

SEQUENCE LISTING

<110> BASF Plant Science GmbH

<120> TRANSGENIC PLANTS WITH INCREASED STRESS TOLERANCE AND YIELD

<130> PF 60360

<160> 468

<170> PatentIn version 3.5

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

Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Leu Cys Cys
195 200 205

Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly Cys Ile Phe
210 215 220

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

Asn Gln Leu Lys Leu Ile Ile Ser Val Leu Gly Ser Gln His Glu Ser
245 250 255

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

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

Arg Ile Asp Ala Lys Arg Thr Leu Arg Glu Ile Lys Leu Leu Arg His
85 90 95

Met Asp His Glu Asn Ile Val Ala Ile Arg Asp Ile Ile Arg Pro Pro
100 105 110

Thr Arg Glu Asn Phe Asn Asp Val Tyr Ile Val Tyr Glu Leu Met Asp
115 120 125

Thr Asp Leu His Gln Ile Ile Arg Ser Asn Gln Pro Leu Thr Glu Asp
130 135 140

His Cys Gln Tyr Phe Leu Tyr Gln Leu Leu Arg Gly Leu Lys Tyr Ile
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His Ser Ala Lys Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu Leu
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Leu Asn Ala Asn Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg
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Tyr Arg Ala Pro Glu Leu Leu Leu Asn Cys Ser Glu Tyr Thr Ala Ala
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Glu Pro Leu Phe Pro Gly Arg Asp Tyr Val Gln Gln Leu Arg Leu Ile
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Thr Glu Leu Ile Gly Ser Pro Glu Asp His Asp Leu Gly Phe Leu Arg
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Ser Asp Asn Ala Arg Arg Tyr Ile Arg Gln Leu Pro Arg Phe Ala Arg
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Gln Pro Leu Asp Arg Lys Phe Pro Asn Met Gly Pro Ala Ala Ile Asp
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Leu Val Glu His Met Leu Arg Phe Asp Pro Ala Arg Arg Ile Thr Val
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Asp Glu Pro Ile Cys His Ser Pro Phe Glu Phe Asp Phe Glu Gln Pro
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Ala Lys Asn Asn Glu Thr Gly Asp Arg Val Ala Ile Lys Lys Ile Thr
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Asn Ala Phe Glu Asn Thr Thr Asp Ala Arg Arg Thr Leu Arg Glu Ile
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Arg Leu Leu Arg His Leu Phe His Glu Asn Ile Ile Ala Val Lys Asp
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Ile Met Lys Pro Val Gly Arg Gln Thr Phe Asn Asp Val Tyr Ile Val
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Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Arg Ser Ser Gln
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Thr Leu Thr Asp Asp His Cys Gln Tyr Phe Ile Tyr Gln Leu Leu Arg
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Gly Leu Lys Tyr Val His Ser Ala Asn Val Leu His Arg Asp Leu Lys
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Pro Ser Asn Leu Leu Leu Asn Ala Ser Cys Asp Leu Lys Ile Cys Asp
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Phe Gly Leu Ala Arg Thr Gly Ser Asp Lys Gly Gln Phe Met Thr Glu
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Asp Glu Tyr Thr Ser Ala Ile Asp Met Trp Ser Val Gly Cys Ile Phe
210 215 220

Ala Glu Leu Leu Gly Arg Lys Pro Leu Phe Pro Gly Lys Asp Tyr Ile
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His Gln Leu Lys Leu Ile Ile Ser Ile Ile Gly Ser Pro Asp Glu Thr
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Asp Leu His Phe Ile Gln Ser Gln Lys Ala Arg Ser Tyr Ile Arg Ser
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Leu Pro Phe Thr Pro Arg Val Ser Leu Ala Arg Leu Tyr Pro Arg Ala
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Asn Pro Leu Ala Ile Gln Leu Ile Asp Lys Met Leu Val Phe Asp Pro
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Arg Lys Arg Ile Thr Val His Glu Ala Leu Glu His Pro Tyr Leu Ser
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Met Leu His Asp Ala Thr Val Glu Pro Ser Ala Pro Ala Pro Phe Glu
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Ser Ile Asn Gln Glu Thr Asn Glu Lys Val Ala Ile Lys Lys Ile Asn
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Asn Val Phe Asp Asn Arg Val Asp Ala Leu Arg Thr Leu Arg Glu Leu
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Lys Leu Leu Arg His Leu Arg His Glu Asn Val Ile Ala Leu Lys Asp
85 90 95

Ile Met Met Pro Ile His Arg Arg Ser Phe Lys Asp Val Tyr Leu Val
100 105 110

Ser Glu Leu Met Asp Thr Asp Leu His Gln Ile Val Lys Ser Ser Gln
115 120 125

Pro Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln Leu Leu Arg
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Gly Leu Lys Tyr Leu His Ser Ala Gly Ile Leu His Arg Asp Leu Lys
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Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys Ile Cys Asp
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Phe Gly Leu Ala Arg Thr Asn Asn Thr Lys Gly Gln Phe Met Thr Glu
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Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Leu Cys Cys
195 200 205

Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly Cys Ile Phe
210 215 220

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

Asp Leu Ala Phe Ile Asp Asn Pro Lys Ala Arg Asn Tyr Ile Lys Ser
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Leu Pro Tyr Thr Pro Gly Ile Pro Leu Ser Ser Met Tyr Pro Gln Ala
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His Pro Leu Ala Ile Asp Leu Leu Gln Lys Met Leu Val Phe Asp Pro
290 295 300

Ser Lys Arg Ile Ser Val Thr Gln Ala Leu Glu His Pro Tyr Met Ser
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Pro Leu Tyr Asp Pro Ser Ala Asn Pro Pro Ala Gln Val Pro Ile Asp
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Ser Val Asn Arg Glu Ile Asn Glu Lys Val Ala Ile Lys Lys Ile Gln
50 55 60

Asn Ala Phe Glu Asn Arg Val Asp Ala Leu Arg Thr Leu Arg Glu Leu
65 70 75 80

Lys Leu Leu Arg His Leu His His Glu Asn Val Ile Ala Leu Lys Asp
85 90 95

Ile Met Met Pro Val His Arg Asn Ser Phe Lys Asp Val Tyr Leu Val
100 105 110

Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys Ser Ser Gln
115 120 125

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

Gly Leu Lys Tyr Leu His Ser Ala Asn Ile Leu His Arg Asp Leu Lys
145 150 155 160

Pro Gly Asn Leu Leu Ile Asn Ala Asn Cys Asp Leu Lys Ile Cys Asp
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Phe Gly Leu Ala Arg Thr Asn Cys Ser Lys Asn Gln Phe Met Thr Glu
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Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Leu Cys Cys
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Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly Cys Ile Phe
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Ala Glu Leu Leu Gly Arg Lys Pro Ile Phe Pro Gly Ser Glu Cys Leu
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Asn Gln Leu Lys Leu Ile Ile Asn Ile Leu Gly Ser Gln Arg Glu Glu
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Asp Ile Glu Phe Ile Asp Asn Pro Lys Ala Lys Lys Tyr Ile Lys Ser
260 265 270

Leu Pro Tyr Ser Pro Gly Ser Pro Leu Ser Arg Leu Tyr Pro Asn Ala
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His Pro Leu Ala Ile Asp Leu Leu Ala Lys Met Leu Val Phe Asp Pro
290 295 300

Thr Lys Arg Ile Ser Val Thr Gln Ala Leu Gln His Pro Tyr Met Ala
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Pro Leu Tyr Asp Pro Asn Cys Asp Pro Pro Ala Val Ile Pro Ile Asp
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ccactttatg atcccaactg taatcctcct gctcagttgc tagtcgatga tcttgagatt 1020
gatgaggagt tgggggaaga aatgatccgt gagactatgt ggaaggagat gttacattac 1080
catcctgagt ttgcagcagc aagtgggtggg gagttctgct accagtag 1128

<210> 12
<211> 375
<212> PRT
<213> L. usitatissimum

<400> 12

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

Val Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Ile Val Cys Ser
35 40 45

Ser Val Asn Arg Glu Thr Asn Glu Lys Val Ala Ile Lys Lys Ile His
50 55 60

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

Lys Leu Leu Arg His Leu Arg His Thr Asn Val Ile Ala Leu Lys Asp
85 90 95

Val Met Met Pro Ile His Arg Arg Ser Phe Lys Asp Val Tyr Phe Val
100 105 110

Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys Ser Ser Gln
115 120 125

Ser Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln Leu Leu Arg
130 135 140

Gly Leu Lys Tyr Leu His Ser Ala Asn Ile Leu His Arg Asp Leu Lys
145 150 155 160

Pro Gly Asn Leu Leu Ile Asn Ala Asn Cys Asp Leu Lys Ile Cys Asp
165 170 175

Phe Gly Leu Ala Arg Thr Ser Thr Gly Lys Gly Gln Phe Met Thr Glu
180 185 190

Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Leu Cys Cys
195 200 205

Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly Cys Ile Phe
210 215 220

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

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

Asp Leu Glu Phe Ile Asp Asn Ala Lys Ala Lys Lys Phe Ile Lys Ser
260 265 270

Leu Pro Tyr Ser Pro Gly Thr Ala Phe Ala His Leu Tyr Pro Asn Ala
275 280 285

His Pro Leu Ala Ile Asp Leu Leu Arg Lys Met Leu Ile Phe Asp Pro
290 295 300

Ser Lys Arg Ile Thr Val Ile Glu Ala Leu Gln His Pro Tyr Leu Ser
305 310 315 320

Pro Leu Tyr Asp Pro Asn Cys Asn Pro Pro Ala Gln Leu Leu Val Asp
325 330 335

Asp Leu Glu Ile Asp Glu Glu Leu Gly Glu Glu Met Ile Arg Glu Thr
340 345 350

Met Trp Lys Glu Met Leu His Tyr His Pro Glu Phe Ala Ala Ala Ser
355 360 365

Gly Gly Glu Phe Cys Tyr Gln
370 375

<210> 13

<211> 1572

<212> DNA

<213> B. napus

<400> 13

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gccaatgatg atttgaccaa agagcattac cagtttttcc tttatcagtt gttgcgtacg	420
ctcaagtaca ttcacacagc taatgtctac catagagatc tgaagccaaa gaatatattg	480
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gatacccca caacaatctt ttggacagac tatgttgcta caagatggta tagagctcct	600
gagctttgtg gatcttttta ctcaaagtat acaccagcaa ttgatatctg gagtataggc	660
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cagcttgatc ttatgactga tctgctcggg acaccttccc tggacaccat ctcccgggtg	780
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cactcaacgg cagttgcaag aggagggcaa ccgaaactta tgaataaacac aaacacattg 1320

aaccctgaaa ctactcaaag cattcctctt aatcaatata caacatcaca agcacctcaa 1380

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<210> 14

<211> 523

<212> PRT

<213> B. napus

<400> 14

Met Met Gln Gln Asp Pro Gln Arg Lys Lys Asn Asn Leu Glu Met Glu

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Phe Phe Ser Asp Tyr Gly Asp Ala Ser Arg Phe Lys Ile Gln Glu Val

20 25 30

Ile Gly Lys Gly Ser Tyr Gly Val Val Cys Ser Ala Ile Asp Thr Leu

35 40 45

Thr Gly Glu Lys Val Ala Ile Lys Lys Ile His Asp Ile Phe Glu His

50 55 60

Ile Ser Asp Ala Ala Arg Ile Leu Arg Glu Ile Lys Leu Leu Arg Leu

65 70 75 80

Leu Arg His Pro Asp Ile Val Glu Ile Lys His Ile Met Leu Pro Pro
85 90 95

Ser Arg Arg Glu Phe Lys Asp Ile Tyr Val Val Phe Glu Leu Met Glu
100 105 110

Ser Asp Leu His Gln Val Ile Lys Ala Asn Asp Asp Leu Thr Lys Glu
115 120 125

His Tyr Gln Phe Phe Leu Tyr Gln Leu Leu Arg Thr Leu Lys Tyr Ile
130 135 140

His Thr Ala Asn Val Tyr His Arg Asp Leu Lys Pro Lys Asn Ile Leu
145 150 155 160

Ala Asn Ala Asn Cys Lys Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg
165 170 175

Val Ala Phe Asn Asp Thr Pro Thr Thr Ile Phe Trp Thr Asp Tyr Val
180 185 190

Ala Thr Arg Trp Tyr Arg Ala Pro Glu Leu Cys Gly Ser Phe Tyr Ser
195 200 205

Lys Tyr Thr Pro Ala Ile Asp Ile Trp Ser Ile Gly Cys Ile Phe Ala
210 215 220

Glu Val Trp Arg Gly Lys Pro Leu Phe Leu Gly Lys Lys Val Val His
225 230 235 240

Gln Leu Asp Leu Met Thr Asp Leu Leu Gly Thr Pro Ser Leu Asp Thr
245 250 255

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

Arg Lys Lys Pro Pro Ile Pro Phe Thr Gln Lys Phe Pro Asn Ala Asp
275 280 285

Pro Leu Ser Leu Lys Leu Phe Glu Arg Leu Leu Ala Phe Asp Pro Lys
290 295 300

Asp Arg Pro Thr Ala Glu Glu Ala Leu Ala Asp Pro Tyr Phe Lys Gly
305 310 315 320

Leu Ala Lys Val Glu Arg Glu Pro Ser Cys Gln Pro Ile Thr Lys Met
325 330 335

Glu Phe Glu Phe Glu Arg Arg Lys Val Thr Lys Glu Asp Ile Arg Glu
340 345 350

Leu Ile Ser Arg Glu Ile Leu Glu Tyr His Pro Gln Leu Leu Lys Asp
355 360 365

His Met Ser Gly Ala Asp Lys Thr Asn Phe Leu Tyr Pro Ser Ala Val
370 375 380

Asp Gln Phe Arg Arg Gln Phe Ala His Leu Glu Glu Asn Ser Gly Lys
385 390 395 400

Thr Gly Pro Val Ala Pro Leu Glu Arg Lys His Ala Ser Leu Pro Arg
405 410 415

Ser Thr Val Ile His Ser Thr Ala Val Ala Arg Gly Gly Gln Pro Lys
420 425 430

Leu Met Asn Asn Thr Asn Thr Leu Asn Pro Glu Thr Thr Gln Ser Ile
435 440 445

Pro Leu Asn Gln Tyr Thr Thr Ser Gln Ala Pro Gln Arg Asn Leu Ser
450 455 460

Gly Thr Lys Pro Ser Thr Phe Met Gly Pro Val Ala Pro Tyr Asp Asn
465 470 475 480

Gly Arg Thr Ser Arg Glu Ala Tyr Asp Pro Arg Ser Leu Ile Arg Ser
485 490 495

Thr Ala Leu Pro Phe Pro Gln Gln Ser Ala Ala Ala Thr Met Gly Lys
500 505 510

Gln Gln Glu Arg Arg Asn Asn Asn His Gly Val
515 520

<210> 15
<211> 1692
<212> DNA
<213> G. max

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tctgcatatg atacacacac tggagaaaag gttgcaataa agaaaataaa tgacatatatt 180
gaacatgttt ctgatgccac tcgcattctt cgtgagatta agcttccttag actttttacgc 240

catccagata ttgtggagat caaacatatt ctgttacctc cttctagaag ggaattcaag	300
gatatatatg ttgtcttcga actcatggaa tctgatttac atcaggtcat caaagcta	360
gatgatctga caccagagca ttaccagttt tttttgtatc agcttcttcg aggc	420
tatattcata cagcaaatgt ttttcaccgt gatctaaagc caaaaaacat tttag	480
gctgactgca aactgaagat ttgcgacttt ggtcttgcca gagtggcttt caat	540
cccactgcta ttttctggac agattatggt gcaaccaggt ggtatagggc tctg	600
tgtggatcct ttttttccaa gtatacacca gctatagaca tatggagcat tggc	660
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gaccttatga ctgatcttct tggaactcca tctcttgaag ccattgctag ggtac	780
gagaaagctc ggagatatatt gagcagcatg cgaaagaaga agcctgttcc tct	840
aagtttcccta atgcagaccc ccttgctctt cgtttgtag aaaaaatggt ggc	900
cctaaggatc ggcctactgc tgaagaggct ctagcggatc catattttaa aggc	960
aaggttgaga gagaaccatc tgctcagcca gttactaaga tggagtttga attt	1020
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 cagtgggtatt ga 1692

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 <211> 563
 <212> PRT
 <213> G. max

<400> 16

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Thr Glu Tyr Gly Glu Gly Ser Arg Tyr Arg Ile Glu Glu Val Ile Gly
 20 25 30

Lys Gly Ser Tyr Gly Val Val Cys Ser Ala Tyr Asp Thr His Thr Gly
 35 40 45

Glu Lys Val Ala Ile Lys Lys Ile Asn Asp Ile Phe Glu His Val Ser
 50 55 60

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

His Pro Asp Ile Val Glu Ile Lys His Ile Leu Leu Pro Pro Ser Arg
 85 90 95

Arg Glu Phe Lys Asp Ile Tyr Val Val Phe Glu Leu Met Glu Ser Asp
 100 105 110

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

Gln Phe Phe Leu Tyr Gln Leu Leu Arg Gly Met Lys Tyr Ile His Thr
130 135 140

Ala Asn Val Phe His Arg Asp Leu Lys Pro Lys Asn Ile Leu Ala Asn
145 150 155 160

Ala Asp Cys Lys Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Val Ala
165 170 175

Phe Asn Asp Thr Pro Thr Ala Ile Phe Trp Thr Asp Tyr Val Ala Thr
180 185 190

Arg Trp Tyr Arg Ala Pro Glu Leu Cys Gly Ser Phe Phe Ser Lys Tyr
195 200 205

Thr Pro Ala Ile Asp Ile Trp Ser Ile Gly Cys Ile Phe Ala Glu Leu
210 215 220

Leu Thr Gly Lys Pro Leu Phe Pro Gly Lys Asn Val Val His Gln Leu
225 230 235 240

Asp Leu Met Thr Asp Leu Leu Gly Thr Pro Ser Leu Glu Ala Ile Ala
245 250 255

Arg Val Arg Asn Glu Lys Ala Arg Arg Tyr Leu Ser Ser Met Arg Lys
260 265 270

Lys Lys Pro Val Pro Leu Ser Gln Lys Phe Pro Asn Ala Asp Pro Leu
275 280 285

Ala Leu Arg Leu Leu Glu Lys Met Leu Ala Phe Glu Pro Lys Asp Arg
290 295 300

Pro Thr Ala Glu Glu Ala Leu Ala Asp Pro Tyr Phe Lys Gly Leu Ala
305 310 315 320

Lys Val Glu Arg Glu Pro Ser Ala Gln Pro Val Thr Lys Met Glu Phe
325 330 335

Glu Phe Glu Arg Arg Arg Ile Thr Lys Glu Asp Val Arg Glu Leu Ile
340 345 350

Tyr Arg Glu Ile Leu Glu Tyr His Pro Lys Met Leu Lys Glu Phe Leu
355 360 365

Glu Gly Ser Glu Pro Thr Gly Phe Met Tyr Pro Ser Ala Val Asp His
370 375 380

Phe Lys Lys Gln Phe Ala Tyr Leu Glu Glu His Tyr Gly Lys Gly Gly
385 390 395 400

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

Val Leu Tyr Ser Asp His Ser Met Gln Asn Thr Ser Glu Val Ala Asp
420 425 430

Asp Leu Ser Lys Cys Cys Ile Lys Glu Val Glu Lys Gln Pro Ile Asp
435 440 445

Ser Ser Ser Ala Ile Pro Met Ser Arg Leu Pro Leu Gln Ala Pro Gln
450 455 460

Asn Ile Gln Gly Val Ala Ala Arg Pro Gly Lys Val Val Gly Ser Val
465 470 475 480

Met Arg Tyr Asn Asn Cys Gly Val Ala Gly Thr Ala Glu Ala Glu Gln
485 490 495

Arg Arg Val Val Arg Asn Pro Ser Val Ser Ala Gln Tyr Ala Ala Ser
500 505 510

Ser Cys Ser Tyr Pro Arg Arg Asn Ser Gly Tyr Lys Ser Glu Arg Gly
515 520 525

Thr Glu Glu Gly Gly Ile Glu Gly Ser Asn Gly Leu Gln Pro Lys Pro
530 535 540

Gln Tyr Met Ala Arg Lys Val Ala Ala Ala Gln Ala Gly Pro Gly Gly
545 550 555 560

Gln Trp Tyr

<210> 17

<211> 1122

<212> DNA

<213> G. max

<400> 17

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cctattcgcc ctgtcggtag aggtgcttat ggtattgttt gcgctgctgt aaatgcagag	180
acaggcgagg aagttgccat taagaagatt ggcaatgcat tcgacaacag aatagatgcc	240
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attaaagata ttatacgtcc tccacagaag gaaaacttca atgatgtgta ccttgtttct	360
gagttaatgg acacagatct gcatcaaata attcgttcca atcagcaatt gactgatgat	420
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gtcactagat ggtaccgagc tcccgaattg cttcttaatt gttcagaata tacagcagcc	660
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<210> 18
 <211> 373
 <212> PRT
 <213> G. max

<400> 18

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Thr His Gly Gly Arg Tyr Val Gln Tyr Asn Ile Tyr Gly Asn Leu Phe
20 25 30

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

Ala Tyr Gly Ile Val Cys Ala Ala Val Asn Ala Glu Thr Gly Glu Glu
50 55 60

Val Ala Ile Lys Lys Ile Gly Asn Ala Phe Asp Asn Arg Ile Asp Ala
65 70 75 80

Lys Arg Thr Leu Arg Glu Ile Lys Leu Leu Arg His Met Asp His Ala
85 90 95

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

Phe Asn Asp Val Tyr Leu Val Ser Glu Leu Met Asp Thr Asp Leu His
115 120 125

Gln Ile Ile Arg Ser Asn Gln Gln Leu Thr Asp Asp His Cys Arg Tyr
130 135 140

Phe Leu Tyr Gln Leu Leu Arg Gly Leu Lys Tyr Val His Ser Ala Asn
145 150 155 160

Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu Leu Leu Asn Ala Asn
165 170 175

Cys Asp Leu Lys Ile Ala Asp Phe Gly Leu Ala Arg Thr Thr Ser Glu
180 185 190

Thr Asp Phe Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro
195 200 205

Glu Leu Leu Leu Asn Cys Ser Glu Tyr Thr Ala Ala Ile Asp Ile Trp
210 215 220

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

Pro Gly Lys Asp Tyr Val His Gln Leu Arg Leu Ile Thr Glu Leu Ile
245 250 255

Gly Ser Pro Asp Asp Ala Ser Leu Gly Phe Leu Arg Ser Asp Asn Ala
260 265 270

Arg Arg Tyr Val Lys Gln Leu Pro Gln Tyr Pro Lys Gln Asn Phe Ser
275 280 285

Ala Arg Phe Pro Thr Met Ser Pro Gly Ala Val Asp Leu Leu Glu Lys
290 295 300

Met Leu Ile Phe Asp Pro Asn Arg Arg Ile Thr Val Asp Glu Ala Leu
305 310 315 320

Ser His Pro Tyr Met Ser Pro Leu His Asp Ile Asn Glu Glu Pro Val
325 330 335

Cys Thr Arg Pro Phe Ser Phe Asp Phe Glu Gln Pro Ser Phe Thr Glu
340 345 350

Glu Asp Ile Lys Glu Leu Ile Trp Arg Glu Ser Val Lys Phe Asn Pro
355 360 365

Val Pro Pro Val Tyr
370

<210> 19
<211> 1134
<212> DNA
<213> L. usitatissimum

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aatcgtaagc cattgtttcc aggcaaagac caagtccacc agatgagggt gttgacagag 780

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catcccctgg ccattgatct tgtggataaa atgatgacat ttgatccac aaaaagaata 960

actgttgagg aagcattagc gcacccttat ctggaacggt tacatgacat agcagatgaa 1020

ccagtttgtc aagagtcatt ctcttttgat tttgagcaac aagtattgag tgaagaacag 1080

atgaaagaga tgatatacag ggaggcattg tcattcaatc cagagtatgc ataa 1134

<210> 20

<211> 377

<212> PRT

<213> L. usitatissimum

<400> 20

Met Ala Gly Gly Tyr Ala His Ser Asn Gly Thr Gly Gly Gln Tyr Pro
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Asp Phe Pro Ala Ile Pro Ile His Gly Gly Gln Phe Val Gln Tyr Asn
20 25 30

Ile Phe Gly Asn Gln Phe Glu Ile Thr Pro Lys Tyr Arg Pro Pro Ile
35 40 45

Met Pro Ile Gly Arg Gly Ala Tyr Gly Ile Val Cys Ser Val Leu Asn
50 55 60

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

Asp Asn His Met Asp Ala Lys Arg Thr Leu Arg Glu Ile Lys Leu Leu
85 90 95

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

Pro Pro Leu Arg Arg Glu Phe Thr Asp Val Tyr Ile Ala Thr Glu Leu
115 120 125

Met Asp Thr Asp Leu His Gln Ile Ile Arg Ser Asn Gln Gly Leu Ser
130 135 140

Glu Glu His Cys Gln Tyr Phe Met Tyr Gln Leu Leu Arg Gly Leu Lys
145 150 155 160

Tyr Ile His Ser Ala His Val Ile His Arg Asp Leu Lys Pro Ser Asn
165 170 175

Leu Leu Leu Asn Ala Asn Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu
180 185 190

Ala Arg Pro Ala Ser Glu Asn Glu Phe Met Thr Glu Tyr Val Val Thr
195 200 205

Arg Trp Tyr Arg Ala Pro Glu Leu Leu Leu Asn Ser Gln Asp Tyr Thr
210 215 220

Ala Ala Ile Asp Val Trp Ser Val Gly Cys Ile Phe Met Glu Leu Met
225 230 235 240

Asn Arg Lys Pro Leu Phe Pro Gly Lys Asp Gln Val His Gln Met Arg
245 250 255

Leu Leu Thr Glu Leu Leu Gly Thr Pro Ser Glu Ser Asp Leu Gly Phe
260 265 270

Val Arg Asn Glu Asp Ala Arg Lys Tyr Ile Arg Gln Leu Ser Pro His
275 280 285

Pro Arg Gln Ser Leu Ala Lys Leu Phe Pro His Val His Pro Leu Ala
290 295 300

Ile Asp Leu Val Asp Lys Met Met Thr Phe Asp Pro Thr Lys Arg Ile
305 310 315 320

Thr Val Glu Glu Ala Leu Ala His Pro Tyr Leu Glu Arg Leu His Asp
325 330 335

Ile Ala Asp Glu Pro Val Cys Gln Glu Ser Phe Ser Phe Asp Phe Glu
340 345 350

Gln Gln Val Leu Ser Glu Glu Gln Met Lys Glu Met Ile Tyr Arg Glu
355 360 365

Ala Leu Ser Phe Asn Pro Glu Tyr Ala
370 375

<210> 21

<211> 1215

<212> DNA

<213> Z. mays

<400> 21

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<213> Z. mays

<400> 22

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

Arg Gly Ala Tyr Gly Ile Val Cys Ser Val Met Asn Ser Glu Thr Lys
50 55 60

Glu Met Val Ala Ile Lys Lys Ile Ala Asn Ala Phe Asp Asn His Met
65 70 75 80

Asp Ala Lys Arg Thr Leu Arg Glu Ile Lys Leu Leu Arg His Leu Asp
85 90 95

His Glu Asn Ile Ile Gly Ile Arg Asp Val Ile Pro Pro Pro Val Pro
100 105 110

Gln Ala Phe Asn Asp Val Tyr Ile Gly Thr Glu Leu Met Asp Thr Asp
115 120 125

Leu His His Ile Ile Arg Ser Asn Gln Glu Leu Ser Glu Glu His Ser
130 135 140

Gln Tyr Phe Met Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser
145 150 155 160

Ala Asn Val Ile His Arg Asp Leu Lys Pro Ser Asn Leu Leu Val Asn
165 170 175

Ala Asn Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Pro Ser
180 185 190

Ser Glu Ser Asp Met Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg
195 200 205

Ala Pro Glu Leu Leu Leu Asn Ser Thr Asp Tyr Ser Ala Ala Ile Asp
210 215 220

Val Trp Ser Val Gly Cys Ile Phe Met Glu Leu Ile Asn Arg Gln Pro
225 230 235 240

Leu Phe Pro Gly Arg Asp His Met His Gln Met Arg Leu Ile Thr Glu
245 250 255

Ala Arg Ala Arg Arg Thr His His Ile Leu Pro Ile Ile Gln Phe Leu
260 265 270

Leu Leu Leu Leu Leu Leu Met Asn Ile Ala Gly Thr Arg Gln Val Ile
275 280 285

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

Arg Lys Tyr Met Arg His Leu Pro Gln Phe Pro Arg Arg Pro Phe Val
 305 310 315 320

Ser Leu Phe Pro Arg Met Gln Pro Val Ala Leu Asp Leu Ile Glu Arg
 325 330 335

Met Leu Thr Phe Asn Pro Leu Gln Arg Ile Thr Val Glu Glu Ala Leu
 340 345 350

Glu His Pro Tyr Leu Glu Arg Leu His Asp Val Ala Asp Glu Pro Ile
 355 360 365

Cys Thr Asp Pro Phe Ser Phe Asp Phe Glu Gln Gln Ala Leu Thr Glu
 370 375 380

Asp Gln Met Lys Gln Leu Ile Phe Asn Glu Ala Ile Glu Leu Asn Pro
 385 390 395 400

Asn Phe Arg Tyr

<210> 23

<211> 1185

<212> DNA

<213> H. annuus

<400> 23

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<211> 394

<212> PRT

<213> H. annuus

<400> 24

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10

15

Ala Pro Pro Pro Pro Pro Pro Gln Gln Gln Pro Val Ala Gly Ile Asp
20 25 30

Asn Ile Pro Ala Thr Leu Ser His Gly Gly Arg Phe Ile Gln Tyr Asn
35 40 45

Ile Phe Gly Asn Ile Phe Glu Val Thr Ala Lys Tyr Lys Pro Pro Ile
50 55 60

Met Pro Ile Gly Lys Gly Ala Tyr Gly Ile Val Cys Ser Ala Leu Asn
65 70 75 80

Ser Glu Thr Asn Glu His Val Ala Ile Lys Lys Ile Ala Asn Ala Phe
85 90 95

Asp Asn Lys Ile Asp Ala Lys Arg Thr Leu Arg Glu Ile Lys Leu Leu
100 105 110

Arg His Met Asp His Glu Asn Val Val Ala Ile Arg Asp Ile Ile Pro
115 120 125

Pro Pro Glu Arg Asn Ala Phe Asn Asp Val Tyr Ile Ala Tyr Glu Leu
130 135 140

Met Asp Thr Asp Leu His Gln Ile Ile Arg Ser Asn Gln Ser Leu Ser
145 150 155 160

Glu Glu His Cys Gln Tyr Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys
165 170 175

Tyr Ile His Ser Ala Asn Val Leu His Arg Asp Leu Lys Pro Ser Asn
180 185 190

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

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

Arg Trp Tyr Arg Ala Pro Glu Leu Leu Leu Asn Ser Ser Asp Tyr Thr
225 230 235 240

Ala Ala Ile Asp Val Trp Ser Val Gly Cys Ile Phe Met Glu Leu Met
245 250 255

Asp Arg Lys Pro Leu Phe Pro Gly Arg Asp His Val His Gln Leu Arg
260 265 270

Leu Leu Met Glu Leu Ile Gly Thr Pro Ser Glu Ala Glu Leu Gly Phe
275 280 285

Leu Asn Glu Asn Ala Lys Arg Tyr Ile Arg Gln Leu Gln His Tyr Pro
290 295 300

Arg Gln Ser Phe Asn Glu Lys Phe Pro Gln Val His Pro Ala Ala Ile
305 310 315 320

Asp Leu Ile Glu Lys Met Leu Thr Phe Asp Pro Arg Gln Arg Ile Thr
325 330 335

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

Ser Asp Glu Pro Val Cys Met Thr Pro Phe Asn Phe Asp Phe Glu His
355 360 365

His Ala Pro Thr Glu Glu Gln Met Lys Glu Met Ile Tyr Arg Glu Ala
370 375 380

Leu Ala Phe Asn Pro Glu Tyr Gln His Leu
385 390

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<212> DNA
<213> L. usitatissimum

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cctccgggag ggatcgagaa tattccggcg acgctaagcc acggcggacg cttcatccaa 180
tacaacattt tcggcaacat tttcgaggtc accgccaagt ataagcctcc aatcatgcct 240
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<211> 415

<212> PRT

<213> L. usitatissimum

<400> 26

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Gln Gln Gln Gln Gln Gln Val Pro Pro Pro Gly Gly Ile Glu Asn Ile
 35 40 45

Pro Ala Thr Leu Ser His Gly Gly Arg Phe Ile Gln Tyr Asn Ile Phe
 50 55 60

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

Ile Gly Lys Gly Ala Tyr Gly Ile Val Cys Ser Ala Leu Asn Ser Glu
85 90 95

Thr Ala Glu His Val Ala Ile Lys Lys Ile Ala Asn Ala Phe Asp Asn
100 105 110

Lys Ile Asp Ala Lys Arg Thr Leu Arg Glu Ile Lys Leu Leu Arg His
115 120 125

Met Asp His Glu Asn Val Val Ala Ile Arg Asp Ile Ile Pro Pro Pro
130 135 140

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

Thr Asp Leu His Gln Ile Ile Arg Ser Asn Gln Gly Leu Ser Glu Glu
165 170 175

His Cys Gln Tyr Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile
180 185 190

His Ser Ala Asn Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu Leu
195 200 205

Leu Asn Ala Asn Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg
210 215 220

Val Thr Ser Glu Thr Asp Phe Met Thr Glu Tyr Val Val Thr Arg Trp
225 230 235 240

Tyr Arg Ala Pro Glu Leu Leu Leu Asn Ser Ser Asp Tyr Thr Ala Ala
245 250 255

Ile Asp Val Trp Ser Val Gly Cys Ile Phe Met Glu Leu Met Asp Arg
260 265 270

Lys Pro Leu Phe Pro Gly Arg Asp His Val His Gln Leu Arg Leu Leu
275 280 285

Met Glu Leu Ile Gly Thr Pro Ser Glu Ala Glu Leu Gly Phe Leu Asn
290 295 300

Glu Asn Ala Lys Arg Tyr Ile Arg Gln Leu Pro Leu Tyr Arg Arg Gln
305 310 315 320

Ser Phe Thr Glu Lys Phe Pro Thr Val His Pro Ser Ala Ile Asp Leu
325 330 335

Val Lys Lys Met Leu Thr Phe Asp Pro Arg Gln Arg Ile Thr Val Glu
340 345 350

Asp Ala Leu Ala His Pro Tyr Leu Asn Ser Leu His Asp Ile Ser Asp
355 360 365

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

Leu Thr Glu Glu Gln Met Lys Glu Leu Ile Tyr Arg Glu Ala Leu Ala
385 390 395 400

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<211> 1146

<212> DNA

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aatgcatttg acaacaaaat tgacgcgaaa aggacattaa gagagattaa gotttctacgc	300
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<211> 381

<212> PRT

<213> L. usitatissimum

<400> 28

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

Pro Pro Ile Arg Pro Ile Gly Arg Gly Ala Tyr Gly Ile Val Cys Ala
50 55 60

Ala Val Asn Ser Asp Thr His Glu Glu Val Ala Ile Lys Lys Ile Gly
65 70 75 80

Asn Ala Phe Asp Asn Lys Ile Asp Ala Lys Arg Thr Leu Arg Glu Ile
85 90 95

Lys Leu Leu Arg His Met Asp His Glu Asn Val Ile Ala Ile Arg Asp
100 105 110

Ile Ile Arg Pro Pro Lys Lys Glu Ala Phe Asn Asp Val Tyr Ile Val
115 120 125

Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Arg Ser Asp Gln
130 135 140

Ser Leu Thr Asp Asp His Cys Gln Tyr Phe Leu Tyr Gln Leu Leu Arg
145 150 155 160

Gly Leu Lys Tyr Val His Ser Ala Asn Val Leu His Arg Asp Leu Lys
165 170 175

Pro Ser Asn Leu Leu Leu Asn Ala Asn Cys Asp Leu Lys Ile Gly Asp
180 185 190

Phe Gly Leu Ala Arg Thr Thr Ser Glu Thr Asp Phe Met Thr Glu Tyr
195 200 205

Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Leu Asn Cys Ser
210 215 220

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

Glu Ile Val Thr Gly Glu Pro Leu Phe Pro Gly Thr Asp Tyr Val His
245 250 255

Gln Leu Lys Leu Ile Thr Glu Leu Ile Gly Thr Pro Asp Asp Ala Ser
260 265 270

Leu Gly Phe Leu Arg Ser Asp Asn Ala Arg Arg Tyr Val Arg Met Leu
275 280 285

Pro Gln Phe Arg Lys Gln Asn Phe Ser Met Arg Phe Leu Asn Thr Ser
290 295 300

Pro Ala Ala Val Asp Leu Leu Glu Lys Met Leu Val Phe Asp Pro Thr
305 310 315 320

Lys Arg Ile Thr Val Asp Asp Ala Leu Ser His Pro Tyr Leu Ser Ala
325 330 335

Leu His Ile Ile Asn Glu Glu Pro Ile Cys Ser Ala Pro Phe His Phe
340 345 350

Asp Phe Glu Gln Pro Ser Cys Thr Glu Glu His Ile Lys Glu Leu Ile
355 360 365

Trp Lys Glu Ala Val Asn Phe Asn Pro Asp His Gln Gln
370 375 380

<210> 29

<211> 1718

<212> DNA

<213> P. patents

<400> 29

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<213> P. patents
<400> 30

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

Ala Tyr Gly Ile Val Cys Ser Leu Phe Asp Thr Val Thr Gly Glu Glu
50 55 60

Val Ala Val Lys Lys Ile Gly Asn Ala Phe Asp Asn Arg Ile Asp Ala
65 70 75 80

Lys Arg Thr Leu Arg Glu Ile Lys Leu Leu Arg His Met Asp His Glu
85 90 95

Asn Val Val Ala Ile Thr Asp Ile Ile Arg Pro Pro Thr Arg Glu Asn
100 105 110

Phe Asn Asp Val Tyr Ile Val Tyr Glu Leu Met Asp Thr Asp Leu His
115 120 125

Gln Ile Ile Arg Ser Asn Gln Ala Leu Thr Glu Asp His Cys Gln Tyr
130 135 140

Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn
145 150 155 160

Val Leu His Arg Asp Leu Lys Pro Thr Asn Leu Leu Val Asn Ala Asn
165 170 175

Cys Asp Leu Lys Ile Ala Asp Phe Gly Leu Ala Arg Thr Leu Ser Glu
180 185 190

Thr Asp Phe Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro
195 200 205

Glu Leu Leu Leu Asn Cys Ser Ala Tyr Thr Ala Ala Ile Asp Ile Trp
210 215 220

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

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

Gly Thr Pro Glu Asp Arg Asp Leu Gly Phe Leu Arg Ser Asp Asn Ala
260 265 270

Arg Arg Tyr Ile Lys His Leu Pro Arg Gln Ser Pro Ile Pro Leu Thr
275 280 285

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

Met Leu Val Phe Asp Pro Ala Lys Arg Ile Thr Val Glu Ala Ala Leu
305 310 315 320

Ala His Pro Tyr Leu Ala Ser Leu His Asp Ile Asn Asp Glu Pro Ala
325 330 335

Ser Val Ser Pro Phe Glu Phe Asp Phe Glu Glu Pro Pro Ile Ser Glu
340 345 350

Glu His Ile Lys Asp Leu Ile Trp Arg Glu Ala Leu Asp Cys Ser Leu
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Gly Pro Asp Asp Met Val Gln
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<213> B. napus

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<210> 32

<211> 368

<212> PRT

<213> B. napus

<400> 32

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20 25 30

Val Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val Val Cys Ser
35 40 45

Ser Ile Asn Arg Glu Thr Asn Glu Lys Val Ala Ile Lys Lys Ile His
50 55 60

Asn Val Phe Glu Asn Arg Val Asp Ala Leu Arg Thr Leu Arg Glu Leu
65 70 75 80

Lys Leu Leu Arg His Val Arg His Asp Asn Val Ile Ala Leu Lys Asp
85 90 95

Val Met Leu Pro Thr Asn Lys Ser Ser Phe Lys Asp Val Tyr Leu Val
100 105 110

Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys Ser Ser Gln
115 120 125

Ser Leu Ser Asp Asp His Cys Lys Tyr Phe Leu Phe Gln Leu Leu Arg
130 135 140

Gly Leu Lys Tyr Leu His Ser Ala Asn Ile Leu His Arg Asp Leu Lys
145 150 155 160

Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys Ile Cys Asp
165 170 175

Phe Gly Leu Ala Arg Thr Ser Gln Gly Asn Glu Gln Phe Met Thr Glu
180 185 190

Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Leu Cys Cys
195 200 205

Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly Cys Ile Phe
210 215 220

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

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

Asp Ile Arg Phe Ile Asp Asn Pro Lys Ala Arg Arg Phe Ile Lys Ser
260 265 270

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

Asn Pro Leu Ala Ile Asp Leu Leu Gln Arg Met Leu Val Phe Asp Pro
290 295 300

Thr Lys Arg Ile Ser Val Thr Asp Ala Leu Ser His Pro Tyr Met Ala
305 310 315 320

Gly Leu Phe Asp Ser Gly Ser Asn Pro Pro Ala His Val Pro Ile Ser
325 330 335

Leu Asp Ile Asp Glu Asn Met Glu Glu Arg Met Ile Arg Glu Met Met
340 345 350

Trp Asp Glu Met Leu Tyr Tyr His Pro Gly Ala Glu Thr Ala Asn Pro
355 360 365

<210> 33

<211> 1119

<212> DNA

<213> B. napus

<400> 33

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gttcctccta tccgtcccat tggtagagga gcttgaggta ttgtctgtgc tgctgtgaac	180
tcagtgaactg gagagaaagt ggctattaag aagatcggta atgcttttga taacatcatt	240
gatgctaaga gagctctacg tgaaatcaag cttctcagga acatggatca tgagaacgtc	300
atagccatca aagatattgt aagacctcca caacgtgata tcttcaacga tgtttacatt	360
gtctatgagt taatggacac tgatctccag cgtatcctcc gttctaagca aaccttaagc	420
cacgaccagt gccgcttctt tgtgtaccag ctcttaagag ggcttaagta cgtgcactcg	480
gccaacatat tacatcgtga tctaaggcca agcaacgtgc tgcttaactc caaacacgag	540
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tatgtgggta cccgttggtg cagagctcct gagctgcttc ttaactgctc ggagtacact	660
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ccagacaact ccagtctcgg tttccttcgc agtgacaacg cgagaagata cgtgaggcaa	840
cttcacgat accctaaaca agagtttgct gctagattcc ccaaaatgcc ccctaccgct	900

attgatttgc tggagagaat gctcgtcttt gatccaaacc gacgtatctc agttgatgaa 960

gctctcggcc atgcatactt atcaccacac cacgatgtgg caaaagaacc tgtatgtcca 1020

actcctttta gcttcgactt cgagcatcct tcatgcacgg aagaacacat aaaagagctt 1080

atctacaagg agtctgtcaa attcaatcct gaccattga 1119

<210> 34

<211> 372

<212> PRT

<213> B. napus

<400> 34

Met Ser Gly Glu Ser Ser Ser Gly Thr Thr Asp His Cys Ile Lys Val

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Val Pro Thr His Gly Gly Arg Tyr Ile Gln Tyr Asn Val Tyr Gly Gln

20 25 30

Leu Phe Glu Val Ser Arg Lys Tyr Val Pro Pro Ile Arg Pro Ile Gly

35 40 45

Arg Gly Ala Cys Gly Ile Val Cys Ala Ala Val Asn Ser Val Thr Gly

50 55 60

Glu Lys Val Ala Ile Lys Lys Ile Gly Asn Ala Phe Asp Asn Ile Ile

65 70 75 80

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

85 90 95

His Glu Asn Val Ile Ala Ile Lys Asp Ile Val Arg Pro Pro Gln Arg

100 105 110

Asp Ile Phe Asn Asp Val Tyr Ile Val Tyr Glu Leu Met Asp Thr Asp
115 120 125

Leu Gln Arg Ile Leu Arg Ser Lys Gln Thr Leu Ser His Asp Gln Cys
130 135 140

Arg Phe Phe Val Tyr Gln Leu Leu Arg Gly Leu Lys Tyr Val His Ser
145 150 155 160

Ala Asn Ile Leu His Arg Asp Leu Arg Pro Ser Asn Val Leu Leu Asn
165 170 175

Ser Lys His Glu Leu Lys Ile Gly Asp Phe Gly Leu Ala Arg Thr Thr
180 185 190

Ser Asp Thr Asp Phe Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg
195 200 205

Ala Pro Glu Leu Leu Leu Asn Cys Ser Glu Tyr Thr Ala Ala Ile Asp
210 215 220

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

Leu Phe Pro Gly Lys Asp Tyr Val His Gln Leu Arg Leu Ile Thr Glu
245 250 255

Leu Val Gly Ser Pro Asp Asn Ser Ser Leu Gly Phe Leu Arg Ser Asp
260 265 270

Asn Ala Arg Arg Tyr Val Arg Gln Leu Pro Arg Tyr Pro Lys Gln Glu
275 280 285

Phe Ala Ala Arg Phe Pro Lys Met Pro Pro Thr Ala Ile Asp Leu Leu
290 295 300

Glu Arg Met Leu Val Phe Asp Pro Asn Arg Arg Ile Ser Val Asp Glu
305 310 315 320

Ala Leu Gly His Ala Tyr Leu Ser Pro His His Asp Val Ala Lys Glu
325 330 335

Pro Val Cys Pro Thr Pro Phe Ser Phe Asp Phe Glu His Pro Ser Cys
340 345 350

Thr Glu Glu His Ile Lys Glu Leu Ile Tyr Lys Glu Ser Val Lys Phe
355 360 365

Asn Pro Asp His
370

<210> 35

<211> 1122

<212> DNA

<213> B. napus

<400> 35

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aagtacgttc ctctcttcg ccccatcggc agaggcgctt acggcatcgt ctgtgctgct 180

acaaactcag agacgggaga ggaagtagct atcaagaaga tcggtaacgc ttttgacaac 240

atcatcgacg ccaagagaac cttgagagag attaagctcc tcaagcacat ggatcacgag	300
aatgttattg ctgtgaagga tataataaga ccaccctga gagagaactt caacgatgtt	360
tacattgttt atgagctcat ggacactgat ctccaccaga ttatacgctc taaccaaccc	420
ttaactgatg atcattgtcg gttcttcttg tatcagttgt tgcgtgggct caagtacgtt	480
cattcagcca atgtgttaca ccgagatcta aagcccagca atttgctcct gaacgcaaac	540
tgtgatctaa agcttgggga tttcgggctt gcgaggacca aatccgagac tgacttcatg	600
actgagtacg ttgttacacg ctggtaccga gctccagagt tacttcttaa ctgctccgag	660
tacacagcag cgatcgatat ctggtccgctc ggttgatttc tcggtgaaac aatgacaaga	720
gagcccttgt ttccgggtaa agattatgtt catcagctta ggcttatcac tgagcttata	780
ggatcacctg atgattcaag cttgggggttc ttaaggagcg acaacgcaag gagatacgtt	840
aaacagcttc cacagtaccc gagacagaac ttcgctgcta ggttcccaaa catgtcagct	900
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gatgaggcgt tgtgccaccc atatttggcg gcgctgcacg atataaacga ggaaccggtg	1020
tgtgtgaggc cgttcaattt cgattttgag caaccttctt tgacagaaga gaacatcaag	1080
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<210> 36

<211> 373

<212> PRT

<213> B. napus

<400> 36

Met Ser Ala Glu Asn Cys Phe Gly Gly Gly Gly Gly Asp Gln Ser Thr

1

5

10

15

Lys Gly Leu Ala Thr His Gly Gly Gln Tyr Val Gln Tyr Asn Val Tyr
20 25 30

Gly Asn Ile Phe Glu Val Thr Arg Lys Tyr Val Pro Pro Leu Arg Pro
35 40 45

Ile Gly Arg Gly Ala Tyr Gly Ile Val Cys Ala Ala Thr Asn Ser Glu
50 55 60

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

Ile Ile Asp Ala Lys Arg Thr Leu Arg Glu Ile Lys Leu Leu Lys His
85 90 95

Met Asp His Glu Asn Val Ile Ala Val Lys Asp Ile Ile Arg Pro Pro
100 105 110

Leu Arg Glu Asn Phe Asn Asp Val Tyr Ile Val Tyr Glu Leu Met Asp
115 120 125

Thr Asp Leu His Gln Ile Ile Arg Ser Asn Gln Pro Leu Thr Asp Asp
130 135 140

His Cys Arg Phe Phe Leu Tyr Gln Leu Leu Arg Gly Leu Lys Tyr Val
145 150 155 160

His Ser Ala Asn Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu Leu
165 170 175

Leu Asn Ala Asn Cys Asp Leu Lys Leu Gly Asp Phe Gly Leu Ala Arg
180 185 190

Thr Lys Ser Glu Thr Asp Phe Met Thr Glu Tyr Val Val Thr Arg Trp
195 200 205

Tyr Arg Ala Pro Glu Leu Leu Leu Asn Cys Ser Glu Tyr Thr Ala Ala
210 215 220

Ile Asp Ile Trp Ser Val Gly Cys Ile Leu Gly Glu Thr Met Thr Arg
225 230 235 240

Glu Pro Leu Phe Pro Gly Lys Asp Tyr Val His Gln Leu Arg Leu Ile
245 250 255

Thr Glu Leu Ile Gly Ser Pro Asp Asp Ser Ser Leu Gly Phe Leu Arg
260 265 270

Ser Asp Asn Ala Arg Arg Tyr Val Lys Gln Leu Pro Gln Tyr Pro Arg
275 280 285

Gln Asn Phe Ala Ala Arg Phe Pro Asn Met Ser Ala Gly Ala Ala Asp
290 295 300

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

Asp Glu Ala Leu Cys His Pro Tyr Leu Ala Ala Leu His Asp Ile Asn
325 330 335

Glu Glu Pro Val Cys Val Arg Pro Phe Asn Phe Asp Phe Glu Gln Pro
340 345 350

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

His Leu Asn Pro Gln
370

<210> 37
<211> 1119
<212> DNA
<213> G. max

<400> 37
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aggttcatcc aatacaacat attcggaac atattcgaag tcaccgcaa atacaagcca 180
cccatcatgc ccatcgaaa aggcgcatac ggcacgtgtt gctcggttt gaactcggag 240
acgaatgagc acgttgccat caagaagatt gcgaatgcat ttgacaaca gattgatgca 300
aagaggaccc tccgtgaaat caagctgctt cgtcacatgg atcatgaaa cgtgggttgca 360
atcagggata tagtgccacc acctcaaagg gagatattca atgatgttta cattgcatat 420
gagttgatgg aactgacct tcaccaaatt attcgttcaa accaaggatt atcagaggag 480
cactgtcagt attttctgta tcaaatactc cgtgggttga agtacatata ttctgccaat 540
gttctgcata gggacttaaa acctagcaac cttctcctga atgccaaactg tgacttaaaa 600
atttgtgatt ttggactggc tcgtgtcacg tctgaaactg attttatgac tgaatatgtt 660
gttacaagat ggtaccgtgc accagagctt ctgttgaact cttctgatta cactgcagca 720
attgatgtat ggtctgttgg ttgtattttc atggaactga tggatcgcaa gcctttgttt 780
cctggcagag atcatgtgca tcagttgcgt ctacttatgg agctgattgg caccocatca 840

gaggctgatt tggggttcct gaatgaaaat gctaagagat acattaggca actaccctt 900

taccgctgtc aatctttcca ggaaaagttt ccacatgtcc atcctgaagc tatagatctt 960

gttgaaaaaa tgttaacttt tgatcctaga aaaaggatta ctgtgaagat gcacttggcg 1020

caccgtact tgacatctct gcatgacatc agtgatgaac cagtgtgcat gactcccttc 1080

tacttgactg tgaacacatg ctcgacggag gacagatga 1119

<210> 38

<211> 372

<212> PRT

<213> G. max

<400> 38

Met Glu Gly Gly Gly Ala Ala Pro Pro Ala Asp Thr Val Met Ser Asp

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Ala Ala Pro Pro Pro Gln Gln Ala Met Ala Met Gly Ile Glu Asn Ile

20 25 30

Pro Ala Thr Leu Ser His Gly Gly Arg Phe Ile Gln Tyr Asn Ile Phe

35 40 45

Gly Asn Ile Phe Glu Val Thr Ala Lys Tyr Lys Pro Pro Ile Met Pro

50 55 60

Ile Gly Lys Gly Ala Tyr Gly Ile Val Cys Ser Ala Leu Asn Ser Glu

65 70 75 80

Thr Asn Glu His Val Ala Ile Lys Lys Ile Ala Asn Ala Phe Asp Asn

85 90 95

Lys Ile Asp Ala Lys Arg Thr Leu Arg Glu Ile Lys Leu Leu Arg His
100 105 110

Met Asp His Glu Asn Val Val Ala Ile Arg Asp Ile Val Pro Pro Pro
115 120 125

Gln Arg Glu Ile Phe Asn Asp Val Tyr Ile Ala Tyr Glu Leu Met Asp
130 135 140

Thr Asp Leu His Gln Ile Ile Arg Ser Asn Gln Gly Leu Ser Glu Glu
145 150 155 160

His Cys Gln Tyr Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile
165 170 175

