

PF5908220081029_F_60204_PCT_Sequence.txt
SEQUENCE LISTING

<110> BASF Plant Science GmbH
<120> Plants having enhanced yield-related traits and a method for making the same
<130> PF60204
<160> 186
<170> PatentIn version 3.4
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<212> PRT
<213> Arabidopsis thaliana

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35 40 45

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Lys Asp Gln Ala Val Asn Cys Pro Arg Cys Asn Ser Thr Asn Thr Lys
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 65 70 75 80
 Lys Gly Cys Arg Arg Tyr Trp Thr Glu Gly Gly Ser Leu Arg Asn Ile
 85 90 95
 Pro Val Gly Gly Gly Ser Arg Lys Asn Lys Arg Ser His Ser Ser Ser
 100 105 110
 Ser Asp Ile Ser Asn Asn His Ser Asp Ser Thr Gln Pro Ala Thr Lys
 115 120 125
 Lys His Leu Ser Asp His His His His Leu Met Ser Met Ser Gln Gln
 130 135 140
 Gly Leu Thr Gly Gln Asn Pro Lys Phe Leu Glu Thr Thr Gln Gln Asp
 145 150 155 160
 Leu Asn Leu Gly Phe Ser Pro His Gly Met Ile Arg Thr Asn Phe Thr
 165 170 175
 Asp Leu Ile His Asn Ile Gly Asn Asn Thr Asn Lys Ser Asn Asn Asn
 180 185 190
 Asn Asn Pro Leu Ile Val Ser Ser Cys Ser Ala Met Ala Thr Ser Ser
 195 200 205
 Leu Asp Leu Ile Arg Asn Asn Ser Asn Asn Gly Asn Ser Ser Asn Ser
 210 215 220
 Ser Phe Met Gly Phe Pro Val His Asn Gln Asp Pro Ala Ser Gly Gly
 225 230 235 240
 Phe Gln Gly Gly Glu Glu Gly Gly Glu Gly Gly Asp Asp Val Asn Gly
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 Arg His Leu Phe Pro Phe Glu Asp Leu Lys Leu Pro Val Ser Ser Ser
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 35 40 45
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PF5908220081029_F_60204_PCT_Sequence.txt

Arg Tyr Trp Thr Ala Gly Gly Ser Leu Arg Asn Ile Pro Val Gly Gly
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 Gly Val Arg Lys Asn Lys Arg Ser Ser Ser Asn Ser Ser Ser Ser
 100 105 110
 Pro Ser Ser Ser Ser Ser Ser Lys Lys Pro Leu Phe Ala Asn Asn Asn
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 130 135 140
 Ala Ala Thr Lys Val Gln Asp Leu Thr Phe Ser Gln Gly Phe Gly Asn
 145 150 155 160
 Ala His Glu Val Lys Asp Leu Asn Leu Ala Phe Ser Gln Gly Phe Gly
 165 170 175
 Ile Gly His Asn His His Ser Ser Ile Pro Glu Phe Leu Gln Val Val
 180 185 190
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 195 200 205
 Leu Glu Leu Leu Gly Ile Ser Ser Ser Ser Ala Ser Ser Asn Ser Arg
 210 215 220
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 245 250 255
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 260 265 270
 Glu Gly Ser Ser Gly Thr Asn Asn Gly Arg Pro Leu Leu Pro Phe Glu
 275 280 285
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 290 295 300
 Asn Gly Asn Leu Lys Glu Asn Asn Asp Glu His Ser Asp His Glu His
 305 310 315 320
 Glu Lys Glu Glu Gly Glu Ala Asp Gln Ser Val Gly Phe Trp Ser Gly
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 aacaacaata acaatacggc ggttgtggcg gagaggaaag caagaccaca agagaaacta 240
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 Asn Thr Thr Ser Asn Ala Arg Pro Asn Thr Ile Leu Thr Ser Asn Gly
 35 40 45
 Val Ser Thr Ala Gly Ala Thr Val Ser Gly Val Ser Asn Asn Asn Asn
 50 55 60

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

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345

350

Asn Gly Tyr Trp Ser Gly Met Phe Ser Thr Thr Gly Gly Gly Ser Ser
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Trp

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<212> DNA
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Asn Ala Thr Ala Ser Asn Gly Gly Ser Gly Gly Asn Thr Asn Asn Thr
35 40 45

Ala Thr Met Glu Thr Arg Lys Ala Arg Pro Gln Glu Lys Val Asn Cys
50 55 60

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Pro Arg Cys Asn Ser Thr Asn Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr
65 70 75 80

Ser Leu Thr Gln Pro Arg Tyr Phe Cys Lys Gly Cys Arg Arg Tyr Trp
85 90 95

Thr Glu Gly Gly Ser Leu Arg Asn Val Pro Val Gly Gly Ser Ser Arg
100 105 110

Lys Asn Lys Arg Ser Ser Thr Pro Leu Ala Ser Pro Ser Asn Pro Lys
115 120 125

Leu Pro Asp Leu Asn Pro Pro Ile Leu Phe Ser Ser Gln Ile Pro Asn
130 135 140

Lys Ser Asn Lys Asp Leu Asn Leu Leu Ser Phe Pro Val Met Gln Asp
145 150 155 160

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

Arg Gly Met Asn Thr Phe Leu Pro Gly Gln Met Met Asp Ser Asn Ser
180 185 190

Val Leu Tyr Ser Ser Leu Gly Phe Pro Thr Met Pro Asp Tyr Lys Gln
195 200 205

Ser Asn Asn Asn Leu Ser Phe Ser Ile Asp His His Gln Gly Ile Gly
210 215 220

His Asn Thr Ile Asn Ser Asn Gln Arg Ala Gln Asp Asn Asn Asp Asp
225 230 235 240

Met Asn Gly Ala Ser Arg Val Leu Phe Pro Phe Ser Asp Met Lys Glu
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<212> DNA
<213> Arabidopsis thaliana

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gattcaacaa cagcaacaac tatgataatg gatgacgaga agaagttgat gacgacaatg 180

PF5908220081029_F_60204_PCT_Sequence.txt

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20 25 30

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35 40 45

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

Gln Glu Pro Arg Asn Cys Pro Arg Cys Asn Ser Ser Asn Thr Lys Phe
65 70 75 80

Cys Tyr Tyr Asn Asn Tyr Ser Leu Ala Gln Pro Arg Tyr Leu Cys Lys
85 90 95

Ser Cys Arg Arg Tyr Trp Thr Glu Gly Gly Ser Leu Arg Asn Val Pro
100 105 110

Val Gly Gly Gly Ser Arg Lys Asn Lys Lys Leu Pro Phe Pro Asn Ser
115 120 125

Ser Thr Ser Ser Ser Thr Lys Asn Leu Pro Asp Leu Asn Pro Pro Phe
130 135 140

Val Phe Thr Ser Ser Ala Ser Ser Ser Asn Pro Ser Lys Thr His Gln
145 150 155 160

Asn Asn Asn Asp Leu Ser Leu Ser Phe Ser Ser Pro Met Gln Asp Lys
165 170 175

Arg Ala Gln Gly His Tyr Gly His Phe Ser Glu Gln Val Val Thr Gly
180 185 190

Gly Gln Asn Cys Leu Phe Gln Ala Pro Met Gly Met Ile Gln Phe Arg
195 200 205

Gln Glu Tyr Asp His Glu His Pro Lys Lys Asn Leu Gly Phe Ser Leu
210 215 220

Asp Arg Asn Glu Glu Glu Ile Gly Asn His Asp Asn Phe Val Val Asn
225 230 235 240

Glu Glu Gly Ser Lys Met Met Tyr Pro Tyr Gly Asp His Glu Asp Arg
245 250 255

Gln Gln His His His Val Arg His Asp Asp Gly Asn Lys Lys Arg Glu
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PF5908220081029_F_60204_PCT_Sequence.txt

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35     40     45

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50     55     60

Phe Cys Tyr Tyr Asn Asn Tyr Ser Leu Thr Gln Pro Arg Tyr Phe Cys
65     70     75     80

Lys Gly Cys Arg Arg Tyr Trp Thr Glu Gly Gly Ser Leu Arg Asn Ile
85     90     95

Pro Val Gly Gly Gly Ser Arg Lys Asn Lys Arg Ser His Ser Ser Ser
100    105    110

Ser Asp Ile Ser Asn Asn His Ser Asp Ser Thr Gln Pro Ala Thr Lys
115    120    125

Lys His Leu Ser Asp His His His His Leu Met Ser Met Ser Gln Gln
130    135    140

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

Leu Asn Leu Gly Phe Ser Pro His Gly Met Ile Arg Thr Asn Phe Thr
165    170    175

Asp Leu Ile His Asn Ile Gly Asn Asn Thr Asn Lys Ser Asn Asn Asn
180    185    190

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PF5908220081029_F_60204_PCT_Sequence.txt

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195 200 205

Leu Asp Leu Ile Arg Asn Asn Ser Asn Asn Gly Asn Ser Ser Asn Ser
210 215 220

Ser Phe Met Gly Phe Pro Val His Asn Gln Asp Pro Ala Ser Gly Gly
225 230 235 240

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

Leu Gly Phe Ser Leu Asp His His His Asn Asn Gly Phe His Gly Gly
260 265 270

Phe Gln Gly Gly Glu Glu Gly Gly Glu Gly Gly Asp Asp Val Asn Gly
275 280 285

Arg His Leu Phe Pro Phe Glu Asp Leu Lys Leu Pro Val Ser Ser Ser
290 295 300

Ser Ala Thr Ile Asn Val Asp Ile Asn Glu His Gln Lys Arg Gly Ser
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Ser Gly Gly Ser Trp Cys
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PF5908220081029_F_60204_PCT_Sequence.txt

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<212> PRT
<213> Glycine max

<400> 14

Met Asp Thr Ala Gln Trp Ala Gln Gly Ile Gly Val Val Lys Gln Pro
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Thr Met Glu Gly Gly Ser Lys Pro Pro Pro Pro Met Leu Glu Arg
20 25 30

Arg Ala Arg Pro Gln Lys Asp Gln Ala Leu Asn Cys Pro Arg Cys Asn
35 40 45

Ser Thr Asn Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Ser Leu Ser Gln
50 55 60

Pro Arg Tyr Phe Cys Lys Thr Cys Arg Arg Tyr Trp Thr Glu Gly Gly
65 70 75 80

Ser Leu Arg Asn Val Pro Val Gly Gly Gly Ser Arg Lys Asn Lys Arg
85 90 95

Ser Thr Pro Ser Ala Pro Pro Pro Ser Ser Ala Ser Ala Gln Ala Lys
100 105 110

Lys Leu Pro Asp Leu Thr Thr Pro Asn Phe Pro Gln Ser Ala Ser Gln
115 120 125

Asp Pro Lys Ile His Gln Gly Gln Asp Leu Asn Leu Ala Tyr Pro Pro
130 135 140

Ala Glu Asp Tyr Asn Thr Val Ser Met Ser Lys Leu Ile Glu Val Pro
145 150 155 160

Tyr Asn Thr Glu Leu Asp Lys Gly Gly Leu His Gln Asn Pro Thr Ser
165 170 175

Ser Ser Thr Pro Thr Ser Ala Ser Ser His His Gln Leu Ser Ala Met
180 185 190

Glu Leu Leu Lys Thr Gly Ile Ala Ala Ala Ser Ser Arg Gly Leu Asn
195 200 205

PF5908220081029_F_60204_PCT_Sequence.txt

Ser Phe Met Pro Met Tyr Asn Ser Thr His His Gly Phe Pro Leu Gln
210 215 220

Asp Phe Lys Pro Pro His His Gly Leu Asn Phe Ser Leu Glu Gly Phe
225 230 235 240

Asp Asn Gly Thr Tyr Gly Gly Leu His Gln Gly Ile Gln Glu Asp Pro
245 250 255

Thr Thr Gly Gly Ala Arg Ile Leu Phe Pro Thr Val Glu Asp Leu Lys
260 265 270

Gln Gln Val Pro Ser Thr Asn Glu Phe Asp His Gln Gln Asn Arg Ser
275 280 285

Gln Glu Gly Ser Ala His Gly Tyr Trp Asn Gly Met Leu Gly Gly Gly
290 295 300

Ser Trp
305

<210> 15
<211> 894
<212> DNA
<213> Glycine max

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caagctttga actgccaag gtgcaattca acaaacacca aattctgcta ctacaacaac 180
tatagcctct ctacagcaag gtacttttgc aagacatgta gaaggatttg gactgagggt 240
ggttctctca gaaatgttcc tgtgggtggg ggctctagaa agaacaagag atcaaccccg 300
ccagcaccac catcagcacc agcaccaaca aagaagcttt ctgatctcgc aacaccaaatt 360
ttccctcaat ctgcttctca ggaccctaag atccaccaag gccaagacct taacctagca 420
tatccaccag ctgaggacta cagcactgtc tccaagttca ttgagggttcc ttacagcact 480
gaattagaca aggggtactac tggctttcat caaaacccta cttcctcatc aacaacaaca 540
tctgcatctt ctcaagtgtc tgccatggag cttctcaaga ctgggattgc agctgcttcc 600
tcaaggggtt tgaactcctt catgccaatg tataattcaa cccatggggt tcccttgcag 660
gactttaagc caccacatgg ccttaacttc agccttgagg ggtttgaaaa tggttatggg 720
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gagggttcag ctcacgggta ttggaatggc atgttaggtg gaggatcatg gtag 894

<210> 16
<211> 297
<212> PRT
<213> Glycine max

<400> 16

Met Asp Thr Ala Gln Trp Ala Gln Gly Ile Gly Val Val Lys Gln Pro
 1 5 10 15

Met Glu Gly Ser Lys Pro Pro Pro Pro Pro Pro Pro Met Leu Glu
 20 25 30

Arg Arg Ala Arg Pro Gln Lys Asp Gln Ala Leu Asn Cys Pro Arg Cys
 35 40 45

Asn Ser Thr Asn Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Ser Leu Ser
 50 55 60

Gln Pro Arg Tyr Phe Cys Lys Thr Cys Arg Arg Tyr Trp Thr Glu Gly
 65 70 75 80

Gly Ser Leu Arg Asn Val Pro Val Gly Gly Gly Ser Arg Lys Asn Lys
 85 90 95

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

Leu Ser Asp Leu Ala Thr Pro Asn Phe Pro Gln Ser Ala Ser Gln Asp
 115 120 125

Pro Lys Ile His Gln Gly Gln Asp Leu Asn Leu Ala Tyr Pro Pro Ala
 130 135 140

Glu Asp Tyr Ser Thr Val Ser Lys Phe Ile Glu Val Pro Tyr Ser Thr
 145 150 155 160

Glu Leu Asp Lys Gly Thr Thr Gly Leu His Gln Asn Pro Thr Ser Ser
 165 170 175

Ser Thr Thr Thr Ser Ala Ser Ser Gln Leu Ser Ala Met Glu Leu Leu
 180 185 190

Lys Thr Gly Ile Ala Ala Ala Ser Ser Arg Gly Leu Asn Ser Phe Met
 195 200 205

Pro Met Tyr Asn Ser Thr His Gly Phe Pro Leu Gln Asp Phe Lys Pro
 210 215 220

Pro His Gly Leu Asn Phe Ser Leu Glu Gly Phe Glu Asn Gly Tyr Gly
 225 230 235 240

Gly Leu Gln Gly Ile Gln Glu Gly Pro Thr Gly Gly Ala Arg Ile Leu
 245 250 255

Phe Pro Thr Val Glu Asp Leu Lys Gln Gln Val Pro Ser Thr Asn Glu
 260 265 270

PF5908220081029_F_60204_PCT_Sequence.txt

Phe Asp Gln Gln Asn Arg Ser Gln Glu Gly Ser Ala His Gly Tyr Trp
 275 280 285

Asn Gly Met Leu Gly Gly Gly Ser Trp
 290 295

<210> 17
 <211> 468
 <212> DNA
 <213> Glycine max

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 aaagaacaag ctattaattg tccaaggtgt cattcaatta acaccaagtt ctgctactac 180
 aacaactaca gcctcacaca gcctaggtat ttctgcaaga cttgtagaag gtattggact 240
 gaaggtggga ccctcaggaa catccctgta ggaggtggct ctaggaagaa caagagatct 300
 tcagcttctt gttccacacc taataatagt cacaataaca ataattcaac caataagaag 360
 cttctctctg atctggtcac cacacctcca actctgtcac acactcaaaa ccctaatagc 420
 aataatgcta ttcataatg ccaagatctc aatctggctt ttccatcc 468

<210> 18
 <211> 156
 <212> PRT
 <213> Glycine max

<400> 18
 Met Asp Thr Ala Gln Trp Pro Gln Glu Met Val Val Lys Pro Ile Glu
 1 5 10 15

Asp Ile Val Val Thr Asn Thr Thr Cys Thr Lys Ala Ala Val Gly Ser
 20 25 30

Val Glu Arg Lys Pro Arg Pro Gln Lys Glu Gln Ala Ile Asn Cys Pro
 35 40 45

Arg Cys His Ser Ile Asn Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Ser
 50 55 60

Leu Thr Gln Pro Arg Tyr Phe Cys Lys Thr Cys Arg Arg Tyr Trp Thr
 65 70 75 80

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

Asn Lys Arg Ser Ser Ala Ser Cys Ser Thr Pro Asn Asn Ser His Asn
 100 105 110

Asn Asn Asn Ser Thr Asn Lys Lys Leu Leu Ser Asp Leu Val Ile Thr

115

120

125

Pro Pro Thr Leu Ser His Thr Gln Asn Pro Asn Ser Asn Asn Ala Ile
130 135 140

His Gln Cys Gln Asp Leu Asn Leu Ala Phe Pro Ser
145 150 155

<210> 19
<211> 726
<212> DNA
<213> Pisum sativum

<400> 19
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aacacaaaat tctgttacta caacaactat agcttaacac aaccaagata tttctgcaaa 180
acatgtagaa ggtactggac tcaaggtggc tccattagaa acattcctgt gggaggtgga 240
acaagaaaaa acaacaaggt tattagatct tcttctaacc ttgtttcaaa tccaacaaaa 300
aacctagtac ctagtattct tggtactagt tctcaaaatc aaaaacatca tgaacaagga 360
caagatctaa atttgatttt cacttctgtt tcttctcata gtttttcagc attggagctt 420
cttactggga taactgcttc aactacaagg ggttttcatt cttttatgcc ggtccaactt 480
caaggtgatt ccaacactag taatattggg tttcctttgc aggattttta gcaagtgcca 540
atgaattttt gtttagatgg gattgggtgga aatgggttatg gaaatgaagg gagggttttg 600
ttcccttttg aggatttaaa acaggatttg gatcagaata acaataaggg agatcaacaa 660
ggttatacaa ctgggttttg gaatggaatg ttgggaggag gaggaggagg atataatggt 720
aattaa 726

<210> 20
<211> 241
<212> PRT
<213> Pisum sativum

<400> 20

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

Thr Asn Thr Ser Glu Lys Lys Pro Arg Pro Glu Lys Gln Gln Ala Val
20 25 30

Asn Cys Pro Arg Cys Asn Ser Ile Asn Thr Lys Phe Cys Tyr Tyr Asn
35 40 45

Asn Tyr Ser Leu Thr Gln Pro Arg Tyr Phe Cys Lys Thr Cys Arg Arg
50 55 60

Tyr Trp Thr Gln Gly Gly Ser Ile Arg Asn Ile Pro Val Gly Gly Gly
65 70 75 80

PF5908220081029_F_60204_PCT_Sequence.txt

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

Asn

<210> 21
<211> 786
<212> DNA
<213> Vitis vinifera

<400> 21
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cctgtggctg agaggagggc aaggccacag aaggatcaag ctttgaactg cccaaggtgc 120
aattcaacca atacaaagtt ctgttactat aacaactaca gtctctcaca gcctagatac 180
ttctgcaaaa cttgtagaag gtattggaca gaggggtggtt ctctcagaaa tgtttcagtt 240
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gcttcttcaa aaaaattgct tcctgatcat cttatcacta gtactcctcc aggggtttcca 360
tcattctgctt ctcaaaaccc taagatccat gaaggccaag atctcaacct agcttttcca 420
cctcctcctg aggattacaa caacagcata tctgaatttg ctgatttgtc ctacaatgcc 480
atggagctgc tcaagagtac tgggattgct tccaggggac tgggttcttt catgcccatg 540

PF5908220081029_F_60204_PCT_Sequence.txt

tcggtttctg attcaaattc aatttactca tctgggtttc ctctgcagga gttcaaacca 600
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 aggctgttgt tcccacttga ggatttgaag caagtttcaa acaccactga gtttgagcaa 720
 agtagaggag ttcaaggaga ctcagctggg tattggaatg gaatgttggg tggaggatca 780
 tggtaa 786

<210> 22
 <211> 261
 <212> PRT
 <213> Vitis vinifera

<400> 22

Met Asp Thr Ala Gln Trp Pro Gln Gly Ile Gly Val Val Lys Pro Met
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Glu Ser Ser Gly Pro Val Ala Glu Arg Arg Ala Arg Pro Gln Lys Asp
 20 25 30

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

Tyr Tyr Asn Asn Tyr Ser Leu Ser Gln Pro Arg Tyr Phe Cys Lys Thr
 50 55 60

Cys Arg Arg Tyr Trp Thr Glu Gly Gly Ser Leu Arg Asn Val Pro Val
 65 70 75 80

Gly Gly Gly Ser Arg Lys Asn Lys Arg Ser Thr Ser Ser Ser Ser Ser
 85 90 95

Ser Ser Ser Pro Ala Ser Ser Lys Lys Leu Leu Pro Asp His Leu Ile
 100 105 110

Thr Ser Thr Pro Pro Gly Phe Pro Ser Ser Ala Ser Gln Asn Pro Lys
 115 120 125

Ile His Glu Gly Gln Asp Leu Asn Leu Ala Phe Pro Pro Pro Pro Glu
 130 135 140

Asp Tyr Asn Asn Ser Ile Ser Glu Phe Ala Asp Leu Ser Tyr Asn Ala
 145 150 155 160

Met Glu Leu Leu Lys Ser Thr Gly Ile Ala Ser Arg Gly Leu Gly Ser
 165 170 175

Phe Met Pro Met Ser Val Ser Asp Ser Asn Ser Ile Tyr Ser Ser Gly
 180 185 190

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

Phe Gln Ser Gly Tyr Gly Ile Gln Glu Ser Gly Ala Arg Leu Leu Phe
210 215 220

Pro Leu Glu Asp Leu Lys Gln Val Ser Asn Thr Thr Glu Phe Glu Gln
225 230 235 240

Ser Arg Gly Val Gln Gly Asp Ser Ala Gly Tyr Trp Asn Gly Met Leu
245 250 255

Gly Gly Gly Ser Trp
260

<210> 23
<211> 603
<212> DNA
<213> Vitis vinifera

<400> 23
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aactgcccac ggtgcaattc aaccaacact aagttctgct attacaacaa ctacagtctc 180
tctcagccaa ggtacttttg caaggcttgt agaaggtatt ggactgaagg tgggtctctc 240
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actagagagc aaggagattc aactgggtac tggactggga tgttaggtgg aggatcatgg 600
taa 603

<210> 24
<211> 200
<212> PRT
<213> Vitis vinifera

<400> 24

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

Glu Ile Val Thr Asn Thr Cys Pro Lys Pro Ala Leu Glu Lys Arg Ala
20 25 30

Arg Pro Gln Lys Glu Gln Ala Leu Asn Cys Pro Arg Cys Asn Ser Thr
35 40 45

Asn Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Ser Leu Ser Gln Pro Arg
50 55 60

PF5908220081029_F_60204_PCT_Sequence.txt

Tyr Phe Cys Lys Ala Cys Arg Arg Tyr Trp Thr Glu Gly Gly Ser Leu
65 70 75 80

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

Ala Ala Gln Asp Phe Arg Thr Leu Glu Leu Leu Thr Gly Ile Thr Ser
100 105 110

Arg Gly Leu Asn Ser Phe Met Pro Met Pro Ile Pro Asp Pro Asn Thr
115 120 125

Val Tyr Thr Thr Gly Phe Pro Met Gln Glu Phe Lys Pro Thr Leu Asn
130 135 140

Phe Ser Leu Asp Gly Leu Gly Ser Gly Tyr Gly Ser Ser Ser Gly Arg
145 150 155 160

Leu Leu Phe Pro Phe Glu Asp Leu Lys Gln Val Ser Ser Thr Ala Asp
165 170 175

His Ile Glu Gln Thr Arg Glu Gln Gly Asp Ser Thr Gly Tyr Trp Thr
180 185 190

Gly Met Leu Gly Gly Gly Ser Trp
195 200

<210> 25
<211> 786
<212> DNA
<213> Nicotiana tabacum

<220>
<221> misc_feature
<222> (653)..(653)
<223> n is a, c, g, or t

<400> 25
atggatactt ctactggcc acagggcata ggactagtga aagctgtgga accctcaaaa 60
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tgcaattcaa caaacacaaa attctgttac tataacaatt atagcctttc tcagccaagg 180
tatttttgca aaacttgtag aaggatttg actgaagggtg gttctttaag aaatgttcct 240
gttggtggcg gttcaagaaa aaacaaaaga tctagttcct cttctaataa ttcttcatcc 300
tccacgtcat catcatacaa aaaaattcca gatctcaca ttccaacttc ttctcaaaac 360
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aatttcagta acatttctga gtttatggcc ttaccttta tgaaccctaa ttccacaact 480
tcatttatgt cctctattat gccacagctt tcggattcta ataattattat gtactcatca 540
tcatcaactg ggctacctaa ttgcatgat ttgaagccta cacttaattt ttctttggat 600

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 ggatca 786

<210> 26
 <211> 262
 <212> PRT
 <213> Nicotiana tabacum

<220>
 <221> UNSURE
 <222> (218)..(218)
 <223> Xaa can be any naturally occurring amino acid

<400> 26

Met Asp Thr Ser His Trp Pro Gln Gly Ile Gly Leu Val Lys Ala Val
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Glu Pro Ser Lys Pro Val Pro Thr Glu Arg Lys Pro Arg Pro Gln Lys
 20 25 30

Glu Gln Ala Ile Asn Cys Pro Arg Cys Asn Ser Thr Asn Thr Lys Phe
 35 40 45

Cys Tyr Tyr Asn Asn Tyr Ser Leu Ser Gln Pro Arg Tyr Phe Cys Lys
 50 55 60

Thr Cys Arg Arg Tyr Trp Thr Glu Gly Gly Ser Leu Arg Asn Val Pro
 65 70 75 80

Val Gly Gly Gly Ser Arg Lys Asn Lys Arg Ser Ser Ser Ser Ser Asn
 85 90 95

Asn Ser Ser Ser Ser Thr Ser Ser Ser Tyr Lys Lys Ile Pro Asp Leu
 100 105 110

Thr Ile Pro Thr Ser Ser Gln Asn Pro Lys Ile Ile Asn Glu Pro His
 115 120 125

Asp Leu Asn Leu Ala Phe Asn Pro Ser Ala Thr Ser Asn Phe Ser Asn
 130 135 140

Ile Ser Glu Phe Met Ala Leu Pro Leu Met Asn Pro Asn Ser Thr Thr
 145 150 155 160

Ser Phe Met Ser Ser Ile Met Pro Gln Leu Ser Asp Ser Asn Asn Ile
 165 170 175

Met Tyr Ser Ser Ser Thr Gly Leu Pro Asn Leu His Asp Leu Lys
 180 185 190

PF5908220081029_F_60204_PCT_Sequence.txt

Pro Thr Leu Asn Phe Ser Leu Asp Gly Phe Asp Asn Asn Asn Gly Tyr
195 200 205

Gly Ser Leu Gln Gly Glu Thr Ala Gly Xaa Lys Leu Phe Phe Pro Leu
210 215 220

Asp Asp Leu Lys Asn Val Ser Thr Pro Asn Asp Asp His Glu Phe Asp
225 230 235 240

Glu Gln Asn Arg Gly Gln Ala Ala Glu Ser His Gly Phe Trp Asn Gly
245 250 255

Met Leu Gly Gly Gly Ser
260

<210> 27
<211> 1419
<212> DNA
<213> Hordeum vulgare

<400> 27
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ttccctcgcc cctacttctc tcctcctgtt catagcgcgg ccggcgagga tttccgctcg 180
cgagcacgag aagcaattgg gatcgatcct tggatggatg cagcccagtg gcaccagggg 240
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tgccgccgct actggaccga gggcggtcgc ctccgcaacg tgcccgtcgg cggcggtcga 600
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catcagcaac accagcagca gcagcagcag cagcaggttc agaacatgct cgggttctcg 1140
ctggacacgg gaggaggtgg cgacggcggg ggatacggcg gcgggttgca gggggcgcag 1200
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PF5908220081029_F_60204_PCT_Sequence.txt

