tacttaaggc tgtggtctca 1140
gaacatagat atctgaaaag aatacaagaa ctcaaggaag cgaaagctgc aggttgctcgt 1200
tcgtctgctg aagttgatag gtacttagaa aggaaaagga agaaggaagt tgaagaaggt 1260
gttccgagaa agggaagctc tcagattggc ccaatgagcc aggaaagcct gaacatacct 1320
gcttcttctg agtcacttgg aatacattca aatagaaaac cttgtagcca ggcgattttg 1380
agttccgaca ccaatgcagg tgttccagct ttttctgcag gagaactggt atctgaacct 1440
gagaaacaac tatgtcaaga aatcaggtta tcgccgcatac attatcttag gatgcaggag 1500
gtccttacaa tacaaattta tagtggtaat atcactagaa aatcagatgc ttatcctttg 1560
tttcaaatag aagcaactaa agtagataga gtttatgata tgcttttgaa gaaaggagtt 1620
gcacccttgt aa 1632
```

<210> 190
 <211> 543
 <212> PRT
 <213> Lycopersicum esculentum

<400> 190

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

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

Ala Thr Thr Gly Gln Gly Thr Ala Asp Gly Lys Arg Ala Leu Tyr His
 35 40 45

Cys Asn Tyr Cys Asn Lys Asp Ile Ser Gly Arg Thr Arg Ile Lys Cys
 50 55 60

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

Ala Glu Val His Pro His Lys Ser His His His Tyr Arg Val Met Asp
 85 90 95

Ile Leu Ala Phe Pro Leu Ile Cys Pro Asp Trp Asn Ala Asp Glu Glu
 100 105 110

Met Leu Leu Leu Glu Gly Ile Glu Met Tyr Gly Met Gly Asn Trp Ala
 115 120 125

Glu Val Gly Glu His Val Gly Thr Lys Thr Lys Glu Ala Cys Ile Asp
 130 135 140

His Phe Lys Asp Ala Tyr Leu Lys Ser Pro Tyr Phe Pro Leu Pro Asp
 145 150 155 160

Met Thr His Val Met Gly Lys Asn Arg Met Glu Leu Leu Ala Met Ala

Lys Gly Asn Phe Thr Asp Lys Lys Gly Leu Ser Ser Leu Gly Asp Val
180 185 190

Ala Pro Lys Asp Glu Ser Phe Ser Pro Ser Arg Ile Lys Val Glu Asp
195 200 205

Thr His Lys Ile Gly Pro Ser Gly Arg Leu Thr Ser Val Ser Asn Ala
210 215 220

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

Gln Asn Glu Pro Val Lys Phe Glu Asp Asn Ser Gly Arg Asn Phe Gly
245 250 255

Gly Lys Lys Pro Lys Ser Leu Lys Asp Asp Gly Ser Ser Leu Met Lys
260 265 270

Leu Ser Gly Tyr Ile Pro Lys Arg Gln Glu Phe Asp Pro Glu Tyr Asp
275 280 285

Asn Asp Ala Glu Gln Leu Leu Ala Asp Met Glu Phe Lys Glu Thr Glu
290 295 300

Thr Glu Glu Glu Arg Glu Leu Lys Leu Arg Val Leu Arg Ile Tyr Ser
305 310 315 320

Lys Arg Leu Asp Glu Arg Lys Arg Arg Lys Val Phe Ile Leu Glu Arg
325 330 335

Asn Leu Leu Gln Pro Ser Glu Phe Glu Lys Asn Leu Ser Pro Glu Glu
340 345 350

Lys Gly Ile Cys Arg Cys Tyr Asp Ala Ile Met Arg Phe Leu Ser Lys
355 360 365

Glu Glu His Glu Glu Leu Leu Lys Ala Val Val Ser Glu His Arg Tyr
370 375 380

Leu Lys Arg Ile Gln Glu Leu Lys Glu Ala Lys Ala Ala Gly Cys Arg
385 390 395 400

Ser Ser Ala Glu Val Asp Arg Tyr Leu Glu Arg Lys Arg Lys Lys Glu
405 410 415

Val Glu Glu Gly Val Pro Arg Lys Gly Ser Ser Gln Ile Gly Pro Met
420 425 430

Ser Gln Glu Ser Leu Asn Ile Pro Ala Ser Ser Glu Ser Leu Gly Ile
435 440 445

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

His Ser Asn Arg Lys Pro Cys Ser Gln Ala Ile Leu Ser Ser Asp Thr
450 455 460

Asn Ala Gly Val Pro Ala Phe Ser Ala Gly Glu Leu Leu Ser Glu Pro
465 470 475 480

Glu Lys Gln Leu Cys Gln Glu Ile Arg Leu Ser Pro His His Tyr Leu
485 490 495

Arg Met Gln Glu Val Leu Thr Ile Gln Ile Tyr Ser Gly Asn Ile Thr
500 505 510

Arg Lys Ser Asp Ala Tyr Pro Leu Phe Gln Ile Glu Ala Thr Lys Val
515 520 525

Asp Arg Val Tyr Asp Met Leu Leu Lys Lys Gly Val Ala Pro Leu
530 535 540

<210> 191
<211> 1548
<212> DNA
<213> Ostreococcus lucimarinus

<400> 191
atggcgagcg cgctcgtgcc gaaacggcga cgggtggcga cggaaaacgc gatgacgaag 60
ctgagtggga acggggagtc gtgcgcactg tttaactgta actattgcca aaaggacatc 120
tcgaacgtgg tgcgcgtacg gtgcgcggag tgcgcaaacg tggatctgtg cacggagtgc 180
ttcgcggtcg gcgtggagcc gcacccgcac aaggcgtatc atcagtatca cgtcatcgac 240
aacatgtcgt ttccgctgtt cacgcgagat tggggggctg acgaagagtt gttattgctg 300
gaggcagtgg agatgttcgg gttgggggaac tggaccgagg tgagcgaaca cgtcgggacg 360
aagacgcgcg cgcagtgtca cgcgcactat tttgaagtct acgtcaagtc tccttgccgcg 420
ccgttaccgg atatgtcgaa gatttttagga aaaggcgtcg cgcgtatgac atcagacgag 480
ctcaaagcgg aggcggagca aaaggcgaac gaaaataagg atgtggagga ggaggagaag 540
cttctcgaat cgcttgctaa cccgaacgca gtgaagacgg agggcaacgt gcaggaactc 600
acaggttaca acatcaagcg caatgagttc gatcccgaat acgacatgga tgccgaactt 660
cccctggcgg agatggaatt tcgcgaaaac gacaccgaag aagacgtcca gatgaagctg 720
cgaatgattg aaatctacaa cagccggctt caagaacgag cgagaagaaa acaattcatt 780
ctcgaacgca atctgctgaa cgtgaaaaag caacaaaacg tggaaaagaa gcgttcacaa 840
tacgagcgcg acttacacgg caccatgcgt atatttgcac gctttctcac gagtaccgag 900
tacgacgtct tgctcgaggg tctcgccgcg gagcaccgaa tccgaacccg catcaccgaa 960
ctgaaagagt acagacgcaa tggatttcac accatcgag agggcgagga ttacgatttg 1020
gagaagcgtc gtcgtgagac ggagttcgct cgtctacacg cgatcgagca tccaactagc 1080
aagaacatag ccagagcgaa caacttaggt cctcgccgctc gaatgtactt gtcacttgat 1140

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```
ctcgccgatc ttccaggcgt agaccttttg aacgacgacg aaaaggagtt gtgcaggagc 1200
tgtcgcttat tgcctgtgca gtatctctcg atgaagggtgg agttgatgcg agaggggtctc 1260
aagtccgaaa agccgctcaa cagaaatcac gttcggaata tgttcaaagt agaccactc 1320
aaggctattc gtgtgtatga gttactccta cagcacggct ggggtgttga agacggcttc 1380
gtgaaccagc gtgaggatga agactccgaa cctgcgccga aaaagtcagc cagcgcagac 1440
gaggaggaag acgaggagga cgatgaagta gattacgaaa ccgacgataa cgacgaagac 1500
gaggacgagg aagacgacga ggaagaggat agcgaggaag acgattag 1548
```

<210> 192
 <211> 515
 <212> PRT
 <213> *Ostreococcus lucimarinus*

<400> 192

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

Ala Met Thr Lys Leu Ser Gly Asn Gly Glu Ser Cys Ala Leu Phe Asn
 20 25 30

Cys Asn Tyr Cys Gln Lys Asp Ile Ser Asn Val Val Arg Val Arg Cys
 35 40 45

Ala Glu Cys Ala Asn Val Asp Leu Cys Thr Glu Cys Phe Ala Val Gly
 50 55 60

Val Glu Pro His Pro His Lys Ala Tyr His Gln Tyr His Val Ile Asp
 65 70 75 80

Asn Met Ser Phe Pro Leu Phe Thr Arg Asp Trp Gly Ala Asp Glu Glu
 85 90 95

Leu Leu Leu Leu Glu Ala Val Glu Met Phe Gly Leu Gly Asn Trp Thr
 100 105 110

Glu Val Ser Glu His Val Gly Thr Lys Thr Arg Ala Gln Cys His Ala
 115 120 125

His Tyr Phe Glu Val Tyr Val Lys Ser Pro Cys Ala Pro Leu Pro Asp
 130 135 140

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

Leu Lys Ala Glu Ala Glu Gln Lys Ala Asn Glu Asn Lys Asp Val Glu
 165 170 175

Glu Glu Glu Lys Leu Leu Glu Ser Leu Ala Asn Pro Asn Ala Val Lys
 180 185 190

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Thr Glu Gly Asn Val Gln Glu Leu Thr Gly Tyr Asn Ile Lys Arg Asn
195 200 205

Glu Phe Asp Pro Glu Tyr Asp Met Asp Ala Glu Leu Pro Leu Ala Glu
210 215 220

Met Glu Phe Arg Glu Asn Asp Thr Glu Glu Asp Val Gln Met Lys Leu
225 230 235 240

Arg Met Ile Glu Ile Tyr Asn Ser Arg Leu Gln Glu Arg Ala Arg Arg
245 250 255

Lys Gln Phe Ile Leu Glu Arg Asn Leu Leu Asn Val Lys Lys Gln Gln
260 265 270

Asn Val Glu Lys Lys Arg Ser Gln Tyr Glu Arg Asp Leu His Gly Thr
275 280 285

Met Arg Ile Phe Ala Arg Phe Leu Thr Ser Thr Glu Tyr Asp Val Leu
290 295 300

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

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

Asp Tyr Asp Leu Glu Lys Arg Arg Arg Glu Thr Glu Phe Ala Arg Leu
340 345 350

His Ala Ile Glu His Pro Thr Ser Lys Asn Ile Ala Arg Ala Asn Asn
355 360 365

Leu Gly Pro Arg Arg Arg Met Tyr Leu Ser Leu Asp Leu Ala Asp Leu
370 375 380

Pro Gly Val Asp Leu Leu Asn Asp Asp Glu Lys Glu Leu Cys Arg Ser
385 390 395 400

Cys Arg Leu Leu Pro Val Gln Tyr Leu Ser Met Lys Val Glu Leu Met
405 410 415

Arg Glu Gly Leu Lys Ser Glu Lys Pro Leu Asn Arg Asn His Val Arg
420 425 430

Asn Met Phe Lys Val Asp Pro Leu Lys Ala Ile Arg Val Tyr Glu Leu
435 440 445

Leu Leu Gln His Gly Trp Val Leu Glu Asp Gly Phe Val Asn Pro Gly
450 455 460

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Glu Asp Glu Asp Ser Glu Pro Ala Pro Lys Lys Ser Ala Ser Ala Asp
465 470 475 480

Glu Glu Glu Asp Glu Glu Asp Asp Glu Val Asp Tyr Glu Thr Asp Asp
485 490 495

Asn Asp Glu Asp Glu Asp Glu Glu Asp Asp Glu Glu Glu Asp Ser Glu
500 505 510

Glu Asp Asp
515

<210> 193
<211> 1704
<212> DNA
<213> Oryza sativa

<400> 193
atgggccggt ctcgcggggt gcccaattcc ggcgacgatg aaacgaacca caggtcgaag 60
cggaggaggg tcgcgtcgag cggcgatgcg ccggactcgc tctcggcggc ctgcggggga 120
gccggagagg gtggtgggaa gaaggcgctg taccactgca actactgcaa taaggatatt 180
tccgggaaga tccgatcaa gtgctccaag tgccccgact tcgacctctg cgtcgagtgc 240
ttctcggtcg gcgccgaggt caccgccgac cgcagcaacc atccttacag ggtcatggac 300
aacctgtctt tccctcttat ttgtccagat tggaatgcag acgaggaaat ctttcttcta 360
gaggggaattg aaatgtatgg tctgggaaat tgggctgaag ttgcggagca tgttggcacc 420
aagaccaagg cacaatgcat tgatcattat acaactgcat acatgaactc accttgttat 480
ccccttccgg atatgtctca tgtaacgggt aagaacagga aggaattgct tgctatggct 540
aaagtacaag gcgagagtaa aaaagtgtta ccaggggatt tgacccttaa ggacgagtct 600
ccattttctc cccaagggt caaggtggaa gatgcacttg gagaagggtt agctggtcga 660
tcaccttcac acatagctgg gggtgcaa atagaaagcat caaatgttgg acaattcaaa 720
gatggtgcta atgtagcaaa agttgaagat ggtcatgttg atagaagtat aggtgtgaaa 780
aaaccccgat attctgcaga tgaagggcct tctttgactg aactgagtgg atacaattca 840
aagagacatg aatttgacc agagtatgat aacgatgctg aacaggcact cgctgagatg 900
gagtttaaag aaactgattc ggaaactgat cgtgaactga agctaagggt attgctgatt 960
tacttgtaa ggcttgatga aagaaaaagg agaaaagagt tcatactgga aagaaactta 1020
ctatttccta atcctttgga gaaggatctc acaaatgaag acaaggaagt ttaccatcgc 1080
tataagggtg tcatgcgttt cttttctaag gaggaacatg aagcacttgt taggagtgtt 1140
cttgaggaaac ggaaaattcg aaggaggatt caagagcttc aggaatgtcg ttctgctgga 1200
tgccgtacat tggctgaagc aaagattcac atagagcaaa agaggaaaaa ggaacatgag 1260
gtgaatgccc aaaaagctaa ggaaagtggc cagctcttat ccaacactaa agtggtgcat 1320
aagacgaatc gacctatgaa aatcgagtca gatggtaatt tggatcagaa gaaagggtgt 1380

```

gccagcttgg attctactgg cagggattct ccaaaaacca cagggcatgc aggcactaaa 1440
cattgggatg actgggatat tgttggtttt cctggggcag agctattaag caccagtga 1500
aaaaatctat gctgtcagaa cagattgcta cccaaccatt acctgaaaat gcaggaggtt 1560
ttgatgcagg aaatattcaa gggtagtgtc gccagaagg aagatgccca tgtattattt 1620
aaggttgacc ctgccaaagt agataacgtt tatgatatgg tgacgaaaaa gttgggtacc 1680
aatgaggagg ccccgactgt ttag 1704

```

<210> 194
 <211> 567
 <212> PRT
 <213> Oryza sativa

<400> 194

Met Gly Arg Ser Arg Gly Val Pro Asn Ser Gly Asp Asp Glu Thr Asn
1 5 10 15

His Arg Ser Lys Arg Arg Arg Val Ala Ser Ser Gly Asp Ala Pro Asp
20 25 30

Ser Leu Ser Ala Ala Cys Gly Gly Ala Gly Glu Gly Gly Gly Lys Lys
35 40 45

Ala Leu Tyr His Cys Asn Tyr Cys Asn Lys Asp Ile Ser Gly Lys Ile
50 55 60

Arg Ile Lys Cys Ser Lys Cys Pro Asp Phe Asp Leu Cys Val Glu Cys
65 70 75 80

Phe Ser Val Gly Ala Glu Val Thr Pro His Arg Ser Asn His Pro Tyr
85 90 95

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

Ala Asp Glu Glu Ile Leu Leu Leu Glu Gly Ile Glu Met Tyr Gly Leu
115 120 125

Gly Asn Trp Ala Glu Val Ala Glu His Val Gly Thr Lys Thr Lys Ala
130 135 140

Gln Cys Ile Asp His Tyr Thr Thr Ala Tyr Met Asn Ser Pro Cys Tyr
145 150 155 160

Pro Leu Pro Asp Met Ser His Val Asn Gly Lys Asn Arg Lys Glu Leu
165 170 175

Leu Ala Met Ala Lys Val Gln Gly Glu Ser Lys Lys Val Leu Pro Gly
180 185 190

Asp Leu Thr Pro Lys Asp Glu Ser Pro Phe Ser Pro Pro Arg Val Lys

195

200

205

Val Glu Asp Ala Leu Gly Glu Gly Leu Ala Gly Arg Ser Pro Ser His
 210 215 220

Ile Ala Gly Gly Ala Asn Lys Lys Ala Ser Asn Val Gly Gln Phe Lys
 225 230 235 240

Asp Gly Ala Asn Val Ala Lys Val Glu Asp Gly His Val Asp Arg Ser
 245 250 255

Ile Gly Val Lys Lys Pro Arg Tyr Ser Ala Asp Glu Gly Pro Ser Leu
 260 265 270

Thr Glu Leu Ser Gly Tyr Asn Ser Lys Arg His Glu Phe Asp Pro Glu
 275 280 285

Tyr Asp Asn Asp Ala Glu Gln Ala Leu Ala Glu Met Glu Phe Lys Glu
 290 295 300

Thr Asp Ser Glu Thr Asp Arg Glu Leu Lys Leu Arg Val Leu Arg Ile
 305 310 315 320

Tyr Leu Ser Arg Leu Asp Glu Arg Lys Arg Arg Lys Glu Phe Ile Leu
 325 330 335

Glu Arg Asn Leu Leu Phe Pro Asn Pro Leu Glu Lys Asp Leu Thr Asn
 340 345 350

Glu Asp Lys Glu Val Tyr His Arg Tyr Lys Val Phe Met Arg Phe Leu
 355 360 365

Ser Lys Glu Glu His Glu Ala Leu Val Arg Ser Val Leu Glu Glu Arg
 370 375 380

Lys Ile Arg Arg Arg Ile Gln Glu Leu Gln Glu Cys Arg Ser Ala Gly
 385 390 395 400

Cys Arg Thr Leu Ala Glu Ala Lys Ile His Ile Glu Gln Lys Arg Lys
 405 410 415

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

Leu Ser Asn Thr Lys Val Val His Lys Thr Asn Arg Pro Met Lys Ile
 435 440 445

Glu Ser Asp Gly Asn Leu Asp Gln Lys Lys Gly Gly Ala Ser Leu Asp
 450 455 460

Ser Thr Gly Arg Asp Ser Pro Lys Thr Thr Gly His Ala Gly Thr Lys
 465 470 475 480

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

His Trp Asp Asp Trp Asp Ile Val Gly Phe Pro Gly Ala Glu Leu Leu
485 490 495

Ser Thr Ser Glu Lys Asn Leu Cys Cys Gln Asn Arg Leu Leu Pro Asn
500 505 510

His Tyr Leu Lys Met Gln Glu Val Leu Met Gln Glu Ile Phe Lys Gly
515 520 525

Ser Val Ala Lys Lys Glu Asp Ala His Val Leu Phe Lys Val Asp Pro
530 535 540

Ala Lys Val Asp Asn Val Tyr Asp Met Val Thr Lys Lys Leu Gly Thr
545 550 555 560

Asn Glu Glu Ala Pro Thr Val
565

<210> 195
<211> 1683
<212> DNA
<213> Populus trichocarpa

<400> 195
atgggtcgtt ctcgaggga ttttactct aatgatgaag accctactca gagatcaaga 60
aggaagaaga atgcggcaag tggagataat tccgaatctt tattggctgg ccaaggaagt 120
ggtgatggga aaagggcatt ataccattgc aattattgca ataaagatat aacaggggaag 180
acccgtatca aatgcgctat gtgccctgat tttgacctat gcttagagtg cttctctgta 240
ggagctgagg ttacacctca taaaagcaat cacccttaca gggttatgga taatttatct 300
ttcccgctta tttgccctga ttggaatgca gatgaagaaa tactgcttct agaggggaatt 360
gaaatgtatg gattggggaa ctgggcagaa attgctgagc acgtggggac aaagagtaaa 420
gacacatgta ttgaacacta taatagtgtt tacatgcaat ccagtgactt ccctctcccg 480
gacatgtcgc ttgttgttgg gaaaaataga aaggaacttc ttgctatggc caagggatat 540
agtgaggaca aaaaaggtgc tgctatgctt ggggatctta ctttgaagga agaattctca 600
ttttctcctt caagagtga agtcgaagaa atgcataaag gaggttcctc tggccgatta 660
tcaacattaa actcagaggt agaattctgct ggccgtccta ctaccacaaa ctctgcagca 720
acagctgcta ataagaaggc atctagcatt gctcgggtta aagatggacc taatgttgtt 780
aaagtgggaag atcctcaggt ggaccgaaat gctaaagga agaaaccgaa ttcctctggg 840
agtgagggtc catctttaat ggagttgagc gggtataacc ccaagaggca ggagtttgat 900
cccgaatatg ataatgatgc tgagcagttg ctagctgaga tggaatttaa agatactgac 960
actgaggaag agcgggagct gaaattgcga gtgctgcata tatattcaaa gcggctcgac 1020
gagagaaagc gcagaaaaga tttcatacta gaaagaaatc tgctgcaacc aagtcctttt 1080
gaaaaggact tgactccaga agagagggca ttatgtcggc gttatgacct tttcatgcgt 1140

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

tttcattcca aggaagagca tgaggaattg cttcaggttg ttatcgaaga gcatcggatg      1200
ctgaaaagga tcgaagagct gaaggaagct caagcagctg gttgccgcac agcagctgag      1260
gcggacaggt accttgagca gaagaggaaa aaagaagccg aggaaaattc cagtagactg      1320
aaagacaatg ctctggttgg tcctagcaac catggtgctc ccaatgcatt tattccgtca      1380
gagtctgtta ggaaggattc gagtactaga cctgtaggac agggctctgc tagctatgcc      1440
aatggtttgg acacaacagg cttttatgaa acgcagctac tatctgaaac tgaaaaacgg      1500
ctatgccgtg agattcacct acctcctcct gtctacctca agatgcaaga ggtcatgacc      1560
aaagagatct tcagcggtaa catcactaag aaattggatg ctcacccctt gttcaagatt      1620
gaagcaagca aagttgatag ggtgtatgat atacttgtga agaaggggat tgctcaacct      1680
tga                                                                           1683

```

```

<210> 196
<211> 540
<212> PRT
<213> Populus trichocarpa
<400> 196

```

```

Met Gly Arg Ser Arg Gly Arg Pro Pro Ser Ser Gly Thr Ser Thr Ala
1           5           10          15

```

```

Ala Ala Ala Ser Asp Asp Pro Asn Asn Arg Ser Ser Lys Arg Lys Lys
          20          25          30

```

```

Thr Thr Ser Asn Val Gly Ser Ile Glu Thr Ala Phe Pro Ala Val Tyr
35          40          45

```

```

Gln Glu Lys Gly Gln Gly Lys Leu Ala Leu Tyr His Cys Asn Tyr Cys
50          55          60

```

```

His Lys Asp Ile Ser Gly Met Val Arg Ile Lys Cys Ala Val Cys Pro
65          70          75          80

```

```

Asp Phe Asp Leu Cys Val Glu Cys Phe Ser Val Gly Ala Glu Val Thr
          85          90          95

```

```

Pro His Lys Ser Asn His Pro Tyr Arg Val Met Asp Asn Leu Ser Phe
100          105          110

```

```

Pro Leu Phe His Pro Asp Trp Asn Thr Asp Glu Glu Ile Leu Leu Leu
115          120          125

```

```

Glu Gly Ile Glu Met Tyr Gly Phe Gly Asn Trp Thr Glu Val Ser Glu
130          135          140

```