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

Leu Asn Ala Asn Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg
195 200 205

Val Thr Ser Glu Thr Asp Phe Met Thr Glu Tyr Val Val Thr Arg Trp
210 215 220

Tyr Arg Ala Pro Glu Leu Leu Leu Asn Ser Ser Asp Tyr Thr Ala Ala
225 230 235 240

Ile Asp Val Trp Ser Val Gly Cys Ile Phe Met Glu Leu Met Asp Arg
245 250 255

Lys Pro Leu Phe Pro Gly Arg Asp His Val His Gln Leu Arg Leu Leu
260 265 270

Met Glu Leu Ile Gly Thr Pro Ser Glu Ala Asp Leu Gly Phe Leu Asn
275 280 285

Glu Asn Ala Lys Arg Tyr Ile Arg Gln Leu Pro Leu Tyr Arg Cys Gln
290 295 300

Ser Phe Gln Glu Lys Phe Pro His Val His Pro Glu Ala Ile Asp Leu
305 310 315 320

Val Glu Lys Met Leu Thr Phe Asp Pro Arg Lys Arg Ile Thr Val Lys
325 330 335

Met His Leu Ala His Pro Tyr Leu Thr Ser Leu His Asp Ile Ser Asp
340 345 350

Glu Pro Val Cys Met Thr Pro Phe Tyr Leu Thr Val Asn Thr Cys Ser
355 360 365

Thr Glu Asp Arg
370

<210> 39

<211> 1176

<212> DNA

<213> G. max

<400> 39

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aggttcaccc aataacaacat attcggaac atattcgaag tcaccgcaa atacaagcca 180

cccatcatcc ccatcgaaa aggcgcatac ggcacgcttt gctcggcttt gaactcggag	240
acgaatgagc acgttgccat caagaagatt gcgaatgcgt ttgataacaa gattgatgca	300
aagaggaccc tccgtgaaat caagctgctt cgtcacatgg atcatgaaaa cgtgggttgca	360
atcagggata tagtgccacc acctcaaagg gagatattca atgatgttta cattgcatat	420
gagttgatgg aactgacct tcaccaaatt attcgttcaa accaaggatt atcagaggag	480
cactgtcagt attttctgta tcaaactctc cgtgggttga agtacatata ttctgccaat	540
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gttacaagat ggtaccgtgc accagagctt ctgttgaact cttctgatta cactgcagca	720
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cctggcagag atcatgtgca tcagttgcgt ctacttatgg agctgattgg caccocatca	840
gaggctgatt tggggttcct gaatgaaaat gctaagagat acattaggca actaccctt	900
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aactttgact ttgaacaaca tgctttgacg gaggaacaga tgaaagaact gatataccga	1140
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<210> 40

<211> 418

<212> PRT

<213> G. max

<400> 40

Met Gly Asn Cys Asn Ala Cys Val Arg Val Asp Asp Val Ala Asp Ser
1 5 10 15

Asn Arg Gly Lys Asn Lys Asn Asn Lys Lys Thr Lys Pro Asn Pro Tyr
20 25 30

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

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

Leu Gly Arg Gly Glu Phe Gly Ile Thr Tyr Leu Cys Thr Asp Arg Glu
65 70 75 80

Thr Lys Gln Glu Leu Ala Cys Lys Ser Ile Ser Lys Arg Lys Leu Arg
85 90 95

Thr Ala Ile Asp Val Glu Asp Val Arg Arg Glu Val Ala Ile Met Ser
100 105 110

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

Asp Glu Glu Asn Val His Leu Val Met Glu Leu Cys Ala Gly Gly Glu
130 135 140

Leu Phe Asp Arg Ile Val Ala Arg Gly His Tyr Ser Glu Arg Ala Ala
145 150 155 160

Ala Tyr Val Ala Arg Thr Ile Ala Glu Val Val Arg Met Cys His Ala
165 170 175

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

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

Val Phe Phe Lys Pro Gly Glu Arg Phe Ser Glu Ile Val Gly Ser Pro
210 215 220

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

Asp Val Trp Ser Ala Gly Val Ile Leu Tyr Ile Leu Leu Cys Gly Val
245 250 255

Pro Pro Phe Trp Ser Glu Asp Glu Arg Gly Val Ala Leu Ala Ile Leu
260 265 270

Arg Gly Val Ile Asp Phe Lys Arg Glu Pro Trp Pro Gln Ile Ser Asp
275 280 285

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

Arg Leu Thr Ala Glu Gln Val Leu Glu His Ser Trp Leu Gln Asn Ala
305 310 315 320

Lys Lys Ala Ser Asn Val Pro Leu Gly Asp Ile Val Arg Thr Arg Leu
325 330 335

Lys Gln Phe Ser Val Met Asn Arg Phe Lys Lys Arg Ala Leu Arg Val
340 345 350

Ile Ala Glu His Leu Ser Val Glu Glu Val Glu Ile Ile Lys Asp Met
355 360 365

Phe Thr Leu Met Asp Thr Asp Lys Asp Gly Lys Val Thr Tyr Glu Glu
370 375 380

Leu Lys Val Gly Leu Arg Lys Val Gly Ser Gln Leu Ala Glu Pro Glu
385 390 395 400

Ile Lys Met Leu Met Glu Val Val Gly Phe Leu Asn Phe Ile Pro Phe
405 410 415

Ile Met

<210> 41

<211> 2135

<212> DNA

<213> P. patents

<400> 41

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gctgggaggc cgaagctcca ggtcaaatac cgaaagatcg cctactgcat ccaaaataga 180

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catgaagaaa gacagagaaa tcaagtccgt ttccgggtcaa agcttaactc actctgttct 360

gcagcggaaa actgaaaacc tgagagactt gtacattttg ggaaagaaac ttggacaagg	420
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actgaagaaa gtgggttcca ttcttaaaga ggaagatata cggcagctga tggatgctgc	1440
ggatgttgat ggcaatggaa cgattgatta cggggagttt ctagccgcca cccttcactt	1500
gaataaaatt gaacgtgatg agaacatgct tgcagctttt tcgtacttgg acaaggacaa	1560
tagtggctat cttacgattg atgagcttca acatgcttta gccagttca acatgggaga	1620

catatctgtg gatgaattgc ttcatgaagt tgatcaaaac aatgacgggc agattgacta	1680
tgctgagttt gttacgatga tgcgcaaggg aaatcctggg gctgctgggc gatcgtcatt	1740
tcggaacagc caaagcttga gcttaaata tgtcttgatg atgggataga ccattgaagg	1800
agtcttgatg aatccttata agtcaagctg accatatttc ttcgtagcat ggtgggctta	1860
agttcccgcc cgtatgttat tcctgttaat cctccatgtg catgagagga aatgattact	1920
gtagactcta aagccgtgga tacgttcctg ttcaatccag cgaagctctc cagctttgtg	1980
gacaaatgta ttaggcatac aatgctgccg gttatgctta ttgttttagac ctgtgatggg	2040
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tgtctatgcg aagagaacat tttctgatga gctcg	2135

<210> 42
 <211> 575
 <212> PRT
 <213> P. patents

<400> 42

Met	Gly	Asn	Thr	Cys	Val	Gly	Ala	Ala	Gly	Tyr	Phe	Gln	Gly	Phe	Thr
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Ser	Ala	Ile	Ala	Leu	Gly	Gly	Arg	Ser	Ser	Arg	Ser	Asn	Ser	Glu	Arg
				20				25					30		

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

Asp	Thr	Pro	Ala	Thr	Gln	Gln	Asn	Pro	Pro	Arg	Gln	Asn	His	Ile	Pro
				50			55				60				

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

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

His Ser Val Leu Gln Arg Lys Thr Glu Asn Leu Arg Asp Leu Tyr Ile
100 105 110

Leu Gly Lys Lys Leu Gly Gln Gly Gln Phe Gly Thr Thr Tyr Leu Cys
115 120 125

Ile Glu Lys Ala Thr Asn Lys Glu Tyr Ala Cys Lys Ser Ile Ala Lys
130 135 140

Arg Lys Leu Ile Ser Lys Glu Asp Val Glu Asp Val Arg Arg Glu Leu
145 150 155 160

Gln Ile Met His His Leu Ser Gly His Pro Asn Ile Val Met Ile Lys
165 170 175

Gly Ala Tyr Glu Asp Pro Ala Ser Val His Leu Val Met Glu Leu Cys
180 185 190

Ala Gly Gly Glu Leu Phe Asp Arg Ile Ile Gln Arg Gly Gln Tyr Ser
195 200 205

Glu Ala Lys Ala Ala Val Leu Thr Arg Thr Ile Val Gly Val Val Glu
210 215 220

Thr Cys His Ser Leu Gly Val Met His Arg Asp Leu Lys Pro Glu Asn
225 230 235 240

Phe Leu Phe Ser Ser Thr Lys Glu Asp Ala Ala Leu Lys Thr Thr Asp
245 250 255

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

Val Gly Ser Pro Tyr Tyr Val Ala Pro Glu Val Leu Arg Lys Asn Tyr
275 280 285

Gly Pro Glu Ala Asp Val Trp Ser Ala Gly Val Ile Leu Tyr Ile Leu
290 295 300

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

Glu Gln Val Leu Lys Ser Glu Leu Asp Phe Ala Ser Asp Pro Trp Pro
325 330 335

Lys Ile Ser Asp Ser Ala Lys Asp Leu Ile Arg Lys Met Leu Asn Pro
340 345 350

Gln Ala Ser Lys Arg Leu Lys Ala His Gln Val Leu Cys His Pro Trp
355 360 365

Ile Cys Glu Asp Gly Val Ala Pro Asp Arg Pro Ile Asp Ser Ala Val
370 375 380

Gln Ser Arg Leu Lys His Phe Ser Ala Met Asn Lys Leu Lys Lys Ile
385 390 395 400

Ala Ile Arg Val Ile Ala Glu Ser Leu Ser Glu Glu Glu Ile Ala Gly
405 410 415

Leu Lys Glu Met Phe Lys Met Met Asp Thr Asp Asn Ser Gly Ser Ile
420 425 430

Ser Tyr Asp Glu Leu Lys Ala Gly Leu Lys Lys Val Gly Ser Ile Leu
435 440 445

Lys Glu Glu Asp Ile Arg Gln Leu Met Asp Ala Ala Asp Val Asp Gly
450 455 460

Asn Gly Thr Ile Asp Tyr Gly Glu Phe Leu Ala Ala Thr Leu His Leu
465 470 475 480

Asn Lys Ile Glu Arg Asp Glu Asn Met Leu Ala Ala Phe Ser Tyr Leu
485 490 495

Asp Lys Asp Asn Ser Gly Tyr Leu Thr Ile Asp Glu Leu Gln His Ala
500 505 510

Leu Ala Gln Phe Asn Met Gly Asp Ile Ser Val Asp Glu Leu Leu His
515 520 525

Glu Val Asp Gln Asn Asn Asp Gly Gln Ile Asp Tyr Ala Glu Phe Val
530 535 540

Thr Met Met Arg Lys Gly Asn Pro Gly Ala Ala Gly Arg Ser Ser Phe
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Arg Asn Ser Gln Ser Leu Ser Leu Asn Asp Val Leu Met Met Gly
565 570 575

<210> 43
<211> 2882
<212> DNA
<213> P. patents

<400> 43

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

Lys Lys Val Glu Lys Leu Ala Glu Ser Lys Gln Pro Glu Pro Trp Lys
65 70 75 80

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

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

Arg Thr Asn Phe Gly Tyr Gly Arg Asp Phe Lys Ser Lys Tyr Thr Leu
115 120 125

Gly Lys Leu Leu Gly His Gly Gln Phe Gly Tyr Thr Tyr Val Ala Ile
130 135 140

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

Gln Met Thr Leu Pro Ile Ser Val Glu Asp Val Lys Arg Glu Val Lys
165 170 175

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

Ser Phe Glu Asp Asp Asp Leu Val Tyr Ile Val Met Glu Leu Cys Glu
195 200 205

Gly Gly Glu Leu Leu Asp Arg Ile Leu Ala Lys Lys Asp Ser Arg Tyr
210 215 220

Ser Glu Lys Asp Ala Ala Lys Ile Val Arg Gln Met Leu Asn Val Ala
225 230 235 240

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

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

Asp Phe Gly Leu Ser Asp Tyr Ile Arg Pro Gly Asn Arg Phe His Asp
275 280 285

Val Val Gly Ser Ala Tyr Tyr Val Ala Pro Glu Val Leu Lys Lys Lys
290 295 300

Ser Gly Pro Glu Ser Asp Val Trp Ser Ile Gly Val Ile Thr Tyr Ile
305 310 315 320

Leu Leu Cys Gly Arg Arg Pro Phe Trp Asp Lys Thr Glu Lys Gly Ile
325 330 335

Phe Asp Glu Val Leu Lys Lys Asn Pro Asp Tyr Gly Glu Lys Pro Trp
340 345 350

Pro Thr Ile Ser Ser Ser Ala Lys Asp Phe Val Lys Lys Leu Leu Val
355 360 365

Lys Asp Pro Ala Ala Arg Leu Thr Ala Ala Gln Ala Leu Ser His Pro
370 375 380

Trp Ala Lys Glu Gly Gly Asp Ala Leu Asp Ile Pro Leu Asp Ile Ser
385 390 395 400

Val Leu Ser Asn Met Arg Glu Phe Val Lys Tyr Ser Arg Leu Lys Gln
405 410 415

Leu Ala Leu Arg Ala Leu Ala Ser Thr Leu Asp Ser Ser Asp Ile Ala
420 425 430

Asp Leu Gln Asp Gln Phe Asn Ala Ile Asp Ile Asp Arg Asn Gly Lys
435 440 445

Ile Thr Leu Glu Glu Met Arg Glu Ala Leu Gln Lys Asp Arg Pro Trp
450 455 460

Ser Ile Gln Glu Ser Arg Ile Val Glu Ile Leu Gln Ala Met Asp Ser
465 470 475 480

Asn Ser Asp Gly Leu Val Asp Phe Asp Glu Phe Val Ala Ala Thr Leu
485 490 495

His Val His Gln Leu Glu Glu Thr Asp Ser Glu Lys Trp Gln Ser Arg
500 505 510

Ser Gln Ala Ala Phe Ser Gln Phe Asp Phe Asp Gly Asp Gly Tyr Ile
515 520 525

Thr Ala Asp Glu Leu Lys Ile Ala Thr Gly Leu Asn Gly Ser Met Asp
530 535 540

Ser Ile Leu Val Glu Ala Asp Ile Asp Gly Asp Gly Lys Ile Ser Leu
545 550 555 560

Ser Glu Phe Gln Lys Leu Leu Arg Gln Ala Ser Leu Gly Ser Arg Thr
565 570 575

Asn Glu His His Thr Leu Val Thr His Asn His Arg Lys Cys
580 585 590

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<211> 1599
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<213> B. napus

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gttgggagtg catactatgt ggccccggag gttttgaaac ggaactatgg accagaggct 780

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gccatgaaca	aactaaagaa	aatggcactg	aatgtaattg	cagagaacct	gtctgaagaa	1140
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accgatcgtg	acgggaaaat	aaactacgaa	gagttcgtag	cgatgatgaa	gaagggaaat	1560
ccagaactgg	tgacgaaccg	acgcagagtc	aacatgtaa			1599

Met Gly His Arg His Ser Lys Ser Lys Ser Ser Gly Pro Pro Pro Ser
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Ser Ser Ser Ser Ser Ser Ser Thr Asn Val Val His His Val Gln Pro
20 25 30

Ser Gly Glu Arg Arg Gly Ser Ser Gly Ser Gly Pro Thr Pro Val Gly
35 40 45

Ser Ser Ser Thr Gly Gly Ser Arg Ser Ala Ala Ser Ala Gln Gln Asn
50 55 60

Gly Arg Ile Leu Gly Arg Pro Met Glu Asn Val Arg Gly Thr Tyr Asp
65 70 75 80

Phe Gly Lys Glu Leu Gly Arg Gly Gln Phe Gly Val Thr Tyr Leu Val
85 90 95

Thr His Lys Glu Thr Lys Lys Leu Phe Ala Cys Lys Ser Ile Pro Thr
100 105 110

Arg Arg Leu Val His Arg Asp Asp Ile Glu Asp Val Arg Arg Glu Val
115 120 125

Gln Ile Met His His Leu Ser Gly His Arg Asn Ile Val Asp Leu Lys
130 135 140

Gly Ala Tyr Glu Asp Arg His Ser Val Asn Leu Ile Met Glu Leu Cys
145 150 155 160

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

Glu Arg Ala Ala Ala Asp Leu Cys Arg Gln Met Val Met Val Val His
180 185 190

Ser Cys His Ser Met Gly Val Met His Arg Asp Leu Lys Pro Glu Asn
195 200 205

Phe Leu Phe Leu Ser Lys Asp Glu Asn Ser Pro Leu Lys Ala Thr Asp
210 215 220

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

Val Gly Ser Ala Tyr Tyr Val Ala Pro Glu Val Leu Lys Arg Asn Tyr
245 250 255

Gly Pro Glu Ala Asp Ile Trp Ser Ala Gly Val Ile Leu Phe Ile Leu
260 265 270

Ile Ser Gly Val Pro Pro Phe Trp Gly Glu Asn Glu Thr Gly Ile Phe
275 280 285

Asp Ala Ile Leu Lys Gly Glu Leu Asp Phe Ser Ala Asp Pro Trp Pro
290 295 300

Thr Val Ser Ala Gly Ala Lys Asp Leu Val Lys Lys Met Leu Lys Tyr
305 310 315 320

Asp Pro Lys Asp Arg Leu Thr Ala Ser Glu Val Leu Asn His Pro Trp
325 330 335

Ile Lys Glu Asp Gly Glu Ala Ser Asp Lys Pro Leu Asp Asn Ala Val
340 345 350

Leu Ser Arg Met Lys Gln Phe Arg Ala Met Asn Lys Leu Lys Lys Met
355 360 365

Ala Leu Asn Val Ile Ala Glu Asn Leu Ser Glu Glu Glu Ile Ile Gly
370 375 380

Leu Lys Glu Met Phe Lys Ala Leu Asp Thr Asp Lys Asn Gly Ile Val
385 390 395 400

Thr Leu Glu Glu Leu Arg Thr Gly Leu Pro Lys Leu Gly Asn Lys Ile
405 410 415

Ser Glu Ala Glu Ile Lys Gln Leu Met Glu Ala Ala Asp Met Asp Gly
420 425 430

Asp Gly Ser Ile Asp Tyr Leu Glu Phe Ile Ser Ala Thr Met His Met
435 440 445

Asn Arg Ile Glu Arg Glu Asp His Leu Tyr Thr Ala Phe Gln Tyr Phe
450 455 460

Asp Lys Asp Asn Ser Gly Tyr Ile Thr Met Glu Glu Leu Glu Gln Ala
465 470 475 480

Met Lys Lys Tyr Asn Met Gly Asp Asp Lys Ser Ile Lys Glu Ile Ile
485 490 495

Ala Glu Val Asp Thr Asp Arg Asp Gly Lys Ile Asn Tyr Glu Glu Phe
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Val Ala Met Met Lys Lys Gly Asn Pro Glu Leu Val Thr Asn Arg Arg
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Arg Val Asn Met

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<211> 1587

<212> DNA

<213> G. max

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<211> 528
<212> PRT
<213> G. max

<400> 48

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Val Tyr Arg His Val Ala Gly Ala Gly Gly Ala Gly Val Tyr Asn Asn
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His Lys Ser His Glu Pro Pro Ser His Gln Pro Tyr Pro Leu Pro Glu
35 40 45

Lys His Ala Pro Trp Arg Pro Pro Pro Ser Pro Lys His Val Tyr Lys
50 55 60

His Asp Thr Ile Thr Gly Lys Pro Phe Glu Asp Val Lys Gln His Tyr
65 70 75 80

Thr Leu Gly Lys Glu Leu Gly Arg Gly Gln Phe Gly Val Thr Tyr Leu
85 90 95

Cys Thr Glu Asn Ser Thr Gly Phe Gln Tyr Ala Cys Lys Ser Ile Ser
100 105 110

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

Ile Gln Ile Met Gln His Leu Ser Gly Gln Ser Asn Ile Val Glu Phe
130 135 140

Lys Gly Ala Phe Glu Asp Lys Gln Ser Val His Val Val Met Glu Leu
145 150 155 160

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

Ser Glu Arg Ala Ala Ala Ser Ile Cys Arg Gln Val Val Lys Val Val
180 185 190

Asn Thr Cys His Phe Met Gly Val Ile His Arg Asp Leu Lys Pro Glu
195 200 205

Asn Phe Leu Leu Ser Ser Lys Asp Asp Lys Gly Leu Leu Lys Ala Thr
210 215 220

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

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

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

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

Phe Asp Val Ile Leu Gln Gly His Ile Asp Phe Glu Ser Ser Pro Trp
290 295 300

Pro Ser Ile Ser Asn Ser Ala Lys Asp Leu Val Arg Lys Met Leu Ile
305 310 315 320

Lys Asp Pro Lys Lys Arg Ile Thr Ala Ala Gln Val Leu Glu His Pro
325 330 335

Trp Leu Lys Glu Gly Gly Asn Ala Ser Asp Lys Pro Ile Asp Ser Ala
340 345 350

Val Leu Ser Arg Met Lys Gln Phe Arg Ala Met Asn Lys Leu Lys Lys
355 360 365

Leu Ala Leu Lys Val Ile Ala Glu Asn Leu Ser Glu Glu Glu Ile Gln
370 375 380

Gly Leu Lys Ala Met Phe Thr Asn Ile Asp Thr Asp Asn Ser Gly Thr
385 390 395 400

Ile Thr Tyr Glu Glu Leu Arg Ala Gly Leu Gln Arg Leu Gly Ser Lys
405 410 415

Leu Thr Glu Ala Glu Val Gln Gln Leu Met Asp Ala Ala Asp Val Asp
420 425 430

Gly Asn Gly Thr Ile Asp Tyr Ile Glu Phe Ile Thr Ala Thr Met His
435 440 445

Arg His Arg Leu Glu Arg Asp Glu His Leu His Lys Ala Phe Gln Tyr
450 455 460

Phe Asp Lys Asp Gly Ser Gly Tyr Ile Thr Arg Asp Glu Leu Glu Thr
465 470 475 480

Ala Met Lys Glu Tyr Gly Met Gly Asn Glu Ala Thr Ile Arg Glu Ile
485 490 495

Ile Ser Glu Val Asp Thr Asp Asn Asp Gly Arg Ile Asn Tyr Asp Glu
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Phe Cys Thr Met Met Arg Ser Gly Thr Gln Gln Gln Gly Lys Leu Phe
515 520 525

<210> 49

<211> 1737

<212> DNA

<213> B. napus

<400> 49

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<211> 578

<212> PRT

<213> B. napus

<400> 50

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Ala Lys Ser Ser Gly Phe Pro Phe Tyr Ser Pro Ser Pro Leu Pro Ser
35 40 45

Leu Phe Lys Ser Ser Pro Ser Val Ser Ser Ser Ala Ser Ser Thr Pro
50 55 60

Leu Arg Ile Phe Lys Arg Pro Phe Pro Pro Pro Ser Pro Ala Lys His
65 70 75 80

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

Ser Glu Val Ser Ile Pro Glu Gly Glu Glu Phe Glu Ile Gly Leu Asp
100 105 110

Lys Ser Phe Gly Phe Ser Lys His Phe Ala Ser His Tyr Glu Ile Asp
115 120 125

Gly Glu Val Gly Arg Gly His Phe Gly Tyr Thr Cys Ser Ala Lys Gly
130 135 140

Lys Lys Gly Ser Leu Lys Gly Gln Glu Val Ala Val Lys Val Ile Pro
145 150 155 160

Lys Ser Lys Met Thr Thr Ala Ile Ala Ile Glu Asp Val Ser Arg Glu
165 170 175

Val Lys Ile Leu Arg Ala Leu Thr Gly His Lys Asn Leu Val Gln Phe
180 185 190

Tyr Asp Ala Phe Glu Asp Asp Glu Asn Val Tyr Ile Val Met Glu Leu
195 200 205

Cys Lys Gly Gly Glu Leu Leu Asp Lys Ile Leu Gln Arg Gly Gly Lys
210 215 220

Tyr Ser Glu Asp Asp Ala Lys Gln Val Met Val Gln Ile Leu Ser Val
225 230 235 240

Val Ala Tyr Cys His Leu Gln Gly Val Val His Arg Asp Leu Lys Pro
245 250 255

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

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

Asp Ile Val Gly Ser Ala Tyr Tyr Val Ala Pro Glu Val Leu His Arg
290 295 300

Thr Tyr Gly Thr Glu Ala Asp Met Trp Ser Ile Gly Val Ile Ala Tyr
305 310 315 320

Ile Leu Leu Cys Gly Ser Arg Pro Phe Trp Ala Arg Thr Glu Ser Gly
325 330 335

Ile Phe Arg Ala Val Leu Lys Ala Glu Pro Asn Phe Glu Glu Ala Pro
340 345 350

Trp Pro Ser Leu Ser Pro Asp Ala Val Asp Phe Val Lys Lys Leu Leu
355 360 365

Asn Lys Asp Tyr Arg Lys Arg Leu Thr Ala Ala Gln Ala Leu Cys His
370 375 380

Pro Trp Leu Val Ala Ser His Glu Leu Lys Ile Pro Ser Asp Met Ile
385 390 395 400

Ile Tyr Lys Leu Val Lys Val Tyr Ile Met Ser Thr Ser Leu Arg Lys
405 410 415

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

Tyr Leu Arg Glu Gln Phe Thr Leu Leu Gly Pro Ser Lys Asn Gly Tyr
435 440 445

Ile Ser Met Gln Asn Tyr Lys Thr Ala Ile Leu Lys Thr Ala Thr Asp
450 455 460

Ala Thr Lys Asp Ser Arg Val Leu Asp Phe Val His Met Ile Ser Cys
465 470 475 480

Leu Gln Tyr Lys Lys Leu Asp Phe Glu Glu Phe Cys Ala Ser Ala Leu
485 490 495

Ser Val Tyr Gln Leu Glu Ala Met Glu Thr Trp Glu Gln His Ala Arg
500 505 510

Arg Ala Tyr Glu Leu Phe Glu Lys Asp Gly Asn Arg Pro Ile Met Ile
515 520 525

Glu Glu Leu Ala Ser Glu Leu Gly Leu Gly Pro Ser Val Pro Val His
530 535 540

Val Val Leu Gln Asp Trp Ile Arg His Ser Asp Gly Lys Leu Ser Phe
545 550 555 560

Leu Gly Phe Val Arg Leu Leu His Gly Val Ser Ser Arg Thr Leu Gln
565 570 575

Lys Ala

<210> 51

<211> 1743

<212> DNA

<213> B. napus

<400> 51

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aactcctacg ccagcagccc gttccagagc cccttaccgg cgggagtagc tccgtcgccg	180
gcgagaactc cgggacggaa gttcaaattg ccgtttccgc cgccgtcccc cgccaagccg	240
atcatggcgg ctctgaggcg gagaagaggc gcgccgccgc ggccgagaga cgagccgac	300
ccggaggaca gcgaggacgt tgacggcgtc ggaggggaga ggctggacaa gaacttcggg	360
ttcggaaga acatggaagg gaagtacgag ttggggaagg aggtggggcg agggcatttt	420
ggtcatactt gctgggctaa ggccaagaaa gggaagatga aggggcagac ggtggctgtc	480
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gtcataagct acatactact ctgtggaagc agacctttct acggaagaac tgaatctgca	1020
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gaacaagaag gaaaccgagt catatccgtc caagaactcg ctggggagat gagcgtggga	1620
ccaaatgcat atcctctgct caaggattgg atccggagtt cagatgggaa gctgagtttc	1680
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tga	1743

<210> 52

<211> 580

<212> PRT

<213> B. napus

<400> 52

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

Gln Ser Pro Val Pro Ser Glu Val Asn Ser Tyr Ala Ser Ser Pro Phe
35 40 45

Gln Ser Pro Leu Pro Ala Gly Val Ala Pro Ser Pro Ala Arg Thr Pro
50 55 60

Gly Arg Lys Phe Lys Trp Pro Phe Pro Pro Pro Ser Pro Ala Lys Pro
65 70 75 80

Ile Met Ala Ala Leu Arg Arg Arg Arg Gly Ala Pro Pro Arg Pro Arg
85 90 95

Asp Glu Pro Ile Pro Glu Asp Ser Glu Asp Val Asp Gly Val Gly Gly
100 105 110

Glu Arg Leu Asp Lys Asn Phe Gly Phe Gly Lys Asn Met Glu Gly Lys
115 120 125

Tyr Glu Leu Gly Lys Glu Val Gly Arg Gly His Phe Gly His Thr Cys
130 135 140

Trp Ala Lys Ala Lys Lys Gly Lys Met Lys Gly Gln Thr Val Ala Val
145 150 155 160

Lys Ile Ile Ser Lys Ala Lys Met Thr Ser Ala Leu Ser Ile Glu Asp
165 170 175

Val Arg Arg Glu Val Lys Leu Leu Lys Ala Leu Ser Gly His Lys His
180 185 190

Met Val Lys Phe Tyr Asp Val Tyr Glu Asp Asn Asp Asn Val Tyr Val
195 200 205

Val Met Glu Leu Cys Glu Gly Gly Glu Leu Leu Asp Arg Ile Leu Ala
210 215 220

Arg Gly Gly Lys Tyr Pro Glu Val Asp Ala Lys Arg Ile Leu Val Gln
225 230 235 240

Ile Leu Ser Ala Thr Ala Phe Phe His Leu Gln Gly Val Val His Arg
245 250 255

Asp Leu Lys Pro Glu Asn Phe Leu Phe Thr Ser Arg Asn Glu Asp Ala
260 265 270

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

Gln Arg Leu Asn Asp Val Val Gly Ser Ala Tyr Tyr Val Ala Pro Glu
290 295 300

Val Leu His Arg Ser Tyr Ser Thr Glu Ala Asp Met Trp Ser Ile Gly
305 310 315 320

Val Ile Ser Tyr Ile Leu Leu Cys Gly Ser Arg Pro Phe Tyr Gly Arg
325 330 335

Thr Glu Ser Ala Ile Phe Arg Cys Val Leu Arg Ala Asn Pro Asn Phe
340 345 350

Glu Asp Met Pro Trp Pro Ser Ile Ser Pro Thr Gly Lys Asp Phe Val
355 360 365

Lys Arg Leu Leu Asn Lys Asp His Arg Lys Arg Met Thr Ala Ala Gln
370 375 380

Ala Leu Ala His Pro Trp Leu Arg Asp Glu Asn Pro Gly Leu Leu Leu
385 390 395 400

Asp Phe Ser Val Tyr Lys Leu Val Arg Ser Tyr Ile Arg Ala Ser Pro
405 410 415

Phe Arg Arg Ser Ala Leu Lys Ala Leu Ala Lys Ala Ile Pro Asp Glu
420 425 430

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

Gly Gly Leu Ser Leu Asn Asn Phe Thr Thr Ala Leu Thr Arg Tyr Ala
450 455 460

Thr Asp Ala Met Met Glu Ser Lys Leu Pro Asp Ile Leu Asn Thr Met
465 470 475 480

Gln Pro Leu Val Gln Lys Lys Leu Asp Phe Glu Glu Phe Cys Ala Ala
485 490 495

Gly Val Ser Val Tyr Gln Leu Glu Ala Leu Glu Glu Trp Glu Gln Ile
500 505 510

Ala Thr Ser Ala Phe Glu His Phe Glu Gln Glu Gly Asn Arg Val Ile
515 520 525

Ser Val Gln Glu Leu Ala Gly Glu Met Ser Val Gly Pro Asn Ala Tyr
530 535 540

Pro Leu Leu Lys Asp Trp Ile Arg Ser Ser Asp Gly Lys Leu Ser Phe
545 550 555 560

Leu Gly Tyr Ala Lys Phe Leu His Gly Val Thr Val Arg Ser Ser Ser
565 570 575

Ser Arg Pro Arg
580

<210> 53
<211> 1725
<212> DNA
<213> B. napus

<400> 53
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tcattcctag cgtttacgat ccagaaagac cacaaggccc aacagcgacg taacgccgcg 180

acgacggcga ataagaaaac gccgccgcag acgcaaacgc gacagacgcc aacgcacggg 240

aaggcgagag agaaggcgaa gagacacgga gaaaagatcc cgtacggtaa gcgcgtggat 300

ttcgggtacg ctaaagattt cgataaccgt tacaccatcg ggaagttgct cggacatggc 360

cagttcggtt atacgtacgt agctaccgat aaaaagacag gagatcgtgt cgctgtgaag 420

aaaatcgata aagccaagat gacactgccg atagctgtgg aagatgttag gagagagggtg 480

aagatacttc aagctttaac tggatcatgaa aacgtggttc ggttctacaa tgccttcgag 540

gacaagaact ctgtttatat agccatggag ttatgcgagg gtggtgaatt gctggatcgg 600

atattagcca agaaagatag tcattatacc gagagagacg cggccgtggt agtgagacag	660
atgctaaaag ttgcagctga atgtcattta cgtggtttgg ttcatagaga tatgaaacca	720
gagaattttc tgttcaaadc aactgaagaa gattcggctc taaaagctac agatttcggt	780
ttatcagact tcataaaacc aggcaagaag ttatcatgata tagtagggag cgcgtattac	840
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gttatcagtt acattcttct ctgcgggaga cgaccttctt gggataagac tgaagatggt	960
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agcaacagcg ccaaagattt cgttaagaag ttgttagtaa aagaccaag agctagatta	1080
acagctgctg aggcactatc acatccatgg gttagagaag gaggagatgc aactgagatt	1140
cccatagaca tatctgttct cagcaatatg cgtcagtttg ttaaattcag ccgcctcaag	1200
caattcgcat taagggtctt tgcaacgacg cttgatgaag aggagttggc tgatcttaga	1260
gaccagtttg gtgcgatgga tgctgataag aatggagcca ttagccttga cgagatgcgg	1320
caggcccttg cgaaagatca tccgtggaag cttaaagatg cacgagtcgc tgagattctt	1380
caagcgattg atagcaacac agatggattt gtggattttg aagagtttgt tgctgctgctg	1440
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gcatttgaga aattcgatat agacggagat ggattttataa cagcagaaga acttcgaatg	1560
catactggct tgaaagggtc cattgagcca ctacttgaag aagcagacat tgatcatgat	1620
ggtaaaatca gtctccatga gtttcgtaga cttttgaaaa ctgcgagtat caaatcaaga	1680
aatgttagaa accctcctgg ttatcttatt tctcggaag cctga	1725

<210> 54

<211> 574

<212> PRT

<213> B. napus

<400> 54

Met Gly Leu Cys Phe Ser Ser Ala Lys Val Ser Gly Arg Gln His Arg
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Ser Pro Arg Ser Pro Asn Pro Pro His His Pro Leu Thr Val Ala Lys
20 25 30

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

Lys Asp His Lys Ala Gln Gln Arg Arg Asn Ala Ala Thr Thr Ala Asn
50 55 60

Lys Lys Thr Pro Pro Gln Thr Gln Thr Arg Gln Thr Pro Thr His Gly
65 70 75 80

Lys Ala Arg Glu Lys Ala Lys Arg His Gly Glu Lys Ile Pro Tyr Gly
85 90 95

Lys Arg Val Asp Phe Gly Tyr Ala Lys Asp Phe Asp Asn Arg Tyr Thr
100 105 110

Ile Gly Lys Leu Leu Gly His Gly Gln Phe Gly Tyr Thr Tyr Val Ala
115 120 125

Thr Asp Lys Lys Thr Gly Asp Arg Val Ala Val Lys Lys Ile Asp Lys
130 135 140

Ala Lys Met Thr Leu Pro Ile Ala Val Glu Asp Val Arg Arg Glu Val
145 150 155 160

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

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

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

Tyr Thr Glu Arg Asp Ala Ala Val Val Val Arg Gln Met Leu Lys Val
210 215 220

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

Glu Asn Phe Leu Phe Lys Ser Thr Glu Glu Asp Ser Ala Leu Lys Ala
245 250 255

Thr Asp Phe Gly Leu Ser Asp Phe Ile Lys Pro Gly Lys Lys Phe His
260 265 270

Asp Ile Val Gly Ser Ala Tyr Tyr Val Ala Pro Glu Val Leu Lys Arg
275 280 285

Arg Ser Gly Pro Glu Ser Asp Val Trp Ser Ile Gly Val Ile Ser Tyr
290 295 300

Ile Leu Leu Cys Gly Arg Arg Pro Phe Trp Asp Lys Thr Glu Asp Gly
305 310 315 320

Ile Phe Lys Glu Val Leu Lys Asn Lys Pro Asp Phe Arg Arg Lys Pro
325 330 335

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

Val Lys Asp Pro Arg Ala Arg Leu Thr Ala Ala Gln Ala Leu Ser His
355 360 365

Pro Trp Val Arg Glu Gly Gly Asp Ala Thr Glu Ile Pro Ile Asp Ile
370 375 380

Ser Val Leu Ser Asn Met Arg Gln Phe Val Lys Phe Ser Arg Leu Lys
385 390 395 400

Gln Phe Ala Leu Arg Ala Leu Ala Thr Thr Leu Asp Glu Glu Glu Leu
405 410 415

Ala Asp Leu Arg Asp Gln Phe Gly Ala Met Asp Ala Asp Lys Asn Gly
420 425 430

Ala Ile Ser Leu Asp Glu Met Arg Gln Ala Leu Ala Lys Asp His Pro
435 440 445

Trp Lys Leu Lys Asp Ala Arg Val Ala Glu Ile Leu Gln Ala Ile Asp
450 455 460

Ser Asn Thr Asp Gly Phe Val Asp Phe Glu Glu Phe Val Ala Ala Ala
465 470 475 480

Leu His Val Asn Gln Leu Glu Glu His Asp Ser Glu Lys Trp Gln Gln
485 490 495

Arg Ser Arg Ala Ala Phe Glu Lys Phe Asp Ile Asp Gly Asp Gly Phe
500 505 510

Ile Thr Ala Glu Glu Leu Arg Met His Thr Gly Leu Lys Gly Ser Ile
515 520 525

Glu Pro Leu Leu Glu Glu Ala Asp Ile Asp His Asp Gly Lys Ile Ser
530 535 540

Leu His Glu Phe Arg Arg Leu Leu Lys Thr Ala Ser Ile Lys Ser Arg
545 550 555 560

Asn Val Arg Asn Pro Pro Gly Tyr Leu Ile Ser Arg Lys Ala
565 570

<210> 55
<211> 1632
<212> DNA
<213> B. napus

<400> 55
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gtcgacgtcg aggacgtccg ccgcgaggtc tcgatcatgt ccacactccc cgaccacccc 360
aacgtcgtca agctcagggc gacttacgag gacggcgaga gcgtgcatct ggtcatggag 420

ctctgcgaag gcggcgagct tttcgacagg atcgtcgcga gggggcatta cacggagcgt	480
gcggctgcgg gagttgcgag gacgatcgct gaggttgtga tgatgtgtca tgtgaatgga	540
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gcgttgaagg ctattgattt tgggttgtct gtgttcttca aacctggaga aaagtttaag	660
gagattgtag gaagtccata ttacatggct cctgaggtgt tgaagagaga ttatggacca	720
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aagagagacc cttggcctca gatatcagag agcgccaaga gccttgtgag gcagatgttg	900
aatcctgatc ccactaagcg tttaactgct cagcaagtgt tagctcacc ttgggtacag	960
aatgcaaaga aagctccaaa tgtaccatta ggggatatag tcagatcaag attgaagcag	1020
ttctctatga tgaatagatt caaaaagaaa gttcttcgtg taatagctga gcaattgtct	1080
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ccagagatca aaatgttgat ggaagtggct gatgttgatg ggaatgggtt totggactac	1260
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ctagctttca tgttctttga caaagatgga agtacatata tcgaacttga tgagctacgg	1380
gaagctttta ctgacgagtt gggcgaacct gatgtcagtg ttctaaacga catcatgcgt	1440
gaagttgatt ctgacaagga tgggcgtata aactatgatg agtttgtgac gatgatgaaa	1500
gcaggaaccg attggagaaa ggcgtcgaga caatactcaa gagagagggt caaaagctta	1560
agcattaact tgatgaaaga tggttcattg catctccatg atgctctcac tggacaatct	1620
gtccctgttt ga	1632

<210> 56
<211> 543
<212> PRT
<213> B. napus

<400> 56

Met Gly Asn Cys Asn Val Cys Val Arg Pro Pro Asn Pro Glu Glu Ser
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Lys Pro Lys Lys Thr Asn Gln Asn Arg Lys Leu Asn Pro Phe Thr Ser
20 25 30

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

Ile Pro Thr Ser His Gln Thr Lys Ile Thr Asp Lys Tyr Ile Leu Gly
50 55 60

Arg Glu Leu Gly Arg Gly Glu Phe Gly Ile Thr Tyr Leu Cys Thr Asp
65 70 75 80

Arg Glu Ser Arg Glu Ala Leu Ala Cys Lys Ser Ile Ser Lys Arg Lys
85 90 95

Leu Arg Thr Ala Val Asp Val Glu Asp Val Arg Arg Glu Val Ser Ile
100 105 110

Met Ser Thr Leu Pro Asp His Pro Asn Val Val Lys Leu Arg Ala Thr
115 120 125

Tyr Glu Asp Gly Glu Ser Val His Leu Val Met Glu Leu Cys Glu Gly
130 135 140

Gly Glu Leu Phe Asp Arg Ile Val Ala Arg Gly His Tyr Thr Glu Arg
145 150 155 160

Ala Ala Ala Gly Val Ala Arg Thr Ile Ala Glu Val Val Met Met Cys
165 170 175

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

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

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

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

Glu Val Asp Val Trp Ser Ala Gly Val Ile Ile Tyr Ile Leu Leu Cys
245 250 255

Gly Val Pro Pro Phe Trp Ala Glu Thr Glu Gln Gly Val Ala Leu Ala
260 265 270

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

Ser Glu Ser Ala Lys Ser Leu Val Arg Gln Met Leu Asn Pro Asp Pro
290 295 300

Thr Lys Arg Leu Thr Ala Gln Gln Val Leu Ala His Pro Trp Val Gln
305 310 315 320

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

Arg Leu Lys Gln Phe Ser Met Met Asn Arg Phe Lys Lys Lys Val Leu
340 345 350

Arg Val Ile Ala Glu His Leu Ser Ile Gln Glu Val Glu Val Ile Lys
355 360 365

Asp Met Phe Ser Leu Met Asp Glu Asp Asn Asp Gly Arg Ile Thr Tyr
370 375 380

Leu Glu Leu Lys Ala Gly Leu Gln Lys Val Gly Ser Gln Leu Gly Glu
385 390 395 400

Pro Glu Ile Lys Met Leu Met Glu Val Ala Asp Val Asp Gly Asn Gly
405 410 415

Phe Leu Asp Tyr Gly Glu Phe Val Ala Val Ile Ile His Leu Gln Lys
420 425 430

Ile Glu Asn Asp Glu Leu Phe Lys Leu Ala Phe Met Phe Phe Asp Lys
435 440 445

Asp Gly Ser Thr Tyr Ile Glu Leu Asp Glu Leu Arg Glu Ala Leu Thr
450 455 460

Asp Glu Leu Gly Glu Pro Asp Val Ser Val Leu Asn Asp Ile Met Arg
465 470 475 480

Glu Val Asp Ser Asp Lys Asp Gly Arg Ile Asn Tyr Asp Glu Phe Val
485 490 495

Thr Met Met Lys Ala Gly Thr Asp Trp Arg Lys Ala Ser Arg Gln Tyr
500 505 510

Ser Arg Glu Arg Phe Lys Ser Leu Ser Ile Asn Leu Met Lys Asp Gly
515 520 525

Ser Leu His Leu His Asp Ala Leu Thr Gly Gln Ser Val Pro Val
530 535 540

<210> 57
<211> 1650
<212> DNA
<213> G. max

<400> 57
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gaagaccatt caaagcccac caccacccat tctgatccct cctccgacca cccctctacc 120
aagcaatctg cagaaaacta caacaacaac aactatcttc ctttcaacgc caagagagag 180
tccatcatgc gccgcggcct cgacaaccaa gcctattatg tcttgggcca taagactccc 240
aacattcgtg atctatacac tcttggccgt aaattgggac agggccaatt tggtaggact 300
tatttatgca ccgagaatgc tacctccatt gaatatgcct gcaaattccat ctccaaaagg 360
aagttgattt ccaaggagga cgttgaggac gtaggaggg aaattcagat aatgcatcat 420
ttagctggtc acaagaacat tgtcaccatc aagggtgctt atgaggatcc actctatggt 480
catattgtca tggagctttg ttccgggggt gagttgtttg atcgcatcat ccagaggggc 540

cactataccg agaggaaggc cgctgacttg accaaaatta ttgttggtgt tgttgaggct	600
tgccattccc ttgggggtcat gcatagagat ctcaagcctg aaaactttct cttggtcaac	660
aaagatgatg atttctctct taaagccatt gactttggcc tctccgtttt cttcaaacc	720
ggtcaagttt tctactgatgt agtcggcagc ccatactatg ttgctcctga gattctcctc	780
aaacattatg ggctgaagc agatgtgtgg acagcgggtg tcatactgta catattgctt	840
agtggagtgc cgccattttg ggcagagacc cagcagggtg tatttgatgc agtattgaag	900
ggacttatag attttgactc agatccttgg cctctaatat ctgacagtgc aaaagatctg	960
attagaaaga tgctgtgttc tcggccttca gaacggttga ctgctcatca agtgttatgt	1020
catccttgga tatgtgaaaa tggagttgcc cctgacaggt cactggacc tgctgttctt	1080
tctcgtctca aacagttttc tgctatgaat aagctaaaga agatggctct gcgagtgatt	1140
gctgaaagtc tatccgaaga ggagattgcc ggtttgagag aaatgtttca ggctatggat	1200
actgataaca gtggtgcaat cactttcgat gaactcaaag ctggtctaag aagatatggg	1260
tctaccctta aggatataga aatacgtgat cttatggaag cggctgatgt ggacaaaagt	1320
ggaaccatag actatgggga gtttattgct gcaacagttc atctcaaca actagagcgt	1380
gaagaacatc tcattgcagc attccaatat ttgacaagg atggtagtgg gtacattaca	1440
gttgatgaac ttcaacaagc ttgtgcagaa caaaacatga ctgacgcttt tcttgaagac	1500
atcattagag aagttgatca agataatgat ggaaggattg attatggtga atttgctgcc	1560
atgatgcaaa aaggcaacgc tggaattggg aggagaacta tgcgcaacag tctgaattta	1620
agcatgagag atgcaccaag tgctcaatag	1650

<210> 58

<211> 549

<212> PRT

<213> G. max

<400> 58

Met	Gly	Asn	Thr	Cys	Arg	Gly	Ser	Leu	Lys	Gly	Lys	Tyr	Ser	Gln	Gly
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Leu	Ser	Gln	Pro	Glu	Asp	His	Ser	Lys	Pro	Thr	Thr	Thr	His	Ser	Asp
			20					25						30	

Pro	Ser	Ser	Asp	His	Pro	Ser	Thr	Lys	Gln	Ser	Ala	Glu	Asn	Tyr	Asn
		35					40					45			

Asn	Asn	Asn	Tyr	Leu	Pro	Phe	Asn	Ala	Lys	Arg	Glu	Ser	Ile	Met	Arg
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Arg	Gly	Leu	Asp	Asn	Gln	Ala	Tyr	Tyr	Val	Leu	Gly	His	Lys	Thr	Pro
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Asn	Ile	Arg	Asp	Leu	Tyr	Thr	Leu	Gly	Arg	Lys	Leu	Gly	Gln	Gly	Gln
				85					90					95	

Phe	Gly	Thr	Thr	Tyr	Leu	Cys	Thr	Glu	Asn	Ser	Thr	Ser	Ile	Glu	Tyr
			100					105					110		

Ala	Cys	Lys	Ser	Ile	Ser	Lys	Arg	Lys	Leu	Ile	Ser	Lys	Glu	Asp	Val
		115					120					125			

Glu	Asp	Val	Arg	Arg	Glu	Ile	Gln	Ile	Met	His	His	Leu	Ala	Gly	His
	130					135					140				

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

His Ile Val Met Glu Leu Cys Ser Gly Gly Glu Leu Phe Asp Arg Ile
165 170 175

Ile Gln Arg Gly His Tyr Thr Glu Arg Lys Ala Ala Glu Leu Thr Lys
180 185 190

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

Arg Asp Leu Lys Pro Glu Asn Phe Leu Leu Val Asn Lys Asp Asp Asp
210 215 220

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

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

Glu Val Leu Leu Lys His Tyr Gly Pro Glu Ala Asp Val Trp Thr Ala
260 265 270

Gly Val Ile Leu Tyr Ile Leu Leu Ser Gly Val Pro Pro Phe Trp Ala
275 280 285

Glu Thr Gln Gln Gly Ile Phe Asp Ala Val Leu Lys Gly His Ile Asp
290 295 300

Phe Asp Ser Asp Pro Trp Pro Leu Ile Ser Asp Ser Ala Lys Asp Leu
305 310 315 320

Ile Arg Lys Met Leu Cys Ser Arg Pro Ser Glu Arg Leu Thr Ala His
325 330 335

Gln Val Leu Cys His Pro Trp Ile Cys Glu Asn Gly Val Ala Pro Asp
340 345 350

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

Met Asn Lys Leu Lys Lys Met Ala Leu Arg Val Ile Ala Glu Ser Leu
370 375 380

Ser Glu Glu Glu Ile Ala Gly Leu Arg Glu Met Phe Gln Ala Met Asp
385 390 395 400

Thr Asp Asn Ser Gly Ala Ile Thr Phe Asp Glu Leu Lys Ala Gly Leu
405 410 415

Arg Arg Tyr Gly Ser Thr Leu Lys Asp Ile Glu Ile Arg Asp Leu Met
420 425 430

Glu Ala Ala Asp Val Asp Lys Ser Gly Thr Ile Asp Tyr Gly Glu Phe
435 440 445

Ile Ala Ala Thr Phe His Leu Asn Lys Leu Glu Arg Glu Glu His Leu
450 455 460

Ile Ala Ala Phe Gln Tyr Phe Asp Lys Asp Gly Ser Gly Tyr Ile Thr
465 470 475 480

Val Asp Glu Leu Gln Gln Ala Cys Ala Glu His Asn Met Thr Asp Ala
485 490 495

Phe Leu Glu Asp Ile Ile Arg Glu Val Asp Gln Asp Asn Asp Gly Arg
500 505 510

Ile Asp Tyr Gly Glu Phe Ala Ala Met Met Gln Lys Gly Asn Ala Gly
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Ala Pro Ser Ala Gln
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<212> PRT

<213> Z. mays

<400> 60

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35 40 45

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

Ile Thr Val Leu Glu Arg Lys Thr Ala Asp Ile Arg Glu His Tyr Ile
65 70 75 80

Ile Gly Arg Arg Leu Gly Gln Gly Gln Phe Gly Thr Thr Phe Leu Cys
85 90 95

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

Arg Lys Leu Ile Thr Lys Glu Asp Val Glu Asp Val Arg Arg Glu Ile
115 120 125

Gln Ile Met His His Leu Ser Gly His Lys Asn Val Val Ser Ile Lys
130 135 140

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

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

Glu Gln Lys Ala Ala Glu Leu Ile Arg Ile Ile Ile Ser Leu Val Ala
180 185 190

Met Cys His Ser Leu Gly Val Met His Arg Asp Leu Lys Pro Glu Asn
195 200 205

Phe Leu Leu Trp Asp Lys Glu Asp Asp Leu Ser Ile Lys Ala Ile Asp
210 215 220

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

Val Gly Ser Pro Tyr Tyr Val Ala Pro Glu Val Leu His Lys Arg Tyr
245 250 255

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

Leu Ser Gly Val Pro Pro Phe Trp Ala Glu Thr Gln Gln Gly Ile Phe
275 280 285

Asp Ala Val Leu Lys Gly His Ile Asp Phe Asp Ser Asp Pro Trp Pro
290 295 300

Lys Ile Ser Glu Ser Ala Lys Asn Leu Ile Arg Lys Met Leu Cys Pro
305 310 315 320

Cys Pro Ser Glu Arg Leu Lys Ala His Glu Val Leu Arg His Pro Trp
325 330 335

Ile Cys Glu Asn Gly Val Ala Thr Asp Gln Ala Leu Asp Pro Gly Val
340 345 350

Leu Ser Arg Leu Lys Gln Phe Ser Thr Met Asn Lys Leu Lys Lys Leu
355 360 365

Ala Leu Arg Val Ile Ala Glu Arg Leu Ser Glu Glu Glu Ile Ala Gly
370 375 380

Leu Arg Gln Met Phe Lys Ala Val Asp Val Gln Asn Arg Gly Val Ile
385 390 395 400

Thr Phe Gly Glu Leu Arg Gln Gly Leu Lys Arg Tyr Gly Ser Glu Leu
405 410 415

Glu Asn Arg Glu Ile Ser Asp Ile Met Glu Val Ala Asp Asn Asp Asn
420 425 430

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

Asn Lys Ile Glu Arg Glu Glu His Leu Met Ala Ala Phe Thr Tyr Phe
450 455 460

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

Cys Gly Glu His Asp Met Asp Asp Thr Phe Leu Glu Glu Ile Ile Leu
485 490 495

Glu Val Asp Gln Asn Asn Asp Gly Gln Ile Asp Tyr Ala Lys Phe Val
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35 40 45