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ggcgggtggcc atgagaccct ggggttcttg aataacagca tgatcgggaa cggcagcagc 1380
aatgacgccg gcggtggcgg tggcggcggc tcgtggtag 1419

<210> 28
<211> 472
<212> PRT
<213> Hordeum vulgare

<400> 28

Met Thr Tyr Gly Gly Glu Arg Arg Gly Ser Asn Pro Thr Thr Val Ile
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His Lys Thr Phe Leu Pro Leu Pro Leu Phe Arg Val Leu Glu Thr Thr
20 25 30

Ser Ser Ser Cys Ser Ser Pro Ser Phe Pro Arg Pro Tyr Phe Ser Pro
35 40 45

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

Ala Ile Gly Ile Asp Pro Trp Met Asp Ala Ala Gln Trp His Gln Gly
65 70 75 80

Leu Gly Leu Val Lys Pro Met Glu Glu Met Ile Met Ala Gly Asn Pro
85 90 95

Asn Pro Asn Pro Asn Gly Asn Pro Ser Pro Gln Pro Ala Pro Pro Ser
100 105 110

Gly Ala Glu Ala Gln Arg Ala Pro Leu Pro Gly Pro Pro Ala Ala Gly
115 120 125

Ala Gly Ala Ala Ala Gly Thr Gly Ser Thr Glu Arg Lys Ala Ala Arg
130 135 140

Pro Gln Lys Glu Lys Ala Ile Asn Cys Pro Arg Cys Asn Ser Thr Asn
145 150 155 160

Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Ser Leu Gln Gln Pro Arg Tyr
165 170 175

Phe Cys Lys Thr Cys Arg Arg Tyr Trp Thr Glu Gly Gly Ser Leu Arg
180 185 190

Asn Val Pro Val Gly Gly Gly Ser Arg Lys Asn Lys Arg Ser Ser Ser
195 200 205

Ser Val Val Ser Ser Ala Ala Gly Ala Val Ser Thr Ser Gly Ala Ala
210 215 220

PF5908220081029_F_60204_PCT_Sequence.txt

Ser Gly Thr Val Pro Val Gly Gly Met Pro Ala Lys Asn Pro Lys Leu
225 230 235 240

Met His Glu Gly Ala His Asp Leu Asn Leu Ala Phe Pro His His His
245 250 255

Gly Arg Val Leu His Pro Ser Glu Phe Ala Ala Phe Pro Ser Leu Glu
260 265 270

Ser Ser Ser Val Cys Asn Pro Gly Gly Ala Met Ala Ala Asn Gly Val
275 280 285

Gly Gly Gly Arg Gly Met Gly Thr Phe Ser Ala Met Glu Leu Leu Arg
290 295 300

Ser Thr Gly Cys Tyr Val Pro Leu Pro Gln Val Gln Leu Gly Met Pro
305 310 315 320

Pro Glu Tyr Ala Ala Ala Gly Phe Ala Leu Gly Glu Phe Arg Met Pro
325 330 335

Leu Gln His Gln Gln Gln His His Gln Gln Gln Gln Gln Gln Gln
340 345 350

Gln His His Gln His Gln His Gln His Gln Gln His Gln Gln Gln Gln
355 360 365

Gln Gln Gln Gln Val Gln Asn Met Leu Gly Phe Ser Leu Asp Thr Gly
370 375 380

Gly Gly Gly Asp Gly Gly Gly Tyr Gly Gly Gly Leu Gln Gly Ala Gln
385 390 395 400

Glu Ser Ala Thr Gly Arg Met Leu Phe Pro Phe Glu Asp Leu Lys Pro
405 410 415

Gly Ala Asn Ala Ala Gly Gly Gly Gly Ala Ser Gly Gly Asp Gln Phe
420 425 430

Glu His Ser Lys Glu Gln Gly Gly Gly Gly Gly His Glu Thr Leu Gly
435 440 445

Phe Trp Asn Asn Ser Met Ile Gly Asn Gly Ser Ser Asn Asp Ala Gly
450 455 460

Gly Gly Gly Gly Gly Gly Ser Trp
465 470

<210> 29
<211> 1128
<212> DNA
<213> Oryza sativa

PF5908220081029_F_60204_PCT_Sequence.txt

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cctatcgccc caccggcggc tggagcggcc gccggcgcgg gcgccgccgg agctggggct    180
ggcacgggagc gccgcgcgcg gccgcagaag gagaaggcgc tcaactgccc gcggtgcaac    240
tcgacgaaca ccaagtcttg ctactacaac aactacagcc tccagcagcc gcgctacttc    300
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cccggaggca acctggcggc ggcgaaacgg gccggtggca ggggcagcgt gggcgcggtc    660
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ggtggtggcg gcggcgtcat cgggtggccat gaggccccag ggttctggaa tagcagcatg   1080
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<210> 30
<211> 375
<212> PRT
<213> Oryza sativa

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<400> 30

Met Trp Gly Leu Gly Leu Val Lys Pro Met Glu Glu Met Leu Met Gly
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Ala Asn Pro Asn Pro Asn Gly Ser Ser Asn Gln Pro Pro Pro Pro Pro
20 25 30

Ser Ser Ala Ala Ser Ala Gln Arg Pro Ile Ala Pro Pro Ala Ala Gly
35 40 45

Ala Ala Ala Gly Ala Gly Ala Ala Gly Ala Gly Ala Gly Thr Glu Arg
50 55 60

Arg Ala Arg Pro Gln Lys Glu Lys Ala Leu Asn Cys Pro Arg Cys Asn
65 70 75 80

Ser Thr Asn Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Ser Leu Gln Gln
Seite 26

Pro Arg Tyr Phe Cys Lys Thr Cys Arg Arg Tyr Trp Thr Glu Gly Gly
100 105 110

Ser Leu Arg Asn Val Pro Val Gly Gly Gly Ser Arg Lys Asn Lys Arg
115 120 125

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

Ala Ala Val Ser Gly Ser Val Pro Val Gly Leu Ala Ala Lys Asn Pro
145 150 155 160

Lys Leu Met His Glu Gly Ala Gln Asp Leu Asn Leu Ala Phe Pro His
165 170 175

His His Gly Arg Ala Leu Gln Pro Pro Glu Phe Thr Ala Phe Pro Ser
180 185 190

Leu Glu Ser Ser Ser Val Cys Asn Pro Gly Gly Asn Leu Ala Ala Ala
195 200 205

Asn Gly Ala Gly Gly Arg Gly Ser Val Gly Ala Phe Ser Ala Met Glu
210 215 220

Leu Leu Arg Ser Thr Gly Cys Tyr Val Pro Leu Pro Gln Met Ala Pro
225 230 235 240

Leu Gly Met Pro Ala Glu Tyr Ala Ala Ala Gly Phe His Leu Gly Glu
245 250 255

Phe Arg Met Pro Pro Pro Pro Gln Gln Gln Gln Gln Gln Ala Gln
260 265 270

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

Gly Ser Gly Val Phe Gly Ala Cys Ser Ala Gly Leu Gln Glu Ser Ala
290 295 300

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

Ala Ala Ala Gly Asp Ala Asn Ser Gly Gly Asp His Gln Tyr Asp His
325 330 335

Gly Lys Asn Gln Gly Gly Gly Gly Gly Val Ile Gly Gly His Glu Ala
340 345 350

Pro Gly Phe Trp Asn Ser Ser Met Ile Gly Asn Gly Ser Ser Asn Gly
355 360 365

Gly Gly Gly Gly Gly Ser Trp
370 375

<210> 31
<211> 1080
<212> DNA
<213> Oryza sativa

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<210> 32
<211> 359
<212> PRT
<213> Oryza sativa

<400> 32
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Ala Ser Ala Leu Asn His Ala Ser Leu Pro Val Val Leu Gln Pro Ile
20 25 30
Val Ser Asn Pro Ser Pro Thr Ser Ser Ser Ser Thr Ser Ser Arg Ser
35 40 45
Ser Ala Gln Ala Thr Gln Gln Arg Ser Ser Ser Ala Thr Ser Ser Pro
Seite 28

50

55

60

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

Cys Pro Arg Cys Asn Ser Ser Asn Thr Lys Phe Cys Tyr Tyr Asn Asn
85 90 95

Tyr Asn Leu Thr Gln Pro Arg His Phe Cys Lys Thr Cys Arg Arg Tyr
100 105 110

Trp Thr Lys Gly Gly Ala Leu Arg Asn Val Pro Ile Gly Gly Gly Cys
115 120 125

Arg Lys Pro Arg Pro Met Pro Ala Pro Val Ala Lys Pro Pro Met Ser
130 135 140

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

Ala Ser Gly Gln Gln Ala Ala Thr Ala His Leu Met Ala Leu Leu Asn
165 170 175

Ser Ala Arg Gly Val Gln Gly His Gly Gly Ser Asn Val His Arg Leu
180 185 190

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

Asn Gly Ala Gly Ala Gly Thr Ala Ala Ser Leu Trp Pro Gln Ser Ala
210 215 220

Pro Arg Pro Val Thr Pro Pro Pro Pro His Met Asp Ser Gln Leu Gly
225 230 235 240

Met Gly Thr Leu Gly His His Asp Val Leu Ser Ser Leu Gly Leu Lys
245 250 255

Leu Pro Ser Ser Ala Ser Ser Ser Pro Ala Ala Ser Tyr Tyr Ser Asp
260 265 270

Gln Leu His Ala Val Val Ser Asn Ala Gly Arg Pro Gln Ala Pro Tyr
275 280 285

Asp Val Ala Thr Ala Ser Leu Pro Cys Thr Thr Ala Val Thr Ser Leu
290 295 300

Pro Ser Ala Leu Ser Ser Val Ser Ala Ala Ala Pro Thr Ser Asn Thr
305 310 315 320

Val Gly Met Asp Leu Pro Pro Val Ser Leu Ala Ala Pro Glu Met Gln
325 330 335

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Tyr Trp Asn Gly Pro Ala Ala Met Ser Val Pro Trp Pro Asp Leu Pro
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Thr Pro Asn Gly Ala Phe Pro
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<210> 33
 <211> 1137
 <212> DNA
 <213> Oryza sativa

<400> 33
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 gtgactgggg gcgcactgag gggcgggcggc gggcgggcggc cgccgccggg ggcaggtggc 180
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 ccgcgctact tctgcaagac gtgccggcgc tactggacgg agggcgggctc gctccgcaac 360
 gtccccgtcg gcggcggtc gcgcaagaac aagcgctcgt cgtcgtcggc ggcatcggcg 420
 tcgcccgcgt ccgcctccac ggcgaattcc gtcgtcacga gcgcgtccat gtccatgtcc 480
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<210> 34
 <211> 378
 <212> PRT
 <213> Oryza sativa

<400> 34

Met Asp Ala Ala His Trp His Gln Gly Leu Gly Leu Val Lys Pro Met
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Glu Glu Met Leu Met Ala Ala Asn Ala Ala Ala Gly Ala Asn Pro Asn
 20 25 30

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

Gly Gly Gly Gly Gly Ala Pro Pro Val Ala Gly Gly Ala Gly Ala Gly
50 55 60

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

Pro Arg Cys Asn Ser Thr Asn Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr
85 90 95

Ser Leu Gln Gln Pro Arg Tyr Phe Cys Lys Thr Cys Arg Arg Tyr Trp
100 105 110

Thr Glu Gly Gly Ser Leu Arg Asn Val Pro Val Gly Gly Gly Ser Arg
115 120 125

Lys Asn Lys Arg Ser Ser Ser Ser Ala Ala Ser Ala Ser Pro Ala Ser
130 135 140

Ala Ser Thr Ala Asn Ser Val Val Thr Ser Ala Ser Met Ser Met Ser
145 150 155 160

Met Ala Ser Thr Gly Gly Gly Ala Ser Lys Asn Pro Lys Leu Val His
165 170 175

Glu Gly Ala Gln Asp Leu Asn Leu Ala Phe Pro His His Gly Gly Leu
180 185 190

Gln Ala Pro Gly Glu Phe Pro Ala Phe Pro Ser Leu Glu Ser Ser Ser
195 200 205

Val Cys Asn Pro Gly Gly Pro Met Gly Thr Asn Gly Arg Gly Gly Gly
210 215 220

Ala Leu Ser Ala Met Glu Leu Leu Arg Ser Thr Gly Cys Tyr Met Pro
225 230 235 240

Leu Gln Val Pro Met Gln Met Pro Ala Glu Tyr Ala Thr Pro Gly Phe
245 250 255

Ala Leu Gly Glu Phe Arg Ala Pro Pro Pro Pro Gln Ser Ser Gln
260 265 270

Ser Leu Leu Gly Phe Ser Leu Asp Ala His Gly Ser Val Gly Gly Pro
275 280 285

Ser Ala Ala Gly Phe Gly Ser Ser Ala Gly Leu Gln Gly Val Pro Glu
290 295 300

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

Ser Ser Gly Thr Gly Gly Gly Gly Ala Ser Gly Gly Gly Ala Gly Val
325 330 335

Asp Gly Gly His Gln Phe Asp His Gly Lys Glu Gln Gln Ala Gly Gly
340 345 350

Gly Gly Gly Gly Pro Gly Gly His Asp Thr Pro Gly Phe Trp Asn Gly
355 360 365

Met Ile Gly Gly Gly Ser Gly Thr Ser Trp
370 375

<210> 35
<211> 29
<212> PRT
<213> Artificial sequence

<220>
<223> core DOF domain of SEQ ID NO: 2
<400> 35

Cys Pro Arg Cys Asn Ser Thr Asn Thr Lys Phe Cys Tyr Tyr Asn Asn
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Tyr Ser Leu Thr Gln Pro Arg Tyr Phe Cys Lys Gly Cys
20 25

<210> 36
<211> 60
<212> PRT
<213> Artificial sequence

<220>
<223> DOF domain of SEQ ID NO: 34
<400> 36

Gln Lys Glu Lys Ala Leu Asn Cys Pro Arg Cys Asn Ser Thr Asn Thr
1 5 10 15

Lys Phe Cys Tyr Tyr Asn Asn Tyr Ser Leu Gln Gln Pro Arg Tyr Phe
20 25 30

Cys Lys Thr Cys Arg Arg Tyr Trp Thr Glu Gly Gly Ser Leu Arg Asn
35 40 45

Val Pro Val Gly Gly Gly Ser Arg Lys Asn Lys Arg
50 55 60

<210> 37
<211> 11
<212> PRT
<213> Artificial sequence

<220>

<223> motif I

<400> 37

Ile Glu Arg Lys Ala Arg Pro Gln Lys Asp Gln
1 5 10

<210> 38

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> motif II

<400> 38

Ile Ile Tyr Trp Ser Gly Met Ile
1 5

<210> 39

<211> 17

<212> PRT

<213> Artificial sequence

<220>

<223> motif III

<400> 39

Ile Ile Ile Arg Leu Leu Phe Pro Phe Glu Asp Leu Lys Pro Leu Val
1 5 10 15

Ser

<210> 40

<211> 11

<212> PRT

<213> Artificial sequence

<220>

<223> motif IV

<400> 40

Ile Val Ile Asn Val Lys Pro Met Glu Glu Ile
1 5 10

<210> 41

<211> 21

<212> PRT

<213> Artificial sequence

<220>

<223> motif V

<400> 41

Val Lys Asn Pro Lys Leu Leu His Glu Gly Ala Gln Asp Leu Asn Leu
1 5 10 15

Ala Phe Pro His His
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<213> Artificial sequence

<220>
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<400> 42

Val Ile Met Glu Leu Leu Arg Ser Thr Gly Cys Tyr Met
1 5 10

<210> 43
<211> 24
<212> PRT
<213> Artificial sequence

<220>
<223> motif VII

<400> 43

Val Ile Ile Met Met Asp Ser Asn Ser Val Leu Tyr Ser Ser Leu Gly
1 5 10 15

Phe Pro Thr Met Pro Asp Tyr Lys
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<210> 44
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<220>
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<220>
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5

<210> 45
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<223> primer 1

<400> 45
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53

<210> 46
<211> 50
<212> DNA

<213> Artificial sequence

<220>

<223> primer 2

<400> 46

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<210> 47

<211> 1827

<212> DNA

<213> Oryza sativa

<400> 47

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tccggcttaa tgcttttctt ttgtcacata tactgcattg caacaattgc catatattca 180

cttctgccat cccattatat agcaactcaa gaatggattg atatatcccc tattactaat 240

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gcgcacatac ttttcaaact actaaatggg gtgtttttta aaaatatatt caatacaaaa 360

gttgctttta aaaattatat tgatccattt ttttaaaaaa aatagctaata acttaattaa 420

tcacgtgtta aaagaccgct ccgttttgcg tgcaggaggg atagggtcac atcctgcatt 480

accgaacaca gcctaaatct tgttgtctag attcgtagta ctggatatat taaatcatgt 540

tctaagttac tatatactga gatgaataga ataagtaaaa ttagaccacac cttagtcctt 600

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gtatacagtt ataaactatt ccctctgttc taaaacataa gggattatgg atggattcga 900

catgtaccag taccatgaat cgaatccaga caagtttttt atgcatattt attctactat 960

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cgataattga atggaacttc cacattcaga ttcgataggt gaccgtcgac tccaagtgtc 1140

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 <212> DNA
 <213> Artificial sequence

<220>
 <223> expression cassette

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tccggcttaa tgcttttctt ttgtcacata tactgcattg caacaattgc catatattca	180
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gttgctttta aaaattatat tgatccattt ttttaaaaaa aatagctaata acttaattaa	420
tcacgtgtta aaagaccgct ccgttttgctg tgcaggaggg ataggttcac atcctgcatt	480
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gcaacaatta	atgtcgacat	taatgaacat	cagaagcgag	gaagcggtag	tgatgcagct	2760
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 <211> 810
 <212> DNA
 <213> Arabidopsis thaliana

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cttcatagcc	tcctaggcaa	caagtggctc	ttgattgcgg	cgagattacc	tggaagaaca	300
gataacgaga	tcaagaacta	ctggaacaca	catataaaga	ggaagctttt	gagcaaaggg	360
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ggggaccaga	agcaaaataa	gtatattcga	aatgggttag	tttgcaaaga	agagagagtt	540
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caaaaccaga gagaaatatt tactttgact gcgtcccgtt ttacatgga aaacgacatg 660
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<210> 50
<211> 269
<212> PRT
<213> Arabidopsis thaliana

<400> 50

Met Gly Arg Ser Pro Cys Cys Glu Lys Glu His Met Asn Lys Gly Ala
1 5 10 15

Trp Thr Lys Glu Glu Asp Glu Arg Leu Val Ser Tyr Ile Lys Ser His
20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Arg Ala Ala Gly Leu Leu Arg
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60

Leu Lys Arg Gly Asn Phe Thr His Asp Glu Asp Glu Leu Ile Ile Lys
65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Ala Arg Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
100 105 110

Lys Arg Lys Leu Leu Ser Lys Gly Ile Asp Pro Ala Thr His Arg Gly
115 120 125

Ile Asn Glu Ala Lys Ile Ser Asp Leu Lys Lys Thr Lys Asp Gln Ile
130 135 140

Val Lys Asp Val Ser Phe Val Thr Lys Phe Glu Glu Thr Asp Lys Ser
145 150 155 160

Gly Asp Gln Lys Gln Asn Lys Tyr Ile Arg Asn Gly Leu Val Cys Lys
165 170 175

Glu Glu Arg Val Val Val Glu Glu Lys Ile Gly Pro Asp Leu Asn Leu
180 185 190

Glu Leu Arg Ile Ser Pro Pro Trp Gln Asn Gln Arg Glu Ile Ser Thr
195 200 205

PF5908220081029_F_60204_PCT_Sequence.txt

Cys Thr Ala Ser Arg Phe Tyr Met Glu Asn Asp Met Glu Cys Ser Ser
210 215 220

Glu Thr Val Lys Cys Gln Thr Glu Asn Ser Ser Ser Ile Ser Tyr Ser
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245 250 255

Lys Thr Arg Ile Leu Asp Phe Arg Ser Leu Glu Met Lys
260 265

<210> 51
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<213> Artificial sequence

<220>
<223> primer: prm05966

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<210> 52
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<220>
<223> primer: prm05967

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<210> 53
<211> 2194
<212> DNA
<213> Oryza sativa

<400> 53
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 <211> 3056
 <212> DNA
 <213> Artificial sequence

<220>
 <223> expression cassette

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PF5908220081029_F_60204_PCT_Sequence.txt

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PF5908220081029_F_60204_PCT_Sequence.txt

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<210> 55
<211> 16
<212> PRT
<213> Artificial sequence

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```

<220>
<223> motif 1

```

```

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

```

```

<220>
<221> UNSURE
<222> (2)..(2)
<223> Xaa can be any naturally occurring amino acid but preferably one
of Lys, Gln, Ala, Pro, Thr, Ile, Ser, more preferably Lys or Gln

```

```

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

```

```

<220>
<221> UNSURE
<222> (6)..(6)
<223> Xaa can be any naturally occurring amino acid but preferably one
of Gln, Glu, Asp, Ala, Ser, more preferably Gln, Glu or Asp

```

```

<220>
<221> UNSURE
<222> (7)..(7)
<223> Xaa can be any naturally occurring amino acid but preferably one
of Arg, Leu, Lys, Met, Ile, more preferably Arg, Leu or Lys

```

```

<220>
<221> UNSURE
<222> (9)..(9)
<223> Xaa can be any naturally occurring amino acid but preferably one
of Ile, Val, Thr, Gly, Leu, Ala, more preferably Ile, Val or Thr

```

<220>
 <221> UNSURE
 <222> (10)..(10)
 <223> Xaa can be naturally occurring any amino acid but preferably one of Asn, Asp, Ala, Ser, Lys, Gly, more preferably Asn, Asp, Ala or Ser

<220>
 <221> VARIANT
 <222> (11)..(11)
 <223> / replace = "His"

<220>
 <221> UNSURE
 <222> (13)..(13)
 <223> Xaa can be any naturally occurring amino acid but preferably one of Arg, Lys, Gln, Glu, Thr, Asn, more preferably Arg, Lys, Gln or Glu

<220>
 <221> UNSURE
 <222> (14)..(14)
 <223> Xaa can be any naturally occurring amino acid but preferably one of Val, Lys, Ala, Ser, Thr, Glu, Asn, more preferably Val, Lys, Ala or Ser

<220>
 <221> UNSURE
 <222> (15)..(15)
 <223> Xaa can be any naturally occurring amino acid but preferably one of Tyr, His, Asn, Asp, more preferably His or Tyr

<400> 55

Thr Xaa Glu Glu Asp Xaa Xaa Leu Xaa Xaa Tyr Ile Xaa Xaa Xaa Gly
 1 5 10 15

<210> 56
 <211> 10
 <212> PRT
 <213> Artificial sequence

<220>
 <223> motif 2

<220>
 <221> VARIANT
 <222> (1)..(1)
 <223> / replace = "Tyr" / replace = "Pro" / replace = "His" / replace = "Leu"

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

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

<220>
 <221> VARIANT
 <222> (5)..(5)
 <223> / replace = "Asn"

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

<220>
 <221> VARIANT
 <222> (7)..(7)
 <223> / replace = "Ile"

<220>
 <221> VARIANT
 <222> (9)..(9)
 <223> / replace = "Arg" / replace = "Thr" / replace = "Ala" / replace =
 "Ser"

<220>
 <221> VARIANT
 <222> (10)..(10)
 <223> / replace = "Ser" / replace = "Lys" / replace = "Asn" / replace =
 "Leu" / replace = "Arg"

<400> 56

Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala
 1 5 10

<210> 57
 <211> 16
 <212> PRT
 <213> Artificial sequence

<220>
 <223> motif 3

<220>
 <221> UNSURE
 <222> (11)..(11)
 <223> Xaa can be any naturally occurring amino acid, preferably one of
 Ile, Met, Leu, or Thr

<400> 57

Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Xaa Asn Tyr Leu Arg Pro
 1 5 10 15

<210> 58
 <211> 11
 <212> PRT
 <213> Artificial sequence

<220>
 <223> motif 4

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

<220>
 <221> VARIANT
 <222> (9)..(9)
 <223> / replace = "His" / replace = "Phe"

<400> 58

Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn
 1 5 10

<210> 59

<211> 14

<212> PRT

<213> Artificial sequence

<220>

<223> motif 5

<220>

<221> VARIANT

<222> (1)..(1)

<223> / replace = "Ser"

<220>

<221> VARIANT

<222> (2)..(2)

<223> / replace = "Asn" / replace = "Arg"

<220>

<221> VARIANT

<222> (3)..(3)

<223> / replace = "Val" / replace = "Leu"

<220>

<221> VARIANT

<222> (4)..(4)

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

<220>

<221> VARIANT

<222> (5)..(5)

<223> / replace = "Lys"

<220>

<221> VARIANT

<222> (6)..(6)

<223> / replace = "Arg"

<220>

<221> VARIANT

<222> (7)..(7)

<223> / replace = "Ile"

<220>

<221> UNSURE

<222> (8)..(8)

<223> Xaa can be any naturally occurring amino acid, preferably one of Ile, Leu, Val, Thr, Ala, Arg, more preferably Ile, Leu, Val or Thr

<220>

<221> UNSURE

<222> (9)..(9)

<223> Xaa can be any naturally occurring amino acid, preferably one of Ser, Asn, Arg, Gly, Ala, Val, Lys, Gln, preferably one of Ser, Asn, Arg, Gly or Ala

<220>

<221> UNSURE

<222> (10)..(10)

<223> Xaa can be any naturally occurring amino acid, preferably one of Arg, Lys, Gln, Met, Thr

```

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

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

<220>
<221> VARIANT
<222> (14)..(14)
<223> / replace = "Leu"

<400> 59
Thr His Ile Lys Arg Lys Leu Xaa Xaa Xaa Gly Ile Asp Pro
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<210> 60
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> motif 6

<220>
<221> UNSURE
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid, preferably one of
Phe, Gly, Cys, Leu, Asp or Tyr

<220>
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<222> (2)..(2)
<223> / replace = "Leu" / replace = "Gln" / replace = "Trp"

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

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

<220>
<221> VARIANT
<222> (7)..(7)
<223> / replace = "Asp"

<220>
<221> UNSURE
<222> (9)..(9)
<223> Xaa can be any naturally occurring amino acid, preferably one of
Arg, Lys, Gly, Thr, Cys, Asp, Ser

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

<220>

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<221> VARIANT
<222> (11)..(11)
<223> / replace = "Asp" / replace = "Asn" / replace = "Gly"

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

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

```

<400> 60

Xaa Pro Asp Leu Asn Leu Glu Leu Xaa Ile Ser Leu Pro
 1 5 10

```

<210> 61
<211> 7
<212> PRT
<213> Artificial sequence

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```

<220>
<223> motif 7

```

```

<220>
<221> VARIANT
<222> (1)..(1)
<223> / replace = "Tyr" / replace = "Cys" / replace = "Asp"

```