```

His Ala Gly Thr Lys Ser Lys Ser Gln Cys Ile Asp His Tyr Asn Ala
145          150          155          160

```


Val Tyr Met Asp Ser Pro Cys Phe Pro Leu Pro Asp Met Ser His Val
165 170 175

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

Glu Met Lys Lys Glu Val Ser Ser His Met Gly Ser Ser Ser Gly Asn
195 200 205

Thr Phe Ser Asp Ala Val Lys Lys Ala Ser Asn Glu Ala Gln Ile Lys
210 215 220

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

Lys Lys Pro Arg Ile Cys Gly Glu Glu Gly Pro Ser Met Thr Glu Leu
245 250 255

Ser Gly Tyr Asn Phe Lys Arg Gln Glu Phe Glu Ile Glu Tyr Asp Asn
260 265 270

Asp Ala Glu Gln Leu Leu Ala Asp Met Glu Phe Lys Asp Thr Asp Thr
275 280 285

Asp Ala Glu Leu Asp Met Lys Leu Gln Val Leu Arg Ile Tyr Ser Lys
290 295 300

Arg Leu Asp Glu Arg Lys Arg Arg Lys Asp Phe Ile Leu Glu Arg Asn
305 310 315 320

Leu Phe Tyr Pro Asp Ala Phe Glu Lys Asn Ile Ser Pro Glu Glu Lys
325 330 335

Glu Ile Tyr Gln Arg Tyr Lys Val Phe Met Arg Phe His Thr Lys Glu
340 345 350

Glu His Glu Glu Leu Met Lys Thr Val Ile Glu Asp His Gln Ile Met
355 360 365

Lys Arg Ile Gln Asp Leu Gln Glu Ala Arg Ala Ala Gly Cys Gln Thr
370 375 380

Ala Gly Glu Ala Gln Gly Phe Ile Glu Gln Lys Arg Lys Lys Glu Ala
385 390 395 400

Glu Glu Ser Ala Gln Arg Ala Lys Glu Ser Met Gln Ala Gly Pro Ala
405 410 415

Gly Lys Leu Leu Pro Lys Pro Asn His Leu Asp Ser Ser Pro Arg Gly
420 425 430

Ala Val Lys Cys Ser Thr Val Phe His Pro Gly Gly Asn Asp Ser Ser
Seite 205

435

440

445

Ser Met Ile Ala Lys Gln Ala Ile Ser Ser Thr Leu Asp Glu Trp Asp
450 455 460

Ile Ala Gly Phe Leu Gly Ala Asp Leu Leu Ser Glu Ser Asp Lys Arg
465 470 475 480

Leu Cys Cys Glu Leu Arg Ile Leu Pro Ala His Tyr Leu Asn Met Leu
485 490 495

His Ile Met Ser Ile Glu Ile Thr Lys Gly Thr Val Thr Asn Lys Thr
500 505 510

Asp Ala His Ser Leu Phe Lys Val Glu Ser Ser Lys Val Asp Arg Val
515 520 525

Tyr Asp Met Leu Val Lys Lys Gly Ile Ala Leu Ala
530 535 540

<210> 197
<211> 1623
<212> DNA
<213> Populus trichocarpa

<400> 197
atgggtcgtt cgcgcggtcg cctccttct tccggaacct ccactgccgc cgccgcctct 60
gatgatccaa acaatagatc ttcaaaaaga aaaaagacga cttccaatgt agggagtata 120
gagactgcat ttccagcagt atatcaagaa aagggtcaag ggaaactggc actataccac 180
tgcaattact gtcataaaga catctctgga atggttcgca ttaagtgtgc agtgtgtcct 240
gatttcgacc tttgcgttga gtgtttttct gttggagccg aagtgactcc tcataaaagc 300
aatcatccct acagggttat ggacaatctg tcttttccgc tctttcatcc agactggaat 360
acagatgaag agatattact tctagagggc attgaaatgt atggatttgg gaactggact 420
gaagtttcag aacatgctgg aaccaagagc aaatctcaat gcattgatca ctataatgct 480
gtatacatgg actcccatg ctttcctctc ccagacatgt ctcattgttat gggaaaaaca 540
agagaggagc tccttgcaat ggccagagga aatgttgaaa tgaagaaaga agtcagctct 600
catatgggtt caagcagtgg caacacattc tcagatgcag ttaagaaagc atctaacgag 660
gcccagatta aggataagat taaagtggaa gaacctctgt ctgacaggag tattcgagag 720
aaaaaaccta gaatttgcgg agaggaagga ctttcaatga cagagttaag tggctataat 780
ttcaagaggc aggaatttga gattgaatat gataatgatg cagagcaact actggcagat 840
atggaattca aagatactga cactgatgct gagcttgaca tgaaactgca agttctgcgc 900
atttactcaa aaaggcttga tgagaggaaa cggaggaaag attttatttt ggaaagaaat 960
ttgttttacc ctgatgcatt tgagaagaac atttcacctg aagagaagga aatatatcag 1020
cgttacaagg tcttcatgag gttccacaca aaagaagagc atgaagaatt gatgaagact 1080

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

gttattgaag atcatcagat tatgaaaaga atacaagatc ttcaggaagc tcgagctgct	1140
ggctgtcaaa cagctggtga ggcccaagga tttattgagc agaagagaaa gaaggaagcc	1200
gaagaaagtg cccaaagagc gaaggaaagt atgcaagcag gccagcagg taaactgttg	1260
ccaaagccaa atcatcttga cagcagccct cgtggagctg tcaagtgttc caccgttttt	1320
catcctggtg gcaacgactc atcttcaatg attgcaaaac aagcaatttc aagcaccctc	1380
gatgagtggg atattgctgg attcctaggg gctgatttgc tctctgaatc tgataagcgt	1440
ctttgttgtg agttgagaat actacctgca cattatctca acatgctgca cataatgtca	1500
atagagataa caaagggtag tgttaccaac aaaaccgatg ctcatagcct gttcaagggtg	1560
gaatcaagca aagtggatag agtatatgat atgttagtga aaaaggggat tgctctagca	1620
tga	1623

<210> 198
 <211> 560
 <212> PRT
 <213> Populus trichocarpa

<400> 198

Met Gly Arg Ser Arg Gly Asn Phe His Ser Asn Asp Glu Asp Pro Thr
 1 5 10 15

Gln Arg Ser Arg Arg Lys Lys Asn Ala Ala Ser Gly Asp Asn Ser Glu
 20 25 30

Ser Leu Leu Ala Gly Gln Gly Ser Gly Asp Gly Lys Arg Ala Leu Tyr
 35 40 45

His Cys Asn Tyr Cys Asn Lys Asp Ile Thr Gly Lys Thr Arg Ile Lys
 50 55 60

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

Gly Ala Glu Val Thr Pro His Lys Ser Asn His Pro Tyr Arg Val Met
 85 90 95

Asp Asn Leu Ser Phe Pro Leu Ile Cys Pro Asp Trp Asn Ala Asp Glu
 100 105 110

Glu Ile Leu Leu Leu Glu Gly Ile Glu Met Tyr Gly Leu Gly Asn Trp
 115 120 125

Ala Glu Ile Ala Glu His Val Gly Thr Lys Ser Lys Asp Thr Cys Ile
 130 135 140

Glu His Tyr Asn Ser Val Tyr Met Gln Ser Gln Tyr Phe Pro Leu Pro
 145 150 155 160

Asp Met Ser Leu Val Val Gly Lys Asn Arg Lys Glu Leu Leu Ala Met

Ala Lys Gly Tyr Ser Glu Asp Lys Lys Gly Ala Ala Met Leu Gly Asp
180 185 190

Leu Thr Leu Lys Glu Glu Ser Pro Phe Ser Pro Ser Arg Val Lys Val
195 200 205

Glu Glu Met His Lys Gly Gly Ser Ser Gly Arg Leu Ser Thr Leu Asn
210 215 220

Ser Glu Val Glu Ser Ala Gly Arg Pro Thr Thr Thr Asn Ser Ala Ala
225 230 235 240

Thr Ala Ala Asn Lys Lys Ala Ser Ser Ile Ala Arg Val Lys Asp Gly
245 250 255

Pro Asn Val Val Lys Val Glu Asp Pro Gln Val Asp Arg Asn Ala Lys
260 265 270

Gly Lys Lys Pro Asn Ser Ser Gly Ser Glu Gly Pro Ser Leu Met Glu
275 280 285

Leu Ser Gly Tyr Asn Pro Lys Arg Gln Glu Phe Asp Pro Glu Tyr Asp
290 295 300

Asn Asp Ala Glu Gln Leu Leu Ala Glu Met Glu Phe Lys Asp Thr Asp
305 310 315 320

Thr Glu Glu Glu Arg Glu Leu Lys Leu Arg Val Leu His Ile Tyr Ser
325 330 335

Lys Arg Leu Asp Glu Arg Lys Arg Arg Lys Asp Phe Ile Leu Glu Arg
340 345 350

Asn Leu Leu Gln Pro Ser Pro Phe Glu Lys Asp Leu Thr Pro Glu Glu
355 360 365

Arg Ala Leu Cys Arg Arg Tyr Asp Pro Phe Met Arg Phe His Ser Lys
370 375 380

Glu Glu His Glu Glu Leu Leu Gln Val Val Ile Glu Glu His Arg Met
385 390 395 400

Leu Lys Arg Ile Glu Glu Leu Lys Glu Ala Gln Ala Ala Gly Cys Arg
405 410 415

Thr Ala Ala Glu Ala Asp Arg Tyr Leu Glu Gln Lys Arg Lys Lys Glu
420 425 430

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

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Ser Asn His Gly Ala Pro Asn Ala Phe Ile Pro Ser Glu Ser Val Arg
450 455 460

Lys Asp Ser Ser Thr Arg Pro Val Gly Gln Gly Ser Ala Ser Tyr Ala
465 470 475 480

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

Thr Glu Lys Arg Leu Cys Arg Glu Ile His Leu Pro Pro Pro Val Tyr
500 505 510

Leu Lys Met Gln Glu Val Met Thr Lys Glu Ile Phe Ser Gly Asn Ile
515 520 525

Thr Lys Lys Leu Asp Ala His Pro Leu Phe Lys Ile Glu Ala Ser Lys
530 535 540

Val Asp Arg Val Tyr Asp Ile Leu Val Lys Lys Gly Ile Ala Gln Pro
545 550 555 560

<210> 199
<211> 1680
<212> DNA
<213> Populus trichocarpa

<400> 199
atgggtcgtt ctcgtgggaa ttttcactct actgatgaag accctactca gagatcaaga 60
aggaaaaaga acgctgcaag tggagagaat tcggaatctt catcggcagg ccaaggaagt 120
agtgatggta aaagggcatt ataccattgc aattattgca ataaagacat aacagggag 180
acccgtatca aatgtgctgt gtgccctgat tttgacctat gtttagagtg cttctctgta 240
ggagctgagg ttacgcctca taaaagcaat cacccttaca gggttatgga taacctatct 300
ttcccactta tttgccctga ctggaatgca gatgaagaaa tactgcttct agaggggaatt 360
gaaatgtatg gattggggaa ttgggcagaa gttgctgagc atgtggggac aaagaataaa 420
gaaacatgta tcaaacacta taatagcgta tacttgcaat ccagttctt ccctctcccg 480
gacatgtctc atgttggttg gaaaaataga aaggagcttc ttgctatggc caagggacat 540
agtgaggaca aaaaaggtag ttctatgctt ggggagcata ctttgaagga agaattctca 600
ttttctcctt caagagtcaa ggtcgaagaa atgcataaag taggttcctc tggccgatta 660
tcaacattaa attcagagtt agaaactgag agccgtccta atagcgcaaa ttctgcagca 720
acagctgcta ataagaaggc atcaagcatg gcccgaaatta atgatggacc cgggtgtaag 780
gtggaagatc ctcaagtgga ccgaaatttc aaggggaaga aaccaagttc ctcaaggagt 840
gaggggtccat cattaatgga gttgagcggg tataatccca agaggcagga gtttgatcct 900
gaatatgaca atgatgctga gcagttgctg gctgagatgg aatttaaaga taatgacact 960
gaggaagagc gtgagctgaa gttgagagt ctgcgtatat attcaaggag gcttgatgag 1020

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

agaaagcgca gaaaagattt cattcttgaa agaaatctac tacatccaag tcctttcgaa      1080
aaggacttga ctccagaaga gagggcatta tgtcggcggtt ttgacccttt catgcgtttt      1140
cattccaagg aagagcatga agaactgctt cgggctggtg tcaaggagca ctggatgctg      1200
aaaagggctc aagagctgaa ggatgcccaa gtggctgggtt gccgcacagc agttgaggca      1260
gacaggtatc ttgagcacia gagaaaaata gaagctgagg aaacttccag gagactgaaa      1320
gacaatgctc agattggtcc tagcagtcag ggtgctccca atgcattcat gtctccagac      1380
tctgttggga aggattcaag caccagacct gcaggacagg gctcttctag ctatgccaat      1440
gatttggaca taatgggctt ttatgaaacg cagctactgt ctgaaactga aaaacggcta      1500
tgctgcgaga ttcacctacc tccacctgtc tacctcaaga tgcaggaggt gatgacaaaa      1560
gagatcttca gcggtaacat cactaagaaa tcagatgctc accccttggt caagattgaa      1620
gcaagcaaag ttgatggggt gtatgatatg cttgtgaaga aggggattgc tcaaccttga      1680

```

```

<210> 200
<211> 559
<212> PRT
<213> Populus trichocarpa

```

<400> 200

```

Met Gly Arg Ser Arg Gly Asn Phe His Ser Thr Asp Glu Asp Pro Thr
1           5           10           15

```

```

Gln Arg Ser Arg Arg Lys Lys Asn Ala Ala Ser Gly Glu Asn Ser Glu
          20          25          30

```

```

Ser Ser Ser Ala Gly Gln Gly Ser Ser Asp Gly Lys Arg Ala Leu Tyr
          35          40          45

```

```

His Cys Asn Tyr Cys Asn Lys Asp Ile Thr Gly Lys Thr Arg Ile Lys
          50          55          60

```

```

Cys Ala Val Cys Pro Asp Phe Asp Leu Cys Leu Glu Cys Phe Ser Val
65          70          75          80

```

```

Gly Ala Glu Val Thr Pro His Lys Ser Asn His Pro Tyr Arg Val Met
          85          90          95

```

```

Asp Asn Leu Ser Phe Pro Leu Ile Cys Pro Asp Trp Asn Ala Asp Glu
          100          105          110

```

```

Glu Ile Leu Leu Leu Glu Gly Ile Glu Met Tyr Gly Leu Gly Asn Trp
          115          120          125

```

```

Ala Glu Val Ala Glu His Val Gly Thr Lys Asn Lys Glu Thr Cys Ile
          130          135          140

```

```

Lys His Tyr Asn Ser Val Tyr Leu Gln Ser Gln Phe Phe Pro Leu Pro
145          150          155          160

```

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Asp Met Ser His Val Val Gly Lys Asn Arg Lys Glu Leu Leu Ala Met
 165 170 175
 Ala Lys Gly His Ser Glu Asp Lys Lys Gly Thr Ser Met Leu Gly Glu
 180 185 190
 His Thr Leu Lys Glu Glu Ser Pro Phe Ser Pro Ser Arg Val Lys Val
 195 200 205
 Glu Glu Met His Lys Val Gly Ser Ser Gly Arg Leu Ser Thr Leu Asn
 210 215 220
 Ser Glu Leu Glu Thr Ala Ser Arg Pro Asn Ser Ala Asn Ser Ala Ala
 225 230 235 240
 Thr Ala Ala Asn Lys Lys Ala Ser Ser Met Ala Arg Ile Asn Asp Gly
 245 250 255
 Pro Gly Val Lys Val Glu Asp Pro Gln Val Asp Arg Asn Phe Lys Gly
 260 265 270
 Lys Lys Pro Ser Ser Ser Gly Ser Glu Gly Pro Ser Leu Met Glu Leu
 275 280 285
 Ser Gly Tyr Asn Pro Lys Arg Gln Glu Phe Asp Pro Glu Tyr Asp Asn
 290 295 300
 Asp Ala Glu Gln Leu Leu Ala Glu Met Glu Phe Lys Asp Asn Asp Thr
 305 310 315 320
 Glu Glu Glu Arg Glu Leu Lys Leu Arg Val Leu Arg Ile Tyr Ser Arg
 325 330 335
 Arg Leu Asp Glu Arg Lys Arg Arg Lys Asp Phe Ile Leu Glu Arg Asn
 340 345 350
 Leu Leu His Pro Ser Pro Phe Glu Lys Asp Leu Thr Pro Glu Glu Arg
 355 360 365
 Ala Leu Cys Arg Arg Phe Asp Pro Phe Met Arg Phe His Ser Lys Glu
 370 375 380
 Glu His Glu Glu Leu Leu Arg Ala Val Val Lys Glu His Trp Met Leu
 385 390 395 400
 Lys Arg Val Glu Glu Leu Lys Asp Ala Gln Val Ala Gly Cys Arg Thr
 405 410 415
 Ala Val Glu Ala Asp Arg Tyr Leu Glu His Lys Arg Lys Ile Glu Ala
 420 425 430

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Glu Glu Thr Ser Arg Arg Leu Lys Asp Asn Ala Gln Ile Gly Pro Ser
435 440 445

Ser Gln Gly Ala Pro Asn Ala Phe Met Ser Pro Asp Ser Val Gly Lys
450 455 460

Asp Ser Ser Thr Arg Pro Ala Gly Gln Gly Ser Ser Ser Tyr Ala Asn
465 470 475 480

Asp Leu Asp Ile Met Gly Phe Tyr Glu Thr Gln Leu Leu Ser Glu Thr
485 490 495

Glu Lys Arg Leu Cys Cys Glu Ile His Leu Pro Pro Pro Val Tyr Leu
500 505 510

Lys Met Gln Glu Val Met Thr Lys Glu Ile Phe Ser Gly Asn Ile Thr
515 520 525

Lys Lys Ser Asp Ala His Pro Leu Phe Lys Ile Glu Ala Ser Lys Val
530 535 540

Asp Gly Val Tyr Asp Met Leu Val Lys Lys Gly Ile Ala Gln Pro
545 550 555

<210> 201
<211> 1722
<212> DNA
<213> Vitis vinifera

<400> 201
atgggtcgtt ctcgcgagc tctgcattct actgacgatg atcaagggtc acacagatcc 60
aagagaagaa agactgcttc aacagcagac aatttagagg gtgcaactgc aggccaagga 120
atgagtgagg ggaagmgagc ttcataccac tgtaattatt gcagcaaaga tatctcagga 180
aagatccgta ccaaagtgt agtttgtccc gattttgacc tttgcattga atgcttttcc 240
attggagctg aggttacacc tcaygtatgc tttcatccat atcgggtcat ggacaattta 300
tcgttcccac tcatttgtcc tgattggaat gcagatgaag agatgttact tctggagggg 360
attgaaatgt acggactggg gaactggagt gaagtttcag aacatgttgg aaccaaagaa 420
aaatcagaat gtatcgatca ctatgttgct atatacatga attcccatg ctttcctctt 480
cctgacatgt cccatgttct tggaaagact agggctgagc tccttgccat ggccagggga 540
gaagatgaag tcaagaaagg atcccctaca catggggagt taactctgaa agtggaatct 600
cccttatctg caagagtcaa gtacggcaaa tgcattgtaa aatgtgtttc tctcatctgt 660
cagagatcca atccgacatg gatttctagc agcactaaaa catctgcagg tgcagttaag 720
agggcatcta acatggccca ggttaaggat ggtcgtgata acattaaagt ggaagaaact 780
caaacagaca gaagtgttgg agagaaaaag cctaggacct cgggggatga ggggccttct 840
gtgacagagc tgagtggata caatttcaag aggcaagagt ttgatgttga gtatgataat 900

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

gatgctgagc agttactggc tgatatggaa ttcaaggatg ctgacactga tgctgagcat	960
gaactgaaac tgcaagttct gcatatttat tccaaaaggc ttgatgagag gaaacgcagg	1020
aaggatttca tattggaaag aaatctactt taccctgacc cttttgagaa gaacctctca	1080
cctgaagaga gggacgtaaa tcagcgcttc aaggctcttta tgcggttcca ctcaaaagaa	1140
gaacatgagg aactgcttag ggttgtgctc gaggaacatt ggattcagaa aagaatacaa	1200
gatcttcagg acgcccagagc tgctggctgc cgtacatctg ctgaggcaga gagatatctt	1260
gaagagaaaag ggaagaaaga agctgaagaa agtgcccaac aagcaaagga aagtgtctgag	1320
gctggtccta gtgggggtaa agtcttacag aggggtgaaca ctgccaaagg agaatctgat	1380
ggcagtcctc ggggaggtgg aagaggttct gcaggtctag aacctggaat caaggacact	1440
tcttcaacaa ctgcaggaca tgctatctta agatccctag atgtttggga tatcactgga	1500
tttccggggg aagatttact ctcaaaaact gagaaacagc tttgcagtga gatcagaatc	1560
ctcccttcac attatctcaa catgctgcac accatgttga cagagacgtt aaatggaaac	1620
atcaccagga aatcagatgc ccatggcctg ttcaagggtg aaccaagcaa agtagacaaa	1680
gtgtacgata tgtttgtgaa gaagggaatt gttaagtcac ag	1722

<210> 202
 <211> 573
 <212> PRT
 <213> Vitis vinifera

<400> 202

Met Gly Arg Ser Arg Ala Val Leu His Ser Thr Asp Asp Asp Gln Gly
 1 5 10 15

Ser His Arg Ser Lys Arg Arg Lys Thr Ala Ser Thr Ala Asp Asn Leu
 20 25 30

Glu Gly Ala Thr Ala Gly Gln Gly Met Ser Glu Gly Lys Arg Ala Ser
 35 40 45

Tyr His Cys Asn Tyr Cys Ser Lys Asp Ile Ser Gly Lys Ile Arg Thr
 50 55 60

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

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

Met Asp Asn Leu Ser Phe Pro Leu Ile Cys Pro Asp Trp Asn Ala Asp
 100 105 110

Glu Glu Met Leu Leu Leu Glu Gly Ile Glu Met Tyr Gly Leu Gly Asn
 115 120 125

Trp Ser Glu Val Ser Glu His Val Gly Thr Lys Arg Lys Ser Glu Cys
 Seite 213

130

135

140

Ile Asp His Tyr Val Ala Ile Tyr Met Asn Ser Pro Cys Phe Pro Leu
 145 150 155 160

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

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

Glu Leu Thr Leu Lys Val Glu Ser Pro Leu Ser Ala Arg Val Lys Tyr
 195 200 205

Gly Lys Cys Met Leu Lys Cys Val Ser Leu Ile Cys Gln Arg Ser Asn
 210 215 220

Pro Thr Trp Ile Ser Ser Ser Thr Lys Thr Ser Ala Gly Ala Val Lys
 225 230 235 240

Arg Ala Ser Asn Met Ala Gln Val Lys Asp Gly Arg Asp Asn Ile Lys
 245 250 255

Val Glu Glu Thr Gln Thr Asp Arg Ser Val Gly Glu Lys Lys Pro Arg
 260 265 270

Thr Ser Gly Asp Glu Gly Pro Ser Val Thr Glu Leu Ser Gly Tyr Asn
 275 280 285

Phe Lys Arg Gln Glu Phe Asp Val Glu Tyr Asp Asn Asp Ala Glu Gln
 290 295 300

Leu Leu Ala Asp Met Glu Phe Lys Asp Ala Asp Thr Asp Ala Glu His
 305 310 315 320

Glu Leu Lys Leu Gln Val Leu His Ile Tyr Ser Lys Arg Leu Asp Glu
 325 330 335

Arg Lys Arg Arg Lys Asp Phe Ile Leu Glu Arg Asn Leu Leu Tyr Pro
 340 345 350

Asp Pro Phe Glu Lys Asn Leu Ser Pro Glu Glu Arg Asp Val Asn Gln
 355 360 365

Arg Phe Lys Val Phe Met Arg Phe His Ser Lys Glu Glu His Glu Glu
 370 375 380

Leu Leu Arg Val Val Leu Glu Glu His Trp Ile Gln Lys Arg Ile Gln
 385 390 395 400

Asp Leu Gln Asp Ala Arg Ala Ala Gly Cys Arg Thr Ser Ala Glu Ala
 405 410 415

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Glu Arg Tyr Leu Glu Glu Lys Gly Lys Lys Glu Ala Glu Glu Ser Ala
420 425 430

Gln Gln Ala Lys Glu Ser Ala Glu Ala Gly Pro Ser Gly Gly Lys Val
435 440 445

Leu Gln Arg Val Asn Thr Ala Lys Gly Glu Ser Asp Gly Ser Pro Arg
450 455 460

Gly Gly Gly Arg Gly Ser Ala Gly Leu Glu Pro Gly Ile Lys Asp Thr
465 470 475 480

Ser Ser Thr Thr Ala Gly His Ala Ile Leu Arg Ser Leu Asp Val Trp
485 490 495

Asp Ile Thr Gly Phe Pro Gly Glu Asp Leu Leu Ser Glu Thr Glu Lys
500 505 510

Gln Leu Cys Ser Glu Ile Arg Ile Leu Pro Ser His Tyr Leu Asn Met
515 520 525

Leu His Thr Met Leu Thr Glu Thr Leu Asn Gly Asn Ile Thr Arg Lys
530 535 540

Ser Asp Ala His Gly Leu Phe Lys Val Glu Pro Ser Lys Val Asp Lys
545 550 555 560

Val Tyr Asp Met Phe Val Lys Lys Gly Ile Val Lys Ser
565 570

<210> 203
<211> 1698
<212> DNA
<213> Zea mays

<400> 203
atggggcggt cgcgaggggt gcagaattcc ggcgacgacg acaccgtaca cagggtcgaag 60
cggaggaggg tcgcatcggg cggggatgcg acggactccg tttccgctgg catcggggga 120
gctggagaag gagggggcaa gaaagcgctc taccactgca attactgcaa caaggacatc 180
tctgggaaga tacggatcaa atgctccaag tgccctgact tcgacctttg cgtggagtgc 240
ttctctgttg gcgctgaagt caccacacat cgcagcaacc atccttacia agtcatggac 300
aacctgtctt tcccacttat ttgccagat tggaatgcag acgaagaaat tctcctcctt 360
gaggggaattg aaatgtatgg tctgggaaac tggcttgaag ttgcagagca tgttggtacc 420
aagtctaagt tacagtgtat tgatcattac acaacagcat acatgaactc acctgttat 480
cccctaccgg atatgtctca tggttaatggc aagaacagga aggagcttct agctatggct 540
aaagtgcagg gtgaaagtaa aaaagggact tctactgttc ctggagagct gactcctaag 600
gctgaatctc ctttttctcc ctccagggtc aaggtggaag atgcacttgg agaaggtcta 660

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

gcaggctgat caccttcgca catagctggt ggtgcaaata aaaaagcttc aaatgtggga 720
catattaaag atgggtctaa tgtatcaaaa gttgaagatg gtcattgtcga tagaagtgtt 780
ggtgtgaaga agcccagata ttctgcagat gaaggccctt cgttgactga actgagtggg 840
tacaatgcaa agagacacga gtttgacca gagtatgata atgatgccga acaagcgctt 900
gctgagatgg aatttaaaga aactgattca gaaactgac gtgaactgaa actccgtgtg 960
ctgcgtatct atctgtccag gcttgatgaa agaaaaagga gaaaagagtt catattggaa 1020
aggaatttat tgtttcctaa tcccttgag aaggatctta caaatgaaga cagggaagtt 1080
taccatcggt ataaggtctt catgcgtttt ctttccaagg aggaacatga agcccttggt 1140
aggagtgtca ttgaagagcg aaaaattcgg aggagaattc aagaactcca ggaatgtcgt 1200
tctgctggat gccgcacact tgctgaagca aagatacaca tagagcaaaa gagggaaaaa 1260
gaatacgagc tgaatgccca aaaagctaag gaaagtaacc accttattgc aaatactaaa 1320
ttggtgcaga agatgaatcg acctatgaag attgagtctg atgggaattt ggatccaaag 1380
aaaggtggtg ttgcgttaga ttctcctaaa actacaggac ttacaagtgt taagcagtgg 1440
gatgactggg atatagttag tcttcctggg gcgaagctat taagtgttag cgaaaagctt 1500
ctatgttgcc agaacagact gctaccagc cattacctga gaatgcagga ggtgctgatg 1560
caggagatat tcaagggtag tgtcctaaag aaggaagacg cacacgtctt gtttaaggtt 1620
gatcctacca aagtagatag tgtttatgat atggtaacaa aaaagctggg caaccatgtg 1680
gagttgccta cggcttag 1698

<210> 204
<211> 565
<212> PRT
<213> Zea mays

<400> 204

Met Gly Arg Ser Arg Gly Val Gln Asn Ser Gly Asp Asp Asp Thr Val
1 5 10 15

His Arg Ser Lys Arg Arg Arg Val Ala Ser Gly Gly Asp Ala Thr Asp
20 25 30

Ser Val Ser Ala Gly Ile Gly Gly Ala Gly Glu Gly Gly Gly Lys Lys
35 40 45

Ala Leu Tyr His Cys Asn Tyr Cys Asn Lys Asp Ile Ser Gly Lys Ile
50 55 60

Arg Ile Lys Cys Ser Lys Cys Pro Asp Phe Asp Leu Cys Val Glu Cys
65 70 75 80

Phe Ser Val Gly Ala Glu Val Thr Pro His Arg Ser Asn His Pro Tyr
85 90 95

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Lys Val Met Asp Asn Leu Ser Phe Pro Leu Ile Cys Pro Asp Trp Asn
100 105 110