Gly Gly Ser Gln Ser Arg His Val Pro Lys Met Lys Ser Ser Ser Thr
50 55 60

Gly Ile Leu Gly Lys Pro Leu Arg Asp Ile Lys Leu His Tyr Thr Leu
65 70 75 80

Gly Arg Glu Leu Gly Arg Gly Gln Phe Gly Val Thr Tyr Leu Cys Thr
85 90 95

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

Lys Leu Thr Asn Lys Asp Asp Ile Glu Asp Val Lys Arg Glu Val Gln
115 120 125

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

Val Phe Glu Asp Lys Gln Asn Val Asn Leu Val Met Glu Leu Cys Ala
145 150 155 160

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

Arg Asp Ala Ala Asp Met Cys Arg Val Ile Val Thr Val Val His Arg
180 185 190

Cys His Ser Leu Gly Val Phe His Arg Asp Leu Lys Pro Glu Asn Phe
195 200 205

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

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

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

Cys Gly Val Pro Pro Phe Trp Ala Glu Thr Glu Lys Glu Ile Phe Asp
275 280 285

Thr Ile Met Arg Gly His Ile Asp Phe Lys Ser Asp Pro Trp Pro Lys
290 295 300

Ile Ser Asp Glu Ala Lys Asp Leu Val Lys Lys Met Leu Asn Ser Asn
305 310 315 320

Val Lys Glu Arg Leu Thr Ala Gln Glu Val Leu Asn His Pro Trp Met
325 330 335

Gln Arg Asp Gly Val Pro Asp Val Pro Leu Asp Asn Ala Val Leu Thr
340 345 350

Arg Leu Arg Asn Phe Ser Ala Ala Asn Lys Met Lys Lys Leu Ala Leu
355 360 365

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

Glu Leu Phe Lys Ser Ile Asp Thr Asp Asn Ser Gly Thr Val Thr Ile
385 390 395 400

Asp Glu Leu Lys Lys Gly Leu Leu Lys Gln Gly Thr Arg Leu Thr Glu
405 410 415

Ala Asp Val Arg Lys Leu Met Glu Ala Ala Asp Val Asp Gly Asn Gly
420 425 430

Lys Ile Asp Phe Asn Glu Phe Ile Ser Ala Thr Met His Met Asn Lys
435 440 445

Thr Gln Lys Glu Asp His Leu His Ala Ala Phe Gln His Phe Asp Thr
450 455 460

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465 470 475 480

Lys Gln Gly Met Gly Asp Pro Glu Thr Leu Gln Glu Ile Ile Asn Glu
485 490 495

Val Asp Thr Asp His Asp Gly Arg Ile Asp Tyr Asp Glu Phe Val Ala
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Ser Pro Arg His Arg Trp
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35 40 45

Asn Asn Asn Asn Asn Lys Ser Pro Val Leu Val Leu Pro Val Lys Glu
50 55 60

Pro Phe Met Arg Arg Asn Met Asp Asn Gln Ala Tyr Tyr Val Leu Gly
65 70 75 80

His Lys Thr Pro Asn Ile Arg Asp Leu Tyr Thr Leu Ser Arg Lys Leu
85 90 95

Gly Gln Gly Gln Phe Gly Thr Thr Tyr Leu Cys Thr Glu Val Ala Thr
100 105 110

Gly Val Asp Tyr Ala Cys Lys Ser Ile Ser Lys Arg Lys Leu Ile Ser
115 120 125

Lys Glu Asp Val Glu Asp Val Arg Arg Glu Ile Gln Ile Met His His
130 135 140

Leu Ala Gly His Lys Asn Ile Val Thr Ile Lys Gly Ala Tyr Glu Asp
145 150 155 160

Pro Leu Tyr Val His Ile Val Met Glu Val Cys Ala Gly Gly Glu Leu
165 170 175

Phe Asp Arg Ile Ile Gln Arg Gly His Tyr Thr Glu Arg Lys Ala Ala
180 185 190

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

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

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

Phe Phe Lys Pro Gly Gln Ile Phe Lys Asp Val Val Gly Ser Pro Tyr
245 250 255

Tyr Val Ala Pro Glu Val Leu Leu Lys His Tyr Gly Pro Glu Ala Asp
260 265 270

Val Trp Thr Ala Gly Val Ile Leu Tyr Ile Leu Leu Ser Gly Val Pro
275 280 285

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

Gly Asp Ile Asp Phe Glu Ser Asp Pro Trp Pro Val Ile Ser Asp Ser
305 310 315 320

Ala Lys Asp Leu Ile Arg Lys Met Leu Cys Ser Asn Pro Ser Glu Arg
325 330 335

Leu Thr Ala His Glu Val Met Arg His Pro Trp Ile Cys Glu Asn Gly
340 345 350

Val Ala Pro Asp Arg Ala Leu Asp Pro Ala Val Leu Ser Arg Leu Lys
355 360 365

Gln Phe Ser Ala Met Asn Lys Leu Lys Lys Met Ala Leu Lys Val Ile
370 375 380

Ala Glu Ser Leu Ser Glu Glu Glu Ile Ala Gly Leu Arg Ala Met Phe
385 390 395 400

Glu Ala Met Asp Thr Asp Asn Ser Gly Ala Ile Thr Phe Asp Glu Leu
405 410 415

Lys Ala Gly Leu Arg Arg Tyr Gly Ser Thr Leu Lys Asp Thr Glu Ile
420 425 430

Gln Asp Leu Met Glu Ala Ala Asp Val Asp Asn Ser Gly Thr Ile Asp
435 440 445

Tyr Ser Glu Phe Ile Ala Ala Thr Ile His Leu Asn Lys Leu Asp Arg
450 455 460

Glu Glu His Leu Val Ser Ala Phe Gln Tyr Phe Asp Lys Asp Gly Ser
465 470 475 480

Gly Tyr Ile Thr Ile Asp Glu Leu Gln Gln Ser Cys Val Glu His Gly
485 490 495

Met Thr Asp Val Phe Leu Glu Asp Val Ile Lys Glu Val Asp Gln Asp
500 505 510

Asn Asp Gly Arg Ile Asp Tyr Gly Glu Phe Val Ala Met Met Gln Lys
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Ser Met Arg Asp Ala
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<212> PRT

<213> B. napus

<400> 66

Met	Gly	Asn	Cys	Cys	Gly	Ser	Pro	Ser	Ser	Ala	Thr	Ile	Glu	Ser	Gly
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His	Gly	Lys	Pro	Lys	Asn	Lys	Asn	Asn	Pro	Phe	His	Ser	Asn	Glu	Ala
			20				25						30		

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

Gly His Asp Ile Ser Ser Gln Tyr Asp Leu Gly Arg Glu Val Gly Arg
50 55 60

Gly Glu Phe Gly Val Thr Tyr Leu Cys Thr Asp Ile Gln Thr Gly Asp
65 70 75 80

Lys Tyr Ala Cys Lys Ser Ile Ser Lys Lys Lys Leu Arg Thr Ala Val
85 90 95

Asp Ile Gly Asp Val Arg Arg Glu Val Glu Ile Met Arg His Met Pro
100 105 110

Lys His Pro Asn Ile Val Ser Leu Lys Asp Ser Phe Glu Asp Asp Asp
115 120 125

Ala Val His Ile Val Met Glu Leu Cys Glu Gly Gly Glu Leu Phe Asp
130 135 140

Arg Ile Val Ala Arg Gly His Tyr Thr Glu Arg Ala Ala Ala Ala Val
145 150 155 160

Met Lys Thr Ile Val Glu Val Val Gln Ile Cys His Lys Gln Gly Val
165 170 175

Met His Arg Asp Leu Lys Pro Glu Asn Phe Leu Phe Ala Asn Lys Lys
180 185 190

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

Lys Pro Gly Glu Gln Phe Asn Glu Ile Val Gly Ser Pro Tyr Tyr Met
210 215 220

Ala Pro Glu Val Leu Arg Arg Asn Tyr Gly Pro Glu Ile Asp Val Trp
225 230 235 240

Ser Ala Gly Val Ile Leu Tyr Ile Leu Leu Cys Gly Val Pro Pro Phe
245 250 255

Trp Ala Glu Thr Glu Gln Gly Val Ala Gln Ala Ile Ile Arg Ser Val
260 265 270

Ile Asp Phe Lys Arg Asp Pro Trp Pro Arg Val Ser Glu Ser Ala Lys
275 280 285

Asp Leu Val Arg Lys Met Leu Glu Pro Asp Pro Lys Lys Arg Leu Ser
290 295 300

Ala Ala Glu Val Leu Glu His Thr Trp Ile Leu Asn Ala Lys Lys Ala
305 310 315 320

Pro Asn Val Ser Leu Gly Glu Thr Val Lys Ala Arg Leu Lys Gln Phe
325 330 335

Ser Val Met Asn Lys Leu Lys Lys Arg Ala Leu Arg Val Ile Ala Glu
340 345 350

His Leu Ser Val Glu Glu Ala Ala Gly Ile Lys Glu Ala Phe Glu Met
355 360 365

Met Asp Val Asn Lys Arg Gly Lys Ile Asn Leu Glu Glu Leu Lys Tyr
370 375 380

Gly Leu Gln Lys Ala Gly Gln Gln Ile Ala Asp Ala Asp Leu Gln Ile
385 390 395 400

Leu Met Glu Ala Thr Asp Val Asp Gly Asp Gly Thr Leu Asn Tyr Gly
405 410 415

Glu Phe Val Ala Val Ser Val His Leu Lys Lys Met Ala Asn Asp Glu
420 425 430

His Leu His Lys Ala Phe Asn Phe Phe Asp Lys Asn Gln Ser Gly Tyr
435 440 445

Ile Glu Pro Glu Glu Leu Arg Glu Ala Leu Asn Asp Glu Leu Asp Glu
450 455 460

Thr Ser Ser Glu Glu Val Ile Ala Ala Ile Met His Asp Val Asp Thr
465 470 475 480

Asp Lys Asp Gly Arg Ile Ser Tyr Glu Glu Phe Ala Ala Met Met Lys
485 490 495

Ala Gly Thr Asp Trp Arg Lys Ala Ser Arg Gln Tyr Ser Arg Glu Arg
500 505 510

Phe Asn Ser Leu Ser Leu Lys Leu Met Arg Asp Gly Ser Leu Gln Leu
515 520 525

Glu Gly Glu Thr
530

<210> 67
<211> 1578
<212> DNA
<213> B. napus

<400> 67
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accgcttcaa acgctggtcc aactgccgaa gcctccgtgc cacaatccaa acacgcccct 120
ccttctcctc ctcccgaac caaacaaggc cccataggac ctgtcttagg ccgctcccatg 180
gaagatgtaa aatcctcata ctctctaggc aaagagctag gccgaggaca gttcggcgtc 240
acgcatctct gactcagaa ggcgacaggt cagcagttcg cttgcaagac cattgccaaa 300
aggaagcttg tgaacaaaga agatattgag gatgtaagaa gggaagtgca gataatgcat 360
cacctgactg gtcagcctaa cattgtggag cttaaaggag cttacgagga taagcattct 420
gtgcatttgg tcatggagct ttgcgctggg ggagagctgt tcgataggat tattgctaaa 480
ggacattact cggagagagc agctgcttcc ttgttgagaa cgattgttca gattgtgcat 540
acttgtcatt ccatgggggt tattcacagg gacttgaagc ctgagaactt tttgttgctc 600
agcaaagatg agaaggctcc tctcaaggcc actgactttg ggctgtctgt attctacaag 660
ccgggagagg tgtttaagga tattgtgggt agtgcttatt acatagcgcc tgagggttttg 720
aaaaggaagt atggaccaga agctgatatt tggagtattg gtgtcatggt gtatatcctc 780
ttatgtggtg tccctccctt ctgggctgaa tcggagaatg ggatattcaa cgccatctta 840
aagagccatg ttgatttctc aagtgatcca tggccatcca tctcacctca ggcgaaggat 900
cttgtaaga agatgctcaa ctctgatccc aagcaaaggc taactgctgc tcaagttctc 960
aatcatccat ggatcaagga agatggagaa gcaccagatg ttcctcttga caatgcgggtg 1020

atgtccaggc tcaagcaatt caaagcaatg aacaatttca agaaagttgc attgaggggtg 1080
 atagcaggct gcttatcaga ggaagagatc atgggggttga aggagatggt taaaggtatg 1140
 gacactgaca acagtggaac gattacactc gaggagctaa gacagggact cgctaagcaa 1200
 ggtacaaggt tgtcagagta cgaagtccag caactaatgg aagctgccga tgctgatggt 1260
 aatggaacaa tagactatgg tgagttttatc gcagccacaa tgcatatcaa cagacttgac 1320
 agagaagaac atctctactc agccttccaa cactttgaca aagacaacag cggatatatt 1380
 actatggaag agctggaaca agccctccgg gagtttggga tgaacgatgg cagagacatt 1440
 aaagagataa tttcagaggt cgatggagac aatgatggtc ggataaacta cgacgagttc 1500
 gtggcaatga tgagaaaagg aaaccctgat cctatcccaa agaagcgacg tgagctttca 1560
 tttaaattggc cagagtag 1578

<210> 68

<211> 525

<212> PRT

<213> B. napus

<400> 68

Met Gly Asn Cys Cys Ser Asn Gly Arg Asp Ser Gly Asp Asn Gly Asp
 1 5 10 15

Thr Arg Gly Ile Thr Ala Ser Asn Ala Gly Pro Thr Ala Glu Ala Ser
 20 25 30

Val Pro Gln Ser Lys His Ala Pro Pro Ser Pro Pro Pro Ala Thr Lys
 35 40 45

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

Ser Ser Tyr Ser Leu Gly Lys Glu Leu Gly Arg Gly Gln Phe Gly Val
65 70 75 80

Thr His Leu Cys Thr Gln Lys Ala Thr Gly Gln Gln Phe Ala Cys Lys
85 90 95

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

Arg Arg Glu Val Gln Ile Met His His Leu Thr Gly Gln Pro Asn Ile
115 120 125

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

Met Glu Leu Cys Ala Gly Gly Glu Leu Phe Asp Arg Ile Ile Ala Lys
145 150 155 160

Gly His Tyr Ser Glu Arg Ala Ala Ala Ser Leu Leu Arg Thr Ile Val
165 170 175

Gln Ile Val His Thr Cys His Ser Met Gly Val Ile His Arg Asp Leu
180 185 190

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

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

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

Lys Arg Lys Tyr Gly Pro Glu Ala Asp Ile Trp Ser Ile Gly Val Met
245 250 255

Leu Tyr Ile Leu Leu Cys Gly Val Pro Pro Phe Trp Ala Glu Ser Glu
260 265 270

Asn Gly Ile Phe Asn Ala Ile Leu Lys Ser His Val Asp Phe Ser Ser
275 280 285

Asp Pro Trp Pro Ser Ile Ser Pro Gln Ala Lys Asp Leu Val Lys Lys
290 295 300

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

Asn His Pro Trp Ile Lys Glu Asp Gly Glu Ala Pro Asp Val Pro Leu
325 330 335

Asp Asn Ala Val Met Ser Arg Leu Lys Gln Phe Lys Ala Met Asn Asn
340 345 350

Phe Lys Lys Val Ala Leu Arg Val Ile Ala Gly Cys Leu Ser Glu Glu
355 360 365

Glu Ile Met Gly Leu Lys Glu Met Phe Lys Gly Met Asp Thr Asp Asn
370 375 380

Ser Gly Thr Ile Thr Leu Glu Glu Leu Arg Gln Gly Leu Ala Lys Gln
385 390 395 400

Gly Thr Arg Leu Ser Glu Tyr Glu Val Gln Gln Leu Met Glu Ala Ala
405 410 415

Asp Ala Asp Gly Asn Gly Thr Ile Asp Tyr Gly Glu Phe Ile Ala Ala
420 425 430

Thr Met His Ile Asn Arg Leu Asp Arg Glu Glu His Leu Tyr Ser Ala
435 440 445

Phe Gln His Phe Asp Lys Asp Asn Ser Gly Tyr Ile Thr Met Glu Glu
450 455 460

Leu Glu Gln Ala Leu Arg Glu Phe Gly Met Asn Asp Gly Arg Asp Ile
465 470 475 480

Lys Glu Ile Ile Ser Glu Val Asp Gly Asp Asn Asp Gly Arg Ile Asn
485 490 495

Tyr Asp Glu Phe Val Ala Met Met Arg Lys Gly Asn Pro Asp Pro Ile
500 505 510

Pro Lys Lys Arg Arg Glu Leu Ser Phe Lys Trp Pro Glu
515 520 525

<210> 69

<211> 1647

<212> DNA

<213> T. aestivum

<400> 69

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gagaagccct ggcccgatgc cgactcgttt aagcccaccg ccgctggtat tctgaggcag	180
ggtttggatc tgacatccat ctctgtcctc gggcgcaaga cggcggacct aagggagcat	240
tatatcattg gccggaagct tgggcagggc cagtttggga cgacatacct ctgcaccgag	300
ataagtacag ggtgcgactt cgcatgcaag accatcctca agcgcaagct cgtcaccaag	360
gtggatgtcg aggatgtgcg ccgtgagatc cagataatgc accatttgtc gggacacaag	420
aacgttgtct cgatcaagga tgtctatgag gacgtgcagg cggtcacat tgtgatggag	480
ctcttgcccg gcggggagct ctttgaccga attcagggga atgggcatta cagcgagatg	540
aaggctgcag agattacaag aattgttgtc agcattgtgg ctatgtgcca ttcacttggt	600
gtgatgcacc gcgatctcaa gccagaaaat ttcctcctcc ttgacaaaga tgatgacctg	660
tccataaaaag caattgattt tggcctatcc gtttacttca agccaggcca ggttttcagt	720
gagctagttag gcagcccgtt ctatgttgct cctgaggtgc tgcacaaacg ctatgggcca	780
gaatctgatg tgtggtcagc tggagtgata ctctatgtgt tgctaagtgg ggttccacca	840
ttttgggcag atacacagaa aggcataattt gatgcagttc tgaaggggca cottgatttg	900
gaatcagacc cttggcctaa gatatctgac ggtgcaaagg atcttataag aaaaatgctt	960
tgcaattgcc cttcagagcg tttgaaagcc catgaagtgc tacggcatcc ctggatctgc	1020
caaatggggg tggccactga tggagttttg gatcctagtg tcatctctcg gctcaagcgg	1080
ttctctgcaa tgaacaatct acagaaatta gctctgagag tgatagctga gcgtctttca	1140
gaagaggaga ttgctggatt aagagaatta ttcaagacag tggacataaa aaatagaggt	1200
gtgatcactt tcggtgagct taggaaaggt ttgacaagat atggcaacga attggtggat	1260
accgagattt gtgatataat ggaagcggct gatacagaca ctgatgtaac cataaattat	1320

gaagaattta ttgctgcaac catgcctcta aacaagatag agcgggaaga gcacttgaag 1380

gcagctttta catatattga caaagatggc agtggctata tcacagtcga caagcttcaa 1440

cgagcctgtg cagaatataa catggagggc actctccttg aagagattat tttagaggcc 1500

gaccagaaca atgacggtca aattgattat gctgaatttg tagccatgat gcaaggcaac 1560

accaacggtg gcaatatttg acttgggcgt ccaacaatgg aaaccagtct gaatgtgacc 1620

ttgagagatg cagctcaagt acattaa 1647

<210> 70

<211> 548

<212> PRT

<213> T. aestivum

<400> 70

Met Gly Asn Gln Asn Gly Thr Pro Gly Asn Asp Tyr Cys Ser Arg Phe

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Pro Arg Glu His Pro Ala Ser Arg Tyr Ala Asp Gly Ile Glu Asp Asp

20 25 30

Ser Tyr Ser Asp Leu Lys Lys Ser Glu Lys Pro Trp Pro Asp Ala Asp

35 40 45

Ser Phe Lys Pro Thr Ala Ala Gly Ile Leu Arg Gln Gly Leu Asp Leu

50 55 60

Thr Ser Ile Ser Val Leu Gly Arg Lys Thr Ala Asp Leu Arg Glu His

65 70 75 80

Tyr Ile Ile Gly Arg Lys Leu Gly Gln Gly Gln Phe Gly Thr Thr Tyr

85 90 95

Leu Cys Thr Glu Ile Ser Thr Gly Cys Asp Phe Ala Cys Lys Thr Ile
100 105 110

Leu Lys Arg Lys Leu Val Thr Lys Val Asp Val Glu Asp Val Arg Arg
115 120 125

Glu Ile Gln Ile Met His His Leu Ser Gly His Lys Asn Val Val Ser
130 135 140

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

Leu Leu Pro Gly Gly Glu Leu Phe Asp Arg Ile Gln Gly Asn Gly His
165 170 175

Tyr Ser Glu Met Lys Ala Ala Glu Ile Thr Arg Ile Val Val Ser Ile
180 185 190

Val Ala Met Cys His Ser Leu Gly Val Met His Arg Asp Leu Lys Pro
195 200 205

Glu Asn Phe Leu Leu Leu Asp Lys Asp Asp Asp Leu Ser Ile Lys Ala
210 215 220

Ile Asp Phe Gly Leu Ser Val Tyr Phe Lys Pro Gly Gln Val Phe Ser
225 230 235 240

Glu Leu Val Gly Ser Pro Phe Tyr Val Ala Pro Glu Val Leu His Lys
245 250 255

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

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

Ile Phe Asp Ala Val Leu Lys Gly His Leu Asp Leu Glu Ser Asp Pro
290 295 300

Trp Pro Lys Ile Ser Asp Gly Ala Lys Asp Leu Ile Arg Lys Met Leu
305 310 315 320

Cys Asn Cys Pro Ser Glu Arg Leu Lys Ala His Glu Val Leu Arg His
325 330 335

Pro Trp Ile Cys Gln Asn Gly Val Ala Thr Asp Gly Val Leu Asp Pro
340 345 350

Ser Val Ile Ser Arg Leu Lys Arg Phe Ser Ala Met Asn Asn Leu Gln
355 360 365

Lys Leu Ala Leu Arg Val Ile Ala Glu Arg Leu Ser Glu Glu Glu Ile
370 375 380

Ala Gly Leu Arg Glu Leu Phe Lys Thr Val Asp Ile Lys Asn Arg Gly
385 390 395 400

Val Ile Thr Phe Gly Glu Leu Arg Lys Gly Leu Thr Arg Tyr Gly Asn
405 410 415

Glu Leu Val Asp Thr Glu Ile Cys Asp Ile Met Glu Ala Ala Asp Thr
420 425 430

Asp Thr Asp Val Thr Ile Asn Tyr Glu Glu Phe Ile Ala Ala Thr Met
435 440 445

Pro Leu Asn Lys Ile Glu Arg Glu Glu His Leu Lys Ala Ala Phe Thr
450 455 460

Tyr Phe Asp Lys Asp Gly Ser Gly Tyr Ile Thr Val Asp Lys Leu Gln
465 470 475 480

Arg Ala Cys Ala Glu Tyr Asn Met Glu Gly Thr Leu Leu Glu Glu Ile
485 490 495

Ile Leu Glu Ala Asp Gln Asn Asn Asp Gly Gln Ile Asp Tyr Ala Glu
500 505 510

Phe Val Ala Met Met Gln Gly Asn Thr Asn Gly Gly Asn Ile Gly Leu
515 520 525

Gly Arg Pro Thr Met Glu Thr Ser Leu Asn Val Thr Leu Arg Asp Ala
530 535 540

Ala Gln Val His
545

<210> 71

<211> 1596

<212> DNA

<213> Z. mays

<400> 71

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tatggctatt ctaaccaggc aaagccggcg caagcacccc cgagttacaa ccctcctcag	120
caggcggccg aggtgaggtg cacaccatcg gcgacgaact cttcggcagt cccacccgtg	180
gctgtgccgc cgaagccaac ggcggaacag attcttggca agcagtacga ggacgtgcgc	240
tctgtctact ccctcgggaa ggagcttggc cggggccagt tcgggggtgac atacctctgc	300
acagagattg cctctggtag gcagtacgcc tgcaagtcca tctccaagcg caagctcgtc	360
agcaaggcag acagggagga cattcgaagg gagatccaga tcatgcagca cctgtctggg	420
cagccaaaca ttgttgagtt ccggggagca tacgaggaca agagcaatgt ccatgtggtg	480
atggagctct gcgcaggtgg ggagctcttc gatcgcatca ttgccaaaggg gcactacaca	540
gagcgtgcag ctgctacaat ctgcagagca gttgtgaatg ttgtcaacat ttgccacttc	600
atgggtgtga tgcaccgtga cctgaaaccg gagaacttct tgcttgcgag caaggaggag	660
aatgcaatgc tcaaggccac tgattttggg ctttcgctct tcatcgaaga aggaaagatg	720
tacagggaca tcgttggaag tgcttattat gttgcgcctg aagtccttaa gcgagctat	780
ggaaaagaga tagatgtttg gagcgcaggt gttattttgt acattcttct cagtgggtgtg	840
cctccatttt gggctgaaac tgaaaagggg atatttgatg ctattctgca tgaggagatt	900
gactttgaaa gtcaaccttg gccatcaatt tctgagagtg ctaaagactt ggtagaaaag	960
atgttgacac gagatccaaa gaaaagactg acttcagctc aagttcttca acattcatgg	1020
ctcagagaag gtggaggtgc atctgataag cctatcgaca gtactgttct ttctagaatg	1080
aagcagttca gagcaatgaa taagctgaaa aagatggccc taaaggttat tgctcaaac	1140
cttaacgagg aagagatcaa ggggctaaag caaatgttca tgaacatgga cacagacaat	1200
agtggcacia tcacgtatga agaactcaaa gcaggactag ccaaacttgg atcaaagctg	1260
tcggaagctg aagtaaagca gttgatggag gctgctgatg ttgatgggaa tggatccatc	1320

gactatgttg agttcatcac tgccacaatg catagacaca agctcgaaaag agacgagtat	1380
ttgtttaagg cattccagta cttcgataaa gataacagcg gtttcatcac aagagatgag	1440
ctggagtctg ctttgatcga gcatgagatg ggtgacacga gtacaataaa ggagatcata	1500
tcagaagtgg acacagacaa tgatgggagg attaactatg aggagttctg cgcaatgatg	1560
agaggaggga tgcagcagcc aatgaggctc aagtag	1596

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

Pro Pro Ser Tyr Asn Pro Pro Gln Gln Ala Ala Glu Val Arg Tyr Thr
35 40 45

Lys Pro Thr Ala Asp Thr Ile Leu Gly Lys Gln Tyr Glu Asp Val Arg
65 70 75 80

Thr Tyr Leu Cys Thr Glu Ile Ala Ser Gly Arg Gln Tyr Ala Cys Lys
100 105 110

Ser Ile Ser Lys Arg Lys Leu Val Ser Lys Ala Asp Arg Glu Asp Ile
115 120 125

Arg Arg Glu Ile Gln Ile Met Gln His Leu Ser Gly Gln Pro Asn Ile
130 135 140

Val Glu Phe Arg Gly Ala Tyr Glu Asp Lys Ser Asn Val His Val Val
145 150 155 160

Met Glu Leu Cys Ala Gly Gly Glu Leu Phe Asp Arg Ile Ile Ala Lys
165 170 175

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

Asn Val Val Asn Ile Cys His Phe Met Gly Val Met His Arg Asp Leu
195 200 205

Lys Pro Glu Asn Phe Leu Leu Ala Ser Lys Glu Glu Asn Ala Met Leu
210 215 220

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

Tyr Arg Asp Ile Val Gly Ser Ala Tyr Tyr Val Ala Pro Glu Val Leu
245 250 255

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

Leu Tyr Ile Leu Leu Ser Gly Val Pro Pro Phe Trp Ala Glu Thr Glu
275 280 285

Lys Gly Ile Phe Asp Ala Ile Leu His Glu Glu Ile Asp Phe Glu Ser
290 295 300

Gln Pro Trp Pro Ser Ile Ser Glu Ser Ala Lys Asp Leu Val Arg Lys
305 310 315 320

Met Leu Thr Arg Asp Pro Lys Lys Arg Leu Thr Ser Ala Gln Val Leu
325 330 335

Gln His Ser Trp Leu Arg Glu Gly Gly Gly Ala Ser Asp Lys Pro Ile
340 345 350

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

Leu Lys Lys Met Ala Leu Lys Val Ile Ala Ser Asn Leu Asn Glu Glu
370 375 380

Glu Ile Lys Gly Leu Lys Gln Met Phe Met Asn Met Asp Thr Asp Asn
385 390 395 400

Ser Gly Thr Ile Thr Tyr Glu Glu Leu Lys Ala Gly Leu Ala Lys Leu
405 410 415

Gly Ser Lys Leu Ser Glu Ala Glu Val Lys Gln Leu Met Glu Ala Ala
420 425 430

Asp Val Asp Gly Asn Gly Ser Ile Asp Tyr Val Glu Phe Ile Thr Ala
435 440 445

Thr Met His Arg His Lys Leu Glu Arg Asp Glu Tyr Leu Phe Lys Ala
450 455 460

Phe Gln Tyr Phe Asp Lys Asp Asn Ser Gly Phe Ile Thr Arg Asp Glu
465 470 475 480

Leu Glu Ser Ala Leu Ile Glu His Glu Met Gly Asp Thr Ser Thr Ile
485 490 495

Lys Glu Ile Ile Ser Glu Val Asp Thr Asp Asn Asp Gly Arg Ile Asn
500 505 510

Tyr Glu Glu Phe Cys Ala Met Met Arg Gly Gly Met Gln Gln Pro Met
515 520 525

Arg Leu Lys
530

<210> 73

<211> 1068

<212> DNA

<213> B. napus

<400> 73

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gaagacagtt ctgggttcga tgaggaagac gaagattcct gcgacgacaa atctgacgaa 120

aagtttccat ttttccatct gggttttctc gatcgggtgta tgtcctggga ggaagacgag 180

ttatcgagtc tgatctccaa ggaaaacgag ttcagaccgt ctcttaccga agaggggtgtc 240

ttagacgacg agtatctggc tttgtgtcgt gaaaaggctg ttgattggat tctcagggtg	300
aaatctcatt acgggttttag ttccttgacg gctcttctcg ctgttaacta cttogatagg	360
ttcatcacia gcaggaagtt tcagacagag tttccgtgga tgtctcagct tacggctttg	420
gcttgtttgt ctttagctgc aaaagttgaa gaggtccgag ttcctctgct cgtagatctc	480
caagtggaag aggcaagcta tgtctttgag gctaaaacca tacagcgaat ggagcttttg	540
attctctcta ctcttcattg gaggggtgcat cccgtgactc caatctcgta tcttgatcat	600
attatccgtc gattcagctt taaatctcac cagcaattgg agtttttgag tagatgtgaa	660
tctctgttgc tctccattgt tcctgattcg aggtttctaa gttatagctc gtctgagtta	720
gcagctgcaa taatgggtctc tgtctttaga ggtttcaaga cgtgtgacga atctgaatac	780
gaatctcagc tcatgacact actcagagtt gattcggaga aagtacataa atgctatgag	840
ttggtgtttg accacattcc aagcacgaag aggatgcaac aacccctag tccaaccggt	900
gtattcgatg catcattcag ctttgatagc tctaacgagt catgggttgt gtctgcatca	960
ccgtctccag agcctctatt caagaggaga agagtgcaag agcagcagat gaagttgtct	1020
tcagtaaaca gagtctttct cgatgtgttc tctagtagtc ctcgctaa	1068

<210> 74

<211> 355

<212> PRT

<213> B. napus

<400> 74

Met	Ala	Leu	Glu	Glu	Glu	Glu	Ile	Gln	Asn	Ala	Pro	Phe	Cys	Met
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Leu	Phe	Cys	Glu	Glu	Asp	Ser	Ser	Gly	Phe	Asp	Glu	Glu	Asp	Glu	Asp
			20					25					30		

Ser Cys Asp Asp Lys Ser Asp Glu Lys Phe Pro Phe Phe His Leu Gly
35 40 45

Phe Leu Asp Arg Cys Met Ser Trp Glu Glu Asp Glu Leu Ser Ser Leu
50 55 60

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

Leu Asp Asp Glu Tyr Leu Ala Leu Cys Arg Glu Lys Ala Val Asp Trp
85 90 95

Ile Leu Arg Val Lys Ser His Tyr Gly Phe Ser Ser Leu Thr Ala Leu
100 105 110

Leu Ala Val Asn Tyr Phe Asp Arg Phe Ile Thr Ser Arg Lys Phe Gln
115 120 125

Thr Glu Phe Pro Trp Met Ser Gln Leu Thr Ala Leu Ala Cys Leu Ser
130 135 140

Leu Ala Ala Lys Val Glu Glu Val Arg Val Pro Leu Leu Val Asp Leu
145 150 155 160

Gln Val Glu Glu Ala Ser Tyr Val Phe Glu Ala Lys Thr Ile Gln Arg
165 170 175

Met Glu Leu Leu Ile Leu Ser Thr Leu His Trp Arg Val His Pro Val
180 185 190

Thr Pro Ile Ser Tyr Leu Asp His Ile Ile Arg Arg Phe Ser Phe Lys
195 200 205

Ser His Gln Gln Leu Glu Phe Leu Ser Arg Cys Glu Ser Leu Leu Leu
210 215 220

Ser Ile Val Pro Asp Ser Arg Phe Leu Ser Tyr Ser Ser Ser Glu Leu
225 230 235 240

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

Glu Ser Glu Tyr Glu Ser Gln Leu Met Thr Leu Leu Arg Val Asp Ser
260 265 270

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

Thr Lys Arg Met Gln Gln Pro Pro Ser Pro Thr Gly Val Phe Asp Ala
290 295 300

Ser Phe Ser Phe Asp Ser Ser Asn Glu Ser Trp Val Val Ser Ala Ser
305 310 315 320

Pro Ser Pro Glu Pro Leu Phe Lys Arg Arg Arg Val Gln Glu Gln Gln
325 330 335

Met Lys Leu Ser Ser Val Asn Arg Val Phe Leu Asp Val Phe Ser Ser
340 345 350

Ser Pro Arg
355

<210> 75
<211> 1083
<212> DNA
<213> G. max

<400> 75
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tcctcatccg acatcggtc ctcaccactt ccgccgtcac ctccgccgtc gccgacgatg 180
acggaggatt gttattccat cgcgagcttc atcgagcacg agcgcaactt cgtccccgga 240
ttcgagtacc tgtcgaggtt ccaatctcgc tccctcgacg ccaacgccag agaagaatcc 300
gttgcatgga ttctcaaggt acacgcgtat tatggctttc agcctttgac ggcgtaacctc 360
gccgtcaact atatggatcg gtttttggat tctagccagt tgccggaaac aaatgggtgg 420
cctctgcaac ttctatctgt tgcagtcttg tctttggcag caaaaatgga ggaacctctt 480
gttccatctc tcttggaact tcagatagaa ggtgccaaagt acatatttga gccgagaaca 540
attcgtagga tggagctact tgttctgggt gtcttggatt ggaggctaag atcagtaacc 600
ccactttgct tctcgccttt ctttgcgtgc aaagtagatt caactggaac ttttatccgg 660
ttcctcattt ccagggcaac agaaatcatc gtatctaata tccaagaggc tagctttctt 720
gcttactggc catcatgcat tgctgctgca gccatactca ctgcagctaa tgaaattcct 780
aattggtctg tggttaagcc cgaaaatgct gagtcatggg gcgagggact aagaaaagaa 840
aaagtaatag ggtgctacca gttgatgcaa gagcttgtga ttaacaataa ccaacggaaa 900
ctccctacta aagtgttgcc gcagctgca gtaacaactc ggaccogaat gaggtcaagt 960
actgtctcat cattctcatc aacatcatca tcatcctctt caacctcctt ctcttgtct 1020

tgtaagagga ggaaattaaa taatcgtttg tgggtagatg atgagaaagg aaactccgag 1080

taa 1083

<210> 76

<211> 360

<212> PRT

<213> G. max

<400> 76

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

Cys Leu Ser Asp Tyr Asp Leu Leu Cys Gly Glu Asp Thr Ser Gly Val
20 25 30

Leu Ser Gly Glu Ser Pro Glu Cys Ser Ser Ser Asp Ile Gly Ser Ser
35 40 45

Pro Leu Pro Pro Ser Pro Pro Pro Ser Pro Thr Met Thr Glu Asp Cys
50 55 60

Tyr Ser Ile Ala Ser Phe Ile Glu His Glu Arg Asn Phe Val Pro Gly
65 70 75 80

Phe Glu Tyr Leu Ser Arg Phe Gln Ser Arg Ser Leu Asp Ala Asn Ala
85 90 95

Arg Glu Glu Ser Val Ala Trp Ile Leu Lys Val His Ala Tyr Tyr Gly
100 105 110

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

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

Leu Ser Val Ala Cys Leu Ser Leu Ala Ala Lys Met Glu Glu Pro Leu
145 150 155 160

Val Pro Ser Leu Leu Asp Leu Gln Ile Glu Gly Ala Lys Tyr Ile Phe
165 170 175

Glu Pro Arg Thr Ile Arg Arg Met Glu Leu Leu Val Leu Gly Val Leu
180 185 190

Asp Trp Arg Leu Arg Ser Val Thr Pro Leu Cys Phe Leu Ala Phe Phe
195 200 205

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

Arg Ala Thr Glu Ile Ile Val Ser Asn Ile Gln Glu Ala Ser Phe Leu
225 230 235 240

Ala Tyr Trp Pro Ser Cys Ile Ala Ala Ala Ala Ile Leu Thr Ala Ala
245 250 255

Asn Glu Ile Pro Asn Trp Ser Val Val Lys Pro Glu Asn Ala Glu Ser
260 265 270

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

Met Gln Glu Leu Val Ile Asn Asn Asn Gln Arg Lys Leu Pro Thr Lys
 290 295 300

Val Leu Pro Gln Leu Arg Val Thr Thr Arg Thr Arg Met Arg Ser Ser
 305 310 315 320

Thr Val Ser Ser Phe Ser Ser Thr Ser Ser Ser Ser Ser Ser Thr Ser
 325 330 335

Phe Ser Leu Ser Cys Lys Arg Arg Lys Leu Asn Asn Arg Leu Trp Val
 340 345 350

Asp Asp Glu Lys Gly Asn Ser Glu
 355 360

<210> 77
 <211> 1200
 <212> DNA
 <213> G. max

<400> 77
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 gatgcccttt actgtgacga aggaaagtgg gaagaggaag aggaggagaa agaagaagaa 120
 gaagatgaag gtgaaaatga aagtgaagtg acaacaaaca ctgcaacttg tcttttccct 180
 ctgctcttgt tggagcaaga cttgttctgg gaagatgagg aactaaactc tatcttttcc 240
 aaagagaagg ttcaacatga agaagcctat ggctataaca atctgaacag tgatgatgat 300
 aataacaaca acaacaatac tagtaataat aatgtgcatt tggactcttg tctctctcag 360
 cctcgtcgtg aggcagtgga atggatgctg aaagtcaatg ctactatgg attctctgct 420
 ctactgcaa cactggccgt tacttatctg gatagggttc ttctaagctt ccattttcaa 480

agggagaagc catggatgat ccagcttgtg gctgtcactt gcattctctt ggctgcaaaa	540
ggtgaagaaa ctcaagtgcc tcttctcttg gaccttcaag tgcaagacac aaagtatgtg	600
tttgaggcaa agactattca gagaatggag ctcttgggtgc tgtccaccct caaatggaag	660
atgcaccccg tgaccctctt ctcttttcta gatcacatta taagaaggct tggattgaaa	720
acacatcttc actgggagtt tctcaggcgc tgtgagcatc ttcttttgtc tgtgctttta	780
gattcaagat ttgttggttg tcttcttctt gtgttggcca ctgcaacaat gctgcatggt	840
atagaccaga ttaaacacaa tgggtgggatg gaatacaaaa atcagcttct gagtgttctc	900
aaaattagca aggagaaagt agatgagtgt tataatgcc a ttctccaact ctcaaattgc	960
aataattatg gtcataacaa caacactagc aagcgcaagt atgagcaa at cccaagcagc	1020
ccaagtggcg ttattgatgc tgcattttgc tctgatgggt ccaacgattc gtgggcagtg	1080
gggtcatcat tatattcacc accagagcct ctcttcaaga agagcagaac ccaaggacaa	1140
caaatgaaat tgtcaccact taaccgggtc attgtcggaa ttgttggcac ctctccttaa	1200

<210> 78
 <211> 399
 <212> PRT
 <213> G. max

<400> 78

Met	Ala	Ile	Gln	His	His	Asn	Asp	Gln	Leu	Glu	His	Asn	Glu	Asn	Val
1				5					10					15	

Ser	Ser	Val	Leu	Asp	Ala	Leu	Tyr	Cys	Asp	Glu	Gly	Lys	Trp	Glu	Glu
			20					25					30		

Glu	Glu	Glu	Glu	Lys	Glu	Glu	Glu	Glu	Asp	Glu	Gly	Glu	Asn	Glu	Ser
				35				40					45		

Glu Val Thr Thr Asn Thr Ala Thr Cys Leu Phe Pro Leu Leu Leu Leu
50 55 60

Glu Gln Asp Leu Phe Trp Glu Asp Glu Glu Leu Asn Ser Ile Phe Ser
65 70 75 80

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

Ser Asp Asp Asp Asn Asn Asn Asn Asn Asn Thr Ser Asn Asn Asn Val
100 105 110

His Leu Asp Ser Cys Leu Ser Gln Pro Arg Arg Glu Ala Val Glu Trp
115 120 125

Met Leu Lys Val Asn Ala His Tyr Gly Phe Ser Ala Leu Thr Ala Thr
130 135 140

Leu Ala Val Thr Tyr Leu Asp Arg Phe Leu Leu Ser Phe His Phe Gln
145 150 155 160

Arg Glu Lys Pro Trp Met Ile Gln Leu Val Ala Val Thr Cys Ile Ser
165 170 175

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

Gln Val Gln Asp Thr Lys Tyr Val Phe Glu Ala Lys Thr Ile Gln Arg
195 200 205

Met Glu Leu Leu Val Leu Ser Thr Leu Lys Trp Lys Met His Pro Val
210 215 220

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

Thr His Leu His Trp Glu Phe Leu Arg Arg Cys Glu His Leu Leu Leu
245 250 255

Ser Val Leu Leu Asp Ser Arg Phe Val Gly Cys Leu Pro Ser Val Leu
260 265 270

Ala Thr Ala Thr Met Leu His Val Ile Asp Gln Ile Lys His Asn Gly
275 280 285

Gly Met Glu Tyr Lys Asn Gln Leu Leu Ser Val Leu Lys Ile Ser Lys
290 295 300

Glu Lys Val Asp Glu Cys Tyr Asn Ala Ile Leu Gln Leu Ser Asn Val
305 310 315 320

Asn Asn Tyr Gly His Asn Asn Asn Thr Ser Lys Arg Lys Tyr Glu Gln
325 330 335

Ile Pro Ser Ser Pro Ser Gly Val Ile Asp Ala Ala Phe Cys Ser Asp
340 345 350

Gly Ser Asn Asp Ser Trp Ala Val Gly Ser Ser Leu Tyr Ser Pro Pro
355 360 365

Glu Pro Leu Phe Lys Lys Ser Arg Thr Gln Gly Gln Gln Met Lys Leu
370 375 380

Ser Pro Leu Asn Arg Val Ile Val Gly Ile Val Gly Thr Ser Pro
 385 390 395

<210> 79
 <211> 1038
 <212> DNA
 <213> Z. mays

<400> 79
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 gactccgtcg tcggcgccgt gttccccgtg gacacagatg aggccgtgcg ggcgttggtg 180
 gagaaggaga cggaccacaa gcctcaagac ggctatgcgg agaggctgga gcgcggcgga 240
 ttggagtact cctggaggag agacgccatg gattggattt gcaaggcca ttogtactac 300
 aggtttggac cactcagtct ttaccttgct gtgaattacc tggatagatt cctctcctca 360
 tatgatctcc cacacgataa gccttggatg cgacagttgt tgtcagttgc ttgcctagca 420
 ctgcgtgtca agatggagga gaccgtgctc cctcttcctg tggaccttca ggtctgcgat 480
 gtgaaatttg agttcgaagc aaggactatt gggaggatgg agcttcttgt gctggccacc 540
 ctgaaatgga gaatgcaggc tgtgaccccc ttcactttca tcagctactt cctcgacaag 600
 ttcaatggtg ggaagccgcc gagtttggca ctacggtcac ggtgcaccga taccataatt 660
 ggcacactca aaggctctac attcttgcga ttacagaccat ctgagattgc cgcggcctca 720
 gctctagcag cagtttttga gaatcaggtt gttggctcct cgagtgcctt ttcagcatct 780
 gaagtccta taaataaggt gatgattgct agatgctatg agctgttgca agagcaagcg 840
 ctggtgagga agacaggga cgtcaatgga agcccttcag tgccgcagag cccgattggc 900

gtgctggatg caacatgctt cagcttttagg agtgaagatg caagactagt atcatcgcaa 960

tcaaacaaca tcagtagtag tagtagtaac gacaatcaag tttctaagag gagaaggcta 1020

agcatatcac caatttga 1038

<210> 80

<211> 345

<212> PRT

<213> Z. mays

<400> 80

Met Gly Ile Leu Cys Leu Gly Ala Ser Ser Thr Leu Leu Cys Gly Glu

1 5 10 15

Asp Arg Asn Asn Val Leu Gly Leu Gly Cys Gly Asn Glu Leu Val Glu

20 25 30

Val Gly Ser Gly His Asp Gly Leu Asp Ser Val Val Gly Ala Val Phe

35 40 45

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

50 55 60

Asp His Lys Pro Gln Asp Gly Tyr Ala Glu Arg Leu Glu Arg Gly Gly

65 70 75 80

Leu Glu Tyr Ser Trp Arg Arg Asp Ala Met Asp Trp Ile Cys Lys Val

85 90 95

His Ser Tyr Tyr Arg Phe Gly Pro Leu Ser Leu Tyr Leu Ala Val Asn

100 105 110

Tyr Leu Asp Arg Phe Leu Ser Ser Tyr Asp Leu Pro His Asp Lys Pro
115 120 125

Trp Met Arg Gln Leu Leu Ser Val Ala Cys Leu Ala Leu Ala Val Lys
130 135 140

Met Glu Glu Thr Val Leu Pro Leu Pro Val Asp Leu Gln Val Cys Asp
145 150 155 160

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

Val Leu Ala Thr Leu Lys Trp Arg Met Gln Ala Val Thr Pro Phe Thr
180 185 190

Phe Ile Ser Tyr Phe Leu Asp Lys Phe Asn Gly Gly Lys Pro Pro Ser
195 200 205

Leu Ala Leu Ala Ser Arg Cys Thr Asp Ile Ile Ile Gly Thr Leu Lys
210 215 220

Gly Ser Thr Phe Leu Ser Phe Arg Pro Ser Glu Ile Ala Ala Ala Ser
225 230 235 240

Ala Leu Ala Ala Val Phe Glu Asn Gln Val Val Gly Ser Ser Ser Ala
245 250 255

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

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

Asn Gly Ser Pro Ser Val Pro Gln Ser Pro Ile Gly Val Leu Asp Ala
 290 295 300

Thr Cys Phe Ser Phe Arg Ser Glu Asp Ala Arg Leu Val Ser Ser Gln
 305 310 315 320

Ser Asn Asn Ile Ser Ser Ser Ser Ser Asn Asp Asn Gln Val Ser Lys
 325 330 335

Arg Arg Arg Leu Ser Ile Ser Pro Ile
 340 345

<210> 81
 <211> 1095
 <212> DNA
 <213> P. patents

<400> 81
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 tgacaagaag acgcgagagc tcgttgcggt gaagtacatc gagcgtgggg agaagattga 180
 cgagaatggt cagcgggaga ttattaatca tcggtcggtg cggcatccca acatagtgag 240
 gttcaaggag gttctgttga caccaactca tttagccatc gtgatggagt atgctgctgg 300
 tggagaactg ttcgagcgaa tttgtaatgc aggtcgggtc agtgaagatg aggccagatt 360
 tttctttcag cagcttattt ctggagtgag ctactgccac tccatgcaaa tttgccatcg 420
 tgatttgaaa ttggaaaaca ctttgttgga tggaagtcct ggcctaggc tgaaaatctg 480
 tgattttggg tattcaaagt cgtctttggt gactcgcaa cccaagtcga ccgtgggaac 540

acctgcctac attgctccag aggtcctgtc gaagaaagag tacgatggca agattgccga	600
tgtgtggtcg tgtggagtga ccttgtagct gatgttagtg ggggcatatc cgtttgagga	660
tcccgatgac ccaaggaatt tcaggaaaac cattgggcgt atcttgagcg tgcagtactc	720
catccccgac tatgtgcaca tttccgtgga gtgcaggcat ttgctgtcta ggatatttgt	780
tgctaaccga gccaaagaga tcaacatcca agaaattaag aaccacgagt ggtttttgaa	840
aaatttacct gcagacttag tagacctggc tgataggagt tacgactttg aggacccgaa	900
tcatccccca cagagcatcg aagagatcat gcgcatcatt ggcgagcta gagagccagg	960
agcaggtgca ccaggaaatt attttgggtga tccgttagat gacatggatg tggagaacga	1020
tgtggacccc gatatcgata gcagtgggga gttcgtatgt gcaatgtagg gtagcagtta	1080
gagcgacggt taacc	1095

<210> 82

<211> 348

<212> PRT

<213> P. patents

<400> 82

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

Arg	Asp	Lys	Lys	Thr	Arg	Glu	Leu	Val	Ala	Val	Lys	Tyr	Ile	Glu	Arg
		35					40					45			

Gly	Glu	Lys	Ile	Asp	Glu	Asn	Val	Gln	Arg	Glu	Ile	Ile	Asn	His	Arg
	50					55					60				

Ser Leu Arg His Pro Asn Ile Val Arg Phe Lys Glu Val Leu Leu Thr
65 70 75 80

Pro Thr His Leu Ala Ile Val Met Glu Tyr Ala Ala Gly Gly Glu Leu
85 90 95

Phe Glu Arg Ile Cys Asn Ala Gly Arg Phe Ser Glu Asp Glu Ala Arg
100 105 110

Phe Phe Phe Gln Gln Leu Ile Ser Gly Val Ser Tyr Cys His Ser Met
115 120 125

Gln Ile Cys His Arg Asp Leu Lys Leu Glu Asn Thr Leu Leu Asp Gly
130 135 140

Ser Pro Ala Pro Arg Leu Lys Ile Cys Asp Phe Gly Tyr Ser Lys Ser
145 150 155 160

Ser Leu Leu His Ser Gln Pro Lys Ser Thr Val Gly Thr Pro Ala Tyr
165 170 175

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

Asp Val Trp Ser Cys Gly Val Thr Leu Tyr Val Met Leu Val Gly Ala
195 200 205

Tyr Pro Phe Glu Asp Pro Asp Asp Pro Arg Asn Phe Arg Lys Thr Ile
210 215 220

Gly Arg Ile Leu Ser Val Gln Tyr Ser Ile Pro Asp Tyr Val His Ile
 225 230 235 240

Ser Val Glu Cys Arg His Leu Leu Ser Arg Ile Phe Val Ala Asn Pro
 245 250 255

Ala Lys Arg Ile Asn Ile Gln Glu Ile Lys Asn His Glu Trp Phe Leu
 260 265 270

Lys Asn Leu Pro Ala Asp Leu Val Asp Leu Ala Asp Arg Ser Tyr Asp
 275 280 285

Phe Glu Asp Pro Asn His Pro Pro Gln Ser Ile Glu Glu Ile Met Arg
 290 295 300

Ile Ile Gly Glu Ala Arg Glu Pro Gly Ala Gly Ala Pro Gly Asn Tyr
 305 310 315 320

Phe Gly Asp Pro Leu Asp Asp Met Asp Val Glu Asn Asp Val Asp Pro
 325 330 335

Asp Ile Asp Ser Ser Gly Glu Phe Val Cys Ala Met
 340 345

<210> 83

<211> 1095

<212> DNA

<213> B. napus

<400> 83

atggataagt atgaggttgt gaaggatctg gggactggga acttcggtgt ggctcgcctt 60

cttaggcaca aggaaaccaa agagcttgtc gccatgaagt acatcgagag aggccgaaag 120

atagatgaga acgtggctag agagattatc aatcacagat cacttaagca tcctaataatc	180
atccgcttca aggaggtgat tctgacacct actcatcttg ccattgtgat ggagtatgct	240
tctgggtggag agctctttga gagaatctgt actgccggta gattcagtga agctgaggct	300
aggtacttct ttcagcagct gatttgtggg gttgactact gccactcctt gcaaataatgc	360
cacagagatc tgaagcttga gaacacattg cttgatggta gccctgctcc gcttttgaaa	420
atctgtgatt ttggttactc caagtcactc atactacatt ctaggcctaa atcgactgtt	480
ggaactccag catacatagc acctgaagtt ctttcccgtg gagaatatga tggcaagcac	540
gcggatgtgt ggtcatgtgg tgtaaccctt tatgtgatgc tggttggagc ttaccattt	600
gaggacccta atgatccaaa gaacttcagg aaaacaatcc aacgtataat ggctatacaa	660
tacaagattc cggactacgt tcacatatct caggaatgca aacaccttct ctctcgcata	720
ttcgtcacta accccgctaa gagaatcacg ctttaaggaga tcaagaatca tccgtggtag	780
ttaaagaatc tgccaaagga gctgctggag tctgctcaag cgggtgtatta caagagagac	840
aacacgagct attctcttca aagcgtagag gacataatga agatagttgg agaagctagg	900
aatccagctt cttcttcaag cgtcagcaaa agcttgggat caggggttga ggaagaagag	960
gatgttgaag ctgaagtga agtggaagaa gaagaggagg aagaagaaga agaagaagat	1020
gaatacgaga agcatgtcaa agaggcacat tcttctattc aagagcctca cgaagcgta	1080
aaggaaaaaa aatga	1095