```

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

```

```

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

```

```

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

```

```

<220>
<221> VARIANT
<222> (5)..(5)
<223> / replace = "Pro"

```

```

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

```

<400> 61

Phe Arg Ser Leu Glu Met Lys
 1 5

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<210> 62
<211> 795
<212> DNA

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<213> Gossypium hirsutum

<400> 62

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<210> 63

<211> 264

<212> PRT

<213> Gossypium hirsutum

<400> 63

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Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
1          5          10          15

Trp Thr Lys Glu Glu Asp Asp Arg Leu Ile Ala Tyr Ile Arg Ala His
20          25          30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
35          40          45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50          55          60

Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
65          70          75          80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
85          90          95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
100         105         110

Arg Arg Lys Leu Leu Ser Arg Gly Ile Asp Pro Ala Thr His Arg Pro
115         120         125

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Leu Asn Glu Ala Ser Gln Asp Val Thr Thr Ile Ser Phe Ser Gly Ala
130 135 140

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

Gly Phe Ile Thr Lys Asp Glu Lys Lys Ile Pro Val Gln Glu Arg Cys
165 170 175

Pro Asp Leu Asn Leu Asp Leu Arg Ile Ser Pro Pro Tyr Tyr Gln Gln
180 185 190

Thr Gln Pro Glu Ser Phe Lys Thr Gly Gly Arg Thr Leu Cys Phe Ile
195 200 205

Cys Ser Leu Gly Val Lys Asn Ser Lys Asp Cys Thr Cys Ser Thr Ile
210 215 220

Thr Thr Ala Ala Gly Ser Ser Ser Ser Ser Ser Ser His Ser Asn Ser
225 230 235 240

Asn Asn Ser Ser Gly Tyr Asp Phe Leu Gly Leu Lys Ser Gly Ile Leu
245 250 255

Glu Tyr Arg Ser Leu Glu Met Lys
260

<210> 64
<211> 756
<212> DNA
<213> Vitis vinifera

<400> 64
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gaagatgatc gcctcatcgc ttatatccgg gcacacggcg agggctgctg gaggtctctc 120
cccaaggccg caggccttct ccgatgtggg aaaagttgcc gcctccgatg gataaactac 180
ctgaggcctg acctcaagcg gggaaacttc accgaggaag aagatgaact catcatcaaa 240
ctgcatagtc tccttggaac caaatggtct cttatagctg ggagattacc aggaagaaca 300
gataatgaaa taaagaatta ctggaacacc cacatacgga gaaagcttct gaaccgaggc 360
atcgatccgt ctactcatcg ccccatcaac gagccctcac cggacgttac aaccatatct 420
ttcgagccg cagttaagga agaggagaag atcaatatca gcagtactgg tggatttggg 480
tgcaaaactg agaaaaacc agttacggaa aagtgtccag acctcaacct tgagctcaga 540
atcagcccac cataccaacc ccaagctgag acgccattga agactggtgg gaggagtagc 600
agcactactc tttgctttgc atgcagtttg ggaataccaa atagttagga gtgcagttgc 660
agtattggta ctagtagtgg aagcagcagc tctgggtatg acttcttagg gttgacatct 720
ggggtttttg attacagagg tttggagatg aaataa 756

<210> 65
 <211> 251
 <212> PRT
 <213> Vitis vinifera

<400> 65

Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
 1 5 10 15

Trp Thr Lys Glu Glu Asp Asp Arg Leu Ile Ala Tyr Ile Arg Ala His
 20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60

Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
 65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110

Arg Arg Lys Leu Leu Asn Arg Gly Ile Asp Pro Ser Thr His Arg Pro
 115 120 125

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

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

Cys Lys Thr Glu Lys Asn Pro Val Thr Glu Lys Cys Pro Asp Leu Asn
 165 170 175

Leu Glu Leu Arg Ile Ser Pro Pro Tyr Gln Pro Gln Ala Glu Thr Pro
 180 185 190

Leu Lys Thr Gly Gly Arg Ser Ser Ser Thr Thr Leu Cys Phe Ala Cys
 195 200 205

Ser Leu Gly Ile Pro Asn Ser Glu Glu Cys Ser Cys Ser Ile Gly Thr
 210 215 220

Ser Ser Gly Ser Ser Ser Gly Tyr Asp Phe Leu Gly Leu Thr Ser
 225 230 235 240

Gly Val Leu Asp Tyr Arg Gly Leu Glu Met Lys
245 250

<210> 66
<211> 735
<212> DNA
<213> Solenostemon scutellarioides

<400> 66
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gaagaagacg atcggctcat ctctacatc cgcgctcacg gcgagggatg ctggcggctct 120
cttcctaagg cagctggcct cctccgctgc ggcaagagct gccgcctgcg ctggatcaac 180
tacttgcgcc cggatctcaa gagaggcaac ttcacagaag acgaagacga actcatcatc 240
aaactccaca gccttctagg caacaaatgg tctcttatag ccggaaggct gccggggcga 300
accgacaacg agatcaagaa ctactggaac actcacatca gaagaaaact ggtgagccaa 360
ggaatcgatc caacgacgca tcgccccatc aatgagcctg ctgcagctgc agctgcacca 420
caggaggaag cagtatcgaa aaccatttcc ttctcccaat cggagagaat cgacaagtgc 480
ccggatttga atcttgatct cagaatcagc cccccatcat catcccagca gcaaaatcaa 540
gaaccgttga aaacaggtac gagtagtggt agtagtagta ccttgtgctt cgcatgtagc 600
atcggcatcc aaaacagcaa ggattgcagc tgcagagacg gaatcatgat cagtgtgagt 660
gggagcagct ctggatatga ttttctgggg ttgaaagcgg gagttttgga ttacagaagc 720
ttggagatga aatga 735

<210> 67
<211> 244
<212> PRT
<213> Solenostemon scutellarioides

<400> 67

Met Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly
1 5 10 15

Ala Trp Thr Lys Glu Glu Asp Asp Arg Leu Ile Ser Tyr Ile Arg Ala
20 25 30

His Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu
35 40 45

Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro
50 55 60

Asp Leu Lys Arg Gly Asn Phe Thr Glu Asp Glu Asp Glu Leu Ile Ile
65 70 75 80

Lys Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg
85 90 95

Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His
Seite 51

100

105

110

Ile Arg Arg Lys Leu Val Ser Gln Gly Ile Asp Pro Thr Thr His Arg
115 120 125

Pro Ile Asn Glu Pro Ala Ala Ala Ala Ala Pro Gln Glu Glu Ala
130 135 140

Val Ser Lys Thr Ile Ser Phe Ser Gln Ser Glu Arg Ile Asp Lys Cys
145 150 155 160

Pro Asp Leu Asn Leu Asp Leu Arg Ile Ser Pro Pro Ser Ser Ser Gln
165 170 175

Gln Gln Asn Gln Glu Pro Leu Lys Thr Gly Thr Ser Ser Gly Ser Ser
180 185 190

Ser Thr Leu Cys Phe Ala Cys Ser Ile Gly Ile Gln Asn Ser Lys Asp
195 200 205

Cys Ser Cys Arg Asp Gly Ile Met Ile Ser Val Ser Gly Ser Ser Ser
210 215 220

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

Leu Glu Met Lys

<210> 68
<211> 822
<212> DNA
<213> Solanum lycopersicum

<400> 68
atgggaaggt caccttggtg tgagaaggca catacaaaca aaggagcatg gactaaagaa 60
gaagatgaaa gactaatttc ttacattaga gtcctggtg aagggttggtg gaggtctctt 120
cctaaagctg ctggacttct tcgatgcggt aaaagttgtc gtctccgatg gattaattac 180
ttaagacctg accttaaagc tggttaacttt actgaagaag aagatgaact cattatcaaa 240
ctccatagcc tccttggaag caagtggctg cttatagcag gaagattacc aggaagaaca 300
gataacgaga taaaaaacta ttggaacaca catataagac gaaagctctt gagtcgaggt 360
attgatccaa caacacatag atcaatcaat gatcctacta caatacaaaa agttacaacg 420
attacttttg ctgctgctca tgaaaatatt aaagatatgg atcaacaaga tgagatgata 480
aatatcaaag ctgaattcgt tgaaacaagc aaagaatcag ataataatga aataattcaa 540
gaaaagtcac catcatgtct tcctgactta aatcttgaac tcagaattag tcctccacat 600
catcaacaac tcgatcatca tcgtcatcat caacgatcaa gctctttatg ttttacatgt 660
agtttgggaa ttcaaaatag taaagattgc agttgtggaa gtgaaagtaa tggaaatgga 720

tggagtaata atatggtaag tatgaacatt atggctggtt atgacttttt gggcttgaag 780
 actaatgggtc ttttggacta tagaactttg gaaactaagt ga 822

<210> 69
 <211> 273
 <212> PRT
 <213> Solanum lycopersicum

<400> 69

Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
 1 5 10 15

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

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60

Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
 65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110

Arg Arg Lys Leu Leu Ser Arg Gly Ile Asp Pro Thr Thr His Arg Ser
 115 120 125

Ile Asn Asp Pro Thr Thr Ile Pro Lys Val Thr Thr Ile Thr Phe Ala
 130 135 140

Ala Ala His Glu Asn Ile Lys Asp Ile Asp Gln Gln Asp Glu Met Ile
 145 150 155 160

Asn Ile Lys Ala Glu Phe Val Glu Thr Ser Lys Glu Ser Asp Asn Asn
 165 170 175

Glu Ile Ile Gln Glu Lys Ser Ser Ser Cys Leu Pro Asp Leu Asn Leu
 180 185 190

Glu Leu Arg Ile Ser Pro Pro His His Gln Gln Leu Asp His His Arg
 195 200 205

His His Gln Arg Ser Ser Ser Leu Cys Phe Thr Cys Ser Leu Gly Ile
 210 215 220

Gln Asn Ser Lys Asp Cys Ser Cys Gly Ser Glu Ser Asn Gly Asn Gly
 Seite 53

225

Trp Ser Asn Asn Met Val Ser Met Asn Ile Met Ala Gly Tyr Asp Phe
245 250 255

Leu Gly Leu Lys Thr Asn Gly Leu Leu Asp Tyr Arg Thr Leu Glu Thr
260 265 270

Lys

<210> 70
<211> 798
<212> DNA
<213> Humulus lupulus

<400> 70
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gaagatgatc gacttattgc atacataagg gctcacggcg agggttgctg gcgctcacta 120
cctaaagccg ccggtctcct aaggtgtggc aagagttgta ggctgcgctg gattaactac 180
ctcagacctg acctcaaacg tggaaacttt acagaagaag aagacgagct tatcatcaag 240
ctccatagtc tccttggaac caaatggtct ttaatagctg gaagactacc aggaagaaca 300
gacaatgaga taaagaacta ctggaacacc cacataagaa gaaagcttct gaacagagga 360
attgaccctg caactcaccg gccactcaac gagtcaggctc aagaaacgac aaacacttcc 420
accactacaa ccgccacaac aaccaccacc accaccgcct ccaacacgac caccacaatc 480
tcgtttgctg cttccactgt taaagaagaa gagaaaacga caagtgtttt gttaaaccac 540
attcaagaac agtgtcctga cttgaacctt gagctcagaa ttagccctcc ttatccgcac 600
cagcaacgcc agccagacca attgaagagc ggtgggtgctt ctctctgctt tgcttgtagt 660
ttgggtttgc agaacagtaa agagtgttgc tgtacaattt caagtatgga tagcaataac 720
ccaagcacca gtgttggtta tgatttcttg ggcttgaaat ctggtgtttt ggattacaga 780
agcttggaac tgaaatag 798

<210> 71
<211> 265
<212> PRT
<213> Humulus lupulus

<400> 71
Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
1 5 10 15
Trp Thr Lys Glu Glu Asp Asp Arg Leu Ile Ala Tyr Ile Arg Ala His
20 25 30
Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
35 40 45

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Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60

Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
100 105 110

Arg Arg Lys Leu Leu Asn Arg Gly Ile Asp Pro Ala Thr His Arg Pro
115 120 125

Leu Asn Glu Ser Gly Gln Glu Thr Thr Asn Thr Ser Thr Thr Thr Thr
130 135 140

Ala Thr Thr Thr Thr Thr Thr Thr Ala Ser Asn Thr Thr Thr Thr Ile
145 150 155 160

Ser Phe Ala Ala Ser Thr Val Lys Glu Glu Glu Lys Thr Thr Ser Val
165 170 175

Leu Leu Asn Pro Ile Gln Glu Gln Cys Pro Asp Leu Asn Leu Glu Leu
180 185 190

Arg Ile Ser Pro Pro Tyr Pro His Gln Gln Arg Gln Pro Asp Gln Leu
195 200 205

Lys Ser Gly Gly Ala Ser Leu Cys Phe Ala Cys Ser Leu Gly Leu Gln
210 215 220

Asn Ser Lys Glu Cys Cys Cys Thr Ile Ser Ser Met Asp Ser Asn Asn
225 230 235 240

Pro Ser Thr Ser Val Gly Tyr Asp Phe Leu Gly Leu Lys Ser Gly Val
245 250 255

Leu Asp Tyr Arg Ser Leu Glu Met Lys
260 265

<210> 72
<211> 813
<212> DNA
<213> Populus tremula x Populus tremuloides

<400> 72
atgggaaggt ctccttgctg tgaaaaagcc catacaaaca aggggtgcgtg gaccaaggag 60
gaagacgatc gccttggtgc ttacattaga gctcatggtg aagggttgctg gcgttcactt 120
cctaaagccg ctggccttct tagatgtggc aagagttgca gacttcgctg gatcaactac 180
ttacgacctg accttaaagc tggcaatttc accgaagcag aagatgagct cattatcaaa 240
Seite 55

PF5908220081029_F_60204_PCT_Sequence.txt

```
ctccatagcc tccttggaac cagtagatgg tcactcatag ctggaagatt accagggaga 300
acagataatg agataaagaa ttattggaac acacatataa gaaggaagct tttgaacaga 360
ggcatagatc ccgcaactca taggccactc aacgaaccgg tacaggaagc cacaacgaca 420
atatctttca ccacaaccac tacttcagtt gaagaagagt ctcgggggttc tataattaaa 480
gaggaaatta aagagaagtt aattagcgca actgctttcg tatgcacaga agcgaaaacc 540
caagttcaag aaaggtgtcc agacttgaat ctcgaacttg gaattagcct tccttcccaa 600
aaccagcctg atcatcacca gccattcaag accggaggaa gtagaagtct ttgttttgct 660
tgcagtttgg ggctacaaaa cagcaaggat tgcagctgca atgttattgt gagcactggt 720
gggagcagtg gcagcactag cacaagaat ggctatgact tcttgggcat gaaaagtggt 780
gttttggtt atagaagttt agagatgaaa taa 813
```

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<210> 73
<211> 270
<212> PRT
<213> Populus tremula x Populus tremuloides
<400> 73
```

```
Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
1 5 10 15
```

```
Trp Thr Lys Glu Glu Asp Asp Arg Leu Val Ala Tyr Ile Arg Ala His
20 25 30
```

```
Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
35 40 45
```

```
Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60
```

```
Leu Lys Arg Gly Asn Phe Thr Glu Ala Glu Asp Glu Leu Ile Ile Lys
65 70 75 80
```

```
Leu His Ser Leu Leu Gly Asn Ser Arg Trp Ser Leu Ile Ala Gly Arg
85 90 95
```

```
Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His
100 105 110
```

```
Ile Arg Arg Lys Leu Leu Asn Arg Gly Ile Asp Pro Ala Thr His Arg
115 120 125
```

```
Pro Leu Asn Glu Pro Val Gln Glu Ala Thr Thr Thr Ile Ser Phe Thr
130 135 140
```

```
Thr Thr Thr Thr Ser Val Glu Glu Glu Ser Arg Gly Ser Ile Ile Lys
145 150 155 160
```


Glu Glu Ile Lys Glu Lys Leu Ile Ser Ala Thr Ala Phe Val Cys Thr
165 170 175

Glu Ala Lys Thr Gln Val Gln Glu Arg Cys Pro Asp Leu Asn Leu Glu
180 185 190

Leu Gly Ile Ser Leu Pro Ser Gln Asn Gln Pro Asp His His Gln Pro
195 200 205

Phe Lys Thr Gly Gly Ser Arg Ser Leu Cys Phe Ala Cys Ser Leu Gly
210 215 220

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

Gly Ser Ser Gly Ser Thr Ser Thr Lys Asn Gly Tyr Asp Phe Leu Gly
245 250 255

Met Lys Ser Gly Val Leu Asp Tyr Arg Ser Leu Glu Met Lys
260 265 270

<210> 74
<211> 762
<212> DNA
<213> Glycine max

<400> 74
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gaagatgaca gactcatatc ttatattcga gctcacggag aaggctgctg gcgttcaactc 120
cccaaagccg ccggccttct ccggtgcggc aagagctgcc gtctccggtg gatcaactac 180
ctccgccccg acctcaaaag aggtaacttt accgaagaag aagatgaact catcatcaaa 240
ctccacagtc tcctcggtaa caagtggctt ttgatagctg gaagattgcc ggggagaaca 300
gacaatgaaa taaagaatta ttggaacacg cacataagaa ggaagctttt gaacagagga 360
atcgaccctg ctactcatag gccactcaac gaggctgctt ctgctgcaac tgttacaact 420
gccaccacta atatatcttt tgggaaacaa caagaacaag agacaagttc tagtaacgga 480
agcgttggtt aaggttccat cttggaacgc tgccctgact tgaaccttga gttaaccatt 540
agtcctcttc gccacaaca acctcagaag aatctttggt ttgtttgcag tttgggtttg 600
aacaacagca aggattgtag ctgcaacggt gccaacactg ttactgttac tgtcagcaac 660
actactcctt cttctgctgc tgctgctgct gctgctgctt atgatttctt gggcatgaaa 720
accaacgggtg tttgggattg caccgccttg gaaatgaaat ga 762

<210> 75
<211> 253
<212> PRT
<213> Glycine max

<400> 75
Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
Seite 57

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

<210> 76
 <211> 885
 <212> DNA
 <213> Brassica rapa

<400> 76

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cccaaagccg ccggccttct cgggtgtggc aaaagctgcc gtctccggtg gatcaactat    180
ctccggcctg accttaagcg tggaaacttc actgaagaag aggacgagct catcatcaag    240
ctccatagtc ttcttggcaa caaatggctg cttattgctg ggagattacc gggaagaaca    300
gataacgaga taaagaacta ttggaacaca catatacgaa gaaagcttat aaaccgaggg    360
attgatccaa caactcatag accaatccaa gaatcgtcag cttctcagga ttctaaaccg    420
acacacctag aagcaatcac aagtaacacc attaatatct ccttcgcctc ttcctcttct    480
actccgaaga tggaaatatt ccaggaaagc acaagttttc ctggaaaaca agagaaaatc    540
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ttgaacctcg agctcagaat cagccttcct gatgttggtg atcatcatca tcaaggcttt    660
gtcgggagagg gaaagacaac aacaccacga cgttgtttca aatgcagttt agggacgata    720
aacgggatgg agtgcagatg cggaagaatg agatgcgatg ttgttgagg tagcaaaggc    780
agtggcaagg ggagtgcacat gagcaacggg ttcgattttt tagggttggc aaagaaagag    840
accaacactt gtcttttttg ttttagaagc ttggagatga aataa                    885

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<210> 77
 <211> 294
 <212> PRT
 <213> Brassica rapa

<400> 77

Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
 1 5 10 15

Trp Thr Lys Glu Glu Asp Glu Arg Leu Ile Ala Tyr Ile Lys Ala His
 20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60

Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
 65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110

Arg Arg Lys Leu Ile Asn Arg Gly Ile Asp Pro Thr Thr His Arg Pro
 115 120 125

PF5908220081029_F_60204_PCT_Sequence.txt

Ile Gln Glu Ser Ser Ala Ser Gln Asp Ser Lys Pro Thr His Leu Glu
130 135 140

Ala Ile Thr Ser Asn Thr Ile Asn Ile Ser Phe Ala Ser Ser Ser Ser
145 150 155 160

Thr Pro Lys Met Glu Ile Phe Gln Glu Ser Thr Ser Phe Pro Gly Lys
165 170 175

Gln Glu Lys Ile Ser Met Val Thr Phe Lys Glu Glu Lys Asp Glu Cys
180 185 190

Pro Val Glu Glu Asn Phe Pro Asp Leu Asn Leu Glu Leu Arg Ile Ser
195 200 205

Leu Pro Asp Val Val Asp His His His Gln Gly Phe Val Gly Glu Gly
210 215 220

Lys Thr Thr Thr Pro Arg Arg Cys Phe Lys Cys Ser Leu Gly Thr Ile
225 230 235 240

Asn Gly Met Glu Cys Arg Cys Gly Arg Met Arg Cys Asp Val Val Gly
245 250 255

Gly Ser Lys Gly Ser Gly Lys Gly Ser Asp Met Ser Asn Gly Phe Asp
260 265 270

Phe Leu Gly Leu Ala Lys Lys Glu Thr Asn Thr Cys Leu Phe Gly Phe
275 280 285

Arg Ser Leu Glu Met Lys
290

<210> 78
<211> 885
<212> DNA
<213> Brassica rapa

<400> 78
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gaggacgaga ggctcatagc ttacattaaa gctcacggcg aaggctgctg gagatctctc 120
cccaaagccg ccggccttct ccggtgtggc aaaagctgcc gtctccggtg gatcaactat 180
ctccggcctg accttaagcg tggaaacttc actgaagaag aggacgagct catcatcaag 240
ctccatagtc ttcttggcaa caaatggctg cttattgctg ggagattacc gggaagaaca 300
gataacgaga taaagaacta ttggaacaca catatacgaa gaaagcttat aaaccgaggg 360
attgatccaa caactcatag accaatccaa gaatcgtcag cttctcagga ttctaaaccg 420
acacacctag aagcaatcac aagtaacacc attaatatct ctttcgcctc ttcctcttct 480
actccgaaga tggaaatatt ccaggaaagc acaagttttc ctggaaaaca agagaaaatc 540

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gtcggagagg gaaagacaac aacaccacga cgttgtttca aatgcagttt agggacgata	720
aacgggatgg agtgcagatg cggaagaatg agatacgatg ttgttgagg tagcaaaggc	780
agtggcaagg ggagtgcacat gagcaacggg ttcgattttt tagggttggc aaagaaagag	840
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<210> 79
 <211> 294
 <212> PRT
 <213> Brassica rapa

<400> 79

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Trp	Thr	Lys	Glu	Glu	Asp	Glu	Arg	Leu	Ile	Ala	Tyr	Ile	Lys	Ala	His
			20					25					30		

Gly	Glu	Gly	Cys	Trp	Arg	Ser	Leu	Pro	Lys	Ala	Ala	Gly	Leu	Leu	Arg
		35					40					45			

Cys	Gly	Lys	Ser	Cys	Arg	Leu	Arg	Trp	Ile	Asn	Tyr	Leu	Arg	Pro	Asp
	50					55					60				

Leu	Lys	Arg	Gly	Asn	Phe	Thr	Glu	Glu	Glu	Asp	Glu	Leu	Ile	Ile	Lys
65					70					75					80

Leu	His	Ser	Leu	Leu	Gly	Asn	Lys	Trp	Ser	Leu	Ile	Ala	Gly	Arg	Leu
			85						90					95	

Pro	Gly	Arg	Thr	Asp	Asn	Glu	Ile	Lys	Asn	Tyr	Trp	Asn	Thr	His	Ile
			100					105					110		

Arg	Arg	Lys	Leu	Ile	Asn	Arg	Gly	Ile	Asp	Pro	Thr	Thr	His	Arg	Pro
		115					120					125			

Ile	Gln	Glu	Ser	Ser	Ala	Ser	Gln	Asp	Ser	Lys	Pro	Thr	His	Leu	Glu
	130					135					140				

Ala	Ile	Thr	Ser	Asn	Thr	Ile	Asn	Ile	Ser	Phe	Ala	Ser	Ser	Ser	Ser
145					150					155					160

Thr	Pro	Lys	Met	Glu	Ile	Phe	Gln	Glu	Ser	Thr	Ser	Phe	Pro	Gly	Lys
				165					170					175	

Gln	Glu	Lys	Ile	Ser	Met	Val	Thr	Phe	Lys	Glu	Glu	Lys	Asp	Glu	Cys
			180					185					190		

Pro	Val	Glu	Glu	Asn	Phe	Pro	Asp	Leu	Asn	Leu	Glu	Leu	Arg	Ile	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

195

200

205

Leu Pro Asp Val Val Asp His His His Gln Gly Phe Val Gly Glu Gly
 210 215 220

Lys Thr Thr Thr Pro Arg Arg Cys Phe Lys Cys Ser Leu Gly Thr Ile
 225 230 235 240

Asn Gly Met Glu Cys Arg Cys Gly Arg Met Arg Tyr Asp Val Val Gly
 245 250 255

Gly Ser Lys Gly Ser Gly Lys Gly Ser Asp Met Ser Asn Gly Phe Asp
 260 265 270

Phe Leu Gly Leu Ala Lys Lys Glu Thr Asn Thr Cys Leu Phe Gly Phe
 275 280 285

Arg Ser Leu Glu Met Lys
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<210> 80
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 <212> DNA
 <213> Eucalyptus gunnii

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

<400> 80
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 ccgaaggccg cgggcctcct ccgctgtggc aagagctgcc gcctccggtg gatcaattac 180
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 ccactcttga gattcactgg taggaaaagt gatttgtgtn tggagtgtaa tttgggggtg 660
 aaaaatagcc aaaattgcag atgcagtgtt ggggtgatcg agagtgaac tagtgttggg 720
 tatgacttct tgggcttgaa ggcaagtgtt ttggattata ggagctga 768

<210> 81
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 <212> PRT

<213> Eucalyptus gunnii

<220>

<221> UNSURE

<222> (214)..(214)

<223> Xaa can be any naturally occurring amino acid

<400> 81

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20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60

Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Ile Ile Ile Lys
65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
100 105 110

Arg Arg Lys Leu Leu Asn Arg Gly Ile Asp Pro Ala Thr His Arg Leu
115 120 125

Ile Asn Glu Pro Ala Gln Asp His His Asp Glu Pro Thr Ile Ser Phe
130 135 140

Ala Ala Asn Ser Lys Glu Ile Lys Glu Met Lys Asn Asn Ala Glu Leu
145 150 155 160

Asn Phe Met Cys Asn Leu Glu Glu Ser Ala Asp Val Ala Ser Ser Ala
165 170 175

Arg Glu Arg Cys Pro Asp Leu Asn Leu Glu Leu Gly Ile Ser Pro Pro
180 185 190

Ser His Gln Leu His Gln Pro Glu Pro Leu Leu Arg Phe Thr Gly Arg
195 200 205

Lys Ser Asp Leu Cys Xaa Glu Cys Asn Leu Gly Leu Lys Asn Ser Gln
210 215 220

Asn Cys Arg Cys Ser Val Gly Val Ile Glu Ser Glu Thr Ser Val Gly
225 230 235 240

PF5908220081029_F_60204_PCT_Sequence.txt

Tyr Asp Phe Leu Gly Leu Lys Ala Ser Val Leu Asp Tyr Arg Ser
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<210> 82
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<212> DNA
<213> Zea mays

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cccaaggccg ccggcctcct gcgctgcggc aagagctgcc gcctccgctg gatcaactac 180
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ctgcacagcg tcctcggcaa caagtgggtcc ctgatcgccg gaaggctgcc cggcaggacg 300
gacaacgaga tcaagaacta ctggaacacg cacatccgga ggaagctgct gagcaggggg 360
atcgacccgg tgacgcaccg cccggtcacg gagcaccacg cgtccaacat caccatatcg 420
ttcgagacgg aagtggccgc cgctgcccgt gatgataaga agggcgccgt cttccggttg 480
gaggacgagg aggaggagga gcgcaacaag gcgacgatgg tcgtcggccg cgaccggcag 540
agccagagcc acagccacag ccaccccgcc ggcgagtggg gccaggggaa gaggccgctc 600
aagtgccccg acctcaacct ggacctctgc atcagcccg cgtgccagga ggaggaggag 660
atggaggagg ctgcgatgag agtgagaccg gcggtgaagc gggaggccgg gctctgcttc 720
ggctgcagcc tggggctccc caggaccgcg gactgcaagt gcagcagcag cagcttcctc 780
gggctcagga ccgccatgct cgacttcaga agcctcgaga tgaaatga 828

<210> 83
<211> 275
<212> PRT
<213> Zea mays

<400> 83
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Trp Thr Lys Glu Glu Asp Glu Arg Leu Val Ala His Ile Arg Ala His
20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60

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

Leu His Ser Val Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
85 90 95

PF5908220081029_F_60204_PCT_Sequence.txt

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
100 105 110

Arg Arg Lys Leu Leu Ser Arg Gly Ile Asp Pro Val Thr His Arg Pro
115 120 125

Val Thr Glu His His Ala Ser Asn Ile Thr Ile Ser Phe Glu Thr Glu
130 135 140

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

Glu Asp Glu Glu Glu Glu Glu Arg Asn Lys Ala Thr Met Val Val Gly
165 170 175

Arg Asp Arg Gln Ser Gln Ser His Ser His Ser His Pro Ala Gly Glu
180 185 190

Trp Gly Gln Gly Lys Arg Pro Leu Lys Cys Pro Asp Leu Asn Leu Asp
195 200 205

Leu Cys Ile Ser Pro Pro Cys Gln Glu Glu Glu Glu Met Glu Glu Ala
210 215 220

Ala Met Arg Val Arg Pro Ala Val Lys Arg Glu Ala Gly Leu Cys Phe
225 230 235 240

Gly Cys Ser Leu Gly Leu Pro Arg Thr Ala Asp Cys Lys Cys Ser Ser
245 250 255

Ser Ser Phe Leu Gly Leu Arg Thr Ala Met Leu Asp Phe Arg Ser Leu
260 265 270

Glu Met Lys
275

<210> 84
<211> 651
<212> DNA
<213> Dendrobium sp.