Ala Asp Glu Glu Ile Leu Leu Leu Glu Gly Ile Glu Met Tyr Gly Leu
115 120 125

Gly Asn Trp Leu Glu Val Ala Glu His Val Gly Thr Lys Ser Lys Leu
130 135 140

Gln Cys Ile Asp His Tyr Thr Thr Ala Tyr Met Asn Ser Pro Cys Tyr
145 150 155 160

Pro Leu Pro Asp Met Ser His Val Asn Gly Lys Asn Arg Lys Glu Leu
165 170 175

Leu Ala Met Ala Lys Val Gln Gly Glu Ser Lys Lys Gly Thr Ser Leu
180 185 190

Leu Pro Gly Glu Leu Thr Pro Lys Ala Glu Ser Pro Phe Ser Pro Ser
195 200 205

Arg Val Lys Val Glu Asp Ala Leu Gly Glu Gly Leu Ala Gly Arg Ser
210 215 220

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

His Ile Lys Asp Gly Ser Asn Val Ser Lys Val Glu Asp Gly His Val
245 250 255

Asp Arg Ser Val Gly Val Lys Lys Pro Arg Tyr Ser Ala Asp Glu Gly
260 265 270

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

Asp Pro Glu Tyr Asp Asn Asp Ala Glu Gln Ala Leu Ala Glu Met Glu
290 295 300

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

Leu Arg Ile Tyr Leu Ser Arg Leu Asp Glu Arg Lys Arg Arg Lys Glu
325 330 335

Phe Ile Leu Glu Arg Asn Leu Leu Phe Pro Asn Pro Leu Glu Lys Asp
340 345 350

Leu Thr Asn Glu Asp Arg Glu Val Tyr His Arg Tyr Lys Val Phe Met
355 360 365

Arg Phe Leu Ser Lys Glu Glu His Glu Ala Leu Val Arg Ser Val Ile
Seite 217

370

375

380

Glu Glu Arg Lys Ile Arg Arg Arg Ile Gln Glu Leu Gln Glu Cys Arg
385 390 395 400

Ser Ala Gly Cys Arg Thr Leu Ala Glu Ala Lys Ile His Ile Glu Gln
405 410 415

Lys Arg Lys Lys Glu Tyr Glu Leu Asn Ala Gln Lys Ala Lys Glu Ser
420 425 430

Asn His Leu Ile Ala Asn Thr Lys Leu Val Gln Lys Met Asn Arg Pro
435 440 445

Met Lys Ile Glu Ser Asp Gly Asn Leu Asp Pro Lys Lys Gly Gly Val
450 455 460

Ala Leu Asp Ser Pro Lys Thr Thr Gly Leu Thr Ser Val Lys Gln Trp
465 470 475 480

Asp Asp Trp Asp Ile Val Gly Leu Pro Gly Ala Lys Leu Leu Ser Ala
485 490 495

Ser Glu Lys Leu Leu Cys Cys Gln Asn Arg Leu Leu Pro Ser His Tyr
500 505 510

Leu Arg Met Gln Glu Val Leu Met Gln Glu Ile Phe Lys Gly Ser Val
515 520 525

Leu Lys Lys Glu Asp Ala His Val Leu Phe Lys Val Asp Pro Thr Lys
530 535 540

Val Asp Ser Val Tyr Asp Met Val Thr Lys Lys Leu Gly Asn His Val
545 550 555 560

Glu Leu Pro Thr Val
565

<210> 205

<211> 1698

<212> DNA

<213> Zea mays

<400> 205

atggggcggt cgcgaggggt gctgagttcc ggcgacgacg acaccgggca caggtcgaag 60

cggaggagag tctcgtcggg cggggatgcg acggactcca tttcagcctc catcggggga 120

gctggagagg gagggggcaa gaaggcgctc tatcactgca actactgcaa caaggacatc 180

tccgggaaga tacggatcaa gtgctccaag tgccctgact tcgacctttg cgtggagtgt 240

ttctctgtcg gcgctgaagt caccgccac cgcagcaacc atccttaca agtcatggac 300

aacttgtctt tcccattat ttgccggat tggaatgcag atgaagaaat tctcctcctt 360

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

gaggggaattg aaatgtatgg tctgggaaac tggcttgaag ttgcagagca tgttggtacc 420
aagtctaagt tacagtgtat tgatcattac acatcagcat acatgaactc accttggttat 480
cccctcccgg atatgtctca tgttaatggc aagaatagga aggaacttct agctatggct 540
aaagtacagg gtgagagtaa aaaagggact ttgctgttac ctggagaact cactcctaag 600
gttgaatctc aattttctcc ctccagggtc aagggtggaag atgcacttgg agaaggtcca 660
gcaggtcgat caccttcaca catggctgtt ggtgcaaata aaaaagcttc aaatgtggga 720
catattaagg atggcgctac tgtatcaaaa gtcgaagatg ttcatgtaga tagaagtgtt 780
ggtgtgaaga agcccagata ttctgcagat gaaggccctt cgttgactga actgagtgga 840
tacaatgcaa agagacatga gtttgacca gaatacgata atgatgccga acaagctctt 900
gctgagatgg aatttaaaga aactgattcg gaaactgac gtgaactgaa actccgtgtg 960
ctgcgtatth acctctccag gcttgatgaa agaaaaagaa gaaaggagt catattggaa 1020
agaaatttgt tgttcctaa tcccttgag aaggatctta cgagtgaaga cagggaactt 1080
taccatcgct ataaagtctt catgcgtttt ctttctaagg aggaacatga agccctcggt 1140
aggagtgtta ttgaggagcg aaaaattcgg aggagaattc aagaactcca ggaatgccgt 1200
tctgctggat gccgcacact ggctgaagca aagatacaca tagagcaaaa gagggaaaaa 1260
gaatacgagc tgaatgcgca aaaagctaag gatagcagtc aacttaatgc aaataataaa 1320
tcagtacaaa agatgaatcg acctatgaaa attgagtccg atgggaattt ggatccaaag 1380
aaagggtgtg ctggcttga ttctcctaag acaacaggac ctacaagtgt taagcagtgg 1440
gatgactggg atatagtttg tcttcctggg gcagagctat taagtgctag cgaaaagctt 1500
ctatgctgtc agaacagatt gctaccagc cattacctga gaatgcagga ggtgctgatg 1560
caggagatat tcaagggtag cgtcctaaag aaggaagacg cccacgtctt atttaaggtc 1620
gatcctacca aagtagatag tgtttatgat atggtatcta aaaaactggg caaccatgag 1680
gaggcccaa cgtctag 1698

```

<210> 206
 <211> 565
 <212> PRT
 <213> Zea mays

<400> 206

Met Gly Arg Ser Arg Gly Val Leu Ser Ser Gly Asp Asp Asp Thr Gly
 1 5 10 15

His Arg Ser Lys Arg Arg Arg Val Ser Ser Gly Gly Asp Ala Thr Asp
 20 25 30

Ser Ile Ser Ala Ser Ile Gly Gly Ala Gly Glu Gly Gly Gly Lys Lys
 35 40 45

Ala Leu Tyr His Cys Asn Tyr Cys Asn Lys Asp Ile Ser Gly Lys Ile
 50 55 60

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

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

Phe Ile Leu Glu Arg Asn Leu Leu Phe Pro Asn Pro Leu Glu Lys Asp
340 345 350

Leu Thr Ser Glu Asp Arg Glu Leu Tyr His Arg Tyr Lys Val Phe Met
355 360 365

Arg Phe Leu Ser Lys Glu Glu His Glu Ala Leu Val Arg Ser Val Ile
370 375 380

Glu Glu Arg Lys Ile Arg Arg Arg Ile Gln Glu Leu Gln Glu Cys Arg
385 390 395 400

Ser Ala Gly Cys Arg Thr Leu Ala Glu Ala Lys Ile His Ile Glu Gln
405 410 415

Lys Arg Lys Lys Glu Tyr Glu Leu Asn Ala Gln Lys Ala Lys Asp Ser
420 425 430

Ser Gln Leu Asn Ala Asn Asn Lys Ser Val Gln Lys Met Asn Arg Pro
435 440 445

Met Lys Ile Glu Ser Asp Gly Asn Leu Asp Pro Lys Lys Gly Gly Ala
450 455 460

Gly Leu Asp Ser Pro Lys Thr Thr Gly Pro Thr Ser Val Lys Gln Trp
465 470 475 480

Asp Asp Trp Asp Ile Val Gly Leu Pro Gly Ala Glu Leu Leu Ser Ala
485 490 495

Ser Glu Lys Leu Leu Cys Cys Gln Asn Arg Leu Leu Pro Ser His Tyr
500 505 510

Leu Arg Met Gln Glu Val Leu Met Gln Glu Ile Phe Lys Gly Ser Val
515 520 525

Leu Lys Lys Glu Asp Ala His Val Leu Phe Lys Val Asp Pro Thr Lys
530 535 540

Val Asp Ser Val Tyr Asp Met Val Ser Lys Lys Leu Gly Asn His Glu
545 550 555 560

Glu Ala Pro Thr Val
565

<210> 207
<211> 46
<212> PRT
<213> Artificial sequence

<220>
<223> Zinc finger ZZ type

<400> 207

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Lys Pro Gly Leu Tyr Cys Cys Asn Tyr Cys Asp Lys Asp Leu Ser Gly
1 5 10 15

Leu Val Arg Phe Lys Cys Ala Val Cys Met Asp Phe Asp Leu Cys Val
20 25 30

Glu Cys Phe Ser Val Gly Val Glu Leu Asn Arg His Lys Asn
35 40 45

<210> 208
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> SANT DNA bindin domain
<400> 208

Val Thr Ser Asp Trp Asn Ala Asp Glu Glu Ile Leu Leu Leu Glu Ala
1 5 10 15

Ile Ala Thr Tyr Gly Phe Gly Asn Trp Lys Glu Val Ala Asp His Val
20 25 30

Gly Ser Lys Thr Thr Thr Glu Cys Ile Lys His Phe Asn Ser Ala Tyr
35 40 45

Met

<210> 209
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> calcium binding EF hand
<400> 209

Asp Asn Asp Ala Glu Gln Leu Leu Ala Asp Met Glu Phe
1 5 10

<210> 210
<211> 88
<212> PRT
<213> Artificial sequence

<220>
<223> SWIRM
<400> 210

Pro Arg Ile Tyr Ser Gly Leu Asp Thr Trp Asp Val Asp Gly Leu Leu
1 5 10 15

Gly Ala Asp Leu Leu Ser Glu Thr Glu Lys Lys Met Cys Asn Glu Thr
20 25 30

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Arg Ile Leu Pro Val His Tyr Leu Lys Met Leu Asp Ile Leu Thr Arg
35 40 45

Glu Ile Lys Lys Gly Gln Ile Lys Lys Lys Ser Asp Ala Tyr Ser Phe
50 55 60

Phe Lys Val Glu Pro Ser Lys Val Asp Arg Val Tyr Asp Met Leu Val
65 70 75 80

His Lys Gly Ile Gly Asp Ser Thr
85

<210> 211
<211> 55
<212> DNA
<213> Artificial sequence

<220>
<223> primer 1

<400> 211
ggggacaagt ttgtacaaaa aagcaggctt aaacaatggg tcgttcgaaa ctagc 55

<210> 212
<211> 52
<212> DNA
<213> Artificial sequence

<220>
<223> primer 2

<400> 212
ggggaccact ttgtacaaga aagctgggtc atgttaggac catgaagcta tg 52

<210> 213
<211> 1130
<212> DNA
<213> Oryza sativa

<400> 213
catgcggcta atgtagatgc tcactgcgct agtagtaagg tactccagta cattatggaa 60
tatacaaagc tgtaatactc gtatcagcaa gagagaggca cacaagttgt agcagtagca 120
caggattaga aaaacgggac gacaaatagt aatggaaaaa caaaaaaaaa caaggaaaca 180
catggcaata taaatggaga aatcacaaga ggaacagaat ccgggcaata cgctgcgaaa 240
gtactcgtac gtaaaaaaaaa gaggcgcatt catgtgtgga cagcgtgcag cagaagcagg 300
gatttgaaac cactcaaact caccactgca aaccttcaaa cgaggccatg gtttgaagca 360
tagaaagcac aggtaagaag cacaacgccc tcgctctcca cctcccacc caatcgcgac 420
gcacctcgcg gatcgggtgac gtggcctcgc ccccaaaaaa tatcccgcgg cgtgaagctg 480
acaccccggg cccaccacc tgtcacgttg gcacatgttg gttatggttc ccggccgcac 540
caaaatatca acgcggcgcg gcccaaaatt tccaaaatcc cgcccaagcc cctggcgcgt 600
gccgctcttc caccagggtc cctctcgtaa tccataatgg cgtgtgtacc ctcggctggt 660

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

tgtacgtggg	cggggttacc	tgggggtgtg	ggtggatgac	gggtgggccc	ggaggaggtc	720
cggccccgcg	cgtcatcgcg	gggcgggggtg	tagcgggtgc	gaaaaggagg	cgatcggtac	780
gaaaattcaa	attaggaggt	ggggggcggg	gcccttggag	aataagcgga	atcgagata	840
tgtccctgac	ttggcttggc	tcctcttctt	cttatccctt	gtcctcgcaa	ccccgcttcc	900
ttctctcctc	tcctcttctc	ttctcttctc	tgggtggtgtg	ggtgtgtccc	tgtctcccct	960
ctccttcctc	ctctccttcc	ccctcctctc	ttccccctc	tcacaagaga	gagagcgcca	1020
gactctcccc	aggtagggtg	agaccagtct	ttttgctcga	ttcgacgcgc	ctttcacgcc	1080
gcctcgcgcg	gatctgaccg	cttcctctcg	ccttctcgca	ggattcagcc		1130

<210> 214
 <211> 1244
 <212> DNA
 <213> Oryza sativa

<400> 214	
aaaaccaccg	agggacctga tctgcaccgg ttttgatagt tgagggaccc gttgtgtctg 60
gttttccgat	cgagggacga aaatcggatt cgggtgtaaag ttaagggacc tcagatgaac 120
ttattccgga	gcatgattgg gaaggagga cataaggccc atgtcgcgatg tgtttggacg 180
gtccagatct	ccagatcact cagcaggatc ggccgcgttc gcgtagcacc cgcggtttga 240
ttcggcttcc	cgcaaggcgg cggccgggtg ccgtgccgcc gtagcttccg ccggaagcga 300
gcacgccgcc	gccgccgacc cggctctgcg tttgcaccgc cttgcacgcg atacatcggg 360
atagatagct	actactctct ccgtttcaca atgtaaataa ttctactatt ttccacattc 420
atattgatgt	taatgaatat agacatatat atctatttag attcattaac atcaatatga 480
atgtaggaaa	tgctagaatg acttacattg tgaattgtga aatggacgaa gtacctacga 540
tggatggatg	caggatcatg aaagaattaa tgcaagatcg tatctgccgc atgcaaaatc 600
ttactaattg	cgctgcatat atgcatgaca gcctgcatgc gggcgtgtaa gcgtgttcat 660
ccattaggaa	gtaaccttgt cattaacttat accagtacta catactatat agtattgatt 720
tcatgagcaa	atctacaaaa ctggaaagca ataagaaata cgggactgga aaagactcaa 780
cattaatcac	caaataatttc gccttctcca gcagaatata tatctctcca tcttgatcac 840
tgtacacact	gacagtgtac gcataaacgc agcagccagc ttaactgtcg tctcacgcgc 900
gcacactggc	cttccatctc aggctagctt tctcagccac ccatcgtaac tgtcaactcg 960
gcgcgcgcac	aggcacaat tacgtacaaa acgcatgacc aaatcaaac caccggagaa 1020
gaatcgctcc	cgcgcgcggc ggcgacgcgc acgtacgaac gcacgcacgc acgccaacc 1080
ccacgacacg	atcgcgcgcg acgccggcga caccggccgt ccacccgcgc cctcacctcg 1140
ccgactataa	atacgtaggc atctgcttga tcttgtcatc catctacca ccaaaaaaaaa 1200
aaggaaaaaa	aaacaaaaca caccaagcca aataaaagcg acaa 1244

<210> 215
 <211> 1482

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

<212> DNA

<213> Arabidopsis thaliana

<400> 215

```

atgttttttg gaccaagtga gtttgatgct gatgaaatgg gttatgcaat gagtagactt      60
gagatagaat ccgatctatg tgatactgga aaagacgttt gtggagttgg tagtagtagt      120
ggtagtcaca gatcaagtga acatttggtg gatctagacc atgaaatcag ccagggttact      180
aaattgaaat ctagtcctca tcaacggtat agccgtgaag tccctgggag acatcagtta      240
cctgtgtcta ctgtgaggat gttggcaggt cgagaaagta atttctctgg aagaggaagg      300
ttttcagccg ctgattgttg ccatatgcta agcagatatt tgcctacaaa aggtccttgg      360
ctttagatc aaatggacag ccgagcatat gtctctcagt tttcaactga tggttctctc      420
tttattgcgg ggtttcaggg tagccgtatt cggatttaca atgtagagaa gggttggaaa      480
gttcaaaagg atattcttgc aaaaagcttg cgttggactg ttactgatac ttctctatcc      540
cctgatcagc gaaatctggt ttacgcaagc atgtcaccta ttgttcacat tgttgatgtt      600
ggatccggtt caaccgagtc tcatgcaaat gttacggaga tccatgatgg cttagacttc      660
tcttctgatg aagatggagg gtactctttt ggaatattct ctgtgaaatt ttcaacagat      720
ggccgagaag ttgttgctgg gagcagtgat gattccattt atgtttatga ccttgaagca      780
aatcgagttt cactccggac tgttgcacac acgtctgatg taaatactgt gtgctttgct      840
gatgaaagtg ggaacctgat tttatctgga agtgatgata atctctgcaa agtggtggat      900
aggcgttggt tcattgggag agataagcca gctggtgttt tagtgggaca cctcgaaggt      960
gttaccttta tcgatagccg tggagatggg cgctattttca tatcaaattg taaagaccaa     1020
actatcaaat tgtgggatat cagaaaaatg tcctcaagcg cacctgcaag gcatgaggtg     1080
ctaagaaact atgaatggga ctacagatgg atggattatc ctactgaagc aagagatcta     1140
aagcaccac tcgatcagtc agtgtcgaca tataaagggtc actcagtttt gcgtactctc     1200
atccgttggt acttctctcc agcgcatagt actggccaaa agtacatcta cacaggatcg     1260
aacgacagtt ccgtctacat atacgacttg gtaagtggag ataaagtggc agtgctaaag     1320
caccatagct cacctgtaag agactgtaat tggcaccat attaccaac gcttataagc     1380
tcttcgtggg acggagatct tgtgaagtgg gaatttccgg ggagcgggtga ggcgccgatt     1440
atgagtaaga agaggggttcg aaggagacat ttctactact ga                        1482

```

<210> 216

<211> 493

<212> PRT

<213> Arabidopsis thaliana

<400> 216

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

Met Ser Arg Leu Glu Ile Glu Ser Asp Leu Cys Asp Thr Gly Lys Asp
20 25 30

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

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

Ile Gly Arg Asp Lys Pro Ala Gly Val Leu Val Gly His Leu Glu Gly
305 310 315 320

Val Thr Phe Ile Asp Ser Arg Gly Asp Gly Arg Tyr Phe Ile Ser Asn
325 330 335

Gly Lys Asp Gln Thr Ile Lys Leu Trp Asp Ile Arg Lys Met Ser Ser
340 345 350

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

Arg Trp Met Asp Tyr Pro Thr Glu Ala Arg Asp Leu Lys His Pro Leu
370 375 380

Asp Gln Ser Val Ser Thr Tyr Lys Gly His Ser Val Leu Arg Thr Leu
385 390 395 400

Ile Arg Cys Tyr Phe Ser Pro Ala His Ser Thr Gly Gln Lys Tyr Ile
405 410 415

Tyr Thr Gly Ser Asn Asp Ser Ser Val Tyr Ile Tyr Asp Leu Val Ser
420 425 430

Gly Asp Lys Val Ala Val Leu Lys His His Ser Ser Pro Val Arg Asp
435 440 445

Cys Asn Trp His Pro Tyr Tyr Pro Thr Leu Ile Ser Ser Ser Trp Asp
450 455 460

Gly Asp Leu Val Lys Trp Glu Phe Pro Gly Ser Gly Glu Ala Pro Ile
465 470 475 480

Met Ser Lys Lys Arg Val Arg Arg Arg His Phe Tyr Tyr
485 490

<210> 217
<211> 1458
<212> DNA
<213> Aquilegia formosa x Aquilegia pubescens

<400> 217
atgtttgtta cagccagtgg ggttgacatt gatgaaatgg ggtacgcat gagtaggcta 60
gagatagaat ccgagttggt cgatggcggg aataccgtcc atgaagccag tagcagtact 120
aggcccgga aactgtttcc taaagtagat gacgagattt cccagcttac aaacctcaga 180
tcagggccta atgatcgact gcatcaactt gtgcccggaa agcagcaatt acctgtttcc 240
ccggtgagga tgttggcagg tcgagaaagt aattattcag gaaaggggaag gttctcgtca 300
gcggatcggt gtcacatgct tagcaggtat ttgcctgtaa atggctcttg gcttgtggac 360
cagacgacca gtcgggccta tgtttctcaa ttttcagctg atggttctct atttgttgcc 420
gggtttcagg gaagcgatat tagaatatac aatgtggata gaggctggaa agttcagaag 480

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

aacattcttg ccaaaagttt gcgttgact gttactgaca catccctttc ccctgatcag      540
cgccatcttg tttataaccag tatgtcaccc atagtccata ttgttaatgt tgggtctgct      600
accacggaat cccttgcaaa tataacagag gtccatgaag gattggactt ctctgctgct      660
gatggagggt attcttttgg aatattctct gtgaaatfff caaccgatgg acgagaactt      720
gttgctggaa gcagtgatga ttcgatatat gtttatgata ttgaagcaaa caagctttcc      780
cttcgaattg cggcacacat ggctgatgtt aatactgtaa cctttgctga tgaaagtggg      840
aatctgatat attcaggaag tgatgataat ctctgcaagg tgtgggacag gcgttgtctc      900
agagcaaagg gaaaaccagc aggggttttg acggggcatt tagaaggcat tacgtttatt      960
gatagccgtg gagatggtcg atattttata tcaaattggaa aagaccaggc cattaactt     1020
tgggacatca ggaaaatgtc ggctaattgct agttgcattg caaaatctag aaattacgaa     1080
tgggactaca gatggatgga ataccact actgagcgagaa agttaaaca tccttgatgat     1140
cagtctttgg ctacatacaa agggcactct gtcttgcgta ctctcatccg ttgttacttt     1200
tcaccggctt acagcactgg ccagaagtac atctacaccg gatcaaata tggttgcgtt     1260
tatatatatg atttggaag tggagcccaa gttgctcgac tagatcatca ttcactcact     1320
gtgagggatt gtagttggca ccctttctac ccaacgcttg tcagcagttc atgggatggg     1380
gtccttgcca gatgtgaatt tcctggcaat ggagaaaaaa ttcggctgaa gagaagcagg     1440
aggagatatg aatcttga                                     1458

```

<210> 218
 <211> 485
 <212> PRT
 <213> Aquilegia formosa x Aquilegia pubescens
 <400> 218

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

Met Ser Arg Leu Glu Ile Glu Ser Glu Leu Phe Asp Gly Gly Asn Thr
 20 25 30

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

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

Asp Arg Leu His Gln Leu Val Pro Gly Lys Gln Gln Leu Pro Val Ser
 65 70 75 80

Pro Val Arg Met Leu Ala Gly Arg Glu Ser Asn Tyr Ser Gly Lys Gly
 85 90 95

Arg Phe Ser Ser Ala Asp Arg Cys His Met Leu Ser Arg Tyr Leu Pro
 100 105 110

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

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

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Thr Tyr Lys Gly His Ser Val Leu Arg Thr Leu Ile Arg Cys Tyr Phe
385 390 395 400

Ser Pro Ala Tyr Ser Thr Gly Gln Lys Tyr Ile Tyr Thr Gly Ser Asn
405 410 415

Asp Gly Cys Val Tyr Ile Tyr Asp Leu Val Ser Gly Ala Gln Val Ala
420 425 430

Arg Leu Asp His His Ser Ser Thr Val Arg Asp Cys Ser Trp His Pro
435 440 445

Phe Tyr Pro Thr Leu Val Ser Ser Ser Trp Asp Gly Val Leu Ala Arg
450 455 460

Cys Glu Phe Pro Gly Asn Gly Glu Lys Ile Arg Leu Lys Arg Ser Arg
465 470 475 480

Arg Arg Tyr Glu Ser
485

<210> 219
<211> 1488
<212> DNA
<213> Brassica napus

<400> 219
atgttttctg gaccaagtga ttctgatact gatgaaatgg gttatgcaat gagtagactc 60
gagattgaat ccgatctatg cgacgctgga aagggctatt acggtgttgg tagcagcagt 120
ggtagtagtc acagatcgag tgagcgtttg ggtgatttag acaatgagat cagccaagtc 180
actaagctga agtcttgtcc tcatgaacgg tttagccgtc aagtaccgg gaggcacag 240
ttgcctgttt ccactgtgaa gatgttggct ggtcgtgaga gtaacttctc tggaagagga 300
ggaaggtttt cttcagctga tcgttgtcat atcttgagta gatatttgcc tgtaagggt 360
ccttggcttg tggatcagat ggacagccga gcttatgtct ctcagttttc aactgatggg 420
tctctcttca ttgctgggtt tcagggaagc catattcgga tttaaatgt agagaaaggt 480
tggaaggttc aaaaggatat tcttgcaaag agcttgcgtt ggactgttac tgatacttct 540
ctgtcccctg atcagcgaaa cctggtttat gcaagcatgt cacctattgt tcacatagtc 600
gatgttggat ctggtacaac cgagtctcac gcaaagtca cggagatcca tgatggatta 660
gacttctctt ctgaagaaga tggaggctac tcttttggga tattctctgt gaaattttca 720
acagatggac gagaactcgt tgctggtagc agtgatgatt ccatttacgt ttatgatctc 780
gaagcaaacc gagtctcact ccggactgtt gcacacacgt ctgatgtgaa cactgtgtgt 840
ttcgccgatg aaagtggaca cctgattctc tctggaggtg atgataatct ctgcaagggtg 900
tgggataggc gttgtttcat tgggagagat aagccagctg gtgttctggt gggacaccta 960
gaaggtgtta catttatcga tagccgcgga gatggtcgct atttcatatc aaatgggaaa 1020

gaccaaacca tcaagctatg ggatattaga aaaatgtcct caactgtacc tgcaaggaat	1080
gaggtgcaca gaaactatga atgggattac agatggatgg attacccttc ggaggcaaga	1140
gatctaaagc acccttatga tcagtctgtg tctacatata agggtcactc agtgttgctg	1200
actctcatcc gttgctactt ctctccagct catagtactg gtcaaaagta catatacaca	1260
ggatccaacg acagttctgt ctacatatat gacttggaaa gtggagataa agcggcggtg	1320
ttaaagcacc atagctcacc tgtgagagac tgtaactggc atccgcatta tccgacgctt	1380
ataagctcgt cgtgggacgg agatcttgtg aaatgggagt ttcctgggag cggtgaggcg	1440
ccgatcatga gcaagaagag ggtccgaagg agacatttct actactga	1488

<210> 220
 <211> 495
 <212> PRT
 <213> Brassica napus

<400> 220

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

Met	Ser	Arg	Leu	Glu	Ile	Glu	Ser	Asp	Leu	Cys	Asp	Ala	Gly	Lys	Gly
			20					25					30		

Tyr	Tyr	Gly	Val	Gly	Ser	Ser	Ser	Gly	Ser	Ser	His	Arg	Ser	Ser	Glu
		35					40					45			

Arg	Leu	Gly	Asp	Leu	Asp	Asn	Glu	Ile	Ser	Gln	Val	Thr	Lys	Leu	Lys
	50					55					60				

Ser	Cys	Pro	His	Glu	Arg	Phe	Ser	Arg	Gln	Val	Pro	Gly	Arg	His	Gln
65					70					75					80

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

Ser	Gly	Arg	Gly	Gly	Arg	Phe	Ser	Ser	Ala	Asp	Arg	Cys	His	Ile	Leu
			100					105					110		

Ser	Arg	Tyr	Leu	Pro	Val	Lys	Gly	Pro	Trp	Leu	Val	Asp	Gln	Met	Asp
		115					120					125			

Ser	Arg	Ala	Tyr	Val	Ser	Gln	Phe	Ser	Thr	Asp	Gly	Ser	Leu	Phe	Ile
		130				135					140				

Ala	Gly	Phe	Gln	Gly	Ser	His	Ile	Arg	Ile	Tyr	Asn	Val	Glu	Lys	Gly
145					150					155					160

Trp	Lys	Val	Gln	Lys	Asp	Ile	Leu	Ala	Lys	Ser	Leu	Arg	Trp	Thr	Val
				165					170					175	

Thr	Asp	Thr	Ser	Leu	Ser	Pro	Asp	Gln	Arg	Asn	Leu	Val	Tyr	Ala	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Met Ser Pro Ile Val His Ile Val Asp Val Gly Ser Gly Thr Thr Glu
195 200 205

Ser His Ala Asn Val Thr Glu Ile His Asp Gly Leu Asp Phe Ser Ser
210 215 220

Glu Glu Asp Gly Gly Tyr Ser Phe Gly Ile Phe Ser Val Lys Phe Ser
225 230 235 240

Thr Asp Gly Arg Glu Leu Val Ala Gly Ser Ser Asp Asp Ser Ile Tyr
245 250 255

Val Tyr Asp Leu Glu Ala Asn Arg Val Ser Leu Arg Thr Val Ala His
260 265 270

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

Ile Leu Ser Gly Gly Asp Asp Asn Leu Cys Lys Val Trp Asp Arg Arg
290 295 300

Cys Phe Ile Gly Arg Asp Lys Pro Ala Gly Val Leu Val Gly His Leu
305 310 315 320

Glu Gly Val Thr Phe Ile Asp Ser Arg Gly Asp Gly Arg Tyr Phe Ile
325 330 335

Ser Asn Gly Lys Asp Gln Thr Ile Lys Leu Trp Asp Ile Arg Lys Met
340 345 350

Ser Ser Thr Val Pro Ala Arg Asn Glu Val His Arg Asn Tyr Glu Trp
355 360 365

Asp Tyr Arg Trp Met Asp Tyr Pro Ser Glu Ala Arg Asp Leu Lys His
370 375 380

Pro Tyr Asp Gln Ser Val Ser Thr Tyr Lys Gly His Ser Val Leu Arg
385 390 395 400

Thr Leu Ile Arg Cys Tyr Phe Ser Pro Ala His Ser Thr Gly Gln Lys
405 410 415

Tyr Ile Tyr Thr Gly Ser Asn Asp Ser Ser Val Tyr Ile Tyr Asp Leu
420 425 430

Glu Ser Gly Asp Lys Ala Ala Val Leu Lys His His Ser Ser Pro Val
435 440 445

Arg Asp Cys Asn Trp His Pro His Tyr Pro Thr Leu Ile Ser Ser Ser
450 455 460

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Trp Asp Gly Asp Leu Val Lys Trp Glu Phe Pro Gly Ser Gly Glu Ala
465 470 475 480

Pro Ile Met Ser Lys Lys Arg Val Arg Arg Arg His Phe Tyr Tyr
485 490 495

<210> 221
<211> 1428
<212> DNA
<213> Glycine max

<400> 221
atgagttggt tgaataaaaa taaaagtact tgtagtgatg gtagtgccaa taatgaatct 60
tcttcaagtg gaatagttgg agaaagggat aatcatcttg atcatgaaat tgcacagctc 120
acaaaactta ggtcaagtcc tcatgagctt ttgggtcgtg ttgttcctgg taagatgagg 180
ttacctgcat ctactgtgag aatgctgggt ggtagagaag gtaattattc tggaagaggg 240
agattttcat cagcagatgg gtgtcatgtg ttaagccgct atttgcctac caaaggctct 300
tggattgtgg atcggatgaa aagtcgtgcc tatgtttcac agttttctgc tgatggttct 360
cttttaattg ctggattcca gggaagccac atcaggatct atgatgttga ccagggtcgg 420
aaagttaaaa aggacatttc tgctagaaag ttacgggtgga cagttactga tacatctctc 480
tcgccagatc aactctatct tgtttatgcc agtatgtcac caattatcca tattgttacc 540
gtgggatctg gcacaacaga atcaatagca aatgttacag aaattcacta tggattaaat 600
ttctcttctg ataatggtga tgatgaattt ggaattttct ctgtcaaatt ttcaacggat 660
gggcgagagc ttgtggctgg aactagtgat tgctcgatat gtgtatatga tcttgagca 720
gataagctga gccttagaat tcctgctcac cagtctgatg ttaacactgt ctgctttgct 780
gatgaatctg gccatcta attttccggt agtgatgata gttttatcaa ggtgtgggat 840
aggcgttggt ttgtcgccaa aggacaacca gctggatatct taatgggaca tttagaaggc 900
attacattca ttgatagccg tggggatggt cgatatTTAA tttctaattg aaaagatcaa 960
actaccaa at tatgggat aaggaagatg tcttctaatt caataaatct tggccttgga 1020
gatgatgagt gggactatcg atggatggac taccctgaat atgcaagaaa tttaaagcat 1080
cctcatgatc agtcattagc aacatataaa ggtcactcag tgttgcgtac tttagtgcgc 1140
tgttatttct ctcttcgta tagcactggc caaaagtaca tttacacagg gtctagtgat 1200
tcatctgttt acatatatga cctggttaagt ggtgcacaag ttgcaaaact tgatcatcat 1260
gaggcacctg taagggattg tagttggcac ccctattatc caatgatgat ctcttcggct 1320
tgggatggtg atgttgtcag gtgggaattt cctgggagtg atgaagcccc tgcttctcca 1380
aataaaagag aaggtcgaat tcgtaggaga aatttgcttt atctatag 1428