<210> 84

<211> 317

<212> PRT

<213> B. napus

<400> 84

Met Asp Lys Tyr Glu Val Val Lys Asp Leu Gly Thr Gly Asn Phe Gly
1 5 10 15

Val Ala Arg Leu Leu Arg His Lys Glu Thr Lys Glu Leu Val Ala Met
20 25 30

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

Ile Ile Asn His Arg Ser Leu Lys His Pro Asn Ile Ile Arg Phe Lys
50 55 60

Glu Val Ile Leu Thr Pro Thr His Leu Ala Ile Val Met Glu Tyr Ala
65 70 75 80

Ser Gly Gly Glu Leu Phe Glu Arg Ile Cys Thr Ala Gly Arg Phe Ser
85 90 95

Glu Ala Glu Ala Arg Tyr Phe Phe Gln Gln Leu Ile Cys Gly Val Asp
100 105 110

Tyr Cys His Ser Leu Gln Ile Cys His Arg Asp Leu Lys Leu Glu Asn
115 120 125

Thr Leu Leu Asp Gly Ser Pro Ala Pro Leu Leu Lys Ile Cys Asp Phe
130 135 140

Gly Tyr Ser Lys Ser Ser Ile Leu His Ser Arg Pro Lys Ser Thr Val
145 150 155 160

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

Asp Gly Lys His Ala Asp Val Trp Ser Cys Gly Val Thr Leu Tyr Val
180 185 190

Met Leu Val Gly Ala Tyr Pro Phe Glu Asp Pro Asn Asp Pro Lys Asn
195 200 205

Phe Arg Lys Thr Ile Gln Arg Ile Met Ala Ile Gln Tyr Lys Ile Pro
210 215 220

Asp Tyr Val His Ile Ser Gln Glu Cys Lys His Leu Leu Ser Arg Ile
225 230 235 240

Phe Val Thr Asn Pro Ala Lys Arg Ile Thr Leu Lys Glu Ile Lys Asn
245 250 255

His Pro Trp Tyr Leu Lys Asn Leu Pro Lys Glu Leu Leu Glu Ser Ala
260 265 270

Gln Ala Val Tyr Tyr Lys Arg Asp Asn Thr Ser Tyr Ser Leu Gln Ser
275 280 285

Val Glu Asp Ile Met Lys Ile Val Gly Glu Ala Arg Asn Pro Ala Ser
290 295 300

Ser Ser Ser Val Ser Lys Ser Leu Gly Ser Gly Ala Glu
305 310 315

<210> 85

<211> 1065

<212> DNA

<213> B. napus

<400> 85

atggacaagt acgagctggt gaaggacata ggcgcgggga atttcggagt ggcgaggctc	60
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atcgatgaga acgtggcgag agagatcata aatcacagat cacttcgcca tcctaacatc	180
atccgcttta aagaggttgt gttgactccg actcatcttg ctattgccat ggagtatgct	240
gctggtggtg aacttttcga gcgtatttgc agtgctggaa gattcagtga agatgaggcg	300
agatacttct tccagcagct tatatcaggt gttagctatt gccatgctat gcaaatatgc	360
catagagatc tgaagctcga gaatacactc cttgatggaa gtctctgctcc acgtctcaaa	420
atctgtgatt ttggttattc caagtcctct ctgctgcact ccaggcccaa atcaacagtt	480
ggaactccag catatattgc acctgaagtc ctttctcgca gagaatacga tggcaagatg	540
gctgatgtat ggtcctgtgg tgtaactctt tatgtcatgc tggttggagc ctacccattc	600
gaagaccagg aagatcccaa aaacttcagg aaaacaatac aaaaaatcat ggctgttcag	660
tacaagatcc cggactacgt ccacatctca caggattgca aacatctcct ttcccgata	720
tttgtggcca actcactcca gaggataacc attgcagaaa tcaagaaaca cccatggttc	780
atgaagaact tgccaaggga actcacagag acagctcaag ctgcgtatct cagaaaagag	840
aatccgacct tctcactcca aaccacagaa gagatcatga agatagtgga tgacgccaaa	900
acgccccgcg ctgtttccag gtccattgga ggttttggct ggggagatga agaagggaaa	960
gaggaagaag aggtggatga agaggaggtg gtggaggacg aggaagatga gtatgataag	1020
actgtaaagc aagtacacgc tagtggagaa gtgaaaatca cttga	1065

<210> 86

<211> 354

<212> PRT

<213> B. napus

<400> 86

Met Asp Lys Tyr Glu Leu Val Lys Asp Ile Gly Ala Gly Asn Phe Gly
1 5 10 15

Val Ala Arg Leu Met Lys Val Lys Asn Ser Lys Glu Leu Val Ala Met
20 25 30

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

Ile Ile Asn His Arg Ser Leu Arg His Pro Asn Ile Ile Arg Phe Lys
50 55 60

Glu Val Val Leu Thr Pro Thr His Leu Ala Ile Ala Met Glu Tyr Ala
65 70 75 80

Ala Gly Gly Glu Leu Phe Glu Arg Ile Cys Ser Ala Gly Arg Phe Ser
85 90 95

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

Tyr Cys His Ala Met Gln Ile Cys His Arg Asp Leu Lys Leu Glu Asn
115 120 125

Thr Leu Leu Asp Gly Ser Pro Ala Pro Arg Leu Lys Ile Cys Asp Phe
130 135 140

Gly Tyr Ser Lys Ser Ser Leu Leu His Ser Arg Pro Lys Ser Thr Val
145 150 155 160

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

Asp Gly Lys Met Ala Asp Val Trp Ser Cys Gly Val Thr Leu Tyr Val
180 185 190

Met Leu Val Gly Ala Tyr Pro Phe Glu Asp Gln Glu Asp Pro Lys Asn
195 200 205

Phe Arg Lys Thr Ile Gln Lys Ile Met Ala Val Gln Tyr Lys Ile Pro
210 215 220

Asp Tyr Val His Ile Ser Gln Asp Cys Lys His Leu Leu Ser Arg Ile
225 230 235 240

Phe Val Ala Asn Ser Leu Gln Arg Ile Thr Ile Ala Glu Ile Lys Lys
245 250 255

His Pro Trp Phe Met Lys Asn Leu Pro Arg Glu Leu Thr Glu Thr Ala
260 265 270

Gln Ala Ala Tyr Phe Arg Lys Glu Asn Pro Thr Phe Ser Leu Gln Thr
275 280 285

Thr Glu Glu Ile Met Lys Ile Val Asp Asp Ala Lys Thr Pro Pro Pro
290 295 300

Val Ser Arg Ser Ile Gly Gly Phe Gly Trp Gly Asp Glu Glu Gly Lys
305 310 315 320

Glu Glu Glu Glu Val Asp Glu Glu Glu Val Val Glu Asp Glu Glu Asp
325 330 335

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

Ile Thr

<210> 87

<211> 1080

<212> DNA

<213> G. max

<400> 87

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gtccgtgata ttgggtctgg gaattttggg gtggcaagge tcatgagaga caagcacact 120

gaggagcttg ttgctgtcaa gtatattgag agaggtgaca agatagatga aaatgtacga 180

agggaaatta taaatcaccg atcactgagg catcccaata ttgtcagggt caaggagatc 240

atattaaccc ctacacattt ggctattgtg atggagtacg cttctggggg agagttatatt 300

gagcggatat gcaatgcagg acggtttagt gaagatgagg cacgcttctt cttccaacaa 360

cttatatcag gggttagcta ctgtcatgca atgcaagtat gccatcgtga cttgaagttg 420

gagaacacat tgttggatgg tagtccagct cctcgtttga agatttgtga ttttgggtat 480

tcaaagtcct ccgtgctaca ttcacaacct aaatctacag tcggtacccc tgcatacatt 540

gctcctgaag ttttgcttaa gaaggaatat gacggcaaga ttgcagatgt gtgggtcttgt 600

ggggtgacct tatatgtcat gttggtgggt gcatatcctt ttgaggatcc agaggaacct 660

aaaaatttcc ggaagacaat tcataggatt ttgaaagtcc agtactcaat tcctgattat 720

gttcatatat cttctgagt cgcgtcatcta atctctagga tctttgtggc agaccctgca 780

cagagaataa gtattcccgga gattcgaaac cacgaatggt ttttgaagaa cctgcccggcc 840

gatctcatgg ttgagaacac gatgaacagg caatttgagg agcctgatca accaatgcag 900

agcattgaag aaatcatgca gataatcagt gaggctacaa ttcttgcagc cggaactcag 960

tctctcaacc agtatcttac tggtagcttg gacattgatg acgacgacat ggacgaggac 1020

ctagagaccg atcccgacct cgacattgat agcagtggag aaatagttta tgcaatatga 1080

<210> 88

<211> 359

<212> PRT

<213> G. max

<400> 88

Met Thr Val Gly Pro Gly Met Asp Met Pro Ile Met His Asp Ser Asp

1 5 10 15

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

20 25 30

Arg Leu Met Arg Asp Lys His Thr Glu Glu Leu Val Ala Val Lys Tyr

35 40 45

Ile Glu Arg Gly Asp Lys Ile Asp Glu Asn Val Arg Arg Glu Ile Ile

50 55 60

Asn His Arg Ser Leu Arg His Pro Asn Ile Val Arg Phe Lys Glu Ile

65 70 75 80

Ile Leu Thr Pro Thr His Leu Ala Ile Val Met Glu Tyr Ala Ser Gly

85 90 95

Gly Glu Leu Phe Glu Arg Ile Cys Asn Ala Gly Arg Phe Ser Glu Asp
100 105 110

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

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

Leu Asp Gly Ser Pro Ala Pro Arg Leu Lys Ile Cys Asp Phe Gly Tyr
145 150 155 160

Ser Lys Ser Ser Val Leu His Ser Gln Pro Lys Ser Thr Val Gly Thr
165 170 175

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

Lys Ile Ala Asp Val Trp Ser Cys Gly Val Thr Leu Tyr Val Met Leu
195 200 205

Val Gly Ala Tyr Pro Phe Glu Asp Pro Glu Glu Pro Lys Asn Phe Arg
210 215 220

Lys Thr Ile His Arg Ile Leu Lys Val Gln Tyr Ser Ile Pro Asp Tyr
225 230 235 240

Val His Ile Ser Ser Glu Cys Arg His Leu Ile Ser Arg Ile Phe Val
245 250 255

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

Trp Phe Leu Lys Asn Leu Pro Ala Asp Leu Met Val Glu Asn Thr Met
275 280 285

Asn Arg Gln Phe Glu Glu Pro Asp Gln Pro Met Gln Ser Ile Glu Glu
290 295 300

Ile Met Gln Ile Ile Ser Glu Ala Thr Ile Pro Ala Ala Gly Thr Gln
305 310 315 320

Ser Leu Asn Gln Tyr Leu Thr Gly Ser Leu Asp Ile Asp Asp Asp Asp
325 330 335

Met Asp Glu Asp Leu Glu Thr Asp Pro Asp Leu Asp Ile Asp Ser Ser
340 345 350

Gly Glu Ile Val Tyr Ala Ile
355

<210> 89

<211> 1083

<212> DNA

<213> G. max

<400> 89

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gaccgttacg atctggtccg cgacatcggg tccggaaatt tcggcgtggc gaggctgatg 120

caggataaac aaaccaagga actcgtcgcc gtcaagtaca tcgaaagggg tgataagatt 180

gatgaaaatg tgaagaggga aattatcaat cacaggtctc tgaggcatcc taacattgtt 240

aggttttaaag aggtaatttt aacacctact catcttgcta ttgtaatgga atatgcatct	300
gggggagagc tctttgagaa aatctgcaat gctgggcgtt ttaccgagga tgaggctcga	360
ttcttctttc agcaactcat atctggggtc agctattgcc atgctatgca agtatgtcat	420
cgggacttga agcttgaaaa cactttgctg gatggaagcc cggcacctcg tttaaagata	480
tgcgattttg ggtactccaa gtcttcagtg cttcattcac aaccaaagtc aactgtggga	540
actcctgcat atattgctcc agaagtattg ctgaaacaag agtatgatgg caagcttgca	600
gatgtctggg catgtggagt aaccttatat gtgatgctag tgggagcata tccttttgag	660
gacctaatag aaccaaagga ctttcggaag acaattcaga gagttcttag tgtccagtat	720
tccattccgg acggagttca aatatctcca gagtgtcttc accttatttc aaggatcttt	780
gtttttgacc cggcagagag aatcaccatg tctgaaatct ggaaccatga atggtttctg	840
aagaatctcc cggcagacct gatggacgag aagataatgg gcaatcaatt tgaagagcca	900
gaccaacca tgcagagcat cgatacgatc atgcagataa tttcagaagc taccgtacca	960
gcagttggga cctattcttt tgaccagttt atggaggaac aaatttatga cttggaatct	1020
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tag	1083

<210> 90
 <211> 360
 <212> PRT
 <213> G. max

<400> 90

Met	Asp	Arg	Ala	Ala	Leu	Thr	Val	Gly	Pro	Gly	Met	Asp	Met	Pro	Ile
1				5				10						15	

Met His Asp Ser Asp Arg Tyr Asp Leu Val Arg Asp Ile Gly Ser Gly
20 25 30

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

Val Ala Val Lys Tyr Ile Glu Arg Gly Asp Lys Ile Asp Glu Asn Val
50 55 60

Lys Arg Glu Ile Ile Asn His Arg Ser Leu Arg His Pro Asn Ile Val
65 70 75 80

Arg Phe Lys Glu Val Ile Leu Thr Pro Thr His Leu Ala Ile Val Met
85 90 95

Glu Tyr Ala Ser Gly Gly Glu Leu Phe Glu Lys Ile Cys Asn Ala Gly
100 105 110

Arg Phe Thr Glu Asp Glu Ala Arg Phe Phe Phe Gln Gln Leu Ile Ser
115 120 125

Gly Val Ser Tyr Cys His Ala Met Gln Val Cys His Arg Asp Leu Lys
130 135 140

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

Cys Asp Phe Gly Tyr Ser Lys Ser Ser Val Leu His Ser Gln Pro Lys
165 170 175

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

Gln Glu Tyr Asp Gly Lys Leu Ala Asp Val Trp Ser Cys Gly Val Thr
195 200 205

Leu Tyr Val Met Leu Val Gly Ala Tyr Pro Phe Glu Asp Pro Asn Glu
210 215 220

Pro Lys Asp Phe Arg Lys Thr Ile Gln Arg Val Leu Ser Val Gln Tyr
225 230 235 240

Ser Ile Pro Asp Gly Val Gln Ile Ser Pro Glu Cys Leu His Leu Ile
245 250 255

Ser Arg Ile Phe Val Phe Asp Pro Ala Glu Arg Ile Thr Met Ser Glu
260 265 270

Ile Trp Asn His Glu Trp Phe Leu Lys Asn Leu Pro Ala Asp Leu Met
275 280 285

Asp Glu Lys Ile Met Gly Asn Gln Phe Glu Glu Pro Asp Gln Pro Met
290 295 300

Gln Ser Ile Asp Thr Ile Met Gln Ile Ile Ser Glu Ala Thr Val Pro
305 310 315 320

Ala Val Gly Thr Tyr Ser Phe Asp Gln Phe Met Glu Glu Gln Ile Tyr
325 330 335

Asp Leu Glu Ser Glu Ser Asp Ala Glu Ser Asp Leu Asp Ile Asp Ser
340 345 350

Ser Gly Glu Ile Val Tyr Ala Ile
355 360

<210> 91
<211> 1011
<212> DNA
<213> G. max

<400> 91
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ttggcaaaag acaagaaaac tggagagctt gttgcggtca aatacataga gaggggcaaa 120
aagattgatg agaatgttca gagggagata attaaccacc gatctTTaag gcatccaaat 180
ataatcaggt ttaaagaggt gttactgacc cctacacatt tagctatcgt cttggagtat 240
gcttcaggtg gtgaactTTt tgagaggata tgtactgctg gtcgatttag cgaagatgag 300
gcaagatatt tcttcagca gctaatatct ggggttagct actgtcattc aatggaaatt 360
tgtcatagag atctaaaatt ggaaaacact ctcttgacg gaaatccatc tccccggctt 420
aaaatttTtg actttggtta ttccaagtct gctctactgc actctcaacc taaatcaaca 480
gttggaactc ctgcatacat tgctccggag gttctgtcgc gaaaggagta tgatggaaag 540
atttcagatg tttggtcctg tggagtgact ctttatgtca tgttagttgg tgcataccca 600
tttgaagatc cagaagatcc tagaaatttc agaaagacta ttgggagaat aatcgggtatt 660
cagtactcca taccgacta tgttcgtgtt tcttctgact gtaggaatct tctctctcgc 720
atctttgttg ctgatcctgc caagaggatc accatcccag agataaaaca gtatccttgg 780
tttctgaaga atatgcctaa agagatcatc gaagctgaaa gaaaaggatt cgaggaaaca 840
accaaagacc aaccaaacca gaaggtggag gaaatcatga ggataattca agcggcaagg 900
ataccaggac aaggatccaa agctggagaa ggtggacaag ctggcactgg atcattagat 960

attgaggatg atgaggaaat tgatgttagt ggtgactatg aacaagtgtg a

1011

<210> 92

<211> 336

<212> PRT

<213> G. max

<400> 92

Met Glu Glu Arg Tyr Glu Pro Leu Lys Glu Leu Gly Ala Gly Asn Phe
1 5 10 15

Gly Val Ala Arg Leu Ala Lys Asp Lys Lys Thr Gly Glu Leu Val Ala
20 25 30

Val Lys Tyr Ile Glu Arg Gly Lys Lys Ile Asp Glu Asn Val Gln Arg
35 40 45

Glu Ile Ile Asn His Arg Ser Leu Arg His Pro Asn Ile Ile Arg Phe
50 55 60

Lys Glu Val Leu Leu Thr Pro Thr His Leu Ala Ile Val Leu Glu Tyr
65 70 75 80

Ala Ser Gly Gly Glu Leu Phe Glu Arg Ile Cys Thr Ala Gly Arg Phe
85 90 95

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

Ser Tyr Cys His Ser Met Glu Ile Cys His Arg Asp Leu Lys Leu Glu
115 120 125

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

Phe Gly Tyr Ser Lys Ser Ala Leu Leu His Ser Gln Pro Lys Ser Thr
145 150 155 160

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

Tyr Asp Gly Lys Ile Ser Asp Val Trp Ser Cys Gly Val Thr Leu Tyr
180 185 190

Val Met Leu Val Gly Ala Tyr Pro Phe Glu Asp Pro Glu Asp Pro Arg
195 200 205

Asn Phe Arg Lys Thr Ile Gly Arg Ile Ile Gly Ile Gln Tyr Ser Ile
210 215 220

Pro Asp Tyr Val Arg Val Ser Ser Asp Cys Arg Asn Leu Leu Ser Arg
225 230 235 240

Ile Phe Val Ala Asp Pro Ala Lys Arg Ile Thr Ile Pro Glu Ile Lys
245 250 255

Gln Tyr Pro Trp Phe Leu Lys Asn Met Pro Lys Glu Ile Ile Glu Ala
260 265 270

Glu Arg Lys Gly Phe Glu Glu Thr Thr Lys Asp Gln Pro Asn Gln Lys
275 280 285

Val Glu Glu Ile Met Arg Ile Ile Gln Ala Ala Arg Ile Pro Gly Gln
290 295 300

Gly	Ser	Lys	Ala	Gly	Glu	Gly	Gly	Gln	Ala	Gly	Thr	Gly	Ser	Leu	Asp
305					310					315					320

Ile	Glu	Asp	Asp	Glu	Glu	Ile	Asp	Val	Ser	Gly	Asp	Tyr	Glu	Gln	Val
				325					330					335	

<210> 93

<211> 1089

<212> DNA

<213> L. usitatissium

<400> 93

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cgggacaagg	tcaccaagga	gctcgtcgct	gtcaaataca	tcgagcgtgg	agataagatt	180
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aggtttaaag	aggtcatcct	gacacctact	catctggcaa	tcgttatgga	atatgcatcc	300
ggtggagagc	tctttgagcg	aatatccagt	gctggccggt	tcggtgagga	tgaggctcgc	360
tttttcttcc	aacaactgat	ttccgggggt	agctattgcc	atgctatgca	agtgtgtcac	420
cgtgatttga	agttggagaa	tacattgtta	gatggaagcc	ctgctcctcg	gttaaaaatt	480
tgtgattttg	ggtactcaaa	gtcatcggtg	cttcattcac	aaccaaagtc	tactgtggga	540
actcctgctt	atattgctcc	tgaagttctg	ttaaggcaag	aatatgatgg	aaagggttgcg	600
gatgtgtggt	cttgccgagt	caccttatat	gtgatgctga	tcggtggata	tccttccgag	660
gacctgaag	agcccaaaga	tttcaggaag	accatacaaa	gaattcttag	tgttcaatat	720
accattccgg	acactattca	cctctctcaa	gagtgccgcg	acctcatagc	caggattttc	780

Glu Tyr Ala Ser Gly Gly Glu Leu Phe Glu Arg Ile Ser Ser Ala Gly
100 105 110

Arg Phe Gly Glu Asp Glu Ala Arg Phe Phe Phe Gln Gln Leu Ile Ser
115 120 125

Gly Val Ser Tyr Cys His Ala Met Gln Val Cys His Arg Asp Leu Lys
130 135 140

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

Cys Asp Phe Gly Tyr Ser Lys Ser Ser Val Leu His Ser Gln Pro Lys
165 170 175

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

Gln Glu Tyr Asp Gly Lys Val Ala Asp Val Trp Ser Cys Gly Val Thr
195 200 205

Leu Tyr Val Met Leu Ile Gly Gly Tyr Pro Phe Glu Asp Pro Glu Glu
210 215 220

Pro Lys Asp Phe Arg Lys Thr Ile Gln Arg Ile Leu Ser Val Gln Tyr
225 230 235 240

Thr Ile Pro Asp Thr Ile His Leu Ser Gln Glu Cys Arg Asp Leu Ile
245 250 255

Ala Arg Ile Phe Val Phe Asp Pro Ala Thr Arg Ile Thr Ile Pro Asp
260 265 270

Ile Lys Asn His Val Trp Phe Leu Arg Asn Leu Pro Ala Asp Leu Met
275 280 285

Asp Glu Arg Thr Met Gly Asn Gln Phe Val Glu Ala Asp Gln Pro Leu
290 295 300

Gln Ser Val Asp Thr Ile Met Gln Ile Ile Ser Glu Ala Thr Ile Pro
305 310 315 320

Pro Ala Gly Ser Gln Arg Leu Asn Gln Tyr Met Ala Asp Asn Leu Asp
325 330 335

Ile Asp Asp Asp Met Glu Asp Leu Asp Ser Glu Ser Glu Leu Asp Ile
340 345 350

Asp Ser Ser Gly Glu Ile Val Tyr Ala Leu
355 360

<210> 95

<211> 1113

<212> DNA

<213> L. usitatissimum

<400> 95

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attgatgaga atgtggcaag agagatcata aatcacagat cgttgcgcca tcctaacata 180

attcgcttca aggagctggt tctgactcca actcatcttg cgatagtgat ggagtatgct 240

gctggaggag agctctttga ggcattttgc aatgctggaa ggttcagcga agatgaggct	300
aggtactttct tccaacaact tatttcaggc gtcagctact gtcattccat gcaaatatgc	360
catagagatt tgaagctgga aaatacttta ctggatggaa gccagctcc acgcttgaag	420
atatgtgatt ttggttattc aaagtcttct ttgcttcatt caagaccaa atctactgtc	480
gggactcctg catatatgtc tcccagggtt ctttctcgca gagaatatga tggcaagctg	540
gcagatgtct ggtcatgtgg agtaacactc tatgttatgc tgggtgggagc atatcccttt	600
gaagaccaag atgacccaaa gaatttcaga aaaacaatta acagaataat ggctgttcag	660
tacaagattc cagactatgt acacatatcg ccagattgca ggcacctcat ttcccacata	720
tttcttgac atccactcaa gaggatcaca atcaaagaaa tcaagagcca cccatggttt	780
ttgaagaatt tgccgagga gctaacagag gcggcacaaa ccatgtacta caggaaagaa	840
aaccagcct tctccttaca aacagtggaa gaaataatga aaatcgtgga cgatgccaaa	900
gttccggcac cagtgtcgag atccatcgga acgtttggct ggggaggaga cgaagacgaa	960
gagacgaagg aagaggaggc agagccggag gctgaaaccg aggcggaggc tgaggctgtg	1020
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<210> 96
 <211> 370
 <212> PRT
 <213> L. usitatissimum

<400> 96

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

Val Ala Arg Leu Met Arg Asn Lys Gln Thr Arg Glu Leu Val Ala Met
20 25 30

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

Ile Ile Asn His Arg Ser Leu Arg His Pro Asn Ile Ile Arg Phe Lys
50 55 60

Glu Leu Val Leu Thr Pro Thr His Leu Ala Ile Val Met Glu Tyr Ala
65 70 75 80

Ala Gly Gly Glu Leu Phe Glu Arg Ile Cys Asn Ala Gly Arg Phe Ser
85 90 95

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

Tyr Cys His Ser Met Gln Ile Cys His Arg Asp Leu Lys Leu Glu Asn
115 120 125

Thr Leu Leu Asp Gly Ser Pro Ala Pro Arg Leu Lys Ile Cys Asp Phe
130 135 140

Gly Tyr Ser Lys Ser Ser Leu Leu His Ser Arg Pro Lys Ser Thr Val
145 150 155 160

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

Asp Gly Lys Leu Ala Asp Val Trp Ser Cys Gly Val Thr Leu Tyr Val
180 185 190

Met Leu Val Gly Ala Tyr Pro Phe Glu Asp Gln Asp Asp Pro Lys Asn
195 200 205

Phe Arg Lys Thr Ile Asn Arg Ile Met Ala Val Gln Tyr Lys Ile Pro
210 215 220

Asp Tyr Val His Ile Ser Pro Asp Cys Arg His Leu Ile Ser His Ile
225 230 235 240

Phe Leu Ala His Pro Leu Lys Arg Ile Thr Ile Lys Glu Ile Lys Ser
245 250 255

His Pro Trp Phe Leu Lys Asn Leu Pro Arg Glu Leu Thr Glu Ala Ala
260 265 270

Gln Thr Met Tyr Tyr Arg Lys Glu Asn Pro Ala Phe Ser Leu Gln Thr
275 280 285

Val Glu Glu Ile Met Lys Ile Val Asp Asp Ala Lys Val Pro Ala Pro
290 295 300

Val Ser Arg Ser Ile Gly Thr Phe Gly Trp Gly Gly Asp Glu Asp Glu
305 310 315 320

Glu Thr Lys Glu Glu Glu Ala Glu Pro Glu Ala Glu Thr Glu Ala Glu
325 330 335

Ala Glu Ala Val Glu Gly Gly Arg Ala Val Glu Gly Gly Gly Val Asp
340 345 350

Glu Tyr Glu Lys Arg Val Lys Glu Ala Gln Ala Ser Gly Glu Phe Arg
355 360 365

Val Ser
370

<210> 97
<211> 1053
<212> DNA
<213> Z. mays

<400> 97
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aagtacatcg agcgtggcga gaagatagat gagaatgtcc agcgcgaaat aattaacat 180
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cttgctattg tcatggaata tgcctctggc ggtgagcttt ttgagagaat atgtaagaac 300
gtgcgattca gtgaagatga ggctcgctac ttcttccaac aactcatttc aggagtaagc 360
tactgccatt caatgcaagt atgccaccgt gatttgaagc tggagaacac acttctagat 420
gggagtgatg ctctcgctt gaagatatgt gacttcggtt attccaagtc atctgttctt 480
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aaaaaagaat atgatggcaa gattgctgac gtttgggtcat gtggtgtaac cctctatgta 600
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attcagcgta tcttgaatgt tcagtagcga attccagaca acgtgaacat atctccagag 720
tgcaggcatc taatttcgag gatttttggt ggcgatcctg ctacgcgaat aacaatccct 780
gaaatccgga atcatagttg gttcctgaag aaccttcctg ctgatctgat ggatgatgat 840

agcatgagca accaatatga ggagcctgac cagccaatgc agaccatgga tcagatcatg 900

cagatttttaa cagaggccac cataccacct gcctgttctc gcagtataaa tgtcctagct 960

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gacagcagcg gtgagattgt gtacgcaatg tga 1053

<210> 98

<211> 350

<212> PRT

<213> Z. mays

<400> 98

Met Asp Met Pro Ile Met His Asp Ser Asp Arg Tyr Glu Leu Val Arg

1 5 10 15

Asp Ile Gly Ser Gly Asn Phe Gly Val Ala Arg Leu Met Arg Asp Arg

20 25 30

Arg Thr Thr Glu Leu Val Ala Val Lys Tyr Ile Glu Arg Gly Glu Lys

35 40 45

Ile Asp Glu Asn Val Gln Arg Glu Ile Ile Asn His Arg Ser Leu Lys

50 55 60

His Pro Asn Ile Ile Arg Phe Lys Glu Val Ile Leu Thr Pro Thr His

65 70 75 80

Leu Ala Ile Val Met Glu Tyr Ala Ser Gly Gly Glu Leu Phe Glu Arg

85 90 95

Ile Cys Lys Asn Val Arg Phe Ser Glu Asp Glu Ala Arg Tyr Phe Phe

100 105 110

Gln Gln Leu Ile Ser Gly Val Ser Tyr Cys His Ser Met Gln Val Cys
115 120 125

His Arg Asp Leu Lys Leu Glu Asn Thr Leu Leu Asp Gly Ser Asp Ala
130 135 140

Pro Arg Leu Lys Ile Cys Asp Phe Gly Tyr Ser Lys Ser Ser Val Leu
145 150 155 160

His Ser Gln Pro Lys Ser Thr Val Gly Thr Pro Ala Tyr Ile Ala Pro
165 170 175

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

Ser Cys Gly Val Thr Leu Tyr Val Met Val Val Gly Ala Tyr Pro Phe
195 200 205

Glu Asp Pro Glu Glu Pro Lys Asn Phe Arg Lys Thr Ile Gln Arg Ile
210 215 220

Leu Asn Val Gln Tyr Ala Ile Pro Asp Asn Val Asn Ile Ser Pro Glu
225 230 235 240

Cys Arg His Leu Ile Ser Arg Ile Phe Val Gly Asp Pro Ala Thr Arg
245 250 255

Ile Thr Ile Pro Glu Ile Arg Asn His Ser Trp Phe Leu Lys Asn Leu
260 265 270

Pro Ala Asp Leu Met Asp Asp Asp Ser Met Ser Asn Gln Tyr Glu Glu
275 280 285

Pro Asp Gln Pro Met Gln Thr Met Asp Gln Ile Met Gln Ile Leu Thr
290 295 300

Glu Ala Thr Ile Pro Pro Ala Cys Ser Arg Ser Ile Asn Val Leu Ala
305 310 315 320

Asp Gly Leu Asp Met Asp Asp Asp Met Asp Asp Leu Asp Ser Asp Ser
325 330 335

Asp Leu Asp Val Asp Ser Ser Gly Glu Ile Val Tyr Ala Met
340 345 350

<210> 99
<211> 1086
<212> DNA
<213> Z. mays

<400> 99
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atgcgcaacc gcgagactcg agagctcgtc gccgtcaagt gcatcgagcg tggccaccgg 120
attgacgaga atgtgtacag ggagatcatc aaccaccgct cgctgcgcca tcccaacatt 180
attcgcttca aggaggtgat acttacacca acacatctta tgattgtgat ggagtttgca 240
gcaggtggag agctttttga tcggatctgt gatcgtgggc ggttttagtga ggatgaggcc 300
cggatatttct ttcagcagtt gatctgtgga gtgagctatt gccattacat gcaaatatgc 360
catagagatc tgaagctgga gaatgttctc ttggatggca gccagctcc acggcttaag 420
atctgcgatt ttggctattc caagtcatca gtgttgcatc caagacccaa atcagcagta 480

ggaacgccag catatatgtgc acctgaggtg ctatcccgtc gcgagtatga tggaaagctt	540
gcagacgtat ggtcctgtgg ggtgactctt tacgtcatgc ttgtgggagc ataccattt	600
gaagaccag atgaccccaa gaatatacgc aagaccattc agcaaataat gcaagtgcaa	660
tacaagatac cagatcatgt ccacatatct acggaatgcc agcaacttat tgcccgtatc	720
tttgttgcca atccaatgag gagaatcaca atgaaggaaa taaagagcca tccatggttt	780
ttgaagaacc taccacggga actcacggag actgcacaag gcatgtacta caggagggat	840
aacaggggtcc cttcttattc agaccaaacy tcggaagaaa tcatgaagat agttcaagat	900
gcaaggacca tgccgaaatc atccagatca ggctatgggt ggagcagtga gtattcggat	960
gaagaagaag agaaggaaga ggaacacaga ccagaggagc atgaggaaga ggaagatgaa	1020
tacgatagga gggatgaaga ggtccatgca agcggagAAC tccgtatgga cgctcttcac	1080
atatga	1086

<210> 100
 <211> 361
 <212> PRT
 <213> Z. mays

<400> 100

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

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

Ile Ile Asn His Arg Ser Leu Arg His Pro Asn Ile Ile Arg Phe Lys
50 55 60

Glu Val Ile Leu Thr Pro Thr His Leu Met Ile Val Met Glu Phe Ala
65 70 75 80

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

Glu Asp Glu Ala Arg Tyr Phe Phe Gln Gln Leu Ile Cys Gly Val Ser
100 105 110

Tyr Cys His Tyr Met Gln Ile Cys His Arg Asp Leu Lys Leu Glu Asn
115 120 125

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

Gly Tyr Ser Lys Ser Ser Val Leu His Ser Arg Pro Lys Ser Ala Val
145 150 155 160

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

Asp Gly Lys Leu Ala Asp Val Trp Ser Cys Gly Val Thr Leu Tyr Val
180 185 190

Met Leu Val Gly Ala Tyr Pro Phe Glu Asp Pro Asp Asp Pro Lys Asn
195 200 205

Ile Arg Lys Thr Ile Gln Gln Ile Met Gln Val Gln Tyr Lys Ile Pro
210 215 220

Asp His Val His Ile Ser Thr Glu Cys Gln Gln Leu Ile Ala Arg Ile
225 230 235 240

Phe Val Ala Asn Pro Met Arg Arg Ile Thr Met Lys Glu Ile Lys Ser
245 250 255

His Pro Trp Phe Leu Lys Asn Leu Pro Arg Glu Leu Thr Glu Thr Ala
260 265 270

Gln Gly Met Tyr Tyr Arg Arg Asp Asn Arg Val Pro Ser Tyr Ser Asp
275 280 285

Gln Thr Ser Glu Glu Ile Met Lys Ile Val Gln Asp Ala Arg Thr Met
290 295 300

Pro Lys Ser Ser Arg Ser Gly Tyr Gly Trp Ser Ser Glu Tyr Ser Asp
305 310 315 320

Glu Glu Glu Glu Lys Glu Glu Glu His Arg Pro Glu Glu His Glu Glu
325 330 335

Glu Glu Asp Glu Tyr Asp Arg Arg Val Lys Glu Val His Ala Ser Gly
340 345 350

Glu Leu Arg Met Asp Ala Leu His Ile
355 360

<210> 101

<211> 745

<212> DNA

<213> B. napus

<400> 101

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atctacgact tcaccgtcaa ggatatctca ggtaacgatg tgagtttgag ccaattcaaa	120
ggcaaaactc ttctgattgt aaacgttgcc tccaaatgtg gactaacgga tgcgaactac	180
aaggaactca atgttctgta cgaaaaatac aaggaacaag ggttggagat attagcgttc	240
ccatgcaatc agtttttggg acaagaacca ggaaacaatg aagagattca gcaaactgtc	300
tgcaacaagg tcaaagctga gttcccatc ttgacaagg tagatgtgaa cgggaagaac	360
acggccccgt tatacaaata cttgaaagca gagaaaggag gattgctaatt tgacgcaatc	420
aaatggaact tcacaaagtt cttggtttct cctgacggca aagtctccca gagatattct	480
cccagaacgt ctctcttca gttcgagaaa gacattcaag ctctgctggg acaggcttct	540
tcttgaatca tcatcgaaag cttcaagaac gggtttatct atttattaaa cgtttttaca	600
tttggtccgt gtcttaagaa tccacaactt tgcaaacttg ttgttcgct taatccttga	660
gaccgctct ttaaataaag tgtcgtttca ttgataagaa ataaaaagaa atcagggccg	720
gcttgacacg aaaaaaaaaa aaaaa	745

<210> 102
 <211> 169
 <212> PRT
 <213> B. napus

<400> 102

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

Leu Ile Val Asn Val Ala Ser Lys Cys Gly Leu Thr Asp Ala Asn Tyr
35 40 45

Lys Glu Leu Asn Val Leu Tyr Glu Lys Tyr Lys Glu Gln Gly Leu Glu
50 55 60

Ile Leu Ala Phe Pro Cys Asn Gln Phe Leu Gly Gln Glu Pro Gly Asn
65 70 75 80

Asn Glu Glu Ile Gln Gln Thr Val Cys Thr Arg Phe Lys Ala Glu Phe
85 90 95

Pro Ile Phe Asp Lys Val Asp Val Asn Gly Lys Asn Thr Ala Pro Leu
100 105 110

Tyr Lys Tyr Leu Lys Ala Glu Lys Gly Gly Leu Leu Ile Asp Ala Ile
115 120 125

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

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

Gln Ala Leu Leu Gly Gln Ala Ser Ser
165

<210> 103

<211> 1121

<212> DNA

<213> Z. mays

<400> 103

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aaccctaataa cgcctccgtg cgtagattcc agaggtggta cgatcatagg ccctctgaac	120
cccaaaacgt ctctgtgcgt agattccaga ggtgatagga tcataggacc cccgtaaatac	180
cgtaataattt tgcattggatc gcttgctttg cgtgcggcgt gcccgggagc tgcaagctcg	240
aggccactgt gctgtgctta gtccgggatt ggggctttat ggttcctgat tctgctggag	300
ctcttagtgt gaatttcgct gtcgaaccgt gtgatttggc ttgcaaaatg actggatttg	360
ctaaccctta cctagcgggtt tttgccgaat ttttagaaga gtagatgccg cggcttatgt	420
ttttgcagag gactctaatt atcgccacct ccgtccacga cttcatcgtc aaggatgcga	480
gcggcaaaga cgttgacctc agcacctaca aggggaaggt tcttctcatt gttaacgtcg	540
catcccagtg tggcttaacc aactccaact aactgagct gggccagctc tatgagaagt	600
acaaggacca aggttttgaa atcctggctt tcccatgcaa ccagtttggt gggcaggagc	660
ctggtaccaa tgaggagatt gtccagtttg cctgcacacg cttcaaggct gactaccca	720
tcttcgacaa ggttgatgtc aacggtagca atgctgcgc catctacaag ttcttgaaat	780
ctagcaaagg tggccttttc ggcgacagca tcaagtggaa cttttccaag ttcttggttg	840
acaaggaggg acgtgttgtg gatcgctatg ctccaaccac ttcaccctg agcattgaga	900
aggatatcaa gaagctgctt gggagctctt aatcagtatc tgggtgcaaa gctgtagaaa	960
aacatgtatc aacaatgccc tgagcgataa aatatatgat aagttgtatt aataaagtat	1020
tgtcgtactt gagaggttg cgtatctgct ctatttccct tgcaaaaaaa aagtacttgt	1080
atatcccctt gtcaccaaata cagccctcga atgaattcca a	1121

<210> 104

<211> 175
<212> PRT
<213> Z. mays

<400> 104

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

Val His Asp Phe Ile Val Lys Asp Ala Ser Gly Lys Asp Val Asp Leu
20 25 30

Ser Thr Tyr Lys Gly Lys Val Leu Leu Ile Val Asn Val Ala Ser Gln
35 40 45

Cys Gly Leu Thr Asn Ser Asn Tyr Thr Glu Leu Ala Gln Leu Tyr Glu
50 55 60

Lys Tyr Lys Asp Gln Gly Phe Glu Ile Leu Ala Phe Pro Cys Asn Gln
65 70 75 80

Phe Gly Gly Gln Glu Pro Gly Thr Asn Glu Glu Ile Val Gln Phe Ala
85 90 95

Cys Thr Arg Phe Lys Ala Glu Tyr Pro Ile Phe Asp Lys Val Asp Val
100 105 110

Asn Gly Ser Asn Ala Ala Pro Ile Tyr Lys Phe Leu Lys Ser Ser Lys
115 120 125

Gly Gly Leu Phe Gly Asp Ser Ile Lys Trp Asn Phe Ser Lys Phe Leu
130 135 140

Val Asp Lys Glu Gly Arg Val Val Asp Arg Tyr Ala Pro Thr Thr Ser
 145 150 155 160

Pro Leu Ser Ile Glu Lys Asp Ile Lys Lys Leu Leu Gly Ser Ser
 165 170 175

<210> 105
 <211> 861
 <212> DNA
 <213> B. napus

<400> 105
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 caaacccaat ccattctctaa accccgcggc ttttctcgtc ccttccttga aattctccac 120
 cgccatatcg aatttcgcga atctgagtaa tgggttctct ctaaaatctc cgattaatcc 180
 tgggtttctc ttcaagtccc gagctttcaa tgttcaagct cgagctgctg ctgagaagac 240
 cgttcacgat ttcaccgtaa aggacattga tgggaatgat gtttctttga acaagtataa 300
 ggggaaagtt atgttgatcg tcaatgtcgc ttcaagatgt ggtttgacat catcaaatta 360
 ctgagagctt tcacatctgt atgagaaata caagagccaa ggatttgaga ttctagcttt 420
 cccttgtaat cagtttggtg gccaaagagcc cggttcaaac cctgagatca aacagtttgc 480
 ttgcaccggg tttaaagcag agttccctat atttgataag gtcgatgtga atggaccgag 540
 cacagcacca atctatcagt tcttgaaatc aaacgcagga ggattcttgg gtgatctcat 600
 taaatggaac ttgagaagt tcttgattga taaaaggga aaggtcgttg agaggtaccc 660
 tcccaccaca tcccctttcc aaatcgagaa ggacatcaag aagttgcttg ctgcttaata 720
 acctctgcga tgagagacca cacagactga ttgtaaaata ttcagtactt gaaactcggc 780
 ttgctggtt atggtttgta tacattgtaa cgatatatat ttattacaa tgctaagtat 840

gattacaaaa aaaaaaaaaa a

861

<210> 106

<211> 236

<212> PRT

<213> B. napus

<400> 106

Met Ala Phe Ser Ser Ser Tyr Tyr Ser Pro Phe Ser Ala Leu Phe Asp
1 5 10 15

Val Ser Lys Pro Asn Pro Ser Leu Asn Pro Ala Ala Phe Leu Val Pro
20 25 30

Ser Leu Lys Phe Ser Thr Ala Ile Ser Asn Phe Ala Asn Leu Ser Asn
35 40 45

Gly Phe Ser Leu Lys Ser Pro Ile Asn Pro Gly Phe Leu Phe Lys Ser
50 55 60

Arg Ala Phe Asn Val Gln Ala Arg Ala Ala Glu Lys Thr Val His
65 70 75 80

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

Tyr Lys Gly Lys Val Met Leu Ile Val Asn Val Ala Ser Arg Cys Gly
100 105 110

Leu Thr Ser Ser Asn Tyr Ser Glu Leu Ser His Leu Tyr Glu Lys Tyr
115 120 125

Lys Ser Gln Gly Phe Glu Ile Leu Ala Phe Pro Cys Asn Gln Phe Gly
130 135 140

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

Arg Phe Lys Ala Glu Phe Pro Ile Phe Asp Lys Val Asp Val Asn Gly
165 170 175

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

Phe Leu Gly Asp Leu Ile Lys Trp Asn Phe Glu Lys Phe Leu Ile Asp
195 200 205

Lys Lys Gly Lys Val Val Glu Arg Tyr Pro Pro Thr Thr Ser Pro Phe
210 215 220

Gln Ile Glu Lys Asp Ile Lys Lys Leu Leu Ala Ala
225 230 235

<210> 107
<211> 848
<212> DNA
<213> B. napus

<400> 107
gagatcctcg tttcggcttc tctatataac aagaaccaat cttctgggttc gagcttcacc 60
atcatcgctc tctcgactcc catctaagtt cacttctgcg aaaccacttg tcagttctca 120
tcacagatt ccgttatcaa caacgggagc taaactttct aggtcggaac attccatggc 180
tgcttcctcc gaacccaaat ccatctatga tttcacgcgc aaggatgcga agggaaacga 240

tgttgatcta agcacttaca aggggaaggt tctgttgatt gtcaacgttg cttctcagtg	300
tggcttgacc aattcgaact atactgagct tgcacagctg taccagaagt acaaagacca	360
tgggtttgag atccttgcat tcccctgtaa ccagtttggt aatcaagaac ctggttctaa	420
tgaagagatt gttcagtttg cttgtacccg tttcaaggcc gagtacccca tcttcgacaa	480
ggttgatgtg aacggtgact cggctgctcc aatctataag ttcttgaaat caagcaaagg	540
agggcttttt ggagacggaa tcaagtggaa cttcgccaag ttcttggttg acaaagatgg	600
gaatgttgtg gaccgttacg ctccaactac ttcccctctc agcattgaga aggacctgaa	660
gaaactgttg ggagttactg cttaagcaac taataggcgc aagtattcaa ataaaagctc	720
ctatagtatt gtaataagct gtgtctatgt tcttgagtgt ctttgggatg agtcgtctcc	780
tactacttaa actcctcctt tttagttact gatgtgtgta acatcgttga cctaaaaaaaa	840
aaaaaaaa	848

<210> 108
 <211> 169
 <212> PRT
 <213> B. napus

<400> 108

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

Asp	Ala	Lys	Gly	Asn	Asp	Val	Asp	Leu	Ser	Thr	Tyr	Lys	Gly	Lys	Val
			20					25					30		

Leu	Leu	Ile	Val	Asn	Val	Ala	Ser	Gln	Cys	Gly	Leu	Thr	Asn	Ser	Asn
		35					40					45			

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

Glu Ile Leu Ala Phe Pro Cys Asn Gln Phe Gly Asn Gln Glu Pro Gly
65 70 75 80

Ser Asn Glu Glu Ile Val Gln Phe Ala Cys Thr Arg Phe Lys Ala Glu
85 90 95

Tyr Pro Ile Phe Asp Lys Val Asp Val Asn Gly Asp Ser Ala Ala Pro
100 105 110

Ile Tyr Lys Phe Leu Lys Ser Ser Lys Gly Gly Leu Phe Gly Asp Gly
115 120 125

Ile Lys Trp Asn Phe Ala Lys Phe Leu Val Asp Lys Asp Gly Asn Val
130 135 140

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

Leu Lys Lys Leu Leu Gly Val Thr Ala
165

<210> 109

<211> 879

<212> DNA

<213> B. napus

<400> 109

aagacttcaa aatgatataa tttaaattgga atattattta aaaaaaatca ggtggtggtg 60

gataatacag caacaaaaaa cagacgtaga acttggttgg agagttccgg ctgcgagaag 120

Val Lys Asp Ser Ser Gly Lys Glu Val Asp Leu Ser Val Tyr Gln Gly
20 25 30

Lys Val Leu Leu Ile Val Asn Val Ala Ser Lys Cys Gly Phe Thr Gln
35 40 45

Thr Asn Tyr Thr Gln Leu Thr Glu Leu Tyr Arg Lys Tyr Lys Asp Gln
50 55 60

Gly Leu Val Ile Leu Ala Phe Pro Cys Asn Gln Phe Leu Asn Gln Glu
65 70 75 80

Pro Gly Thr Ser Gln Asp Ala His Glu Phe Ala Cys Thr Arg Phe Lys
85 90 95

Ala Glu Tyr Pro Val Phe Gln Lys Val Arg Val Asn Gly Gln Asn Ala
100 105 110

Ala Pro Val Tyr Lys Phe Leu Lys Ser Lys Lys Pro Ser Phe Leu Gly
115 120 125

Ser Arg Ile Lys Trp Asn Phe Thr Lys Phe Leu Val Gly Lys Asp Gly
130 135 140

Gln Val Ile Asp Arg Tyr Gly Pro Thr Val Pro Pro Leu Ser Ile Glu
145 150 155 160

Lys Asp Ile Lys Lys Ala Leu Gly Asp Glu Gly Ala Phe Pro Ser Thr
165 170 175

<210> 111

<211> 752

<212> DNA

<213> G. max

<400> 111

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tcacactatg gccacctcaa acgccaaatc attccatgat ttcaccgtta tagatgccaa	120
gggaaatgat attaaccttg gtgactacaa aggaaaggtc cttatcattg tcaatgttgc	180
ctcacaatgt ggcttgacta attcaaatta cactgagctc agtcagttgt atgagaaata	240
caaacagaaa ggtctggaaa ttctggcggt cccatgcaat cagtttgggg cacaggagcc	300
tggatctaata gaacagatac aagagtttgt ttgtactcgc ttcaaggctg agtttcccgt	360
ttttgacaag gttgatgtga atggtgacaa ggctgctcca ctgtacaaat atctaaaatc	420
aagcaaaggt ggactccttg gggatggcat caaatggaac ttcgccaagt tccttgttga	480
taaagagggg aatgttgttg atcgctatgc acccacaact tctcctctga gcattgagaa	540
ggacttgctg aagttgttgg atgcatgaag ttatgaatgt ttggagttgc caataaataa	600
actatgaata agaaatgtac tgcagatgct gctgcaattt cctgtgtgcc ttatatgtac	660
cgaacagtt gctctttag ctttgacatt agattcataa ccatgatatt gtgtacttat	720
tatagtgtga atgtgaagtt aagctacctt ta	752

<210> 112
 <211> 166
 <212> PRT
 <213> G. max

<400> 112

Met	Ala	Thr	Ser	Asn	Ala	Lys	Ser	Phe	His	Asp	Phe	Thr	Val	Ile	Asp
1				5				10					15		

Ala	Lys	Gly	Asn	Asp	Ile	Asn	Leu	Gly	Asp	Tyr	Lys	Gly	Lys	Val	Leu
			20					25					30		

Ile Ile Val Asn Val Ala Ser Gln Cys Gly Leu Thr Asn Ser Asn Tyr
35 40 45

Thr Glu Leu Ser Gln Leu Tyr Glu Lys Tyr Lys Gln Lys Gly Leu Glu
50 55 60

Ile Leu Ala Phe Pro Cys Asn Gln Phe Gly Ala Gln Glu Pro Gly Ser
65 70 75 80

Asn Glu Gln Ile Gln Glu Phe Val Cys Thr Arg Phe Lys Ala Glu Phe
85 90 95

Pro Val Phe Asp Lys Val Asp Val Asn Gly Asp Lys Ala Ala Pro Leu
100 105 110

Tyr Lys Tyr Leu Lys Ser Ser Lys Gly Gly Leu Leu Gly Asp Gly Ile
115 120 125

Lys Trp Asn Phe Ala Lys Phe Leu Val Asp Lys Glu Gly Asn Val Val
130 135 140

Asp Arg Tyr Ala Pro Thr Thr Ser Pro Leu Ser Ile Glu Lys Asp Leu
145 150 155 160

Leu Lys Leu Leu Asp Ala
165

<210> 113

<211> 1046

<212> DNA

<213> G. max

<400> 113

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cgccagagct ccatcacccg aacaagaccc aggcaggtgt cgcagtagcg ggagaaagga	120
cgctatataa atatatttgt ccccgatgct ctctatttca gccactcgta tattcttctt	180
ccgctcaaca actataagat tatctttctt ttctttcttct ctccaattct tctccaatcc	240
caaccgcacc ctcttcgct cctttcttca cacttcgctc aacaactata ataacatctt	300
tctctctccg aacagatcac actatggcca cctcaagcgc caaatcagtc catgatttca	360
ccgttaaaga tgccaaggga aatgatatta atcttgggtga ctacaaagga aaggctcctta	420
tcattgtcaa tgttgcctca caatgtggct tgactaatte aaattacact gagctcagtc	480
agttgtatga gaaatacaaa cagaaaggtc tggaaattct ggcatttcca tgcaatcagt	540
ttggggcaca ggagcctgga tctaataaac agatacaaga gtttgtttgt actcgcttca	600
aggctgagtt tcccgttttt gacaagggtg atgtgaatgg tgacaaagct gctccactgt	660
acaagtatct aaaatcaagc aaagggtggac tctttgggga tggatatcaa tggaacttct	720
ccaagttcct tgttgataaa gagggaaatg tggttgatcg ctatgcaccc acaacttctc	780
ctctgagcat tgagaaggac ttgctgaagt tgttggatgc atgaatgaag ctatgaatga	840
ctggagctgc caataaatga attgtgatta gaatataaat tatgaataag aaatgtattg	900
cagatgctgc tgcaatttcc tgtgtgcctt gtatgtgtac cgaaacaggt actctttag	960
ctctgacatt aggttcataa ccataagatt gtgtgcttaa tattgtgtga atgtaaactt	1020
aagcttcctt taataaaaaa aaaaaa	1046