<400> 84
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cctaaggcgg caggtctcct tcgttggtggg aagagttgcc gccttcgatg gatcaattac 180
ctccgtcctg atcttaagcg cggaaacttt accgaggagg aagatgaact catcatcaag 240
cttcatagtt tacttggaat taaatggctg ttgatagcgg ggagggttaca agggaggacg 300
gacaacgaga tcaagaacta ctggaacacg catattcgtc ggaaactggt gagtaggggg 360
atagatccga cgacgcaccg ccctcttcac ggccaagccg acgcatcctt cgtgaatgag 420

PF5908220081029_F_60204_PCT_Sequence.txt

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ttggagctct gcataagccc tcctctacag aagcaggagg attcagaaga agatatgatg 600
agagaagagt ttggcctttg cttcacaac gggttgctgg aattcagatg a 651

<210> 85
<211> 216
<212> PRT
<213> Dendrobium sp.

<400> 85

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

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60

Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
85 90 95

Gln Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
100 105 110

Arg Arg Lys Leu Leu Ser Arg Gly Ile Asp Pro Thr Thr His Arg Pro
115 120 125

Leu His Gly Gln Ala Asp Ala Ser Phe Val Asn Glu Val Glu Lys Val
130 135 140

Val Ser Phe Arg Arg Arg Glu Asp Glu Asn Lys Ser Ser Asn Ser Ser
145 150 155 160

Ser Ser Asn Ser Arg Ser Asn Ser Glu Glu Ala Lys Arg Trp Arg Cys
165 170 175

Pro Asp Leu Asn Leu Glu Leu Cys Ile Ser Pro Pro Leu Gln Lys Gln
180 185 190

Glu Asp Ser Glu Glu Asp Met Met Arg Glu Glu Phe Gly Leu Cys Phe
195 200 205

Thr Asn Gly Leu Leu Glu Phe Arg
210 215

<210> 86
<211> 798
<212> DNA
<213> Triticum aestivum

<400> 86
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gaggacgacc ggctcaccgc ctacatcaag gcgcacggcg agggctgctg gcgctccctg 120
cccaaggccg cgggggttgct ccgctgcggc aagagctgcc gcctccgctg gatcaactac 180
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ctccacagcc tcctgggcaa caaatggtct ctgatagccg ggagactccc agggaggacg 300
gacaacgaga tcaagaacta ctggaacacg cacatcagga ggaagctcac gagccggggg 360
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tccttcgaga cggcgagag ggacgacaag ggcgccgtgt tccggcgaga cgccgagccc 480
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gtggtgaaga gggaggccgt cgtgggcctc tgcttcagct gcagcatggg gctccccagg 720
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agcatcgaga tgaaatga 798

<210> 87
<211> 265
<212> PRT
<213> Triticum aestivum

<400> 87

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Trp Thr Lys Glu Glu Asp Asp Arg Leu Thr Ala Tyr Ile Lys Ala His
20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60

Leu Lys Arg Gly Asn Phe Ser Asp Glu Glu Asp Glu Leu Ile Ile Lys
65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
85 90 95

PF5908220081029_F_60204_PCT_Sequence.txt

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
100 105 110

Arg Arg Lys Leu Thr Ser Arg Gly Ile Asp Pro Val Thr His Arg Ala
115 120 125

Ile Asn Ser Asp His Ala Ala Ser Asn Ile Thr Ile Ser Phe Glu Thr
130 135 140

Ala Gln Arg Asp Asp Lys Gly Ala Val Phe Arg Arg Asp Ala Glu Pro
145 150 155 160

Thr Lys Val Ala Ala Ala Ala Ala Ile Thr His Val Asp His His
165 170 175

His His His Arg Ser Asn Pro Leu His Gln Met Glu Trp Gly Gln Gly
180 185 190

Lys Pro Leu Lys Cys Pro Asp Leu Asn Leu Asp Leu Cys Ile Ser Pro
195 200 205

Pro Ser His Glu Asp Pro Met Val Asp Thr Lys Pro Val Val Lys Arg
210 215 220

Glu Ala Val Val Gly Leu Cys Phe Ser Cys Ser Met Gly Leu Pro Arg
225 230 235 240

Ser Ala Asp Cys Lys Cys Ser Ser Phe Met Gly Leu Arg Thr Ala Met
245 250 255

Leu Asp Phe Arg Ser Ile Glu Met Lys
260 265

<210> 88
<211> 804
<212> DNA
<213> Hordeum vulgare

<400> 88
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cccaaggccg ccggcctgct ccgctgcggc aagagctgcc gcctccgctg gatcaactac 180
ctccgccccg acctcaagcg cggcaacttc agccacgagg aggacgagct catcatcaag 240
ctccacagcc tcctgggaaa caaatggtcc ctgatagccg ggagactgcc ggggaggacg 300
gacaacgaga tcaagaacta ctggaacacg cacatccgga ggaagctgac gagccggggg 360
atcgacccgg tgaccaccg cgcgatcaac agcgaccacg ccgctgcca catcaccata 420
tcctttgagt cggcgagag ggacgacaag ggcgccgtgt tccggcgaga cgccgagccc 480
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PF5908220081029_F_60204_PCT_Sequence.txt

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 agggaggccg gcgtcggcgt cggcgtggtg ggcctctgct tcagctgcag catggggctc 720
 cccaggagct cggactgcaa gtgcagcagc ttcatggggc tccggaccgc catgctcgac 780
 ttcagaagca tcgagatgaa atga 804

<210> 89
 <211> 267
 <212> PRT
 <213> Hordeum vulgare

<400> 89

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Trp Thr Lys Glu Glu Asp Asp Arg Leu Thr Ala Tyr Ile Lys Ala His
 20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60

Leu Lys Arg Gly Asn Phe Ser His Glu Glu Asp Glu Leu Ile Ile Lys
 65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110

Arg Arg Lys Leu Thr Ser Arg Gly Ile Asp Pro Val Thr His Arg Ala
 115 120 125

Ile Asn Ser Asp His Ala Ala Ser Asn Ile Thr Ile Ser Phe Glu Ser
 130 135 140

Ala Gln Arg Asp Asp Lys Gly Ala Val Phe Arg Arg Asp Ala Glu Pro
 145 150 155 160

Ala Lys Ala Ala Ala Ala Ala Ala Ala Ile Ser His His Val Asp His
 165 170 175

His His Arg Ser Asn Pro Gln Leu Asp Trp Gly Gln Gly Lys Pro Leu
 180 185 190

Lys Cys Pro Asp Leu Asn Leu Asp Leu Cys Ile Ser Pro Pro Ile His
 195 200 205

PF5908220081029_F_60204_PCT_Sequence.txt

Glu Asp Pro Met Val Asp Thr Lys Pro Val Val Lys Arg Glu Ala Gly
210 215 220

Val Gly Val Gly Val Val Gly Leu Cys Phe Ser Cys Ser Met Gly Leu
225 230 235 240

Pro Arg Ser Ser Asp Cys Lys Cys Ser Ser Phe Met Gly Leu Arg Thr
245 250 255

Ala Met Leu Asp Phe Arg Ser Ile Glu Met Lys
260 265

<210> 90
<211> 813
<212> DNA
<213> Tradescantia fluminensis

<400> 90
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cccaagtccg caggccttct tcgttgcggg aagagctgtc gtcttcgatg gattaattac 180
cttaggcctg acctcaagag aggcaacttc accgaagaag aggatgaagt tatcatcaaa 240
cttcatgcct tactgggaaa caagtgggtc ctgatagcag gcagattgcc gggaagaacc 300
gacaatgaga ttaagaacta ctggaacaca cacataaaac gaaagctaata cagtcgagga 360
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gtatcaccat attttcagcc tatttgcttg tgttatcgtc ttgggtttttc gagaactgag 720
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<210> 91
<211> 270
<212> PRT
<213> Tradescantia fluminensis

<400> 91
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20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ser Ala Gly Leu Leu Arg
35 40 45

PF5908220081029_F_60204_PCT_Sequence.txt

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60

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

Leu His Ala Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
100 105 110

Lys Arg Lys Leu Ile Ser Arg Gly Ile Asp Pro Gln Thr His Arg Pro
115 120 125

Val Asn Ser Gly Ala Gln Phe Thr Ile Ser Ser Ala Asn Asn Gln Ala
130 135 140

Asn Ser Thr Lys Ile Pro Val Asn Glu Ala Leu Lys Gln Ser Thr Asp
145 150 155 160

Ser Ser Ser Ser Gln Asp Met Gln Ser Ser Asn Ser Val Leu Asp Val
165 170 175

Val Glu Arg Cys Pro Asp Leu Asn Leu Asp Leu Ser Ile Asn Ile Ala
180 185 190

Tyr Ser Thr Asp Arg Lys Pro Phe Ser Ser Ser Thr Glu Met Gln Ile
195 200 205

Thr Pro Ala Ala Thr Glu Ala Thr Thr Pro Thr Ser Val Ser Pro Tyr
210 215 220

Phe Gln Pro Ile Cys Leu Cys Tyr Arg Leu Gly Phe Ser Arg Thr Glu
225 230 235 240

Ala Cys Ser Cys Lys Ala Ile Ser Asn Ser Asn Ser Gln Asn Val Phe
245 250 255

Arg Tyr Tyr Arg Pro Leu Lys Glu Glu Gly His Gln Thr Asn
260 265 270

<210> 92
<211> 774
<212> DNA
<213> Picea glauca

<400> 92
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gaggacgacc gcctcatcgc ccacattcga gccacggcg aaggttgctg gcgctcgctt 120
cccaaggccg cagggtgat gcgatgcggg aagagctgca ggctccgatg gataaactac 180
Seite 71

PF5908220081029_F_60204_PCT_Sequence.txt

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gacaacgaga taaagaacta ctggaatact cacatcaaga gaaaattgct aaacaaggga 360
ctcgaccccc agtcccatcg ccccttggc caggtccaca gcagcaacac tacctgttcc 420
tctctgcccc cccctgagca cgaaattctg gcgttccaga gcccgagaac gccggagata 480
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cccgccgcaa gcagggttc gagcgctgat agaaccgtgg attcaaaacc taattctggc 660
agcgaactgt gctgtcccat ggggctgcaa gtaaattatg gcgcgcaatg cgagaacaga 720
tatagtgaag agaatgcttc aggtttctcg agtcattaca ggcttgtctt atag 774

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<210> 93
 <211> 257
 <212> PRT
 <213> Picea glauca

<400> 93

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

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PF5908220081029_F_60204_PCT_Sequence.txt

Ala Asp Phe Phe Gln Tyr Glu Arg Ser Glu Ser Ser Pro Ile Glu Pro
165 170 175

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

Ile Ser Leu Pro Val His Ser Ala Pro Ala Ala Ser Arg Ala Ser Ser
195 200 205

Val Asp Arg Thr Val Asp Ser Lys Pro Asn Ser Gly Ser Glu Leu Cys
210 215 220

Cys Pro Met Gly Leu Gln Val Asn Tyr Gly Ala Gln Cys Glu Asn Arg
225 230 235 240

Tyr Ser Glu Glu Asn Ala Ser Gly Phe Ser Ser His Tyr Arg Leu Val
245 250 255

Leu

<210> 94
<211> 702
<212> DNA
<213> Pinus taeda

<400> 94
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cccaaggccg cagggttgct gcggtgcggg aaaagttgca ggctccgatg gataaactac 180
ctgctccccg atttgaagcg tggaaacttc tctgaacaag aagacgagct catcatcaaa 240
ttccactccc gtctcgggaa caaatggtct cttattgcac ggattttgcc cgggcggacg 300
gacaacgaga taaagaacca ctggaacacg cacatcaaga aaaaattggt gagaatggga 360
ctcgatccca agtctcatct ccacttgggt gaaccccgctg acagcaacac tacctacacc 420
gttctggcct ctccaagca caaaattccg ccgttccaga gcccgagaac cccggacata 480
gcagatttct ttcaatacga ccgctctgga agctcgacaa tggagctcgt cgcttctaaa 540
gccgaagagc atccggaact gaatcttgat ttgtctataa gcttgccgctc tcattcgacc 600
cccgccacaa ccagagcttc gacagtccat agaaccgtag actcaaactc taattctgga 660
agtggacttt ggtgtctcac agggatggaa gcgatatcgt ga 702

<210> 95
<211> 233
<212> PRT
<213> Pinus taeda

<400> 95

Met Gly Arg Thr Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
1 5 10 15

PF5908220081029_F_60204_PCT_Sequence.txt

Trp Thr Gln Glu Glu Asp Ala Arg Leu Val Ala His Ile Gln Ala His
20 25 30

Gly Glu Gly Gly Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60

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

Phe His Ser Arg Leu Gly Asn Lys Trp Ser Leu Ile Ala Arg Ile Leu
85 90 95

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

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

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

Pro Lys His Lys Ile Pro Pro Phe Gln Ser Pro Arg Thr Pro Asp Ile
145 150 155 160

Ala Asp Phe Phe Gln Tyr Asp Arg Ser Gly Ser Ser Thr Met Glu Leu
165 170 175

Val Ala Ser Lys Ala Glu Glu His Pro Glu Leu Asn Leu Asp Leu Ser
180 185 190

Ile Ser Leu Pro Ser His Ser Thr Pro Ala Thr Thr Arg Ala Ser Thr
195 200 205

Val His Arg Thr Val Asp Ser Asn Ser Asn Ser Gly Ser Gly Leu Trp
210 215 220

Cys Leu Thr Gly Met Glu Ala Ile Ser
225 230

<210> 96
<211> 807
<212> DNA
<213> Gossypium raimondii

<400> 96
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aggctgctgg cgttccctcc ccaaagctgc tgggctgctt agatgtggta agagttgcag 120
attaagatgg ataaactact tgaggcctga tcttaagaga ggaaatttca ctgaggaaga 180

PF5908220081029_F_60204_PCT_Sequence.txt

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agatgagctt atcatcaagc ttcacagttt acttggaac aaatgggtcat tgattgctgg 240
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aaagcttata agcagaggaa ttgatccaca aactcatcgt cctctcaatc aaaccgcca 360
taccaacacg gtcacagccc ccaccgaatt ggatttcaga aacatgccta catccgtttc 420
caaatccagt tccatcaaaa acccatctct ggatttcaat tacaatgaat ttcaattcaa 480
gtccaacaca gattcccttg aagaacccaa ctgtacagcc agcagtggaa tgactacaga 540
tgaagaacaa caagaacagc tgcacaagca gcagcaatac gatccaagca atgggcaaga 600
cttaaatttg gagctgtcga ttgggattgt ttcagctgac tcatctcggg tatcaagtgc 660
caactcggcc gagtcgaaac caaaggtaga taacaacaat ttccagtttc ttgaacaagc 720
tatggtggct aaggcggtat gtttgtgttg gcaattaggt tttggaacaa gtgaaatttg 780
taggaactgt caaaattcaa attcaaa 807

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<210> 97
 <211> 268
 <212> PRT
 <213> Gossypium raimondii
 <400> 97

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

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PF5908220081029_F_60204_PCT_Sequence.txt

Ser Asn Thr Asp Ser₁₆₅ Leu Glu Glu Pro Asn₁₇₀ Cys Thr Ala Ser Ser₁₇₅ Gly

Met Thr Thr Asp₁₈₀ Glu Glu Gln Gln Glu₁₈₅ Gln Leu His Lys Gln₁₉₀ Gln Gln

Tyr Asp Pro₁₉₅ Ser Asn Gly Gln Asp₂₀₀ Leu Asn Leu Glu Leu₂₀₅ Ser Ile Gly

Ile Val Ser Ala Asp Ser Ser₂₁₅ Arg Val Ser Ser Ala₂₂₀ Asn Ser Ala Glu

Ser Lys Pro Lys Val Asp₂₃₀ Asn Asn Asn Phe Gln₂₃₅ Phe Leu Glu Gln Ala₂₄₀

Met Val Ala Lys Ala₂₄₅ Val Cys Leu Cys Trp₂₅₀ Gln Leu Gly Phe Gly₂₅₅ Thr

Ser Glu Ile Cys₂₆₀ Arg Asn Cys Gln Asn₂₆₅ Ser Asn Ser

<210> 98
<211> 793
<212> DNA
<213> Gossypioides kirkii

<400> 98
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gctgctggcg ttccctcccc aaagctgctg ggctgcttag atgtggtgtaag agttgcagat 120
taagatggat aaactacttg aggcctgatac ttaagagagg aaatttcact gaagaagaag 180
atgagcttat catcaagctt cacagttttac tcggaacaaa atgggtctttg attgctggaa 240
gattaccagg aagaacagat aatgagataa agaactactg gaacacacac atcaaaagaa 300
agcttataag cagaggaatt gatccacaaa ctcatcgatc tctcaatcaa accgccaata 360
ccaacacagt cacagcccc accgaattgg atttcagaaa cagccccaca tcagttttcca 420
aatccagttc catcaaaaac ccaaatttca attacaatga atttcaattc aagtccaaca 480
cagattccct tgaagaacc aactgtacag ccagcagtg catgactaca gatgaagaac 540
aacaagaaca gctgcacaag aagcagcaac acgatccatg taacgggcaa gacctaaatt 600
tgagagctatc gattgggatt gtttcagctg actcatctcg gggtttcaagt gccaaactcg 660
cggagtcgaa accaaagcta gataacaaca atttccagtt tctggaacaa gctatggtgg 720
caaaggccgt atgtttgtgt tggcaattag gtttccgaac aagtgaatt ttaggaact 780
gtcaaaattc aaa 793

<210> 99
<211> 263
<212> PRT
<213> Gossypioides kirkii

<400> 99

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

PF5908220081029_F_60204_PCT_Sequence.txt

<210> 100
<211> 565
<212> DNA
<213> Sorghum bicolor

<400> 100
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cccaaggcgg cgggcctgct gcgctgcggc aagagctgcc gcctccggtg gatcaactac 180
ctccgccccg acctcaagcg cggcaacttc acccaggagg aagacgaact catcatcaag 240
ctccaccaga tcctcggaag caagtggctg ctgatcgccg ggcggctgcc ggggaggacg 300
gacaacgaga tcaagaacta ctggaacacg ccatttcaa gcgcaagctc atcgcccgcg 360
gcatcgaccc acggacgcac cagccggcga gtgcaggcgc cgttgctccc gccccggcg 420
ccgccgcttt cgccgccgcg ccaagcaagc cattcgccag catggcgacg acaaggcggc 480
ggcgggtggt gcggtccaac cggctgcagc ttgcgagaca agcaagcggg gacgatgaca 540
gcacgttccg ggtcgttccg tgccc 565

<210> 101
<211> 188
<212> PRT
<213> Sorghum bicolor

<400> 101
Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
1 5 10 15
Trp Thr Lys Glu Glu Asp Gln Arg Leu Val Ala Tyr Ile Lys Ala His
20 25 30
Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
35 40 45
Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60
Leu Lys Arg Gly Asn Phe Thr Gln Glu Glu Asp Glu Leu Ile Ile Lys
65 70 75 80
Leu His Gln Ile Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
85 90 95
Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr Pro Ile
100 105 110
Gln Ser Ala Ser Ser Ser Pro Ala Ala Ser Thr His Gly Arg Thr Ser
115 120 125
Arg Arg Val Gln Ala Pro Leu Leu Pro Pro Pro Ala Pro Pro Leu Ser
130 135 140

PF5908220081029_F_60204_PCT_Sequence.txt

Pro Pro Arg Gln Ala Ser His Ser Pro Ala Trp Arg Arg Gln Gly Gly
145 150 155 160

Gly Gly Trp Cys Gly Pro Thr Gly Cys Ser Leu Arg Asp Lys Gln Ala
165 170 175

Val Thr Met Thr Ala Arg Ser Gly Ser Phe Arg Ala
180 185

<210> 102
<211> 797
<212> DNA
<213> Gossypium herbaceum

<400> 102
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cgttccctcc ccaaagctgc tgggctgctt agatgtggta agagttgcag attaagatgg 120
ataaactact tgaggcctga tcttaagaga ggaaatttca ctgaagaaga agatgagctt 180
atcatcaagc ttcacagttt acttggaac aaatgggtcat tgattgctgg aagattacca 240
ggaagaacag ataatgagat aaagaactac tggaacacac acatcaaaag aaagcttata 300
agcagaggaa ttgatccaca aactcatcgt cctctcaatc aaacggccaa taccaacaca 360
gtcacagccc ccaccgaatt ggatttcaga aactcgccca catccgtttc caaatccagt 420
tccatcaaaa acccgctctt ggatttcaat tacaatgaat ttcaattcaa gtccaacaca 480
gattcccttg aagaaccaa ctgtacagcc agcagtggca tgactacaga tgaagaacaa 540
caagaacagc tgcacaagaa gcagcaatac ggtccgagca atgggcaaga cataaatttg 600
gagctgtcga ttgggattgt ttcagctgac tcatctcggg tatcaagtgc caactcggcc 660
gagtcgaaac caaaggtaga taacaacaat ttccagtttc ttgaacaagc tatggtggct 720
aaggcgggtat gtttgtgttg gcaattaggt tttggaacaa gtgaaatttg taggaactgt 780
caaaattcaa attcaaa 797

<210> 103
<211> 265
<212> PRT
<213> Gossypium herbaceum

<400> 103
Thr Lys Glu Glu Asp Gln Arg Leu Ile Asn Tyr Ile Arg Val His Gly
1 5 10 15

Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg Cys
20 25 30

Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp Leu
35 40 45

Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys Leu
Seite 79

50

55

60

His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu Pro
65 70 75 80

Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile Lys
85 90 95

Arg Lys Leu Ile Ser Arg Gly Ile Asp Pro Gln Thr His Arg Pro Leu
100 105 110

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

Phe Arg Asn Ser Pro Thr Ser Val Ser Lys Ser Ser Ser Ile Lys Asn
130 135 140

Pro Ser Leu Asp Phe Asn Tyr Asn Glu Phe Gln Phe Lys Ser Asn Thr
145 150 155 160

Asp Ser Leu Glu Glu Pro Asn Cys Thr Ala Ser Ser Gly Met Thr Thr
165 170 175

Asp Glu Glu Gln Gln Glu Gln Leu His Lys Lys Gln Gln Tyr Gly Pro
180 185 190

Ser Asn Gly Gln Asp Ile Asn Leu Glu Leu Ser Ile Gly Ile Val Ser
195 200 205

Ala Asp Ser Ser Arg Val Ser Ser Ala Asn Ser Ala Glu Ser Lys Pro
210 215 220

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

Lys Ala Val Cys Leu Cys Trp Gln Leu Gly Phe Gly Thr Ser Glu Ile
245 250 255

Cys Arg Asn Cys Gln Asn Ser Asn Ser
260 265

<210> 104
<211> 2162
<212> DNA
<213> Physcomitrella patens

<400> 104
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aggtagtaca cagaccacag tgataggagt tattctgaga gcgataaaga atctgcgaga 120
gagccattga ggcatgggga ggaaaccatg ctgtgagaaa gtcgggctga ggagagggcc 180
atggacgtcc gaagaggatc agaagctagt ctctcacatc accaacaatg gcctcagctg 240

PF5908220081029_F_60204_PCT_Sequence.txt

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tctgattctt gatctacatg ccaccttggg aaacaggtgg tctcggattg cggcgcaact	420
cccaggccgc acggataacg aaatcaagaa ctattggaac acgagactaa agaagaggct	480
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caccgaggat gacactgatg atgaaggcgg ggactcctcc gacgttacta tgagcgacgc	600
ttctaagtcc gagaagagat ccaagaaaa atcgaaaccc aaggagactg tcaaggttcg	660
tcaacccaaa ggtccaaagc cagccccgca gctcaagatg tgtcagagtg atgaaggacc	720
agtgctactt aagggtgccta aggctccgaa atcaccatt agtgtaaacc ctggaccggg	780
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tgaagaccat cgagattcga gtgattttat caaggctctc accagtgtgt cttctttccc	900
tgaagctgaa ttatggagtt gcatcaagcc gattacgaat tcgttctcct caactgcgtt	960
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aatgcaattc agttcccagc tgactcatga gattgggcag aattacggtg ggattttcca	1200
ggagacatgt tatcctcaac cagacatggg gatgtcatgg agtatgcatg cagagttgag	1260
ccactgtggg acggagtcct tgttcgctac cccaatccc gctaattgctc ctagtaattt	1320
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catctgctcg agagtgtagt tgtacatgtt cctgctgccag gagagtgatt ttgcaggttt	1560
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accgaagcta tgcaatcact ctaatccatc cggacgaaac atgcttgctt actgcggaga	1680
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ccttaccaga gacaagtttt gaggcagaga attgtgtaaa ttctttcact atgaaaggaa	2040
accgaaagtt actgtggagt gtagttgttg acgaggatgg tttagagcga tcctgtgctt	2100
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aa	2162

<210> 105
<211> 421

<212> PRT

<213> *Physcomitrella patens*

<400> 105

Met Gly Arg Lys Pro Cys Cys Glu Lys Val Gly Leu Arg Arg Gly Pro
 1 5 10 15

Trp Thr Ser Glu Glu Asp Gln Lys Leu Val Ser His Ile Thr Asn Asn
 20 25 30

Gly Leu Ser Cys Trp Arg Ala Ile Pro Lys Leu Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp
 50 55 60

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

Leu His Ala Thr Leu Gly Asn Arg Trp Ser Arg Ile Ala Ala Gln Leu
 85 90 95

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

Lys Lys Arg Leu Arg Ser Gln Gly Leu Asp Pro Asn Thr His Leu Pro
 115 120 125

Leu Glu Asp Ser Lys Leu Asp Asp Thr Glu Asp Asp Thr Asp Asp Glu
 130 135 140

Gly Gly Asp Ser Ser Asp Val Thr Met Ser Asp Ala Ser Lys Ser Glu
 145 150 155 160

Lys Arg Ser Lys Lys Lys Ser Lys Pro Lys Glu Thr Val Lys Val Arg
 165 170 175

Gln Pro Lys Gly Pro Lys Pro Ala Pro Gln Leu Lys Met Cys Gln Ser
 180 185 190

Asp Glu Gly Pro Val Leu Leu Lys Val Pro Lys Ala Pro Lys Ser Pro
 195 200 205

Ile Ser Val Asn Pro Gly Pro Gly Cys Asn Tyr Asp Asp Asp Ser Glu
 210 215 220

His Ser Ser Ser Ser Thr Val Thr Thr Lys Ser His Glu Asp His Arg
 225 230 235 240

Asp Ser Ser Asp Phe Ile Lys Ala Leu Thr Ser Val Ser Ser Phe Pro
 245 250 255

PF5908220081029_F_60204_PCT_Sequence.txt

Glu Ala Glu Leu Trp Ser Cys Ile Lys Pro Ile Thr Asn Ser Phe Ser
260 265 270

Ser Thr Ala Leu Leu Ser Glu Trp Asp Ser Tyr Arg Ala Phe Asp Ser
275 280 285

Ser Leu Phe Pro Ser Ser Tyr Pro Gln Leu Asn Ser Gly Leu Pro Lys
290 295 300

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

Gly Met Leu Pro Ala Tyr Asn Pro Met Gly Met Glu Met Gln Thr Arg
325 330 335

Met Gln Phe Ser Ser Gln Leu Thr His Glu Ile Gly Gln Asn Tyr Gly
340 345 350

Gly Ile Phe Gln Glu Thr Cys Tyr Pro Gln Pro Asp Met Gly Met Ser
355 360 365

Trp Ser Met His Ala Glu Leu Ser His Cys Gly Thr Glu Ser Leu Phe
370 375 380

Ala Thr Pro Asn Pro Ala Asn Ala Pro Ser Asn Phe Glu Glu Val Pro
385 390 395 400

Gln Pro Ser Pro Cys Thr Thr Ser Gln Glu Leu Gln Arg Leu Ala Ala
405 410 415

Leu Leu Asp Leu Ile
420

<210> 106

<211> 1104

<212> DNA

<213> Malus x domestica

<400> 106

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gaagatgcc a tgctagttaa ttatattcag aagcatggac ctggaaattg gagaaacctt 120

ccaaagaatg caggactcca gagatgcggg aagagttgcc gcctcagatg gactaactac 180

cttagacctg atataaagag aggaaggttc tcctttgaag aagaagagac tataatccaa 240

ctacatagca tccttgga aa caagtgg tca gctattgctg ctcgcttgcc aggaaggaca 300

gacaatgaaa taaaaaacta ctggaacacg cacatccgaa aaaggctcct tcgaatggga 360

attgatcccg tgactcatgc tccacgcac gatcttcttg atctgtcctc aattctcagc 420

tcatatgtgt gcaacaaccc agctgctgca ctactcaatt tgtcaaactt gttgaatagt 480

acccatcagc gacaaccact tgttaatcca gaaatgttaa ggctagcaac aagtctgtta 540

tcaatcaaac aagcaaaccc ggaaatgtgt tccaaaatt ataatctcca tcaaaaccag 600

PF5908220081029_F_60204_PCT_Sequence.txt

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atttccaatt ctcaggaaca aaataatcaa gttctccac ctttacaatc caatgatcag 660
tttcaaaatc tcatccaagg gggagacttt tctgctgaca tggcaaaaca tctgatgcaa 720
cagatcaatg tggaagggtt ctcaccaaac atgaccaact tgagctgccc cttttcccaa 780
gaaaacatag tcccccgaa tttgagtgcc gatcatcatc aaacagctgt ctccaagca 840
aactatgtgc cttgcagtac tacttctggt aaccctgggtc ctgattttcc ggaaaattca 900
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acgccttatt cgagcccgac tcctttgaat tcatcaggta catacataaa cagcagcaca 1020
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ttggacatca gtgatcatcat gtaa 1104