<210> 222
<211> 475
<212> PRT
<213> Glycine max

<400> 222

Met Ser Trp Leu Asn Lys Asn Lys Ser Thr Cys Ser Asp Gly Ser Ala
1 5 10 15

Asn Asn Glu Ser Ser Ser Ser Gly Ile Val Gly Glu Arg Asp Asn His
20 25 30

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

Glu Leu Leu Gly Arg Val Val Pro Gly Lys Met Arg Leu Pro Ala Ser
50 55 60

Thr Val Arg Met Leu Val Gly Arg Glu Gly Asn Tyr Ser Gly Arg Gly
65 70 75 80

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

Thr Lys Gly Pro Trp Ile Val Asp Arg Met Lys Ser Arg Ala Tyr Val
100 105 110

Ser Gln Phe Ser Ala Asp Gly Ser Leu Leu Ile Ala Gly Phe Gln Gly
115 120 125

Ser His Ile Arg Ile Tyr Asp Val Asp Gln Gly Trp Lys Val Lys Lys
130 135 140

Asp Ile Ser Ala Arg Lys Leu Arg Trp Thr Val Thr Asp Thr Ser Leu
145 150 155 160

Ser Pro Asp Gln Leu Tyr Leu Val Tyr Ala Ser Met Ser Pro Ile Ile
165 170 175

His Ile Val Thr Val Gly Ser Gly Thr Thr Glu Ser Ile Ala Asn Val
180 185 190

Thr Glu Ile His Tyr Gly Leu Asn Phe Ser Ser Asp Asn Gly Asp Asp
195 200 205

Glu Phe Gly Ile Phe Ser Val Lys Phe Ser Thr Asp Gly Arg Glu Leu
210 215 220

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

Asp Lys Leu Ser Leu Arg Ile Pro Ala His Gln Ser Asp Val Asn Thr
245 250 255

Val Cys Phe Ala Asp Glu Ser Gly His Leu Ile Phe Ser Gly Ser Asp
260 265 270

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Asp Ser Phe Ile Lys Val Trp Asp Arg Arg Cys Phe Val Ala Lys Gly
275 280 285

Gln Pro Ala Gly Ile Leu Met Gly His Leu Glu Gly Ile Thr Phe Ile
290 295 300

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

Thr Thr Lys Leu Trp Asp Ile Arg Lys Met Ser Ser Asn Ala Ile Asn
325 330 335

Leu Gly Leu Gly Asp Asp Glu Trp Asp Tyr Arg Trp Met Asp Tyr Pro
340 345 350

Glu Tyr Ala Arg Asn Leu Lys His Pro His Asp Gln Ser Leu Ala Thr
355 360 365

Tyr Lys Gly His Ser Val Leu Arg Thr Leu Val Arg Cys Tyr Phe Ser
370 375 380

Pro Ser Tyr Ser Thr Gly Gln Lys Tyr Ile Tyr Thr Gly Ser Ser Asp
385 390 395 400

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

Leu Asp His His Glu Ala Pro Val Arg Asp Cys Ser Trp His Pro Tyr
420 425 430

Tyr Pro Met Met Ile Ser Ser Ala Trp Asp Gly Asp Val Val Arg Trp
435 440 445

Glu Phe Pro Gly Ser Asp Glu Ala Pro Ala Ser Pro Asn Lys Arg Glu
450 455 460

Gly Arg Ile Arg Arg Arg Asn Leu Leu Tyr Leu
465 470 475

<210> 223
<211> 1467
<212> DNA
<213> Gossypium hirsutum

<400> 223	
atgtttgtta cagccagtgg ggttgacatt gatgaaatgg ggtacgcat gagtaggcta	60
gagatagaat ccgagttgtt cgatggcggg aataccgtcc atgaagccag tagcagtact	120
aggcccgga aactgtttcc taaagtagat gacgagattt cccagcttac aaacctcaga	180
tcagggccta atgatcgact gcatcaactt gtgcccggaa agcagcaatt acctgtttcc	240
ccggtgagga tgttggcagg tcgagaaagt aattattcag gaaagggaag gttctcgta	300

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

gcggatcgtt gtcacatgct tagcaggtat ttgcctgtaa atggtccttg gcttgtggac      360
cagacgacca gtcgggccta tgtttctcaa ttttcagctg atggttctct atttgttgcc      420
gggtttcagg gaagcaatat taggatatac aatgtggata gaggttggaa agttcaaaag      480
aacattcttg ctaaaagttt gcgttggaca gttaccgaca catccctttc tccggatcag      540
cggtaccttg tttataccag catgtcgcct gtagttcaca ttgttaatgt tgggtcttct      600
accacggaat cttttgcaa tgtcacggag atccacgaag gattggactt ttcttctaata      660
gatcgaaggt attcttttgg aatattctcc gtgaaatttt caactgatgg acgagaactt      720
gtggctggaa gcagtgatga ctcgatatat gtttatgatc tggaagcaaa caagctttcc      780
cttcgaatta tggcacacac ggctgatgtt aacacggcaa ctttgccga tgaaagcggc      840
aatttgatat attctgggag tgatgattat ctctgcatgg tgtgggatag gcgttgcttt      900
ggagcaaaag ataagccggc aggagttttg gtgggacacc tggaaggat tatattcctc      960
gacagtcgtg gggatggtcg ttacttcata tcaaacggta aagatcagac tatcaagctt     1020
tgggatatcc ggaaaatgtc ctccgatacc tcttgcaatt tagggatatc gaatttcgaa     1080
tgggattaca gatggatgga ctaccctcca caggctagag atttgaaaca cccaagtgc      1140
ggatcagtgg ctacttataa aggtcactca gtgttgcgca ctcttattcg ctgttatttt     1200
tcacccgaat actgcacggg ccaaaagtac atttacaccg gatctcacga ttctcgggtt     1260
tatatttatg atgtggtcac cggagcccaa gttgcggtac tgaagcacca tacatcacca     1320
gtaagagact gtagttggca cccgcattac cctgtgttgg tcagctcctc ttgggacggg     1380
gacgtgggta agtgggaatt ccctggtaaa ggagaagcgc cggtccttgc gaacgagagg     1440
agagtcagga ggcaatatca cgattga                                           1467

```

```

<210> 224
<211> 488
<212> PRT
<213> Gossypium hirsutum
<400> 224

```

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

Met Ser Arg Leu Glu Ile Glu Ser Glu Leu Phe Asp Gly Gly Asn Thr
20 25 30

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

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

Asp Arg Leu His Gln Leu Val Pro Gly Lys Gln Gln Leu Pro Val Ser
65 70 75 80

Pro Val Arg Met Leu Ala Gly Arg Glu Ser Asn Tyr Ser Gly Lys Gly
85 90 95

Arg Phe Ser Ser Ala Asp Arg Cys His Met Leu Ser Arg Tyr Leu Pro
100 105 110

Val Asn Gly Pro Trp Leu Val Asp Gln Thr Thr Ser Arg Ala Tyr Val
115 120 125

Ser Gln Phe Ser Ala Asp Gly Ser Leu Phe Val Ala Gly Phe Gln Gly
130 135 140

Ser Asn Ile Arg Ile Tyr Asn Val Asp Arg Gly Trp Lys Val Gln Lys
145 150 155 160

Asn Ile Leu Ala Lys Ser Leu Arg Trp Thr Val Thr Asp Thr Ser Leu
165 170 175

Ser Pro Asp Gln Arg Tyr Leu Val Tyr Thr Ser Met Ser Pro Val Val
180 185 190

His Ile Val Asn Val Gly Ser Ser Thr Thr Glu Ser Phe Ala Asn Val
195 200 205

Thr Glu Ile His Glu Gly Leu Asp Phe Ser Ser Asn Asp Arg Arg Tyr
210 215 220

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

Val Ala Gly Ser Ser Asp Asp Ser Ile Tyr Val Tyr Asp Leu Glu Ala
245 250 255

Asn Lys Leu Ser Leu Arg Ile Met Ala His Thr Ala Asp Val Asn Thr
260 265 270

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

Asp Tyr Leu Cys Met Val Trp Asp Arg Arg Cys Phe Gly Ala Lys Asp
290 295 300

Lys Pro Ala Gly Val Leu Val Gly His Leu Glu Gly Ile Thr Phe Leu
305 310 315 320

Asp Ser Arg Gly Asp Gly Arg Tyr Phe Ile Ser Asn Gly Lys Asp Gln
325 330 335

Thr Ile Lys Leu Trp Asp Ile Arg Lys Met Ser Ser Asp Thr Ser Cys
340 345 350

Asn Leu Gly Tyr Arg Asn Phe Glu Trp Asp Tyr Arg Trp Met Asp Tyr
Seite 237

355

360

365

Pro Pro Gln Ala Arg Asp Leu Lys His Pro Ser Asp Gly Ser Val Ala
 370 375 380

Thr Tyr Lys Gly His Ser Val Leu Arg Thr Leu Ile Arg Cys Tyr Phe
 385 390 395 400

Ser Pro Glu Tyr Cys Thr Gly Gln Lys Tyr Ile Tyr Thr Gly Ser His
 405 410 415

Asp Ser Arg Val Tyr Ile Tyr Asp Val Val Thr Gly Ala Gln Val Ala
 420 425 430

Val Leu Lys His His Thr Ser Pro Val Arg Asp Cys Ser Trp His Pro
 435 440 445

His Tyr Pro Val Leu Val Ser Ser Ser Trp Asp Gly Asp Val Val Lys
 450 455 460

Trp Glu Phe Pro Gly Lys Gly Glu Ala Pro Val Leu Ala Asn Glu Arg
 465 470 475 480

Arg Val Arg Arg Gln Tyr His Asp
 485

<210> 225
 <211> 1464
 <212> DNA
 <213> Helianthus annuus

<400> 225
 atgtactcta ggggttggac cacacttata ggtgacatgg gatatgccct aagtagattg 60
 gaaatcgacc cagattattc tgataacgga tctgttggag acgataatga cagccaccag 120
 tcttcatcac aaaatgatgt ggatcctgaa gttgctcagt taacaaagct gaaatcagca 180
 ccccatgatg gattgaaacg cgttcttcca cgaagggggg aatttgatgt ttcgcctgtg 240
 aagatgttag cgggtcgaga agggaattat tcgggtcgtg ggaagttttc tttagcagat 300
 cgttgtcata tgctaaacaa atattttacct gttaaagggtc cttctattgt tgaccaattg 360
 accacccggg cttatgtctc acagttttca aaagacgggt ccctttttgt tgctgcattt 420
 caggggaagtc agattaaaat ttataatgct gaaatggggt ggaaacttca caagaaaatt 480
 gttgctgaaa gctttaattg gacggttact gacacatcta tttcaccaga taaacgtttc 540
 ctgatttatt caactttgtc tcctatagtc aacattgtaa atattggatc tgctggaaca 600
 gagtctcatg caaatgtcac ggacatacac gaagggctag aatttgcagc tgatgatgaa 660
 gaaggatatg catttggaat tttttctgta aaattttcta gtgatggtag agaacttgta 720
 gccggaagta gtgatgattc aatttatgtt tatgatattg aagcaaaaag attttccctt 780
 cgaattcaag cgcatacgtc agatgtaaac agtgtatgct ttgctgatga agccagcaat 840

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

ctgatatatt ctgggagtga tgataatctc tgtaaggttt gggacagacg ttccatcaga	900
tcaaaaggaa agccagttgg aatcctcacg gggcatctag aaggaattac acatcttgat	960
agccgtaatg atggtcgtta tttcatttca aatggaaaag atcagactat taagctttgg	1020
gatatcagaa aaatgtcctc taatgctggt cgcgctccta tatccaggaa ctatgaatgg	1080
gactacagat ggatggacta tctacttagg gcacgagatg taaagcatcc atctgaccag	1140
tccgttgcta catacaaagg tcattcagta ttgcgtacac tcatacgctg ctatTTTTca	1200
ccagaatata gcactggcca aaggtatatt tatactggat ctcatgattc ttgtgtgtat	1260
gtttatgatt tggttactgg ggcccgggtt gcaagacttg tgcaccataa gtcaaccgtg	1320
cgggactgca gctggcacc ttactatcca atgctcgtca gttcttcgtt tgatggagat	1380
atcgcaaagt gggaatttcc tggaacgga gagaaccga ttcccgtgaa taacagtagg	1440
cctcgacgac aatattatga ttaa	1464

<210> 226
 <211> 487
 <212> PRT
 <213> Helianthus annuus

<400> 226

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

Leu	Ser	Arg	Leu	Glu	Ile	Asp	Pro	Asp	Tyr	Ser	Asp	Asn	Gly	Ser	Val
			20					25					30		

Gly	Asp	Asp	Asn	Asp	Ser	His	Gln	Ser	Ser	Ser	Gln	Asn	Asp	Val	Asp
		35					40					45			

Pro	Glu	Val	Ala	Gln	Leu	Thr	Lys	Leu	Lys	Ser	Ala	Pro	His	Asp	Gly
	50					55					60				

Leu	Lys	Arg	Val	Leu	Pro	Arg	Arg	Gly	Glu	Phe	Asp	Val	Ser	Pro	Val
65					70					75					80

Lys	Met	Leu	Ala	Gly	Arg	Glu	Gly	Asn	Tyr	Ser	Gly	Arg	Gly	Lys	Phe
				85					90					95	

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

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

Phe	Ser	Lys	Asp	Gly	Ser	Leu	Phe	Val	Ala	Ala	Phe	Gln	Gly	Ser	Gln
	130					135					140				

Ile	Lys	Ile	Tyr	Asn	Ala	Glu	Met	Gly	Trp	Lys	Leu	His	Lys	Lys	Ile
145					150					155					160

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Val Ala Glu Ser Phe Asn Trp Thr Val Thr Asp Thr Ser Ile Ser Pro
 165 170 175
 Asp Lys Arg Phe Leu Ile Tyr Ser Thr Leu Ser Pro Ile Val Asn Ile
 180 185 190
 Val Asn Ile Gly Ser Ala Gly Thr Glu Ser His Ala Asn Val Thr Asp
 195 200 205
 Ile His Glu Gly Leu Glu Phe Ala Ala Asp Asp Glu Glu Gly Tyr Ala
 210 215 220
 Phe Gly Ile Phe Ser Val Lys Phe Ser Ser Asp Gly Arg Glu Leu Val
 225 230 235 240
 Ala Gly Ser Ser Asp Asp Ser Ile Tyr Val Tyr Asp Ile Glu Ala Lys
 245 250 255
 Arg Phe Ser Leu Arg Ile Gln Ala His Thr Ser Asp Val Asn Ser Val
 260 265 270
 Cys Phe Ala Asp Glu Ala Ser Asn Leu Ile Tyr Ser Gly Ser Asp Asp
 275 280 285
 Asn Leu Cys Lys Val Trp Asp Arg Arg Ser Ile Arg Ser Lys Gly Lys
 290 295 300
 Pro Val Gly Ile Leu Thr Gly His Leu Glu Gly Ile Thr His Leu Asp
 305 310 315 320
 Ser Arg Asn Asp Gly Arg Tyr Phe Ile Ser Asn Gly Lys Asp Gln Thr
 325 330 335
 Ile Lys Leu Trp Asp Ile Arg Lys Met Ser Ser Asn Ala Ala Arg Ala
 340 345 350
 Pro Ile Ser Arg Asn Tyr Glu Trp Asp Tyr Arg Trp Met Asp Tyr Leu
 355 360 365
 Leu Arg Ala Arg Asp Val Lys His Pro Ser Asp Gln Ser Val Ala Thr
 370 375 380
 Tyr Lys Gly His Ser Val Leu Arg Thr Leu Ile Arg Cys Tyr Phe Ser
 385 390 395 400
 Pro Glu Tyr Ser Thr Gly Gln Arg Tyr Ile Tyr Thr Gly Ser His Asp
 405 410 415
 Ser Cys Val Tyr Val Tyr Asp Leu Val Thr Gly Ala Arg Val Ala Arg
 420 425 430

Leu Val His His Lys Ser Thr Val Arg Asp Cys Ser Trp His Pro Tyr
435 440 445

Tyr Pro Met Leu Val Ser Ser Ser Phe Asp Gly Asp Ile Ala Lys Trp
450 455 460

Glu Phe Pro Gly Asn Gly Glu Asn Pro Ile Pro Val Asn Asn Ser Arg
465 470 475 480

Pro Arg Arg Gln Tyr Tyr Asp
485

<210> 227
<211> 1410
<212> DNA
<213> Hordeum vulgare

<400> 227
atggcagcgg cagggaggct gcggggacgg cggcgggagc agaaggaggt ggagcgcgag 60
ctcgagccgt tcactatcga ggaagagggtg tcccacctca cccgggcttt gtcggagccg 120
tgcccgggca cccgcgccgc cgtccgtggc gccaggcgga agaggggagc ctcggctttc 180
gacatgctgt cgtcgagga gtccggccgg tccggtggcg gcgggttctg ctcggccgac 240
cgcgccctacg ccgcccggag gcacctgcc gcggtagggc cgtggtgctg cgaagacatg 300
gatagcgagg cctatgtttc gcagttctcc agcgatggct cactgctcgt tgctgggttt 360
cggggaagcc gcatcagagt ttacgatgtc gataaagggt ggaagggtgca taagaacata 420
agctgcagaa gtatgagggtg gacggtttca gacattgctc tctcccctga ccagcgatac 480
cttgcttatt ccagtttgtc gcctattgtt cacattgtga atgtgcagaa tgctggaagg 540
gaatcatatg ctaatgttac tgaaattcac gaggggtttg aattctgtga tgatgatgaa 600
tactctttcg ggatattctc tgtgaaattt tcgaaagatg gtagagaagt tgttggtggg 660
aacaatgatt gttcaatata tgtctatgat cttggagcaa ataaagtatc agaccgtatc 720
cgtgctcata tgggtgatgt caacacggtt acctttgctg atgaaagtgg caatttggtg 780
tactctggaa gtgatgataa tctctgtaag gtctgggata ggcgttgctt tgtaagagag 840
aaaccagcag gtgttttgac aggtcattta gatgggatta cttttattga tagccgtggt 900
gatgggaggt atctaattct gaactgcaag gaccagacta tcaaactttg ggacgtcaga 960
aagatgtccg ccaccgtcaa aggacgacaa ccgagattat atgactggga ctacagatgg 1020
atgtcgctcc catcacacgc tagatattat aagcatccag atgatctgtc tctggcaact 1080
tacaggggtc attcagttct gcggacactt atccgctgct acttctctcc aatgcacagc 1140
acgggcccaga ggtacatata cactggatca agtgatgatt cagtgcataa ttacgatgtg 1200
gtaaccgggg cgaccgtcaa gaagctctcg tggcacggtt cgatcatcag agactgcacc 1260
tggcatcctt accgtccaac acttgctcagc tcttcctggg acggctatct ggcccgggtg 1320
gaggcatcag gcgacaacga ggaccctcgt gtgctcacgt gcgacgagca gaggaatagc 1380
ccttaccacg agacatacgg gctgttgtaa 1410

<210> 228
 <211> 469
 <212> PRT
 <213> Hordeum vulgare

<400> 228

Met Ala Ala Ala Gly Arg Leu Arg Gly Arg Arg Arg Ala Gln Lys Glu
 1 5 10 15

Val Glu Arg Glu Leu Glu Pro Phe Thr Ile Glu Glu Glu Val Ser His
 20 25 30

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

Arg Gly Ala Arg Arg Lys Arg Gly Val Ser Ala Phe Asp Met Leu Ser
 50 55 60

Ser Arg Glu Ser Gly Arg Ser Gly Gly Gly Gly Phe Cys Ser Ala Asp
 65 70 75 80

Arg Ala Tyr Ala Ala Gly Arg His Leu Pro Ala Val Gly Pro Trp Cys
 85 90 95

Val Glu Asp Met Asp Ser Glu Ala Tyr Val Ser Gln Phe Ser Ser Asp
 100 105 110

Gly Ser Leu Leu Val Ala Gly Phe Arg Gly Ser Arg Ile Arg Val Tyr
 115 120 125

Asp Val Asp Lys Gly Trp Lys Val His Lys Asn Ile Ser Cys Arg Ser
 130 135 140

Met Arg Trp Thr Val Ser Asp Ile Ala Leu Ser Pro Asp Gln Arg Tyr
 145 150 155 160

Leu Ala Tyr Ser Ser Leu Ser Pro Ile Val His Ile Val Asn Val Gln
 165 170 175

Asn Ala Gly Arg Glu Ser Tyr Ala Asn Val Thr Glu Ile His Glu Gly
 180 185 190

Leu Glu Phe Cys Asp Asp Asp Glu Tyr Ser Phe Gly Ile Phe Ser Val
 195 200 205

Lys Phe Ser Lys Asp Gly Arg Glu Val Val Val Gly Asn Asn Asp Cys
 210 215 220

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

Arg Ala His Met Gly Asp Val Asn Thr Val Thr Phe Ala Asp Glu Ser
245 250 255

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

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

His Leu Asp Gly Ile Thr Phe Ile Asp Ser Arg Gly Asp Gly Arg Tyr
290 295 300

Leu Ile Ser Asn Cys Lys Asp Gln Thr Ile Lys Leu Trp Asp Val Arg
305 310 315 320

Lys Met Ser Ala Thr Val Lys Gly Arg Gln Pro Arg Leu Tyr Asp Trp
325 330 335

Asp Tyr Arg Trp Met Ser Leu Pro Ser His Ala Arg Tyr Tyr Lys His
340 345 350

Pro Asp Asp Leu Ser Leu Ala Thr Tyr Arg Gly His Ser Val Leu Arg
355 360 365

Thr Leu Ile Arg Cys Tyr Phe Ser Pro Met His Ser Thr Gly Gln Arg
370 375 380

Tyr Ile Tyr Thr Gly Ser Ser Asp Asp Ser Val His Ile Tyr Asp Val
385 390 395 400

Val Thr Gly Ala Thr Val Lys Lys Leu Ser Trp His Gly Ser Ile Ile
405 410 415

Arg Asp Cys Thr Trp His Pro Tyr Arg Pro Thr Leu Val Ser Ser Ser
420 425 430

Trp Asp Gly Tyr Leu Ala Arg Trp Glu Ala Ser Gly Asp Asn Glu Asp
435 440 445

Pro Ser Val Leu Thr Cys Asp Glu Gln Arg Asn Ser Pro Tyr His Glu
450 455 460

Thr Tyr Gly Leu Leu
465

<210> 229
<211> 1479
<212> DNA
<213> Linum usitatissimum

<400> 229
atgttcttcg tagcttcaac tgacgggatg ggttatgcca tgagtagatt ggagatagaa 60
tctcagctgt gtgacgagga agagactgtc aatgaagttg gtggtggaag ccaacagcac 120
Seite 243

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

aagtctctta acaaatcggg agagaaattg gaccatgaag ttgccagga cactaaccta      180
aaatctcagc cccatagacg gctcgagaag gagatacctg ggaagagaca gttcccagtc      240
tctcctgtaa agatgttggc cggtcgagaa ggtaatTTTT ccggaagggg gaggttctcg      300
cgagctgatc ggtgtcatat gctcagcaga tatttgccctg ctgatggccc atggcttgct      360
gatcgaatga atagccgagc ttatgtctcg cagttttctt ctgatggtac cttgtttggt      420
gctggctttc aggggaagcca tattaaagta tacaatgtcg agaaaggggtg gaaagttcag      480
aaggatatta ttgccagaag tttgcgttgg acagttacgg atacctctct gtctccggat      540
caacggtttc ttgtctatgc cagtatgtgc cctattgtgc acattgttaa tatcgcatca      600
tcaacaacgg aatcagttgc aaatgtaacg gagattcacg atggttttaga cttttctgat      660
gaagacgatg ggggctatgc tttcgggatc ttctcagtaa aattttctac tgatggctcg      720
gaactagttg ctggaagtag tgatgatgct atatgtgtct atgatctcga aactaataag      780
ctctctctca gaatcctagc acacacatct gatgtgaaca ccgtctgttt tgctgacgag      840
agtgggcatc tgatatactc cgggagtgat gataatctct gcaaggtgtg ggatagacgt      900
tgcttcatag caaaagggaa gcctgcagga gtcctaacgg gacatatcga aggaattaca      960
gatatagaca gccgtggaga tggccgatat ttaatatcaa atggaaaaga tcagacaatc     1020
aaactttggg atatcaggaa aatggccccc aatgctacaa gctcttttagg gatcaggaat     1080
tatgaatggg attacagatg gatggactac ccaccaccag ctagagactt gaagcatcca     1140
tgcgatctgt ccgtggctac ttataaaggt cactcggttc tccgaacgct tattcgtgc      1200
tatttctcac caacctatag caccggccag aaatacatTT acaccggatc tcacgactct      1260
tctgtttata tttatgatgt ggcgactggg gaggtagctg gagtgctgaa acaccataac      1320
tcgccggtaa gagattgcag ttggcacccg cactatccta tgctggtgag ctcttcatgg      1380
gatggggata tagtgaggtg ggagttcgtc ggcaatggag aagctccgat gcctatggcc      1440
aagaaacgac tacgcagaag gcaatactac gatgtctga      1479

```

<210> 230
 <211> 490
 <212> PRT
 <213> Linum usitatissum

<400> 230

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

Leu Glu Ile Glu Ser Gln Leu Cys Asp Glu Glu Glu Thr Val Asn Glu
 20 25 30

Val Gly Gly Gly Ser Gln Gln His Lys Ser Leu Asn Lys Ser Val Glu
 35 40 45

Lys Leu Asp His Glu Val Ala Gln Asp Thr Asn Leu Lys Ser Gln Pro
 50 55 60

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

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

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Asp Gln Thr Ile Lys Leu Trp Asp Ile Arg Lys Met Ala Pro Asn Ala
340 345 350

Thr Ser Ser Leu Gly Ile Arg Asn Tyr Glu Trp Asp Tyr Arg Trp Met
355 360 365

Asp Tyr Pro Pro Pro Ala Arg Asp Leu Lys His Pro Cys Asp Leu Ser
370 375 380

Val Ala Thr Tyr Lys Gly His Ser Val Leu Arg Thr Leu Ile Arg Cys
385 390 395 400

Tyr Phe Ser Pro Thr Tyr Ser Thr Gly Gln Lys Tyr Ile Tyr Thr Gly
405 410 415

Ser His Asp Ser Ser Val Tyr Ile Tyr Asp Val Ala Thr Gly Glu Val
420 425 430

Ala Gly Val Leu Lys His His Asn Ser Pro Val Arg Asp Cys Ser Trp
435 440 445

His Pro His Tyr Pro Met Leu Val Ser Ser Ser Trp Asp Gly Asp Ile
450 455 460

Val Arg Trp Glu Phe Val Gly Asn Gly Glu Ala Pro Met Pro Met Ala
465 470 475 480

Lys Lys Arg Leu Arg Arg Arg Gln Tyr Tyr
485 490

<210> 231
<211> 1422
<212> DNA
<213> Lithospermum erythrorhizon

<400> 231
atggggtatg ctatgagtag atttgaaact gatgtatctg taatcttttag ttcaagttct 60
gattctgaga cttctcatga ttctcttattc aataagccag tgaaaaattt ggatcatgaa 120
attgctcagc ttactaggct tagatcagca cccacgaga atctaagtag agacctacta 180
gttaagaggg tattgccgct ttcgacaatg aaaatgctgg ctggcagaga agctaattgtt 240
tcaggaagag ggaggttttc atctgcagat tgttgtcatg tagtcagtcg acatttgcct 300
gttaacgatc cttgtgttgt cgatcaaattg acatctagag tttatttgtc acagttttcgt 360
actgatgggt ctcttttcat tgctggcttt cagggatgcc acatcagaat atacaatgta 420
gataaagggg ggaaagttca aaacgacatt atagcaaaat gtgtgagatg gacaattact 480
gatgcatctc tttctccaga tcaaaagttc cttgcctatg ctagcttgac accaattgca 540
catattgtaa aatttggttc tgctgctacg gaatctcatg caaatgttac ggatatacat 600
gatggattgg atttttcatc taacgatgat gggggatact cttttgggggt attttccatc 660