<210> 114
 <211> 166
 <212> PRT
 <213> G. max

<400> 114

Met Ala Thr Ser Ser Ala Lys Ser Val His Asp Phe Thr Val Lys Asp
1 5 10 15

Ala Lys Gly Asn Asp Ile Asn Leu Gly Asp Tyr Lys Gly Lys Val Leu
20 25 30

Ile Ile Val Asn Val Ala Ser Gln Cys Gly Leu Thr Asn Ser Asn Tyr
35 40 45

Thr Glu Leu Ser Gln Leu Tyr Glu Lys Tyr Lys Gln Lys Gly Leu Glu
50 55 60

Ile Leu Ala Phe Pro Cys Asn Gln Phe Gly Ala Gln Glu Pro Gly Ser
65 70 75 80

Asn Glu Gln Ile Gln Glu Phe Val Cys Thr Arg Phe Lys Ala Glu Phe
85 90 95

Pro Val Phe Asp Lys Val Asp Val Asn Gly Asp Lys Ala Ala Pro Leu
100 105 110

Tyr Lys Tyr Leu Lys Ser Ser Lys Gly Gly Leu Phe Gly Asp Gly Ile
115 120 125

Lys Trp Asn Phe Ser Lys Phe Leu Val Asp Lys Glu Gly Asn Val Val
130 135 140

Asp Arg Tyr Ala Pro Thr Thr Ser Pro Leu Ser Ile Glu Lys Asp Leu
145 150 155 160

Leu Lys Leu Leu Asp Ala

165

<210> 115

<211> 789

<212> DNA

<213> G. max

<400> 115

tatctagcta gcgttaccac tttcaattcc aaattcactc tcagaaatta gaatggctag	60
ccaatcaaac actaaatcag ttcacgattt cacagttaaa gatgccaggg gaaatgatgt	120
taatctcgcc gattacaaag gaaaggctct tctccttgct aatgttgctt cacaatgcgg	180
cttgactaat tcaaactaca cagagcttaa tcaattgtat gagaaataca aagggaaagg	240
acttgaaatt ctggcattcc cgtgcaatca gtttggggct caggagccag gaactaatga	300
agagattgtg gagtttgctt gtactcgctt caaagctgag tttcccattt tcgacaaggt	360
ggatgtgaat ggtgacaatg ctgctccact gtacaagttt ctgaaatcaa gcaaagggtg	420
actctttggg gatagtatca aatggaactt ctccaaattc cttgttgata aggatggaaa	480
tgtcgttgac cgttatgcac ccacaacttc tcctcttagc attgagaaag acataaagaa	540
gctgctagat gcatgaatga ctggagtggc cactaaatga aaaataatga ttagaataac	600
atcatgaata atgtactgca gatcagatat tagtggaatt tcctccgaat ttgtactgaa	660
acagttgctc tgctcatgta cctctgaatt actatttgct tcttcatcta tatataaatt	720
gtgttggtga tcaatttata tatgtaaagc aaattcattg ctcgtttcat tcttaaaaaa	780
aaaaataaaa	789

<210> 116

<211> 167

<212> PRT

<213> G. max

<400> 116

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

Asp Ala Arg Gly Asn Asp Val Asn Leu Ala Asp Tyr Lys Gly Lys Val
20 25 30

Leu Leu Leu Val Asn Val Ala Ser Gln Cys Gly Leu Thr Asn Ser Asn
35 40 45

Tyr Thr Glu Leu Asn Gln Leu Tyr Glu Lys Tyr Lys Gly Lys Gly Leu
50 55 60

Glu Ile Leu Ala Phe Pro Cys Asn Gln Phe Gly Ala Gln Glu Pro Gly
65 70 75 80

Thr Asn Glu Glu Ile Val Glu Phe Ala Cys Thr Arg Phe Lys Ala Glu
85 90 95

Phe Pro Ile Phe Asp Lys Val Asp Val Asn Gly Asp Asn Ala Ala Pro
100 105 110

Leu Tyr Lys Phe Leu Lys Ser Ser Lys Gly Gly Leu Phe Gly Asp Ser
115 120 125

Ile Lys Trp Asn Phe Ser Lys Phe Leu Val Asp Lys Asp Gly Asn Val
130 135 140

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

Ile Lys Lys Leu Leu Asp Ala

165

<210> 117

<211> 924

<212> DNA

<213> G. max

<400> 117

gaaaatagtt tcagatacgt tgcgttgatt gattggatatg aagtgattga ctttttttct	60
tcttctattc tcacacatac ccatctactc cttccctcat ggctgaacaa tcttccaact	120
ccattttacga tttcactgtc aaggacatca gtggaaatga tgtgagtctg aatgattaca	180
gcgggaaggt tctactgatt gtgaatgtcg cctctcaatg tggtttgaca cagacaaatt	240
acaagaatt gaatgtattg tacgagaagt acaagaatca aggatttgaa atottggcat	300
ttccgtgcaa ccagtttgct ggacaggaac caggaaacaa tgaagaaatt caggaagtag	360
tttgacaaag gttcaaggct gaatttccta tctttgataa ggttgaagtc aatgggaaga	420
atgcagtgcc actttacaag tttttaaagg agaagaaagg gggaatattt ggcgatggta	480
tcaagtggaa cttcaciaag ttcttagtaa acaagaagg gaaggttgtg gacagatatg	540
cacctaccac ctcacctctg aaaatcgaga aagacataga gaagctcttg caatcttgaa	600
tagtaagatt tgattctaca tatctaattg gctgaggaca tagggaatct gtccggtgcc	660
ttcgaaggac aagtagcaat atgtatcata agttaatata tgcctgaaa agttcttaat	720
gtatctctgtg tatttgatt ttggattgct caataagtat aaattggtgt tctcactctg	780
ttaccaaaac cataaaataa taatatattt ggatgcatct ttatgttaaa aaaaaaaaaa	840
aaaaacatag aaaggacaaa aatgaacta gtgttaaaca atgaagagaa taaggagaaa	900

<210> 118

<211> 166

<212> PRT

<213> G. max

<400> 118

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

Ile Ser Gly Asn Asp Val Ser Leu Asn Asp Tyr Ser Gly Lys Val Leu
20 25 30

Leu Ile Val Asn Val Ala Ser Gln Cys Gly Leu Thr Gln Thr Asn Tyr
35 40 45

Lys Glu Leu Asn Val Leu Tyr Glu Lys Tyr Lys Asn Gln Gly Phe Glu
50 55 60

Ile Leu Ala Phe Pro Cys Asn Gln Phe Ala Gly Gln Glu Pro Gly Asn
65 70 75 80

Asn Glu Glu Ile Gln Glu Val Val Cys Thr Arg Phe Lys Ala Glu Phe
85 90 95

Pro Ile Phe Asp Lys Val Glu Val Asn Gly Lys Asn Ala Val Pro Leu
100 105 110

Tyr Lys Phe Leu Lys Glu Lys Lys Gly Gly Ile Phe Gly Asp Gly Ile
115 120 125

Lys Trp Asn Phe Thr Lys Phe Leu Val Asn Lys Glu Gly Lys Val Val
130 135 140

Asp Arg Tyr Ala Pro Thr Thr Ser Pro Leu Lys Ile Glu Lys Asp Ile
145 150 155 160

Glu Lys Leu Leu Gln Ser
165

<210> 119
<211> 957
<212> DNA
<213> G. max

<400> 119
aattcggcac gagcccaacc actcaaaatg tcctccatgg ctctctccac cgctttcttc 60
acaccctcc atgatttcac tcaagccaga acaaccccat caccctctt gcctttcacc 120
aaatcctcct ttgcttcctc caagtcaacc ttttttcacc ctgccctttc cctacaaacc 180
tcttccaact ttcccaggct ttttgaaaag cctaagtttt tctctgttca tgcaagggct 240
gccacagaaa aaaccattta tgattttact gtcaaggata ttgacagaaa ggatgtttct 300
cttagcaagt ttaaggggaa ggttctattg attgtcaatg ttgcttcacg atgtggtttg 360
acatcatcaa attactcgga gctgtcacgc ttgtatgaaa aatataagaa tcaaggtttg 420
gagatttttag ctttcccctg caatcaattt ggtatgcagg aacctggatc aaatgaagat 480
attaagcaat ttgcttgcac tcgatataaa gcagaatttc caatttttga taaggttgat 540
gtcaatggac catttacaac tccagtgtac cagtttctga aatcgagtgc tggaggcttt 600
ttgggtgatc ttataaagtg gaattttgag aaattcttgg ttgacaaaaa tggtaaagtt 660
attgaaagat acccaccaac aacgtctcct tttcaaattg agaaggatat ccagaagtta 720

cttgctgcct gagtgttaatt cagaacacaa acgagagctg tatgtaagag cacgaaccga	780
gtgatgtgtg cacaataagt taaaactgaa gatgagcaat aagtatagct atgcaattta	840
ctttggtgtc ttactaaag aaattatcag tttagggaag aaaattatac tgtattaccc	900
caaatgatt gaatatagta tatgtttctc tctttttctt tcaaaaaaaaa aaaaaaa	957

<210> 120
 <211> 234
 <212> PRT
 <213> G. max

<400> 120

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

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

Ser	Ser	Phe	Ala	Ser	Ser	Lys	Ser	Thr	Phe	Phe	His	Pro	Ala	Leu	Ser
		35						40					45		

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

Phe	Ser	Val	His	Ala	Arg	Ala	Ala	Thr	Glu	Lys	Thr	Ile	Tyr	Asp	Phe
65					70					75					80

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

Gly	Lys	Val	Leu	Leu	Ile	Val	Asn	Val	Ala	Ser	Arg	Cys	Gly	Leu	Thr
			100						105					110	

Ser Ser Asn Tyr Ser Glu Leu Ser Arg Leu Tyr Glu Lys Tyr Lys Asn
115 120 125

Gln Gly Leu Glu Ile Leu Ala Phe Pro Cys Asn Gln Phe Gly Met Gln
130 135 140

Glu Pro Gly Ser Asn Glu Asp Ile Lys Gln Phe Ala Cys Thr Arg Tyr
145 150 155 160

Lys Ala Glu Phe Pro Ile Phe Asp Lys Val Asp Val Asn Gly Pro Phe
165 170 175

Thr Thr Pro Val Tyr Gln Phe Leu Lys Ser Ser Ala Gly Gly Phe Leu
180 185 190

Gly Asp Leu Ile Lys Trp Asn Phe Glu Lys Phe Leu Val Asp Lys Asn
195 200 205

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

Glu Lys Asp Ile Gln Lys Leu Leu Ala Ala
225 230

<210> 121
<211> 997
<212> DNA
<213> G. max

<400> 121

aagaaatcaa agagacagaa agttgagaga gaagtgttca cgtcttttgag aaatgggtgc

ttcggcatcg gtcacagaaa aatccatcca tgaattcatg gtcaaggatg ctaagggcag	120
agacgtgaac ctcagcacct acaaagggaa ggttcttctt gtagttaacg tcgcttcaaa	180
atgtggattt acaaattcca attacacca gttaactgag ctttacagca aatataaaga	240
cagaggtctt gagatactgg catttccatg caaccagttt ctgaaacaag agcccgggag	300
tagccaggag gcagaggaat ttgcctgtac aagggtacaag gctgagtatc ccatttttgg	360
aaaggtacgt gtcaatggac ctgatacagc acctgtctac aaattcctta aagcaaataa	420
aacaggattt ctgggtagta ggataaagtg gaatttcact aagtttttgg ttgacaagga	480
agggcatgtc ctcgctcggt atggtccaac cacctcacg ttgtccattg aaaatgacat	540
caagacagca ttgggggagg cttgaaagac tctacaatca cttcaaattg gtgctcttgt	600
tgaagatgat tgaaacataa ggaatgtata tttgtagatg tttcttctag tgattatttc	660
ttacatattt catgcctagg tttttttgtg tttgttgtat tagaattctg ttttgtttgt	720
gatttttagtc gttattttaa aattaattaa tgggcattag tttgagttgt gtgttagaag	780
tgtgttttca tgtatcactt actaaatgca tgcaatcttc atggcctcat gtgtattaat	840
gtctaggaag ttgcatcact tgttataatg ctagggaaca gtccctacca agtctatcaa	900
gagtctatat atatggatga tatgaagaac ctatgtactg tatttttaca gaacaaaaag	960
cttttcattc tgtaaattgt acgaaatcgt cgacccg	997

<210> 122
 <211> 170
 <212> PRT
 <213> G. max

<400> 122

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

Val Lys Asp Ala Lys Gly Arg Asp Val Asn Leu Ser Thr Tyr Lys Gly
20 25 30

Lys Val Leu Leu Val Val Asn Val Ala Ser Lys Cys Gly Phe Thr Asn
35 40 45

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

Gly Leu Glu Ile Leu Ala Phe Pro Cys Asn Gln Phe Leu Lys Gln Glu
65 70 75 80

Pro Gly Ser Ser Gln Glu Ala Glu Glu Phe Ala Cys Thr Arg Tyr Lys
85 90 95

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

Ala Pro Val Tyr Lys Phe Leu Lys Ala Asn Lys Thr Gly Phe Leu Gly
115 120 125

Ser Arg Ile Lys Trp Asn Phe Thr Lys Phe Leu Val Asp Lys Glu Gly
130 135 140

His Val Leu Ala Arg Tyr Gly Pro Thr Thr Ser Pro Leu Ser Ile Glu
145 150 155 160

Asn Asp Ile Lys Thr Ala Leu Gly Glu Ala
165 170

<210> 123
<211> 735
<212> DNA
<213> G. max

<400> 123
gcagagtgtg gcatcctaaa ttaagaaaaa caaagagaga aaattgtgag aggagttttc 60
acgtctttga gaaatgggtg cttcgctatc ggtctcggaa aaatccatcc atgaattcat 120
ggtcaaggat gctaagggca gagacgtgaa cctcagcatc taciaaggga aggttcttct 180
tgtagtaa at gtcgcttcaa aatgtggatt tacgaatacc aattacaccc agttaactga 240
gctttacagc aaatacaaag acagaggcct tgagatactg gcattttccat gcaaccagtt 300
tctgaagcag gagcctggga gtagccagga cgtagaggaa tttgcctgca caagatacaa 360
ggccgcgtat cccatttttg gaaaggtacg tgtcaatgga cctgatacag cacctgtcta 420
caaattcctt aaagcaaata aatcaggatt tctgggttct aggataaagt ggaatttcac 480
caagtttttg gttgacaagg aagggaatgt cctccggcgt tatggttcaa ccacctcacc 540
gttttccatt gaaaatgaca tcaagagagc attgtgggag gcttgaaaaa ctctacaatc 600
acttcaaatt ggtgctcttg ttgaagatga ttgacacata aggaatgtat atttgagat 660
gtttcttcta gtgattattt gctaaaaaat tcatgtctac gtttttttgt gtctgctgat 720
tagaaatccg ttttg 735

<210> 124
<211> 170
<212> PRT
<213> G. max

<400> 124

Met Gly Ala Ser Leu Ser Val Ser Glu Lys Ser Ile His Glu Phe Met
1 5 10 15

Val Lys Asp Ala Lys Gly Arg Asp Val Asn Leu Ser Ile Tyr Lys Gly
20 25 30

Lys Val Leu Leu Val Val Asn Val Ala Ser Lys Cys Gly Phe Thr Asn
35 40 45

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

Gly Leu Glu Ile Leu Ala Phe Pro Cys Asn Gln Phe Leu Lys Gln Glu
65 70 75 80

Pro Gly Ser Ser Gln Asp Val Glu Glu Phe Ala Cys Thr Arg Tyr Lys
85 90 95

Ala Ala Tyr Pro Ile Phe Gly Lys Val Arg Val Asn Gly Pro Asp Thr
100 105 110

Ala Pro Val Tyr Lys Phe Leu Lys Ala Asn Lys Ser Gly Phe Leu Gly
115 120 125

Ser Arg Ile Lys Trp Asn Phe Thr Lys Phe Leu Val Asp Lys Glu Gly
130 135 140

Asn Val Leu Arg Arg Tyr Gly Ser Thr Thr Ser Pro Phe Ser Ile Glu
145 150 155 160

Asn Asp Ile Lys Arg Ala Leu Trp Glu Ala
165 170

<210> 125
<211> 681
<212> DNA
<213> L. usitatissimum

<400> 125
ggttctgcaa aaatgtcgag cgaagaacaa cagagccgc attccattta cgatttcact 60
gtaaagaatg ctaagggaca tgctgtaagt ctcggtatct acaaggggaa ggtcctgctt 120
attatcaatg ttgcttcaa atgtggcatg accaactcaa actacacgga gctgaatgct 180
ttgtatcaca agtacaaaga tcaagggttg gagatactgg cattcccttg caaccagttt 240
ggagcagaag aaccaggaaa caatgacgag attgaagaat tcgtttgcag tagattcaag 300
tccgagttcc ccatattcga caagactgag gtgaatggag agaatgcac cccactgtac 360
aagttgttga agacagggaa atggggaatt ttcggcgacg acatccaatg gaactttgtc 420
aagttccttg tcaacaaaca aggccaagtt gttgatcggt actaccaac aacttctccc 480
ctaagcatcg agtatgatat aaagaagctg ttgggagtct gaaagagagt agctatgctg 540
atgggaaact ctgtcatggg gattcaattc aagcacttgt tcttcagaga ttctttgtca 600
ttgctatcgg aagtgacctg ctgcttgtgt gtggtttgaa aagcctgaga aatggtgtat 660
gatgggttga ctactaatgg g 681

<210> 126
<211> 169
<212> PRT
<213> L. usitatissimum

<400> 126

Met Ser Ser Glu Glu Gln Gln Ser Pro His Ser Ile Tyr Asp Phe Thr
1 5 10 15

Val Lys Asn Ala Lys Gly His Ala Val Ser Leu Gly Ile Tyr Lys Gly
20 25 30

Lys Val Leu Leu Ile Ile Asn Val Ala Ser Lys Cys Gly Met Thr Asn
35 40 45

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

Gly Leu Glu Ile Leu Ala Phe Pro Cys Asn Gln Phe Gly Ala Glu Glu
65 70 75 80

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

Ser Glu Phe Pro Ile Phe Asp Lys Thr Glu Val Asn Gly Glu Asn Ala
100 105 110

Ser Pro Leu Tyr Lys Leu Leu Lys Thr Gly Lys Trp Gly Ile Phe Gly
115 120 125

Asp Asp Ile Gln Trp Asn Phe Val Lys Phe Leu Val Asn Lys Gln Gly
130 135 140

Gln Val Val Asp Arg Tyr Tyr Pro Thr Thr Ser Pro Leu Ser Ile Glu
145 150 155 160

Tyr Asp Ile Lys Lys Leu Leu Gly Val
165

<210> 127

<211> 716

<212> DNA

<213> O. sativa

<400> 127

ttcgtagata gggagagggga tttcgatttt tttttctcca cggcgaaatc cgcgaggcgg	60
aggaggagga ggagggcgag atgggggcgg cggaatccgt gccggagacc tccatacacg	120
aattcacctg caaggattgc aacggcaagg aggtgagcct ggagatgtac aaggggaagg	180
tgctaatacgt cgtcaacgtc gcctccaaat gtgggttcac ggagaccaac tacacgcagc	240
tgacggagct ctatcagaaa cacagggaca aagattttga gattctagca tttccctgca	300
atcagttctt gcgacaagag ccaggatctg accagcaaat aaaggatttt gcttgcacaa	360
gatttaaagc tgaatatccc gtttttcaga aggtgcgtgt aaatggtcct gatgctgcac	420
cactttacaa atttttgaaa gctagcaagc ctggcttggt tggatctaga atcaagtgga	480
actttaccaa atttcttatt gataagaatg gcaaagtcac taacagatac tcgaactgga	540
ccagtccttt gtcttttgag aaagacatcc tgaaggcgct cgaggattag atctcgtacc	600
ctcccccatc cttcatttgc agaagtaggc aaagtatctg gttgtaatat ctagacctat	660
gggatgctca atagtgaatt tttgcaatat attccttctt ttgtgtaaaa aaaaaa	716

<210> 128

<211> 169

<212> PRT

<213> O. sativa

<400> 128

Met	Gly	Ala	Ala	Glu	Ser	Val	Pro	Glu	Thr	Ser	Ile	His	Glu	Phe	Thr
1				5					10					15	

Val	Lys	Asp	Cys	Asn	Gly	Lys	Glu	Val	Ser	Leu	Glu	Met	Tyr	Lys	Gly
				20				25					30		

Lys Val Leu Ile Val Val Asn Val Ala Ser Lys Cys Gly Phe Thr Glu
35 40 45

Thr Asn Tyr Thr Gln Leu Thr Glu Leu Tyr Gln Lys His Arg Asp Lys
50 55 60

Asp Phe Glu Ile Leu Ala Phe Pro Cys Asn Gln Phe Leu Arg Gln Glu
65 70 75 80

Pro Gly Ser Asp Gln Gln Ile Lys Asp Phe Ala Cys Thr Arg Phe Lys
85 90 95

Ala Glu Tyr Pro Val Phe Gln Lys Val Arg Val Asn Gly Pro Asp Ala
100 105 110

Ala Pro Leu Tyr Lys Phe Leu Lys Ala Ser Lys Pro Gly Leu Phe Gly
115 120 125

Ser Arg Ile Lys Trp Asn Phe Thr Lys Phe Leu Ile Asp Lys Asn Gly
130 135 140

Lys Val Ile Asn Arg Tyr Ser Thr Ala Thr Ser Pro Leu Ser Phe Glu
145 150 155 160

Lys Asp Ile Leu Lys Ala Leu Glu Asp
165

<210> 129

<211> 625

<212> DNA

<213> O. sativa

<400> 129

cgtctccacg ctaccgtttc gcaaccaccc gcttcctcct ccggagaccg ctgggcgcgc	60
gctcgtcca gcatggccgc cgcgccgtcc gccacctccg tccacgactt caccgtcaag	120
gatgcaagcg gaaaagacgt gaacctgagc acctacaagg ggaaggttct cctcatcggt	180
aacgtcgcac cccaatgtgg cttaactaac tccaactaca ctgagctgag ccagctgtat	240
gagaagtaca aggtccaagg ctttgagata ttggctttcc cgtgcaatca gtttgaggagg	300
caggaacccg gctccaatga ggagattgtc cagtttgctt gcactcgctt caaggctgag	360
tatcccattt ttgacaaggt tgatgtcaac ggtaacaatg ctgcaccctt gtacaagtat	420
ctgaagtcta acaaaggtgg gcttttcggt gatagcatca agtggaactt ctccaaattc	480
ttggttgaca aggagggtcg cgtggtgctt cgttatacgc ccaccacctc ccctcttaga	540
attgaggtaa tgacctgcac taccacttgc aatctctttc tacagcctcg acttgatagg	600
ctctcattat aacatttcca tacta	625

<210> 130
 <211> 179
 <212> PRT
 <213> O. sativa

<400> 130

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

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

Glu Ile Leu Ala Phe Pro Cys Asn Gln Phe Gly Gly Gln Glu Pro Gly
65 70 75 80

Ser Asn Glu Glu Ile Val Gln Phe Ala Cys Thr Arg Phe Lys Ala Glu
85 90 95

Tyr Pro Ile Phe Asp Lys Val Asp Val Asn Gly Asn Asn Ala Ala Pro
100 105 110

Leu Tyr Lys Tyr Leu Lys Ser Asn Lys Gly Gly Leu Phe Gly Asp Ser
115 120 125

Ile Lys Trp Asn Phe Ser Lys Phe Leu Val Asp Lys Glu Gly Arg Val
130 135 140

Val Leu Arg Tyr Thr Pro Thr Thr Ser Pro Leu Arg Ile Glu Val Met
145 150 155 160

Thr Cys Thr Thr Thr Cys Asn Leu Phe Leu Gln Pro Arg Leu Asp Arg
165 170 175

Leu Ser Leu

<210> 131

<211> 1158

<212> DNA

<213> Z. mays

<400> 131

cggtccggat tcccgggtcg acgttttcgta ccactcgtaa ccagaatcgc cgcaagccaa	60
tctgtctccg ccaggcgcca agccaaccct caccaccacc cgtccacccc catcagtga	120
tcaccgctca cagcctttac tcgccaccgc agcaccacct gctcggccgc ccgctccgc	180
gttcccatat ctctctctct ctggctctct gctcgccacg cgccgtacca ggcgcgcgcg	240
ccacatggct cctcgttca ctagcctcct ctcgccgcgc aactccgcgc ccgcctcgcg	300
gctcccctcg gccgcgcgcg gacgggcac cacttttcgt cgcttccgc atcaccgcac	360
gggctgggct ggggcctccg tcgcgccgc gcgtacggcg cgcaagcggg caccgcgcgt	420
cgctacgcc accgcagcta ccgagaagag catctacgac tacaccgtta aggacattga	480
tggaaaagat gttcctctta aaaagttcaa gaataaggtg ttgctgattg ttaacgttgc	540
ttctcaatgt gggttgacaa cagcaaatta cactgaacta tctcatatct atgagaagta	600
caagactcaa gggtttgaga tccttgcat tcttgcaat caatttggtg cacaagaacc	660
tggatcaa atcagatta agcagtttgc atgtacaaga ttcaaagctg aatttccgat	720
ttttgacaag gttgatgtca atggacctaa tacagctccc atctataaat ttctgaagtc	780
cagtgtgga ggatttttgg gtgatctcgt gaaatggaat tttgagaagt tcttagtgga	840
taagaatggc aaagtcattg agagatatcc accaacaact tcacctttcc agattgagaa	900
ggacatccag aaactgctcg cggcataagt acttccaagt ctttcagctc cgacacttca	960
gaagttcttt tgaatggcgt ccctgggaaa cgatttcaca gcaaacgtgg agtcagacaa	1020
ggagatcctc tgcccccttc tttttgttct tgcgacagat ctctgcagt cgattgtcaa	1080
caaggcttgt gattgtggca tcctccggct ccctctaccg aacacttggt gttctaattt	1140
ccctattatt caatatgc	1158

<210> 132
<211> 227
<212> PRT
<213> Z. mays

<400> 132

Met Ala Pro Ser Phe Thr Ser Leu Leu Ser Ala Ala Asn Ser Ala Ala
1 5 10 15

Ala Ser Arg Leu Pro Ser Ala Ala Ala Gly Arg Ala Ser Thr Phe Val
20 25 30

Arg Phe Pro His His Pro Thr Gly Trp Ala Gly Ala Ser Val Ala Ala
35 40 45

Pro Arg Thr Ala Arg Lys Arg Ala Pro Gly Val Ala Tyr Ala Thr Ala
50 55 60

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

Lys Asp Val Pro Leu Lys Lys Phe Lys Asn Lys Val Leu Leu Ile Val
85 90 95

Asn Val Ala Ser Gln Cys Gly Leu Thr Thr Ala Asn Tyr Thr Glu Leu
100 105 110

Ser His Ile Tyr Glu Lys Tyr Lys Thr Gln Gly Phe Glu Ile Leu Ala
115 120 125

Phe Pro Cys Asn Gln Phe Gly Ala Gln Glu Pro Gly Ser Asn Thr Gln
130 135 140

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

Asp Lys Val Asp Val Asn Gly Pro Asn Thr Ala Pro Ile Tyr Lys Phe
 165 170 175

Leu Lys Ser Ser Ala Gly Gly Phe Leu Gly Asp Leu Val Lys Trp Asn
 180 185 190

Phe Glu Lys Phe Leu Val Asp Lys Asn Gly Lys Val Ile Glu Arg Tyr
 195 200 205

Pro Pro Thr Thr Ser Pro Phe Gln Ile Glu Lys Asp Ile Gln Lys Leu
 210 215 220

Leu Ala Ala
 225

<210> 133
 <211> 848
 <212> DNA
 <213> Z. mays

<400> 133
 caacctcagc tagtcagctc cgccgctttt gctttctctc tccaggetct cggettcgctc 60
 cacaagctac agccgcgcgc tcctccttga cccggcctga ccccgctagt tcgccgcctg 120
 ccgtctgccg cccagcatg gccgcgcgct cgtccgccac ctccgtccac gacttcaccg 180
 tcaaggattc gagcggcaag gacgttgacc tcagcgtcta cagggggaag gttctttctca 240
 tcgttaacgt cgcattccaa tgtggcttaa ccaactccaa ctacactcag caggcccagc 300

tctatgagaa gtacaagaac caaggctttg aaatcctcgc tttcccgtgc aaccagtttg	360
gtgggcagga gcctggtacc aacgaggaga ttgccagtt tgctgcaca cgcttcaagg	420
ctgactaccc catctttgac aaggttgatg tcaatggtaa caatgctgcg cccatctaca	480
agtttctgaa atctagcaag ggtggccttt tcggcgacag catcaagtgg aacttttcca	540
agttcttggg tgacaaggag gggcgtggtg tggatcgcta tgctccaacc acttcacctc	600
tgagcattga gaaggatc aagaagctgc ttgggagctc ttaaacgata tctggctgca	660
aaactgtaga aaaaactgta tgaacattgc tctgagagct gaagtatata acaatcttgt	720
cttaataaag tagttttagt atttgagagg ttgcagtacc tgctttatct cccttgcatg	780
cactctgtac ttgtacttgc gacacgatcc gatagaaatg atattccttt tccttgcaaa	840
aaaaaaaa	848

<210> 134
 <211> 168
 <212> PRT
 <213> Z. mays

<400> 134

Met	Ala	Ala	Ala	Ser	Ser	Ala	Thr	Ser	Val	His	Asp	Phe	Thr	Val	Lys
1				5					10					15	

Asp	Ser	Ser	Gly	Lys	Asp	Val	Asp	Leu	Ser	Val	Tyr	Arg	Gly	Lys	Val
			20					25					30		

Leu	Leu	Ile	Val	Asn	Val	Ala	Ser	Gln	Cys	Gly	Leu	Thr	Asn	Ser	Asn
		35					40					45			

Tyr	Thr	Gln	Gln	Ala	Gln	Leu	Tyr	Glu	Lys	Tyr	Lys	Asn	Gln	Gly	Phe
		50				55					60				

Glu Ile Leu Ala Phe Pro Cys Asn Gln Phe Gly Gly Gln Glu Pro Gly
65 70 75 80

Thr Asn Glu Glu Ile Ala Gln Phe Ala Cys Thr Arg Phe Lys Ala Asp
85 90 95

Tyr Pro Ile Phe Asp Lys Val Asp Val Asn Gly Asn Asn Ala Ala Pro
100 105 110

Ile Tyr Lys Phe Leu Lys Ser Ser Lys Gly Gly Leu Phe Gly Asp Ser
115 120 125

Ile Lys Trp Asn Phe Ser Lys Phe Leu Val Asp Lys Glu Gly Arg Val
130 135 140

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

Ile Lys Lys Leu Leu Gly Ser Ser
165

<210> 135

<211> 735

<212> DNA

<213> Z. mays

<400> 135

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atctggaaat gacttaatga caaatgaagt tgttccactc agcaacttca aaggcaaggt 180

atgtttggtt gtcaatgtat caagcaaatg tggattaact ccaaagaatt atccagagct	240
tgaacagttg tacaagacat atggtccaag aggatttggt gtgttggcat tccaacaaa	300
tcaattcgca aatcaagaac caggtacacc agaggatatc agaaaattgg ttgatggata	360
tggagtcaca tttccaatgt ttgctaaaac tgatgttaat ggcctaactg ctcatccagt	420
gttcaagttc ttgaaacaaa accttggtgg agtacttgga agttcaatca aatggaattt	480
caccaagttc ttatgtgaca gaaatggtaa accagtcaag agatacatgc caaccacca	540
accattgtca tttgttgctg atattgaagc acttcttgat caagaatgag aaacaagcaa	600
cacattggca catccattga tcaagaatat ataaatattt acatatgata caacaaggca	660
tattcaaaat gaaatcattc tatatatatg attacaacat ttacatttaa ttatttggag	720
ttataaaaaa aaaaa	735

<210> 136
 <211> 182
 <212> PRT
 <213> Z. mays

<400> 136

Met	Phe	Ala	Met	Gln	Ala	Gly	Gly	Leu	Glu	Phe	Glu	Lys	Val	Glu	Glu
1			5					10						15	

Gly	Glu	Val	Lys	Ala	Thr	Ser	Leu	Phe	Glu	Leu	Ser	Gly	Asn	Asp	Leu
		20					25					30			

Met	Thr	Asn	Glu	Val	Val	Pro	Leu	Ser	Asn	Phe	Lys	Gly	Lys	Val	Cys
		35					40					45			

Leu	Val	Val	Asn	Val	Ser	Ser	Lys	Cys	Gly	Leu	Thr	Pro	Lys	Asn	Tyr
	50						55				60				

Pro Glu Leu Glu Gln Leu Tyr Lys Thr Tyr Gly Pro Arg Gly Phe Val
65 70 75 80

Val Leu Ala Phe Pro Thr Asn Gln Phe Ala Asn Gln Glu Pro Gly Thr
85 90 95

Pro Glu Asp Ile Arg Lys Leu Val Asp Gly Tyr Gly Val Thr Phe Pro
100 105 110

Met Phe Ala Lys Thr Asp Val Asn Gly Leu Thr Ala His Pro Val Phe
115 120 125

Lys Phe Leu Lys Gln Asn Leu Gly Gly Val Leu Gly Ser Ser Ile Lys
130 135 140

Trp Asn Phe Thr Lys Phe Leu Cys Asp Arg Asn Gly Lys Pro Val Lys
145 150 155 160

Arg Tyr Met Pro Thr Thr Gln Pro Leu Ser Phe Val Ala Asp Ile Glu
165 170 175

Ala Leu Leu Asp Gln Glu
180

<210> 137

<211> 960

<212> DNA

<213> B. napus

<400> 137

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gttaaggatt ttcagatcgt ggtcgcttcc gacaaggaac cgaacatcag taagaagccg	180
ccgcagcagc agcagcagca gaaccagctt ggtcccaaga gaagctctaa caaagacaga	240
cacatcaaag tcgaaggcag gggtcggaga atcaggatgc ctgctctctg cgccgctagg	300
atcttccaat tgactagaga attgggccac aaatccgacg gcgagacaat ccagtggctg	360
cttcagcagg ctgagccgtc gattatcgca gccaccggtt cgggaaccat accggcctct	420
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ggtttgatga tcagtcatga gttggacggt ggtggtgggt ctagtagtgg gaggccaaat	540
tggggtggtg gcggcggaga tggagtagga ggagcttcta ggtcgagttt accaacaggg	600
ctgtggccaa atgtagctgg gtttgagct ggtgtgcaga ccactgggat gatgagtgat	660
ggaggtggtt acagaattgg gtttcctggg tttgattatc ctggtggagc tatgagtttt	720
gcgtccattc ttggtggtgg taataacaat cagatgcctg gacttgagtt agggttggct	780
caggaaggga atgttggtgt cttgaatccg cactcttttg cacagattta tcagcagcag	840
atgagtcaag ctcaggctca gggtaggggt cttcaccata ctcttctgca taaccatca	900
catgaggagc atcagcaaga gagtggtag aaagatgatt ctcaaggctc cgggcgttaa	960

<210> 138
 <211> 319
 <212> PRT
 <213> B. napus

<400> 138

Met	Asp	Pro	Lys	Asn	Pro	Asn	Arg	His	Gln	Val	Pro	Asn	Phe	Leu	Asn
1				5						10				15	

Pro Pro Pro Arg His Gln Ser Ile Gly Asp Ala Ser Lys Asp Asp Asn
20 25 30

His His His Ser Lys Pro Ala Glu Val Lys Asp Phe Gln Ile Val Val
35 40 45

Ala Ser Asp Lys Glu Pro Asn Ile Ser Lys Lys Pro Pro Gln Gln Gln
50 55 60

Gln Gln Gln Asn Gln Leu Gly Pro Lys Arg Ser Ser Asn Lys Asp Arg
65 70 75 80

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

Cys Ala Ala Arg Ile Phe Gln Leu Thr Arg Glu Leu Gly His Lys Ser
100 105 110

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

Ile Ala Ala Thr Gly Ser Gly Thr Ile Pro Ala Ser Ala Leu Ala Ser
130 135 140

Ala Ala Ala Val Ser Ser His His Leu Gln Gly Gly Ser Leu Thr Ala
145 150 155 160

Gly Leu Met Ile Ser His Glu Leu Asp Gly Gly Gly Gly Ser Ser Ser
165 170 175

Gly Arg Pro Asn Trp Gly Val Gly Gly Gly Asp Gly Val Gly Gly Ala
180 185 190

Ser Arg Ser Ser Leu Pro Thr Gly Leu Trp Pro Asn Val Ala Gly Phe
195 200 205

Gly Ala Gly Val Gln Thr Thr Gly Met Met Ser Asp Gly Gly Gly Tyr
210 215 220

Arg Ile Gly Phe Pro Gly Phe Asp Tyr Pro Gly Gly Ala Met Ser Phe
225 230 235 240

Ala Ser Ile Leu Gly Gly Gly Asn Asn Asn Gln Met Pro Gly Leu Glu
245 250 255

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

Phe Ala Gln Ile Tyr Gln Gln Gln Met Ser Gln Ala Gln Ala Gln Gly
275 280 285

Arg Val Leu His His Thr Leu Leu His Asn Pro Ser His Glu Glu His
290 295 300

Gln Gln Glu Ser Gly Glu Lys Asp Asp Ser Gln Gly Ser Gly Arg
305 310 315

<210> 139

<211> 936

<212> DNA

<213> B. napus

<400> 139

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aaggattttc agatcgtggt cgcttccgac aaagaaccga acaagaagcc gcagcagcag	180
cagaaccagc ttggctcctaa gagaagctct aacaaagaca gacacatcaa agtgaaggc	240
aggggtcggg gaatcaggat gcctgctctc tgcgccgcta ggatcttcca attgactaga	300
gaattgggtc acaaatccga cggcgagaca atccagtggc tgcttcagca ggctgagccg	360
tcgattatcg cagccaccgg ttcaggaact ataccggcct ctgctttagc ctcagccgct	420
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gatggagggt ctaggtcgag tttaccaacg gggctgtggc caaatgtagc tgggtttgga	600
gctgggggtc agaccatgag tgatggaggt gggtacagga ttgggtttcc tgggtttgat	660
tatcctggtg gagctatgag ttttgcattc attcttgggt gtggtagtaa caatcagatg	720
cctggacttg agttagggtt ggctcaggaa gggaatgttg gtgtcttgaa tctcagttc	780
tttgacaga tttatcagca gcagatgagt caggctcagg ctcaggctca agctcagggt	840
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ggtgagaaaag atgattctca agggtcaggg cgtaa	936

<210> 140
 <211> 311
 <212> PRT
 <213> B. napus

<400> 140

Met	Asp	Pro	Lys	Asn	Pro	Asn	Arg	His	Gln	Val	Pro	Asn	Phe	Leu	Asn
1				5						10				15	

Pro Pro Pro Arg Asn Gln Ser Leu Gly Asp Ala Ser Lys Asp Asp Asn
20 25 30

His His Ser Lys Pro Ala Glu Val Lys Asp Phe Gln Ile Val Val Ala
35 40 45

Ser Asp Lys Glu Pro Asn Lys Lys Pro Gln Gln Gln Gln Asn Gln Leu
50 55 60

Gly Pro Lys Arg Ser Ser Asn Lys Asp Arg His Ile Lys Val Glu Gly
65 70 75 80

Arg Gly Arg Arg Ile Arg Met Pro Ala Leu Cys Ala Ala Arg Ile Phe
85 90 95

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

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

Gly Thr Ile Pro Ala Ser Ala Leu Ala Ser Ala Ala Ala Val Ser
130 135 140

Ser His His Leu Gln Gly Gly Gly Ser Leu Thr Ala Gly Leu Met Ile
145 150 155 160

Ser His Glu Leu Asp Gly Gly Ser Ser Ser Gly Arg Pro Asn Trp Gly
165 170 175

Val Gly Gly Gly Asp Gly Gly Ser Arg Ser Ser Leu Pro Thr Gly Leu
180 185 190

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

Gly Gly Gly Tyr Arg Ile Gly Phe Pro Gly Phe Asp Tyr Pro Gly Gly
210 215 220

Ala Met Ser Phe Ala Ser Ile Leu Gly Gly Gly Ser Asn Asn Gln Met
225 230 235 240

Pro Gly Leu Glu Leu Gly Leu Ala Gln Glu Gly Asn Val Gly Val Leu
245 250 255

Asn Pro Gln Ser Phe Ala Gln Ile Tyr Gln Gln Gln Met Ser Gln Ala
260 265 270

Gln Ala Gln Ala Gln Ala Gln Gly Arg Val Leu His His Thr Leu Gln
275 280 285

His Asn Pro Ser His Glu Glu His Gln Gln Glu Ser Gly Glu Lys Asp
290 295 300

Asp Ser Gln Gly Ser Gly Arg
305 310

<210> 141
<211> 1556
<212> DNA
<213> Z. mays

<400> 141
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aacgggaatg gatcgggggc cgtcggaggt gagatgcagc aggtgcggaa ggcggcaccc	180
aagcggagct ccaccaagga ccggcacacc aaggtggagg gcagggggcg tcgcatccgg	240
atgccagcgc tgtgcgcggc ccgggtgttc cagctgacgc gggagctcgg gcacaagacg	300
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gcccggttcg gccgtgctga cgcgtgggac cgggttgctg gccttgccct cccttcggag	540
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acaaggaaga ggcggtggga acaagaaatg cagcagcagc agcagcagca agcgcagcaa	720
tatcagcagc agatggcggg gtacacgcag agccaaatgc cgggcaccgt gtggatggtg	780
ccgagcagca acaacacgca ggggtggtggt acaccttcca gcggcggcag tggcggtatgc	840
accggcgagt ctatctggac gttcccgag atgggcagcg ccaccgccgc ggctgccgtg	900
taccggggga gcgtgccgag cgggctacat ttcatgaact tccccgcacc ggtggcgctg	960
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<210> 142
 <211> 400
 <212> PRT
 <213> Z. mays

<400> 142

Met	Asp	Val	Ala	Gly	Asp	Gly	Gly	Gly	Gly	Arg	Arg	Pro	Asn	Phe	Pro
1				5						10				15	

Leu	Gln	Leu	Leu	Glu	Lys	Lys	Glu	Glu	Gln	Pro	Cys	Ser	Ile	Ser	Ala
				20					25					30	

Ala	Val	Gly	Ala	Ser	Ala	Gly	Gly	Asn	Gly	Asn	Gly	Ser	Gly	Ala	Val
		35						40					45		

Gly	Gly	Glu	Met	Gln	Gln	Val	Arg	Lys	Ala	Ala	Pro	Lys	Arg	Ser	Ser
		50						55					60		

Thr	Lys	Asp	Arg	His	Thr	Lys	Val	Glu	Gly	Arg	Gly	Arg	Arg	Ile	Arg
65						70				75					80

Met	Pro	Ala	Leu	Cys	Ala	Ala	Arg	Val	Phe	Gln	Leu	Thr	Arg	Glu	Leu
				85						90					95

Gly	His	Lys	Thr	Asp	Gly	Glu	Thr	Ile	Glu	Trp	Leu	Leu	Gln	Gln	Ala
				100				105						110	

Glu Pro Ala Val Ile Ala Ala Thr Gly Thr Gly Thr Ile Pro Ala Asn
115 120 125

Phe Thr Ser Leu Asn Ile Ser Leu Arg Ser Ser Gly Ser Ser Phe Ser
130 135 140

Ala Pro Ala His Leu Arg Ala Ala Leu Pro Ala Ser Pro Ala Thr Ala
145 150 155 160

Ala Arg Phe Gly Arg Ala Asp Ala Trp Asp Arg Val Val Gly Leu Ala
165 170 175

Phe Pro Ser Glu Gly Pro Ala Ser Ser Ser Ser Ser Pro Ser Pro Leu
180 185 190

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

Pro Ser Ala Ala Ala Ala Ala Ala Ala Asp Met Thr Arg Lys Arg
210 215 220

Arg Trp Glu Gln Glu Met Gln Gln Gln Gln Gln Gln Gln Ala Gln Gln
225 230 235 240

Tyr Gln Gln Gln Met Ala Gly Tyr Thr Gln Ser Gln Met Pro Gly Thr
245 250 255

Val Trp Met Val Pro Ser Ser Asn Asn Thr Gln Gly Gly Gly Thr Pro
260 265 270

Ser Ser Gly Gly Ser Gly Gly Cys Thr Gly Glu Ser Ile Trp Thr Phe
275 280 285

Pro Gln Met Gly Ser Ala Thr Ala Ala Ala Ala Val Tyr Arg Gly Ser
290 295 300

Val Pro Ser Gly Leu His Phe Met Asn Phe Pro Ala Pro Val Ala Leu
305 310 315 320

Leu Pro Gly Gln Gln Leu Gly Leu Gly Ser Val Gly Gly Gly Gly Gly
325 330 335

Gly Ser Gly Gly Gly Ser Gly Gly Glu Gly His Met Gly Ile Leu Ala
340 345 350

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

Gln Gly Gly Gly Gly Gly Gly Gly Gly Gly Ser Gly Gln Gln Gln Gln His
370 375 380

Gly Gly Gly Arg Gly Asp Arg His Glu Ser Met Ser Thr Ser Asp Ser
385 390 395 400

<210> 143
<211> 1194
<212> DNA
<213> B. napus

<400> 143
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agcttcttga ttcttcttcc tctctttcca cttccttagc tatcatcca tcagcttcgt	180
cttccgaacc taactccgac cctaacgttc tctccaagaa accacctcca aagcgaacct	240
caacaaagga cagacacacc aaagtcgaag gccggggccg taggatccgt atgccggcca	300
tgtgcgccgc acgtgtcttt cagctcacac gcgagctcg tcataaatcc gacggtgaaa	360
ccatcgagtg gcttctccag caagctgaac cggcggttat agccgctacg gggactggaa	420
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aacatcatca tcagcagcag cttcaccagg tgcgtcccaa gaatgagtcg gattcttgtt	600
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gatctttgcc tactagccag actcctgcc cggcgccgtt ttggagtagt ggtgataata	720
cgcagaatct atgggctttt catcattccg gtgacgttta caacacaagc agcggtggtg	780
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cgtttgcttt gttttccgga cagcctttgg cgtctggtta tggaggaggt ggtggaggag	900
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gcacaagtca tcattcctag gccaaaaaaa cacacacaaa caatatatct gtgagattta	1080
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ttttgcattg cttttttcat atggagtatt ttttttctta aaaaaaaaaa aaaa	1194

<210> 144
 <211> 321
 <212> PRT
 <213> B. napus

<400> 144

Met Asp Pro Asp Pro Asp His His Gln Arg Pro Asn Phe Pro Leu Gln
1 5 10 15

Leu Leu Asp Ser Ser Ser Ser Ser Thr Ser Leu Ala Ile Ile Pro
20 25 30

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

Lys Pro Pro Pro Lys Arg Thr Ser Thr Lys Asp Arg His Thr Lys Val
50 55 60

Glu Gly Arg Gly Arg Arg Ile Arg Met Pro Ala Met Cys Ala Ala Arg
65 70 75 80

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

Ile Glu Trp Leu Leu Gln Gln Ala Glu Pro Ala Val Ile Ala Ala Thr
100 105 110

Gly Thr Gly Thr Ile Pro Ala Asn Phe Thr Ser Leu Asn Ile Ser Leu
115 120 125

Arg Ser Ser Arg Ser Ser Leu Ser Ala Ala His Leu Arg Thr Thr Pro
130 135 140

Ser Asn Tyr Tyr Phe His Ser Pro Ala Met Ala Gln His His His Gln
145 150 155 160

Gln Gln Leu His Gln Val Arg Pro Lys Asn Glu Ser Asp Ser Cys Ser
165 170 175

Ser Ser Gln Leu Val Asp His Asn Gln Met Gly Asn Tyr Leu Val Gln
180 185 190

Ser Thr Ala Gly Ser Leu Pro Thr Ser Gln Thr Pro Ala Thr Ala Pro
195 200 205

Phe Trp Ser Ser Gly Asp Asn Thr Gln Asn Leu Trp Ala Phe His His
210 215 220

Ser Gly Asp Val Tyr Asn Thr Ser Ser Gly Gly Gly Gly Gly Gly Gly
225 230 235 240

Gly Ala Gly Gly Gly Gly Gly Val His Leu Met Asn Phe Pro Ala Pro
245 250 255

Phe Ala Leu Phe Ser Gly Gln Pro Leu Ala Ser Gly Tyr Gly Gly Gly
260 265 270

Gly Gly Gly Gly Gly Glu His Asn His Tyr Gly Val Leu Ser Ala Leu
275 280 285

Asn Ala Ala Tyr Arg Pro Val Gln Glu Thr Ala Asn Gln Gln Asn His
290 295 300

Gly Asp His His His Asn His Gln Glu Asp Gly Ser Thr Ser His His
305 310 315 320

Ser

<210> 145
<211> 1750
<212> DNA
<213> B. napus

<400> 145
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ggacacccta accaaatctg ttgaaagctt ttctctgtga ttgagaacaa tatggtttcc 180
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aatcatgctg agtatatgaa ggctgagcgt gatattctta cgaagattga tcatcctttc 720
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gctcgggtgt aactgcgga gatcgtctct gcagtttccc atctccatga gaatgggata 900
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actactgagt atatggcacc tgagatcggt agaggaaagg ggcatagataa ggctgctgac	1080
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tcaaataaag ctcatgcgtt gctgaaaggg ttgctgcaaa aagagccaga gagaagactt	1260
ggaagcggac cgagcggagc agaggagata aaagggcaca aatgggtcaa gggaatgaac	1320
tggaagaagc tggaggcaag agaagtgaag ccaagtttca agccggaggt atctgggagg	1380
caatgcatag cgaattttga caagtgttgg actgatatgt ctgtgctgga ttgccagca	1440
agcagtccta gctcggatcc taaggccaac cttttacca acttcacata cgtcaggcct	1500
cctcattcat tcctcaacca aaccacatcg acttcgtaga ggaaagatgg gtttatggaa	1560
atacattgtt tttatgtttg ataaaaagat acataatctg atcttgtgtt tctattattt	1620
cttctcatgc ttgtcaaaac cattgtggtt gtttctttct caacatgtac attcgttttt	1680
accttttcat caaactgtat ttatactatt aaactaatca agttagagtg catgcaaaaa	1740
aaaaaaaaaa	1750

<210> 146
 <211> 455
 <212> PRT
 <213> B. napus

<400> 146

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

His	Leu	Phe	Leu	Thr	Ile	Thr	Pro	Pro	Gln	Ala	Val	Leu	Lys	Glu	Asn
			20					25					30		

Leu Glu Leu Asp Phe Ser Asp Val Phe Gly Pro Leu Pro Glu Asp Pro
35 40 45

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

Ser Leu Val Gly Pro Ser Leu Ile Thr Ser His Ser Phe Lys Leu Ser
65 70 75 80

Lys Leu Thr Leu Arg Glu Thr Asn Asp Ser Val Asp Leu Val Glu Cys
85 90 95

Leu Glu Glu Gly Glu Ser Ser Cys Asn Ser Asp Thr Glu Ala Val Ser
100 105 110

Lys Val Ser Gly Gly Val Val Gly Ile Glu Asp Phe Glu Val Leu Lys
115 120 125

Val Val Gly Gln Gly Ala Phe Gly Lys Val Tyr Gln Val Arg Lys Lys
130 135 140

Glu Ser Ser Glu Ile Tyr Ala Met Lys Val Met Arg Lys Asp Lys Ile
145 150 155 160

Met Glu Lys Asn His Ala Glu Tyr Met Lys Ala Glu Arg Asp Ile Leu
165 170 175

Thr Lys Ile Asp His Pro Phe Ile Val Gln Leu Lys Tyr Ser Phe Gln
180 185 190

Thr Lys Tyr Arg Leu Tyr Leu Val Leu Asp Phe Ile Asn Gly Gly His
195 200 205

Leu Phe Phe Gln Leu Tyr His Gln Gly Leu Phe Arg Glu Asp Leu Ala
210 215 220

Arg Val Tyr Thr Ala Glu Ile Val Ser Ala Val Ser His Leu His Glu
225 230 235 240

Asn Gly Ile Met His Arg Asp Leu Lys Pro Glu Asn Ile Leu Met Asp
245 250 255

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

Glu Glu Asn Lys Arg Ser Asn Ser Met Cys Gly Thr Thr Glu Tyr Met
275 280 285

Ala Pro Glu Ile Val Arg Gly Lys Gly His Asp Lys Ala Ala Asp Trp
290 295 300

Trp Ser Val Gly Ile Leu Leu Tyr Glu Met Leu Thr Gly Lys Pro Pro
305 310 315 320

Phe Leu Gly Ser Lys Gly Lys Ile Gln Gln Lys Ile Val Lys Asp Lys
325 330 335

Ile Lys Leu Pro Gln Phe Leu Ser Asn Glu Ala His Ala Leu Leu Lys
340 345 350

Gly Leu Leu Gln Lys Glu Pro Glu Arg Arg Leu Gly Ser Gly Pro Ser
355 360 365

Gly Ala Glu Glu Ile Lys Gly His Lys Trp Phe Lys Gly Met Asn Trp
 370 375 380

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

Ser Gly Arg Gln Cys Ile Ala Asn Phe Asp Lys Cys Trp Thr Asp Met
 405 410 415

Ser Val Leu Asp Ser Pro Ala Ser Ser Pro Ser Ser Asp Pro Lys Ala
 420 425 430

Asn Pro Phe Thr Asn Phe Thr Tyr Val Arg Pro Pro His Ser Phe Leu
 435 440 445

Asn Gln Thr Thr Ser Thr Ser
 450 455

<210> 147
 <211> 2019
 <212> DNA
 <213> G. max

<400> 147
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 cagcagcagc atatttagat cccttattgt tgagtgggtg gagaaatggt gtcctctcag 360