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<210> 107
 <211> 367
 <212> PRT
 <213> Malus x domestica

<400> 107

Met Gly Arg Ala Pro Cys Cys Asp Lys Asn Gly Leu Lys Lys Gly Pro
 1 5 10 15

Trp Thr Thr Glu Glu Asp Ala Met Leu Val Asn Tyr Ile Gln Lys His
 20 25 30

Gly Pro Gly Asn Trp Arg Asn Leu Pro Lys Asn Ala Gly Leu Gln Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp
 50 55 60

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

Leu His Ser Ile Leu Gly Asn Lys Trp Ser Ala Ile Ala Ala Arg Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110

Arg Lys Arg Leu Leu Arg Met Gly Ile Asp Pro Val Thr His Ala Pro
 115 120 125

Arg Ile Asp Leu Leu Asp Leu Ser Ser Ile Leu Ser Ser Tyr Val Cys
 130 135 140

Asn Asn Pro Ala Ala Ala Leu Leu Asn Leu Ser Asn Leu Leu Asn Ser
 145 150 155 160

Thr His Gln Arg Gln Pro Leu Val Asn Pro Glu Met Leu Arg Leu Ala
 165 170 175

PF5908220081029_F_60204_PCT_Sequence.txt

Thr Ser Leu Leu Ser Ile Lys Gln Ala Asn Pro Glu Met Cys Ser Gln
180 185 190

Asn Tyr Asn Leu His Gln Asn Gln Ile Ser Asn Ser Gln Glu Gln Asn
195 200 205

Asn Gln Val Leu Pro Pro Leu Gln Ser Asn Asp Gln Phe Gln Asn Leu
210 215 220

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

Gln Ile Asn Val Glu Gly Phe Ser Pro Asn Met Thr Asn Leu Ser Cys
245 250 255

Pro Leu Ser Gln Glu Asn Ile Val Pro Pro Asn Leu Ser Ala Asp His
260 265 270

His Gln Thr Ala Val Ser Gln Ala Asn Tyr Val Pro Cys Ser Thr Thr
275 280 285

Ser Gly Asn Pro Gly Pro Asp Phe Pro Glu Asn Ser Tyr Phe Gln Ser
290 295 300

Phe Asn Tyr Asn Lys Asn His Asp Phe Ser Phe Asp Ser Val Met Ser
305 310 315 320

Thr Pro Tyr Ser Ser Pro Thr Pro Leu Asn Ser Ser Gly Thr Tyr Ile
325 330 335

Asn Ser Ser Thr Glu Asp Glu Lys Glu Ser Tyr Cys Ser Ser Trp Leu
340 345 350

Lys Phe Glu Ile Pro Glu Ser Thr Leu Asp Ile Ser Asp Ile Met
355 360 365

<210> 108
<211> 1167
<212> DNA
<213> Picea mariana

<400> 108
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cttcggccat gtatcaagcg gggaaatatt acagcagatg aagaagaact tattattaga 240
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gacaacgaaa taaagaacta ctggaacact aacttgagca agaaacttgc tgtcagagga 360
atcgatccca agactcataa aaaagtcaca actgacagca ttaacagagc cagtgatcgt 420

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gatcctgatt tcatgcagcc tcagccagtt gtcagctcag aggccggcaa gcaaaccgat 720
gatagtactg tatattgcag cagcgactca gctgctagct gtgccttgat cgaccatttg 780
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<210> 109
 <211> 388
 <212> PRT
 <213> Picea mariana

<400> 109

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

Gly Glu Gly Asn Trp Arg Ser Leu Pro Lys Lys Ala Gly Leu Arg Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Cys
 50 55 60

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

Met His Ala Leu Leu Gly Asn Arg Trp Ser Ile Ile Ala Gly Arg Val
 85 90 95

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

Ser Lys Lys Leu Ala Val Arg Gly Ile Asp Pro Lys Thr His Lys Lys
 115 120 125

Val Thr Thr Asp Ser Ile Asn Arg Ala Ser Asp Arg Phe Asn Gln Arg
 130 135 140

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

<210> 110
 <211> 564
 <212> DNA

<213> Fragaria x ananassa

<400> 110

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gatcagaaac tcattgacta catccaaaaa cacggcgaag gttgctggaa ttcgcttcct      120
aaggctgcag ggttgctgcg ttgtggtaag agttgtcgac tgagatggat aaactatcta      180
cgaccagatc ttaaacgagg aagctttggg gaagatgaag aggatctcat catcaggcct      240
cataaactcc ttgggaatag gtggtcgcta atagctggaa gactgcctgg aaggacagat      300
aacgaagtga agaactactg gaactctcat ttaaagaaga agatactgaa gacaggcact      360
actcttcgtc caaataagcc ccatgagaat aaccatgcac ctaataacaa acttgctcaag      420
ctcttcaata agatggacga tgaggctggt gatgaggtct catcagccga ttctgctgct      480
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<210> 111

<211> 187

<212> PRT

<213> Fragaria x ananassa

<400> 111

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Ser Ile Gln Glu Asp Gln Lys Leu Ile Asp Tyr Ile Gln Lys His Gly
 20          25          30

Glu Gly Cys Trp Asn Ser Leu Pro Lys Ala Ala Gly Leu Arg Arg Cys
 35          40          45

Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp Leu
 50          55          60

Lys Arg Gly Ser Phe Gly Glu Asp Glu Glu Asp Leu Ile Ile Arg Leu
 65          70          75          80

His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro
 85          90          95

Gly Arg Thr Asp Asn Glu Val Lys Asn Tyr Trp Asn Ser His Leu Lys
100          105          110

Lys Lys Ile Leu Lys Thr Gly Thr Thr Leu Arg Pro Asn Lys Pro His
115          120          125

Glu Asn Asn His Ala Pro Asn Asn Lys Leu Val Lys Leu Phe Asn Lys
130          135          140

Met Asp Asp Glu Val Val Asp Glu Val Ser Ser Ala Asp Ser Ala Ala
145          150          155          160
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Gly Cys Leu Val Pro Glu Leu Asn Leu Asp Leu Thr Leu Ser Ile Lys
 165 170 175

Thr Ser Thr Gly Met Ala Asp Pro Gln Val Ala
 180 185

<210> 112
 <211> 1266
 <212> DNA
 <213> Petunia hybrida

<400> 112
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 cctgcaaaag ccggtcttca aagatgtggg aagagttgca ggcttaggtg gactaattac 180
 ttgaggcctg atatcaagag aggaaaattc actttacaag aagaacaaac cattattcaa 240
 ctccatgctc tcttagggaa taggtggctg gctattgcaa ctcacttgcc aaaaagaaca 300
 gacaatgaga taaagaatta ttggaataca catcttaaga aacggctagt aaaaatgggc 360
 attgatccag tgactcaca gcccaagaat gatgccctct tgtcccatga tggatcaatcc 420
 aagaatgcag ctaaccttag ccacatggct cagtgggaga gtgctcggct cgaagccgaa 480
 gctcgactag ttagacaatc caagcttcgg tccaatagtt tccaaaatcc tcttgcttct 540
 catgaattat ttacatctcc tacccttct agtcctctcc acaagccaat tgtcacacct 600
 acaaaggccc ctggatcccc tcgatgtttg gacgtgctta aagcctggaa cgggtgtttgg 660
 accaaaccaa tgaatgatgt tcttcatgcc gatggtagca ctagtgctag tgctactggt 720
 tcagtcaatg cactcggctt ggacctggaa tctcctactt ctacactaag ctactttgaa 780
 aatgcgcaac atatttctac tgggatgatt caagaaaact ctacttcttt attcgaattc 840
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 gaaaattcaa tgtcactcac ttcaacactt caagatttga ctatgccaat ggacactaca 1020
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 ttctaa 1266

<210> 113
 <211> 421
 <212> PRT
 <213> Petunia hybrida

<400> 113
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 Seite 89

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

PF5908220081029_F_60204_PCT_Sequence.txt

Glu Gly Gly Ile Met Asn Glu Glu Ser Glu Glu Asp Trp Lys Gly Phe
 290 295 300
 Gly Asn Ser Ser Thr Gly His Leu Pro Glu Tyr Lys Asp Gly Ile Asn
 305 310 315 320
 Glu Asn Ser Met Ser Leu Thr Ser Thr Leu Gln Asp Leu Thr Met Pro
 325 330 335
 Met Asp Thr Thr Trp Thr Ala Glu Ser Leu Arg Ser Asn Ala Glu Asp
 340 345 350
 Ile Ser His Gly Asn Asn Phe Val Glu Thr Phe Thr Asp Leu Leu Leu
 355 360 365
 Ser Thr Ser Gly Asp Gly Gly Leu Ser Gly Asn Gly Thr Asp Ser Asp
 370 375 380
 Asn Gly Gly Gly Ser Gly Asn Asp Pro Ser Glu Thr Cys Gly Asp Asn
 385 390 395 400
 Lys Asn Tyr Trp Asn Ser Ile Phe Asn Leu Val Asn Ser Ser Pro Ser
 405 410 415
 Asp Ser Ala Met Phe
 420

<210> 114
 <211> 1047
 <212> DNA
 <213> Lotus japonicus

<400> 114
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 ccgaagcttg caggactgaa caggtgcggg aagagttgca ggctaaggtg gactaactac 180
 ttgaggcctg atattaaaag aggaaagttc actgaggaag aagagcaact catcatcaat 240
 ttacatgctg ttcttgggaa taagtgttct gccatagcag gtcatttgcc agggaggact 300
 gataatgaaa tcaagaattt ctggaacacc catttgaaga aaaagcttct gcaaatgggg 360
 ttagatccag tctcatcg tccaagatta gatcacctta atcttctatc caatctccaa 420
 cagttcctag ctgccacaaa catggtcact agtttcacaa acactttgga ttctaattgct 480
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 cttcaagttc ttggaaccaa tcctgcctca aacttgagc tacttaatca acttggaaca 600
 tcatttcaa ttccagacac ttttcttcat gaagctttag gattgaatca atctaagctc 660
 caagaacttt ataagagttc aattggtttt ctttctcatc aaaatctgtc taatttgcaa 720
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actataccat taaattcact tccaaatctg gtttcagcat cacctcaatg ttccactgtc 900
aaggaaatgg aaaacaaggt gaatccaaat gagtgtctcca acccttcttc cacttcaacc 960
acctttgaaa tgtggggaga tttcatgtgt gaggaagtaa acgatgatta ttggaaagac 1020
cttatagacc aagagtctaa ccggttaa 1047

<210> 115
<211> 348
<212> PRT
<213> Lotus japonicus

<400> 115

Met Gly Arg Thr Pro Cys Cys Asp Glu Ile Gly Leu Lys Lys Gly Pro
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Trp Thr Pro Glu Glu Asp Ala Ile Leu Val Asp Tyr Ile Gln Lys His
20 25 30

Gly His Gly Ser Trp Arg Ala Leu Pro Lys Leu Ala Gly Leu Asn Arg
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp
50 55 60

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

Leu His Ala Val Leu Gly Asn Lys Trp Ser Ala Ile Ala Gly His Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Asn Thr His Leu
100 105 110

Lys Lys Lys Leu Leu Gln Met Gly Leu Asp Pro Val Thr His Arg Pro
115 120 125

Arg Leu Asp His Leu Asn Leu Leu Ser Asn Leu Gln Gln Phe Leu Ala
130 135 140

Ala Thr Asn Met Val Thr Ser Phe Thr Asn Thr Leu Asp Ser Asn Ala
145 150 155 160

Ala Leu Arg Leu Gln Ser Asp Ala Thr Gln Leu Ala Lys Leu Gln Leu
165 170 175

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

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

PF5908220081029_F_60204_PCT_Sequence.txt

Leu His Glu Ala Leu Gly Leu Asn Gln Ser Lys Leu Gln Glu Leu Tyr
 210 215 220

Lys Ser Ser Ile Gly Phe Pro Ser His Gln Asn Leu Ser Asn Leu Gln
 225 230 235 240

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

Ser Thr Ile Asn Ser Cys Met Gln Ser Arg Lys Val Val Asp Glu Gln
 260 265 270

Leu Asp Ala Thr Asn Ser Ser Ser Thr Ile Pro Leu Asn Ser Leu Pro
 275 280 285

Asn Leu Val Ser Ala Ser Pro Gln Cys Ser Thr Val Lys Glu Met Glu
 290 295 300

Asn Lys Val Asn Pro Asn Glu Cys Ser Asn Pro Ser Ser Thr Ser Thr
 305 310 315 320

Thr Phe Glu Met Trp Gly Asp Phe Met Cys Glu Glu Val Asn Asp Asp
 325 330 335

Tyr Trp Lys Asp Leu Ile Asp Gln Glu Ser Asn Arg
 340 345

<210> 116
 <211> 1128
 <212> DNA
 <213> Populus x canescens

<400> 116
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 ccaaagaatg ctgagttgca gaggtgtgga aagagttgtc gtcttcgttg gactaactat 180
 ttgaggcctg atatcaagag aggtcggttt tctttcgagg aagaagagac aataattcag 240
 ctacatggta tattgggaaa caagtgggtc gccattgctg ctcggctgcc tggaagaacc 300
 gacaacgaaa tcaagaacta ctggaacaca cacatcagga agaggcttct gagaatggga 360
 atcgatccag tgactcatag tccaaggctt gatcttctag acctctctc gatcctcaac 420
 tcacctctt acgactcctc caggatgaac atgtcaagaa ttcttgaggt tcaacctcta 480
 ggcgatccag aactcttaag gctagccaca tctctcttat cttctcaacg tgaccaaacc 540
 caagattttg caatcccaa tggtcatcaa gaaaaccatc tttccagccc tcaagtccat 600
 caaaaccaga accaatcgat aattcatcaa gtaaccagt ttcaaccgc aggtcaagaa 660
 atgcctgcgt gactgcatt gactaccacc ctttgtgtaa ctttttctaa tgaagcacag 720
 caaatggacc ccaacggaga ccaataccac ttaagcacca ttaccacctt tagctctcca 780

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<210> 117
 <211> 375
 <212> PRT
 <213> Populus x canescens
 <400> 117

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 1 5 10 15

Trp Thr Pro Asp Glu Asp Gln Lys Leu Ile Gly Tyr Ile Gln Lys His
 20 25 30

Gly Tyr Gly Asn Trp Arg Thr Leu Pro Lys Asn Ala Glu Leu Gln Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp
 50 55 60

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

Leu His Gly Ile Leu Gly Asn Lys Trp Ser Ala Ile Ala Ala Arg Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110

Arg Lys Arg Leu Leu Arg Met Gly Ile Asp Pro Val Thr His Ser Pro
 115 120 125

Arg Leu Asp Leu Leu Asp Leu Ser Ser Ile Leu Asn Ser Pro Leu Tyr
 130 135 140

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

Gly Asp Pro Glu Leu Leu Arg Leu Ala Thr Ser Leu Leu Ser Ser Gln
 165 170 175

Arg Asp Gln Thr Gln Asp Phe Ala Ile Pro Asn Gly His Gln Glu Asn
 180 185 190

PF5908220081029_F_60204_PCT_Sequence.txt

His Leu Ser Ser Pro Gln Val His Gln Asn Gln Asn Gln Ser Ile Ile
195 200 205

His Gln Ala Asn Gln Phe Gln Pro Ala Gly Gln Glu Met Pro Ala Cys
210 215 220

Thr Ala Leu Thr Thr Thr Pro Cys Val Thr Phe Ser Asn Glu Ala Gln
225 230 235 240

Gln Met Asp Pro Asn Gly Asp Gln Tyr His Leu Ser Thr Ile Thr Thr
245 250 255

Phe Ser Ser Pro Asn Ser Gln Val Ser Thr His Asp Gln Trp Gln Ser
260 265 270

Asn Arg Met Gly Ser Asn Leu Ser Glu Asp Tyr Tyr Val Pro Ala Val
275 280 285

Ser Ser Tyr Asn Ser Ala Asp Asn Cys Arg Gly Thr Asp Leu Val Asp
290 295 300

Pro Ser Ser Glu Ala Ser Thr Phe Ile Ser Asn Asn Ser Asn Gln Thr
305 310 315 320

Phe Gly Phe Ala Ser Val Leu Ser Thr Pro Ser Ser Ser Pro Ala Pro
325 330 335

Leu Asn Ser Asn Ser Thr Tyr Ile Asn Cys Ser Ser Thr Glu Asp Glu
340 345 350

Arg Asp Ser Tyr Cys Ser Asn Phe Leu Lys Phe Glu Ile Pro Asp Ile
355 360 365

Leu Asp Val Ser Asn Phe Met
370 375

<210> 118
<211> 1128
<212> DNA
<213> Daucus carota

<400> 118
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gaagatcaga aactcttggc ttacattgaa gaacatggtc atggtagctg gcgcgccttg 120
ccttctaaag ccgggcttca gagatgcgga aaaagctgca gactgagatg gactaattat 180
ctgagacctg atatcaagag aggcaagttc agtctgcagg aagaacaaac aatcattcaa 240
cttcatgctc tcttgggaaa caggtggtct gccatagcga ctcaattgcc gaaaagaact 300
gacaacgaga tcaaaaacta ctggaacact catctcaaga aaagattaac caaatggga 360
atcgatcccc tcaactcaca gcctaaaaac gatgccatct tgtcctcaca cgatgggtcac 420
ctcaaaagca cggctaattct cagccacatg gcacaatggg agagtgctcg cctcgaggcc 480

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aaggcatgga acggcgtttg gactagtaac aacgaagccg gaggaagaag tagtggtttt      660
gttggcaatg gcattggcca ccatgagtct cctacatcaa ctactgttag ttacgatatt      720
acaaatggtg tggagaataa tgcgagtttc aaagaagagg gtaatattga ggatgacgga      780
aagcgattag tttcggaatt taaacaagga atcgagaatg caatttcggg actaagtgat      840
gtgccgatac ttcctatgga aattgcatgg ccaaccgaag aatccctaata aagggttgat      900
catgacgatg atattactga aaatattaat gatcagcatg tccaagtgg taatttcgtg      960
gagaatttca ccgatctttt gctcaacaat tccggcaagg ctgaccggag cccatcggac     1020
ggcgatcaga gtcctgtgat attgctggtg cgccgttgcc aatgggaagt gcgagtggat     1080
acttcaaga taacaagaat tattggaata gtattcttaa tttggtga                     1128

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<210> 119
 <211> 375
 <212> PRT
 <213> Daucus carota

<400> 119

Met Gly Arg Ser Pro Cys Cys Asp Lys Val Gly Leu Lys Lys Gly Pro
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Trp Thr Pro Glu Glu Asp Gln Lys Leu Leu Ala Tyr Ile Glu Glu His
 20 25 30

Gly His Gly Ser Trp Arg Ala Leu Pro Ser Lys Ala Gly Leu Gln Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp
 50 55 60

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

Leu His Ala Leu Leu Gly Asn Arg Trp Ser Ala Ile Ala Thr His Leu
 85 90 95

Pro Lys Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Leu
 100 105 110

Lys Lys Arg Leu Thr Lys Met Gly Ile Asp Pro Val Thr His Lys Pro
 115 120 125

Lys Asn Asp Ala Ile Leu Ser Ser His Asp Gly His Leu Lys Ser Thr
 130 135 140

Ala Asn Leu Ser His Met Ala Gln Trp Glu Ser Ala Arg Leu Glu Ala
 145 150 155 160

PF5908220081029_F_60204_PCT_Sequence.txt

Glu Ala Arg Leu Val Arg Gln Ser Lys Leu Arg Ser Asn Ser Pro Pro
165 170 175

Pro Asn Thr Thr Thr Thr Thr Thr Thr Leu Asn Lys Pro Met Ala Pro
180 185 190

Pro Pro Leu Cys Leu Asp Ile Leu Lys Ala Trp Asn Gly Val Trp Thr
195 200 205

Ser Asn Asn Glu Ala Gly Gly Arg Ser Ser Gly Phe Val Gly Asn Gly
210 215 220

Ile Gly His His Glu Ser Pro Thr Ser Thr Thr Val Ser Tyr Asp Ile
225 230 235 240

Thr Asn Gly Val Glu Asn Asn Ala Ser Phe Lys Glu Glu Gly Asn Ile
245 250 255

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

Asn Ala Ile Ser Gly Leu Ser Asp Val Pro Ile Leu Pro Met Glu Ile
275 280 285

Ala Trp Pro Thr Gln Glu Ser Leu Ile Arg Val Asp His Asp Asp Asp
290 295 300

Ile Thr Glu Asn Ile Asn Asp Gln His Val Pro Ser Gly Asn Phe Val
305 310 315 320

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

Ser Pro Ser Asp Gly Asp Gln Ser Pro Val Ile Leu Leu Val Arg Arg
340 345 350

Cys Gln Trp Glu Val Arg Val Asp Thr Ser Lys Ile Thr Arg Ile Ile
355 360 365

Gly Ile Val Phe Leu Ile Trp
370 375

<210> 120
<211> 801
<212> DNA
<213> Fagopyrum cymosum

<400> 120
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gggttgaaga gggggccatg gactcctgaa gaagacgagc gtctcgccaa ttacatcaac 120
aaagatggag aaggaagatg gagaacactt cccaaacgcg ctggcctcct ccgatgtggg 180
Seite 97

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ctcatagctg gcaggattcc gggaagaaca gataacgaga ttaagaacta ctggaacact 360
catctgagta agaaattgat aagtcaaggc atagatccaa gaactcaca accattatcc 420
tcagctccaa accctaata tggcgttgta caaaccccca aaattgcaga tactccatca 480
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<210> 121
 <211> 265
 <212> PRT
 <213> Fagopyrum cymosum

<400> 121

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

Ser Lys Val Gly Leu Lys Arg Gly Pro Trp Thr Pro Glu Glu Asp Glu
 20 25 30

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

Leu Pro Lys Arg Ala Gly Leu Leu Arg Cys Gly Lys Ser Cys Arg Leu
 50 55 60

Arg Trp Met Asn Tyr Leu Arg Pro Asn Val Lys Arg Gly Gln Ile Ala
 65 70 75 80

Pro Asp Glu Glu Asp Leu Ile Leu Arg Leu His Arg Leu Leu Gly Asn
 85 90 95

Arg Trp Ser Leu Ile Ala Gly Arg Ile Pro Gly Arg Thr Asp Asn Glu
 100 105 110

Ile Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys Leu Ile Ser Gln
 115 120 125

Gly Ile Asp Pro Arg Thr His Lys Pro Leu Ser Ser Ala Pro Asn Pro
 130 135 140

Asn His Gly Val Val Gln Thr Pro Lys Ile Ala Asp Thr Pro Ser Thr
 145 150 155 160

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

Phe Val Leu Pro Ser Thr Thr Ser Pro Leu Asp Ser Phe His Gly Asn
180 185 190

Ser Asn Thr Ser His Asp Pro Ala Ser Val Glu Asp Asp Gln Asp Thr
195 200 205

Asp Pro Asn Tyr Cys Thr Asp Asp Val Phe Ser Ser Phe Leu Asn Ser
210 215 220

Leu Ile Asn Glu Asp Leu Tyr Thr Thr Gln Thr Gln Gln Gln Tyr His
225 230 235 240

Phe Gly Ala Ala Gly Trp Asp Ala Pro Leu Met Ser Ala Ser Asp Pro
245 250 255

Leu Arg Gln Thr Pro Pro His Gln Asp
260 265

<210> 122
<211> 1023
<212> DNA
<213> Boea crassifolia

<400> 122
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actcttccaa ctaatgctgg gctgcaacga tgtggaaaga gctgccggtt gcggtggact 180
aattatctcc ggccagatat taaaagaggg aggttttcat ttgaagaaga agagaccatt 240
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ctaaactcgt ctctgtgcaa caattcacca acccagatga atttttcaag gttgcaacct 480
cgttttaacc ccgagttgct aagattcgcc gcttcccttt tttcttccaa ctgccaatcc 540
caagattttc cgatgcaaaa ccagataacc agcaataatc aaatcccacc acccttcatg 600
caaacttcag ttcaagatgt tgcagtgttg cccgatttat gtgccgatac taacctcggg 660
acctcattct ccgttcatga tgaggttcaa gaatttcaac aaaaccagc tggatatgga 720
atgccttctg cttaacagg agagtatgtg ccagtgtcga acgacgggta ttacgggtcg 780
ggtagaccaac cattttaga cccgactcca tcgtccgtga cttcaaattt tcaatcttat 840
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taa

1023

<210> 123
 <211> 340
 <212> PRT
 <213> Boea crassifolia

<400> 123

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

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

Lys Tyr Gly Tyr Gly Asn Trp Arg Thr Leu Pro Thr Asn Ala Gly Leu
 35 40 45

Gln Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg
 50 55 60

Pro Asp Ile Lys Arg Gly Arg Phe Ser Phe Glu Glu Glu Glu Thr Ile
 65 70 75 80

Ile Arg Leu His Ser Ile Leu Gly Asn Lys Trp Ser Leu Ile Ala Ala
 85 90 95

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

Asn Ile Arg Lys Arg Leu Leu Arg Met Gly Ile Asp Pro Val Thr His
 115 120 125

Ser Pro Arg Leu Gln Leu Leu Asp Leu Ser Thr Ile Leu Asn Ser Ser
 130 135 140

Leu Cys Asn Asn Ser Pro Thr Gln Met Asn Phe Ser Arg Leu Gln Pro
 145 150 155 160

Arg Phe Asn Pro Glu Leu Leu Arg Phe Ala Ala Ser Leu Phe Ser Ser
 165 170 175

Asn Cys Gln Ser Gln Asp Phe Pro Met Gln Asn Gln Ile Thr Ser Asn
 180 185 190

Asn Gln Ile Pro Pro Pro Phe Met Gln Thr Ser Val Gln Asp Val Ala
 195 200 205

Val Leu Pro Asp Leu Cys Ala Asp Thr Asn Leu Gly Thr Ser Phe Ser
 210 215 220

Val His Asp Glu Val Gln Glu Phe Gln Gln Asn Pro Ala Gly Tyr Gly
 225 230 235 240

PF5908220081029_F_60204_PCT_Sequence.txt

Met Pro Ser Ala Leu Thr Gly Glu Tyr Val Pro Val Leu Asn Asp Gly
245 250 255

Tyr Tyr Gly Ser Gly Asp Gln Pro Phe Val Asp Pro Thr Pro Ser Ser
260 265 270

Val Thr Ser Asn Phe Gln Ser Tyr Cys Ser Asn Ser Leu Gly Phe Gln
275 280 285

Ser Ile Phe Ser Thr Pro Pro Ser Ser Pro Thr Pro Leu Asn Ser Asn
290 295 300

Ser Thr Tyr Val Asn Ser Cys Ser Ser Thr Glu Asp Glu Thr Glu Ser
305 310 315 320

Tyr Tyr Asn Ser Met Trp Lys Phe Glu Ile Pro Asp Asn Leu Arg Ile
325 330 335

Asn Asp Phe Met
340

<210> 124
<211> 1083
<212> DNA
<213> Medicago truncatula

<400> 124
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ctcccaaaga atgctggtgc aggattacaa agatgtggaa agagttgtcg tctacgttgg 180
acaaactatc tccgaccgga tataaagaga ggacgattct cttttgaaga agaagaaacc 240
ataattcagc tgcatagcat acttggcaac aagtggctct caattgcttc taggctacca 300
ggaagaacag acaatgaaat caagaattat tggaacactc acattaggaa aagactctta 360
agaatgggaa ttgatcctgt gacacataat ccacgttttg atcttttgga cctatcttct 420
atcctaaatt catctctcta tgcctctacc tcatcatcac aaatgaacat ccaaaggcta 480
attggtacac aatcaatagt gaaccctgag attctaaagt tggcttcac actcttctct 540
tctcaaaatg gacaagagaa tcaccaaatt gatcacaaac aacaaattag ctcacacatg 600
gatcaagaag catgcacat gttgttgaat ccaccttttg ataataattc aatgtctttc 660
attcaaacac acttgagaa tatatactca tcatttttac ctgaatttgg cttccaacaa 720
catcatgaaa atgttcaatt aaattatttg cattgcaatg gaattgcttc aagtaatgta 780
acagaggatt ttgttcatca attaccatgc tataactact taagttctga ttatcatgca 840
aatgatttaa atgtggaccc tcacatatca gaaacttcaa cttttcattg caataacaac 900
aaccagaatt ttaatttcgc ttcagttcta tctacacctt catcaagtcc cacacagttg 960
aattcaaatt ctgcgaatat gaatgaaagc agtagtactg aagatgagac agagagctat 1020