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

aagttttcaa ccgatggacg ggaaattgta gctggtacca gtgatgaatc aatttgtgtt 720
tatgatctag aagcagatag actttccctt agaatttcag cccacgagtc agatgttaac 780
tctgtatgct ttgctgatga aagcggccat cttatttatt ctggaagtga tgacaatctc 840
tgcaaggttt gggacagacg ttgcttcaat gccaaaggaa aaccagcagg catcttgatg 900
ggacacctcg aaggaattac atttattgat agccgaggag atgggcgata ttttatttca 960
aatggtaaag atcagacaat caaactctgg gatatccgca aaatgtcctc gaatgctggc 1020
ggcacaattc aaagcagaaa tagtgaatgg gactacagat ggatggaata tccacaagag 1080
gcaagagatt tgaagcatcc atctgatcta tcgggtgcta cttacaaagg ccaactccgtc 1140
ttgtgtactc ttattcgctg ctacttctcc ccagactata gtactggcca gaaatacatc 1200
tacactggat ctcatgatgc aaatgtttat atctacgact tggttaactgg agatcaagtt 1260
tctacacttc agtaccataa ggcaactgta agggattgta gttggcacc aaactatcct 1320
atgcttgta gctcatcgtt tgacggagaa attgtcaaat ggggaatatcg tggaaacgat 1380
gaagctcccg tccaaggaaa caatcagcgg cttcaaagat ga 1422

```

```

<210> 232
<211> 473
<212> PRT
<213> Lithospermum erythrorhizon

```

<400> 232

```

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

```

```

Ser Ser Ser Ser Asp Ser Glu Thr Ser His Asp Ser Leu Ile Asn Lys
20          25          30

```

```

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

```

```

Ser Ala Pro His Glu Asn Leu Ser Arg Asp Leu Leu Val Lys Arg Val
50          55          60

```

```

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

```

```

Ser Gly Arg Gly Arg Phe Ser Ser Ala Asp Cys Cys His Val Val Ser
85          90          95

```

```

Arg His Leu Pro Val Asn Asp Pro Cys Val Val Asp Gln Met Thr Ser
100         105         110

```

```

Arg Val Tyr Leu Ser Gln Phe Ser Thr Asp Gly Ser Leu Phe Ile Ala
115        120        125

```

```

Gly Phe Gln Gly Cys His Ile Arg Ile Tyr Asn Val Asp Lys Gly Trp
130        135        140

```

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

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

Gly Asp Gln Val Ser Thr Leu Gln Tyr His Lys Ala Thr Val Arg Asp
420 425 430

Cys Ser Trp His Pro Asn Tyr Pro Met Leu Val Ser Ser Ser Phe Asp
435 440 445

Gly Glu Ile Val Lys Trp Glu Tyr Arg Gly Asn Asp Glu Ala Pro Val
450 455 460

Gln Gly Asn Asn Gln Arg Leu Gln Arg
465 470

<210> 233
<211> 1464
<212> DNA
<213> Lycopersicon esculentum

<400> 233
atgtattttg atttcttaca cccagagtcc attgaagaca tgggggtattc tctaagtaag 60
ttagaagtag acaccggact ctttgatggg tcaagttcca atcatggggg tgctagcagt 120
gttcatcatg aaagaccaac aaattatttg gaccatgaaa tttctcaact tactaagctt 180
agatcaggac cccatgaaaa tctcagtaga atcctaccag ggaaaaagga agttcctgta 240
tccgcattca agatgttagc tgctcgagaa gccaatatatt ccggtagagg aaggttttcg 300
aaggcagatt gttgtcatgt tctaagtaaa tatttgccag ttagtggtcc ttggattgtg 360
gaccagatgg aaaccagagc ttatgtatca caattttcag cagatgggtc cttttttgtt 420
gctgcctttc aggggaagtca tattagaata tacaatgtgg aaagaggggtg gaaagttcac 480
aagaatattc atgcaaaaag tttgagatgg acagttactg atacatctct ttctccggat 540
caacgtcatt tgggtctatgc tactatgtca cccatcgtag atattgtaga tgtaggatct 600
gctgcctctg aatctgtagc caacatcaca gaaattcatg atgggttgct tttgtctact 660
gacaatgatg attttggaat tttctctgtg aaattttcta ctgaagggtc ggaagttgtt 720
gctggaagta gtgatgatgc gatctatgtt tatgatcttg aagcaaaca actctctctt 780
cgaatatccg cacacaattc tgatgtcaat tctgtatgtt ttgctgacga aagtggccat 840
ctcatttatt ctggaagtga tgacaatctg tgtaagggtc gggatagacg ttgttttagg 900
gccaaagaaa agccagccgg agtcttgatg ggacacctag aaggcgttac gttccttgat 960
agtcgggggg atggtcgtta tttcatttct aacagtaaag atcagtccat caagctctgg 1020
gatatccgca aaatgtcttc tcatgctgct cgcaatatct gggttcaggaa ttatgagtgg 1080
gactatagat ggatggacta ccctgctcaa gctagagacg tgaagcacc ttatgatcag 1140
tcaatatcca cttataaggg tcattctgtc ttgcgtactc taattcgctg ctactttctca 1200
ccagaatata gactgggca gagatacatt tacacaggat cccatgatgc ctgcgtatac 1260
atctatgatt tggtaagtgg agagcaagtc gcgaaattgc agcaccaccg gtcgaccatt 1320
agagattgta gctggcacc tacttatcca atgcttggtta gctcttcttg ggatggagat 1380
gttgtcaaat gggaattccc tggaaatggg gaagcaccac tccctccaaa aaggaagcag 1440

atcagaagaa ggcatttctt ttaa

1464

<210> 234
 <211> 487
 <212> PRT
 <213> Lycopersicon esculentum

<400> 234

Met Tyr Phe Asp Phe Leu His Pro Glu Ser Ile Glu Asp Met Gly Tyr
 1 5 10 15

Ser Leu Ser Lys Leu Glu Val Asp Thr Gly Leu Phe Asp Gly Ser Ser
 20 25 30

Ser Asn His Gly Val Ala Ser Ser Val His His Glu Arg Pro Thr Asn
 35 40 45

Tyr Leu Asp His Glu Ile Ser Gln Leu Thr Lys Leu Arg Ser Gly Pro
 50 55 60

His Glu Asn Leu Ser Arg Ile Leu Pro Gly Lys Lys Glu Val Pro Val
 65 70 75 80

Ser Ala Phe Lys Met Leu Ala Ala Arg Glu Ala Asn Ile Ser Gly Arg
 85 90 95

Gly Arg Phe Ser Lys Ala Asp Cys Cys His Val Leu Ser Lys Tyr Leu
 100 105 110

Pro Val Ser Gly Pro Trp Ile Val Asp Gln Met Glu Thr Arg Ala Tyr
 115 120 125

Val Ser Gln Phe Ser Ala Asp Gly Ser Leu Phe Val Ala Ala Phe Gln
 130 135 140

Gly Ser His Ile Arg Ile Tyr Asn Val Glu Arg Gly Trp Lys Val His
 145 150 155 160

Lys Asn Ile His Ala Lys Ser Leu Arg Trp Thr Val Thr Asp Thr Ser
 165 170 175

Leu Ser Pro Asp Gln Arg His Leu Val Tyr Ala Thr Met Ser Pro Ile
 180 185 190

Val His Ile Val Asp Val Gly Ser Ala Ala Ser Glu Ser Val Ala Asn
 195 200 205

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

Phe Gly Ile Phe Ser Val Lys Phe Ser Thr Glu Gly Arg Glu Val Val
 225 230 235 240

Ala Gly Ser Ser Asp₂₄₅ Asp Ala Ile Tyr Val₂₅₀ Tyr Asp Leu Glu Ala₂₅₅ Asn
 Lys Leu Ser Leu₂₆₀ Arg Ile Ser Ala His₂₆₅ Asn Ser Asp Val₂₇₀ Asn Ser Val
 Cys Phe Ala₂₇₅ Asp Glu Ser Gly His₂₈₀ Leu Ile Tyr Ser Gly₂₈₅ Ser Asp Asp
 Asn Leu₂₉₀ Cys Lys Val Trp Asp₂₉₅ Arg Arg Cys Phe Arg₃₀₀ Ala Lys Glu Lys
 Pro Ala Gly Val Leu Met₃₁₀ Gly His Leu Glu Gly₃₁₅ Val Thr Phe Leu Asp₃₂₀
 Ser Arg Gly Asp Gly₃₂₅ Arg Tyr Phe Ile Ser₃₃₀ Asn Ser Lys Asp Gln₃₃₅ Ser
 Ile Lys Leu Trp₃₄₀ Asp Ile Arg Lys Met₃₄₅ Ser Ser His Ala Ala₃₅₀ Arg Asn
 Ile Trp Phe₃₅₅ Arg Asn Tyr Glu Trp₃₆₀ Asp Tyr Arg Trp Met₃₆₅ Asp Tyr Pro
 Ala Gln₃₇₀ Ala Arg Asp Val Lys₃₇₅ His Pro Tyr Asp Gln₃₈₀ Ser Ile Ser Thr
 Tyr Lys Gly His Ser Val₃₉₀ Leu Arg Thr Leu Ile₃₉₅ Arg Cys Tyr Phe Ser₄₀₀
 Pro Glu Tyr Ser Thr₄₀₅ Gly Gln Arg Tyr Ile₄₁₀ Tyr Thr Gly Ser His₄₁₅ Asp
 Ala Cys Val Tyr₄₂₀ Ile Tyr Asp Leu Val₄₂₅ Ser Gly Glu Gln Val₄₃₀ Ala Lys
 Leu Gln His₄₃₅ His Arg Ser Thr Ile₄₄₀ Arg Asp Cys Ser Trp₄₄₅ His Pro Thr
 Tyr Pro₄₅₀ Met Leu Val Ser Ser₄₅₅ Ser Trp Asp Gly Asp₄₆₀ Val Val Lys Trp
 Glu Phe Pro Gly Asn Gly₄₇₀ Glu Ala Pro Leu Pro₄₇₅ Pro Lys Arg Lys Gln₄₈₀
 Ile Arg Arg Arg His₄₈₅ Phe Phe

<210> 235
 <211> 1488
 <212> DNA

<213> Medicago truncatula

<400> 235

```

atgtacgcta tatccggtgc actttacgtt gaccaaattg gctatgctat gagtagatta      60
gacgtggact ctagtgatac tgaagatgga aatgcaatcc ttgaagattc tagtactgga      120
aaagctaaaa aggcatattga aaatttagac aatgaaattg ctcaaataac caagttgaaa      180
tcaacacctc atcaactgct agtacatgat ggatctggaa ggaaagagtt gcctgtttcc      240
ccggtgaaga tgctggcagg ccgcgaatct aattgttcag gacggggaag gttttcttcc      300
gctgatcgct gtcattcttt gagcagggtat ttacctgtaa atggtccttg gcctatcgac      360
caaatgccta gtcgagcata cgtgtctcag ttttcagctg atggttctct tttgtttgct      420
gggttccagg gaaaccacat aaaaatatac aatgtggaga aaggttggaa agttcaaaaa      480
aacattctaa ccaagagttt gagatggaca atcactgata cttctctttc ccctgatcaa      540
agtcattctag tttatgccag catgtcaccc attgtacaca ttgtgaatgt tggatcttct      600
gagacagagt cactagcaaa tgtgacggag atccacgatg ggttggattt ttcacaaac      660
gacgatggag gatactcttt tggaattttc tctttgaaat tttcaacaga tgggaaggaa      720
ttagttgcag gaactagtgg cgattctata tatgtatacg atcttgaaac aaataagggt      780
tcacttcgaa ttttagcaca cacggctgat gtaaactctg tatgttttgc tgatgaaact      840
ggccatctta tttactctgg aagtgatgat agtttctgca aggtctggga tcggcggttg      900
ttaaatgcta aagacaagcc agcaggggtt ttgatgggac accttgaggg cattacgttt      960
attgattccc gtggagatgg acgctatttc atttcaaacg gtaaagatca gaccatcaaa     1020
ctttgggaca tacgtaaaat gtcattcaat gttaccagta accgtgtccg tggatatagg     1080
agttttgaat gggattacag gtggatggat taccgccac aagcaaaaga cttgaatcat     1140
ccttgtgata agtcagtggc tacatataga ggccattcag tcttacgcac tcttgtccgc     1200
tgcttttttt ctccagcttt tagcactggc cagaagtaca tctatactgg atcacacaac     1260
gcatgtgttt atgtatatga tttggtgagt ggagcacaag ttgcaacatt gaagcaccat     1320
aatcacctg taagagattg tagttggcat cccttcacc ctatgcttgt tagctcttct     1380
tgggatggag atgttgtaaa atggcaatct gctggaagct ctgatatggc agcctcgtcg     1440
gttaagaaga gggtaaaca aagacatttt tatgaagatt acctatga                     1488

```

<210> 236

<211> 495

<212> PRT

<213> Medicago truncatula

<400> 236

```

Met Tyr Ala Ile Ser Gly Ala Leu Tyr Val Asp Gln Met Gly Tyr Ala
1           5           10          15

```

```

Met Ser Arg Leu Asp Val Asp Ser Ser Asp Thr Glu Asp Gly Asn Ala
          20          25          30

```


Ile Leu Glu Asp Ser Ser Thr Gly Lys Ala Lys Lys Ala Phe Glu Asn
 35 40 45
 Leu Asp Asn Glu Ile Ala Gln Ile Thr Lys Leu Lys Ser Thr Pro His
 50 55 60
 Gln Leu Leu Val His Asp Gly Ser Gly Arg Lys Glu Leu Pro Val Ser
 65 70 75 80
 Pro Val Lys Met Leu Ala Gly Arg Glu Ser Asn Cys Ser Gly Arg Gly
 85 90 95
 Arg Phe Ser Ser Ala Asp Arg Cys His Leu Leu Ser Arg Tyr Leu Pro
 100 105 110
 Val Asn Gly Pro Trp Pro Ile Asp Gln Met Pro Ser Arg Ala Tyr Val
 115 120 125
 Ser Gln Phe Ser Ala Asp Gly Ser Leu Phe Val Ala Gly Phe Gln Gly
 130 135 140
 Asn His Ile Lys Ile Tyr Asn Val Glu Lys Gly Trp Lys Val Gln Lys
 145 150 155 160
 Asn Ile Leu Thr Lys Ser Leu Arg Trp Thr Ile Thr Asp Thr Ser Leu
 165 170 175
 Ser Pro Asp Gln Ser His Leu Val Tyr Ala Ser Met Ser Pro Ile Val
 180 185 190
 His Ile Val Asn Val Gly Ser Ser Glu Thr Glu Ser Leu Ala Asn Val
 195 200 205
 Thr Glu Ile His Asp Gly Leu Asp Phe Ser Ser Asn Asp Asp Gly Gly
 210 215 220
 Tyr Ser Phe Gly Ile Phe Ser Leu Lys Phe Ser Thr Asp Gly Lys Glu
 225 230 235 240
 Leu Val Ala Gly Thr Ser Gly Asp Ser Ile Tyr Val Tyr Asp Leu Glu
 245 250 255
 Thr Asn Lys Val Ser Leu Arg Ile Leu Ala His Thr Ala Asp Val Asn
 260 265 270
 Thr Val Cys Phe Ala Asp Glu Thr Gly His Leu Ile Tyr Ser Gly Ser
 275 280 285
 Asp Asp Ser Phe Cys Lys Val Trp Asp Arg Arg Cys Leu Asn Ala Lys
 290 295 300
 Asp Lys Pro Ala Gly Val Leu Met Gly His Leu Glu Gly Ile Thr Phe
 Seite 253

305

310

315

320

Ile Asp Ser Arg Gly Asp Gly Arg Tyr Phe Ile Ser Asn Gly Lys Asp
 325 330 335

Gln Thr Ile Lys Leu Trp Asp Ile Arg Lys Met Ser Ser Asn Val Thr
 340 345 350

Ser Asn Arg Val Arg Gly Tyr Arg Ser Phe Glu Trp Asp Tyr Arg Trp
 355 360 365

Met Asp Tyr Pro Pro Gln Ala Lys Asp Leu Asn His Pro Cys Asp Gln
 370 375 380

Ser Val Ala Thr Tyr Arg Gly His Ser Val Leu Arg Thr Leu Val Arg
 385 390 395 400

Cys Phe Phe Ser Pro Ala Phe Ser Thr Gly Gln Lys Tyr Ile Tyr Thr
 405 410 415

Gly Ser His Asn Ala Cys Val Tyr Val Tyr Asp Leu Val Ser Gly Ala
 420 425 430

Gln Val Ala Thr Leu Lys His His Lys Ser Pro Val Arg Asp Cys Ser
 435 440 445

Trp His Pro Phe His Pro Met Leu Val Ser Ser Ser Trp Asp Gly Asp
 450 455 460

Val Val Lys Trp Gln Ser Ala Gly Ser Ser Asp Met Ala Ala Ser Ser
 465 470 475 480

Val Lys Lys Arg Val Asn Lys Arg His Phe Tyr Glu Asp Tyr Leu
 485 490 495

<210> 237
 <211> 1392
 <212> DNA
 <213> Oryza sativa

<400> 237
 atgggttatg gcatgagtag gatggaggag gaatacagcg agcatgaaga tcagaataat 60
 ggtggatcta attcacaagt gaataatgag ttcttaaaca cacataatga tattttccat 120
 atgactcaaa taagatcagg acctagttaa agtcttcgca agtctattgg tacaagcaaa 180
 gatgtgatat cgacaaccag gttattgtct ggaagggaaa ttaattcttc aggaaatggg 240
 aagttctctt cagttgatcg tgcgtttctt cttggtcgtt atcttccagt tgatggccct 300
 gaaatagtgg acaggatgga ttcccagact tatgtttcac agttttctgc tgatggatct 360
 ctttttgttg ctggttttca gggaagccac ataagaatat atgatgttga taaaggttgg 420
 aaagtacata gggacattca tgctagaagt ttgagatgga ccattagtga cgcatactt 480

tcccctgatc aacagtttct tgtctactcc agtctagcac cgattatcca tatcgtcaat	540
gttgggactg ctgcaaaaca atcatatgct aatatcactg acatccacga tggactagat	600
ttttcacagc atgaagatgt tcgatataca tttggaatat tttctgttaa attctcttct	660
gatggccgag agcttgttgc tggcagtaac gatgattcaa tatatgttta tgaccttgtg	720
gcaaacaaac taacgttgcg tttgcctgct catcattctg atgtcaaacac agtagcattt	780
gctgacgaaa ctggccatct catatattct ggaagtgatg ataatttatg caaggtctgg	840
gataggcgat gtttatccac agaagaacct gctggagttt tgactgggca tttgcatggc	900
attactcata ttgatagccg tggagatggg cgggtgtttca tatcaaattg aaaagaccaa	960
gctatcaaaa tgtgggacat caggaaaatg acatccaatg ctgatagtta tgaagacaga	1020
acctcaaatt gggactatag atattcaaga tatccacaac agtataagca actaaagcat	1080
ccccatgac agtcaatagc tacatactgg ggccattcag ttcttcgtac attgatccgt	1140
tgctatTTTT ctctgcata tagcacagga cagaagtaca tatatacagg atcctatgat	1200
tctagtgttt gtatctacga tgtggtgagc ggatcacaag ttgcaaaact caaaggatat	1260
catcagctgg caattcgaga ctgcagttgg catcccttcg accctatgct tgtcagctca	1320
tcctgggacg gccgggttgc caagtgggcc aggtcttcct gtcagcaaga agagactact	1380
gatctcgatt ga	1392

<210> 238
 <211> 463
 <212> PRT
 <213> Oryza sativa

<400> 238

Met	Gly	Tyr	Gly	Met	Ser	Arg	Met	Glu	Glu	Glu	Tyr	Ser	Glu	His	Glu
1				5				10						15	

Asp	Gln	Asn	Asn	Gly	Gly	Ser	Asn	Ser	Gln	Val	Asn	Asn	Glu	Phe	Leu
		20						25					30		

Asn	Thr	His	Asn	Asp	Ile	Phe	His	Met	Thr	Gln	Ile	Arg	Ser	Gly	Pro
		35					40					45			

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

Thr	Thr	Arg	Leu	Leu	Ser	Gly	Arg	Glu	Ile	Asn	Ser	Ser	Gly	Asn	Gly
65					70					75				80	

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

Val	Asp	Gly	Pro	Glu	Ile	Val	Asp	Arg	Met	Asp	Ser	Arg	Ala	Tyr	Val
			100					105					110		

Ser	Gln	Phe	Ser	Ala	Asp	Gly	Ser	Leu	Phe	Val	Ala	Gly	Phe	Gln	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115

120

125

Ser His Ile Arg Ile Tyr Asp Val Asp Lys Gly Trp Lys Val His Arg
130 135 140

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

Ser Pro Asp Gln Gln Phe Leu Val Tyr Ser Ser Leu Ala Pro Ile Ile
165 170 175

His Ile Val Asn Val Gly Thr Ala Ala Lys Gln Ser Tyr Ala Asn Ile
180 185 190

Thr Asp Ile His Asp Gly Leu Asp Phe Ser Gln His Glu Asp Val Arg
195 200 205

Tyr Thr Phe Gly Ile Phe Ser Val Lys Phe Ser Ser Asp Gly Arg Glu
210 215 220

Leu Val Ala Gly Ser Asn Asp Asp Ser Ile Tyr Val Tyr Asp Leu Val
225 230 235 240

Ala Asn Lys Leu Thr Leu Arg Leu Pro Ala His His Ser Asp Val Asn
245 250 255

Thr Val Ala Phe Ala Asp Glu Thr Gly His Leu Ile Tyr Ser Gly Ser
260 265 270

Asp Asp Asn Leu Cys Lys Val Trp Asp Arg Arg Cys Leu Ser Thr Glu
275 280 285

Glu Pro Ala Gly Val Leu Thr Gly His Leu His Gly Ile Thr His Ile
290 295 300

Asp Ser Arg Gly Asp Gly Arg Cys Phe Ile Ser Asn Gly Lys Asp Gln
305 310 315 320

Ala Ile Lys Met Trp Asp Ile Arg Lys Met Thr Ser Asn Ala Asp Ser
325 330 335

Tyr Glu Asp Arg Thr Ser Asn Trp Asp Tyr Arg Tyr Ser Arg Tyr Pro
340 345 350

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

Tyr Trp Gly His Ser Val Leu Arg Thr Leu Ile Arg Cys Tyr Phe Ser
370 375 380

Pro Ala Tyr Ser Thr Gly Gln Lys Tyr Ile Tyr Thr Gly Ser Tyr Asp
385 390 395 400

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Ser Ser Val Cys Ile Tyr Asp Val Val Ser Gly Ser Gln Val Ala Lys
405 410 415

Leu Lys Gly Tyr His Gln Leu Ala Ile Arg Asp Cys Ser Trp His Pro
420 425 430

Phe Asp Pro Met Leu Val Ser Ser Ser Trp Asp Gly Arg Val Ala Lys
435 440 445

Trp Ser Arg Ser Ser Cys Gln Gln Glu Glu Thr Thr Asp Leu Asp
450 455 460

<210> 239
<211> 1476
<212> DNA
<213> Pinus radiata

<400> 239
atgaatacgg caatgcattt tggctgctggt tggcgatcga ttgctgagat ggggtatacgg 60
atgagcagac tagagattga gcctgagtcg tgtgaggacg agaagagcctt ggatgggggtt 120
ggtaacagcc agggaccgaa tgagttgccg agatgcttgg atcatgagtt ggcgcatttg 180
acgaatctga agtcgaggcc ccatgaacat ttgatccgag atttccctgg gaggcgggct 240
ctgcctgttt ccaccgttaa gatgctggcg ggtcgagagt gtaattattc acgaagaggg 300
aggttctcct ccgctgattg ctgtcacatg ctgagcagat atgtgcctgt taatggctct 360
tcgcccctgg atcagatgaa tagtcgagct tatgtttcgc aattttcagc tgatggttct 420
ctatttgttg ctggctttca gggtagccac attagaattt ataatgttga taaaggatgg 480
aaatgtcaga agaacattct taccaagagt ttacgggtgga cgatcactga tacatctctt 540
tctcctgacc aacgttacct tgtgtatgcc agtatgtcac ccacgtcca tattgttgac 600
atcggctccg ctgctatgga ttctcttgca aacatcacgg agatccatga gggtttggat 660
ttttccgctg acagtggacc atattctttt ggaatcttct ctgttaaatt ttctaccgat 720
ggacgagaag tcgtcgtgag aagcagcgac gattctatat atgtctatga tcttgtggca 780
aataagcttt ccctcagaat tccagcacat gagtctgatg tgaacacagt atgctttgct 840
gatgaaagtg gtcataataa ttattctggg agtgatgata catactgcaa ggtgtgggat 900
agacgttgcc tgagtgccag aaataaacct gcaggagttc taatgggaca ccttgaaggc 960
attacgttca ttgatagccg tggatgatgg cgttatttca tatcaaattg caaagatcag 1020
acgatcaaac tttgggatat ccggaaaatg ggctctgata tctgtcgtcg aggccttagg 1080
aatttcgaat gggattacag atggatggac taccaccccc gggctaggga ttcgaaacac 1140
ccttttgatc tgtcagtggc aacatataaa ggccattcgg tgttgctgac tcttattcgg 1200
tgctacttct cccagtaga tagcactggc caaaagtata tctacactgg atcccatgat 1260
tcctgtgttt atatctatga tgtgggtgact ggagctcaag ttgcggccct caagcaccat 1320
aaatcgccgg tcagagactg cagttggcac ccggagtacc cgatgattgt gagctcttct 1380

tgggatgggg atattgtgaa atgggaattc tttgggaacg gagaaactga gatcccggcg 1440
atgaagaaga ggatccggag gcggcatttg tattaa 1476

<210> 240
<211> 491
<212> PRT
<213> Pinus radiata

<400> 240

Met Asn Thr Ala Met His Phe Gly Ala Gly Trp Arg Ser Ile Ala Glu
1 5 10 15

Met Gly Tyr Thr Met Ser Arg Leu Glu Ile Glu Pro Glu Ser Cys Glu
20 25 30

Asp Glu Lys Ser Leu Asp Gly Val Gly Asn Ser Gln Gly Pro Asn Glu
35 40 45

Leu Pro Arg Cys Leu Asp His Glu Leu Ala His Leu Thr Asn Leu Lys
50 55 60

Ser Arg Pro His Glu His Leu Ile Arg Asp Phe Pro Gly Arg Arg Ala
65 70 75 80

Leu Pro Val Ser Thr Val Lys Met Leu Ala Gly Arg Glu Cys Asn Tyr
85 90 95

Ser Arg Arg Gly Arg Phe Ser Ser Ala Asp Cys Cys His Met Leu Ser
100 105 110

Arg Tyr Val Pro Val Asn Gly Pro Ser Pro Leu Asp Gln Met Asn Ser
115 120 125

Arg Ala Tyr Val Ser Gln Phe Ser Ala Asp Gly Ser Leu Phe Val Ala
130 135 140

Gly Phe Gln Gly Ser His Ile Arg Ile Tyr Asn Val Asp Lys Gly Trp
145 150 155 160

Lys Cys Gln Lys Asn Ile Leu Thr Lys Ser Leu Arg Trp Thr Ile Thr
165 170 175

Asp Thr Ser Leu Ser Pro Asp Gln Arg Tyr Leu Val Tyr Ala Ser Met
180 185 190

Ser Pro Ile Val His Ile Val Asp Ile Gly Ser Ala Ala Met Asp Ser
195 200 205

Leu Ala Asn Ile Thr Glu Ile His Glu Gly Leu Asp Phe Ser Ala Asp
210 215 220

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

Gly Arg Glu Val Val Ala Gly Ser Ser Asp Asp Ser Ile Tyr Val Tyr
 245 250 255

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

Asp Val Asn Thr Val Cys Phe Ala Asp Glu Ser Gly His Ile Ile Tyr
 275 280 285

Ser Gly Ser Asp Asp Thr Tyr Cys Lys Val Trp Asp Arg Arg Cys Leu
 290 295 300

Ser Ala Arg Asn Lys Pro Ala Gly Val Leu Met Gly His Leu Glu Gly
 305 310 315 320

Ile Thr Phe Ile Asp Ser Arg Gly Asp Gly Arg Tyr Phe Ile Ser Asn
 325 330 335

Gly Lys Asp Gln Thr Ile Lys Leu Trp Asp Ile Arg Lys Met Gly Ser
 340 345 350

Asp Ile Cys Arg Arg Gly Phe Arg Asn Phe Glu Trp Asp Tyr Arg Trp
 355 360 365

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

Ser Val Ala Thr Tyr Lys Gly His Ser Val Leu Arg Thr Leu Ile Arg
 385 390 395 400

Cys Tyr Phe Ser Pro Val His Ser Thr Gly Gln Lys Tyr Ile Tyr Thr
 405 410 415

Gly Ser His Asp Ser Cys Val Tyr Ile Tyr Asp Val Val Thr Gly Ala
 420 425 430

Gln Val Ala Ala Leu Lys His His Lys Ser Pro Val Arg Asp Cys Ser
 435 440 445

Trp His Pro Glu Tyr Pro Met Ile Val Ser Ser Ser Trp Asp Gly Asp
 450 455 460

Ile Val Lys Trp Glu Phe Phe Gly Asn Gly Glu Thr Glu Ile Pro Ala
 465 470 475 480

Met Lys Lys Arg Ile Arg Arg Arg His Leu Tyr
 485 490

<210> 241

<211> 1467

<212> DNA

<213> *Populus tremuloides*

<400> 241