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cctgttacgt tagatttgaa taacattgat tccactacca gtgagcctat ggaagaagtg	540
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tcctttgttg aggaatcatt gaaagatgaa gatgggaatc tcatgaagat ccacagagtt	780
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caggtgagga aaaaggttac ttctgaaata tatgctatga aggttatgcg gaaggacaag	900
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caagctaggc gcttaggttg tggacctcgg ggtgttgagg aaattaaaag ccacaagtgg	1560
tttaaaccaa tcaattggag aaagttggaa gcaagagaaa tccaaccaag ctttaggcc	1620

gaagtagctg gtgtgcactg tgttgccaac ttgagaagc gctggactga tatgcctgtt 1680

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gttggtctaa gatgccaaca tgaaacattt tcatgtgcc ttgacttgtg tgaactttgc 1860

aggttgtggg ttcattcact tattatgtgc accttgctgc ggctctctgc aaatgtattg 1920

agctgtcatg tatgcagaaa ataaattact ttatttataa gtggtatctt ctattaggga 1980

caaaaaaaaa caaaaaagag agagagagac cgacacgca 2019

<210> 148

<211> 479

<212> PRT

<213> G. max

<400> 148

Met Val Ser Ser Gln Phe Ser Ala Phe Thr Leu Ala Gly Tyr Lys Pro

1 5 10 15

Ser Gln Thr Gln Leu Leu Phe Pro Ala Lys Leu Val Asp Thr Val Asn

20 25 30

Thr Glu His Ile Glu Leu Asp Phe Ser Asp Val Phe Gly Pro Val Thr

35 40 45

Leu Asp Leu Asn Asn Ile Asp Ser Thr Thr Ser Glu Pro Met Glu Glu

50 55 60

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

65 70 75 80

His Ser Leu Val Gly Pro Ser Thr Cys Val Ser Gln Ser Leu Lys Leu
85 90 95

Gly Lys Leu Thr Ile His Glu Thr Glu Asp Ser Leu Glu Leu Val Glu
100 105 110

His Val Asn Gly Glu Ala Ile Lys Asp Ile Lys Glu Ser Ser Phe Val
115 120 125

Glu Glu Ser Leu Lys Asp Glu Asp Gly Asn Leu Met Lys Ile His Arg
130 135 140

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

Phe Ala Lys Val Tyr Gln Val Arg Lys Lys Gly Thr Ser Glu Ile Tyr
165 170 175

Ala Met Lys Val Met Arg Lys Asp Lys Ile Met Glu Lys Asn His Ala
180 185 190

Glu Tyr Met Lys Ala Glu Arg Asp Ile Trp Thr Lys Ile Glu His Pro
195 200 205

Phe Val Val Gln Leu Arg Tyr Ser Phe Gln Thr Lys Tyr Arg Leu Tyr
210 215 220

Leu Val Leu Asp Phe Val Asn Gly Gly His Leu Phe Phe Gln Leu Tyr
225 230 235 240

His Gln Gly Leu Phe Arg Glu Asp Leu Ala Arg Ile Tyr Thr Ala Glu
245 250 255

Ile Val Ser Ala Val Ser His Leu His Ala Asn Gly Ile Met His Arg
260 265 270

Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Ala Asp Gly His Val Met
275 280 285

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

Asn Ser Met Cys Gly Thr Leu Glu Tyr Met Ala Pro Glu Ile Ile Leu
305 310 315 320

Gly Lys Gly His Asp Lys Ala Ala Asp Trp Trp Ser Val Gly Val Leu
325 330 335

Leu Phe Glu Met Leu Thr Gly Lys Pro Pro Phe Cys Gly Gly Asn Arg
340 345 350

Asp Lys Ile Gln Gln Lys Ile Val Lys Asp Lys Ile Lys Leu Pro Ala
355 360 365

Phe Leu Ser Ser Glu Ala His Ser Leu Leu Lys Gly Leu Leu Gln Lys
370 375 380

Glu Gln Ala Arg Arg Leu Gly Cys Gly Pro Arg Gly Val Glu Glu Ile
385 390 395 400

Lys Ser His Lys Trp Phe Lys Pro Ile Asn Trp Arg Lys Leu Glu Ala
405 410 415

Arg Glu Ile Gln Pro Ser Phe Arg Pro Glu Val Ala Gly Val His Cys
420 425 430

Val Ala Asn Phe Glu Lys Arg Trp Thr Asp Met Pro Val Val Asp Ser
435 440 445

Pro Ala Ala Ser Pro Asn Gly Gly Asn Pro Phe Lys Asp Phe Ser Tyr
450 455 460

Val Arg Pro Ala Ala Ser Phe Leu Gln Arg Asn Asn Pro Ala Tyr
465 470 475

<210> 149
<211> 1684
<212> DNA
<213> Z. mays

<400> 149
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aacctctgtt acagcagcgc gtgcacaggc cccaagctt tttagaggga agatacttct 180
gccagggggc ccccagatg ttgtgccttc tgaaaatgtt gagttcgact tttctgatgt 240
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cgttggacta gatgacttcg aagttctgaa gctcgttggc caaggggcat ttggcaaagt 600

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caagattgtg gagaagaatc atgctgagta catgaaagct gagagagata tacttacaaa	720
ggttgaccat ccttttgtcg tgcagctgag gtactccttt cagacgaagt accgacttta	780
ccttgtcctg gacttcataa atgggggcca tctcttcttc cagctttacc accagggttt	840
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cgtggtctga gatctgcccc ggagttcaaa tatttatctt ttgactccg aatcctatgt	1620
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gatt	1684

<210> 150

<211> 481

<212> PRT

<213> Z. mays

<400> 150

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

Val Val Pro Ser Glu Asn Val Glu Phe Asp Phe Ser Asp Val Phe Gly
35 40 45

Pro Ser Ala Val Gln Thr His Thr Glu Val Ser Ile Leu Thr Pro Asp
50 55 60

Ser Pro Ala Pro Val Ala Glu Ser Asn Asp Glu Val Tyr Asn Asp Pro
65 70 75 80

Asp Val Ile Val Lys Arg Ser His Ser Leu Val Gly Pro Ser Ser Leu
85 90 95

Val Ser Gln Ser Leu Pro Phe Ser Lys Leu Thr Leu His Lys Thr Glu
100 105 110

Ser Pro Leu Glu Leu Ser Glu Cys Pro Ser Lys Gly Lys Gln Ile Asn
115 120 125

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

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

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

Ile Tyr Ala Met Lys Val Met Arg Lys Asp Lys Ile Val Glu Lys Asn
180 185 190

His Ala Glu Tyr Met Lys Ala Glu Arg Asp Ile Leu Thr Lys Val Asp
195 200 205

His Pro Phe Val Val Gln Leu Arg Tyr Ser Phe Gln Thr Lys Tyr Arg
210 215 220

Leu Tyr Leu Val Leu Asp Phe Ile Asn Gly Gly His Leu Phe Phe Gln
225 230 235 240

Leu Tyr His Gln Gly Leu Phe Arg Glu Glu Leu Ala Arg Ile Tyr Ala
245 250 255

Ala Glu Ile Val Ser Ala Val Ala His Leu His Ala Asn Gly Ile Met
260 265 270

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

Ala Met Leu Thr Asp Phe Gly Met Ala Lys Glu Phe Asp Glu Asn Thr
290 295 300

Arg Ser Asn Ser Met Cys Gly Thr Val Glu Tyr Met Ala Pro Glu Ile
305 310 315 320

Phe Gln Gly Arg Gly His Asp Lys Ala Ala Asp Trp Trp Ser Val Gly
325 330 335

Ile Leu Leu Phe Glu Met Leu Thr Gly Lys Pro Pro Phe Val Gly Gly
340 345 350

Asn Arg Cys Lys Ile Gln Gln Lys Ile Val Lys Glu Lys Ile Lys Leu
355 360 365

Pro Thr Tyr Leu Ser Ser Glu Val His Ser Leu Leu Lys Gly Leu Leu
370 375 380

His Lys Glu Ala Gly Arg Arg Leu Gly Ser Gly Pro Gly Gly Ser Asp
385 390 395 400

Glu Ile Gln Lys His Lys Trp Phe Lys Ser Val Asn Trp Lys Arg Leu
405 410 415

Glu Ala Arg Gln Ile Glu Pro Ser Phe Arg Pro Asn Val Ala Gly Lys
420 425 430

Thr Cys Ile Ala Asn Phe Asp Lys Cys Trp Thr Asn Met Ser Val Leu
435 440 445

Asp Ser Pro Val Ala Ser Pro Val Ala Ala Asn Ser Asn Phe Val Gly
450 455 460

Tyr Ser Tyr Val Arg Pro Ala Pro Phe Leu Gln Lys Pro Ser Pro Leu
465 470 475 480

Gly

<210> 151
<211> 1226
<212> DNA
<213> G. max

<400> 151
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ttctcctgcg ccaaggacca caaccctacc gtctggtttg ccgacaacgg cgaacgcttg 180
ggcacttata gcggccacaa cggcgccgtt tggacctgcg acgtctcaag agattcggct 240
cgactcatca cgggaagtgc cgatcagacc gccaaagctat gggacgtgca aagcggcctg 300
caattatata ccttcaactt cgattccccg gccagggtccg tcgattttctc tgcggcgat 360
aagctcgccg ttatcaccac tgacccttc atggagttgc cctcgcgaat ccatgtcaaa 420
cgcatcgcta acgatccatc ccaacagatc ggggaatctg tgctttctcat taagggtcct 480
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gaagatgctg ttattcgtat ttgggattcc gagaccggaa aactgttca agagtccgac 600
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ttccttactg gttcccttga taagtctgcc aggctttggg atactaggtc attgactctt 720
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tttttaatga atttatgcat ttttggttta tgttgatcg acatggtcaa ttttggttg 1200

agtggcactc ttaattaagg agtttt 1226

<210> 152

<211> 326

<212> PRT

<213> G. max

<400> 152

Met Arg Pro Ile Leu Met Lys Gly His Glu Arg Pro Leu Thr Phe Leu

1 5 10 15

Lys Tyr Asn Arg Asp Gly Asp Leu Leu Phe Ser Cys Ala Lys Asp His

20 25 30

Asn Pro Thr Val Trp Phe Ala Asp Asn Gly Glu Arg Leu Gly Thr Tyr

35 40 45

Arg Gly His Asn Gly Ala Val Trp Thr Cys Asp Val Ser Arg Asp Ser

50 55 60

Ala Arg Leu Ile Thr Gly Ser Ala Asp Gln Thr Ala Lys Leu Trp Asp

65 70 75 80

Val Gln Ser Gly Leu Gln Leu Tyr Thr Phe Asn Phe Asp Ser Pro Ala

85 90 95

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

100 105 110

Asp Pro Phe Met Glu Leu Pro Ser Ala Ile His Val Lys Arg Ile Ala
115 120 125

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

Pro Gln Gly Arg Ile Asn Arg Ala Ile Trp Gly Pro Leu Asn Thr Thr
145 150 155 160

Ile Ile Ser Ala Gly Glu Asp Ala Val Ile Arg Ile Trp Asp Ser Glu
165 170 175

Thr Gly Lys Leu Leu Gln Glu Ser Asp Lys Glu Ser Gly His Lys Lys
180 185 190

Thr Val Thr Ser Leu Ala Lys Ser Ala Asp Asp Ser His Phe Leu Thr
195 200 205

Gly Ser Leu Asp Lys Ser Ala Arg Leu Trp Asp Thr Arg Ser Leu Thr
210 215 220

Leu Ile Lys Thr Tyr Val Thr Glu Arg Pro Val Asn Ala Val Thr Met
225 230 235 240

Ser Pro Leu Leu Asp His Val Val Ile Gly Gly Gly Gln Asp Ala Ser
245 250 255

Ala Val Thr Thr Thr Asp His Arg Ala Gly Lys Phe Glu Ala Lys Phe
260 265 270

Phe Asp Lys Ile Leu Gln Glu Glu Ile Gly Gly Val Lys Gly His Phe
275 280 285

Gly Pro Ile Asn Ala Leu Ala Phe Asn Pro Asp Gly Lys Ser Phe Ser
290 295 300

Ser Gly Gly Glu Asp Gly Tyr Val Arg Leu His His Phe Asp Pro Asp
305 310 315 320

Tyr Phe Asn Ile Lys Ile
325

<210> 153

<211> 1271

<212> DNA

<213> Z. mays

<400> 153

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ccgctgacgt tcttgcgcta caaccgcgac ggggacctcc tgttctcctg cgctaaggac 180

cacaccccca cggctctggtta cgccgacaac ggcgatcgcc tcggcaccta ccgcggccac 240

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accgacaact tcatggacca cgttcccacc gttcaggtca agcgcacgcg cgaggacatc 480

gacgaccaga cggaggagtc tgcactcgtc atcacgggca tcaagggaag gatcaacagg 540

gccgtttggg gcccgctgaa caggaccatt atcactgccg gggaggatgc caccattcgc 600

atctgggact cagagactgg acagctgctg aaagagtctg ataaagaatc tggacatcag	660
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gataaatctg caaagctatg ggatacaaga acgctaaccg tgatcaagac gtatgtcaca	780
gagagacctg ttaatgctgt tgacatctct cccactcatg atactgtggt tctaggaggt	840
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tcactggtct gttgcaacaa atggcaacgc tgaagtatcc taagaaatcc atttcttgcg	1260
aaaaaaaaa a	1271

<210> 154
 <211> 326
 <212> PRT
 <213> Z. mays

<400> 154

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

Thr	Pro	Thr	Val	Trp	Tyr	Ala	Asp	Asn	Gly	Asp	Arg	Leu	Gly	Thr	Tyr
		35						40				45			

Arg Gly His Asn Gly Ala Val Trp Thr Cys Asp Val Ser Arg Asp Ser
50 55 60

Ala Arg Leu Ile Thr Gly Ser Ala Asp Gln Thr Ala Lys Leu Trp Glu
65 70 75 80

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

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

Asp Asn Phe Met Asp His Val Pro Thr Val Gln Val Lys Arg Ile Ala
115 120 125

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

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

Ile Ile Thr Ala Gly Glu Asp Ala Thr Ile Arg Ile Trp Asp Ser Glu
165 170 175

Thr Gly Gln Leu Leu Lys Glu Ser Asp Lys Glu Ser Gly His Gln Lys
180 185 190

Thr Ile Ser Ser Leu Ser Lys Ser Leu Asp Trp Ser His Phe Ile Thr
195 200 205

Gly Ser Leu Asp Lys Ser Ala Lys Leu Trp Asp Thr Arg Thr Leu Thr
 210 215 220

Leu Ile Lys Thr Tyr Val Thr Glu Arg Pro Val Asn Ala Val Asp Ile
 225 230 235 240

Ser Pro Thr His Asp Thr Val Val Leu Gly Gly Gly Gln Asp Ala Met
 245 250 255

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

Tyr His Lys Ile Leu Gln Glu Glu Ile Gly Gly Val Lys Gly His Phe
 275 280 285

Gly Pro Ile Asn Ala Leu Ala Phe Asn Pro Asp Gly Arg Ser Phe Ser
 290 295 300

Ser Gly Gly Glu Asp Gly Tyr Val Arg Leu His His Phe Asp Ser Asp
 305 310 315 320

Tyr Phe Ser Ile Lys Met
 325

<210> 155
 <211> 1241
 <212> DNA
 <213> G. max

<400> 155
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gccgacaatg gcgaacgctt gggcacttat cgcgggccaca acggcgccgt ttggacctgc	180
gacgtctcaa gagattcggg tegtctgatc acgggtagtg ccgatcagac cgccaagcta	240
tgggacgtgc aaagcgggtct gcaattgtac accttcaatt tcgattcccc tgccaggtcc	300
gtcgatttct ccgtcgggtga taggctggcc gttatcacca ccgacccctt catggagtta	360
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aagtctgccg atgattcaca tttccttact ggttcccttg ataagtctgc taggctttgg	660
gatactaggt cattgactct tatcaagacc tatgtcacgg aacgccctgt caatgcagtt	720
acgatgtcac ctcttcttga tcatgtggtt attggagggtg gtcaggatgc gtcagctgtt	780
acaactactg atcatcgtgc tggcaaattt gaagccaaat tctttgacaa gattcttcaa	840
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gatggaaaaa gtttttcaag tggaggtgaa gatgggttatg tacggttgca ccacttcgac	960
ccagattatt tcaacatcaa aatatagtgc ctgatggttt gtggttaaaa ttaggtgggt	1020
cctagaagtt agcatttaat tattctcaac caacatttaa ttatatattg gtaatatgga	1080
agagtttttt ttttaaataa aattatgcat ttttggctta tgttgtatta acattattat	1140
catttttggt tggagtggca ctcttaatta aggagttttt ctccccacgt cacaagattt	1200
tgacaatatt agaagtatgg catatattag gcgtaaaaaa a	1241

<210> 156

<211> 326

<212> PRT

<213> G. max

<400> 156

Met Arg Pro Ile Leu Met Lys Gly His Glu Arg Pro Leu Thr Phe Leu
1 5 10 15

Lys Tyr Asn Arg Asp Gly Asp Leu Leu Phe Ser Cys Ala Lys Asp His
20 25 30

Asn Pro Thr Val Trp Phe Ala Asp Asn Gly Glu Arg Leu Gly Thr Tyr
35 40 45

Arg Gly His Asn Gly Ala Val Trp Thr Cys Asp Val Ser Arg Asp Ser
50 55 60

Val Arg Leu Ile Thr Gly Ser Ala Asp Gln Thr Ala Lys Leu Trp Asp
65 70 75 80

Val Gln Ser Gly Leu Gln Leu Tyr Thr Phe Asn Phe Asp Ser Pro Ala
85 90 95

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

Asp Pro Phe Met Glu Leu Ser Ser Ala Ile His Val Lys Arg Ile Ala
115 120 125

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

Pro Leu Gly Arg Ile Asn Arg Ala Ile Trp Gly Pro Leu Asn Ser Thr
145 150 155 160

Ile Ile Ser Ala Gly Glu Asp Ala Val Ile Arg Ile Trp Asp Ser Glu
165 170 175

Thr Gly Lys Leu Leu Lys Glu Ser Asp Lys Glu Ser Gly His Lys Lys
180 185 190

Thr Val Thr Ser Leu Ala Lys Ser Ala Asp Asp Ser His Phe Leu Thr
195 200 205

Gly Ser Leu Asp Lys Ser Ala Arg Leu Trp Asp Thr Arg Ser Leu Thr
210 215 220

Leu Ile Lys Thr Tyr Val Thr Glu Arg Pro Val Asn Ala Val Thr Met
225 230 235 240

Ser Pro Leu Leu Asp His Val Val Ile Gly Gly Gly Gln Asp Ala Ser
245 250 255

Ala Val Thr Thr Thr Asp His Arg Ala Gly Lys Phe Glu Ala Lys Phe
260 265 270

Phe Asp Lys Ile Leu Gln Glu Glu Ile Gly Gly Val Lys Gly His Phe
275 280 285

Gly Pro Ile Asn Ala Leu Ala Phe Asn Pro Asp Gly Lys Ser Phe Ser
290 295 300

Ser Gly Gly Glu Asp Gly Tyr Val Arg Leu His His Phe Asp Pro Asp
305 310 315 320

Tyr Phe Asn Ile Lys Ile

325

<210> 157

<211> 1044

<212> DNA

<213> A. thaliana

<400> 157

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tcgcgttcca agtttagggg tccttgctga actgttttct ctctgctct taccaagatt	120
tcccctttaa ctgcttcttc accttctaag tccgccaagc ataaatggaa gattttgtgt	180
tttagaaatg aagattctgc tcccgagaat ccggagcatt ttgtgcctga ggaattagtt	240
aagccagatc aagattctcc atgtacagat aaaacagatt ggaaggcaac ttttcaaag	300
gctgcagatg cagttttgaa ggccattggg actcgttgga aggtaccatg gaactgtcag	360
accattgtgc aggtaatgct tctgtgggta gccgctttct ggttcattgg ttcattgatg	420
atcccattca tggctcatat atcaggtttc cacaagaat ccctaacatt tagaggccaa	480
gctttgttca gtctgataac cgatgtaaca gaaggcctag ccgggattgc tatcctccac	540
cgttgcctct ccatgttccg tccacttgca agtgattggg tccgctttac ccttaaagga	600
aactggcaac tagatgttat cataggctgt ttcattgtcc ctttcgttaa ccggctctcc	660
caattaaacc taaacctctt gccactcca ccaacctcaa gtccagtctc actctcaagt	720
gtcgagcagt ctataatggc tagagaccct gtggcaatgg cactgtatgc agttgtagta	780
tcaatttgtg caccggtttg ggaagagata gtgttcagag gggtcttggt accgtctcta	840
actaggtaca tgccagtttg gtgtgcgatt cttgtgagtt cgattgcatt tgctttggca	900
catttcaatg tgcagaggat gttaccattg gtgttccttg gagtggtatt gggtttgata	960

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gtattcatgg aattgatgcg atga 1044

<210> 158

<211> 347

<212> PRT

<213> A. thaliana

<400> 158

Met Leu Thr Ser Ser Cys Ser Ser Ser Ser Leu Leu Cys His Arg Pro
1 5 10 15

Ala Leu Ser Ser Ser Arg Ser Lys Phe Arg Val Pro Cys Arg Thr Val
20 25 30

Phe Ser Pro Ala Leu Thr Lys Ile Ser Pro Leu Thr Ala Ser Ser Pro
35 40 45

Ser Lys Ser Ala Lys His Lys Trp Lys Ile Leu Cys Phe Arg Asn Glu
50 55 60

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

Lys Pro Asp Gln Asp Ser Pro Cys Thr Asp Lys Thr Asp Trp Lys Ala
85 90 95

Thr Phe Gln Lys Ala Ala Asp Ala Val Leu Lys Ala Ile Gly Thr Arg
100 105 110

Trp Lys Val Pro Trp Thr Val Glu Thr Ile Val Gln Val Met Leu Leu
115 120 125

Trp Val Ala Ala Phe Trp Phe Ile Gly Ser Trp Met Ile Pro Phe Met
130 135 140

Ala His Ile Ser Gly Phe His Lys Glu Ser Leu Thr Phe Arg Gly Gln
145 150 155 160

Ala Leu Phe Ser Leu Ile Thr Asp Val Thr Glu Gly Leu Ala Gly Ile
165 170 175

Ala Ile Leu His Arg Cys Leu Ser Met Phe Arg Pro Leu Ala Ser Asp
180 185 190

Trp Phe Arg Phe Thr Leu Lys Gly Asn Trp Gln Leu Asp Val Ile Ile
195 200 205

Gly Cys Phe Met Phe Pro Phe Val Asn Arg Leu Ser Gln Leu Asn Leu
210 215 220

Asn Leu Leu Pro Leu Pro Pro Thr Ser Ser Pro Val Ser Leu Ser Ser
225 230 235 240

Val Glu Gln Ser Ile Met Ala Arg Asp Pro Val Ala Met Ala Leu Tyr
245 250 255

Ala Val Val Val Ser Ile Cys Ala Pro Val Trp Glu Glu Ile Val Phe
260 265 270

Arg Gly Phe Leu Leu Pro Ser Leu Thr Arg Tyr Met Pro Val Trp Cys
275 280 285

Ala Ile Leu Val Ser Ser Ile Ala Phe Ala Leu Ala His Phe Asn Val
 290 295 300

Gln Arg Met Leu Pro Leu Val Phe Leu Gly Val Val Leu Gly Leu Ile
 305 310 315 320

Phe Ala Arg Ser Arg Asn Leu Leu Pro Ser Met Leu Leu His Ser Leu
 325 330 335

Trp Asn Gly Phe Val Phe Met Glu Leu Met Arg
 340 345

<210> 159
 <211> 1224
 <212> DNA
 <213> B. napus

<400> 159
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 atttgcaagc cgccggttat ctacggttta ccgtagaaaa tggagatcag cgtgcatttc 180
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 ttgtggttta agttttgttt tgacaggggt aactgagatg gtagccttac catatctagg 360
 gatcgacgtt cagaagctga gcttgacga caaggcggag atcttattcc tggatcaagg 420
 ttttaacaact ctagcagtac ttgctgttat attcaccgtt gctaaaacat tcgagccgct 480
 tcctgaagac attttgcgct atgatttgaa acagcccttt aacttgcaaa aaggatggct 540
 ggtgtggagt gggataggtc tggttgagc tggtggggct attgcgttaa caggtgttgc 600

tttatccttg tttaggacag agacaccaga aagagaggtg gactctttga tgaagcttct	660
cccatthaatc ggatcctcaa acataagcac gttaagctta gtggggataa ctggagtcct	720
tgctccactt cttgaggaga cgggtgtttcg cggattcttc atggtctctc ttaccaaagt	780
ggtgccgact ccaatagcga tcatcatcag ctgagctgcg tttgcacttg cgcacctcac	840
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aaccgcgaat ctattaccc cgatgggtcat acacggtttc tggaactcgg gagttgtctt	960
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ctagctttgc tcttcctttc tgtccgcagt taacatgtaa aagcttcttg tacgatgctg	1080
gatcttagta aattttgttt gtattcgacc aaagaattca aaacttgatg caagagtttg	1140
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aaaaaaaaa gagaccgaca cgca	1224

<210> 160
 <211> 337
 <212> PRT
 <213> B. napus

<400> 160

Met	Ile	Ser	Cys	Leu	Ser	Lys	Ser	Ser	Ser	Leu	Phe	Cys	Ile	Ser	Gly
1				5					10					15	

Ser	Arg	Ser	Leu	Ile	Pro	Pro	Lys	Thr	Tyr	Asn	Arg	Gly	Gly	Leu	Cys
			20					25					30		

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

Arg Lys Trp Arg Ser Ala Cys Ile Ser Asn Ser Gly Lys Glu Thr Glu
50 55 60

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

Arg Trp Glu Val Pro Trp Glu Trp Gln Thr Val Ser Leu Thr Ser Leu
85 90 95

Ala Cys Gly Leu Ser Phe Val Leu Thr Gly Leu Thr Glu Met Val Ala
100 105 110

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

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

Ala Val Ile Phe Thr Val Ala Lys Thr Phe Glu Pro Leu Pro Glu Asp
145 150 155 160

Ile Leu Arg Tyr Asp Leu Lys Gln Pro Phe Asn Leu Gln Lys Gly Trp
165 170 175

Leu Val Trp Ser Gly Ile Gly Leu Val Gly Ala Val Gly Ala Ile Ala
180 185 190

Leu Thr Gly Val Ala Leu Ser Leu Phe Arg Thr Glu Thr Pro Glu Arg
195 200 205

Glu Val Asp Ser Leu Met Lys Leu Leu Pro Leu Ile Gly Ser Ser Asn
210 215 220

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

Leu Glu Glu Thr Val Phe Arg Gly Phe Phe Met Val Ser Leu Thr Lys
245 250 255

Trp Val Pro Thr Pro Ile Ala Ile Ile Ile Ser Ser Ala Ala Phe Ala
260 265 270

Leu Ala His Leu Thr Pro Gly Glu Phe Pro Gln Leu Phe Ile Leu Gly
275 280 285

Ser Val Leu Gly Leu Ser Tyr Ala Gln Thr Arg Asn Leu Ile Thr Pro
290 295 300

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

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

Asn

<210> 161

<211> 1564

<212> DNA

<213> Z. mays

<400> 161

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cgctcgtgc ctcgccatc ccgctccaag gttccgggtt cggctcctgc ctctcccctc	180
ctccgtcgcc gcgaggccgt tgcttggctt caggcctcgg tgtggggctc cagcgaaggg	240
atgggcattg tggcacgtct catgcttcag aaatggtcag gatgggcca caacatctga	300
cgaaggtgat gacttcaagt atgttgccca atcacagagc tctggtggtg cagaggtgaa	360
aaaggaagtg gtgagtagct taaacgggga gcaggagcag aatttgaagg acgacgattg	420
gttcctgcaa ctgcagaaga taaaagaaaa ttactaggc aggatagtaa aatttcagac	480
agaacgctgg atagtacctt ggactggaca aaccattgct caggtgatga ttttatggat	540
tgccacattt tggtttgtgg gttcctggat agtgccattg ttggctcatg ctgctgggtt	600
tagcaaggaa acattgacgc acagaggcca ggcactatac agtctcttga cagacataac	660
agagggcctt gccgggatcg caatccttca ccaatgcctt ggtagattcc ggcccccttc	720
tccaggggtg ttcgagttca atctgaaggg caaatggcac ttggacgtag catttgggtg	780
cctgctattc ccactagtta atctactctc acacataaac atcagcctag ttccagcgtc	840
accaggtcca gctgtcgggg tttccagcgt agaacagtcc atcgtggccc gggatccagt	900
ggcaatggct ttgtatgctg tggtagtcac ggtatgcgcg cctatatggg aagaaatcgt	960
gttccgagga ttcttctcc cgtctctaac acggtacatg ccactcccat ggtcgatcct	1020
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gtttcttgga gtggtgatgg gaggagtctt tgcaaggctc cgcaacctgc tggcgctgat	1140
ggtgctgcac agcttgtgga atggatttgt gttcttggat ttgatgaagt gagcagctga	1200
gctggagtta ttgtttcggg tccaaccttg gacatatctg cttgagcctc gtctgaaaat	1260
gttttgaca agattggttc tattcttttt tcaggattaa aagcaaggca tctaattgcag	1320

cggcggaaca gaaggaatcg tgtaagtctg aagcgaagag ataacaattt gtgcaggaaa	1380
atagaccaca gaacagaaga aatgtttatt tttttgagaa ttttatgtag aatgatcagt	1440
cgctgcagtc ttaggacctg tgcccagctt ccataagcat ctgccacatt tttgtaaatt	1500
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aaaa	1564

<210> 162
 <211> 359
 <212> PRT
 <213> Z. mays

<400> 162

Met	Ser	Ser	Ala	Ser	Cys	Leu	Val	His	Pro	Ala	Pro	Arg	Phe	Arg	Val
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Arg	Leu	Leu	Pro	Leu	Pro	Ser	Ser	Val	Ala	Ala	Arg	Pro	Leu	Leu	Gly
			20					25					30		

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

Val	Ser	Cys	Phe	Arg	Asn	Gly	Gln	Asp	Gly	Pro	Thr	Thr	Ser	Asp	Glu
	50					55					60				

Gly	Asp	Asp	Phe	Lys	Tyr	Val	Ala	Gln	Ser	Gln	Ser	Ser	Gly	Gly	Ala
65					70					75					80

Glu	Val	Lys	Lys	Glu	Val	Val	Ser	Ser	Leu	Asn	Gly	Glu	Gln	Glu	Gln
				85						90				95	

Asn Leu Lys Asp Asp Asp Trp Phe Leu Gln Leu Gln Lys Ile Lys Glu
100 105 110

Asn Leu Leu Gly Arg Ile Val Lys Phe Gln Thr Glu Arg Trp Ile Val
115 120 125

Pro Trp Thr Gly Gln Thr Ile Ala Gln Val Met Ile Leu Trp Ile Ala
130 135 140

Thr Phe Trp Phe Val Gly Ser Trp Ile Val Pro Leu Leu Ala His Ala
145 150 155 160

Ala Gly Phe Ser Lys Glu Thr Leu Thr His Arg Gly Gln Ala Leu Tyr
165 170 175

Ser Leu Leu Thr Asp Ile Thr Glu Gly Leu Ala Gly Ile Ala Ile Leu
180 185 190

His Gln Cys Leu Gly Arg Phe Arg Pro Leu Pro Pro Gly Trp Phe Glu
195 200 205

Phe Asn Leu Lys Gly Lys Trp His Leu Asp Val Ala Phe Gly Cys Leu
210 215 220

Leu Phe Pro Leu Val Asn Leu Leu Ser His Ile Asn Ile Ser Leu Val
225 230 235 240

Pro Ala Ser Pro Gly Pro Ala Val Gly Val Ser Ser Val Glu Gln Ser
245 250 255

Ile Val Ala Arg Asp Pro Val Ala Met Ala Leu Tyr Ala Val Val Val
260 265 270

Thr Val Cys Ala Pro Ile Trp Glu Glu Ile Val Phe Arg Gly Phe Leu
 275 280 285

Leu Pro Ser Leu Thr Arg Tyr Met Pro Leu Pro Trp Ser Ile Leu Ala
 290 295 300

Ser Ala Ala Ala Phe Ala Leu Ala His Phe Asn Ala Gln Arg Val Met
 305 310 315 320

Pro Leu Val Phe Leu Gly Val Val Met Gly Gly Val Phe Ala Arg Ser
 325 330 335

Arg Asn Leu Leu Ala Ser Met Val Leu His Ser Leu Trp Asn Gly Phe
 340 345 350

Val Phe Leu Asp Leu Met Lys
 355

<210> 163
 <211> 1480
 <212> DNA
 <213> B. napus

<400> 163
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 taaacacatc gcttcgaatc ttcgagagct ttgtcagaga tgagttccga cgatgagaga 180
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gtcgatatct gcgagaaagg agacgccttt atcaaagagc aaacagggag catgtacaag	360
aatgcaaaga agaagattga cagaggcgtc gcttttccca cgtgcgtttc tgtgaacaac	420
gtcgttggtc atttctcacc tcttgctggt gatgagtcag tgttggaaga gggtgacatg	480
gtcaaaattg atatgggatg tcatattgat gggttcattg ctcttgttgg ccacacgcat	540
gttcttcaag aaggaccctg tactggacgc aaagctgatg ttattgctgc tgogaatacc	600
gccgctgaag ttgctttgag actcgtagct cctgggaaga agaaccatgc tgtcactgaa	660
gctattcaga aggtgtctga agcgtacgac tgcaaaattg tggaaggggt tatttccac	720
cagatgaaac agaacgtgat agatggaagc aagagtttcc taagtgtatc cactccagaa	780
acgaggggtg atgatgctga gtttgaagag aatgaagtct atgcaatcga tattgtggca	840
agcactggtg atggcaagcc taagctatta gacgagaagc aaacaactat ttaccggaaa	900
gatgagagta ttactatca gttgaagatg aaggcctcca gatccttaat aagogaagtt	960
aaagagaact tccccacat gccattcact tcaaggctgc tggaggagaa aagggcacgt	1020
cttggaacttg tggagtgtgt gaaccatggt catttgcaac catatcctgt tctttacgag	1080
aagcctggtg attttgttgc ccagattaaa ttcacagttt tgctgatgcc aaatggatcg	1140
gataagatca cttcacatac acttcaggag ctgcaaccta cgaagaccat tgatgaccct	1200
gagatcaaag gatggttagc cttgggtatc aaaaagaaga aggggtggtgg aaagaagaag	1260
aaagccaaga atgcaggaga ggctcaacg gaggctgagc caatggaagc aagtagcaat	1320
gctgaagcat gagatctttc tttttttttt tttttctctt aaagaatttt tgaaacttca	1380
gttcttatgt atgttttgag ttttaagagtt tcttagataa aaagaacaga aaagaagtac	1440
ttatcaaaat gtctcctttt ccaaaaaaaaa aaaaaaaaaa	1480

<211> 390
<212> PRT
<213> B. napus

<400> 164

Met Ser Ser Asp Asp Glu Arg Asp Glu Lys Glu Leu Asp Leu Thr Ser
1 5 10 15

Pro Glu Val Val Thr Lys Tyr Lys Ser Ala Ala Glu Ile Val Asn Lys
20 25 30

Ala Leu Gln Val Val Leu Ala Glu Cys Lys Pro Gly Ala Lys Ile Val
35 40 45

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

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

Thr Cys Val Ser Val Asn Asn Val Val Gly His Phe Ser Pro Leu Ala
85 90 95

Gly Asp Glu Ser Val Leu Glu Glu Gly Asp Met Val Lys Ile Asp Met
100 105 110

Gly Cys His Ile Asp Gly Phe Ile Ala Leu Val Gly His Thr His Val
115 120 125

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

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

Lys Asn His Ala Val Thr Glu Ala Ile Gln Lys Val Ser Glu Ala Tyr
165 170 175

Asp Cys Lys Ile Val Glu Gly Val Ile Ser His Gln Met Lys Gln Asn
180 185 190

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

Arg Val Asp Asp Ala Glu Phe Glu Glu Asn Glu Val Tyr Ala Ile Asp
210 215 220

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

Gln Thr Thr Ile Tyr Arg Lys Asp Glu Ser Ile His Tyr Gln Leu Lys
245 250 255

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

His Met Pro Phe Thr Ser Arg Ser Leu Glu Glu Lys Arg Ala Arg Leu
275 280 285

Gly Leu Val Glu Cys Val Asn His Gly His Leu Gln Pro Tyr Pro Val
290 295 300

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

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

Glu Leu Gln Pro Thr Lys Thr Ile Asp Asp Pro Glu Ile Lys Gly Trp
340 345 350

Leu Ala Leu Gly Ile Lys Lys Lys Lys Gly Gly Gly Lys Lys Lys Lys
355 360 365

Ala Lys Asn Ala Gly Glu Ala Ser Thr Glu Ala Glu Pro Met Glu Ala
370 375 380

Ser Ser Asn Ala Glu Ala
385 390

<210> 165
<211> 1413
<212> DNA
<213> G. max

<400> 165
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agatgggttc attgctgctg tggcacacac tcatgttctt caggaggggc cagttacagg	480
acgggcagcc gatgctcttg cagcagcaaa caccgctgcc gaagtggcct tgcggcttgt	540
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tgattgtaaa attggtgagg gtgttcttag ccaccaaattg aaacagtttg tgattgatgg	660
gaataagggtt gtgctaagtg tatccaatcc agatacaagg gttgatgatg cagagtttga	720
ggagaatgaa gtttatgcaa ttgatatcgt agcaagtact ggagatggca agcctaagct	780
tttgatgaa aagcagacaa ctatttataa gagagctgtt gacaagagct atcacttgaa	840
gatgaaagca tctaggttca ttttcagtga aataagccaa aagtttccca tcatgccctt	900
ctctgcaagg gctttggaag agaaaagagc tcgtttgggt ttagtggaat gtgtgaatca	960
tgagctcctg caaccttatc ctgttctgca tgaaaagcct ggtgattatg ttgcacatat	1020
caaattcact gtcttgctaa tgcccaatgg atcagatcgt gttacgtctc actcaactcca	1080
ggagttgcag cccaccaaaa caatagatga tcccgaaatc aaggcgtggc tagcattggg	1140
cacaaagaca aagaagaaag gcggtggaaa gaagaagaaa ggtaagaagg gggcagaagc	1200
tgaaccaatg gatgcaacaa atgatgctac accccaagaa caagattgag agacaaaaac	1260
cctttgattt tgcttttgat ccctttcaat tttggtacat ttttcaccaa gttgtatctg	1320
cttgattgtg aatttagtac agctttcgga catccaatgt taataggaat ttgatttcoct	1380
tggctattgt acttgacctg aatgctgtac tcc	1413

<210> 166

<211> 390

<212> PRT

<213> G. max

<400> 166

Met Ser Asp Asp Glu Arg Glu Lys Lys Glu Leu Asp Leu Thr Ser Pro
1 5 10 15

Glu Val Val Thr Lys Tyr Lys Ser Ala Ala Glu Ile Val Asn Lys Ala
20 25 30

Leu Gln Leu Val Ile Ser Glu Cys Lys Pro Lys Thr Lys Ile Val Asp
35 40 45

Leu Cys Glu Lys Gly Asp Ser Tyr Ile Arg Glu Gln Thr Gly Asn Met
50 55 60

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

Cys Val Ser Val Asn Asn Thr Val Cys His Phe Ser Pro Leu Ala Ser
85 90 95

Asp Glu Thr Val Leu Glu Asp Gly Asp Ile Val Lys Ile Asp Met Ala
100 105 110

Cys His Ile Asp Gly Phe Ile Ala Ala Val Ala His Thr His Val Leu
115 120 125

Gln Glu Gly Pro Val Thr Gly Arg Ala Ala Asp Ala Leu Ala Ala Ala
130 135 140

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

Asn Lys Asp Val Thr Glu Ala Ile Gln Lys Ile Ala Ala Ala Tyr Asp
165 170 175

Cys Lys Ile Val Glu Gly Val Leu Ser His Gln Met Lys Gln Phe Val
180 185 190

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

Val Asp Asp Ala Glu Phe Glu Glu Asn Glu Val Tyr Ala Ile Asp Ile
210 215 220

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

Thr Thr Ile Tyr Lys Arg Ala Val Asp Lys Ser Tyr His Leu Lys Met
245 250 255

Lys Ala Ser Arg Phe Ile Phe Ser Glu Ile Ser Gln Lys Phe Pro Ile
260 265 270

Met Pro Phe Ser Ala Arg Ala Leu Glu Glu Lys Arg Ala Arg Leu Gly
275 280 285

Leu Val Glu Cys Val Asn His Glu Leu Leu Gln Pro Tyr Pro Val Leu
290 295 300

His Glu Lys Pro Gly Asp Tyr Val Ala His Ile Lys Phe Thr Val Leu
305 310 315 320

Leu Met Pro Asn Gly Ser Asp Arg Val Thr Ser His Ser Leu Gln Glu
325 330 335

Leu Gln Pro Thr Lys Thr Ile Asp Asp Pro Glu Ile Lys Ala Trp Leu
340 345 350

Ala Leu Gly Thr Lys Thr Lys Lys Lys Gly Gly Gly Lys Lys Lys Lys
355 360 365

Gly Lys Lys Gly Ala Glu Ala Glu Pro Met Asp Ala Thr Asn Asp Ala
370 375 380

Thr Pro Gln Glu Gln Asp
385 390

<210> 167
<211> 1517
<212> DNA
<213> G. max

<400> 167
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acttctcac aaggttacaa ggactaaaga gttgtgccac catgtcggac gatgaaaggg 180
aggagaaaga gttgatctc tcttctgccg aagttgtcac caaatacaaa accgctgctg 240
agatcgtaa caaggccttg aagctagtta tttcagaatg taaaccaaag gcgaagattg 300
tgatatttg tgagaaagg gattcataca ttcgagagca aactggaaat gtgtacaaga 360
atgtgaagag gaagattgag agaggtgttg ctttcccaac atgtttatca atcaacaacg 420
ttgtctgcca tttctctcca ctagccagtg atgaggccgt gttggaagaa ggtgatatat 480
tgaaaattga tatggcatgc catatagatg ggttcattgc tgtggtagct cacacccatg 540
ttcttcagga aggtcctgtt acaggaaggg cagctgatgt cattgctgct gctaatactg 600

ctgctgaggt ggccttgagg cttgtcaggc cgggaaagaa gaacaaggat gtaagtgatg	660
caattcaaaa ggttgctgct gcctatgact gtaaaattgt tgaggggtgtt cttagccacc	720
aaatgaagca gtttggttatt gatgggaata aagttgtgct tagtttgtct aatccagaca	780
caagggttga cgaagcagag tttgaggaga acgaagttta tgcaattgat atagtaacaa	840
gcactgggga tggcaagcct aagctggttg atgagaagca gacaactatt tataagaggg	900
ctgttgacaa gagttatcac ttgaagatga aagcgtctag gttcattttc agtgaaataa	960
gccaaaaatt tccaatcatg ccattctctg ctagggcttt ggaagagaaa agagctcgac	1020
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agcctggtga tttggttgcg cacatcaaat tcacagtctt gttgatgcca aatggatcgg	1140
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atattaaggc ctggctagcc ttgggcacaa agacaaagaa gaaagggtggg gggaagaaga	1260
aaaaaggtaa gaaaggggac aaggcagatg agacaactga agctgaggct atggactcaa	1320
caaacggggc cactcctcaa gagtgactta actacccttc cctctcctct cctctcctct	1380
cccaaacaa tgaaagaagc tttttcgttt ctttttcgac acctcttttc aattttggta	1440
cattgttcac caaattgtat tttgcttgct tggatgtcaa ttttagtata gtgttccgac	1500
attaaaaaaaa aaaaaaa	1517

<210> 168

<211> 394

<212> PRT

<213> G. max

<400> 168

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

1

5

10

15

Glu Val Val Thr Lys Tyr Lys Thr Ala Ala Glu Ile Val Asn Lys Ala
20 25 30

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

Ile Cys Glu Lys Gly Asp Ser Tyr Ile Arg Glu Gln Thr Gly Asn Val
50 55 60

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

Cys Leu Ser Ile Asn Asn Val Val Cys His Phe Ser Pro Leu Ala Ser
85 90 95

Asp Glu Ala Val Leu Glu Glu Gly Asp Ile Leu Lys Ile Asp Met Ala
100 105 110

Cys His Ile Asp Gly Phe Ile Ala Val Val Ala His Thr His Val Leu
115 120 125

Gln Glu Gly Pro Val Thr Gly Arg Ala Ala Asp Val Ile Ala Ala Ala
130 135 140

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

Asn Lys Asp Val Ser Asp Ala Ile Gln Lys Val Ala Ala Ala Tyr Asp
165 170 175

Cys Lys Ile Val Glu Gly Val Leu Ser His Gln Met Lys Gln Phe Val
180 185 190

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

Val Asp Glu Ala Glu Phe Glu Glu Asn Glu Val Tyr Ala Ile Asp Ile
210 215 220

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

Thr Thr Ile Tyr Lys Arg Ala Val Asp Lys Ser Tyr His Leu Lys Met
245 250 255

Lys Ala Ser Arg Phe Ile Phe Ser Glu Ile Ser Gln Lys Phe Pro Ile
260 265 270

Met Pro Phe Ser Ala Arg Ala Leu Glu Glu Lys Arg Ala Arg Leu Gly
275 280 285

Leu Val Glu Cys Val Asn His Glu Leu Leu Gln Pro Tyr Pro Val Leu
290 295 300

His Glu Lys Pro Gly Asp Leu Val Ala His Ile Lys Phe Thr Val Leu
305 310 315 320

Leu Met Pro Asn Gly Ser Asp Arg Ile Thr Thr His Pro Leu Gln Glu
325 330 335

Leu Gln Pro Thr Lys Thr Ile Asp Asp Pro Asp Ile Lys Ala Trp Leu
340 345 350

Ala Leu Gly Thr Lys Thr Lys Lys Lys Gly Gly Gly Lys Lys Lys Lys
 355 360 365

Gly Lys Lys Gly Asp Lys Ala Asp Glu Thr Thr Glu Ala Glu Ala Met
 370 375 380

Asp Ser Thr Asn Gly Ala Thr Pro Gln Glu
 385 390

<210> 169
 <211> 1366
 <212> DNA
 <213> Z. mays

<400> 169
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 gagctcgacc tctcctccaa cgatgtcgtc accaagtaca agactgccgc cgaaatcctg 180
 aacaacgctc tgaagctggt tgtgtctgag tgcaagccaa aagcaaagat tgttgacctt 240
 tgtgagaagg gtgactcttt cataagagag caaactggga atgtctacaa gaatgcaaag 300
 aggaagattg aaaggggcat tgctttccca acctgtgttt ctgtgaacaa cacagtctgc 360
 cacttctccc cgcttaccac agatgatgca gttctggaag aaaatgatat gggttaaatt 420
 gacatggggg gtcattattga tggctttatt gctgtgggtg cacatacaca tgtaattgca 480
 aatgggcctg tcacaggaag agcagctgat gttcttgctg ctgccaacac agcagcagaa 540
 gttgcaatga ggcttgctcag acctgggaag aagaataagg atgttactga agcaattcag 600
 aaagttgctg ctgtttatga ttgcaaaatt gtggaagggtg ttcttagcca tcaactgaag 660

caatttgtga ttgatggtaa caaagttgtg ctaagtgtct ccaatgctga taaaagggtt	720
gatgatgctg aatttgaaga aaatgaagtc tatgcaatcg atattgtcac cagcactggg	780
gaggggaagc ccaagttatt ggatgagaag cagaccacca tctacaaaag ggctgtagac	840
aagaattata acctgaagat gaaagcgtca agatttattt tcagtgaaat cagccagaag	900
ttcccaatca tgcccttcac tgctagggca ttagaagaga agcgtgcacg cttaggcttg	960
gtggaatgca tgaaccatga gctattgcag ccgtaccctg tacttcatga gaagccaggt	1020
gaccttggtg cacacataaa gttcactgtg ctgctaattgc ccaatggatc ggataggatt	1080
acatcatatc cgctacagga gttaaagcca aaaaaatcca ttgaagacaa tgctgagata	1140
aaggcatggc ttgctttggg gacgaaatca aagaagaagg gtggtggaaa gaagaagaaa	1200
ggcaagaaag gagatgcagc aggagatccc atggaggcga caaacgatgc tacaagccaa	1260
gaataattct gatttttggg attactgcac ccagcatttt ctctcttgtt tottgcgtgc	1320
atctgatggg gttatattac attcagttgc gaaaaaaaaa aaaaaa	1366

<210> 170
 <211> 392
 <212> PRT
 <213> Z. mays

<400> 170

Met	Ser	Ser	Asp	Asp	Glu	Val	Arg	Glu	Glu	Lys	Glu	Leu	Asp	Leu	Ser
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Ser	Asn	Asp	Val	Val	Thr	Lys	Tyr	Lys	Thr	Ala	Ala	Glu	Ile	Leu	Asn
			20					25					30		

Asn	Ala	Leu	Lys	Leu	Val	Val	Ser	Glu	Cys	Lys	Pro	Lys	Ala	Lys	Ile
			35					40					45		

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

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

Pro Thr Cys Val Ser Val Asn Asn Thr Val Cys His Phe Ser Pro Leu
85 90 95

Thr Thr Asp Asp Ala Val Leu Glu Glu Asn Asp Met Val Lys Ile Asp
100 105 110

Met Gly Cys His Ile Asp Gly Phe Ile Ala Val Val Ala His Thr His
115 120 125

Val Ile Ala Asn Gly Pro Val Thr Gly Arg Ala Ala Asp Val Leu Ala
130 135 140

Ala Ala Asn Thr Ala Ala Glu Val Ala Met Arg Leu Val Arg Pro Gly
145 150 155 160

Lys Lys Asn Lys Asp Val Thr Glu Ala Ile Gln Lys Val Ala Ala Val
165 170 175

Tyr Asp Cys Lys Ile Val Glu Gly Val Leu Ser His Gln Leu Lys Gln
180 185 190

Phe Val Ile Asp Gly Asn Lys Val Val Leu Ser Val Ser Asn Ala Asp
195 200 205

Thr Lys Val Asp Asp Ala Glu Phe Glu Glu Asn Glu Val Tyr Ala Ile
210 215 220

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

Lys Gln Thr Thr Ile Tyr Lys Arg Ala Val Asp Lys Asn Tyr Asn Leu
245 250 255

Lys Met Lys Ala Ser Arg Phe Ile Phe Ser Glu Ile Ser Gln Lys Phe
260 265 270

Pro Ile Met Pro Phe Thr Ala Arg Ala Leu Glu Glu Lys Arg Ala Arg
275 280 285

Leu Gly Leu Val Glu Cys Met Asn His Glu Leu Leu Gln Pro Tyr Pro
290 295 300

Val Leu His Glu Lys Pro Gly Asp Leu Val Ala His Ile Lys Phe Thr
305 310 315 320

Val Leu Leu Met Pro Asn Gly Ser Asp Arg Ile Thr Ser Tyr Pro Leu
325 330 335

Gln Glu Leu Lys Pro Thr Lys Ser Ile Glu Asp Asn Ala Glu Ile Lys
340 345 350

Ala Trp Leu Ala Leu Gly Thr Lys Ser Lys Lys Lys Gly Gly Gly Lys
355 360 365

Lys Lys Lys Gly Lys Lys Gly Asp Ala Ala Gly Asp Pro Met Glu Ala
370 375 380

Thr Asn Asp Ala Thr Ser Gln Glu
385 390

<210> 171
<211> 1492
<212> DNA
<213> Z. mays

<400> 171
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cgacttcata tcggattgaa gcaatgtcgt cggacgatga ggtcagggag gagaaggagc 180
tcgacctctc ctccaacgac gttgtcacca agtacaaggc tgccgccgaa atcctcaaca 240
acgctctgaa gattgttgtg tctcagtgc aagcaaaagt caagattggt gacctttgcg 300
agaagggcga ctctttcata agagagcaaa ctgggaatgt ttacaagaac gcaaagagga 360
agattgaaag gggatttgct ttcccaacct gtgtatccgt caatgacaca gtttgccact 420
tctcaccgct tgcaaccgat gatgccgttc tggaagaaaa tgacatggtt aaaattgata 480
tgggctgtca tattgatggc tttattgctg tgggtggcaca tacacatgta attacaaatg 540
ggcctgtcac aggaagggct ggtgatgtgc ttgctgctgc caacacagca gcagaagtgc 600
caatgcggct tgtgagacct gggaagaaaa ataaggatgt tactgaagca attcagaaag 660
ttgctgctgc ttatgattgc aaaattgtgg aagggtgttct tagccatcaa ctgaaacaat 720
ttgtgattga tggtaacaaa gttgtgctca gtgtctccaa tgctgataca aagggtgatg 780
atgctgaatt tgaagaaaat gaagtatatg caatcgatat tgtcaccagc actggggagg 840
ggaagcccaa gttattggat gagaaacaga ccaccatcta caaaagggcc gtagacaaga 900

attatcactt gaagatgaaa gcgtcaaggt ttattttcag tgagatcagc cagaagttcc 960
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 aatgcatgaa ccatgaacta ttgcagccgt accctgtact tcatgagaag ccaggcgatc 1080
 ttgttgaca cataaagttc actgtgctgc tgatgccaa tggatcagat aagataacat 1140
 cacatcctct acaggagtta aagcccacca aatccattga agacaatgca gagataaagg 1200
 catggcttgc tttggggacg aaatcaaaga agaaggggtg tgggaagaag aagaaaggca 1260
 agaaaggaga tgcagcagaa gcagatccca tggaggaggc gacaaacggt gctacaagcc 1320
 aagaataatt ctgatttttg gaattactgc caccagcttt tttcttgttt cttoctgca 1380
 tctgatggtg ttatattaca ttcagttgtg gaaaaattga gtactatttc tagcttctaa 1440
 gaaatgaagc atcctattat cgcaaaaaaa aaaacaaaga taatcgacaa gg 1492