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gtttagcaata acatgtttga atttcatatc tcagatatct taggtgtgaa tgagttcatg 1080
taa 1083

<210> 125
<211> 360
<212> PRT
<213> Medicago truncatula

<400> 125

Met Gly Arg Ala Pro Cys Cys Glu Lys Asn Asn Gly Leu Lys Arg Gly
1 5 10 15

Pro Trp Thr Gln Glu Glu Asp Gln Lys Leu Ile Asp Tyr Ile Gln Lys
20 25 30

His Gly Tyr Gly Asn Trp Arg Leu Leu Pro Lys Asn Ala Val Ala Gly
35 40 45

Leu Gln Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu
50 55 60

Arg Pro Asp Ile Lys Arg Gly Arg Phe Ser Phe Glu Glu Glu Glu Thr
65 70 75 80

Ile Ile Gln Leu His Ser Ile Leu Gly Asn Lys Trp Ser Ser Ile Ala
85 90 95

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

Thr His Ile Arg Lys Arg Leu Leu Arg Met Gly Ile Asp Pro Val Thr
115 120 125

His Asn Pro Arg Phe Asp Leu Leu Asp Leu Ser Ser Ile Leu Asn Ser
130 135 140

Ser Leu Tyr Ala Ser Thr Ser Ser Ser Gln Met Asn Ile Gln Arg Leu
145 150 155 160

Ile Gly Thr Gln Ser Ile Val Asn Pro Glu Ile Leu Lys Leu Ala Ser
165 170 175

Ser Leu Phe Ser Ser Gln Asn Gly Gln Glu Asn His Gln Ile Asp His
180 185 190

Lys Gln Gln Ile Ser Ser His Met Asp Gln Glu Ala Cys Thr Met Leu
195 200 205

Leu Asn Pro Pro Phe Asp Asn Asn Ser Met Ser Phe Ile Gln Thr His
210 215 220

PF5908220081029_F_60204_PCT_Sequence.txt

Leu Glu Asn Ile Tyr Ser Ser Phe Leu Pro Glu Phe Gly Phe Gln Gln
225 230 235 240

His His Glu Asn Val Gln Leu Asn Tyr Leu His Cys Asn Gly Ile Ala
245 250 255

Ser Ser Asn Val Thr Glu Asp Phe Val His Gln Leu Pro Cys Tyr Asn
260 265 270

Tyr Leu Ser Ser Asp Tyr His Ala Asn Asp Leu Asn Val Asp Pro His
275 280 285

Ile Ser Glu Thr Ser Thr Phe His Cys Asn Asn Asn Asn Gln Asn Phe
290 295 300

Asn Phe Ala Ser Val Leu Ser Thr Pro Ser Ser Ser Pro Thr Gln Leu
305 310 315 320

Asn Ser Asn Ser Ala Asn Met Asn Glu Ser Ser Ser Thr Glu Asp Glu
325 330 335

Thr Glu Ser Tyr Val Ser Asn Asn Met Phe Glu Phe His Ile Ser Asp
340 345 350

Ile Leu Gly Val Asn Glu Phe Met
355 360

<210> 126
<211> 944
<212> DNA
<213> Arabidopsis thaliana

<400> 126
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ggagcttgga ctaaggaaga agacgataag ctcatctctt acatcaaagc tcacggtgaa 180
ggttggtggc gttctcttcc tagatccgcc ggtcttcaac gttgcggaaa aagctgtcgt 240
ctccgatgga ttaactatct ccgacctgat ctcaagaggg gtaacttcac cctcgaagaa 300
gatgatctca tcatcaaact acatagcctt ctcggttaaca agtgggtctt tattgcgacg 360
agattaccag gaagaacaga taacgagatt aagaattact ggaacacaca tgtaagagg 420
aagctattaa gaaaagggat tgatccggcg actcatcgac ctatcaacga gacaaaaact 480
tctcaagatt cgtctgattc tagtaaaaca gaggaccctc ttgtcaagat tctctctttt 540
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tactcagttg ttgaagaaag atgtctggac ttgaatcttg agcttaggat cagtccacca 660
tggcaagaca agtccatga tgagaggaac ctaaggtttg ggagagtga gtaggtgc 720
agtgcgtgcc gttttggatt cgggaacggc aaggagtgt gctgtaataa tgtgaaatgt 780
caaacagagg acagtagtag cagcagttat tcttcaaccg acattagtag tagcattggt 840

PF5908220081029_F_60204_PCT_Sequence.txt

tatgacttct tgggtctaaa caacactagg gttttggatt ttagcacttt ggaaatgaaa 900
tgaaatgaaa tactatatta atcaatttat agctgtgaat tgtg 944

<210> 127
<211> 274
<212> PRT
<213> Arabidopsis thaliana

<400> 127

Met Gly Arg Ser Pro Cys Cys Glu Lys Asp His Thr Asn Lys Gly Ala
1 5 10 15

Trp Thr Lys Glu Glu Asp Asp Lys Leu Ile Ser Tyr Ile Lys Ala His
20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Arg Ser Ala Gly Leu Gln Arg
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60

Leu Lys Arg Gly Asn Phe Thr Leu Glu Glu Asp Asp Leu Ile Ile Lys
65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Thr Arg Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Val
100 105 110

Lys Arg Lys Leu Leu Arg Lys Gly Ile Asp Pro Ala Thr His Arg Pro
115 120 125

Ile Asn Glu Thr Lys Thr Ser Gln Asp Ser Ser Asp Ser Ser Lys Thr
130 135 140

Glu Asp Pro Leu Val Lys Ile Leu Ser Phe Gly Pro Gln Leu Glu Lys
145 150 155 160

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

Val Val Glu Glu Arg Cys Leu Asp Leu Asn Leu Glu Leu Arg Ile Ser
180 185 190

Pro Pro Trp Gln Asp Lys Leu His Asp Glu Arg Asn Leu Arg Phe Gly
195 200 205

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

PF5908220081029_F_60204_PCT_Sequence.txt

Lys Glu Cys Ser Cys Asn Asn Val Lys Cys Gln Thr Glu Asp Ser Ser
225 230 235 240

Ser Ser Ser Tyr Ser Ser Thr Asp Ile Ser Ser Ser Ile Gly Tyr Asp
245 250 255

Phe Leu Gly Leu Asn Asn Thr Arg Val Leu Asp Phe Ser Thr Leu Glu
260 265 270

Met Lys

<210> 128
<211> 1287
<212> DNA
<213> Arabidopsis thaliana

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agtgccccac caaatgcttc aatcctcttc cactacacaa aaaaacaact taatcccttt      180
ataccctttt agccaaaacc ctcgctaaaa gccaatccct caatataaaa taacaagtag      240
aattgatctg cctatatata agattttgag acgaaataag atctaaacca caagaaagaa      300
agtaaacata aaagtatggg aaggtcaccg tgctgtgaga aagctcacac aaacaaagga      360
gcatggacga aagaagagga cgagaggctc gtcgcctaca ttaaagctca tggagaaggc      420
tgctggagat ctctcccaa agccgccgga cttcttcgct gtggcaagag ctgccgtctc      480
cggtg gatca actatctccg gcctgacctt aagcgtggaa acttcaccga ggaagaagac      540
gaactcatca tcaagctcca tagccttctt ggcaacaaat ggtcgcttat tgccgggaga      600
ttaccgggaa gaacagataa cgagataaag aactattgga acacgcatat acgaagaaag      660
cttataaaca gagggattga tccaacgagt catagaccaa tccaagaatc atcagcttct      720
caagattcta aacctacaca actagaacca gttacgagta ataccattaa tatctcattc      780
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aaaatctcaa tgcttacgtt caaagaagaa aaagatgagt gccagttca agaaaagttc      900
ccagatttga atcttgagct cagaatcagt cttcctgatg atgttgatcg tcttcaaggg      960
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gagtgcagat gcggaagaat gagatgcatg gtagtcggag gtagcagcaa ggggagtgac     1080
atgagcaatg gatttgattt tttagggttg gcaaagaaag agaccacttc tcttttgggc     1140
tttcgaagct tggagatgaa ataattattgt caaatttttag gcgtaactgt acaaaacttt     1200
tgcctagata atttgaaagt atatcttcaa cttgtatgag aaatttaact ggtgaattat     1260
aatatataga atttgttttt ttttctc                                     1287
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<210> 129
<211> 282

<212> PRT

<213> Arabidopsis thaliana

<400> 129

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

Ser Asn Gly Phe Asp Phe Leu Gly Leu Ala Lys Lys Glu Thr Thr Ser
260 265 270

Leu Leu Gly Phe Arg Ser Leu Glu Met Lys
275 280

<210> 130
<211> 1077
<212> DNA
<213> Arabidopsis thaliana

<400> 130
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agctcacatg aacaaaggag cttggactaa agaagaagat cagcttcttg ttgattacat 180
ccgtaaacac ggtgaaggtt gctggcgatc tctccctcgc gccgctggat tacaagatg 240
tggttaagagt tgtagattga gatggatgaa ttatctaaga ccagatctca aaagaggcaa 300
ttttactgaa gaagaagatg aactcatcat caagctccat agcttgctcg gtaacaaatg 360
gtctttaata gctgggagat taccaggaag aacagataac gagatcaaga actattggaa 420
cactcatatc aagaggaagc ttctcagccg tgggattgat ccaaactctc accgtctgat 480
caacgaatcc gtcgtgtctc cgtcgtctct tcaaaacgat gtcgttgaga ctatacatct 540
tgatttctct ggaccgggta aaccggaacc ggtgcgtaga gagattggta tggttaataa 600
ttgtgagagt agtgaacga cgtcggagaa ggattatggg aacgaggaag attgggtggt 660
gaatttggaa ctctctgttg gaccgagtta tcggtacgag tcgactcgga aagtgagtgt 720
tgttgactcg gctgagtcga ctcgacggtg gggttccgag ttgtttggag ctcagagag 780
tgatgcggtg tgtttgtgtt gtcggattgg gttgtttcgt aatgagtcgt gtcggaattg 840
tcgggtttct gatgttagaa ctcattagag agtcaatcga gaattcttta ggaatctttt 900
tatatattta gatcgtcaat tgtgtttttt tttgtttcac atttgttatg taacatcaag 960
taagaaacta gcataattat ttgatggcaa agccaaaaga ttgtgctcaa agaaatttat 1020
aaaaacaaca attagggcat gttgtacttg cagatgctaa aaaacggtaa tttttat 1077

<210> 131
<211> 257
<212> PRT
<213> Arabidopsis thaliana

<400> 131
Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Met Asn Lys Gly Ala
1 5 10 15

Trp Thr Lys Glu Glu Asp Gln Leu Leu Val Asp Tyr Ile Arg Lys His
20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Arg Ala Ala Gly Leu Gln Arg
35 40 45

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Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Arg Pro Asp
50 55 60

Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
100 105 110

Lys Arg Lys Leu Leu Ser Arg Gly Ile Asp Pro Asn Ser His Arg Leu
115 120 125

Ile Asn Glu Ser Val Val Ser Pro Ser Ser Leu Gln Asn Asp Val Val
130 135 140

Glu Thr Ile His Leu Asp Phe Ser Gly Pro Val Lys Pro Glu Pro Val
145 150 155 160

Arg Glu Glu Ile Gly Met Val Asn Asn Cys Glu Ser Ser Gly Thr Thr
165 170 175

Ser Glu Lys Asp Tyr Gly Asn Glu Glu Asp Trp Val Leu Asn Leu Glu
180 185 190

Leu Ser Val Gly Pro Ser Tyr Arg Tyr Glu Ser Thr Arg Lys Val Ser
195 200 205

Val Val Asp Ser Ala Glu Ser Thr Arg Arg Trp Gly Ser Glu Leu Phe
210 215 220

Gly Ala His Glu Ser Asp Ala Val Cys Leu Cys Cys Arg Ile Gly Leu
225 230 235 240

Phe Arg Asn Glu Ser Cys Arg Asn Cys Arg Val Ser Asp Val Arg Thr
245 250 255

His

<210> 132
<211> 1054
<212> DNA
<213> Oryza sativa

<400> 132
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aaaggaaaga atcaagaaag cttcatcgtc ttcatgggga ggtcaccgtg ctgcgagaag 120
gcacacacca acaaggagc atggaccaag gaggaagatg accggctcat tgcctacatc 180

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ttcaccgagg aggaggatga gctgatcatc aagcttcaca gccttttagg caacaaatgg	360
tctctgatag ccgggagggtt gccaggaaga acggacaacg agatcaagaa ctactggaac	420
acgcacatca ggaggaagct gctgagccgt ggcacgacc cggtgacaca ccggccgac	480
aacgacagcg cgtccaacat caccatatca ttcgaggcgg ccgcggcggc ggcgagggac	540
gacaaggccg ccgtgttccg gcgagaggac catcctcatc agccgaaggc ggtgacagt	600
gcacaggagc agcaggcagc cgccgattgg ggccatggga agccactcaa gtgccctgac	660
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gtgaagaggg agaccggcgt ctgcttcagc tgcagcctgg ggctcccaa gagcacagac	780
tgcaagtgca gcagcttcc	840
atgaaatgag cacctcctcc tctgtagttt cttctttcgt tttgtcactt ggatattggt	900
tagcttttct tctaggtgaa aacacacaga gagagagaga gagagagaga gagagagaga	960
taacatctcc tctgtgctc ttgctgctcc attttgtctc tgttgtaatt accatatatt	1020
gactaatcat gacaaataat acttgatgct aagt	1054

<210> 133
 <211> 251
 <212> PRT
 <213> Oryza sativa

<400> 133

Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
 1 5 10 15

Trp Thr Lys Glu Glu Asp Asp Arg Leu Ile Ala Tyr Ile Lys Ala His
 20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60

Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
 65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110

Arg Arg Lys Leu Leu Ser Arg Gly Ile Asp Pro Val Thr His Arg Pro
 115 120 125

PF5908220081029_F_60204_PCT_Sequence.txt

Ile Asn Asp Ser Ala Ser Asn Ile Thr Ile Ser Phe Glu Ala Ala Ala
130 135 140

Ala Ala Ala Arg Asp Asp Lys Ala Ala Val Phe Arg Arg Glu Asp His
145 150 155 160

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

Ala Asp Trp Gly His Gly Lys Pro Leu Lys Cys Pro Asp Leu Asn Leu
180 185 190

Asp Leu Cys Ile Ser Leu Pro Ser Gln Glu Glu Pro Met Met Met Lys
195 200 205

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

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

Ala Met Leu Asp Phe Arg Ser Leu Glu Met Lys
245 250

<210> 134
<211> 732
<212> DNA
<213> Oryza sativa

<400> 134
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gaggacgagc gcctcgtcgc ctacatccgc gccacggcg agggctgctg gcgctcgctc 120
cccaaggccg ccggcctcct ccgctgcggc aagagctgcc gcctccgctg gatcaactac 180
ctccgccccg acctcaagcg cggcaacttc accgccgacg aggacgacct catcatcaag 240
ctccacagcc tcctcggcaa caagtgggtct ctgatcgcg cgaggctgcc ggggaggagc 300
gacaacgaga tcaagaacta ctggaacacg cacatccgcc ggaagcttct cggcaggggg 360
atcgacccccg tcacgcaccg ccccgtaac gccgccgcc ccaccatctc cttccatccc 420
cagccgccgc caacgacgaa ggaggagcag ctcatactca gcaagccgcc caagtgcccc 480
gacctcaacc tggacctctg catcagcccc cgtcgtgcc aggaagaaga cgatgactat 540
gaggcgaagc cggcgatgat cgtgaggcg cggagctgc agcgccgcc cggcggcctc 600
tgcttcggct gcagcctcg cctccagaag gaggcaagt gcagcgcgcg cggcgccggc 660
gccggcgccg gcaacaactt cctcggcctc agggctggca tgctcgactt cagaagcctc 720
cccatgaaat ga 732

<210> 135
<211> 243
<212> PRT

<213> Oryza sativa

<400> 135

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

<210> 136

PF5908220081029_F_60204_PCT_Sequence.txt

<211> 1033
<212> DNA
<213> Oryza sativa

<400> 136
gctattacta ctagtataaaa accaacgcga agctctcgtc ggcgacaacc aactcgacac 60
cgcgggcgagg cgaaccaacg cgcgggcgtg gcatggggag gtcgccatgc tgcgagaagg 120
cgcacacgaa caagggggcg tggacgaagg aggaggacca gcggtgatc gcctacatca 180
aggcgcacgg cgaggggttc tggcggtcgc tgcccaaggc ggcggggctc ctccgctgcg 240
gcaagagctg ccgcctccgc tggatgaact acctccgccc cgacctcaag cgcggaact 300
tcaccgacga cgacgacgag ctcatcatca agctccacgc ctttctcggc aacaagtggg 360
cgttgattgc ggggcagctg ccggggagga cggacaacga gatcaagaac tactggaaca 420
cgcacatcaa gcgcaagctc ctgagccggg gcatcgacct gcagacgcac cggccgggtca 480
gcgcccgggag cagcgccgcc gcggcgagcg ggctgaccac gacggccagc accgccgcct 540
ttccgtccct tgcgccggcg ccgccgccgc agcagcacag gctacacaac ccggtgcacg 600
ccgcccgcgc gagcaatgag agcttcgcca ggtccgcggc gtccccgcgc tcggaggagc 660
gccacagcag cagcgggcgc agctcgagc cgccgcggtg ccccgacctc aacctcgacc 720
tcgacctcga cctgtccatg agcctgccga gctcgccgcc caagacgccg gccgccgcgt 780
cgtccacgac cgcgtcgcgc caccatcacc accagcagca gaagaccatc tgcctctgct 840
accacctcgg cgtccgcaac ggcgacgtct gcagctgcaa ggcggccgcg ccatcgccgg 900
ccggcccacg cgcgttcggg tttctcaggc cactggagga gggccagtac atatagcaca 960
gcaggcttta gggaaaaaaa acctgtaaaa aacacaaaaa aaaacggtgg gcaatagagt 1020
tttttctaag ttc 1033

<210> 137
<211> 287
<212> PRT
<213> Oryza sativa

<400> 137
Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
1 5 10 15
Trp Thr Lys Glu Glu Asp Gln Arg Leu Ile Ala Tyr Ile Lys Ala His
20 25 30
Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
35 40 45
Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Arg Pro Asp
50 55 60
Leu Lys Arg Gly Asn Phe Thr Asp Asp Asp Asp Glu Leu Ile Ile Lys
65 70 75 80

PF5908220081029_F_60204_PCT_Sequence.txt

Leu His Ala Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Gln Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
100 105 110

Lys Arg Lys Leu Leu Ser Arg Gly Ile Asp Pro Gln Thr His Arg Pro
115 120 125

Val Ser Ala Gly Ser Ser Ala Ala Ala Ala Ser Gly Leu Thr Thr Thr
130 135 140

Ala Ser Thr Ala Ala Phe Pro Ser Leu Ala Pro Ala Pro Pro Pro Gln
145 150 155 160

Gln His Arg Leu His Asn Pro Val His Ala Ala Ala Pro Ser Asn Ala
165 170 175

Ser Phe Ala Arg Ser Ala Ala Ser Pro Pro Ser Glu Asp Gly His Ser
180 185 190

Ser Ser Gly Gly Ser Ser Asp Ala Pro Arg Cys Pro Asp Leu Asn Leu
195 200 205

Asp Leu Asp Leu Asp Leu Ser Met Ser Leu Pro Ser Ser Pro Pro Lys
210 215 220

Thr Pro Ala Ala Ala Ser Ser Thr Thr Ala Ser Arg His His His His
225 230 235 240

Gln Gln Gln Lys Thr Ile Cys Leu Cys Tyr His Leu Gly Val Arg Asn
245 250 255

Gly Asp Val Cys Ser Cys Lys Ala Ala Ala Pro Ser Pro Ala Gly Pro
260 265 270

Arg Ala Phe Arg Phe Leu Arg Pro Leu Glu Glu Gly Gln Tyr Ile
275 280 285

<210> 138
<211> 1179
<212> DNA
<213> Oryza sativa

<400> 138
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gggcatggg gaggtcgccg tgctgcgaga aggcgcacac gaacaagggg gcgtggacga 180
aggaggagga ccagcggctc atcgctaca tcagggcgca tggcgaaggc tgctggcgct 240
cgctgcccga ggcggcgggc ctcttcgct gcggcaagag ctgccgcctc cggtggatga 300
actacctccg ccccgacctc aagcgcggca acttcaccga cgacgaggac gagctcatca 360
Seite 113

PF5908220081029_F_60204_PCT_Sequence.txt

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ggacggacaa cgagatcaag aactactgga acacgcacat caagcgcaag ctctctgccc 480
gcggcatcga cccgcagacg caccgcccgc tgctcagcgg cggtgacggc atcgcgggca 540
gcaacaaggc ggcaccaccg ccgccgcata ccatatccgt cccggcgaag gcggcgggcg 600
cggcgatctt cgccgtggcg aagccgccgc cgccgccgcg cccggtcgac tcctcggacg 660
acggctgccc cagcagcagc ggcacaacga gcacggggga gccgcggtgc cccgacctca 720
acctcgagct ctcggtcggg ccgacgccga gctcgccgcc ggcgagagacg cccaccagcg 780
cgcgggccgg ctgcctctgc taccacctcg gcttcgcggg cggggaggcg tgcagctgtc 840
aggctgacag caagggccca cagagttta gatatttcag gccgttgga caaggccagt 900
acatatgaga tatgaccatg agatgtgaga tggcttaatt agcttcaatt cccaacatgt 960
gtaacacagg gagtttttct agtgagcagc aatactgttt aatttcagaa aaaaaaggg 1020
aaagaaaaag gttctaactt gttcatattt cttactatta tccaatcttc atgatctcaa 1080
tctctctctc tctttattat ttttctttgt agtaattaac ttcattgttg ttcctctaaa 1140
aaagattggt cgatgttatt cagtataaaa tattcctag 1179
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<210> 139
 <211> 260
 <212> PRT
 <213> Oryza sativa

<400> 139

Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
 1 5 10 15

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

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Arg Pro Asp
 50 55 60

Leu Lys Arg Gly Asn Phe Thr Asp Asp Glu Asp Glu Leu Ile Ile Arg
 65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Gln Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110

Lys Arg Lys Leu Leu Ala Arg Gly Ile Asp Pro Gln Thr His Arg Pro
 115 120 125

Leu Leu Ser Gly Gly Asp Gly Ile Ala Ala Ser Asn Lys Ala Ala Pro
130 135 140

Pro Pro Pro His Pro Ile Ser Val Pro Ala Lys Ala Ala Ala Ala Ala
145 150 155 160

Ile Phe Ala Val Ala Lys Pro Pro Pro Pro Pro Arg Pro Val Asp Ser
165 170 175

Ser Asp Asp Gly Cys Arg Ser Ser Ser Gly Thr Thr Ser Thr Gly Glu
180 185 190

Pro Arg Cys Pro Asp Leu Asn Leu Glu Leu Ser Val Gly Pro Thr Pro
195 200 205

Ser Ser Pro Pro Ala Glu Thr Pro Thr Ser Ala Arg Pro Val Cys Leu
210 215 220

Cys Tyr His Leu Gly Phe Arg Gly Gly Glu Ala Cys Ser Cys Gln Ala
225 230 235 240

Asp Ser Lys Gly Pro His Glu Phe Arg Tyr Phe Arg Pro Leu Glu Gln
245 250 255

Gly Gln Tyr Ile
260

<210> 140
<211> 232
<212> PRT
<213> Antirrhinum majus
<400> 140

Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
1 5 10 15

Trp Thr Lys Glu Glu Asp Asp Arg Leu Val Ala Tyr Ile Arg Ala His
20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60

Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
100 105 110

PF5908220081029_F_60204_PCT_Sequence.txt

Arg Arg Lys Leu Leu Ser Arg Gly Ile Asp Pro Thr Thr His Arg Ser
115 120 125

Ile Asn Asp Gly Thr Ala Ser Gln Asp Gln Val Thr Thr Ile Ser Phe
130 135 140

Ser Asn Ala Asn Ser Lys Glu Glu Asp Thr Lys His Lys Val Ala Val
145 150 155 160

Asp Ile Met Ile Lys Glu Glu Asn Ser Pro Val Gln Glu Arg Cys Pro
165 170 175

Asp Leu Asn Leu Asp Leu Lys Ile Ser Pro Pro Cys Gln Gln Gln Ile
180 185 190

Asn Tyr His Gln Glu Asn Leu Lys Thr Gly Gly Arg Asn Gly Ser Ser
195 200 205

Thr Leu Cys Phe Val Cys Arg Leu Gly Ile Gln Asn Ser Lys Asp Cys
210 215 220

Ser Cys Ser Asp Gly Val Gly Asn
225 230

<210> 141
<211> 1014
<212> DNA
<213> Oryza sativa

<400> 141
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cggaagcggc cggcggcgct gcgcggcggg gaggaggcgg cggcggcggc gctgaagcgt 120
gggccgtgga cgcccagga ggacgaggtg ctggcgcggt tcgtggcgcg ggaggggtgc 180
gaccggtggc gcacgctgcc gcggcgcgcg ggcctgctgc gctgcggcaa gagctgccgc 240
ctccggtgga tgaactacct ccgccccgac atcaagcgct gccccatcgc cgacgacgag 300
gaggacctca tcctccgcct ccaccgcctc ctcggaacc ggtggtcgct gatcgccggg 360
aggttgccgg ggcgacgga caacgagatc aagaactact ggaactcgca tctcagcaag 420
aagctcatcg cgcagggcat cgacccgcgg acgcacaagc cgctgacggc cgccgccgat 480
cactccaacg ccgccgtgc cgtcgccgcc acttcttaca agaaggcggg gccggccaag 540
ccgccgagga cggcatcctc gccggccgct ggcattgagt gcagcgacga tcgtgcccga 600
ccggccgacg gtggcggtga cttcgacgag atggtgagcg ccgccgatgc cgagggattc 660
gaaggaggat ttggcgatca gttctgtgcc gaggatgcag ttcattggtg cttcgacatg 720
ggttccgctt ccgccatggt ggggtgacgac gacttctcct cgtttcttga ttctctgac 780
aacgacgagc agttaggcga tctcttcgtc gtcgagggca acgatcacga gcatggcaat 840
ggtgagattg gtcattggaga cgtcatggaa tccaacagc aatctttcgg gagattgatc 900

PF5908220081029_F_60204_PCT_Sequence.txt

aggggaataag ttgaccatga gaaaacatgt aagaacagct tgtctgctga gtcatgaccg 960
gtgatgtgta tgtgatggaa gaaaacgtat gtacgactta atgcttgcac ctat 1014