```

atgtattttt ttgctagaag aacttcggta gacgaaatgg gttacgctat gagcagactg      60
gagactgaat ctgaactctg tgatggtggc aagaccattc ctgaggctgg tagcagcaag      120
agagccagca attggttgaa taacttagac catgaaattg ctcaggttac gaagttgaaa      180
tctagtccgc ataaacagct ggccgaactt gttcccggca tgcataagtc atctgtttcc      240
actgttaaga tgttggttgg tcgagaagct aattattcag caaggggaag attctctgca      300
gctgatcggt gtcacatgct tagcagatat ttgcctgtca atggaccttg gcttggtgac      360
cagatgagta cccgagccta tgtctcgag ttttcagctg atggctctct atttgttgct      420
gggttttcagg gaagctatat tagaatatac aatgtggaga aggggtggaa agttcagaag      480
aacattcttg ccaaaagttt gcgttggact gttaccgata catctctttc cccagatcag      540
cgccatctcg tttatgcaag catgtcacct attgtccata ttgttgatgc tgggtctgcc      600
gaaacagagt cgcttgcaaa cgttacggag tttcatgacg gattggactt ttcttctggt      660
gatgggggct attcttttgg aatcttctct gtgaaatfff ccactgatgg gcgagaactt      720
gttgaggaa gtaatgatga ctccatatat gtctacgacc ttgaacaaaa taagctctcc      780
ctcagaatff tggcacacac gtctgatggt aacactgtat gttttgctga tgaaagtggc      840
caccttatct tttctgggag tgatgataat ctttgcaagg tgtgggatag acgctgcttt      900
attgcaaaaag ggaagccagc tggagtccta acaggacact tagaaggcat aacattttatt      960
gacagccatg gagatggtcg gtattttatc tcaaatggta aagatcagac tatcaaaact      1020
tgggatattc ggaaaatggc ccctaattgct actagctatt cagggttag gaattatgaa      1080
tgggactaca ggtggatgga ctacccatat gaggcaagag atttgaaaca cccctgcgat      1140
caatcagtag ccacatataa aggtcattcg gttctgcgca ctcttatccg ctgctacttt      1200
tctcctgtat atagtactgg ccagaagtac atctacactg gatctcatga ttcttgtggt      1260
tatattttatg acttggtgac tggagaacta gtttcattac tacaacatca taaatcacct      1320
gtaagagatt gtagttggca cccatattat cccatgctcg tcagctcttc ttgggacgga      1380
gatgtcgtaa aatgggagtt tcctggcaat ggagaagctc cagtcccttc aaccaagaag      1440
agaattcgaa ggagacaatt tgattga      1467

```

<210> 242

<211> 488

<212> PRT

<213> *Populus tremuloides*

<400> 242

```

Met Tyr Phe Phe Ala Arg Arg Thr Ser Val Asp Glu Met Gly Tyr Ala
1           5           10          15

```

```

Met Ser Arg Leu Glu Thr Glu Ser Glu Leu Cys Asp Gly Gly Lys Thr
          20          25          30

```


PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Ile Pro Glu Ala Gly Ser Ser Lys Arg Ala Ser Asn Trp Leu Asn Asn
35 40 45

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

Lys Gln Leu Ala Glu Leu Val Pro Gly Met His Lys Ser Ser Val Ser
65 70 75 80

Thr Val Lys Met Leu Val Gly Arg Glu Ala Asn Tyr Ser Ala Arg Gly
85 90 95

Arg Phe Ser Ala Ala Asp Arg Cys His Met Leu Ser Arg Tyr Leu Pro
100 105 110

Val Asn Gly Pro Trp Leu Val Asp Gln Met Ser Thr Arg Ala Tyr Val
115 120 125

Ser Gln Phe Ser Ala Asp Gly Ser Leu Phe Val Ala Gly Phe Gln Gly
130 135 140

Ser Tyr Ile Arg Ile Tyr Asn Val Glu Lys Gly Trp Lys Val Gln Lys
145 150 155 160

Asn Ile Leu Ala Lys Ser Leu Arg Trp Thr Val Thr Asp Thr Ser Leu
165 170 175

Ser Pro Asp Gln Arg His Leu Val Tyr Ala Ser Met Ser Pro Ile Val
180 185 190

His Ile Val Asp Ala Gly Ser Ala Glu Thr Glu Ser Leu Ala Asn Val
195 200 205

Thr Glu Phe His Asp Gly Leu Asp Phe Ser Ser Gly Asp Gly Gly Tyr
210 215 220

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

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

Asn Lys Leu Ser Leu Arg Ile Leu Ala His Thr Ser Asp Val Asn Thr
260 265 270

Val Cys Phe Ala Asp Glu Ser Gly His Leu Ile Phe Ser Gly Ser Asp
275 280 285

Asp Asn Leu Cys Lys Val Trp Asp Arg Arg Cys Phe Ile Ala Lys Gly
290 295 300

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Lys Pro Ala Gly Val Leu Thr Gly His Leu Glu Gly Ile Thr Phe Ile
305 310 315 320

Asp Ser His Gly Asp Gly Arg Tyr Phe Ile Ser Asn Gly Lys Asp Gln
325 330 335

Thr Ile Lys Leu Trp Asp Ile Arg Lys Met Ala Pro Asn Ala Thr Ser
340 345 350

Tyr Ser Gly Leu Arg Asn Tyr Glu Trp Asp Tyr Arg Trp Met Asp Tyr
355 360 365

Pro Tyr Glu Ala Arg Asp Leu Lys His Pro Cys Asp Gln Ser Val Ala
370 375 380

Thr Tyr Lys Gly His Ser Val Leu Arg Thr Leu Ile Arg Cys Tyr Phe
385 390 395 400

Ser Pro Val Tyr Ser Thr Gly Gln Lys Tyr Ile Tyr Thr Gly Ser His
405 410 415

Asp Ser Cys Val Tyr Ile Tyr Asp Leu Val Thr Gly Glu Leu Val Ser
420 425 430

Leu Leu Gln His His Lys Ser Pro Val Arg Asp Cys Ser Trp His Pro
435 440 445

Tyr Tyr Pro Met Leu Val Ser Ser Ser Trp Asp Gly Asp Val Val Lys
450 455 460

Trp Glu Phe Pro Gly Asn Gly Glu Ala Pro Val Pro Ser Thr Lys Lys
465 470 475 480

Arg Ile Arg Arg Arg Gln Phe Asp
485

<210> 243
<211> 1428
<212> DNA
<213> Prunus armeniaca

<400> 243	
atgagttaca gaacaagggtt tggaaaagat aatagcgctt gtgatagtgg aaatgctggt	60
gaaggttctg gttcaagtaa aggaccaat gaagtatcaa atgattttga tcatgaaatt	120
gctcaactca ctaagcatag atcaagaccc catcagcttt tgagccagga catgcctgga	180
aagtcgaggt tactggtttc aacaatgaaa atgttggttg gtcgtgaaag taatcattca	240
ggacgtggga gattctcgtc tgctgacggt tgccatgttt tgagccggta tctgcccac	300
aatggtcctt ggggggtgga ccagtcaaca agtcctgctt atgtttctca attttcaaat	360
gatggtttgt tttttgttgc tggatttcag ggcggccata ttagaatata taatgttgat	420

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

aagggatgga aagttcagaa ggacatccta accaaaagct tgagatggac aattactgat      480
acatctctat ctccagatca acgttatctt gtttatgcta gcatgacacc cattgtcaat      540
attgtcaatg ttggatcttc tatgacagag tcacttgcaa atgttacgga aattcatgaa      600
ggctctggatt tttctgttgg tggatgatgag gacgaatttg gaattttctc agtttagattt      660
tcaactgatg ggcgagagct tgtagctgca agtagagatg cttcaatata tgtttatgat      720
ctccaagcaa ataaagttaa cctccgaata ccagcacact cgtctgatgt aaacactgta      780
tgctttgcgg atgagactgg acatctcata tattctggca gtgacgataa tctctgtaag      840
gtttgggata gacgctgctt taatcacaaa ggacagccag ctgggggtcct gatgggacat      900
cttgaagggtg ttacatttat tgatagtagg ggagatgggc gttacttcat atcaaaggg      960
aaggaccaga ctaccaact ctgggatata agaaagatgt cctctagagc catgtacagc     1020
ccaaggctta gagatcatga ctgggattac agatggatgg agtaccagc tcatgcaaaa     1080
actttgaaac atccaaatga tcagtcactg gctacatata gaggtcatgg agtcctgcgt     1140
actttaattc gctgttacct ttctccagca tatagtactg gacaaaagta catctacact     1200
ggatctagtg atcatttgtt ctatatatat gatctggtga ccggtgctca agttgcgaga     1260
ctcaaccatc acgaaggacc tgtaagagac tgtagttggc atcctctcta tccgatgttg     1320
gtcagctctt cttgggatgg gacgattgcc agatgggaat ttcctgggga tgaccaagta     1380
cccaccctgg agaggccgag agcgcgccgg aaggagaggc tactataa                    1428

```

<210> 244
 <211> 475
 <212> PRT
 <213> Prunus armeniaca

<400> 244

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

Gly Asn Ala Val Glu Gly Ser Gly Ser Ser Lys Gly Pro Asn Glu Val
20 25 30

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

Arg Pro His Gln Leu Leu Ser Gln Asp Met Pro Gly Lys Ser Arg Leu
50 55 60

Leu Val Ser Thr Met Lys Met Leu Val Gly Arg Glu Ser Asn His Ser
65 70 75 80

Gly Arg Gly Arg Phe Ser Ser Ala Asp Gly Cys His Val Leu Ser Arg
85 90 95

Tyr Leu Pro Ile Asn Gly Pro Trp Gly Val Asp Gln Ser Thr Ser Pro
100 105 110

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Ala Tyr Val Ser Gln Phe Ser Asn Asp Gly Leu Phe Phe Val Ala Gly
115 120 125

Phe Gln Gly Gly His Ile Arg Ile Tyr Asn Val Asp Lys Gly Trp Lys
130 135 140

Val Gln Lys Asp Ile Leu Thr Lys Ser Leu Arg Trp Thr Ile Thr Asp
145 150 155 160

Thr Ser Leu Ser Pro Asp Gln Arg Tyr Leu Val Tyr Ala Ser Met Thr
165 170 175

Pro Ile Val Asn Ile Val Asn Val Gly Ser Ser Met Thr Glu Ser Leu
180 185 190

Ala Asn Val Thr Glu Ile His Glu Gly Leu Asp Phe Ser Val Gly Gly
195 200 205

Asp Glu Asp Glu Phe Gly Ile Phe Ser Val Arg Phe Ser Thr Asp Gly
210 215 220

Arg Glu Leu Val Ala Ala Ser Arg Asp Ala Ser Ile Tyr Val Tyr Asp
225 230 235 240

Leu Gln Ala Asn Lys Val Asn Leu Arg Ile Pro Ala His Ser Ser Asp
245 250 255

Val Asn Thr Val Cys Phe Ala Asp Glu Thr Gly His Leu Ile Tyr Ser
260 265 270

Gly Ser Asp Asp Asn Leu Cys Lys Val Trp Asp Arg Arg Cys Phe Asn
275 280 285

His Lys Gly Gln Pro Ala Gly Val Leu Met Gly His Leu Glu Gly Val
290 295 300

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

Lys Asp Gln Thr Thr Gln Leu Trp Asp Ile Arg Lys Met Ser Ser Arg
325 330 335

Ala Met Tyr Ser Pro Arg Leu Arg Asp His Asp Trp Asp Tyr Arg Trp
340 345 350

Met Glu Tyr Pro Ala His Ala Lys Thr Leu Lys His Pro Asn Asp Gln
355 360 365

Ser Leu Ala Thr Tyr Arg Gly His Gly Val Leu Arg Thr Leu Ile Arg
370 375 380

Cys Tyr Leu Ser Pro Ala Tyr Ser Thr Gly Gln Lys Tyr Ile Tyr Thr
385 390 395 400

Gly Ser Ser Asp His Cys Val Tyr Ile Tyr Asp Leu Val Thr Gly Ala
405 410 415

Gln Val Ala Arg Leu Asn His His Glu Gly Pro Val Arg Asp Cys Ser
420 425 430

Trp His Pro Leu Tyr Pro Met Leu Val Ser Ser Ser Trp Asp Gly Thr
435 440 445

Ile Ala Arg Trp Glu Phe Pro Gly Asp Asp Gln Val Pro Thr Leu Glu
450 455 460

Arg Pro Arg Ala Arg Arg Lys Glu Arg Leu Leu
465 470 475

<210> 245
<211> 1437
<212> DNA
<213> Saccharum officinarum

<400> 245
atgcgcggag tgcggcggag cgcgcgcggg gaatcgtccc ggaaggcggc ggcggaccgg 60
gaccgggagg tggagcgggt cacgctgtgc gccaatgtgt cccacctcac caggaccacg 120
tcggagccgt gccgcagggc tcgcggcgcc gctccggcgc tccggaagag gcccttctcg 180
gcgttcgagc tgggtgtcggc gagggaggcc ggccgcgcgg gcggcgccgg gttctccgcg 240
gccgaccgag cctacgtcgg caggcagcac atccccacca aggggccctg gggcgctcgac 300
gacgtggaca gcgaggccta cgtctcgcag ttctccgctg atggctcctt gctcatcgct 360
gggtttcggg gaagccgcat cagagtctac gacgccgaga aagggtggaa gattcataag 420
gatataagct gccaatggt gactggacg gtttcagaca ttgctctctc acctgaccaa 480
cgattccttg cctatgcaag tttgtcgcct actgttcaca ttgtgaacgt gcagagtgtc 540
ggaaaggaat cacatgctaa tattactgaa attcatgagg gactggattt aactgggtgg 600
gatgaggatg aggactttgg aatattttct gttaaattct caaaagatgg taaagaaatt 660
gttggtggga acaatgaaag atcaatatat gtttatgacc ttgcaacaaa taaagtgtca 720
gcccgcaccc gtgctcataa agctgatgtc aatgctgtta ccttcgctga tgaaagtgga 780
aatgtgttgt actctggaag tgatgatagt ttctgtaagg tgtgggacag acgttgcctt 840
tcaggggaaa agtcagcagg tactttaaca ggtcatttag atggagttac atttatcgat 900
agccgtggtg atgggcgtta tttcatctcc aattgcaagg atcagagaat caaactttgg 960
gacatcagga aaatgtcttc cgtcgtgaga gctcgcccag tgagtctagt ggactgggac 1020
tataggtggg agctatttcc atcagaagcc cacaatttta agcatccaga tgatcagtct 1080
gtggccacat acagaggcca ttcagttctg cgaacactta tccgttgcta tttctcccct 1140
gtgcacagca cgggtcagag gtacatatac acaggatcca gtgacaagtc tgtacatatt 1200

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

tatgatgtgg taagcgggaa gactgtcaag aggctttctt ggcatggctc gatcatcaga	1260
gactgcacct ggcatccata ctacccaacg ctcgtcagct cctcctggga cggctatgtt	1320
gcccgtctggg aggcatcagg cgacgacgac gacccttcag tgctcgtcca cgacgagaag	1380
agggcaaccc gttactttcg gagatacgcc aatcccttca cagatccctt catgtga	1437

<210> 246
 <211> 478
 <212> PRT
 <213> Saccharum officinarum

<400> 246

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

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

Met Ser His Leu Thr Arg Thr Thr Ser Glu Pro Cys Arg Arg Ala Arg
 35 40 45

Gly Ala Ala Pro Ala Leu Arg Lys Arg Pro Phe Ser Ala Phe Glu Leu
 50 55 60

Val Ser Ala Arg Glu Ala Gly Arg Ala Gly Gly Ala Gly Phe Ser Ala
 65 70 75 80

Ala Asp Arg Ala Tyr Val Gly Arg Gln His Ile Pro Thr Lys Gly Pro
 85 90 95

Trp Gly Val Asp Asp Val Asp Ser Glu Ala Tyr Val Ser Gln Phe Ser
 100 105 110

Ala Asp Gly Ser Leu Leu Ile Ala Gly Phe Arg Gly Ser Arg Ile Arg
 115 120 125

Val Tyr Asp Ala Glu Lys Gly Trp Lys Ile His Lys Asp Ile Ser Cys
 130 135 140

Gln Met Val His Trp Thr Val Ser Asp Ile Ala Leu Ser Pro Asp Gln
 145 150 155 160

Arg Phe Leu Ala Tyr Ala Ser Leu Ser Pro Thr Val His Ile Val Asn
 165 170 175

Val Gln Ser Ala Gly Lys Glu Ser His Ala Asn Ile Thr Glu Ile His
 180 185 190

Glu Gly Leu Asp Leu Thr Gly Gly Asp Glu Asp Glu Asp Phe Gly Ile
 195 200 205

Phe Ser Val Lys Phe Ser Lys Asp Gly Lys Glu Ile Val Val Gly Asn
210 215 220

Asn Glu Arg Ser Ile Tyr Val Tyr Asp Leu Ala Thr Asn Lys Val Ser
225 230 235 240

Ala Arg Ile Arg Ala His Lys Ala Asp Val Asn Ala Val Thr Phe Ala
245 250 255

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

Lys Val Trp Asp Arg Arg Cys Leu Ser Gly Glu Lys Ser Ala Gly Thr
275 280 285

Leu Thr Gly His Leu Asp Gly Val Thr Phe Ile Asp Ser Arg Gly Asp
290 295 300

Gly Arg Tyr Phe Ile Ser Asn Cys Lys Asp Gln Arg Ile Lys Leu Trp
305 310 315 320

Asp Ile Arg Lys Met Ser Ser Val Val Arg Ala Arg Pro Val Ser Leu
325 330 335

Val Asp Trp Asp Tyr Arg Trp Glu Leu Phe Pro Ser Glu Ala His Asn
340 345 350

Phe Lys His Pro Asp Asp Gln Ser Val Ala Thr Tyr Arg Gly His Ser
355 360 365

Val Leu Arg Thr Leu Ile Arg Cys Tyr Phe Ser Pro Val His Ser Thr
370 375 380

Gly Gln Arg Tyr Ile Tyr Thr Gly Ser Ser Asp Lys Ser Val His Ile
385 390 395 400

Tyr Asp Val Val Ser Gly Lys Thr Val Lys Arg Leu Ser Trp His Gly
405 410 415

Ser Ile Ile Arg Asp Cys Thr Trp His Pro Tyr Tyr Pro Thr Leu Val
420 425 430

Ser Ser Ser Trp Asp Gly Tyr Val Ala Arg Trp Glu Ala Ser Gly Asp
435 440 445

Asp Asp Asp Pro Ser Val Leu Val His Asp Glu Lys Arg Ala Thr Arg
450 455 460

Tyr Phe Arg Arg Tyr Ala Asn Pro Phe Thr Asp Pro Phe Met
465 470 475

<210> 247

<211> 1380

<212> DNA

<213> Triticum aestivum

<400> 247

```

atgggttatg gcatgagtag gctacatgag ggatacagtg agcctgaagg gctgaatagt      60
gatggatcta gttcagtcga agtgaataat gattttctcaa agttacacaa tgatattttc      120
catatgactc gactaagatc aggacctagt gaaagcatcc gcaagtccat ggatagagtc      180
tcagtgacta ggttggttacg tggaagggaa gttaattctt caggaaatgg aaagttctct      240
ccggttgatc gtgcattcgt tcttggtcat tatcttccag tggatggtcc tgaaacgggtg      300
gatacaatgg attcacgagc ttatgtttca cagttttctg ccgatgggtc tctttttggt      360
gctgggtttc aggggaagcca cataagaata tatgatgtcg ataaagggtg ggaaatacac      420
aaggacattc atgctagaag tttagatgg acaattagt atgcagcggt atcacctgat      480
caaagggtcc ttgtctactc tagtctggca cccattatcc atattgtcaa tgttggcact      540
gcttcaagag aatcatatgc taatgtcact gacatccatg atggattaga tttttcagag      600
catgaagatg ttagatattc atttggtcctc ttttctgtta aattttccac tgatgggagg      660
gagcttggtg ctggcagtaa tgatgattca atatatgtct atgaccttca gaccaacaaa      720
gtgacattgc gtttgctgc ccatacatct gatgtcaaca cagtagcatt tgctgatgaa      780
tctggtaacc tactttattc tggaagcgat gataacttgt gcaagggtctg ggacagacgt      840
tgtttgcca caggggaagc ggctgggggtt ttgactggac atctgcatgg cattactcat      900
attgacagcc gtggagatgg tcgatgtttc atatcaaatg gaaaagatca agctattaag      960
atgtgggaca tccggaaaat gacatccaat gctgatgggt cggaaaacag agtccctgcc     1020
tgggactaca gatattcaag atatccacaa cagtacaagc aacaaaagca tccacatgac     1080
cagtcagtag ctacataccg gggccattca gttctccgta cattgattcg ttgctatttt     1140
tctcccacat atagcacagg acagaagtac atatatacag gatcttatga tgctagtgtc     1200
tgcatctatg atgtggtaag tgggtcgcaa gttgccaaac tgcaaggaca tcatcatttg     1260
gcagttcgag actgcagctg gcatccgtcc gatccaatgc ttgtcagttc atcatgggac     1320
ggccagggtg ccgatgggtc caggactcgc tccaagcaag atacttgtga actcgattaa     1380

```

<210> 248

<211> 459

<212> PRT

<213> Triticum aestivum

<400> 248

Met Gly Tyr Gly Met Ser Arg Leu His Glu Gly Tyr Ser Glu Pro Glu
 1 5 10 15

Gly Leu Asn Ser Asp Gly Ser Ser Ser Val Glu Val Asn Asn Asp Phe
 20 25 30

Ser Lys Leu His Asn Asp Ile Phe His Met Thr Arg Leu Arg Ser Gly
 35 40 45

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

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

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Met Trp Asp Ile Arg Lys Met Thr Ser Asn Ala Asp Gly Ser Glu Asn
325 330 335

Arg Val Pro Ala Trp Asp Tyr Arg Tyr Ser Arg Tyr Pro Gln Gln Tyr
340 345 350

Lys Gln Gln Lys His Pro His Asp Gln Ser Val Ala Thr Tyr Arg Gly
355 360 365

His Ser Val Leu Arg Thr Leu Ile Arg Cys Tyr Phe Ser Pro Thr Tyr
370 375 380

Ser Thr Gly Gln Lys Tyr Ile Tyr Thr Gly Ser Tyr Asp Ala Ser Val
385 390 395 400

Cys Ile Tyr Asp Val Val Ser Gly Ser Gln Val Ala Lys Leu Gln Gly
405 410 415

His His His Leu Ala Val Arg Asp Cys Ser Trp His Pro Ser Asp Pro
420 425 430

Met Leu Val Ser Ser Ser Trp Asp Gly Gln Val Ala Arg Trp Ser Arg
435 440 445

Thr Arg Ser Lys Gln Asp Thr Cys Glu Leu Asp
450 455

<210> 249
<211> 1416
<212> DNA
<213> Triticum aestivum

<400> 249
atggcggcgg caggagact gcggggacgg cggcggacaa aggaggtgga gcgcgagccc 60
gagccgttca ccatcgagga ggaggtgtcc cacctcacc ggggccggtc ggagccgtgc 120
cccggcacc gcgccgcat ccatggcgcc aagcgggaaga gggacgtctc ggctttcgag 180
atgctgtcgt cgaggagtc cggcctctcg ggaggcggcg ggttctgttc ggccgaccgc 240
gcctacgccg ccggaagca cctcccgtcg gaaggaccct ggtgcgtgga agacatggat 300
agcgaggcct atgtctcgca gttctccagc gatggctcga tgctcgttgc cgggtttcgg 360
ggaagccgca tcagagttta cgatgtcgat agagggtgga aggttcataa gaacataagc 420
tgcagaagta tgaggtggac ggtttcagat attgcgtctt cccctgacca gcgatatctt 480
gcctattcca gtttgtcgcc tattgttcac attgttaatg tgcagaatgc tggaagggaa 540
tcggatgcta atgttactga aattcacgat ggtttggaat tctgtgatga cgatgaatac 600
tctttcggga tattctctgt gaaattttcg aaagatggta gagaagtagt tgttgggaac 660
aatgattgtt caatatatgt ctatgatctt ggagcaaata aagtgtcaga ccgtatccgt 720
gctcatacgt ctgatgtcaa cacggtcacc tttgctgatg aaagtggcaa tttattgtac 780

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

tctggaagtg atgataatct ctgtaagggtc tgggataggc gttgccttgt aagagagaaa	840
ccagcaggtg ttttgacagg tcacttagat gggattacat gtattgatag ccgtggtgat	900
gggcgttatc taatctccaa ctgcaaggat cagactatca aactttggga catcagaaa	960
atgtccgccca ccgtaaaagg acgacaacca agattgtatg actgggacta cagatggatg	1020
tcgttcccgt cacacgctag atattataag catccaaatg atctatctct ggcaacatac	1080
aggggtcatt cagttctgcg gacacttatc cgctgctact tctctccaat gcacagcacg	1140
ggccagaggt acatatacac tggatcaagt gacgattcag tgcataattta cgatgtggta	1200
acaggggcca ccgtcaagaa gctctcgtgg cagggttcga tcacagaga ctgcacctgg	1260
catccttacc gtccaacgct cgtaagctct tcctgggacg gctatctggc ccggtgggag	1320
gcatcaggca acaatgagga cccctcgtg ctcacgtgcg acgagcagag gactagccct	1380
tacgaccaga catacgggct ctcttttgcc ctgtag	1416

<210> 250
 <211> 471
 <212> PRT
 <213> Triticum aestivum

<400> 250

Met	Ala	Ala	Ala	Gly	Arg	Leu	Arg	Gly	Arg	Arg	Arg	Thr	Lys	Glu	Val
1				5				10						15	

Glu	Arg	Glu	Pro	Glu	Pro	Phe	Thr	Ile	Glu	Glu	Glu	Val	Ser	His	Leu
			20					25					30		

Thr	Arg	Val	Arg	Ser	Glu	Pro	Cys	Pro	Gly	Thr	Arg	Ala	Ala	Ile	His
		35					40					45			

Gly	Ala	Lys	Arg	Lys	Arg	Asp	Val	Ser	Ala	Phe	Glu	Met	Leu	Ser	Ser
	50					55					60				

Arg	Glu	Ser	Gly	Leu	Ser	Gly	Gly	Gly	Gly	Phe	Cys	Ser	Ala	Asp	Arg
65					70					75					80

Ala	Tyr	Ala	Ala	Gly	Lys	His	Leu	Pro	Ser	Glu	Gly	Pro	Trp	Cys	Val
				85					90					95	

Glu	Asp	Met	Asp	Ser	Glu	Ala	Tyr	Val	Ser	Gln	Phe	Ser	Ser	Asp	Gly
			100					105					110		

Ser	Met	Leu	Val	Ala	Gly	Phe	Arg	Gly	Ser	Arg	Ile	Arg	Val	Tyr	Asp
		115					120					125			

Val	Asp	Arg	Gly	Trp	Lys	Val	His	Lys	Asn	Ile	Ser	Cys	Arg	Ser	Met
	130					135					140				

Arg	Trp	Thr	Val	Ser	Asp	Ile	Ala	Leu	Ser	Pro	Asp	Gln	Arg	Tyr	Leu
145					150					155					160

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Ala Tyr Ser Ser Leu Ser Pro Ile Val His Ile Val Asn Val Gln Asn
165 170 175