<210> 172
 <211> 394
 <212> PRT
 <213> Z. mays

<400> 172

Met Ser Ser Asp Asp Glu Val Arg Glu Glu Lys Glu Leu Asp Leu Ser
 1 5 10 15

Ser Asn Asp Val Val Thr Lys Tyr Lys Ala Ala Ala Glu Ile Leu Asn
 20 25 30

Asn Ala Leu Lys Ile Val Val Ser Gln Cys Lys Pro Lys Val Lys Ile
 35 40 45

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

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

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

Ala Thr Asp Asp Ala Val Leu Glu Glu Asn Asp Met Val Lys Ile Asp
100 105 110

Met Gly Cys His Ile Asp Gly Phe Ile Ala Val Val Ala His Thr His
115 120 125

Val Ile Thr Asn Gly Pro Val Thr Gly Arg Ala Gly Asp Val Leu Ala
130 135 140

Ala Ala Asn Thr Ala Ala Glu Val Ala Met Arg Leu Val Arg Pro Gly
145 150 155 160

Lys Lys Asn Lys Asp Val Thr Glu Ala Ile Gln Lys Val Ala Ala Ala
165 170 175

Tyr Asp Cys Lys Ile Val Glu Gly Val Leu Ser His Gln Leu Lys Gln
180 185 190

Phe Val Ile Asp Gly Asn Lys Val Val Leu Ser Val Ser Asn Ala Asp
195 200 205

Thr Lys Val Asp Asp Ala Glu Phe Glu Glu Asn Glu Val Tyr Ala Ile
210 215 220

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

Lys Gln Thr Thr Ile Tyr Lys Arg Ala Val Asp Lys Asn Tyr His Leu
245 250 255

Lys Met Lys Ala Ser Arg Phe Ile Phe Ser Glu Ile Ser Gln Lys Phe
260 265 270

Pro Ile Met Pro Phe Thr Ala Arg Ala Leu Glu Glu Lys Arg Ala Arg
275 280 285

Leu Gly Leu Val Glu Cys Met Asn His Glu Leu Leu Gln Pro Tyr Pro
290 295 300

Val Leu His Glu Lys Pro Gly Asp Leu Val Ala His Ile Lys Phe Thr
305 310 315 320

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

Gln Glu Leu Lys Pro Thr Lys Ser Ile Glu Asp Asn Ala Glu Ile Lys
340 345 350

Ala Trp Leu Ala Leu Gly Thr Lys Ser Lys Lys Lys Gly Gly Gly Lys
355 360 365

Lys Lys Lys Gly Lys Lys Gly Asp Ala Ala Glu Ala Asp Pro Met Glu
370 375 380

Glu Ala Thr Asn Gly Ala Thr Ser Gln Glu
385 390

<210> 173
<211> 1053
<212> DNA
<213> B. napus

<400> 173
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accaacttag cttcttccat tacaaagctt gtccccaagg aaaagtccca gatcctcacc 180
ctttcatgga tgagtcaagc gatggcatct ctttgccaga cccacaacgc tatcaagact 240
cttataaccg atctagagct tcctgtctca gattgggagg acaagtgggt cgacatctac 300
ctagacatca gcgtcaagct cctcgacctc tgcaacgcct tcagctcgga gctaagccgc 360
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cagaatctgc cgaaagctca atcctccctc gacgcctgga agcagcacat cgtttccaag 480
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gtcaagactc tgtacatctc tgggtgtctt gctgctgcct tctcaggctc atcgcagaac 660
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gagctcgagg ctgttgattc aggtgttaag aaccttgccc ctgcgatcca acaagggctc 840
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gaccttgttt ccaaggaggt ggattgcttc ttcaagattc tgttatcggg gagggacact 960
ttgctggaga acctcaggtc gatgggagca ccaacaacgg tgctgacgac gtcacaaaaa 1020

aaggctgccg gaaaaaagca gagaggattc tga

1053

<210> 174

<211> 350

<212> PRT

<213> B. napus

<400> 174

Met Ala Arg Pro Gln Asp Pro Pro Arg Gly Phe Phe Pro Phe Gly Asn
1 5 10 15

Pro Phe Lys Asn Leu Ser Ser Lys Asn Pro Val Leu Ser Ser Asn Leu
20 25 30

Leu Ser Leu Leu Asn Thr Phe Glu Thr Asn Leu Ala Ser Ser Ile Thr
35 40 45

Lys Leu Val Pro Lys Glu Lys Ser Gln Ile Leu Thr Leu Ser Trp Met
50 55 60

Ser Gln Ala Met Ala Ser Leu Cys Gln Thr His Asn Ala Ile Lys Thr
65 70 75 80

Leu Ile Thr Asp Leu Glu Leu Pro Val Ser Asp Trp Glu Asp Lys Trp
85 90 95

Val Asp Ile Tyr Leu Asp Ile Ser Val Lys Leu Leu Asp Leu Cys Asn
100 105 110

Ala Phe Ser Ser Glu Leu Ser Arg Leu Asn Gln Gly His Leu Phe Leu
115 120 125

Gln Phe Ala Leu His Asn Leu Gly Thr Asn Ala Pro Gln Asn Leu Pro
130 135 140

Lys Ala Gln Ser Ser Leu Asp Ala Trp Lys Gln His Ile Val Ser Lys
145 150 155 160

Asn Pro Arg Leu Glu Ser Cys His Ala Ile Leu Thr Ser Leu Val Gln
165 170 175

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

Met Arg Ala Leu Tyr Gly Val Lys Val Lys Thr Leu Tyr Ile Ser Gly
195 200 205

Val Phe Ala Ala Ala Phe Ser Gly Ser Ser Gln Asn Leu Leu Tyr Val
210 215 220

Thr Val Ser Asn Glu Leu Pro Trp Ala Pro Ser Phe Met Asp Met Gln
225 230 235 240

Asn Thr Met Asn Ser Glu Met Lys Ser Ile Phe Leu Ser Asp Gly Leu
245 250 255

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

Ala Pro Ala Ile Gln Gln Gly Ser Ile Asp Ser Ile Ser Leu Gln Pro
275 280 285

Leu Lys Asp Ser Val Thr Glu Leu Thr Ser Gly Ile Asp Leu Val Ser
290 295 300

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

Leu Leu Glu Asn Leu Arg Ser Met Gly Ala Pro Thr Thr Val Leu Thr
 325 330 335

Thr Ser Pro Lys Lys Ala Ala Gly Lys Lys Gln Arg Gly Phe
 340 345 350

<210> 175
 <211> 1173
 <212> DNA
 <213> B. napus

<400> 175
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 gtcgagaagt tcgatccggc gtggaatccg acgggcatgc tcgaagtcag ctcatctctc 180
 acgctcttcc ctcagtacag agagaagtat cttcaggact cttggcccac gatcgaatcc 240
 gctctcaaac aatacggcgt cgcttgcaaa ctcaacctgg ttgaaggatc tatgactggt 300
 tcgacgacga ggaagacgag agatccgtat atcattgtca aagctaggga tttgattaag 360
 cttcttttga gaagtgttcc tgctcctcag gcaatcaaga ttctggaaga tgaagtgcaa 420
 tgtgatatca tcaagattgg aagcttggtt cggaataagg aaaggtttgt gaaaagaagg 480
 cagcggccttg tgggtcctaa ttcttctacc ttgaaggcga tggagatatt aaccgactgt 540
 tacattctag ttcagggaag tactgtagct gcaatggggt cttttaaaagg tctaaaacaa 600
 gtccgaaggg ttgtggaaca gtgtatgcgt aatgaattac atcctgtata ccagataaag 660

gatctcatga tgagaaggga actagcaaag gatccagcgc ttgcaacgga aagctgggat	720
aggtttcttc ctaagttcag gaagagtaat gttcagcaaa agaagcccaa gagcaaggag	780
aagaaggaat acacaccatt ccctcctcct caaccgccta gcaaggttga taagcaattg	840
gagtctggag aatacttcct gaatgaaaac aagaagtcag agaagaagtg gcaggagaag	900
caagagaagc agacagagaa gactatagag aagaaaagaa tgagagatgc ctcgttcgtc	960
ccacctgagg aacctgtgca gagcagcaac aactcaaaca aatacgagga ggggaagaaa	1020
gatctaaccg agttaacaca atccttaaag agcaagacaa aagagttgaa gaagcagaag	1080
aagactcaag agaaagtgaa tgcagaggag tacattgccg ttatgtctgg tgataaatct	1140
tccaagaaga aatccaaagt cgtgagagat taa	1173

<210> 176
 <211> 390
 <212> PRT
 <213> B. napus

<400> 176

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

Lys	Pro	Arg	Tyr	Lys	Gly	Lys	His	Asp	Lys	Pro	Lys	Pro	Trp	Asp	Asp
			20					25					30		

Asp	Pro	Asn	Ile	Asp	Arg	Trp	Lys	Val	Glu	Lys	Phe	Asp	Pro	Ala	Trp
		35					40					45			

Asn	Pro	Thr	Gly	Met	Leu	Glu	Val	Ser	Ser	Phe	Ser	Thr	Leu	Phe	Pro
	50					55					60				

Gln Tyr Arg Glu Lys Tyr Leu Gln Asp Ser Trp Pro Thr Ile Glu Ser
65 70 75 80

Ala Leu Lys Gln Tyr Gly Val Ala Cys Lys Leu Asn Leu Val Glu Gly
85 90 95

Ser Met Thr Val Ser Thr Thr Arg Lys Thr Arg Asp Pro Tyr Ile Ile
100 105 110

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

Pro Gln Ala Ile Lys Ile Leu Glu Asp Glu Val Gln Cys Asp Ile Ile
130 135 140

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

Gln Arg Leu Val Gly Pro Asn Ser Ser Thr Leu Lys Ala Met Glu Ile
165 170 175

Leu Thr Asp Cys Tyr Ile Leu Val Gln Gly Ser Thr Val Ala Ala Met
180 185 190

Gly Ser Phe Lys Gly Leu Lys Gln Val Arg Arg Val Val Glu Gln Cys
195 200 205

Met Arg Asn Glu Leu His Pro Val Tyr Gln Ile Lys Asp Leu Met Met
210 215 220

Arg Arg Glu Leu Ala Lys Asp Pro Ala Leu Ala Thr Glu Ser Trp Asp
225 230 235 240

Arg Phe Leu Pro Lys Phe Arg Lys Ser Asn Val Gln Gln Lys Lys Pro
245 250 255

Lys Ser Lys Glu Lys Lys Glu Tyr Thr Pro Phe Pro Pro Pro Gln Pro
260 265 270

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

Glu Asn Lys Lys Ser Glu Lys Lys Trp Gln Glu Lys Gln Glu Lys Gln
290 295 300

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

Pro Pro Glu Glu Pro Val Gln Ser Ser Asn Asn Ser Asn Lys Tyr Glu
325 330 335

Glu Gly Lys Lys Asp Leu Thr Glu Leu Thr Gln Ser Leu Lys Ser Lys
340 345 350

Thr Lys Glu Leu Lys Lys Gln Lys Lys Thr Gln Glu Lys Val Asn Ala
355 360 365

Glu Glu Tyr Ile Ala Val Met Ser Gly Asp Lys Ser Ser Lys Lys Lys
370 375 380

Ser Lys Val Val Arg Asp
385 390

<210> 177
<211> 1455
<212> DNA
<213> G. max

<220>
<221> misc_feature
<222> (1449)..(1449)
<223> n is a, c, g, or t

<400> 177
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actcagagga ggagaatggc gtagcgaacg agtcacaagc acttgagcag aaggagaagc 120

gaaaggggaa gcacgacaag cccaagccat gggacgacga cccaacatc gaccactgga 180

agatcgagaa gttcgaccct tcatggaacg acggcggcat gctcgaagtg agtccttctt 240

ccactctctt tcctcagtac cgcgaaaagt acctccaaga agcttgcccc atgggtcaaat 300

cctcactcaa ggagttcggg gttgcttgcg aactcaacct cgttgagggt tccatgactg 360

tttcaaccac caggaagact agggaccctt atattatcat caaagccagg gatcttatca 420

agcttctatc acgaagtatt cctgctctc aggcgataaa aatacttgac gatgagatgc 480

aatgtgacat cattaatac agtggcatgg ttcgcaataa ggagcgattt gtaaaaagaa 540

gacaacatct tgtgggcccc aattcttcca ccttgaaggc tcttgaaata ctactgggt 600

gctacattct cgtccaggga aacacagttg ctgctatggg ttcatcaca ggcttgaagc 660

aagtcagaag aattgttgaa gaatgcatgc tgaataaaat gcatcctgta tacaacatta 720

aggttcttat gatgaagaaa gaacttgaaa aggatccagc acttgcccag gagaactggg 780

ataggttcct tccaaaattc aagaagaaaa atgttaagca aaagaagggt aacactaaac 840

agaagaaacc atacactcct ttccctccac ctcaacagcc cagtaagatt gatatacaat 900

tagaaactgg agaatacttt ttaagtaaca aaaggaaatc agcaaagata tggcaagaga	960
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tcccacccaa ggagcctgca aatctggtgg ataaatctga ggatgctaac aataatgtag	1080
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aaaatataaa tgccgagaca tatattatag gatcatcaga acaagcatcg ggaaagaaat	1200
ccaagaagca aaggtcttaa acataatctt cattttggag atgaaaaatg agcatgtgat	1260
gtctatgtta attcaatcaa gatcttctgc atccaatgtc tttgcagtaa cagttttgac	1320
accaatgtat tttgaggcat agttgttcat tccatttgtc atggagatga gtgcgtggca	1380
ttgtgtatct tattgtactt gccaatagac agtaagtcag tatcatgtac actacctgtt	1440
atttaagtnt acatc	1455

<210> 178
 <211> 389
 <212> PRT
 <213> G. max

<400> 178

Met	Glu	Ile	His	Ser	Glu	Glu	Glu	Asn	Gly	Val	Ala	Asn	Glu	Ser	Gln
1				5					10					15	

Ala	Leu	Glu	Gln	Lys	Glu	Lys	Arg	Lys	Gly	Lys	His	Asp	Lys	Pro	Lys
				20				25					30		

Pro	Trp	Asp	Asp	Asp	Pro	Asn	Ile	Asp	His	Trp	Lys	Ile	Glu	Lys	Phe
		35					40				45				

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

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

Met Val Lys Ser Ser Leu Lys Glu Phe Gly Val Ala Cys Glu Leu Asn
85 90 95

Leu Val Glu Gly Ser Met Thr Val Ser Thr Thr Arg Lys Thr Arg Asp
100 105 110

Pro Tyr Ile Ile Ile Lys Ala Arg Asp Leu Ile Lys Leu Leu Ser Arg
115 120 125

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

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

Val Lys Arg Arg Gln His Leu Val Gly Pro Asn Ser Ser Thr Leu Lys
165 170 175

Ala Leu Glu Ile Leu Thr Gly Cys Tyr Ile Leu Val Gln Gly Asn Thr
180 185 190

Val Ala Ala Met Gly Ser Phe Lys Gly Leu Lys Gln Val Arg Arg Ile
195 200 205

Val Glu Glu Cys Met Leu Asn Lys Met His Pro Val Tyr Asn Ile Lys
210 215 220

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

Glu Asn Trp Asp Arg Phe Leu Pro Lys Phe Lys Lys Lys Asn Val Lys
245 250 255

Gln Lys Lys Val Asn Thr Lys Gln Lys Lys Pro Tyr Thr Pro Phe Pro
260 265 270

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

Tyr Phe Leu Ser Asn Lys Arg Lys Ser Ala Lys Ile Trp Gln Glu Lys
290 295 300

Gln Glu Lys Gln Ala Glu Lys Thr Ala Glu Asn Lys Arg Lys Arg Glu
305 310 315 320

Glu Ala Phe Ile Pro Pro Lys Glu Pro Ala Asn Leu Val Asp Lys Ser
325 330 335

Glu Asp Ala Asn Asn Asn Val Ala Asp Met Ala Ile Ser Leu Lys Lys
340 345 350

Lys Thr Lys Lys Phe Gly Lys Arg Lys Ser Glu Glu Asn Ile Asn Ala
355 360 365

Glu Thr Tyr Ile Ile Gly Ser Ser Glu Gln Ala Ser Gly Lys Lys Ser
370 375 380

Lys Lys Gln Arg Ser
385

<210> 179
<211> 1466
<212> DNA
<213> Z. mays

<400> 179
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ctgctgcgcc ggcagagggg aagaactggc ggcggaaggg gaagcacgac aagcccaagc 180
cgtgggacga ggaccccaac atcgaccgct ggaagatcga caagtctgac cctgcctgga 240
acgagggcgg catgctcgaa gtcagctcct tctccaccct ctttccccag taccgagaga 300
agtacctaca ggaggcgtgg ccggtcgtga agggcgcatc gaaggagtac gggatctcgt 360
gcgagctcaa tttggtggag ggatccatga ctgtgtcgac gaccagaaag acaagggatc 420
ccttcgctat tatcaaggcc agggaactaa ttaagctttt gtccaggagc gtccctgcac 480
ctcaggcaat caaaattctt gatgatgaga tgaactgcga tattattaag attggtggtc 540
ttgtgagaaa taaggagcgg tttgttaaaa ggagggaacg gcttttaggc cctaacttgt 600
ctacactcaa ggctattgag attttgactg gctgctacat cttagtgcag ggaaatactg 660
ttgcagccat gggcaactat aggggaaggg gactgaaaca agtgagaagg attgtagagg 720
attgcatgaa gaatgtaaag catccagtgt accacatcaa ggaactacta atcaaactg 780
agctagcaaa aaatcctgct ctagccaatg aaaattggga cagatttctc ccgaagttca 840
agaagaagaa tgtcaagcag aagaagcctc aaactaagga gaagaaaccg tacacaccct 900
ttccaccgcc tcaacagcct agcaagattg atcttgaact tgagaacggg gagtatttca 960
tgagtgacaa aaagaaatca gcaaagaaat ggcaagagaa gctggacaag caatctggga 1020

gagctgaaga aaataaaaga aaaagagagg ctgcatttgt tcctccaaag gagaacactg	1080
cagggtccatc caaatctgac aagaatgccg gtgacaacag tgagatagcc gatatagcga	1140
agtcattaata gagaaaggcg aaggaattta gaaagaacga ggcccaggag agtgtcatag	1200
ctgaatcata tatcgcaagt aatgatgaat tgcggcaaaa aaagaaaaag aaatcaacta	1260
agtccaagta gcctaatacct catgcataat gacactggca attgagaagg attgcatgag	1320
ccatccctat aattatgtca ttcatgctgt gatcgtatta gatgatgaaa caaaattcga	1380
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ccatgataac caagcaaaaa aaaaaa	1466

<210> 180
 <211> 391
 <212> PRT
 <213> Z. mays

<400> 180

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

Asn	Trp	Arg	Arg	Lys	Gly	Lys	His	Asp	Lys	Pro	Lys	Pro	Trp	Asp	Glu
			20					25					30		

Asp	Pro	Asn	Ile	Asp	Arg	Trp	Lys	Ile	Asp	Lys	Phe	Asp	Pro	Ala	Trp
		35					40					45			

Asn	Glu	Gly	Gly	Met	Leu	Glu	Val	Ser	Ser	Phe	Ser	Thr	Leu	Phe	Pro
	50					55					60				

Gln	Tyr	Arg	Glu	Lys	Tyr	Leu	Gln	Glu	Ala	Trp	Pro	Val	Val	Lys	Gly
65						70				75					80

Ala Leu Lys Glu Tyr Gly Ile Ser Cys Glu Leu Asn Leu Val Glu Gly
85 90 95

Ser Met Thr Val Ser Thr Thr Arg Lys Thr Arg Asp Pro Phe Ala Ile
100 105 110

Ile Lys Ala Arg Glu Leu Ile Lys Leu Leu Ser Arg Ser Val Pro Ala
115 120 125

Pro Gln Ala Ile Lys Ile Leu Asp Asp Glu Met Asn Cys Asp Ile Ile
130 135 140

Lys Ile Gly Gly Leu Val Arg Asn Lys Glu Arg Phe Val Lys Arg Arg
145 150 155 160

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

Leu Thr Gly Cys Tyr Ile Leu Val Gln Gly Asn Thr Val Ala Ala Met
180 185 190

Gly Asn Tyr Arg Gly Arg Gly Leu Lys Gln Val Arg Arg Ile Val Glu
195 200 205

Asp Cys Met Lys Asn Val Lys His Pro Val Tyr His Ile Lys Glu Leu
210 215 220

Leu Ile Lys Arg Glu Leu Ala Lys Asn Pro Ala Leu Ala Asn Glu Asn
225 230 235 240

Trp Asp Arg Phe Leu Pro Lys Phe Lys Lys Lys Asn Val Lys Gln Lys
245 250 255

Lys Pro Gln Thr Lys Glu Lys Lys Pro Tyr Thr Pro Phe Pro Pro Pro
260 265 270

Gln Gln Pro Ser Lys Ile Asp Leu Glu Leu Glu Asn Gly Glu Tyr Phe
275 280 285

Met Ser Asp Lys Lys Lys Ser Ala Lys Lys Trp Gln Glu Lys Leu Asp
290 295 300

Lys Gln Ser Gly Arg Ala Glu Glu Asn Lys Arg Lys Arg Glu Ala Ala
305 310 315 320

Phe Val Pro Pro Lys Glu Asn Thr Ala Gly Pro Ser Lys Ser Asp Lys
325 330 335

Asn Ala Ser Asp Asn Ser Glu Ile Ala Asp Ile Ala Lys Ser Leu Lys
340 345 350

Arg Lys Ala Lys Glu Phe Arg Lys Asn Glu Ala Gln Glu Ser Val Ile
355 360 365

Ala Glu Ser Tyr Ile Ala Ser Asn Asp Glu Leu Arg Gln Lys Lys Lys
370 375 380

Lys Lys Ser Thr Lys Ser Lys
385 390

<210> 181

<211> 1127

<212> DNA

<213> G. max

<400> 181

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cgttcgagaa atgcagcagc acctgatgca gatgcagccc atgatggctg cctactaccc	120
caacaacgtc accactgatc acattcaaca gtacctggat gagaacaagt ccttgattct	180
gaagattgtt gaaagccaga attctggcaa gctgagcgag tgtgccgaga accaatcaag	240
gctgcagaga aatctcatgt acctagctgc aatagctgat tctcaaccac aaccatctcc	300
attggctggg cagtatcctt ctagtggact tgtgcagcag ggagcacact acatgcaggc	360
tcaacaggct cagcagatgt cacaacaaca gctaattggct tcgcgctcct cgctcctgta	420
ctcccaacag cttttctcag tgcttcaaca gcagcaaggc atgcacagcc aacttggcat	480
gagctccagt ggaagtcaag gcctccacat gctgcaaagt gaagccacta atgttggagg	540
caatgcaacc ataggaaccg gaggaggggt tccggacttt gtacgcattg gtagtggcaa	600
gcaagatatt ggaatctctg gtgaaggcag aggaggaaac tctagtggcc actctggtga	660
tgggtgtgag aacttaatt acctgaaagc tgctggtgat ggaaactgaa ctagccaggg	720
agaatggtaa aagtttcctt ggcctttagc cgtttattga gtgaattatg agaattaggc	780
aatggagatt aagtagggaa gggaaggagg aaagggaaaa gttgctgctt agatatcttg	840
tttgttaatc ttgtgctaaa ggcaaactgc cttaacgttt ctgtagtact agtaactagt	900
aagtaacatg atgcatgctt tatttttctt gtgtaaagtt ctagtcataa atgtcagggt	960
cacaagttcc ttccctttct gttctgtttc tgtatgcaca cttgttggcc aagagggtta	1020
tttggatgaac gatgacagat gtaattttga cgatgttcct gctttaagga gtttgatgca	1080
tcaaagttca attacaagct aaaccatta cgaaaaaaaa aaaaaaa	1127

<210> 182
<211> 212
<212> PRT
<213> G. max

<400> 182

Met Gln Gln His Leu Met Gln Met Gln Pro Met Met Ala Ala Tyr Tyr
1 5 10 15

Pro Asn Asn Val Thr Thr Asp His Ile Gln Gln Tyr Leu Asp Glu Asn
20 25 30

Lys Ser Leu Ile Leu Lys Ile Val Glu Ser Gln Asn Ser Gly Lys Leu
35 40 45

Ser Glu Cys Ala Glu Asn Gln Ser Arg Leu Gln Arg Asn Leu Met Tyr
50 55 60

Leu Ala Ala Ile Ala Asp Ser Gln Pro Gln Pro Ser Pro Leu Ala Gly
65 70 75 80

Gln Tyr Pro Ser Ser Gly Leu Val Gln Gln Gly Ala His Tyr Met Gln
85 90 95

Ala Gln Gln Ala Gln Gln Met Ser Gln Gln Gln Leu Met Ala Ser Arg
100 105 110

Ser Ser Leu Leu Tyr Ser Gln Gln Pro Phe Ser Val Leu Gln Gln Gln
115 120 125

Gln Gly Met His Ser Gln Leu Gly Met Ser Ser Ser Gly Ser Gln Gly
130 135 140

Leu His Met Leu Gln Ser Glu Ala Thr Asn Val Gly Gly Asn Ala Thr
 145 150 155 160

Ile Gly Thr Gly Gly Gly Phe Pro Asp Phe Val Arg Ile Gly Ser Gly
 165 170 175

Lys Gln Asp Ile Gly Ile Ser Gly Glu Gly Arg Gly Gly Asn Ser Ser
 180 185 190

Gly His Ser Gly Asp Gly Gly Glu Thr Leu Asn Tyr Leu Lys Ala Ala
 195 200 205

Gly Asp Gly Asn
 210

<210> 183
 <211> 912
 <212> DNA
 <213> B. napus

<400> 183
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 agttgagtct caaaactcag gaaagctcag cgagtgtgcc gagaatcagg caaggcttca 180
 acgcaacctc atgtacttgg ctgcaatagc agattctcag cctcaacctc caagcgtgca 240
 tagccagtat ggatctgctg gtggtgggtt gattcaggga gaaggagcgt cacactatatt 300
 gcagcagcaa caggcgactc aacagcagca gatgactcag cagtctctta tggcagctcg 360
 ttcttcaatg atgtatcagc agcagcaaca gccttatgca acgcttcagc atcagcagtt 420

gcaccatagc cagcttggga tgagctctag cagcggagga ggaagcagtg gtctccatat	480
ccttcaggga gaggctgggtg ggtttcatga atttggccgt ggaagccgg agatgggaag	540
tggatgaaggc aggggtggaa gctcagggga tggtaggagaa acactctact tgaagtcac	600
agatgatggg aactgaaaga gtgttcgaca agtaagggtcc agtgaagaag cagcagcaga	660
agtagtagta gtaagagtct gaagtttggt tgttttggt tagttgcttg ttgaagaagc	720
aaagaacttg tttattttat ttctatgttt gttccctaaa aatatgaact cttacgtggt	780
gaagtgtacc atgcatatct gctcgctaca agttatgtcg taatcttagt atgttatttc	840
ttaggacaat aatttctgga gatcattggt tgtgaaatgt gacgtagttt gaatttcaaa	900
aaaaaaaaaa aa	912

<210> 184
 <211> 203
 <212> PRT
 <213> B. napus

<400> 184

Met	Gln	Gln	His	Leu	Met	Gln	Met	Gln	Pro	Met	Met	Ala	Gly	Tyr	Tyr
1				5					10					15	

Pro	Ser	Asn	Val	Thr	Ser	Asp	His	Ile	Gln	Gln	Tyr	Leu	Asp	Glu	Asn
			20					25					30		

Lys	Ser	Leu	Ile	Leu	Lys	Ile	Val	Glu	Ser	Gln	Asn	Ser	Gly	Lys	Leu
		35					40					45			

Ser	Glu	Cys	Ala	Glu	Asn	Gln	Ala	Arg	Leu	Gln	Arg	Asn	Leu	Met	Tyr
	50					55					60				

Leu Ala Ala Ile Ala Asp Ser Gln Pro Gln Pro Pro Ser Val His Ser
65 70 75 80

Gln Tyr Gly Ser Ala Gly Gly Gly Leu Ile Gln Gly Glu Gly Ala Ser
85 90 95

His Tyr Leu Gln Gln Gln Gln Ala Thr Gln Gln Gln Gln Met Thr Gln
100 105 110

Gln Ser Leu Met Ala Ala Arg Ser Ser Met Met Tyr Gln Gln Gln Gln
115 120 125

Gln Pro Tyr Ala Thr Leu Gln His Gln Gln Leu His His Ser Gln Leu
130 135 140

Gly Met Ser Ser Ser Ser Gly Gly Gly Ser Ser Gly Leu His Ile Leu
145 150 155 160

Gln Gly Glu Ala Gly Gly Phe His Glu Phe Gly Arg Gly Lys Pro Glu
165 170 175

Met Gly Ser Gly Glu Gly Arg Gly Gly Ser Ser Gly Asp Gly Gly Glu
180 185 190

Thr Leu Tyr Leu Lys Ser Ser Asp Asp Gly Asn
195 200

<210> 185

<211> 1245

<212> DNA

<213> G. max

<400> 185

gggaccagag agaaaacagg gggatttgtt tctctctgca gttgcactct tgcaggcagg	60
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tttatacttt agaaccagct agcgagcaag tgagcgagtg tcatatatat atatacatag	180
tgcgttcgag aaatgcagca gcacctgatg cagatgcagc ccatgatggc tgcctactac	240
cccaacaacg tcaccactga tcacattcaa cagtacctgg atgagaacaa gtccttgatt	300
ctgaagattg ttgaaagcca gaattctggc aagctgagcg agtgtgccga gaaccaatca	360
aggctgcaga gaaatctcat gtacctagct gcaatagctg attctcaacc acaaccatct	420
ccattggctg gtcagtatcc ttctagtgga cttgtgcagc agggagcaca ctacatgcag	480
gctcaacagg ctgagcagat gtcacaacaa cagctaattg cttcgcgctc ctgctcctg	540
tactcccaac agcctttctc agtgcttcaa cagcagcaag gcatgcacag ccaacttggc	600
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ggcaatgcaa ccataggaac cggaggaggg tttccggact ttgtacgcat tggtagtggc	720
aagcaagata ttggaatctc tggatgaaggc agaggaggaa actctagtgg ccactctggt	780
gatggtggtg agacacttaa ttacctgaaa gctgctggtg atggaaactg aactagccag	840
ggagaatggt aaaagtttcc ttggccttta gccgtttatt gagtgaatta tgagaattag	900
gcaatggaga ttaagtaggg aagggaagga ggaaagggaa aagttgctgc ttagatatct	960
tgtttgttaa tcttgctgta aaggcaaact gccttaacgt ttctgtagta ctagtaacta	1020
gtaagtaaca tgatgcatgc tttatTTTTt ttgtgtaaag ttctagtcac aaatgtcagg	1080
gtcacaagtt ccttcccttt ctgttctgtt tctgtatgca cacttggttg ccaagagggg	1140
tatttggtga acgatgacag atgtaatttt gacgatgttc ctgctttaag gagtttgatg	1200
catcaaagtt caattacaag ctaaaccat tatgaaataa aaaaa	1245

<210> 186
<211> 212
<212> PRT
<213> G. max

<400> 186

Met Gln Gln His Leu Met Gln Met Gln Pro Met Met Ala Ala Tyr Tyr
1 5 10 15

Pro Asn Asn Val Thr Thr Asp His Ile Gln Gln Tyr Leu Asp Glu Asn
20 25 30

Lys Ser Leu Ile Leu Lys Ile Val Glu Ser Gln Asn Ser Gly Lys Leu
35 40 45

Ser Glu Cys Ala Glu Asn Gln Ser Arg Leu Gln Arg Asn Leu Met Tyr
50 55 60

Leu Ala Ala Ile Ala Asp Ser Gln Pro Gln Pro Ser Pro Leu Ala Gly
65 70 75 80

Gln Tyr Pro Ser Ser Gly Leu Val Gln Gln Gly Ala His Tyr Met Gln
85 90 95

Ala Gln Gln Ala Gln Gln Met Ser Gln Gln Gln Leu Met Ala Ser Arg
100 105 110

Ser Ser Leu Leu Tyr Ser Gln Gln Pro Phe Ser Val Leu Gln Gln Gln
115 120 125

Gln Gly Met His Ser Gln Leu Gly Met Ser Ser Ser Gly Ser Gln Gly
130 135 140

Leu His Met Leu Gln Ser Glu Ala Thr Asn Val Gly Gly Asn Ala Thr
 145 150 155 160

Ile Gly Thr Gly Gly Gly Phe Pro Asp Phe Val Arg Ile Gly Ser Gly
 165 170 175

Lys Gln Asp Ile Gly Ile Ser Gly Glu Gly Arg Gly Gly Asn Ser Ser
 180 185 190

Gly His Ser Gly Asp Gly Gly Glu Thr Leu Asn Tyr Leu Lys Ala Ala
 195 200 205

Gly Asp Gly Asn
 210

<210> 187
 <211> 1342
 <212> DNA
 <213> G. max

<400> 187
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 aacctctgtt ctcaactgtg tttctttacc tctcacctac tttcagacca taccagatt 180
 gactaggctg agaagatgca gcagacaccg cctatgattc ctatgatgcc ttcgttccca 240
 cctacgaaca taaccaccga gcagattcaa aaataccttg atgagaacaa gaagctgatt 300
 ctggcaatat tggacaatca aaatcttgga aaacttgag aatgtgcca gtaccaagct 360
 cagcttcaaa agaatttgat gtatttagct gcaattgctg atgccagcc tcaaaccgcg 420

gccatgcctc cgcagatggc accgcaccct gccatgcaac caggattcta tatgcaacat	480
cctcaggctg ctgcagcagc aatggctcag cagcagcaag gaatgttccc ccagaaaatg	540
ccattgcaat ttggcaatcc acatcaaatg caggaacaac aacagcagct acaccagcag	600
gccatccaag gtcaaatggg acttagacct ggagatataa ataatggcat gcatccaatg	660
cacagtgagg ctgctcttgg aggtggaaac agcggtggtc caccttcggc tactgggtcca	720
aacgatgcac gtggtggaag caagcaagat gcctctgagg ctggaacagc tgggtggagac	780
ggccaaggca gctccgcggc tgctcataac agtggagatg gtgaagaggc aaagtgacat	840
gtttttatgt gcttttcatg agatacatat gactgttgat agtaggtttt cttaaaaggg	900
taggactagt gtgatctgat gacctttgat aggtcgacca aaggacaaaa gggcttctct	960
tgtttgatag cttaggtagt tgtgttggtta gaattttggc acgaagcaag tttgcatcaa	1020
ctgaaacggc tggtgccaca acatactgta cttgtcactg gaagggtgtaa gcatgtggta	1080
tttgtgatca cctaaattgc ttctggtttt taacaatttt tctttgcagt ttgttgtggt	1140
catataaaca aaaatgtttg cttttggtgc aattctactg gattctaggc gtcaattgaa	1200
acatgaaatg ccgtggatgg attcacggtc tgaatttagt ttaggggtcta atottcatta	1260
ggcccggaac ttgcaattca ggaacaagta ctttgagatg cttctaaagg atatttgcct	1320
ttattacagt tattattttg aa	1342

<210> 188
 <211> 213
 <212> PRT
 <213> G. max

<400> 188

Met	Gln	Gln	Thr	Pro	Pro	Met	Ile	Pro	Met	Met	Pro	Ser	Phe	Pro	Pro
1				5				10					15		

Thr Asn Ile Thr Thr Glu Gln Ile Gln Lys Tyr Leu Asp Glu Asn Lys
20 25 30

Lys Leu Ile Leu Ala Ile Leu Asp Asn Gln Asn Leu Gly Lys Leu Ala
35 40 45

Glu Cys Ala Gln Tyr Gln Ala Gln Leu Gln Lys Asn Leu Met Tyr Leu
50 55 60

Ala Ala Ile Ala Asp Ala Gln Pro Gln Thr Pro Ala Met Pro Pro Gln
65 70 75 80

Met Ala Pro His Pro Ala Met Gln Pro Gly Phe Tyr Met Gln His Pro
85 90 95

Gln Ala Ala Ala Ala Ala Met Ala Gln Gln Gln Gln Gly Met Phe Pro
100 105 110

Gln Lys Met Pro Leu Gln Phe Gly Asn Pro His Gln Met Gln Glu Gln
115 120 125

Gln Gln Gln Leu His Gln Gln Ala Ile Gln Gly Gln Met Gly Leu Arg
130 135 140

Pro Gly Asp Ile Asn Asn Gly Met His Pro Met His Ser Glu Ala Ala
145 150 155 160

Leu Gly Gly Gly Asn Ser Gly Gly Pro Pro Ser Ala Thr Gly Pro Asn
165 170 175

Asp Ala Arg Gly Gly Ser Lys Gln Asp Ala Ser Glu Ala Gly Thr Ala
180 185 190

Gly Gly Asp Gly Gln Gly Ser Ser Ala Ala Ala His Asn Ser Gly Asp
195 200 205

Gly Glu Glu Ala Lys
210

<210> 189
<211> 1451
<212> DNA
<213> H. annuus

<400> 189

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aatcatgacc ttcgatcaga tgggaattaa ggacgatctc ctccgtggaa tctaccaaca	180
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aaaaaaaaa a	1451

<210> 190
 <211> 408
 <212> PRT
 <213> H. annuus

<400> 190

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

Pro Ile Met Thr Phe Asp Gln Met Gly Ile Lys Asp Asp Leu Leu Arg
35 40 45

Gly Ile Tyr Gln His Gly Phe Glu Lys Pro Ser Ala Ile Gln Gln Arg
50 55 60

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

Ser Gly Thr Gly Lys Thr Ser Met Ile Ala Leu Thr Val Cys Gln Ile
85 90 95

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

Arg Glu Leu Ala Ala Gln Thr Glu Lys Gln Ile Leu Ala Ile Gly Asp
115 120 125

Phe Ile Ser Ile Gln Ala His Ala Cys Ile Gly Gly Lys Ser Val Gly
130 135 140

Glu Asp Ile Arg Lys Leu Glu Asn Gly Val His Val Val Ser Gly Thr
145 150 155 160

Pro Gly Arg Val Cys Asp Met Ile Lys Arg Arg Thr Leu Arg Thr Arg
165 170 175

Ala Ile Lys Leu Leu Ile Leu Asp Glu Ser Asp Glu Met Leu Ser Arg
180 185 190

Gly Phe Lys Asp Gln Ile Tyr Asp Val Tyr Arg Tyr Leu Pro Pro Glu
195 200 205

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

Met Thr Ser Lys Phe Met Thr Asp Pro Val Arg Ile Leu Val Lys Arg
225 230 235 240

Asp Glu Leu Thr Leu Glu Gly Ile Lys Gln Phe Phe Val Ala Val Glu
245 250 255

Arg Glu Asn Trp Lys Phe Asp Thr Leu Cys Asp Leu Tyr Asp Thr Leu
260 265 270

Thr Ile Thr Gln Ala Val Ile Phe Cys Asn Thr Lys Arg Lys Val Asp
275 280 285

Trp Leu Thr Glu Lys Met Arg Glu Asn Asn Phe Thr Val Ser Ala Met
290 295 300

His Gly Asp Met Pro Gln Lys Glu Arg Asp Ala Ile Met Glu Glu Phe
305 310 315 320

Arg Ser Gly Val Thr Arg Val Leu Ile Thr Thr Asp Val Trp Ala Arg
325 330 335

Gly Leu Asp Val Gln Gln Val Ser Leu Val Ile Asn Tyr Asp Leu Pro
340 345 350

Asn Asn Arg Glu Leu Tyr Ile His Arg Ile Gly Arg Ser Gly Arg Phe
355 360 365

Gly Arg Lys Gly Val Ala Ile Asn Phe Val Lys Thr Asp Asp Ile Lys
 370 375 380

Ile Leu Arg Asp Ile Glu Gln Tyr Tyr Ser Thr Gln Ile Asp Glu Met
 385 390 395 400

Pro Met Asn Val Ala Asp Leu Ile
 405

<210> 191
 <211> 1521
 <212> DNA
 <213> G. max

<400> 191
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 taagatgagt gaattgcttt cactgatgg gcaagaattc ttcacctcat atgacgaagt 180
 ctatgacagc tttgatgcca tgggattgca agagaatctt ctgcgaggca tatatgctta 240
 tggttttgag aggcttctg caatccagca aaggggaatt gttcctttct gcaaaggtct 300
 ggatgtgatt caacaggctc agtctggaac aggaaagaca gcaacatttt gttctggaat 360
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 ggagctagca cagcagattg agaaagttat gcgagctctt ggtgattacc tgggagttaa 480
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gttctctgct acaatgccac cagaagccct tgagattaca agaaagttca tgaataagcc	780
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tggaattctat aaattttgtt taatcaatta attagcaggt tgctgctcaa gcctgcattt	1500
gctttcaaaa aaaaaaaaaa a	1521

<210> 192
 <211> 413
 <212> PRT
 <213> G. max

<400> 192

Met	Ala	Gly	Leu	Ala	Pro	Glu	Gly	Thr	Gln	Phe	Asp	Gly	Arg	Gln	Tyr
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Asp	Ala	Lys	Met	Ser	Glu	Leu	Leu	Ser	Thr	Asp	Gly	Gln	Glu	Phe	Phe
					20				25					30	

Thr Ser Tyr Asp Glu Val Tyr Asp Ser Phe Asp Ala Met Gly Leu Gln
35 40 45

Glu Asn Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Arg Pro Ser
50 55 60

Ala Ile Gln Gln Arg Gly Ile Val Pro Phe Cys Lys Gly Leu Asp Val
65 70 75 80

Ile Gln Gln Ala Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Cys Ser
85 90 95

Gly Ile Leu Gln Gln Leu Asp Tyr Gly Leu Val Gln Cys Gln Ala Leu
100 105 110

Val Leu Ala Pro Thr Arg Glu Leu Ala Gln Gln Ile Glu Lys Val Met
115 120 125

Arg Ala Leu Gly Asp Tyr Leu Gly Val Lys Val His Ala Cys Val Gly
130 135 140

Gly Thr Ser Val Arg Glu Asp Gln Arg Ile Leu Gln Ala Gly Val His
145 150 155 160

Thr Val Val Gly Thr Pro Gly Arg Val Phe Asp Met Leu Arg Arg Gln
165 170 175

Ser Leu Arg Pro Asp Cys Ile Lys Met Phe Val Leu Asp Glu Ala Asp
180 185 190

Glu Met Leu Ser Arg Gly Phe Lys Asp Gln Ile Tyr Asp Ile Phe Gln
195 200 205

Leu Leu Pro Ser Lys Ile Gln Val Gly Val Phe Ser Ala Thr Met Pro
210 215 220

Pro Glu Ala Leu Glu Ile Thr Arg Lys Phe Met Asn Lys Pro Val Arg
225 230 235 240

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

Tyr Val Asn Val Asp Lys Glu Glu Trp Lys Leu Glu Thr Leu Cys Asp
260 265 270

Leu Tyr Glu Thr Leu Ala Ile Thr Gln Ser Val Ile Phe Val Asn Thr
275 280 285

Arg Arg Lys Val Asp Trp Leu Thr Asp Lys Met Arg Ser Asn Asp His
290 295 300

Thr Val Ser Ala Thr His Gly Asp Met Asp Gln Asn Thr Arg Asp Ile
305 310 315 320

Ile Met Arg Glu Phe Arg Ser Gly Ser Ser Arg Val Leu Ile Thr Thr
325 330 335

Asp Leu Leu Ala Arg Gly Ile Asp Val Gln Gln Val Ser Leu Val Ile
340 345 350

Asn Tyr Asp Leu Pro Thr Gln Pro Glu Asn Tyr Leu His Arg Ile Gly
355 360 365

Arg Ser Gly Arg Phe Gly Arg Lys Gly Val Ser Ile Asn Phe Val Thr
370 375 380

Thr Asp Asp Ala Arg Met Leu Ser Asp Ile Gln Lys Phe Tyr Asn Val
385 390 395 400

Thr Val Glu Glu Leu Pro Ser Asn Val Ala Asp Leu Leu
405 410

<210> 193
<211> 1635
<212> DNA
<213> G. max

<400> 193
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cgagagctat caagatgcta gttcttgatg aatctgatga aatgttgagc agagggttta 660

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<210> 194

<211> 407

<212> PRT

<213> G. max

<400> 194

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Asn Pro Ala Glu Asp Met Asp Phe Glu Thr Thr Glu Gly Val Lys Ala
20 25 30

Ile Ala Ser Phe Glu Glu Met Gly Ile Lys Asp Asp Leu Leu Arg Gly
35 40 45

Ile Tyr Gln Tyr Gly Phe Glu Lys Pro Ser Ala Ile Gln Gln Arg Ala
50 55 60

Val Thr Pro Ile Ile Gln Gly Arg Asp Val Ile Ala Gln Ala Gln Ser
65 70 75 80

Gly Thr Gly Lys Thr Ser Met Ile Ala Leu Thr Val Cys Gln Val Val
85 90 95

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

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

Ile Asn Ile Gln Ala His Ala Cys Val Gly Gly Lys Ser Val Gly Glu
130 135 140

Asp Ile Arg Lys Leu Glu Tyr Gly Val His Val Val Ser Gly Thr Pro
145 150 155 160

Gly Arg Val Cys Asp Met Ile Lys Arg Arg Thr Leu Arg Thr Arg Ala
165 170 175

Ile Lys Met Leu Val Leu Asp Glu Ser Asp Glu Met Leu Ser Arg Gly
180 185 190

Phe Lys Asp Gln Ile Tyr Asp Val Tyr Arg Tyr Leu Pro Pro Asp Leu
195 200 205

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

Thr Asn Lys Phe Met Thr Asp Pro Val Arg Ile Leu Val Lys Arg Asp
225 230 235 240

Glu Leu Thr Leu Glu Gly Ile Lys Gln Phe Phe Val Ala Val Glu Arg
245 250 255

Glu Glu Trp Lys Phe Asp Thr Leu Cys Asp Leu Tyr Asp Thr Leu Thr
260 265 270

Ile Thr Gln Ala Val Ile Phe Cys Asn Thr Lys Arg Lys Val Asp Trp
275 280 285

Leu Thr Glu Lys Met Arg Asn Asn Asn Phe Thr Val Ser Ser Met His
290 295 300

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

Ala Gly Thr Thr Arg Val Leu Ile Thr Thr Asp Val Trp Ala Arg Gly
325 330 335

Leu Asp Val Gln Gln Val Ser Leu Val Ile Asn Tyr Asp Leu Pro Asn
340 345 350

Asn Arg Glu Leu Tyr Ile His Arg Ile Gly Arg Ser Gly Arg Phe Gly
355 360 365

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

Leu Arg Asp Ile Glu Gln Tyr Tyr Ser Thr Gln Ile Asp Glu Met Pro
385 390 395 400

Met Asn Val Ala Asp Leu Ile
405

<210> 195
<211> 1569
<212> DNA
<213> G. max

<400> 195
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gagaatcctg gtaaagcgtg atgaattgac ccttgagggt atcaaacagt tttatgtgaa	900
tgttgataag gaagactgga aactagagac attatgtgac ctttatgaga ctttggctat	960
caccagagt gtcacttttg tgaacacaag gcgtaagggt gactggctca ctgacaagat	1020
gcgaagcaat gaccatacag tctcagccac ccatggagac atggaccaa acactcgtga	1080
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gctctagag	1569

<210> 196

<211> 413

<212> PRT

<213> G. max

<400> 196

Met	Ala	Gly	Leu	Ala	Pro	Glu	Gly	Ser	Gln	Phe	Asp	Ala	Arg	Gln	Tyr
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Asp	Ser	Lys	Met	Asn	Glu	Leu	Leu	Ser	Ala	Asp	Gly	Gln	Glu	Phe	Phe
			20					25					30		

Thr	Ser	Tyr	Asp	Glu	Val	Tyr	Asp	Ser	Phe	Asp	Ala	Met	Gly	Leu	Gln
		35					40						45		

Glu	Asn	Leu	Leu	Arg	Gly	Ile	Tyr	Ala	Tyr	Gly	Phe	Glu	Arg	Pro	Ser
	50					55					60				

Ala	Ile	Gln	Gln	Arg	Gly	Ile	Val	Pro	Phe	Cys	Lys	Gly	Leu	Asp	Val
65					70					75					80

Ile	Gln	Gln	Ala	Gln	Ser	Gly	Thr	Gly	Lys	Thr	Ala	Thr	Phe	Cys	Ser
				85					90					95	

Gly	Ile	Leu	Gln	Gln	Leu	Asp	Tyr	Gly	Leu	Val	Gln	Cys	Gln	Ala	Leu
			100					105					110		

Val	Leu	Ala	Pro	Thr	Arg	Glu	Leu	Ala	Gln	Gln	Ile	Glu	Lys	Val	Met
			115				120						125		

Arg	Ala	Leu	Gly	Asp	Tyr	Leu	Gly	Val	Lys	Val	His	Ala	Cys	Val	Gly
		130					135				140				

Gly	Thr	Ser	Val	Arg	Glu	Asp	Gln	Arg	Ile	Leu	Gln	Ala	Gly	Val	His
145					150					155				160	

Thr Val Val Gly Thr Pro Gly Arg Val Phe Asp Met Leu Arg Arg Gln
165 170 175

Ser Leu Arg Pro Asp His Ile Lys Met Phe Val Leu Asp Glu Ala Asp
180 185 190

Glu Met Leu Ser Arg Gly Phe Lys Asp Gln Ile Tyr Asp Ile Phe Gln
195 200 205

Leu Leu Pro Gly Gln Ile Gln Val Gly Val Phe Ser Ala Thr Met Pro
210 215 220

Pro Glu Ala Leu Glu Ile Thr Arg Lys Phe Met Asn Lys Pro Val Arg
225 230 235 240

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

Tyr Val Asn Val Asp Lys Glu Asp Trp Lys Leu Glu Thr Leu Cys Asp
260 265 270

Leu Tyr Glu Thr Leu Ala Ile Thr Gln Ser Val Ile Phe Val Asn Thr
275 280 285

Arg Arg Lys Val Asp Trp Leu Thr Asp Lys Met Arg Ser Asn Asp His
290 295 300

Thr Val Ser Ala Thr His Gly Asp Met Asp Gln Asn Thr Arg Asp Ile
305 310 315 320

Ile Met Arg Glu Phe Arg Ser Gly Ser Ser Arg Val Leu Ile Thr Thr
325 330 335

Asp Leu Leu Ala Arg Gly Ile Asp Val Gln Gln Val Ser Leu Val Ile
340 345 350

Asn Tyr Asp Leu Pro Thr Gln Pro Glu Asn Tyr Leu His Arg Ile Gly
355 360 365

Arg Ser Gly Arg Phe Gly Arg Lys Gly Val Ala Ile Asn Phe Val Thr
370 375 380

Leu Asp Asp Ala Arg Met Leu Ser Asp Ile Gln Lys Phe Tyr Asn Val
385 390 395 400

Thr Val Glu Glu Leu Pro Ser Asn Val Ala Asp Leu Leu
405 410

<210> 197
<211> 1703
<212> DNA
<213> G. max

<400> 197
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agggacttga tgttattcaa caggctcaat ctggaactgg gaagacggct actttctgct	420
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caactcgtga gcttgctcag cagattgaga aagttatgcg ggcacttgga gattatcaag	540
gtgtgaaggt tcatgcttgt gtgggaggta ccagtgtgcg tgaggaccag cgcattctat	600
ctagtgggtg tcatgtttgt gttggtagcc ctggctgtgt gtttgatatg ctgcgccgac	660
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ctgacaagat gagaagccgt gaccacacag tctcagcaac ccacggagac atggaccaga	1080
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gcttagtaat ttatgttaaa ttgtgagttt gtctgaatat ccaagtaatt attacttgc	1560
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<211> 413

<212> PRT

<213> G. max

<400> 198

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Thr Ser Tyr Asp Glu Val Tyr Asp Ser Phe Asp Ala Met Gly Leu Gln
35 40 45

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

Ala Ile Gln Gln Arg Gly Ile Val Pro Phe Cys Lys Gly Leu Asp Val
65 70 75 80

Ile Gln Gln Ala Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Cys Ser
85 90 95