<210> 142
<211> 275
<212> PRT
<213> Oryza sativa

<400> 142

Met Lys Arg Lys Arg Pro Ala Ala Leu Arg Gly Gly Glu Glu Ala Ala
1 5 10 15

Ala Ala Ala Leu Lys Arg Gly Pro Trp Thr Pro Glu Glu Asp Glu Val
20 25 30

Leu Ala Arg Phe Val Ala Arg Glu Gly Cys Asp Arg Trp Arg Thr Leu
35 40 45

Pro Arg Arg Ala Gly Leu Leu Arg Cys Gly Lys Ser Cys Arg Leu Arg
50 55 60

Trp Met Asn Tyr Leu Arg Pro Asp Ile Lys Arg Cys Pro Ile Ala Asp
65 70 75 80

Asp Glu Glu Asp Leu Ile Leu Arg Leu His Arg Leu Leu Gly Asn Arg
85 90 95

Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile
100 105 110

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

Ile Asp Pro Arg Thr His Lys Pro Leu Thr Ala Ala Ala Asp His Ser
130 135 140

Asn Ala Ala Ala Ala Val Ala Ala Thr Ser Tyr Lys Lys Ala Val Pro
145 150 155 160

Ala Lys Pro Pro Arg Thr Ala Ser Ser Pro Ala Ala Gly Ile Glu Cys
165 170 175

Ser Asp Asp Arg Ala Arg Pro Ala Asp Gly Gly Gly Asp Phe Ala Ala
180 185 190

Met Val Ser Ala Ala Asp Ala Glu Gly Phe Glu Gly Gly Phe Gly Asp
195 200 205

Gln Phe Cys Ala Glu Asp Ala Val His Gly Gly Phe Asp Met Gly Ser
210 215 220

PF5908220081029_F_60204_PCT_Sequence.txt

Ala Ser Ala Met Val Gly Asp Asp Asp Phe Ser Ser Phe Leu Asp Ser
225 230 235 240

Leu Ile Asn Asp Glu Gln Leu Gly Asp Leu Phe Val Val Glu Gly Asn
245 250 255

Asp His Glu His Gly Asn Gly Glu Ile Gly His Gly Asp Val Met Glu
260 265 270

Ser Lys Gln
275

<210> 143
<211> 1003
<212> DNA
<213> B. napus

<400> 143
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tctccatata accctagcta gtttcatcat cacaagaacc agaagaagaa gaagaagatg 120
gggagggtctc cttgctgcga gaaggaccac acgaacaaag gagcttggac taaagaagaa 180
gacgataagc tcgtctctta catcaaactc cacggcgaag gctgttggcg ctctcttccg 240
agatccgccc gtcttctccg ctgcggcaaa agctgccgtc ttcggtggat taactatctc 300
cgacctgatc tcaagagggg taacttcacc ctcgaagaag atgatctcat catcaaaactc 360
catagcctcc ttggaaacaa atggtctctt atcgcgacga gattaccggg aagaacagat 420
aacgagatca agaactactg gaatacacac gtaaagagga agcttttgag aggagggatt 480
gatcccacga ctcataggcc gatcaacgaa tccaaagctc ctcgtgattc gcctgagact 540
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gatcagaaaag gactgatatg caaaaaagag agagttgagt attctgtagt tgaagaaaag 660
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gatgagacca aactttggtt tgggagagag aagtacaagt gcaactgcatg ccgttttggg 780
ttgggaaacg gcaaggagt tagctgcgat aatgtttaat gtcaagtcga ggacagtagt 840
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<210> 144
<211> 279
<212> PRT
<213> B. napus

<400> 144

Met Gly Arg Ser Pro Cys Cys Glu Lys Asp His Thr Asn Lys Gly Ala
1 5 10 15

Trp Thr Lys Glu Glu Asp Asp Lys Leu Val Ser Tyr Ile Lys Ser His
Seite 118

20

25

30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Arg Ser Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60

Leu Lys Arg Gly Asn Phe Thr Leu Glu Glu Asp Asp Leu Ile Ile Lys
 65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Thr Arg Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Val
 100 105 110

Lys Arg Lys Leu Leu Arg Gly Gly Ile Asp Pro Thr Thr His Arg Pro
 115 120 125

Ile Asn Glu Ser Lys Ala Pro Arg Asp Ser Pro Glu Thr Arg Glu Thr
 130 135 140

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

Asn Asp Gln Lys Gly Leu Ile Cys Lys Lys Glu Arg Val Glu Tyr Ser
 165 170 175

Val Val Glu Glu Lys Cys Leu Asp Leu Asn Leu Glu Leu Arg Ile Ser
 180 185 190

Pro Pro Trp Gln Asp Gln Gln His His Asp Glu Thr Lys Leu Trp Phe
 195 200 205

Gly Arg Glu Lys Tyr Lys Cys Thr Ala Cys Arg Phe Gly Leu Gly Asn
 210 215 220

Gly Lys Glu Cys Ser Cys Asp Asn Val Lys Cys Gln Val Glu Asp Ser
 225 230 235 240

Ser Ser Ser Ser Ser Tyr Ser Ser Ser Asp Ile Ser Ser Ser Val Ile
 245 250 255

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

Phe Ser Thr Ser Glu Met Asn
 275

<210> 145
 <211> 1082

PF5908220081029_F_60204_PCT_Sequence.txt

<212> DNA
<213> B. napus

<400> 145
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aacaaggtg cttggactaa agaagaagac gagagactcg tctcttacat caaatcccac 120
ggcgaaggct gctggcgatc tctccctaga gccgccgggc tcctccgttg cggcaagagc 180
tgccgtctcc ggtggattaa ctatctccgg cctgatctca aaagaggaaa cttcacccgc 240
gacgaagatg aagttatcat caatcttcat agcctcattg gcaacaagtg gtctttaatt 300
gcggcgagat tgcctggaag aacagataac gagataaaga attactggaa cacgcatata 360
aagaggaaac tcttgagtaa agggattgat cccaacactc acagatcgat caacgcaggg 420
aaagtttctg attcgaagaa aacagaggac caagttgtaa aagatgtttc ttttgggtct 480
ctgtttgata aaacagaaaa gtccgaggag cagaagcaaa ataaaaaaca aaagcagaat 540
ctaataatg ggtagtttg caaagaagag agggttgagc atcacccagc tgttgttggt 600
caagaaatth tttgccc aaa tttgaatctc gagcttagga tcagtccacc atggcacaac 660
aagaatcatg atgatcatac aagagagaaa tctactacct acactgcac cgtctttac 720
gtgcaaaacg gcatggagtc tagtagtgat actgcaaaat gtcaaacaga ggatagcagt 780
agcattagcc attcttctact tgacattagt agtattagca gcgttggtta tgacttcttg 840
ggtttgaata cgaggtttat ggattttcgg agcttgga aa tgaactaaac aaaaaacaaa 900
aaataaatth gtagatctga tactgttact cttaatctcg cttttacttt attttaatgg 960
ttttcctaath tttgtacata aacttaaaaa tattatgatc aaatgtatcg ctgtctcatt 1020
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aa 1082

<210> 146
<211> 287
<212> PRT
<213> B. napus

<400> 146
Met Gly Arg Ser Pro Cys Cys Glu Lys Glu His Met Asn Lys Gly Ala
1 5 10 15
Trp Thr Lys Glu Glu Asp Glu Arg Leu Val Ser Tyr Ile Lys Ser His
20 25 30
Gly Glu Gly Cys Trp Arg Ser Leu Pro Arg Ala Ala Gly Leu Leu Arg
35 40 45
Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60
Leu Lys Arg Gly Asn Phe Thr Arg Asp Glu Asp Glu Val Ile Ile Asn
65 70 75 80

PF5908220081029_F_60204_PCT_Sequence.txt

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

<210> 147
<211> 909
<212> DNA
<213> B. napus

<400> 147
ccataaaacc ctggtttcat cataacaaga tcatcatcag aagatatggg gaggtctcca 60
tgctgcgaga aagaccacac gaacaaagga gcttggacca aggaagaaga ccagaagctc 120
atctcttaca tcaaattcca cggcgaaggt tgttggcgct ctctccctgc atccgccggc 180
cttctccgct gcggcaaaag ctgccgtctc cgttggatta actatctccg tcctgatctc 240
aagagaggtg acttcaccct cgaagaagac gatctcatca tcaaactaca tagcctcctc 300

PF5908220081029_F_60204_PCT_Sequence.txt

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ggcaacaagt ggtctcttat tgcgacgagg ttaccgggaa gaacagataa cgagattaag 360
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catcggccga tcaaagctcg tcgggatgcg tctgaagcta gagaaacaga ggactcgctt 480
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aggttttaaaa agagtctgac ttgcaaaacg aagagcttgg atttgaatct tgagctaaga 600
atcagcccg cgtggcaaga ccaacaccga cgtgatgaga ggaaactctt gtttaggaaa 660
gagaagtatc tctgcagtgc gtgtcgtttt gggttgggaa acggtaagga gtgtagctgt 720
gagaatgtga gatgtcatat agatgactct agtagtagca gctactcttc aagcgacata 780
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<210> 148
 <211> 271
 <212> PRT
 <213> B. napus

<400> 148

Met Gly Arg Ser Pro Cys Cys Glu Lys Asp His Thr Asn Lys Gly Ala
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Trp Thr Lys Glu Glu Asp Gln Lys Leu Ile Ser Tyr Ile Lys Ser His
 20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Ala Ser Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60

Leu Lys Arg Gly Asn Phe Thr Leu Glu Glu Asp Asp Leu Ile Ile Lys
 65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Thr Arg Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Met
 100 105 110

Lys Arg Lys Leu Leu Arg Gly Gly Ile Asp Pro Ala Thr His Arg Pro
 115 120 125

Ile Lys Ala Arg Arg Asp Ala Ser Glu Ala Arg Glu Thr Glu Asp Ser
 130 135 140

Leu Val Lys Val Ile Ser Phe Gly Pro Gln Leu Glu Lys Glu Glu Ser
 145 150 155 160

PF5908220081029_F_60204_PCT_Sequence.txt

Ser Arg Glu Glu Gly Arg Phe Lys Lys Ser Leu Thr Cys Lys Thr Lys
165 170 175

Ser Leu Asp Leu Asn Leu Glu Leu Arg Ile Ser Pro Pro Trp Gln Asp
180 185 190

Gln His Arg Arg Asp Glu Arg Lys Leu Leu Phe Arg Lys Glu Lys Tyr
195 200 205

Leu Cys Ser Ala Cys Arg Phe Gly Leu Gly Asn Gly Lys Glu Cys Ser
210 215 220

Cys Glu Asn Val Arg Cys His Ile Asp Asp Ser Ser Ser Ser Ser Tyr
225 230 235 240

Ser Ser Ser Asp Ile Ser Ser Ser Val Val Gly Phe Asp Phe Leu Gly
245 250 255

Leu Asn Thr Ser Ser Val Leu Asp Tyr Thr Ser Leu Glu Met Asn
260 265 270

<210> 149
<211> 812
<212> DNA
<213> G. max

<220>
<221> misc_feature
<222> (748)..(748)
<223> n is a, c, g, or t

<400> 149
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gctggcgctc tctcccaaaa gccgccggcc ttctccgttg cggcaagagc tgtcgtctcc 180
gctggatcaa ctatctccgc cctgacctca agcgccggcaa tttctccctc gaagaagacc 240
aactcatcat caaactccac agcctccttg gcaacaagtg gtctctaatt gctggtagat 300
tgcccggtag aactgacaat gagatcaaga attactggaa tactcacata cgcaggaagc 360
ttctgagcag aggtattgac cctgccactc acaggcctct caacgattct tctcatcaag 420
aacctgctgc tgtctctgcc cctcctaaac atcaagagtc ctttcaccat gaacgctgcc 480
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atagcaaaga ttgtagctgt gccctccaca ctagtactgc caacgctact gctactggct 660
atgattttctt ggccttgaaa accaccgtcg ttttggatta cagaaccttg cacatgaaat 720
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tttcttactt acttacttac ttacttactt ac 812

<210> 150
 <211> 235
 <212> PRT
 <213> G. max

<400> 150

Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
 1 5 10 15

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

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60

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

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110

Arg Arg Lys Leu Leu Ser Arg Gly Ile Asp Pro Ala Thr His Arg Pro
 115 120 125

Leu Asn Asp Ser Ser His Gln Glu Pro Ala Ala Val Ser Ala Pro Pro
 130 135 140

Lys His Gln Glu Ser Phe His His Glu Arg Cys Pro Asp Leu Asn Leu
 145 150 155 160

Glu Leu Thr Ile Ser Pro Pro His His Pro Gln Pro Asp His Pro His
 165 170 175

Leu Lys Thr Leu Val Thr Asn Ser Asn Leu Cys Phe Pro Cys Ser Leu
 180 185 190

Gly Leu His Asn Ser Lys Asp Cys Ser Cys Ala Leu His Thr Ser Thr
 195 200 205

Ala Asn Ala Thr Ala Thr Gly Tyr Asp Phe Leu Ala Leu Lys Thr Thr
 210 215 220

Val Val Leu Asp Tyr Arg Thr Leu His Met Lys
 225 230 235

<210> 151

<211> 1227

<212> DNA

<213> S. lycopersicum

<400> 151

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aaggaccttg gacacctgaa gaagatcaaa aactcttagc ttatatcgaa gaacatgggtc      180
atggtagctg gcgcgcatta cctaccaaag ctggacttca aagatgtggt aagagttgca      240
ggctcagggtg gactaattac cttaggcctg atatcaagag aggaaaattc actttacaag      300
aagaacaaac catcattcaa cttcatgctc tcttagggaa taggtgggtcg gccatagcca      360
ctcatttatc caaacgaaca gataatgaga ttaaaaatta ttggaatact catctcaaga      420
aacggctagt gaaaatgggg atcgaccag tgaccacaa gccgaagaac gatgccttgt      480
tgtccaatga cggtcagtct aaaaacgcag ctaaccttag ccacatggct cagtgggaaa      540
gtgcccggct tgaagccgaa gctagactcg ctagacaatc taaactccgg tccaatagtt      600
tccaaaattc actcgcatct caagaattta ccgctccttc accttctagt cctcttagta      660
aaccgcttgt ggccccagca cgttgtctca acgtgctgaa agcctgaaac ggggtgtttgg      720
accaaaccaa tgaatgaagg gttccgtcgc gagcgctagt gctgggtattt cagttgcggg      780
agcactcgcg agggatttgg aatctcctac ttctacacta ggctatttcg aaaatgcgca      840
acatattaca tcatcaggaa ttggaggaag ttctaataca gttttgtatg aatttgttgg      900
aaattcatca gggcttagtg aagggtggaat tatgaacaat gatgaaagtg aagaagattg      960
gaaggaattt gggaactcat caactggaca tttgcctcaa tacagaaaag atgttattaa      1020
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atggacaaca gaatcctcaa ggtcaaatac agagcaaatt tcccctgcca attttgtgga      1140
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cacggaatcc gatacggagg ggaaagg                                     1227

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<210> 152

<211> 208

<212> PRT

<213> S. lycopersicum

<400> 152

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Met Gly Arg Ser Pro Cys Cys Asp Lys Val Gly Leu Lys Lys Gly Pro
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20          25          30

Gly His Gly Ser Trp Arg Ala Leu Pro Thr Lys Ala Gly Leu Gln Arg
35          40          45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp
50          55          60

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

Leu His Ala Leu Leu Gly Asn Arg Trp Ser Ala Ile Ala Thr His Leu
85 90 95

Ser Lys Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Leu
100 105 110

Lys Lys Arg Leu Val Lys Met Gly Ile Asp Pro Val Thr His Lys Pro
115 120 125

Lys Asn Asp Ala Leu Leu Ser Asn Asp Gly Gln Ser Lys Asn Ala Ala
130 135 140

Asn Leu Ser His Met Ala Gln Trp Glu Ser Ala Arg Leu Glu Ala Glu
145 150 155 160

Ala Arg Leu Ala Arg Gln Ser Lys Leu Arg Ser Asn Ser Phe Gln Asn
165 170 175

Ser Leu Ala Ser Gln Glu Phe Thr Ala Pro Ser Pro Ser Ser Pro Leu
180 185 190

Ser Lys Pro Val Val Ala Pro Ala Arg Cys Leu Asn Val Leu Lys Ala
195 200 205

<210> 153
<211> 1042
<212> DNA
<213> T. aestivum

<400> 153
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ggcgcgtgga cgaggaggga ggacgagagg ctgggtggccc acgtccgggc gcacggggag 180
ggctgctggc gctcgctgcc cagcgccgcc ggcctgctgc gctgcggcaa gagctgccgc 240
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gacgagctca tcgtcaagct ccacagcctc ctcggcaaca agtggtcgct catcgccgcg 360
cgctccccg ggaggaccga caacgagatc aagaactact ggaacacgca catccggagg 420
aagctgctgg gcagggggat cgaccccgtc acgcaccgcc ccctcaccga cgccaccacc 480
gtctccttcg tccatcctgc agaggcgcca aagacgcagc cggtgacgga ggagaggaag 540
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ggccgcctct gcttccgctg cagcatcctg agagtgcagc gagcggcgac ggagtgcagc 720
tgcggcagca acttcctggg cctcagggcc ggcattgctc acttcagagg cctcgagatg 780

PF5908220081029_F_60204_PCT_Sequence.txt

aaatagaaat ttgggaataa ttattcgatc aaactttctg ctgtaaattg ttgctccctc 840
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gaggaggaga ctggtatggt attattaggt gaggatttgt agcgatatcc tccctgcctt 960
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gaaataatac agtacgatac tt 1042

<210> 154
<211> 235
<212> PRT
<213> T. aestivum

<400> 154

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

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60

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

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Ala Arg Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
100 105 110

Arg Arg Lys Leu Leu Gly Arg Gly Ile Asp Pro Val Thr His Arg Pro
115 120 125

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

Lys Thr Gln Pro Val Thr Glu Glu Arg Lys Pro Pro Arg Cys Pro Asp
145 150 155 160

Leu Asn Leu Asp Leu Cys Ile Ser Leu Pro Phe Gln Gln Glu Glu Glu
165 170 175

Arg Pro Pro Ala Arg Ala Cys Ala Lys Pro Val Lys Met Glu Gln Leu
180 185 190

Gln Gln Gly Arg Leu Cys Phe Arg Cys Ser Ile Leu Arg Val Arg Gly
195 200 205

PF5908220081029_F_60204_PCT_Sequence.txt

Ala Ala Thr Glu Cys Ser Cys Gly Ser Asn Phe Leu Gly Leu Arg Ala
 210 215 220

Gly Met Leu Asp Phe Arg Gly Leu Glu Met Lys
 225 230 235

<210> 155
 <211> 1177
 <212> DNA
 <213> T. aestivum

<400> 155
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 tcacggcgg cggcgcacca tctaaagaga tagcgagatg gggaggtcgc cgtgctgcga 180
 gaaggcgcac accaacaagg ggcctggac caaggaggag gacgaccggc tcaccgccta 240
 catcaaggcg cacggcgagg gctgctggcg ctccctgccc aaggccgccc ggctgctccg 300
 ctgcggaag agctgccgc tccgctggat caactacctc cccccgacc tcaagcgcg 360
 caacttcagc gacgaggagg acgagctcat catcaagctc cacagcctcc tgggcaacaa 420
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 gtaggtgaaa aaattacagc gagtgaaaga caagaagaag ggtgaggatg atcttgtgtt 1080
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<210> 156
 <211> 263
 <212> PRT
 <213> T. aestivum

<400> 156
 Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
 1 5 10 15

Trp Thr Lys Glu Glu Asp Asp Arg Leu Thr Ala Tyr Ile Lys Ala His
 Seite 128

20

25

30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60

Leu Lys Arg Gly Asn Phe Ser Asp Glu Glu Asp Glu Leu Ile Ile Lys
 65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110

Arg Arg Lys Leu Thr Ser Arg Gly Ile Asp Pro Val Thr His Arg Ala
 115 120 125

Ile Asn Ser Asp His Ala Ala Ser Asn Ile Thr Ile Ser Phe Glu Ala
 130 135 140

Ala Gln Arg Asp Asp Lys Gly Ala Val Phe Arg Arg Asp Ala Glu Pro
 145 150 155 160

Thr Lys Val Ala Ala Ala Ala Ala Ile Thr His Val Asp His His
 165 170 175

His Arg Ser Asn Pro His His Gln Met Glu Trp Gly Gln Gly Lys Pro
 180 185 190

Leu Lys Cys Pro Asp Leu Asn Leu Asp Leu Cys Ile Ser Pro Pro Ser
 195 200 205

His Glu Asp Ser Met Val Asp Thr Lys Pro Val Val Lys Arg Glu Ala
 210 215 220

Val Val Gly Leu Cys Phe Ser Cys Ser Met Gly Leu Pro Arg Ser Ala
 225 230 235 240

Asp Cys Lys Cys Ser Ser Phe Met Gly Leu Arg Thr Ala Met Leu Asp
 245 250 255

Phe Arg Ser Ile Glu Met Lys
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<210> 157

<211> 1035

<212> DNA

<213> T. aestivum

<400> 157

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<210> 158
 <211> 235
 <212> PRT
 <213> T. aestivum

<400> 158

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Gly Glu Gly Cys Trp Arg Ser Leu Pro Ser Ala Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60

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

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Ala Arg Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 Seite 130

100

105

110

Arg Arg Lys₁₁₅ Leu Leu Gly Arg Gly₁₂₀ Ile Asp Pro Val Thr₁₂₅ His Arg Pro

Leu Thr₁₃₀ Asp Ala Thr Thr Val₁₃₅ Ser Phe Val His Pro Ala Glu Ala Pro

Lys₁₄₅ Thr Gln Pro Val Thr₁₅₀ Glu Glu Arg Lys Pro₁₅₅ Pro Arg Cys Pro Asp₁₆₀

Leu Asn Leu Asp Leu₁₆₅ Cys Ile Ser Leu Pro₁₇₀ Phe Gln Gln Glu Glu₁₇₅ Glu

Arg Pro Pro Ala₁₈₀ Arg Ala Cys Ala Lys₁₈₅ Pro Val Lys Met Glu₁₉₀ Gln Leu

Gln Gln Gly₁₉₅ Arg Leu Cys Phe Arg₂₀₀ Cys Ser Ile Leu Arg₂₀₅ Val Arg Gly

Ala Ala₂₁₀ Thr Glu Cys Ser Cys₂₁₅ Gly Ser Asn Phe Leu₂₂₀ Gly Leu Arg Ala

Gly₂₂₅ Met Leu Asp Phe Arg₂₃₀ Gly Leu Glu Met Lys₂₃₅

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<212> DNA
<213> T. aestivum

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tgaggcaaga gctgccgct cagggtgatc aactacctc gccccgacct caagcgggc 240
aacttcaccc gcgacgagga cgacctcatc gtcaagctcc acagcctgct cggcaacaag 300
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<210> 160
 <211> 240
 <212> PRT
 <213> T. aestivum

<400> 160

Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
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Trp Thr Arg Glu Glu Asp Glu Arg Leu Val Ala His Val Arg Ala His
 20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Gly Ala Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60

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

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Ala Arg Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110

Arg Arg Lys Leu Leu Gly Arg Gly Ile Asp Pro Val Thr His Arg Pro
 115 120 125

Leu Thr His Ala Ala Ser Ala Thr Thr Val Ser Phe Leu His Pro Ala
 130 135 140

Glu Pro Pro Lys Thr Gln Pro Ala Thr Glu Glu Ser Lys Pro Pro Arg
 145 150 155 160

Cys Pro Asp Leu Asn Leu Asp Leu Cys Ile Ser Leu Pro Phe Gln Gln
 165 170 175

Glu Glu Glu Arg Pro Pro Ala Arg Ala Cys Ala Lys Pro Val Lys Met
 180 185 190

Glu Gln Leu Gln Gln Gly Gly Gly Leu Cys Phe Arg Cys Ser Ile
 195 200 205

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

Leu Gly Leu Arg Ala Gly Met Leu Asp Phe Arg Gly Leu Arg Met Lys
 225 230 235 240

<210> 161

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<211> 1092
<212> DNA
<213> T. aestivum

<400> 161
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gccgagccca ccaaggtagc ggcagcggca gcggcgatca cccacgtgga ccaccatcac 540
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<210> 162
<211> 268
<212> PRT
<213> T. aestivum

<400> 162
Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
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Trp Thr Lys Glu Glu Asp Asp Arg Leu Thr Ala Tyr Ile Lys Ala His
20 25 30
Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
35 40 45
Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60
Leu Lys Arg Gly Asn Phe Ser Asp Glu Glu Asp Glu Leu Ile Ile Lys
65 70 75 80

PF5908220081029_F_60204_PCT_Sequence.txt

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
100 105 110

Arg Arg Lys Leu Thr Ser Arg Gly Ile Asp Pro Val Thr His Arg Ala
115 120 125

Ile Asn Ser Asp His Ala Ala Ser Asn Ile Thr Ile Ser Phe Glu Thr
130 135 140

Ala Gln Arg Asp Asp Lys Gly Ala Val Phe Arg Arg Asp Ala Glu Pro
145 150 155 160

Thr Lys Val Ala Ala Ala Ala Ala Ile Thr His Val Asp His His
165 170 175

His His His Arg Ser Asn Pro Gln Met Asp Trp Gly Gln Gly Lys Pro
180 185 190

Leu Lys Cys Pro Asp Leu Asn Leu Asp Leu Cys Ile Ser Pro Pro Ser
195 200 205

His Glu Asp Pro Met Val Asp Thr Lys Pro Val Val Lys Arg Glu Ala
210 215 220

Gly Val Gly Val Gly Val Val Gly Leu Cys Phe Ser Cys Ser Met Gly
225 230 235 240

Leu Pro Arg Ser Val Glu Cys Lys Cys Ser Ser Phe Met Gly Leu Arg
245 250 255

Thr Ala Met Leu Asp Phe Arg Ser Ile Glu Met Lys
260 265

<210> 163
<211> 2604
<212> DNA
<213> P. patens

<400> 163
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acagacttcg agggcatggg gaggaacca tgctgtgaga aagcggggtt gaagagaggg 240
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PF5908220081029_F_60204_PCT_Sequence.txt

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 gtctagcatg aatttgtact aatg 2604

<210> 164
 <211> 421
 <212> PRT
 <213> P. patens

<400> 164

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 20 25 30

Gly Leu Gly Cys Trp Arg Ala Thr Pro Lys Leu Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60

Leu Lys Arg Gly Ile Phe Ser Glu Glu Glu Glu Asn Leu Ile Leu Asp
 65 70 75 80

Ala His Ala Thr Leu Gly Asn Arg Trp Ser Arg Ile Ala Ala Gln Leu
 85 90 95

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

Lys Lys Arg Leu Arg Ser Gln Gly Leu Asp Pro Asn Thr His Leu Pro
 115 120 125

Leu Arg Thr Asp Arg Ser Asp Gly Thr Gly Gly Asp Thr Asp Val Glu
 130 135 140

Asp Gly Asp Cys Ser Asp Ala Thr Met Ser Asp Ala Thr Lys Ser Lys
 145 150 155 160

Ile Lys Val Lys Arg Lys Ala Lys Phe Gln Glu Thr Val Lys Val Arg
 165 170 175

Gln Pro Lys Gly Pro Lys Pro Ala Pro Gln Leu Lys Met Cys Gln Ser
 180 185 190

Glu Glu Gly Pro Val Leu Leu Lys Val Ser Lys Cys Pro Gln Ser Ser
 195 200 205

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

PF5908220081029_F_60204_PCT_Sequence.txt

His Ser Ser Ser Ser Pro Ala Ser Ser Thr Ile Thr Thr Lys Ser Ala
 225 230 235 240

Glu Asp His Gln Asp Ser Ser Ser Phe Val Arg Ser Leu Thr Ser Ala
 245 250 255

Pro Ser Phe Pro Glu Ala Glu Leu Trp Asn Cys Ile Lys Pro Ser Thr
 260 265 270

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

Gly Leu Asp Ser Ser Leu Pro Cys Pro Tyr Leu His Ser Asn Thr Glu
 290 295 300

Pro Pro Lys Leu Glu Glu Cys Lys Pro Leu Val Thr Pro Pro Leu Thr
 305 310 315 320

Gln Gly Val Ser Pro Ser His Asp Thr Met Asp Ile Gly Met Gln Arg
 325 330 335

Asn Met His Val Ser Ser Gln Pro Ser Leu Glu Val Gly Glu Asn Tyr
 340 345 350

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

Ser Trp Thr Met Glu Gly Glu Ile Ser His Ala Thr Pro Glu Pro Ile
 370 375 380

Phe Ala Leu Ala Pro Pro Ile Ser Ala Gly Leu Tyr Gly Glu Val Leu
 385 390 395 400

Pro Pro Ala Pro Arg Asp Ser Ser Gln Glu Met Gln Arg Leu Ala Ala
 405 410 415

Leu Leu Asp Leu Ile
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<210> 165
 <211> 926
 <212> DNA
 <213> P. trichocarpa

<400> 165
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 gctcacggtg aagggttgctg gcgctcactt cctaaagccg ctggccttct tagatgtggc 180
 aagagttgca gacttcgttg gatcaactat ttaagacctg accttaaacg tggcaatttc 240
 accgaagcag aagatgagct cattatcaaa ctccatagcc tccttggaac caaatggtca 300

PF5908220081029_F_60204_PCT_Sequence.txt

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gaaccagcag tacaagaagc cacaacaaca atatctttca ccacgactac tacttcagta 480
cttgaagaag agtctctggg ttctataatt aaagaggaaa ataaagagaa gataattagc 540
gcaactgctt tcgtatgcaa agaagagaaa acccaagttc aagaaagggtg tccagacttg 600
aatctcgagc ttggaattag ccttccttcc caaaaccagc ctgatcatca ccagccattc 660
aaaactggag gaagtagaag tctttgtttt gcttgcagtt tggggctaca aaacagcaag 720
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aggagaaagg gattgcctat taaatt 926
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<210> 166
 <211> 271
 <212> PRT
 <213> P. trichocarpa