Ala Gly Arg Glu Ser Asp Ala Asn Val Thr Glu Ile His Asp Gly Leu
180 185 190

Glu Phe Cys Asp Asp Asp Glu Tyr Ser Phe Gly Ile Phe Ser Val Lys
195 200 205

Phe Ser Lys Asp Gly Arg Glu Val Val Val Gly Asn Asn Asp Cys Ser
210 215 220

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

Ala His Thr Ser Asp Val Asn Thr Val Thr Phe Ala Asp Glu Ser Gly
245 250 255

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

Arg Arg Cys Leu Val Arg Glu Lys Pro Ala Gly Val Leu Thr Gly His
275 280 285

Leu Asp Gly Ile Thr Cys Ile Asp Ser Arg Gly Asp Gly Arg Tyr Leu
290 295 300

Ile Ser Asn Cys Lys Asp Gln Thr Ile Lys Leu Trp Asp Ile Arg Lys
305 310 315 320

Met Ser Ala Thr Val Lys Gly Arg Gln Pro Arg Leu Tyr Asp Trp Asp
325 330 335

Tyr Arg Trp Met Ser Phe Pro Ser His Ala Arg Tyr Tyr Lys His Pro
340 345 350

Asn Asp Leu Ser Leu Ala Thr Tyr Arg Gly His Ser Val Leu Arg Thr
355 360 365

Leu Ile Arg Cys Tyr Phe Ser Pro Met His Ser Thr Gly Gln Arg Tyr
370 375 380

Ile Tyr Thr Gly Ser Ser Asp Asp Ser Val His Ile Tyr Asp Val Val
385 390 395 400

Thr Gly Ala Thr Val Lys Lys Leu Ser Trp His Gly Ser Ile Ile Arg
405 410 415

Asp Cys Thr Trp His Pro Tyr Arg Pro Thr Leu Val Ser Ser Ser Trp
420 425 430

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Asp Gly Tyr Leu Ala Arg Trp Glu Ala Ser Gly Asn Asn Glu Asp Pro
435 440 445

Ser Val Leu Thr Cys Asp Glu Gln Arg Thr Ser Pro Tyr Asp Gln Thr
450 455 460

Tyr Gly Leu Ser Phe Ala Leu
465 470

<210> 251
<211> 1461
<212> DNA
<213> Vitis vinifera

```

<400> 251
atgtatttta cagccagtga ggggtctgct aatgaaatgg ggtatgccat gagtagattg      60
gagctagatt ctgatttctg tgatgctggc aaggacatcc atggaaatga taacactgaa      120
agactcaaca aagaattgaa tcatttagat catgaaattht cccagctcac aaagcttaga      180
tcgggacctc acgaatgtct gagtcagatt attcctggaa agcgggactc acctgtttcg      240
acgggttaaga tgctggcggg tcgagaaggg aattattcag gaaggggaag gttctcatca      300
gctgattgtt gtcatatgtt aagtagatat ttgcctgtca atggtccttg gcttgtggac      360
caaatgacaa gtcgagctta tgtgtcgcaa ttttctgctg atggttccct gtttgttgca      420
gggtttcagg gaagccatat tagaatatac aatgtggata gaggggtgaa agtgcagaag      480
aatattcttg caaaaagctt gcgatggaca gtcactgata catctctctc ccctgatcaa      540
cgccatcttg tttatgccag catgtcacct attgtccata ttgttaatat tggatctgct      600
gcaacagaat ctcttgcaaa cattacggag attcatgatg gtttggattt ttctgctgct      660
gatgatgagg gttattcttt cggaatcttc tcagtgaat tttccacaga tgggcgagag      720
ctttagtagtg gaagtagtga tgattcaata tatgtttatg atcttgaagc aaataagctt      780
tcccttagaa tttcggcaca cacgtctgat gtcaatactg tatgctttgc tgatgaaagt      840
gggcatctta tttattccgg gagtgatgat agtttgtgca aggtttggga cagacgttgc      900
ttcatatcaa aagggaagcc tgcaggagtc ctgatgggac acctagaagg aattactttt      960
attgatagcc gtagagatgg tcgtcatctc atttcaaata gtaaagacca gtctatcaaa     1020
ctttgggaca tccgaaaaat gtcctccaat gctacttgca ctccaggggtt caggaattat     1080
gaatgggatt atagatggat ggattatcca acccaggcaa gagagttgaa acacccatgt     1140
gatcaatcac tttccactta taaaggatcat tcagtcctgc gtactctcat acgctgctac     1200
ttctccccgt cttatagcac tggtcagaaa tacatctact ctggatctag cgattcttgc     1260
atttatattt atgatttgct gaccggagcc caagttgcaa cactggagca ccataaatca     1320
gtcgtaagag attgtaattg gcaccctaata tatccaatcc tggttagctc ttcattgggat     1380
ggagacattg tcaagtggga attccctggg aatggagagc cccctttgat caagaaacga     1440
atccggcgga aatatttata g                                     1461

```

<210> 252

<211> 486

<212> PRT

<213> Vitis vinifera

<400> 252

Met Tyr Phe Thr Ala Ser Glu Gly Ala Ala Asn Glu Met Gly Tyr Ala
 1 5 10 15

Met Ser Arg Leu Glu Leu Asp Ser Asp Phe Cys Asp Ala Gly Lys Asp
 20 25 30

Ile His Gly Asn Asp Asn Thr Glu Arg Leu Asn Lys Glu Leu Asn His
 35 40 45

Leu Asp His Glu Ile Ser Gln Leu Thr Lys Leu Arg Ser Gly Pro His
 50 55 60

Glu Cys Leu Ser Gln Ile Ile Pro Gly Lys Arg Asp Ser Pro Val Ser
 65 70 75 80

Thr Val Lys Met Leu Ala Gly Arg Glu Gly Asn Tyr Ser Gly Arg Gly
 85 90 95

Arg Phe Ser Ser Ala Asp Cys Cys His Met Leu Ser Arg Tyr Leu Pro
 100 105 110

Val Asn Gly Pro Trp Leu Val Asp Gln Met Thr Ser Arg Ala Tyr Val
 115 120 125

Ser Gln Phe Ser Ala Asp Gly Ser Leu Phe Val Ala Gly Phe Gln Gly
 130 135 140

Ser His Ile Arg Ile Tyr Asn Val Asp Arg Gly Trp Lys Val Gln Lys
 145 150 155 160

Asn Ile Leu Ala Lys Ser Leu Arg Trp Thr Val Thr Asp Thr Ser Leu
 165 170 175

Ser Pro Asp Gln Arg His Leu Val Tyr Ala Ser Met Ser Pro Ile Val
 180 185 190

His Ile Val Asn Ile Gly Ser Ala Ala Thr Glu Ser Leu Ala Asn Ile
 195 200 205

Thr Glu Ile His Asp Gly Leu Asp Phe Ser Ala Ala Asp Asp Glu Gly
 210 215 220

Tyr Ser Phe Gly Ile Phe Ser Val Lys Phe Ser Thr Asp Gly Arg Glu
 225 230 235 240

Leu Val Ala Gly Ser Ser Asp Asp Ser Ile Tyr Val Tyr Asp Leu Glu
 245 250 255

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Ala Asn Lys Leu Ser Leu Arg Ile Ser Ala His Thr Ser Asp Val Asn
260 265 270

Thr Val Cys Phe Ala Asp Glu Ser Gly His Leu Ile Tyr Ser Gly Ser
275 280 285

Asp Asp Ser Leu Cys Lys Val Trp Asp Arg Arg Cys Phe Ile Ser Lys
290 295 300

Gly Lys Pro Ala Gly Val Leu Met Gly His Leu Glu Gly Ile Thr Phe
305 310 315 320

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

Gln Ser Ile Lys Leu Trp Asp Ile Arg Lys Met Ser Ser Asn Ala Thr
340 345 350

Cys Thr Pro Gly Phe Arg Asn Tyr Glu Trp Asp Tyr Arg Trp Met Asp
355 360 365

Tyr Pro Thr Gln Ala Arg Glu Leu Lys His Pro Cys Asp Gln Ser Leu
370 375 380

Ser Thr Tyr Lys Gly His Ser Val Leu Arg Thr Leu Ile Arg Cys Tyr
385 390 395 400

Phe Ser Pro Ser Tyr Ser Thr Gly Gln Lys Tyr Ile Tyr Ser Gly Ser
405 410 415

Ser Asp Ser Cys Ile Tyr Ile Tyr Asp Leu Leu Thr Gly Ala Gln Val
420 425 430

Ala Thr Leu Glu His His Lys Ser Val Val Arg Asp Cys Asn Trp His
435 440 445

Pro Asn Tyr Pro Ile Leu Val Ser Ser Ser Trp Asp Gly Asp Ile Val
450 455 460

Lys Trp Glu Phe Pro Gly Asn Gly Glu Pro Pro Leu Ile Lys Lys Arg
465 470 475 480

Ile Arg Arg Lys Tyr Leu
485

<210> 253

<211> 1431

<212> DNA

<213> Zea mays

<400> 253

atgcaaggaa ggatgcgagg cgcgcggcgg agcgcgcgcg gggaatcgtc ccggaaggcg

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

gcgggcccgcg aggtggagcc attcacgctg tgcggcgaga tgtcccatct caccagggcc      120
acgtcagagc cgtgccgcag ggctcgcggc gccgccttcg cccgccgggc gaggcccttc      180
tcggcgtagc agctggtgtc ggcgcgggag gccggccgcg cgggcggcgc cgggttctcc      240
gcggccgatc gagcctacct cggcaggcag cacatcccca ccaaggggcc gtggggcgtc      300
gacgacgtgg aaagcgaggc ctacgtctcg cagttctccg ccgatggctc gttgctcatc      360
gcgggggtttc ggggaagccg catcagagtc tacgacgccg agaaaggggtg gaagatccac      420
aaggatataa gctgcagaag tgtgcaactg acggtttcag atattgctct ctcacctgac      480
caacgattcc ttgcctatgc aagtctgaca cctattgttc acattgtgaa tgttcagaat      540
gctggaaagg aatcacatgc taatattact gaaattcatg agggattgga tttaacgggt      600
ggtgatgagg atgaggactt tggaatattt tctgttaaata tctccaaaga tggtaaagaa      660
gttgttgttg ggaacaatga aaagtcaata tatgtttatg acctttcagc aaataaagtg      720
tcagcccgca tccgtgctca taaagctgat gtcaatgctg ttaccttcgc tgatgaaact      780
ggaaacgtgt tgtactctgg aagtgatgat agtctctgta aggtgtggga caggcgttgc      840
ctttcagggg aaaagtcagc aggtattttg acaggtcatt tagatggagt tacatttatac      900
gatagccgtg gtgatgggcg ttatttcatac tctcattgca aggatcagag aatcaaactt      960
tgggacatca ggaaaatgtc ttccgtcgtg agatctcgcc cagtgagtct agtggactgg     1020
gactataggt ggatgccatt tccatcagaa gtcataatc ttaagcatcc aggtgatcag     1080
tctgtggcca catacagagg ccattcagtt ttgcgaacac ttatccgttg ctatTTTTTcc     1140
cctgtgcaca gcacgggtca gaggtacata tacacgggat ccagtgacaa gtctgtacat     1200
atttatgacg tggtaacccg ggaggctgtc aagaggcttt cgtggcatgg ctccatcatc     1260
agagactgca cctggcatcc atactacca acgctcgtca gctcctcctg ggacggcttc     1320
gttgcccggg gggaggcctc gggcgacgac gacgaccatt cgggtgctcgt tgccgacgag     1380
atgagaggaa gcccttacta ccggagatac ggcgatccct tggatgatgta g              1431

```

<210> 254
 <211> 460
 <212> PRT
 <213> Zea mays

<400> 254

Met Gly Tyr Gly Met Ser Arg Leu Asp Asp Glu Tyr Tyr Glu Ala Glu
 1 5 10 15

Gly Gln Asn Thr Gly Gly Ser Gly Ser Val Gln Val Asn Asp Glu Phe
 20 25 30

Ala Thr Leu His Asn Asp Ile Phe His Met Thr Arg Met Arg Ser Gly
 35 40 45

Leu Thr Glu Ser Tyr Lys Ser Met Gly Thr Asn Arg Gly Ile Ile Ser
 50 55 60

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

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

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Cys Ala Asp Gly Ala Pro Ala Trp Asp Tyr Arg Tyr Ser Arg Tyr Pro
340 345 350

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

Tyr Arg Gly His Thr Val Leu Arg Thr Leu Ile Arg Cys Tyr Phe Ser
370 375 380

Pro Ser Tyr Ser Thr Gly Gln Lys Tyr Ile Tyr Thr Gly Ser Tyr Asp
385 390 395 400

Ser Asn Val Cys Ile Tyr Asp Val Val Ser Gly Ser Gln Val Ala Lys
405 410 415

Leu Lys Trp His Gln Met Ala Ile Arg Asp Cys Ser Trp His Pro Phe
420 425 430

Glu Pro Thr Leu Val Ser Ser Ser Trp Asp Gly Arg Val Val Lys Trp
435 440 445

Thr Ser Ala Arg Asp Glu Gly Ala Ser Asp Val Asp
450 455 460

<210> 255
<211> 1383
<212> DNA
<213> Zea mays

<400> 255
atgggttatg gcatgagtag gctagacgat gaatactatg aggctgaagg gcagaatact 60
ggtggatctg gctcagttca agtgaacgat gagtttgcaa cactacataa tgatattttt 120
catatgaccc gaatgagatc aggacttact gaaagctaca agtccatggg taccaacaga 180
ggcataatat caactgcaa gttattatct cgaagggaaa ttgattgttc tggaaagggg 240
atgttctctt ctggtgaccg tgcatttggt ctaggtcgtc atgttccgat gaacaatcct 300
gaattattgg ataggatgga ttctcgtgct tacgtttcac agttttctgc tgatggtact 360
ctttttgttg ctggttttca gggaagtcac ataagaatat acgatgttga tagaggctgg 420
agcatacaca aagacattca tgctaggtgt ttaagatgga caatcagtga tgtatcctta 480
tcacctgatc agcggtatct tgcctactct agtctggcac ctattatcca tattgtcaat 540
gttgggaatg cggcaagaga atcctatgct aacgtcactg acatccatga tggattggat 600
ttttcacagc atgaagatgt tcaatattca tttggaatat tttctgtaaa attttcctct 660
gatggacggg aacttggtgc tggcagcaat gatgactcaa tatatgtcta tgatcttcat 720
gcaaacaaat tgacattacg tttatctgct catacatctg atgtcaatac agtagcattt 780
gctgatgaaa ccggccatct catatattct ggaagtgacg acactttatg caaggtctgg 840
gacaggcggg gtttgtccgc aggacaggct gccggagttt tgactggaca tttgcatggg 900

ataacacata ttgatagtcg tggagatggc cgaagtttca tatccaatgg aaaagatcaa	960
gcaatcaaac tgtgggatat caggaaaatg atgtccaatg ctgatagttg tgcagatgga	1020
gccccagcct gggactacag atattcaagg tatccgcac aacataaaca gttaaagcat	1080
ccgcatgata agtcaatagc gacgtaccgt ggacatacag tcctccggac attgatccgt	1140
tgctactttt ctccttcgta tagcactggg caaaagtaca tatatacagg gtcgtatgat	1200
tccaatgttt gcatctatga tgtggtaagt ggatcccagg ttgcgaagct gaaatggcat	1260
caaatggcga ttcgggactg cagttggcac ccatttgagc ccacgcttgt gagctcatcc	1320
tgggacggcc gggtagtgaa atggaccagc gcacgtgatg aaggggcttc tgatgtcgat	1380
tga	1383

<210> 256
 <211> 476
 <212> PRT
 <213> Zea mays

<400> 256

Met	Gln	Gly	Arg	Met	Arg	Gly	Ala	Arg	Arg	Ser	Ala	Arg	Gly	Glu	Ser
1				5					10					15	

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

Glu	Met	Ser	His	Leu	Thr	Arg	Ala	Thr	Ser	Glu	Pro	Cys	Arg	Arg	Ala
		35					40					45			

Arg	Gly	Ala	Ala	Phe	Ala	Arg	Arg	Ala	Arg	Pro	Phe	Ser	Ala	Tyr	Glu
	50					55					60				

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

Ala	Ala	Asp	Arg	Ala	Tyr	Leu	Gly	Arg	Gln	His	Ile	Pro	Thr	Lys	Gly
				85					90					95	

Pro	Trp	Gly	Val	Asp	Asp	Val	Glu	Ser	Glu	Ala	Tyr	Val	Ser	Gln	Phe
			100					105					110		

Ser	Ala	Asp	Gly	Ser	Leu	Leu	Ile	Ala	Gly	Phe	Arg	Gly	Ser	Arg	Ile
		115					120					125			

Arg	Val	Tyr	Asp	Ala	Glu	Lys	Gly	Trp	Lys	Ile	His	Lys	Asp	Ile	Ser
	130					135					140				

Cys	Arg	Ser	Val	His	Trp	Thr	Val	Ser	Asp	Ile	Ala	Leu	Ser	Pro	Asp
145					150					155					160

Gln	Arg	Phe	Leu	Ala	Tyr	Ala	Ser	Leu	Thr	Pro	Ile	Val	His	Ile	Val
			165						170					175	

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

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

Asp Asp Asp Asp His Ser Val Leu Val Ala Asp Glu Met Arg Gly Ser
450 455 460

Pro Tyr Tyr Arg Arg Tyr Gly Asp Pro Leu Val Met
465 470 475

<210> 257
<211> 1357
<212> DNA
<213> Citrus sinensis

<220>
<221> Unsure
<222> (665)..(665)
<223> n can be a stretch of 105 to 135 nucleotides

<220>
<221> misc_feature
<222> (665)..(665)
<223> n is a, c, g, or t

<400> 257
atgttcgtaa cagcaagtgg agttgacttt gacgaaatgg gatatgccat gagtagattc 60
gagatagaat ctgaattcta tgatgctgcc gatactgtca atcaagctag taatagtcgt 120
agcaaattca agaaaccctt gagtgcttta gaccatgaaa ttgccagct cacgaagctg 180
aaatcggaac ccaaggagca ttttagcaaa gaagtacctg ggaagcggca cttgcctgtt 240
tccactgtga aaatgttggc tggtagggaa ggcaattatt caggaagagg gaggttctca 300
gctgcagatt gttgtcatat gcttagtaga tatttgcctg ttaatgggcc ctggcctgtg 360
gaccagacaa ctagccgagc atatgtctct cagttttcgg ctgatggttc tttatttgtt 420
gctggatttc aggctagtca aattagaatc tatgatgtgg agagaggttg gaaaatacag 480
aaagacattc ttgctaaaag tttgcgttgg acagtcacag atacatctct tccccggat 540
cagcgccatc ttgtttatgc aagcatgtca cctatagtgc acattgttga tgttggttct 600
gggacaatgg agtctcttgc aaatgttacg gagatacatg atggattgga cttttctgct 660
gcagnctctc agaattttgg cacacacgtc tgatgttaac actgtatgtt ttggtgatga 720
aagtggccat ctaatctatt ctgggagtga tgacaatcta tgcaagggtat gggatagacg 780
ctgtctaaat gtgaaaggga agccagcagg agtcctgatg ggacacctag aagggatcac 840
gttcattgat agccgtggag atggtcgtta tctgatctca aatggtaaag atcaggccat 900
caaactttgg gatattcgga aaatgtcctc taatgcatcc tgcaatttag gatttaggag 960
ttatgaatgg gattacagat ggatggacta cccaccccag gcaagagatt tgaaacaccc 1020
atgtgatcaa tccgttgcta cgtataaagg tcattctgtc ttgcgtactc ttatccggtg 1080
ccacttttcc cctgtataca gcactggcca aaagtatatc tacactggat cccatgattc 1140
ttgtgtttat gtttatgacc tggtagagtg tgagcaagtt gctgcactca agtaccatac 1200
ttcacccgtt agagactgta gttggcaccc aagtcaacca atgcttggtta gctcttcttg 1260
ggatggagat gttgtcaggt gggagtttcc gggtaatgga gaagctgctc ctctctctaaa 1320

caagaagagg atccggagga gacagtttta cttgtga

<210> 258
 <211> 451
 <212> PRT
 <213> Citrus sinensis

<220>
 <221> UNSURE
 <222> (222)..(222)
 <223> X can be a stretch of 35 to 45 amino acids

<400> 258

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

Met Ser Arg Phe Glu Ile Glu Ser Glu Phe Tyr Asp Ala Ala Asp Thr
 20 25 30

Val Asn Gln Ala Ser Asn Ser Arg Ser Lys Phe Lys Lys Pro Leu Ser
 35 40 45

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

Lys Glu His Phe Ser Lys Glu Val Pro Gly Lys Arg His Leu Pro Val
 65 70 75 80

Ser Thr Val Lys Met Leu Ala Gly Arg Glu Gly Asn Tyr Ser Gly Arg
 85 90 95

Gly Arg Phe Ser Ala Ala Asp Cys Cys His Met Leu Ser Arg Tyr Leu
 100 105 110

Pro Val Asn Gly Pro Trp Pro Val Asp Gln Thr Thr Ser Arg Ala Tyr
 115 120 125

Val Ser Gln Phe Ser Ala Asp Gly Ser Leu Phe Val Ala Gly Phe Gln
 130 135 140

Ala Ser Gln Ile Arg Ile Tyr Asp Val Glu Arg Gly Trp Lys Ile Gln
 145 150 155 160

Lys Asp Ile Leu Ala Lys Ser Leu Arg Trp Thr Val Thr Asp Thr Ser
 165 170 175

Leu Ser Pro Asp Gln Arg His Leu Val Tyr Ala Ser Met Ser Pro Ile
 180 185 190

Val His Ile Val Asp Val Gly Ser Gly Thr Met Glu Ser Leu Ala Asn
 195 200 205

Val Thr Glu Ile His Asp Gly Leu Asp Phe Ser Ala Ala Xaa Leu Arg
 Seite 282

210

215

220

Ile Leu Ala His Thr Ser Asp Val Asn Thr Val Cys Phe Gly Asp Glu
 225 230 235 240

Ser Gly His Leu Ile Tyr Ser Gly Ser Asp Asp Asn Leu Cys Lys Val
 245 250 255

Trp Asp Arg Arg Cys Leu Asn Val Lys Gly Lys Pro Ala Gly Val Leu
 260 265 270

Met Gly His Leu Glu Gly Ile Thr Phe Ile Asp Ser Arg Gly Asp Gly
 275 280 285

Arg Tyr Leu Ile Ser Asn Gly Lys Asp Gln Ala Ile Lys Leu Trp Asp
 290 295 300

Ile Arg Lys Met Ser Ser Asn Ala Ser Cys Asn Leu Gly Phe Arg Ser
 305 310 315 320

Tyr Glu Trp Asp Tyr Arg Trp Met Asp Tyr Pro Pro Gln Ala Arg Asp
 325 330 335

Leu Lys His Pro Cys Asp Gln Ser Val Ala Thr Tyr Lys Gly His Ser
 340 345 350

Val Leu Arg Thr Leu Ile Arg Cys His Phe Ser Pro Val Tyr Ser Thr
 355 360 365

Gly Gln Lys Tyr Ile Tyr Thr Gly Ser His Asp Ser Cys Val Tyr Val
 370 375 380

Tyr Asp Leu Val Ser Gly Glu Gln Val Ala Ala Leu Lys Tyr His Thr
 385 390 395 400

Ser Pro Val Arg Asp Cys Ser Trp His Pro Ser Gln Pro Met Leu Val
 405 410 415

Ser Ser Ser Trp Asp Gly Asp Val Val Arg Trp Glu Phe Pro Gly Asn
 420 425 430

Gly Glu Ala Ala Pro Pro Leu Asn Lys Lys Arg Ile Arg Arg Arg Gln
 435 440 445

Phe Tyr Leu
 450

<210> 259
 <211> 1119
 <212> DNA
 <213> Glycine max

<400> 259

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

atgtctagta gggcttatgt ctcccagttt tcagctgatg gctctctttt tattgctggg      60
ttccagggaa gtcacataag aatatacaac gtggacagag gttggaaagt tcagaagaac      120
attctagcta aaaatttgag atggacaatc actgatacat ctctttcacc tgatcaacgc      180
tatctagttt atgccagtat gtcacctatt gtacacattg taaatgccgg atctgctgaa      240
acgggagtccc tagcaaatgt tacagagata catgatgggt tggatttttc atcaaagtat      300
gatggaggat actccttttg aattttctgt gtgaaattct caaaagatgg gaaagaatta      360
gttgcaggaa gtagtggtga ttctatatat gtatacgatc ttgaagcaaa taagctctca      420
cttcgaattt tagctcacac gtgtgatgtg aacactgtat gttttgctga tgaaactagc      480
catcttattt actctgggag tgatgatagt ttctgcaagg tctgggatcg gcgttgcttg      540
attgctaaag gcaagccagc aggggtttta atgggacacc ttgaggcat tacatttatt      600
gatactcgag gagatggacg ctatttcatt tcaaattgga aagatcaaac cattaaactt      660
tgggacatac gcaaaatgtc atccaatgtt accagcaatc ctgggtatag gagttacgaa      720
tgggattaca ggtggatgga ttatccaccc caagcaaaag acttgactca cccttgatgat      780
cagtcagtgg ctacttatag aggccattcg gtcttacgca ctctcatccg ctgctatttc      840
tccccagcgt ttagcacggg ccagaagtac atctatactg gatcacacaa cgcatgtgtt      900
tatatatatg atttggtaag tggagctcaa gtcgcaacgc tgaagcacca taaatcacct      960
gtaagagatt gtagctggca ccccttcac actacacttg ttagctcttc ttgggatgga     1020
gatgttgatg aatgggaatt tgctgggagt ggtgatacac caggctcttc aactaagaag     1080
agggtatgga caagacattt ttatgaacat tacctatga                               1119

```

<210> 260
 <211> 372
 <212> PRT
 <213> Glycine max
 <400> 260

Met Ser Ser Arg Ala Tyr Val Ser Gln Phe Ser Ala Asp Gly Ser Leu
 1 5 10 15

Phe Ile Ala Gly Phe Gln Gly Ser His Ile Arg Ile Tyr Asn Val Asp
 20 25 30

Arg Gly Trp Lys Val Gln Lys Asn Ile Leu Ala Lys Asn Leu Arg Trp
 35 40 45

Thr Ile Thr Asp Thr Ser Leu Ser Pro Asp Gln Arg Tyr Leu Val Tyr
 50 55 60

Ala Ser Met Ser Pro Ile Val His Ile Val Asn Ala Gly Ser Ala Glu
 65 70 75 80

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

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

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

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

Ile Tyr Val Tyr Asp Leu Glu Ala Asn Lys Leu Ser Leu Arg Ile Leu
130 135 140

Ala His Thr Cys Asp Val Asn Thr Val Cys Phe Ala Asp Glu Thr Ser
145 150 155 160

His Leu Ile Tyr Ser Gly Ser Asp Asp Ser Phe Cys Lys Val Trp Asp
165 170 175

Arg Arg Cys Leu Ile Ala Lys Gly Lys Pro Ala Gly Val Leu Met Gly
180 185 190

His Leu Glu Gly Ile Thr Phe Ile Asp Thr Arg Gly Asp Gly Arg Tyr
195 200 205

Phe Ile Ser Asn Gly Lys Asp Gln Thr Ile Lys Leu Trp Asp Ile Arg
210 215 220

Lys Met Ser Ser Asn Val Thr Ser Asn Pro Gly Tyr Arg Ser Tyr Glu
225 230 235 240

Trp Asp Tyr Arg Trp Met Asp Tyr Pro Pro Gln Ala Lys Asp Leu Thr
245 250 255

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

Arg Thr Leu Ile Arg Cys Tyr Phe Ser Pro Ala Phe Ser Thr Gly Gln
275 280 285

Lys Tyr Ile Tyr Thr Gly Ser His Asn Ala Cys Val Tyr Ile Tyr Asp
290 295 300

Leu Val Ser Gly Ala Gln Val Ala Thr Leu Lys His His Lys Ser Pro
305 310 315 320

Val Arg Asp Cys Ser Trp His Pro Phe His Thr Thr Leu Val Ser Ser
325 330 335

Ser Trp Asp Gly Asp Val Val Lys Trp Glu Phe Ala Gly Ser Gly Asp
340 345 350

Thr Pro Gly Ser Ser Thr Lys Lys Arg Val Trp Thr Arg His Phe Tyr
355 360 365

Glu His Tyr Leu
370

<210> 261
<211> 448
<212> DNA
<213> Hordeum vulgare

<400> 261
atgggttatg gcatgagtag gctgcatgag ggatacagtg aacatgaagg gcagaatagt 60
gatggatcta gttcagtcga agtgaataat gactttctcaa aattaaataa tgatattttc 120
cacatgactc gactaagatc aggacctagt gaaagcatcc gcaagtccat ggatagagtc 180
tcagtaacta ggttggttacg tggaagggaa gttaactctt caggaaatgg aaagttttct 240
ccggttgatc gtgcattcgt tcttggtcat tatcttccag tggatgggcc tgaaacagtg 300
gacaggatgg attcacgagc ttatgtttca catttttctg ccgatgggtc tctttttggt 360
gctgggtttc aggggaagcca cataagaata tatgatgtcg ataaaggctg ggaagtacac 420
aaggatattc atgctagaag tttgagat 448

<210> 262
<211> 149
<212> PRT
<213> Hordeum vulgare

<400> 262

Met Gly Tyr Gly Met Ser Arg Leu His Glu Gly Tyr Ser Glu His Glu
1 5 10 15

Gly Gln Asn Ser Asp Gly Ser Ser Ser Val Glu Val Asn Asn Asp Phe
20 25 30

Ser Lys Leu Asn Asn Asp Ile Phe His Met Thr Arg Leu Arg Ser Gly
35 40 45

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

Leu Leu Arg Gly Arg Glu Val Asn Ser Ser Gly Asn Gly Lys Phe Ser
65 70 75 80

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

Pro Glu Thr Val Asp Arg Met Asp Ser Arg Ala Tyr Val Ser His Phe
100 105 110

Ser Ala Asp Gly Ser Leu Phe Val Ala Gly Phe Gln Gly Ser His Ile
115 120 125

Arg Ile Tyr Asp Val Asp Lys Gly Trp Glu Val His Lys Asp Ile His
130 135 140

Ala Arg Ser Leu Arg
145

<210> 263
<211> 1029
<212> DNA
<213> Hordeum vulgare

<400> 263
aactcgtgca tgccttcatg ctggcaagag ccatactctt acattcaagc tgttgtcatc 60
aagagaatcc aatcgctccg gatttggttag attctcttca gccgattgct cttatgctct 120
tcgcaaacac ctaccagtaa gaggcccggtg gtgtgttgat agcatggatt gcgcagcata 180
catctcacia ttctcttttg atggttctct actaattggg aggcgtatca gaatctataa 240
cgctgacaaa aaatggaaga tccacaagga tataacctgc aaaagtctgc ggtggacagt 300
atcagatatt gctctctcac ctgatcaaca atacctagca tattccagtc tgtcccctac 360
tgttcacata gtaaatgttc agaatgctcc gaagcagtca catgctaata ttacaatgca 420
ggatgttcat gaggggttga atttttctgc tgctgctgat gaatcctcct ttggaatatt 480
ttcaataaag ttttcaaaag atgggcatga acttggtggt ggaaacagca atgagtcaat 540
atgtatttat gatcttgag caaacaagt gacagagcga attcatgctc atgtggctga 600
tgtaaatgcg gtcacgttcg ctgatgaatc tgggtggtgct ttgtactccg gaagtgatga 660
tagcctctgt aagggtgtggg ataggcgttg ccacaacaga gcgaaaccag taggtgtttt 720
ggcagggtcat ttagatggag ttacatttat tgatagccat ggagacgggc attatttcat 780
ctccaactgc aaggatcaga ctattaaact atgggatatc agaaaattgt cctcggctac 840
gaaggactgc acacaaaag catacgaatg ggattacaga tggatgacct atccatcaga 900
agccccgattt ttgaagcatc catatgatca atcgttagcc acattcagag gccattcggt 960
gttgcgca cttatccgtt gctacttttc cccaatgcac agcacaggtc agaggtatat 1020
atacacagg 1029

<210> 264
<211> 342
<212> PRT
<213> Hordeum vulgare

<400> 264

Thr Arg Ala Cys Leu His Ala Gly Lys Ser His Ile Ser Thr Phe Lys
1 5 10 15

Leu Leu Ser Ser Arg Glu Ser Asn Arg Ser Gly Phe Gly Arg Phe Ser
20 25 30

Ser Ala Asp Cys Ser Tyr Ala Leu Arg Lys His Leu Pro Val Arg Gly
35 40 45

Pro Trp Cys Val Asp Ser Met Asp Cys Ala Ala Tyr Ile Ser Gln Phe
50 55 60

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

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

Gln Arg Tyr Ile Tyr Thr
340

<210> 265
<211> 1226
<212> DNA
<213> Pinus taeda

<220>
<221> Unsure
<222> (730)..(730)
<223> n can be a stretch of 315 to 330 nucleotides

<220>
<221> misc_feature
<222> (730)..(730)
<223> n is a, c, g, or t

```

<400> 265
gctcgtagac attgaaggtc cggaagcttt gccaaacagaa ctgcaagcac      60
aggacaaagg gagagaatgg gaaactcaca gtttcaaaat catcattttg acaaagatga      120
taacagtaac agaaatgatg aagtccaaaa tatggatgat gcttctgaag atcccaacaa      180
acttcaccat gaacttgaac atataacaaa gctgagggtca gcaccaaagt gtatgctgtc      240
caggatgaat ggtaagagcc agaatggcta tgtttcaaca ttatctatgt tggcaggcag      300
agaagccaat atttctggga gagggaaatt tagtgtagct gattgctgtc atgttgcaag      360
tagatatttg ccatcttggt gccagatat aatggatatg atggacagta gagcatatat      420
tggaacaatt tcagcagatg gctccctttt tgtcacagga tttcaggatc atcggataag      480
aatatacaat gtggagaatg gatggacaat tcaaaaggat gtgcttgcta gaaacttgcg      540
ttggactatc actgacactt ctctttcacc tgatcagcgt taccttgtgt atgctactat      600
cactcctatt gtccacattg tgaatgttgg aagcagtgtc agagaatcct tagcaaacgt      660
cacagaaatt catgaagcgc tggatttctc tatgtacgaa gaacattgct catttggaat      720
tttctgcgtn cttactttc atcgatagtc gtggagatgg acgctatatt atttctaattg      780
gaaaagacca gacgacaaag atgtgggata ttcgcaaaat gactgcagga aatcctagca      840
taaagtcaag gagttcctct ggtaatgaat gggattatcg ttggatggag tatccaaaga      900
ataggaagaa tgctaagcat ccatatgacc agtctctgat gacttacagg ggacatgctg      960
tcttgcgtac tcttgtccgc tgctacttct ctccatcctt cagcactggc cagaaataca     1020
tctacacagg atcacacgat ggctgtgttt atatttatga tgtggtaagt gggaacctca     1080
ttaagaaact cgactatcat aggtccactg tgagggactg cagctggcat ccgttctatc     1140
caactcttgt aagctgttca tgggatggag ttgttgccaa atgggaccat tcaacagcaa     1200
gaagtcgcag aagccgcagc ccgtga                                     1226

```

<210> 266
<211> 361
<212> PRT
<213> Pinus taeda

<220>
 <221> UNSURE
 <222> (197)..(197)
 <223> X can be a stretch of 105 to 110 amino acids

<400> 266

```

Met Gly Asn Ser Gln Phe Gln Asn His His Phe Asp Lys Asp Asp Asn
 1          5          10          15

Ser Asn Arg Asn Asp Glu Val Gln Asn Met Asp Asp Ala Ser Glu Asp
          20          25          30

Pro Asn Lys Leu His His Glu Leu Glu His Ile Thr Lys Leu Arg Ser
          35          40          45

Ala Pro Asn Gly Met Leu Ser Arg Met Asn Gly Lys Ser Gln Asn Gly
 50          55          60

Tyr Val Ser Thr Leu Ser Met Leu Ala Gly Arg Glu Ala Asn Ile Ser
 65          70          75          80

Gly Arg Gly Lys Phe Ser Val Ala Asp Cys Cys His Val Ala Ser Arg
          85          90          95

Tyr Leu Pro Ser Cys Gly Pro Asp Ile Met Asp Met Met Asp Ser Arg
          100          105          110

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

Phe Gln Asp His Arg Ile Arg Ile Tyr Asn Val Glu Asn Gly Trp Thr
 130          135          140

Ile Gln Lys Asp Val Leu Ala Arg Asn Leu Arg Trp Thr Ile Thr Asp
 145          150          155          160

Thr Ser Leu Ser Pro Asp Gln Arg Tyr Leu Val Tyr Ala Thr Ile Thr
          165          170          175

Pro Ile Val His Ile Val Asn Val Gly Ser Ser Val Arg Glu Ser Leu
          180          185          190

Ala Asn Val Thr Xaa Ile Thr Phe Ile Asp Ser Arg Gly Asp Gly Arg
 195          200          205

Tyr Phe Ile Ser Asn Gly Lys Asp Gln Thr Thr Lys Met Trp Asp Ile
 210          215          220

Arg Lys Met Thr Ala Gly Asn Pro Ser Ile Lys Ser Arg Ser Ser Ser
 225          230          235          240
    
```

Gly Asn Glu Trp Asp Tyr Arg Trp Met Glu Tyr Pro Lys Asn Arg Lys
245 250 255

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

Ala Val Leu Arg Thr Leu Val Arg Cys Tyr Phe Ser Pro Ser Phe Ser
275 280 285

Thr Gly Gln Lys Tyr Ile Tyr Thr Gly Ser His Asp Gly Cys Val Tyr
290 295 300

Ile Tyr Asp Val Val Ser Gly Asn Leu Ile Lys Lys Leu Asp Tyr His
305 310 315 320

Arg Ser Thr Val Arg Asp Cys Ser Trp His Pro Phe Tyr Pro Thr Leu
325 330 335

Val Ser Cys Ser Trp Asp Gly Val Val Ala Lys Trp Asp His Ser Thr
340 345 350

Ala Arg Ser Arg Arg Ser Arg Ser Pro
355 360

<210> 267
<211> 1269
<212> DNA
<213> Saccharum officinarum

<220>
<221> Unsure
<222> (566)..(566)

<220>
<221> misc_feature
<222> (566)..(566)
<223> n is a, c, g, or t

<400> 267
atgggttatg gcatgagtag gctagaagat gaatattatg agcctgaagg gcagaatact 60
gatggatctg gctcagttca agtgaacgat gagtttgcaa aactgcacaa cgatattttt 120
catatgacac gaatgagatc aagacttact gaaaggtaca agtccatgga taccaacaga 180
ggcataatat caacggccaa gttattatct cgaagggaaa ttgattgttc tggaaagggg 240
atgttctctt cttgtgaccg tgcatttggt ctaggtcgct atgttccaat gaatggccct 300
gaattattgg ataggatgga ttctcgtgct tatgtttcac agttttctgc tgatgggtact 360
ctttttggtg ctggttttca gggaagtcac ataagaatat atgatgctga tagaggctgg 420
agcatacaca aagacattca tgctaagtgt ttgagatgga caatcagtga tgtattccta 480
tcacctgatc aacggtatct tgcctactct agtctggcac ctattaatca tattggcaat 540
gtcggaaatg ctggaagaga atcctngtcg acccagcgt cgggccggca gcaatgatga 600
atcaatatat gtctatgacc ttcaagcaaa caaattgaca ttacgtttac ctgctcatac 660

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

atctgatgtc aatacagtag catttgctga tgaaaccggc catctcatat attcaggaag      720
tgacgacact ttatgcaagg tctgggacag gcggtgtttg tccacaggac aagctgccgg      780
agttttgact ggacatttgc atggggtaac acacattgat agtcgtggag atggccgaag      840
tttcatatcc aatggaaaag accaagcaat caaactgtgg gatgtcagga aaatgacgtc      900
caatgctgat agttgtgcag acggagcccc aacttgggac tacagatatt caaggtatcc      960
gcagcagcat aaacagttaa agcatccgca tgatcagtca ttagcgacat accgtggaca     1020
ttcagtcctc cggacattga tccgttgcta cttttctcct gcttacagca ctgggcaaaa     1080
gtacatatat acagggtcgt atgattcctg cgttcacatc tatgatgtgg taagtggatc     1140
gcaagttgcg aagctgaaat ggcacaaat ggcgatacgt gactgcagct ggcacccatt     1200
tgagcccacg cttgtgagct catcctggga cggccatgta gcgaaatgga ccagtgcacg     1260
tgatcaaaa                                     1269

```

```

<210> 268
<211> 422
<212> PRT
<213> Saccharum officinarum

```

```

<220>
<221> UNSURE
<222> (189)..(189)
<223> Xaa can be a stretch of 30 to 40 amino acids
<400> 268

```

```

Met Gly Tyr Gly Met Ser Arg Leu Glu Asp Glu Tyr Tyr Glu Pro Glu
1           5           10           15

```

```

Gly Gln Asn Thr Asp Gly Ser Gly Ser Val Gln Val Asn Asp Glu Phe
          20           25           30

```

```

Ala Lys Leu His Asn Asp Ile Phe His Met Thr Arg Met Arg Ser Arg
          35           40           45

```

```

Leu Thr Glu Arg Tyr Lys Ser Met Asp Thr Asn Arg Gly Ile Ile Ser
50           55           60

```

```

Thr Ala Lys Leu Leu Ser Arg Arg Glu Ile Asp Cys Ser Gly Lys Gly
65           70           75           80

```

```

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

```

```

Met Asn Gly Pro Glu Leu Leu Asp Arg Met Asp Ser Arg Ala Tyr Val
100           105           110

```

```

Ser Gln Phe Ser Ala Asp Gly Thr Leu Phe Gly Ala Gly Phe Gln Gly
115           120           125

```


PF5908220081125_F_60259_PCT_Sequence_Listing.txt

Ser His Ile Arg Ile Tyr Asp Ala Asp Arg Gly Trp Ser Ile His Lys
130 135 140

Asp Ile His Ala Lys Cys Leu Arg Trp Thr Ile Ser Asp Val Phe Leu
145 150 155 160

Ser Pro Asp Gln Arg Tyr Leu Ala Tyr Ser Ser Leu Ala Pro Ile Asn
165 170 175

His Ile Gly Asn Val Gly Asn Ala Gly Arg Glu Ser Xaa Arg Pro Thr
180 185 190

Arg Pro Ala Gly Ser Asn Asp Glu Ser Ile Tyr Val Tyr Asp Leu Gln
195 200 205

Ala Asn Lys Leu Thr Leu Arg Leu Pro Ala His Thr Ser Asp Val Asn
210 215 220

Thr Val Ala Phe Ala Asp Glu Thr Gly His Leu Ile Tyr Ser Gly Ser
225 230 235 240

Asp Asp Thr Leu Cys Lys Val Trp Asp Arg Arg Cys Leu Ser Thr Gly
245 250 255

Gln Ala Ala Gly Val Leu Thr Gly His Leu His Gly Val Thr His Ile
260 265 270

Asp Ser Arg Gly Asp Gly Arg Ser Phe Ile Ser Asn Gly Lys Asp Gln
275 280 285

Ala Ile Lys Leu Trp Asp Val Arg Lys Met Thr Ser Asn Ala Asp Ser
290 295 300

Cys Ala Asp Gly Ala Pro Thr Trp Asp Tyr Arg Tyr Ser Arg Tyr Pro
305 310 315 320

Gln Gln His Lys Gln Leu Lys His Pro His Asp Gln Ser Leu Ala Thr
325 330 335

Tyr Arg Gly His Ser Val Leu Arg Thr Leu Ile Arg Cys Tyr Phe Ser
340 345 350

Pro Ala Tyr Ser Thr Gly Gln Lys Tyr Ile Tyr Thr Gly Ser Tyr Asp
355 360 365

Ser Cys Val His Ile Tyr Asp Val Val Ser Gly Ser Gln Val Ala Lys
370 375 380

Leu Lys Trp His Gln Met Ala Ile Arg Asp Cys Ser Trp His Pro Phe
385 390 395 400

Glu Pro Thr Leu Val Ser Ser Ser Trp Asp Gly His Val Ala Lys Trp
Seite 293

Thr Ser Ala Arg Asp Gln
420

<210> 269
<211> 1173
<212> DNA
<213> Sorghum bicolor

<220>
<221> Unsure
<222> (528)..(528)
<223> n can be a stretch of 135 to 165 nucleotides

<220>
<221> misc_feature
<222> (528)..(528)
<223> n is a, c, g, or t

<400> 269
atgggttatg gcatgagtag gctagaagat gaatactatg agcctgaagg gcagaatact 60
gatggatctg gctcagttca agtgaacaat gagtttgcag aactgcataa cgatattttt 120
catatgaccc gaatgagatc aagacttact gaaagctaca agtccatggg taccaacaga 180
ggcataatat caacggccaa gttattatct caaagggaaa ttgattgttc tggaaagaag 240
atgttctctt ctggtgaccg tgcatttggt ctaggtcgct atgttccaat gaacggccct 300
cagttattgg ataggatgga ttctcgtgct tatgtttcgc agttttctgc tgatggcact 360
ctttttgttg ctggttttca gggaagtcac ataagaatat atgatgctga tagaggctgg 420
agcatacaca aagacattca tgctaggtgg ttgagatgga caatcagtga tgtatcctta 480
tcacctgatc agcggtatct tgcctactct agtctggcac ctattgtncg tttacctgct 540
catacatctg atgtcaatac agtagcattt gctgatgaaa ctggccatct catatattct 600
ggaagtgacg acactttatg caaggtctgg gacaggcggg gtttgtccac aggacaagct 660
gccggagttc tgactggaca tttgcatggg gtaacacata ttgatagtcg tggagatggc 720
cgaagtttca tatcgaatgg aaaagaccaa gcaatcaaac tgtgggatgt caggaaaatg 780
acgtccaatg ctgatagttg tgcagacgga gcccgaagtt gggactacag atattcgagg 840
tatccgcagc agcataaaca gttaaagcat ccgcatgac agtcattagc gacataccgt 900
ggacatgcag tcctccggac attgatccgt tgctactttt ctcttgctta cagcactggg 960
caaaagtaca tatatacagg gtcgtatgat tcctgcgttt acatctatga tgtggtaagt 1020
ggatcgcaag ttgcgaagct gaaatggcat caaatggcga ttcgtgactg cagttggcac 1080
ccatttgagc ccacgcttgt gagctcatcc tgggacggcc aggtagcaaa atggaccagt 1140
gcacgtgatc aacaggcttc tgatatagat tga 1173

<210> 270
<211> 391
<212> PRT
<213> Sorghum bicolor

<220>
 <221> UNSURE
 <222> (177)..(177)
 <223> Xaa can be a stretch of 45 to 55 amino acids
 <400> 270
 Met Gly Tyr Gly Met Ser Arg Leu Glu Asp Glu Tyr Tyr Glu Pro Glu
 1 5 10 15
 Gly Gln Asn Thr Asp Gly Ser Gly Ser Val Gln Val Asn Asn Glu Phe
 20 25 30
 Ala Glu Leu His Asn Asp Ile Phe His Met Thr Arg Met Arg Ser Arg
 35 40 45
 Leu Thr Glu Ser Tyr Lys Ser Met Gly Thr Asn Arg Gly Ile Ile Ser
 50 55 60
 Thr Ala Lys Leu Leu Ser Gln Arg Glu Ile Asp Cys Ser Gly Lys Lys
 65 70 75 80
 Met Phe Ser Ser Gly Asp Arg Ala Phe Val Leu Gly Arg Tyr Val Pro
 85 90 95
 Met Asn Gly Pro Gln Leu Leu Asp Arg Met Asp Ser Arg Ala Tyr Val
 100 105 110
 Ser Gln Phe Ser Ala Asp Gly Thr Leu Phe Val Ala Gly Phe Gln Gly
 115 120 125
 Ser His Ile Arg Ile Tyr Asp Ala Asp Arg Gly Trp Ser Ile His Lys
 130 135 140
 Asp Ile His Ala Arg Trp Leu Arg Trp Thr Ile Ser Asp Val Ser Leu
 145 150 155 160
 Ser Pro Asp Gln Arg Tyr Leu Ala Tyr Ser Ser Leu Ala Pro Ile Val
 165 170 175
 Xaa Arg Leu Pro Ala His Thr Ser Asp Val Asn Thr Val Ala Phe Ala
 180 185 190
 Asp Glu Thr Gly His Leu Ile Tyr Ser Gly Ser Asp Asp Thr Leu Cys
 195 200 205
 Lys Val Trp Asp Arg Arg Cys Leu Ser Thr Gly Gln Ala Ala Gly Val
 210 215 220
 Leu Thr Gly His Leu His Gly Val Thr His Ile Asp Ser Arg Gly Asp
 225 230 235 240

Gly Arg Ser Phe Ile Ser Asn Gly Lys Asp Gln Ala Ile Lys Leu Trp
245 250 255

Asp Val Arg Lys Met Thr Ser Asn Ala Asp Ser Cys Ala Asp Gly Ala
260 265 270

Pro Ser Trp Asp Tyr Arg Tyr Ser Arg Tyr Pro Gln Gln His Lys Gln
275 280 285

Leu Lys His Pro His Asp Gln Ser Leu Ala Thr Tyr Arg Gly His Ala
290 295 300

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

Gly Gln Lys Tyr Ile Tyr Thr Gly Ser Tyr Asp Ser Cys Val Tyr Ile
325 330 335

Tyr Asp Val Val Ser Gly Ser Gln Val Ala Lys Leu Lys Trp His Gln
340 345 350

Met Ala Ile Arg Asp Cys Ser Trp His Pro Phe Glu Pro Thr Leu Val
355 360 365

Ser Ser Ser Trp Asp Gly Gln Val Ala Lys Trp Thr Ser Ala Arg Asp
370 375 380

Gln Gln Ala Ser Asp Ile Asp
385 390

<210> 271
<211> 336
<212> PRT
<213> Artificial sequence

<220>
<223> Conserved Domain comprised in SEQ ID NO: 02

<400> 271

Tyr Val Ser Gln Phe Ser Thr Asp Gly Ser Leu Phe Ile Ala Gly Phe
1 5 10 15

Gln Gly Ser Arg Ile Arg Ile Tyr Asn Val Glu Lys Gly Trp Lys Val
20 25 30

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

Ser Leu Ser Pro Asp Gln Arg Asn Leu Val Tyr Ala Ser Met Ser Pro
50 55 60

Ile Val His Ile Val Asp Val Gly Ser Gly Ser Thr Glu Ser His Ala
65 70 75 80

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

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

Gly Gly Tyr Ser Phe Gly Ile Phe Ser Val Lys Phe Ser Thr Asp Gly
100 105 110

Arg Glu Val Val Ala Gly Ser Ser Asp Asp Ser Ile Tyr Val Tyr Asp
115 120 125

Leu Glu Ala Asn Arg Val Ser Leu Arg Thr Val Ala His Thr Ser Asp
130 135 140

Val Asn Thr Val Cys Phe Ala Asp Glu Ser Gly Asn Leu Ile Leu Ser
145 150 155 160

Gly Ser Asp Asp Asn Leu Cys Lys Val Trp Asp Arg Arg Cys Phe Ile
165 170 175

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

Thr Phe Ile Asp Ser Arg Gly Asp Gly Arg Tyr Phe Ile Ser Asn Gly
195 200 205

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

Ala Pro Ala Arg His Glu Val Leu Arg Asn Tyr Glu Trp Asp Tyr Arg
225 230 235 240

Trp Met Asp Tyr Pro Thr Glu Ala Arg Asp Leu Lys His Pro Leu Asp
245 250 255

Gln Ser Val Ser Thr Tyr Lys Gly His Ser Val Leu Arg Thr Leu Ile
260 265 270

Arg Cys Tyr Phe Ser Pro Ala His Ser Thr Gly Gln Lys Tyr Ile Tyr
275 280 285

Thr Gly Ser Asn Asp Ser Ser Val Tyr Ile Tyr Asp Leu Val Ser Gly
290 295 300

Asp Lys Val Ala Val Leu Lys His His Ser Ser Pro Val Arg Asp Cys
305 310 315 320

Asn Trp His Pro Tyr Tyr Pro Thr Leu Ile Ser Ser Ser Trp Asp Gly
325 330 335

<210> 272
<211> 2194
<212> DNA
<213> Oryza sativa

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

```

<400> 272
aatccgaaaa gtttctgcac cgttttcacc ccctaactaa caatataggg aacgtgtgct      60
aaatataaaa tgagacctta tatatgtagc gctgataact agaactatgc aagaaaaaact      120
catccaccta ctttagtggc aatcgggcta aataaaaaaag agtcgctaca ctagtttcgt      180
tttccttagt aattaagtgg gaaaatgaaa tcattattgc ttagaatata cgttcacatc      240
tctgtcatga agttaaatga 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 tagcaatatc      660
tgaattcaag cactccacca tcaccagacc actttttaata atatctaaaa tacaaaaaat      720
aattttacag aatagcatga aaagtatgaa acgaactatt taggtttttc acatacaaaa      780
aaaaaaagaa ttttgctcgt gcgcgagcgc caatctccca tattgggcac acaggcaaca      840
acagagtggc tgcccacaga acaaccaca aaaaacgatg atctaacgga ggacagcaag      900
tccgcaacaa cttttaaca gcaggctttg cggccaggag agaggaggag aggcaaagaa      960
aaccaagcat cctccttctc ccatctataa attcctcccc ctttttcccc tctctatata     1020
ggaggcatcc aagccaagaa gagggagagc accaaggaca cgcgactagc agaagccgag     1080
cgaccgcctt ctcgatccat atcttccggt cgagttcttg gtcgatctct tccctcctcc     1140
acctcctcct cacagggtat gtgcctccct tcggttggtc ttggatttat tgttctaggt     1200
tgtgtagtac gggcgttgat gttaggaaag gggatctgta tctgtgatga ttctgtttct     1260
tggatttggg atagaggggt tcttgatggt gcatgttatc ggttcgggtt gattagtagt     1320
atggttttca atcgtctgga gagctctatg gaaatgaaat ggtttaggga tcggaatctt     1380
gcgattttgt gagtaccttt tgtttgaggt aaaatcagag caccggtgat ttgcttggt     1440
gtaataaagt acggttggtt ggtcctcgat tctggtagtg atgcttctcg atttgacgaa     1500
gctatccttt gtttattccc tattgaacaa aaataatcca actttgaaga cgggtcccgtt     1560
gatgagattg aatgattgat tcttaagcct gtccaaaatt tcgcagctgg cttgtttaga     1620
tacagtagtc cccatcacga aattcatgga aacagttata atcctcagga acaggggatt     1680
ccctgttctt ccgatttgct ttagtcccag aatttttttt cccaaatatc ttaaaaagtc     1740
actttctggt tcagttcaat gaattgattg ctacaaataa tgcttttata gcgttatcct     1800
agctgtagtt cagttaatag gtaatacccc tatagtttag tcaggagaag aacttatccg     1860
atttctgatc tccattttta attatatgaa atgaactgta gcataagcag tattcatttg     1920
gattattttt tttattagct ctcaccctt cattattctg agctgaaagt ctggcatgaa     1980
ctgtcctcaa ttttgttttc aaattcacat cgattatcta tgcattatcc tcttgatatc     2040

```

PF5908220081125_F_60259_PCT_Sequence_Listing.txt

acctgtagaa gtttcttttt ggttattcct tgactgcttg attacagaaa gaaatttatg	2100
aagctgtaat cgggtagatt atactgcttg ttcttatgat tcatttcctt tgtgcagttc	2160
ttggtgtagc ttgccacttt caccagcaaa gttc	2194

<210> 273
 <211> 1245
 <212> DNA
 <213> Oryza sativa

<400> 273 cttgttggtg atctgtgccc ccaagaagaa taacactcta ctcttacttg ttggaaaaaa	60
atagtattag caaccacgca tatgcaaatt ttaatgcagt aataataaga gatggatcga	120
tcgttttcca gctcttgat atgtgactgg ccctgcttta tgtgtgtagt gttaatttca	180
gcttttagcag tacgtgatta gtgatggaca ataattgtcg cagacgtatc tatcaattgc	240
tcctgttggtg tgatgcttta actgttggaa tcaaagttgc gttgcctttg ttgttatgag	300
gaggaatata tatgttgggg caggaaaaga atggaggaga gatcgttctc catatcctta	360
tcacggcct cgtcactgct cgcagtttaa ctttttggtg atgcgagcga tggtcagcca	420
tatatatact cccatgctgc atgctagtaa tcaatatacg ctttgtaaaa gtaaacgac	480
gtctagtaat tgcaatatca taggggtagc cattgacaga gatctacata gatagagggg	540
gaacaagaat tgacactcca cagatgctcc actcattcac ctttactaat ttatatcttt	600
tgatgtttga tcgatcgatc gatccgtccg tcggtgtctc gacgaataaa aactgcaaat	660
cgaactgtat gtatataata tagcgtcgta aattaaatta aattaaatcg aactgaatac	720
tacatgtcga agcaagaatt agttcaacta aaagatttag tttttccggt tgcaatatct	780
gtgaaattaa ttgaagaaat taagaagaaa actggagaga tatatatatg gatgagacaa	840
aatgagataa gacgcatgat ggtccctcgg atgatgtcgt ccgttcctta tttccattcc	900
atggcagctg ctatcgctat ctagtgcgcg cggcatctcc aatcccatcc attctagtgg	960
tcgatctagc tactactgag tattgttttt tcttcttttt actactgttg attattctgc	1020
aactgcagtt agatgcttgc tactcctaca tcgatctctc tcgcgcgggc gtatgcattg	1080
cattcactac tgatgatccg tgggtgtagt gtgggtggct ataaataggg caggggtgcgg	1140
ttgccattgc tcctcaggcc agcaactgag aagctccata caagtaagca gcagctagtt	1200
gccgacaagg ccagagaagg aagaagaagc tctcatcatc atcac	1245

<210> 274
 <211> 56
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: prm09100

<400> 274 ggggacaagt ttgtacaaaa aagcaggctt aaacaatggt ttttggacca agttag	56
--	----

<210> 275
<211> 50
<212> DNA
<213> Artificial sequence

<220>
<223> primer: prm09101

<400> 275
ggggaccact ttgtacaaga aagctggggtt gtgtagagag acgcatcagt

50