<400> 166

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

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60

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

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110

Arg Arg Lys Leu Leu Asn Arg Gly Ile Asp Pro Ala Thr His Arg Pro
 115 120 125

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

Thr Thr Thr Thr Ser Val Leu Glu Glu Glu Ser Leu Gly Ser Ile Ile
 145 150 155 160

PF5908220081029_F_60204_PCT_Sequence.txt

Lys Glu Glu Asn Lys Glu Lys Ile Ile Ser Ala Thr Ala Phe Val Cys
165 170 175

Lys Glu Glu Lys Thr Gln Val Gln Glu Arg Cys Pro Asp Leu Asn Leu
180 185 190

Glu Leu Gly Ile Ser Leu Pro Ser Gln Asn Gln Pro Asp His His Gln
195 200 205

Pro Phe Lys Thr Gly Gly Ser Arg Ser Leu Cys Phe Ala Cys Ser Leu
210 215 220

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

Val Gly Ser Ser Gly Ser Thr Ser Thr Lys Thr Gly Tyr Asp Phe Leu
245 250 255

Gly Met Lys Ser Gly Val Leu Asp Tyr Arg Ser Leu Glu Met Lys
260 265 270

<210> 167
<211> 917
<212> DNA
<213> P. trichocarpa

<400> 167
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accacaggtg aaggttgctg gcgttcactt cctaaagctg ctggccttct aagatgcggc 180
aagagctgca gacttcgttg gatcaactat ttaagacctg accttaaacg tggcaatttt 240
actgaagaag aagatgagct cattatcaaa ctccatagtc tcctcggcaa caaatgggtca 300
cttatagccg gaaggttacc agggagaaca gataatgaga taaagaatta ttggaacaca 360
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gaaccagccc aagaagcttc aacaacaata tctttcagca ctactacctc agttaaagaa 480
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gacttcctag ggatgaaaag tgggtgtgtg gattatagag gtttggagat gaaatgatta 840
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<210> 168

<211> 268

<212> PRT

<213> P. trichocarpa

<400> 168

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

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60

Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
 65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110

Arg Arg Lys Leu Leu Asn Arg Gly Ile Asp Pro Ala Thr His Arg Pro
 115 120 125

Leu Asn Glu Pro Ala Gln Glu Ala Ser Thr Thr Ile Ser Phe Ser Thr
 130 135 140

Thr Thr Ser Val Lys Glu Glu Ser Leu Ser Ser Val Lys Glu Glu Ser
 145 150 155 160

Asn Lys Glu Lys Ile Ile Ser Ala Ala Ala Phe Ile Cys Lys Glu Glu
 165 170 175

Lys Thr Pro Val Gln Glu Arg Cys Pro Asp Leu Asn Leu Glu Leu Arg
 180 185 190

Ile Ser Leu Pro Cys Gln Asn Gln Pro Asp Arg His Gln Ala Phe Lys
 195 200 205

Thr Gly Gly Ser Thr Ser Leu Cys Phe Ala Cys Ser Leu Gly Leu Gln
 210 215 220

Asn Ser Lys Asp Cys Ser Cys Ser Val Ile Val Gly Thr Ile Gly Ser
 225 230 235 240

Ser Ser Ser Ala Gly Ser Lys Thr Gly Tyr Asp Phe Leu Gly Met Lys
 245 250 255

PF5908220081029_F_60204_PCT_Sequence.txt

Ser Gly Val Leu Asp Tyr Arg Gly Leu Glu Met Lys
260 265

<210> 169
<211> 858
<212> DNA
<213> M. truncatula

<400> 169
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ctccatagtc ttcttggtta caaatggtct ttgatagctg gaagattacc aggaagaaca 300
gataatgaga taaagaatta ttggaacact catataagaa gaaagctttt gaatagagga 360
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caatatcatc atcatcatca tcatcaagaa atgaacacaa acatgggtta aggggttggtg 600
ttagaacgtt gtcctgattt gaatcttgag ttaacaatta gtccaccacg tgttcaagaa 660
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ggcttagaaa tgaaatga 858

<210> 170
<211> 285
<212> PRT
<213> M. truncatula

<400> 170
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Trp Thr Lys Glu Glu Asp Asp Arg Leu Ile Ser Tyr Ile Arg Ala His
20 25 30
Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
35 40 45
Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60
Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
65 70 75 80

PF5908220081029_F_60204_PCT_Sequence.txt

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
100 105 110

Arg Arg Lys Leu Leu Asn Arg Gly Ile Asp Pro Ala Thr His Arg Pro
115 120 125

Leu Asn Glu Val Ser His Ser Gln Ser Gln Ser Gln Thr Leu His Leu
130 135 140

Gln Asn Gln Glu Ala Val Thr Ile Ala Val Ala Ala Ser Thr Ser Thr
145 150 155 160

Pro Thr Ala Thr Lys Thr Leu Pro Thr Thr Ile Ser Phe Ala Ser Ser
165 170 175

Ile Lys Gln Glu Gln Tyr His His His His His His Gln Glu Met Asn
180 185 190

Thr Asn Met Val Lys Gly Leu Val Leu Glu Arg Cys Pro Asp Leu Asn
195 200 205

Leu Glu Leu Thr Ile Ser Pro Pro Arg Val Gln Glu His Asp Glu Gln
210 215 220

Phe Arg Asn Arg Glu Arg Asn Asn Leu Cys Phe Val Cys Ser Leu Gly
225 230 235 240

Leu Gln Asn Ser Lys Asp Cys Thr Cys Asp Glu Ile Val Gly Asn Ser
245 250 255

Ser Ser Gly Asn Gly Ser Thr Ala Pro Ala Tyr Asp Phe Leu Gly Leu
260 265 270

Lys Gly Gly Val Trp Asp Tyr Lys Gly Leu Glu Met Lys
275 280 285

<210> 171
<211> 879
<212> DNA
<213> Z. mays

<400> 171
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ggcccacggc gaaggctgct ggaggtcgct cccaaggcc gcgggcctgc tgcgctgcgg 180
caagagctgc cgcctccggt ggatcaacta cctgcgcccc gacctcaagc gcggcaactt 240
caccaggag gaggacgacg tcatcatcaa gctccaccag gtcctcgga acaagtggtc 300
gctgatcgcc gccagctgc cggggcggac ggacaacgag atcaagaact actggaacac 360
Seite 142

PF5908220081029_F_60204_PCT_Sequence.txt

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ggcgcacagc agcgacgacg acgacagcac gtccgggtcc ctgccacacc aacatgctgt 600
cggcggcatc gacctcaacc tctcgctaag cccaccgacg agccaaccgt catcgccggc 660
cgccgccaag ggagttgtag ctagcggata tggccaaggg agtgagagct agctgtacct 720
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ttcttccatg caggccgga gacctaag agaacgtgtg cgtgcgtgtg agaattaaac 840
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<210> 172
 <211> 226
 <212> PRT
 <213> Z. mays

<400> 172

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

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60

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

Leu His Gln Val Leu Gly Asn Lys Trp Ser Leu Ile Ala Ala Gln Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110

Lys Arg Lys Leu Ile Ala Arg Gly Ile Asp Pro Arg Thr His Gln Pro
 115 120 125

Ala Ser Ala Ala Ala Val Ala Pro Ala Ala Ala Ala Ala Ala Ala Ala
 130 135 140

Gln Ser Ser Phe Arg His His Gly Asp Asp Glu Ala Val Ala Arg Arg
 145 150 155 160

Ser Cys Ser Arg Asp Ser Gly Cys Ile Ala Ala His Ser Ser Asp Asp
 165 170 175

PF5908220081029_F_60204_PCT_Sequence.txt

Asp Asp Ser Thr Ser Gly Ser Leu Pro His Gln His Ala Val Gly Gly
180 185 190

Ile Asp Leu Asn Leu Ser Leu Ser Pro Pro Thr Ser Gln Pro Ser Ser
195 200 205

Pro Ala Ala Ala Lys Gly Val Val Ala Ser Gly Tyr Gly Gln Gly Ser
210 215 220

Glu Ser
225

<210> 173
<211> 1405
<212> DNA
<213> Z. mays

<400> 173
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tcttttacgt actactacta ctactagctg tagttaacta ctatccctgc tcagctctgc 180
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gcctcgtccg gcgagttcga gatgacgacg acctccaagt ggtcctggtg cggatggcct 660
gctggaccgc cgccggccgc tcgcttctgc ggctcctgca gctggtaatg ctgctgcccc 720
gcggtcgcgc tggcgagcgg gcggtgcgtc tgcgggtcca tgccgcgggc gaggagcttg 780
cgcttgatgt gcgtgttcca gtagttcttg atctcgttgt ccgtcctgcc cggcagcctc 840
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tcctcctcgg tgaagttgcc gcgcttgagg tccgggcgca ggtagttgat ccaccgcagc 960
cggcagctct tcccgcagcg cagcagacct gcggcttttg gtagcgatct ccagcagccc 1020
tcgccgtggg cttgatgta ggcgacgagg cgctggctct cctccttggg ccacgcgccc 1080
ttgttggtgt gcgcctgctc gcagcacggg gacctcccca tgccggccgc ccgccaggca 1140
gagatcgacg acagccacgc cgcgcacaga cagagaggcc tcgctgctgc cggagtgggt 1200
gggagtacgt agtcgatcgg aggatgctgg actggtggcg gcgatcgatg gcgtggtttt 1260
gctgcgagcc tttcggaat ggagaacaga acaaaggcaa ggagccgggg aggagcgggg 1320
gaggagtggg tggttttata cgaaagaggg gtcgaggtgg agagcgtgga ggagcgaggg 1380

ccgaggggtgc ccgccccatt gaccc

1405

<210> 174
 <211> 288
 <212> PRT
 <213> Z. mays

<400> 174

Met Gly Arg Ser Pro Cys Cys Glu Gln Ala His Thr Asn Lys Gly Ala
 1 5 10 15

Trp Thr Lys Glu Glu Asp Gln Arg Leu Val Ala Tyr Ile Lys Ala His
 20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60

Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Asp Leu Ile Ile Lys
 65 70 75 80

Phe His Glu Leu Phe Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110

Lys Arg Lys Leu Leu Ala Arg Gly Met Asp Pro Gln Thr His Arg Pro
 115 120 125

Leu Ala Ser Ala Thr Ala Gly Gln Gln His Tyr Gln Leu Gln Glu Pro
 130 135 140

Gln Lys Arg Ala Ala Gly Gly Gly Pro Ala Gly His Pro His Gln Asp
 145 150 155 160

His Leu Glu Val Val Val Ile Ser Asn Ser Pro Asp Glu Ala Tyr Ser
 165 170 175

Arg Ser Ser Asp Asp Glu Pro Arg Ser Ala Thr Pro Pro Arg Arg His
 180 185 190

Leu Asp Ile Asp Leu Asn Leu Ser Ile Ser Leu Ala Ala Tyr Gln Pro
 195 200 205

Pro Glu Glu Thr Gly Ile Ile Lys Gln Pro Leu Val Met Lys Gln Glu
 210 215 220

Gln Glu Thr Ala Ala Gly Gly Thr Asn Ala Ala Ala Val Cys Leu Cys
 225 230 235 240

PF5908220081029_F_60204_PCT_Sequence.txt

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

Gly Ser Ser Ser Ser Ser Ser His Ser His Ser His Ser His Gln
260 265 270

Trp Ala Leu Asn Phe Leu Gln Ala Ala Ala Pro Cys Tyr Arg Gly Gln
275 280 285

<210> 175
<211> 940
<212> DNA
<213> Z. mays

<400> 175
gcgcgcaagc aagcacacga gggagcagcg ggcaggcagg caggcagcca tggggagggtc 60
tccgtgctgc gagaaggcac acacgaacaa gggcgcctgg accaaggagg aggaccagcg 120
cctgatcgcc tacatcaggg cgcacggcga ggggagctgg cgctcgctgc ccaaggccgc 180
gggactcctc cgctgcggca agagctgcag gctccgctgg atgaactacc tccgcccgga 240
cctcaagcgc ggcaacttca ccggcgacga cgacgagctc atcatcaagc tccacgcctt 300
gctcggcaac aagtggctgc tcatcgctgg gcagctgccc ggccggacgg acaacgagat 360
caagaactac tggaacacgc acatcaagcg caagctgctc agccgcggca tcgacccgca 420
gacgcaccgc ccgctcagcg gcggcgctgg cagcgcgctc accaccacgt ccagcaccgc 480
cggcttcccc tccccgcgc cggcgtccag gccacgccc acgccccgc ccgccgtcgt 540
cgtcccgcgc aatgcgatct tcgcgcgccc ggcgcgctcg gaggacggcc acagcagcag 600
cggcgcgagc acggacgcgc cgcgctgccc cgacctaac ctggacctgg acctgtccgt 660
gggcccgcgc cccaagacgc cggcggccac gcccgctcg cagcagcggc ggcggacgac 720
catctgcctg tgctaccacc tcggtgtccg cggcggcgag gcctgcagct gcgagaccgc 780
gtcgtcgtg gcgggcttcc ggtttctccg gccgctggag gagggccagt acatataggt 840
aaaggtaggc gtcgttaaata cactgtaggc aggcagaggc aaccctaccc tcgcaaacct 900
gtaaaaacag ccagggaaaa aaaatggaga gtttttaatg 940

<210> 176
<211> 262
<212> PRT
<213> Z. mays

<400> 176
Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
1 5 10 15

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

Gly Glu Gly Ser Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
Seite 146

35

40

45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Arg Pro Asp
 50 55 60

Leu Lys Arg Gly Asn Phe Thr Gly Asp Asp Asp Glu Leu Ile Ile Lys
 65 70 75 80

Leu His Ala Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Gln Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110

Lys Arg Lys Leu Leu Ser Arg Gly Ile Asp Pro Gln Thr His Arg Pro
 115 120 125

Leu Ser Gly Gly Ala Gly Ser Ala Leu Thr Thr Thr Ser Ser Thr Ala
 130 135 140

Gly Phe Pro Ser Pro Ala Pro Ala Ser Arg Pro Thr Pro Thr Pro Pro
 145 150 155 160

Pro Ala Val Val Val Pro Pro Asn Ala Ile Phe Ala Arg Pro Ala Pro
 165 170 175

Ser Glu Asp Gly His Ser Ser Ser Gly Ala Ser Thr Asp Ala Pro Arg
 180 185 190

Cys Pro Asp Leu Asn Leu Asp Leu Asp Leu Ser Val Gly Pro Pro Pro
 195 200 205

Lys Thr Pro Ala Ala Thr Pro Ala Ser Gln Gln Arg Arg Arg Thr Thr
 210 215 220

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

Cys Glu Thr Ala Ser Ser Leu Ala Gly Phe Arg Phe Leu Arg Pro Leu
 245 250 255

Glu Glu Gly Gln Tyr Ile
 260

<210> 177
 <211> 824
 <212> DNA
 <213> Z. mays

<400> 177
 gcgggctct gggagaggta gggagccatg gggaggtcgc cgtgctgcga gaaggggcac 60

accaacaagg gcgcgtggac caaggaggag gacgagcggc tgggtggcgta catccggtcg 120

PF5908220081029_F_60204_PCT_Sequence.txt

cacggggaag ggtgctggcg gtcgctgccc agcgcggcgg gtctgctgcg ctgcggcaag	180
agctgcaggc tgcggtggat gaactacctc cggccggacc tcaagcgcg gaacttcacc	240
gacgacgagg acgagctcat catccgcctg cacgccctcc tcggcaacaa gtgggtctctg	300
atcgccgggc agctgccggg ccggacggac aacgagatca agaactactg gaacacgcac	360
atcaaacgca agctcctggc ccgcggcac gacccgcacg cgcaccaccg cccgcaggcg	420
ctgcaccacg tggcagcagc agccctcgtc ccggcccccg ccgcaagcc gaagccgaag	480
ccggcggagt cgtccgacga cggcgggcgc agcagctgca gctgcagcgg cagcggcagc	540
agcgcggggg agccgcggtg ccccgacctc aacctcgacc tgtccgttgg tccgcccggac	600
gcgcccacct cgccgccgcc gccgtgcctg tgccaccgcg cctgggaagc gtgcggctgc	660
caggcaggct gacggctgag gcagcaagag ttcagatttt tttttgtta ggcagttgaa	720
acaaggctag tgtgaaccga gaggatca gtagctagga cactgtctca gagaaagaaa	780
gaaaaaaaaa aaccaaagg attctcgaaa aaaaaaaaaa aaaa	824

<210> 178
 <211> 214
 <212> PRT
 <213> Z. mays

<400> 178

Met Gly Arg Ser Pro Cys Cys Glu Lys Gly His Thr Asn Lys Gly Ala
 1 5 10 15

Trp Thr Lys Glu Glu Asp Glu Arg Leu Val Ala Tyr Ile Arg Ser His
 20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Ser Ala Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Arg Pro Asp
 50 55 60

Leu Lys Arg Gly Asn Phe Thr Asp Asp Glu Asp Glu Leu Ile Ile Arg
 65 70 75 80

Leu His Ala Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Gln Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110

Lys Arg Lys Leu Leu Ala Arg Gly Ile Asp Pro His Ala His His Arg
 115 120 125

Pro Gln Ala Leu His His Val Ala Ala Ala Ala Leu Val Pro Ala Pro
 130 135 140

Ala Ala Lys Pro Lys Pro Lys Pro Ala Glu Ser Ser Asp Asp Gly Gly
 Seite 148

145 150 155 160

Arg Ser Ser Cys Ser Cys Ser Gly Ser Gly Ser Ser Ala Gly Glu Pro
165 170 175

Arg Cys Pro Asp Leu Asn Leu Asp Leu Ser Val Gly Pro Pro Asp Ala
180 185 190

Pro Thr Ser Pro Pro Pro Pro Cys Leu Cys His Arg Ala Trp Glu Ala
195 200 205

Cys Gly Cys Gln Ala Gly
210

<210> 179
<211> 1276
<212> DNA
<213> Z. mays

<400> 179
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ggcggcaaaa ggacgataca aaagcagcca gggttgctgg caacagcgtc ggtcgcccgc 120
ccgctcgcca tggggaggtc gccgtgctgc gagaaggcgc acaccaacaa gggcgcgctgg 180
accaaggagg aggacgagcg cctggctcgcg cacatcaggg cgacaggcga ggggtgctgg 240
cgctcgctgc ccaaggccgc cggcctcctg cgctgcggca agagctgccg cctccgctgg 300
atcaactacc tccgccccga cctcaagcgc ggcaacttca cggaggagga ggacgagctc 360
atcgtcaagc tgcacagcgt cctcggcaac aagtgggtccc tgatcgccgg aaggctgccc 420
ggcaggacgg acaacgagat caagaactac tggaacacgc acatccggag gaagctgctg 480
agcaggggga tcgacccggt gacgcaccgc ccggtcacgg agcaccacgc gtccaacatc 540
accatatcgt tcgagacgga ggtggccgcc gctgcccgtg atgataagaa gggcgccgctc 600
ttccggctgg aggaggagga ggagcgcaac aaggcgacga tggtcgtcgg ccgcgaccgg 660
cagagccaga gccagagcca cagccacccc gccggcgagt gggggccagg gaagaggccg 720
ctcaagtgcc ccgacctcaa cctggacctc tgcacagacc cgccgtgcca ggaggaggag 780
gagatggagg aggctgcgat gagagtgaga ccggcggtga agcgggaggc cgggctctgc 840
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tctggaaatt gacgct 1276

PF5908220081029_F_60204_PCT_Sequence.txt

<210> 180
 <211> 273
 <212> PRT
 <213> Z. mays

<400> 180

Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
 1 5 10 15

Trp Thr Lys Glu Glu Asp Glu Arg Leu Val Ala His Ile Arg Ala His
 20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60

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

Leu His Ser Val Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110

Arg Arg Lys Leu Leu Ser Arg Gly Ile Asp Pro Val Thr His Arg Pro
 115 120 125

Val Thr Glu His His Ala Ser Asn Ile Thr Ile Ser Phe Glu Thr Glu
 130 135 140

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

Glu Glu Glu Glu Glu Arg Asn Lys Ala Thr Met Val Val Gly Arg Asp
 165 170 175

Arg Gln Ser Gln Ser Gln Ser His Ser His Pro Ala Gly Glu Trp Gly
 180 185 190

Gln Gly Lys Arg Pro Leu Lys Cys Pro Asp Leu Asn Leu Asp Leu Cys
 195 200 205

Ile Ser Pro Pro Cys Gln Glu Glu Glu Glu Met Glu Glu Ala Ala Met
 210 215 220

Arg Val Arg Pro Ala Val Lys Arg Glu Ala Gly Leu Cys Phe Gly Cys
 225 230 235 240

Ser Leu Gly Leu Pro Arg Thr Ala Asp Cys Lys Cys Ser Ser Ser Ser
 Seite 150

Phe Leu Gly Leu Arg Thr Ala Met Leu Asp Phe Arg Ser Leu Glu Met
260 265 270

Lys

<210> 181
<211> 1328
<212> DNA
<213> Z. mays

<400> 181
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accgccaccg gcagaaccag aacacatcga gcggcatcgg agcgcgaatc tgtgcggcgg 180
cgtcgcctct gccgggaggg tgggcggcat ggggaggtcc ccgtgctgcg agcaggcgca 240
caccaacaag ggcgcgtgga ccaaggagga ggaccagcgc ctcatcgcct acatcaaggc 300
ccacggcgag ggctgctgga ggtcgctacc aaaagccgca gggctgctgc ggtgcgggaa 360
gagctgccgg ctgcggtgga tcaactacct gcgcccggac ctcaagcgcg gcaacttcag 420
cgaggaggag gacgagctga tcatcaagtt ccacgagctg ttcggcaaca agtggtcgct 480
catcgccggg aggctgccgg gcaggacgga caacgagata aaaaactact ggaacacgca 540
catcaagcgg aagctgctcg cccgcggcat ggacccgcag acccaccgcc cgctggccgc 600
agcgccagca ggagggccgc agcagcagca ttgccattac cagatggagc cacagaagcg 660
ggcggcgccg gcggaccatt ccgaggccgc cgttgccacc aactcgccgg aggccagcag 720
ccgcagcagc gacgacgacg aggcgcgggc gctggcgcca ccgccgcggc ggcggcagcg 780
ccacctgac atcgacctga acctgtccat cagcctcgcg gcctaccagc cgccggaggg 840
aaccggcagc gccatcgagc cactgacggc gacgacgaag cgggaggagg gaacggcggc 900
ggcgggtgtg ctctgcctca acagcctcg gtaccgggca ggcgtcgagt gcgcctgtgg 960
cagcggcggc tcgccgtcgt cccgttcgca gtgggctcgg gatTTTTTtac aggcggcgcc 1020
ctgctacaga ggctagcatt gatcagtgag acagtgacat gatcgggagg gcttttactg 1080
aggggagggg cagagcagat atagttaact agtagtacta ttagtaaaaa ggcaagcgtg 1140
cttagtaggc tttagcagct catgcattgc atgcatcatg ggttatttac gaggagatgt 1200
gctctttgtc tttgtcgat tctggctctg gcctcggaca cagactgatc gatcatgcct 1260
tggcgacatg acatgcatac tgtagagtgg tttagtcgca gcatgcgtgc agttcatgac 1320
ttttgtgc 1328

<210> 182
<211> 275
<212> PRT
<213> Z. mays

<400> 182

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

Tyr Arg Gly
275

<210> 183
<211> 1103
<212> DNA
<213> Z. mays

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<400> 183
ctcgtctgcct tctcaaatcc aaacgcgaag tagcaacaag caaaagccca gatcgataat    60
acgatggggc ggtcgccgtg ctgcgagaag gcgcacacca acagggggcgc gtggaccaag    120
gaggaggacg agcggctggt ggcctacgtc cgcgcgcacg gcgaaggggtg ctggcgctcg    180
ctgcccaggg cggcgggcct gctgcgctgc ggcaagagct gccgcctgcg ctggatcaac    240
tacctccgcc cggacctcaa gcgaggcaac ttcaccgccg acgaggacga cctcatcgtc    300
aagctgcaca gcctcctcgg gaacaagtgg tcgctcatcg ccgcgcgggt cccggggcgg    360
acggacaacg agatcaagaa ctactggaac acgcacatcc ggcgcaagct gctgggcagc    420
ggcatcgacc ccgtcacgca ccgccgcgtc gcggggggcg ccgcgaccac catctcgttc    480
cagcccagcc ccaacaccgc cgtcgccgcc gccgcagaaa cagcagcgca ggcgccgatc    540
aaggccgagg agacggcggc cgtcaaggcg cccaggtgcc ccgacctcaa cctggacctc    600
tgcacagcc cgccgtgcc gcatgaggac gacggcgagg aggaggagga ggagctggac    660
ctcatcaagc ccgccgtcgt caagcgggag gcgctgcagg ccggccacgg ccacggccac    720
ggcctctgcc tcggctgcgg cctgggcgga cagaaggag cggccgggtg cagctgcagc    780
aacggccacc acttcctggg gctcaggacc agcgtgctcg acttcagagg cctggagatg    840
aagtgaacga aacgaagccc acacgtcctt tcttctcctt ttgttgctcg ttgtagtctt    900
ggcttgttgg atttggatag agctagttgg ttactagttg ttagttagaa gatagtgcag    960
gatgatcact agtactggc tacctcgaca cagtagctgc tcccttctct tccattctat   1020
gtaaaaaaga aaaaaaata cttagggggg gtttggtttc tagggactaa tgtttagtcc   1080
ctacatttta aaaaaaaaaa aaa                                     1103
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<210> 184
<211> 260
<212> PRT
<213> Z. mays

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<400> 184
Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Arg Gly Ala
1          5          10          15

Trp Thr Lys Glu Glu Asp Glu Arg Leu Val Ala Tyr Val Arg Ala His
          20          25          30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Arg Ala Ala Gly Leu Leu Arg
35          40          45
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Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60

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

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Ala Arg Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
100 105 110

Arg Arg Lys Leu Leu Gly Ser Gly Ile Asp Pro Val Thr His Arg Arg
115 120 125

Val Ala Gly Gly Ala Ala Thr Thr Ile Ser Phe Gln Pro Ser Pro Asn
130 135 140

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

Ala Glu Glu Thr Ala Ala Val Lys Ala Pro Arg Cys Pro Asp Leu Asn
165 170 175

Leu Asp Leu Cys Ile Ser Pro Pro Cys Gln His Glu Asp Asp Gly Glu
180 185 190

Glu Glu Glu Glu Glu Leu Asp Leu Ile Lys Pro Ala Val Val Lys Arg
195 200 205

Glu Ala Leu Gln Ala Gly His Gly His Gly His Gly Leu Cys Leu Gly
210 215 220

Cys Gly Leu Gly Gly Gln Lys Gly Ala Ala Gly Cys Ser Cys Ser Asn
225 230 235 240

Gly His His Phe Leu Gly Leu Arg Thr Ser Val Leu Asp Phe Arg Gly
245 250 255

Leu Glu Met Lys
260

<210> 185
<211> 608
<212> DNA
<213> Zea mays

<400> 185
gcctcttccc tgctgcatct gcacgccgcc cacacatgct atttttgttc acttggttatt 60
gcttcttgct gtggtctggt aaaccgactt ggtcctgata atcctccgcg ttctactgat 120
gtgctgtcgc tgcacatgc gcgtgttgct gtcagagcct agggctggtg aagcccatgg 180
aggagatgct gatggcggcc agcgcgggcg ctgcaaatcc gagccaaggc tcgaatccga 240
Seite 154

PF5908220081029_F_60204_PCT_Sequence.txt

acccgccgcc ggcggcgccc gtaacgggag cgggtagcac cgagcggcgc gcgcggccgc 300
 agaaggagaa gacgctcacc tgcccgcggt gcaactccac caacaccaa ttctgtact 360
 acaacaacta cagcctccag cagccacgct acttctgcaa gacgtgccgc cgctactgga 420
 cggagggcgg atccctccgc agcgtccccg tgggcggcgg ctcccgcaag aacaagcgct 480
 cctcctcctc ctctctctcg tcggcgggcg cgtccgcctc cacctcctcc tcggccacga 540
 gctcgtccat ggccagcaca ccggggggcg cgtccaagag tccggagctg gcgcacgacc 600
 tcaaccta 608

<210> 186
 <211> 163
 <212> PRT
 <213> Zea mays
 <400> 186

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