Gly Ile Leu Gln Gln Leu Asp Tyr Ser Leu Thr Gln Cys Gln Ala Leu
100 105 110

Val Leu Ala Pro Thr Arg Glu Leu Ala Gln Gln Ile Glu Lys Val Met
115 120 125

Arg Ala Leu Gly Asp Tyr Gln Gly Val Lys Val His Ala Cys Val Gly
130 135 140

Gly Thr Ser Val Arg Glu Asp Gln Arg Ile Leu Ser Ser Gly Val His
145 150 155 160

Val Val Val Gly Thr Pro Gly Arg Val Phe Asp Met Leu Arg Arg Gln
165 170 175

Ser Leu Gln Pro Asp His Ile Lys Met Phe Val Leu Asp Glu Ala Asp
180 185 190

Glu Met Leu Ser Arg Gly Phe Lys Asp Gln Ile Tyr Asp Ile Phe Gln
195 200 205

Leu Leu Pro Ser Lys Ile Gln Val Gly Val Phe Ser Ala Thr Met Pro
210 215 220

Pro Glu Ala Leu Glu Ile Thr Arg Lys Phe Met Asn Lys Pro Val Arg
225 230 235 240

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

Tyr Val Asn Val Glu Lys Glu Glu Trp Lys Leu Asp Thr Leu Cys Asp
260 265 270

Leu Tyr Glu Thr Leu Ala Ile Thr Gln Ser Val Ile Phe Val Asn Thr
275 280 285

Arg Arg Lys Val Asp Trp Leu Thr Asp Lys Met Arg Ser Arg Asp His
 290 295 300

Thr Val Ser Ala Thr His Gly Asp Met Asp Gln Asn Thr Arg Asp Ile
 305 310 315 320

Ile Met Arg Glu Phe Arg Ser Gly Ser Ser Arg Val Leu Ile Thr Thr
 325 330 335

Asp Leu Leu Ala Arg Gly Ile Asp Val Gln Gln Val Ser Leu Val Ile
 340 345 350

Asn Phe Asp Leu Pro Thr Gln Pro Glu Asn Tyr Leu His Arg Ile Gly
 355 360 365

Arg Ser Gly Arg Phe Gly Arg Lys Gly Val Ala Ile Asn Phe Val Thr
 370 375 380

Lys Asp Asp Glu Lys Met Leu Phe Asp Ile Gln Lys Phe Tyr Asn Val
 385 390 395 400

Gln Val Glu Glu Leu Pro Ser Asn Val Ala Glu Leu Leu
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 <211> 413
 <212> PRT
 <213> G. max

<400> 200

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			20					25					30		

Thr	Ser	Tyr	Asp	Glu	Val	Tyr	Asp	Ser	Phe	Asp	Ala	Met	Gly	Leu	Gln
		35					40						45		

Glu	Asn	Leu	Leu	Arg	Gly	Ile	Tyr	Ala	Tyr	Gly	Phe	Glu	Arg	Pro	Ser
	50					55					60				

Ala	Ile	Gln	Gln	Arg	Gly	Ile	Val	Pro	Phe	Cys	Lys	Gly	Leu	Asp	Val
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Ile	Gln	Gln	Ala	Gln	Ser	Gly	Thr	Gly	Lys	Thr	Ala	Thr	Phe	Cys	Ser
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Gly	Ile	Leu	Gln	Gln	Leu	Asp	Tyr	Gly	Leu	Val	Gln	Cys	Gln	Ala	Leu
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Val Leu Ala Pro Thr Arg Glu Leu Ala Gln Gln Ile Glu Lys Val Met
115 120 125

Arg Ala Leu Gly Asp Tyr Leu Gly Val Lys Val His Ala Cys Val Gly
130 135 140

Gly Thr Ser Val Arg Glu Asp Gln Arg Ile Leu Gln Ala Gly Val His
145 150 155 160

Thr Val Val Gly Thr Pro Gly Arg Val Phe Asp Met Leu Arg Arg Gln
165 170 175

Ser Leu Arg Pro Asp Cys Ile Lys Met Phe Val Leu Asp Glu Ala Asp
180 185 190

Glu Met Leu Ser Arg Gly Phe Lys Asp Gln Ile Tyr Asp Ile Phe Gln
195 200 205

Leu Leu Pro Ser Lys Ile Gln Val Gly Val Phe Ser Ala Thr Met Pro
210 215 220

Pro Glu Ala Leu Glu Ile Thr Arg Lys Phe Met Asn Lys Pro Val Arg
225 230 235 240

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

Tyr Val Asn Val Asp Lys Glu Glu Trp Lys Leu Glu Thr Leu Cys Asp
260 265 270

Leu Tyr Glu Thr Leu Ala Ile Thr Gln Ser Val Ile Phe Val Asn Thr
275 280 285

Arg Arg Lys Val Asp Trp Leu Thr Asp Lys Met Arg Ser Asn Asp His
290 295 300

Thr Val Ser Ala Thr His Gly Asp Met Asp Gln Asn Thr Arg Asp Ile
305 310 315 320

Ile Met Arg Glu Phe Arg Ser Gly Ser Ser Arg Val Leu Ile Thr Thr
325 330 335

Asp Leu Leu Ala Arg Gly Ile Asp Val Gln Gln Val Ser Leu Val Ile
340 345 350

Asn Tyr Asp Leu Pro Thr Gln Pro Glu Asn Tyr Leu His Arg Ile Gly
355 360 365

Arg Ser Gly Arg Phe Gly Arg Lys Gly Val Ala Ile Asn Phe Val Thr
370 375 380

Thr Asp Asp Ser Arg Met Leu Ser Asp Ile Gln Lys Phe Tyr Asn Val
385 390 395 400

Thr Val Glu Glu Leu Pro Ser Asn Val Ala Asp Leu Leu
405 410

<210> 201

<211> 1675

<212> DNA

<213> H. vulgare

<400> 201

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<211> 447

<212> PRT

<213> H. vulgare

<400> 202

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Ser Arg Asn Ala Lys Trp Gly Tyr Ser Ala Phe His Asn Val Thr Ala

35 40 45

Met Val Gly Ala Gly Val Leu Ser Leu Pro Phe Ala Met Ser Glu Leu

50 55 60

Gly Trp Gly Pro Gly Ile Ala Val Leu Ile Ile Ser Trp Val Ile Thr

65 70 75 80

Leu Tyr Thr Leu Trp Gln Met Val Glu Met His Glu Met Val Pro Gly
85 90 95

Lys Arg Phe Asp Arg Tyr His Glu Leu Gly Gln His Ala Phe Gly Asp
100 105 110

Lys Leu Gly Leu Trp Ile Val Val Pro Gln Gln Leu Ile Val Glu Val
115 120 125

Gly Val Asn Ile Val Tyr Met Val Thr Gly Gly Arg Ser Leu Lys Lys
130 135 140

Phe His Asp Val Ile Cys Asp Gly Lys Cys Lys Asp Ile Lys Leu Ser
145 150 155 160

Phe Phe Ile Met Ile Phe Ala Ser Val His Phe Val Leu Ser Gln Leu
165 170 175

Pro Asn Phe Asn Ser Ile Ser Gly Val Ser Leu Ala Ala Ala Val Met
180 185 190

Ser Leu Ser Tyr Ser Thr Ile Ala Trp Gly Ala Ser Val Asp Lys Gly
195 200 205

Lys Met Val Asn Val Asp Tyr Asn Leu Arg Ala Thr Thr Met Pro Gly
210 215 220

Lys Val Phe Gly Phe Phe Gly Ala Leu Gly Glu Val Ala Phe Ala Tyr
225 230 235 240

Ala Gly His Asn Val Val Leu Glu Ile Gln Ala Thr Ile Pro Ser Thr
245 250 255

Pro Glu Lys Pro Ser Lys Lys Pro Met Trp Lys Gly Val Val Val Ala
260 265 270

Tyr Ile Val Val Ala Leu Cys Tyr Phe Pro Val Ala Leu Ile Gly Tyr
275 280 285

Trp Ala Phe Gly Asn Ser Val Asp Asp Asn Ile Leu Ile Thr Leu Asn
290 295 300

Lys Pro Lys Trp Leu Ile Ala Met Ala Asn Met Met Val Val Ile His
305 310 315 320

Val Ile Gly Ser Tyr Gln Ile Tyr Ala Met Pro Val Phe Asp Met Ile
325 330 335

Glu Thr Val Leu Val Lys Lys Leu Arg Phe Pro Pro Gly Leu Thr Leu
340 345 350

Arg Leu Ile Ala Arg Ser Leu Tyr Val Ala Phe Thr Met Phe Val Ala
355 360 365

Ile Thr Phe Pro Phe Phe Gly Gly Leu Leu Gly Phe Phe Gly Gly Phe
370 375 380

Ala Phe Ala Pro Thr Thr Tyr Phe Leu Pro Cys Ile Met Trp Leu Ala
385 390 395 400

Ile Tyr Lys Pro Lys Arg Phe Ser Leu Ser Trp Cys Thr Asn Trp Val
405 410 415

Cys Ile Val Leu Gly Val Cys Leu Met Ile Leu Ser Pro Ile Gly Gly
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435 440 445

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<211> 2445
<212> DNA
<213> P. patents

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<400> 204

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Pro	Lys	Thr	Pro	Leu	Arg	Ser	Ser	Phe	Ser	Val	Asp	Ser	Ser	Gly	Val
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Ala	Thr	Gly	Arg	Arg	Gly	Trp	Gln	Arg	Ser	Ser	Lys	Gly	Phe	Phe	Lys
		50				55					60				

Leu	Gly	Gln	Ser	Leu	Lys	Phe	Lys	Ser	Ser	Ser	Gln	Glu	Tyr	Asp	Glu
65					70					75					80

Asp	Met	Pro	Lys	Asp	Leu	Gln	Trp	Lys	Thr	Leu	Asp	Pro	Ser	Ser	Pro
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Ser Leu Tyr Lys Trp Asn Thr Phe Phe Leu Val Ser Cys Leu Val Ala
100 105 110

Ile Phe Val Asp Pro Leu Phe Phe Tyr Leu Pro Lys Val Asp Tyr Ser
115 120 125

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

Phe Arg Thr Ile Ser Asp Phe Phe Tyr Val Val His Met Val Leu Arg
145 150 155 160

Phe Arg Thr Ala Phe Val Arg Pro Ser Thr Arg Val Phe Gly Arg Gly
165 170 175

Glu Leu Val Thr Asp Pro Arg Glu Ile Ala Ile Arg Tyr Leu Lys Phe
180 185 190

Asp Phe Trp Ile Asp Phe Val Ala Val Leu Pro Ile Pro Gln Val Val
195 200 205

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

Asn Thr Lys Asp Ala Leu Arg Tyr Ile Val Val Phe Gln Tyr Val Pro
225 230 235 240

Arg Met Leu Arg Ile Phe Pro Leu Leu Ser Lys Met Ile Asn Ser Thr
245 250 255

Gly Val Leu Leu Glu Thr Ala Trp Ala Gly Ala Ala Phe Asn Leu Ile
260 265 270

Leu Tyr Met Leu Ala Ser His Ile Leu Gly Ala Thr Trp Tyr Leu Leu
275 280 285

Ser Val Glu Arg Gln Asp Thr Cys Trp Thr Asp Val Cys Leu Arg Asn
290 295 300

Ala Pro Asp Lys Ala Leu Cys Arg Arg Glu Ile Phe Asp Cys Ala Trp
305 310 315 320

Gln Gly Ala Ala Val Asn Ala Trp Tyr Gly Asn Phe Thr Thr Asp Ser
325 330 335

Asn Val Phe Cys Asn Tyr Ile Ala Val Pro Met Gly Ala Asp Thr Phe
340 345 350

Asn Tyr Gly Ile Tyr Asn Asn Ala Ile Ser Asn Thr Ile Ser Ser Ser
355 360 365

Asp Leu Ala Phe Ser Gln Thr Tyr Phe Phe Cys Leu Trp Gln Gly Leu
370 375 380

Leu Ala Leu Ser Ser Leu Ser Gln Thr Leu Asn Val Ser Thr Phe Val
385 390 395 400

Gly Glu Ile Ile Phe Thr Ile Ile Ile Ile Ile Val Gly Leu Phe Leu
405 410 415

Phe Ala Phe Leu Ile Gly Asn Met Gln Thr Tyr Leu Gln Ser Leu Thr
420 425 430

Leu Arg Leu Glu Glu Met Arg Val Lys Arg Arg Asp Thr Glu Gln Trp
435 440 445

Met Arg His Arg Asn Leu Pro His Asp Ile Val Gln Arg Val Arg Arg
450 455 460

Tyr Asp Gln Tyr Lys Trp Val Ala Thr Arg Gly Val Asp Glu Glu Thr
465 470 475 480

Leu Val Gln Ser Leu Pro Ser Asp Leu Arg Arg Asp Ile Lys Arg His
485 490 495

Leu Cys Leu Arg Leu Val Arg Asn Val Pro Phe Cys Asp Gln Met Asp
500 505 510

Glu Ser Leu Leu Asp Ala Met Cys Glu Arg Leu Arg Pro Ala Leu Cys
515 520 525

Thr Glu Gly Thr His Ile Leu Arg Glu Gly Asp Pro Val Asn Glu Met
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Phe Phe Val Ile Arg Gly Glu Leu Lys Ser Glu Thr Thr Asn Gly Gly
545 550 555 560

Arg Thr Gly Phe Tyr Asn Lys Ala Val Leu Ser Ser Gly Asp Phe Cys
565 570 575

Gly Glu Glu Leu Leu Thr Trp Ala Leu Asp Pro Lys Pro Gln Ser His
580 585 590

Leu Pro Thr Ser Thr Ser Ser Val Lys Ala Leu Lys Glu Val Glu Ala
595 600 605

Phe Ser Leu Ser Ser Asp Asp Leu Lys Phe Ile Ala Ser Gln Phe Arg
610 615 620

Arg Leu His Ser Lys Gln Leu Gln His Thr Phe Arg Tyr Tyr Ser Asn
625 630 635 640

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Tyr Gln Arg Arg Arg Leu Ala Glu Leu Arg Arg Lys Glu Glu Asp Gln
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Tyr Leu Ser Leu Gln Gly Glu Pro Thr Asp Arg Ile Ser Leu Gly Ala
675 680 685

Thr Ile Leu Ala Gly Arg Phe Ala Lys Asn Ala Met Arg Gly Val Gln
690 695 700

Arg Leu Arg Ser Met His Ala Ala Glu Leu Ala Arg Ile Ser Asn Ile
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Pro Lys Pro Ser Glu Ser Asp Phe Ser Gln Asp Asn
725 730

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<211> 1113

<212> DNA

<213> Z. mays

<400> 205

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tcgcccgact tccgccgtgg gtgctggccg ggcgccgggt ccccgctcaa cgacgtgctc	780
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gtcagcttcg gcggcgacga cgagcccgct gagagggctg agtcgggcg cgccctccgc	1020
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<210> 206

<211> 370

<212> PRT

<213> Z. mays

<400> 206

Met Met Met Met Gly Glu Gly Val Ser Met Pro Pro Trp Ser His His
1 5 10 15

Val Pro Val Ser Gly Val Asp Glu Gly Asp Glu Met Thr Pro Tyr Leu
20 25 30

Leu Ala Ala Leu Arg Gln Tyr Leu Pro Cys Asn Asp Ala Gly Ala Glu
35 40 45

Ala Glu Glu Asp Glu Ala Ala Ala Ala Ala Ala Met Ala Ala Gly
50 55 60

Val Asp Gly Tyr Gly Cys Asp Glu Phe Arg Met Tyr Glu Phe Lys Val
65 70 75 80

Arg Arg Cys Ala Arg Ala Arg Ser His Asp Trp Thr Glu Cys Pro Phe
85 90 95

Ala His Pro Gly Glu Lys Ala Arg Arg Arg Asp Pro Arg Lys Tyr His
100 105 110

Tyr Ser Gly Ala Ala Cys Pro Asp Phe Arg Lys Gly Gly Cys Lys Arg
115 120 125

Gly Asp Gly Cys Asp Met Ala His Gly Val Phe Glu Cys Trp Leu His
130 135 140

Pro Ala Arg Tyr Arg Thr Gln Pro Cys Lys Asp Gly Thr Ala Cys Arg
145 150 155 160

Arg Arg Val Cys Phe Phe Ala His Thr Ala Asp Gln Leu Arg Val Leu
165 170 175

Pro Pro Thr Pro Gln Gln Gln Ser Ser Pro Arg Gly Ala Ala Cys Ser
180 185 190

Ser Pro Leu Ala Glu Ser Tyr Asp Gly Ser Pro Leu Arg Arg Gln Ala
195 200 205

Phe Glu Ser Tyr Leu Thr Lys Ser Ile Met Cys Ser Ser Pro Thr Ser
210 215 220

Thr Leu Leu Ser Pro Pro Lys Ser Pro Pro Ser Glu Ser Pro Pro Leu
225 230 235 240

Ser Pro Asp Phe Arg Arg Gly Cys Trp Pro Gly Ala Gly Ser Pro Val
245 250 255

Asn Asp Val Leu Ala Ser Leu Arg Gln Leu Arg Leu Ser Arg Ala Asn
260 265 270

Ser Ser Pro Ser Gly Gly Trp Cys Gly Tyr Pro Ala Ser Ala Val Ala
275 280 285

Tyr Gly Ser Pro Thr Gly Gly Ala Leu Tyr Gly Leu Ser Ser Thr Pro
290 295 300

Arg Ala Thr Ala Ala Ser Cys Tyr Met Ala Asn Leu Asp Pro Leu Asp
305 310 315 320

Val Ser Phe Gly Gly Asp Asp Glu Pro Val Glu Arg Val Glu Ser Gly
325 330 335

Arg Ala Leu Arg Ala Lys Val Phe Glu Arg Leu Ser Arg Glu Gly Ala
340 345 350

Val Ser Gly Asp Ala Gly Gly Pro Asp Val Gly Trp Val Ser Asp Leu
355 360 365

Ile Asn
370

<210> 207

<211> 1672

<212> DNA

<213> P. patents

<400> 207

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gagaaagaaa aagagggaga ttgggacgtt atttcgaggt ttctgtagcg tgttgaggtt 180

tgtaattgtc tctggctcgg ttagtgaact tgcttgaggg cataggagtt caggagtagc 240

cacttgttgc gtgttcagtc ttcaggaaac gtgcgcgtca agacttggtg tttattaaga 300

gatcatcttg tagtcgttct gtgacgtata gcgatcaata agcagtttca gatttccagt 360

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<210> 208

<211> 231

<212> PRT

<213> P. patents

<400> 208

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

Gly Ala Arg His Tyr Leu Ala Pro Val Lys Lys Asp Leu Lys Ser Ala
20 25 30

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

Met Arg Gln Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Asn Lys
50 55 60

Arg Ser Arg Ile Trp Leu Gly Ser Phe Pro Thr Ala Glu Met Ala Ala
65 70 75 80

Arg Ala Tyr Asp Ala Ala Val Val Cys Leu Arg Gly Pro Gly Ala Thr
85 90 95

Leu Asn Phe Pro Asp Ser Pro Pro Gln Leu Leu Pro Glu Cys Asn Ser
100 105 110

Pro Lys Asp Ile Gln Val Ala Ala Ala Ala Ala Ala Ala Ala Lys
115 120 125

Pro Cys Thr Pro Val Ala Leu Pro Ala Lys Ala Lys Met Gln Leu Leu
130 135 140

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

Ser His Gln Thr Pro Ala Glu Ser Asp Cys Ser Gly Thr Thr Gly Glu
165 170 175

Gly Ser Ser Arg Ser Gly Ala Lys Ser Glu Ile Thr Gln Asp Glu Glu
180 185 190

Leu Asp Phe Thr Gly Glu Ser Ser Ser Pro Val Val Ala Glu Glu Phe
195 200 205

Val Ser Leu Glu Asp Val Glu Leu Ala Trp Glu Asp Ala Lys Phe Asp
210 215 220

Asp Ile Asn Phe Leu Asp Leu
225 230

<210> 209
<211> 1193
<212> DNA
<213> B. napus

<400> 209
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ttggtgtctt tgggtataaag ctcttcttac aagaaagatc accaatgata ggttttagaga 180
gtacgtccaa gaactcttcg actaactcag ttagtcaaga gaacacgaga gagaccaaac 240
cggtttagaga ttctggtaag catccggttt acaggggtgt ccgaaagagg agctggggaa 300
aatgggtgtc ggagataaga gagccgagga agaaatctcg tatatggctc ggaacgtttc 360
cttcaccgga gatggcgggc cgtgcacacg acgtagctgc tttgagcatc aaaggaacct 420
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ctcgagacat ccaagccgca gctctcaaag ctgcacacat ggagatcatt atgacgacct	540
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cctctgcgac tggctcggag gagctagagg agattgttga gctgccgagt ttaggggtcta	660
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accatatgtt gaatgatgtt gaatgttagt tgttgatttg ggattatcaa tattcctttt	1140
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<210> 210
 <211> 217
 <212> PRT
 <213> B. napus

<400> 210

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

His	Pro	Val	Tyr	Arg	Gly	Val	Arg	Lys	Arg	Ser	Trp	Gly	Lys	Trp	Val
			35					40					45		

Ser Glu Ile Arg Glu Pro Arg Lys Lys Ser Arg Ile Trp Leu Gly Thr
50 55 60

Phe Pro Ser Pro Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu
65 70 75 80

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

Ser Phe Pro Arg Pro Ser Ser Leu Ser Pro Arg Asp Ile Gln Ala Ala
100 105 110

Ala Leu Lys Ala Ala His Met Glu Ile Ile Met Thr Thr Ser Gln Ser
115 120 125

Ser Ser Ser Ser Ser Leu Thr Ser Ser Ser Ser Leu Glu Ser Leu Val
130 135 140

Ser Ser Ser Ala Thr Gly Ser Glu Glu Leu Glu Glu Ile Val Glu Leu
145 150 155 160

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

Phe Ile Phe Phe Asp Ser Ala Asp Phe Trp Val Tyr Pro Pro His Gln
180 185 190

Leu Ser Glu Val Asp Tyr Glu Met Ile Pro Gly Ser Leu Ser Gln Asp
195 200 205

Trp Asp Leu Pro Gly Leu Phe Asn Tyr
210 215

<210> 211
<211> 366
<212> DNA
<213> Z. mays

<400> 211
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ccaccaagc ggccggcggg gcggaccaag ttccgggaga cgcggcaccc cgtgtaccgc 180
ggcgtgcggc ggcgcgggcc cgcggggcgc tgggtgtgcg aggtccgcga gcccaacaag 240
aagtcgcgca tctggctcgg caccttcgcc acccccgagg ccgccgcgcg cgcgcacgac 300
gtggccgcgc tggccctgcg gggccgcgcc gcgtgectca acttcgcga ctgggcgcgc 360
cactag 366

<210> 212
<211> 121
<212> PRT
<213> Z. mays

<400> 212

Met Glu Tyr Ala Ala Val Gly Tyr Gly Tyr Gly Tyr Gly Tyr Asp Glu
1 5 10 15

Arg Gln Glu Pro Ala Glu Ser Ala Asp Gly Gly Gly Gly Gly Asp Asp
20 25 30

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

Thr Lys Phe Arg Glu Thr Arg His Pro Val Tyr Arg Gly Val Arg Arg
50 55 60

Arg Gly Pro Ala Gly Arg Trp Val Cys Glu Val Arg Glu Pro Asn Lys
65 70 75 80

Lys Ser Arg Ile Trp Leu Gly Thr Phe Ala Thr Pro Glu Ala Ala Ala
85 90 95

Arg Ala His Asp Val Ala Ala Leu Ala Leu Arg Gly Arg Ala Ala Cys
100 105 110

Leu Asn Phe Ala Asp Ser Ala Arg His
115 120

<210> 213
<211> 884
<212> DNA
<213> B. napus

<400> 213
cttccacca aagtagcctt ttcgtaacat ttgatggatc actcatcttc ttcggaatca 60
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aataaaaata tcaagaagaa aagagtcaaa gaagatcttg atgatgatga aaagattaat 180
gtttcaaagc atcaaagttt tagaggggtg agaatgaggc aatggggaaa atgggtctcg 240
gagatcagag agccaaagaa gaaatctaga atctggcttg gtaccttccc cacggcggag 300
atggctgctc gtgctcacga cgtggcggct ttagccataa aaggtgactc tgctcatctc 360
aacttcccgg agctagccta ccacctcct agaccggcta gtgccacccc taaagacatc 420

caagcagccg cagcggaggc tgcagcttca gtagtcattg atatggacat agagacgtcg 480
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 gagtccttcc cttacgagga acccttcttc tcgggaagtt actagaaaac aaagacggtg 660
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 cttttacgtg ggtaaagtca tgtgtgatat gtaagttttt ttttgcttaa agatatgtaa 840
 gctataaatg ttatttgttt tgtaacaaaa aaaaaaaaaa aaaa 884

<210> 214
 <211> 203
 <212> PRT
 <213> B. napus

<400> 214

Met Asp His Ser Ser Ser Ser Glu Ser His Leu Asp Asp Tyr Arg Arg
 1 5 10 15

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

Ile Lys Lys Lys Arg Val Lys Glu Asp Leu Asp Asp Asp Glu Lys Ile
 35 40 45

Asn Val Ser Lys His Gln Ser Phe Arg Gly Val Arg Met Arg Gln Trp
 50 55 60

Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Lys Lys Lys Ser Arg Ile
 65 70 75 80

Trp Leu Gly Thr Phe Pro Thr Ala Glu Met Ala Ala Arg Ala His Asp
85 90 95

Val Ala Ala Leu Ala Ile Lys Gly Asp Ser Ala His Leu Asn Phe Pro
100 105 110

Glu Leu Ala Tyr His Leu Pro Arg Pro Ala Ser Ala His Pro Lys Asp
115 120 125

Ile Gln Ala Ala Ala Glu Ala Ala Ala Ser Val Val Ile Asp Met
130 135 140

Asp Ile Glu Thr Ser Ser Pro Ser Thr Gly Ala Thr Glu Leu Ser Pro
145 150 155 160

Pro Ala Val Ala Ser Thr Ala Asp Asp Ala Phe Ser Asp Leu Pro Asp
165 170 175

Leu Phe Leu Asp Val Asn His Lys Asn Asp Gly Phe Trp Glu Ser Phe
180 185 190

Pro Tyr Glu Glu Pro Phe Phe Ser Gly Ser Tyr
195 200

<210> 215

<211> 958

<212> DNA

<213> B. napus

<400> 215

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ctcaatatca agaaggaaat gtcattgtca cctccgtctt ctccaaagat caagagcaag	180
aagaataaga ttaagaagta caaaggagtg aggatgagaa gttggggatc atgggtgtct	240
gagattaggg caccaaataa aaagataagg atttggttg gctcttactc aacagctgaa	300
gcagcagcta gggcttatga tgttgcactc ttgtgtctaa aaggccctca agccaatctc	360
aacttcccca gctctgcttc ttctcgctt ctgttagatg aaaagacca tttgtcccc	420
aaatccatcc aaaaaattgc cgctcaagca gccacaatt catttgacct tttgtctcca	480
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gataatgac ataatgggat gttcttcttc gatgatggag ctccgtttaa ttactctcct	660
ccactgaact cgaccacgaa tatggtcgat gggatattct acgaagatgc tgatattcca	720
ctttggagtt tcagttgatc tgacggtcca gaatacatac ttactatat atgttttatt	780
atttacaaaa ttatTTTTat atgttaatta atttacctta cacaaaaatg ataactaatt	840
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa	958

<210> 216
 <211> 210
 <212> PRT
 <213> B. napus

<400> 216

Met	Val	Lys	Gln	Glu	Leu	Asn	Ile	Lys	Lys	Glu	Met	Ser	Leu	Ser	Pro
1				5				10					15		

Pro Ser Ser Pro Lys Ile Lys Ser Lys Lys Asn Lys Ile Lys Lys Tyr
20 25 30

Lys Gly Val Arg Met Arg Ser Trp Gly Ser Trp Val Ser Glu Ile Arg
35 40 45

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

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

Pro Gln Ala Asn Leu Asn Phe Pro Ser Ser Ala Ser Ser Arg Leu Leu
85 90 95

Leu Asp Glu Lys Thr His Leu Ser Pro Lys Ser Ile Gln Lys Ile Ala
100 105 110

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

Ala Asp Ser Ser Pro Phe Asp His Asp Gln His Pro Asp Asp Met Gln
130 135 140

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

Ser Ser Ser Trp Tyr Asp Asn Asp His Asn Gly Met Phe Phe Phe Asp
165 170 175

Asp Gly Ala Pro Phe Asn Tyr Ser Pro Pro Leu Asn Ser Thr Thr Asn
180 185 190

Met Val Asp Gly Tyr Phe Tyr Glu Asp Ala Asp Ile Pro Leu Trp Ser
195 200 205

Phe Ser
210

<210> 217
<211> 821
<212> DNA
<213> B. napus

<400> 217
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agtttgata tgtttatttt ttttgtaact tccccccact ttttgggaca tcatcttacc 780

atactaaaaa ggaaaataag cccaaaaaaa aaaaaaaaaa a

821

<210> 218

<211> 177

<212> PRT

<213> B. napus

<400> 218

Met Asp Gln Gly Pro Ser Ser Ser Lys Tyr Lys Gly Val Arg Lys Arg
1 5 10 15

Lys Trp Gly Lys Trp Val Ser Glu Ile Arg Leu Pro Asn Ser Arg Glu
20 25 30

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

Phe Asp Ala Ala Leu Tyr Cys Leu Arg Gly Ser Gly Thr Lys Phe Asn
50 55 60

Phe Pro Asp Asn Pro Pro Ala Ile Ser Gly Gly Gly Asn Met Ser Arg
65 70 75 80

Ser Glu Ile Arg Asp Ala Ala Ala Arg Phe Ala Asn Ser Glu Glu Ser
85 90 95

Val Ala Ser Glu Met Val Val Gln Gln Gln Glu Ser Pro Ser Thr Thr
100 105 110

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

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

Ala Asp Glu Phe Leu Gly Asp Arg Phe Val Glu Gln Val Ser Pro Thr
145 150 155 160

Trp Asn Gly Asp Glu Ser Cys Tyr Asp Gly Ser Val Ser Leu Trp Asn
165 170 175

Phe

<210> 219

<211> 878

<212> DNA

<213> B. napus

<400> 219

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accggaaga actcgaagtc taaaaatgag caaaagagtg tttccaagca toccaatttt	180
cgtgggggtca gaatgagaca atggggaaaa tgggtgtctg agatcagaga gccaaagaa	240
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gtggcggtt tagccatcaa aggcggctct gtcacctca atttcctga gctcgttgc	360
catttgccga gaccggccag cgcagatcct aaagacattc aagccgccgc tgcagcagcc	420
gcagtggaat ggaaagcccc ggagtcaccg tctagcacgg ggacgtcatc tatgacgtca	480
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cacaaagtgg acggtttctg ggactcgttt ccctacgaag aacctttctt catgggaaac	600

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<210> 220
 <211> 181
 <212> PRT
 <213> B. napus

<400> 220

Met	Gln	Asp	Ser	Ser	Leu	Pro	Arg	Ser	Glu	Arg	Asn	Leu	Arg	Ser	Leu
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Val	Pro	Glu	Arg	Thr	Gly	Lys	Asn	Ser	Lys	Ser	Lys	Asn	Glu	Gln	Lys
			20					25					30		

Ser	Val	Ser	Lys	His	Pro	Asn	Phe	Arg	Gly	Val	Arg	Met	Arg	Gln	Trp
		35					40					45			

Gly	Lys	Trp	Val	Ser	Glu	Ile	Arg	Glu	Pro	Arg	Lys	Lys	Ser	Arg	Ile
	50					55				60					

Trp	Leu	Gly	Thr	Phe	Ser	Thr	Pro	Glu	Met	Ala	Ala	Arg	Ala	His	Asp
65					70					75				80	

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

Glu Leu Ala Cys His Leu Pro Arg Pro Ala Ser Ala Asp Pro Lys Asp
100 105 110

Ile Gln Ala Ala Ala Ala Ala Val Glu Trp Lys Ala Pro Glu
115 120 125

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

Asp Asp Ala Phe Ser Asp Leu Pro Asp Leu Leu Val Asp Ala Asn Asp
145 150 155 160

His Lys Val Asp Gly Phe Trp Asp Ser Phe Pro Tyr Glu Glu Pro Phe
165 170 175

Phe Met Gly Asn Tyr
180

<210> 221
<211> 968
<212> DNA
<213> B. napus

<400> 221
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tctccggtgg aagaggagac tcatcaccac cgagaagatg aagagaccca tcgaacaaat 180
aagaagaaac gggctagacc cgacccgtgt tatagaggcg tacggatgcg aacgtggggc 240
aatgggtct ccgagatccg cgagccacgc aagaagagcc gaatctggct cggcaccttc 300
tccacggcgg agatggcggc gcgtg'gcac gacgcagctg ctttaaccat caaaggaccc 360

Arg Thr Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Arg Lys Lys
50 55 60

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

Ala His Asp Ala Ala Ala Leu Thr Ile Lys Gly Pro Ser Ala Val Leu
85 90 95

Asn Phe Pro Glu Leu Ala Thr Phe Leu Pro Arg Pro Ala Ser Ser Ser
100 105 110

Pro Arg Asp Val Gln Ala Ala Ala Val Ala Ala Ala Met Asp Phe
115 120 125

Ser Ser Ser Ser Ser Ser Ala Gly Val Ile Ser Asp Pro Thr Thr Val
130 135 140

Val Pro Glu Ser Gln Leu Ser Ser Ser Ser Ser Tyr Leu Ser Phe Thr
145 150 155 160

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

Ala Glu Glu Leu Ser Glu Ile Val Glu Leu Pro Ser Leu Glu Thr Ser
180 185 190

Tyr Asp Glu Pro Trp Ser Glu Phe Val Tyr Val Asp Pro Ala Tyr Pro
195 200 205

Pro Ser Ser Pro Trp Tyr Phe Asn Asn Cys Tyr Ser Phe Tyr Tyr His
210 215 220

Ser	Asp	Glu	Thr	Gly	Thr	Ser	Met	Gly	Glu	Pro	Phe	Asp	Ser	Ser	Asn
225					230					235					240

Phe	Cys	Leu	Phe	Pro
				245

<210> 223
 <211> 983
 <212> DNA
 <213> G. max

<400> 223	
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ctttctattc cttaaaccat ggtcgagcct gcagtagcag caagctcaga attatcagac	120
tcaacacgaa acaccaacac caacaccctt tcacctctt cctcatcgtc gttatctccg	180
tcgccatcac cgtcatcatc aagctctaaa aagcgagcga gagacaacaa caatagtaga	240
aacaacagca acaagcattc tgtgtataga ggtgtccgaa tgcgcacgtg gggcaaattg	300
gtgtcggaaa tccgcgagcc gcgaaagaag aaccgaatct ggctcggcac ctctgccacc	360
gccgagatgg cggcgcgtgc ccacgacgtg gcggcgctga cgataaaagg ctcatccgcc	420
atccttaact tccccgaact cgccgcctcc ctgccccggc cggcctccaa ctcgccccgc	480
gacgtgcagg ccgcggcagc caaggcggcg tccatggagg cgccgcgcgc gacccctccg	540
tcgccggccg ccacgccgga ggatgacctc ggcgagatcg tggagctgcc gccgctcgga	600
acgagtttcg actcgcccga ccggagttcc gagtttgtgt tcctggacat ggacgacggg	660
tggccctatt ctacccgtg gtaccacagc atttatgatg gtgggtactt cattagcgac	720
atgaacaaca tggtttcgat gcaagagtca gagagcatgg ttctttccct gtggccttga	780

agttaagcca atgctactca ttgcagtatg gttatatattt ggttcttttt tttttttttt	840
gcgtgagaca gataatcatg tttctgttct taagtatgcg attagggatt ggattttcat	900
gtccgtatat atgaaataac atttatttgc cgatatcaat ctcttgaatg aacatcaata	960
cattgaaaaa aaaaaaaaaa aaa	983

<210>	224
<211>	233
<212>	PRT
<213>	G. max

<400> 224

Met Val Glu Pro Ala Val Ala Ala Ser Ser Glu Leu Ser Asp Ser Thr
1 5 10 15

Arg Asn Thr Asn Thr Asn Thr Pro Ser Pro Ser Ser Ser Ser Ser Ser Leu
20 25 30

Ser Pro Ser Pro Ser Pro Ser Ser Ser Ser Ser Ser Lys Lys Arg Ala Arg
35 40 45

Asp Asn Asn Asn Ser Arg Asn Asn Ser Asn Lys His Ser Val Tyr Arg
50 55 60

Gly Val Arg Met Arg Thr Trp Gly Lys Trp Val Ser Glu Ile Arg Glu
65 70 75 80

Pro Arg Lys Lys Asn Arg Ile Trp Leu Gly Thr Phe Ala Thr Ala Glu
85 90 95

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

Ser Ala Ile Leu Asn Phe Pro Glu Leu Ala Ala Ser Leu Pro Arg Pro
115 120 125

Ala Ser Asn Ser Pro Arg Asp Val Gln Ala Ala Ala Lys Ala Ala
130 135 140

Ser Met Glu Ala Pro Pro Arg Thr Pro Pro Ser Pro Ala Ala Thr Pro
145 150 155 160

Glu Asp Asp Leu Gly Glu Ile Val Glu Leu Pro Pro Leu Gly Thr Ser
165 170 175

Phe Asp Ser Pro Asp Arg Ser Ser Glu Phe Val Phe Leu Asp Met Asp
180 185 190

Asp Gly Trp Pro Tyr Ser His Pro Trp Tyr His Ser Ile Tyr Asp Gly
195 200 205

Gly Tyr Phe Ile Ser Asp Met Asn Asn Met Val Ser Met Gln Glu Ser
210 215 220

Glu Ser Met Val Leu Ser Leu Trp Pro
225 230

<210> 225

<211> 1097

<212> DNA

<213> G. max

<400> 225

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tgtaaaaatg attcattttc ctctaactac agcattgata cttgcaagat gtacaaaggg	180
gtaaggaaga gaaaatgggg caaatgggtg tccgaaattc ggcttcccaa cagccgtgag	240
cgcatatggt tggggctcta tgacacccaa gtgaaggcgg ccagagcatt tgatgtcgca	300
ctttattgcc tacgtggcaa aagtgcgagt ttcaactttc ctgacacacc tcgacacttg	360
gaaattaata tgggtgttacc atgtgacata caacaacaac ctctctccca tccggagatt	420
caagagatag cctcgaagtt tgcgaacaac gaccacgtcc ctttggagga ggagagtgct	480
tttcaagaac aagaacaaga cccctcgatg gagtcacaaa gtgacgagtc taaatctgcc	540
aatacaataa cggagatgag caacttcctt aatatttatg atggtggaac tcatactaat	600
gtacaagtgg atcaattaca aggggattgg gacagcatgg attggacatt ttttaacatg	660
ttggatgact tgaatggctc ggatttttggc ctctatttgg ggccagacaa gttgcacccg	720
ggtgagtttt tgtgtcccac tcaagctcca atgctttttc atgaggatga aattgaaggt	780
gatgatgac atgatgcttt ttctaaccat tccttacttt ggagttggaa cttttgattc	840
acctgcaa attaacttagat accctctact ttgcataagt ttcaactagt aaataattac	900
tagcaagcaa gcctctctat tatgtttttt tgtagccatt tatacatggc tgtttctcaa	960
ttataatagt taggctatga ctagagttta tgtcaaattg accataaaga caaaaagaaa	1020
aaagaccata taccatgcc aataataat tatagaaagt ggcccggttt ttattgccta	1080
aaaaaaaaa aaaaaaa	1097

<210> 226

<211> 254

<212> PRT

<213> G. max

<400> 226

Met Val Lys Pro Ala Met Ala Ser Val Asp Ser Ser Ser Phe Ser Ser
1 5 10 15

Cys Lys Asn Asp Ser Phe Ser Ser Asn Tyr Ser Ile Asp Thr Cys Lys
20 25 30

Met Tyr Lys Gly Val Arg Lys Arg Lys Trp Gly Lys Trp Val Ser Glu
35 40 45

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

Thr Gln Val Lys Ala Ala Arg Ala Phe Asp Val Ala Leu Tyr Cys Leu
65 70 75 80

Arg Gly Lys Ser Ala Ser Phe Asn Phe Pro Asp Thr Pro Arg His Leu
85 90 95

Glu Ile Asn Met Val Leu Pro Cys Asp Ile Gln Gln Gln Pro Leu Ser
100 105 110

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

Val Pro Leu Glu Glu Glu Ser Ala Phe Gln Glu Gln Glu Gln Asp Pro
130 135 140

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

Glu Met Ser Asn Phe Pro Asn Ile Tyr Asp Gly Gly Thr His Thr Asn
165 170 175

Val Gln Val Asp Gln Leu Gln Gly Asp Trp Asp Ser Met Asp Trp Thr
180 185 190

Phe Phe Asn Met Leu Asp Asp Leu Asn Gly Ser Asp Phe Gly Leu Tyr
195 200 205

Leu Gly Pro Asp Lys Leu His Pro Gly Glu Phe Leu Cys Pro Thr Gln
210 215 220

Ala Pro Met Leu Phe His Glu Asp Glu Ile Glu Gly Asp Asp Asp His
225 230 235 240

Asp Ala Phe Ser Asn His Ser Leu Leu Trp Ser Trp Asn Phe
245 250

<210> 227
<211> 1181
<212> DNA
<213> G. max

<400> 227
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caaacctgca gcatcagaaa tcaggcattg caatcaccaa aggtggcaag ttcaaaggga 120
gaagcagaaa caacaacacc acaaatttg ttggggtgag acaaaggccc tcaggagat 180
gggtagctga gatcaaagac acaactcaga agataagaat gtggcttggc acatttgaga 240
cagctgagga agcagcaaga gcctatgatg aagccgctg cttcttctgc ggatccaaca 300
ctcgaccaa cttcatcact catgtctcct tggattcccc tcttgcttct cgaattcgaa 360

atcttcttaa caacagaaaa ggtatcaaaa aagaggaaga tgctaattgct aatgctaata	420
atgcacctgc cccaagagtt agcactacta gcagtgtac tagcactggg actagtagta	480
attcaagcaa tggaaatgac aacaatgacc agtctctttc taccgtaaca actcaaagtt	540
caaatctggt tgatgatgcc tataaaccag atttgagcaa ttgcagggag gagtttgagt	600
caggatcatca gtccaatact tcatgggtgt ttggacctgt ctttgatcgt ttccctatgg	660
ctcaaatatt cgatatacca aagattgatg atggcctcac taatgcagct gatttggatc	720
tttcagaatt tgaaagaatg aaagttgaaa gacaaatatc agcttcactc tatgcaatta	780
atgggggtgca agagtacatg gaaactgttc aggactccaa tgaaactctc tgggatcttc	840
cacccttatg ctcatgttc tgttaatctt gaaggtttta atgacctgc aattattcct	900
tctcaatgtc ctatttattt tactattatt gaagatttga ggaaggggtg tgggatctaa	960
ggattgattg aaatattaca ataacaatat agctttgggtg agatataatt ttgtttttct	1020
aactgcttaa tgtcagcagg aagatccatg agttgcattt tgtgaaagct ctttttcaat	1080
cattattatg taaaaagtct aagcatttat gttccttttt tcacatccta aatgtcaaaa	1140
agtaaatctt caaatctttt tgcaaaaaaa aaaaaaaaaa a	1181

<210> 228
 <211> 275
 <212> PRT
 <213> G. max

<400> 228

Met	Glu	Ile	Gln	Phe	Gln	Gln	Pro	Asn	Leu	Gln	His	Gln	Lys	Ser	Gly
1				5					10					15	

Ile	Ala	Ile	Thr	Lys	Gly	Gly	Lys	Phe	Lys	Gly	Arg	Ser	Arg	Asn	Asn
				20				25						30	

Asn Thr Asn Lys Phe Val Gly Val Arg Gln Arg Pro Ser Gly Arg Trp
35 40 45

Val Ala Glu Ile Lys Asp Thr Thr Gln Lys Ile Arg Met Trp Leu Gly
50 55 60

Thr Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Glu Ala Ala
65 70 75 80

Cys Leu Leu Arg Gly Ser Asn Thr Arg Thr Asn Phe Ile Thr His Val
85 90 95

Ser Leu Asp Ser Pro Leu Ala Ser Arg Ile Arg Asn Leu Leu Asn Asn
100 105 110

Arg Lys Gly Ile Lys Lys Glu Glu Asp Ala Asn Ala Asn Ala Asn Asn
115 120 125

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

Thr Ser Ser Asn Ser Ser Asn Gly Asn Asp Asn Asn Asp Gln Ser Leu
145 150 155 160

Ser Thr Val Thr Thr Gln Ser Ser Asn Leu Phe Asp Asp Ala Tyr Lys
165 170 175

Pro Asp Leu Ser Asn Cys Arg Glu Glu Phe Glu Ser Gly His Gln Ser
180 185 190

Asn Thr Ser Trp Cys Phe Gly Pro Val Phe Asp Arg Phe Pro Met Ala
195 200 205

Gln Ile Phe Asp Ile Pro Lys Ile Asp Asp Gly Leu Thr Asn Ala Ala
210 215 220

Asp Leu Asp Leu Ser Glu Phe Glu Arg Met Lys Val Glu Arg Gln Ile
225 230 235 240

Ser Ala Ser Leu Tyr Ala Ile Asn Gly Val Gln Glu Tyr Met Glu Thr
245 250 255

Val Gln Asp Ser Asn Glu Thr Leu Trp Asp Leu Pro Pro Leu Cys Ser
260 265 270

Leu Phe Cys
275

<210> 229
<211> 1095
<212> DNA
<213> G. max

<400> 229
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aacaacaaaaa gtaacacaca cgcacacacg catcatcgta taacatttgt tttatttttt 120
ttaaagagcg agtggtgtaa caaatggtga agtcgaagag cgtggagaaa cctgcggagg 180
aacaacaacg aggtggtggt tcagcgtaca gaggagtacg gaagaggaag tgggggaagt 240
acgtgtcggg aattaggctg cccaacagcc gtcaaaggat ttggttgggt tcttacgaca 300
gcgccgaaaa ggcggcgcgt gcattcgacg cggccatggt ctgcttacgt ggcagcgggtg 360

ccaacttta	tttcccgagc	gaccggccca	acatcgctgg	cgggaggaac	atgacgccct	420
cgcagattca	gatcgccgcg	gcgcgtttcg	ccaattcgga	gccccgaaag	gagtgttcgg	480
gtaaaccctg	ggagtctttg	acttcgattg	aggaaacgac	gtcgtttcca	gtaaattcgg	540
atacggatac	atcttctcct	ctatcagtag	tgacgatcca	aaacgacacc	gaagtagcaa	600
ccgggtcgtt	tccgggtata	ttttcgggtt	tcgggtcggg	taatttcgtc	cccgaattct	660
ccgattttcc	gagcttcgat	gatttcggcc	acgatttctt	cgtgcatgag	cttcggggtt	720
tcgattacgg	agaagagaac	ttggatgggt	tgataattca	ggactcgttc	ctgtggaatt	780
tctaagcggg	tcggggtttag	gataatttta	ttatatccca	accgtgttta	gaattcggat	840
cggatccgga	tttgggttgg	tcaatttttg	tgagaccatg	ccctctgtgt	tagtagttag	900
tgatggtaat	gtttttttta	tgtacctagt	agtcaagggt	tcgatttttt	gggatgagaa	960
tcataattta	tttatttgtc	atgactcatg	tcattaattg	taaagttgtc	tgctgatagt	1020
gtaattttct	tttggccatt	cattcaatta	taaaaatgat	aagatatttt	cgtctgcaaa	1080
aaaaaaaaaa	aaaaa					1095

<210> 230
 <211> 213
 <212> PRT
 <213> G. max

<400> 230

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

Gly	Gly	Val	Ser	Ala	Tyr	Arg	Gly	Val	Arg	Lys	Arg	Lys	Trp	Gly	Lys
			20					25					30		

Tyr Val Ser Glu Ile Arg Leu Pro Asn Ser Arg Gln Arg Ile Trp Leu
35 40 45

Gly Ser Tyr Asp Ser Ala Glu Lys Ala Ala Arg Ala Phe Asp Ala Ala
50 55 60

Met Phe Cys Leu Arg Gly Ser Gly Ala Asn Phe Asn Phe Pro Ser Asp
65 70 75 80

Arg Pro Asn Ile Ala Gly Gly Arg Asn Met Thr Pro Ser Gln Ile Gln
85 90 95

Ile Ala Ala Ala Arg Phe Ala Asn Ser Glu Pro Arg Lys Glu Cys Ser
100 105 110

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

Pro Val Asn Ser Asp Thr Asp Thr Ser Ser Pro Leu Ser Val Val Thr
130 135 140

Ile Gln Asn Asp Thr Glu Val Ala Thr Gly Ser Phe Pro Gly Ile Phe
145 150 155 160

Ser Gly Phe Gly Ser Gly Asn Phe Val Pro Glu Phe Ser Asp Phe Pro
165 170 175

Ser Phe Asp Asp Phe Gly His Asp Phe Phe Val His Glu Leu Pro Gly
180 185 190

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

Phe Leu Trp Asn Phe

210

<210> 231

<211> 1174

<212> DNA

<213> H. annuus

<400> 231

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aacactagcg aaatggaagg agtacaataa taaaatcgat tcgttggacg agaaagcgaa	120
gcctgtacgg aaagtgcccg caaaagggtc gaaaaaaggg tgtatgaaag gttaaaggcgg	180
gcccgaaaac tcgcggtgca aataccgagg cgtaagacaa cgaacatggg gaaaatgggt	240
ggccgagatt cgggaaccca atcgagggag gaggttatgg ttagggactt ttgggtctgc	300
ggttgaagca gcccgggctt atgatgaagc ggcccggggt atgtatgggc cctgtgcgcg	360
cctcaatatg cccgattctg gttcgggtcc gggttcgggt tcgatgaacg agtggttcgaa	420
gatggggtct aatggtgctt ctagttgtga ttcgaccaca acgtgtagtc actcggagga	480
gattataccg tgggtcaaac gacaaacggt taatcaggat gaaggcgagt caaacagcgg	540
tcaactgttg accatggtca gacaagaagt taaagaagaa ccattgaag aaaaagttga	600
aatgacaaag gatgttgatt ttcaaaatat ggaagagctt acggaaacga tggcgcaaag	660
ggacacagga cccacgtag atcacgtggg gtcccttgag cctcctgatg aggctgagaa	720
cgaacctatg agccaagatg gtagtgagcc aacatctggt tatgggttcg gtttctctaa	780
ccgagaaccc cctgatgtgt tcagggggct cgatgatatg ctttggcttg agccagcgag	840
acaagacggg tgtgggggtg tagcggatta cgggttcgat ttcttgaagc cggggcggcc	900

cgaagagtgc aacttcacat tggaagagtt ggggttcaat ttgggggctg attttggtgt 960

gtgagcagag acaagagtga aacattacta attgtttaca tgtttttttaa gaatttttag 1020

gcaacatatt gataaagttg gtgtattgta ggtggaacaa agatactatt gtgccttgta 1080

gatcgttcgt aggtttgtat aaattggttc gtgttggttaa cccgaagcta gtttgtatag 1140

aacttaaatt ttcggaacaaa aaaaaaaaaa aaaa 1174

<210> 232

<211> 266

<212> PRT

<213> H. annuus

<400> 232

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

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

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

Ala Ala Arg Ala Tyr Asp Glu Ala Ala Arg Val Met Tyr Gly Pro Cys
50 55 60

Ala Arg Leu Asn Met Pro Asp Ser Gly Ser Gly Pro Gly Ser Gly Ser
65 70 75 80

Met Asn Glu Cys Ser Lys Met Gly Ser Asn Gly Ala Ser Ser Cys Asp
85 90 95

Ser Thr Thr Thr Cys Ser His Ser Glu Glu Ile Ile Pro Trp Ser Asn
100 105 110

Arg Gln Thr Val Asn Gln Asp Glu Gly Glu Ser Asn Ser Gly Gln Leu
115 120 125

Leu Thr Met Val Arg Gln Glu Val Lys Glu Glu Pro Ile Glu Glu Lys
130 135 140

Val Glu Met Thr Lys Asp Val Asp Phe Gln Asn Met Glu Glu Leu Thr
145 150 155 160

Glu Thr Met Ala Gln Arg Asp Thr Gly Pro His Val Asp His Val Gly
165 170 175

Ser Leu Glu Pro Pro Asp Glu Ala Glu Asn Glu Pro Cys Ser Gln Asp
180 185 190

Gly Ser Glu Pro Thr Ser Gly Tyr Gly Phe Gly Phe Ser Asn Arg Glu
195 200 205

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

Ala Arg Gln Asp Gly Cys Gly Val Val Ala Asp Tyr Gly Phe Asp Phe
225 230 235 240

Leu Lys Pro Gly Arg Pro Glu Glu Cys Asn Phe Thr Leu Glu Glu Leu
245 250 255

Gly Phe Asn Leu Gly Ala Asp Phe Gly Val
260 265

<210> 233
<211> 847
<212> DNA
<213> H. annuus

<400> 233
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acaataacat gaatcacaac accgccaccg ctaccacaac caccaccaa cgccccaac 120
ccggggacct taacgatgaa gttacaaaa aaacaagaa aaccgacatt gatcaataa 180
accaccctgt ataccgcggt gtacgcaagc ggagttgggg aaaatgggtg tcagaaatcc 240
gcgagccaaa gaaaaaatca agaatatggc ttgggacttt tgacaccca gagatggcgg 300
cccgggcca tgatgtagct gcggtcgcca tcaaaggtaa ctcgccatc ctcaacttcc 360
ctgagctggc tcaccaactc cccaagccgg cttcaaactc ccctagagat atccaagccg 420
cggctcttaa agccgccacg ttggtccttc gaagccttaa ttccgataaa gatgatcaat 480
ccgagccaac ccggattgat caacttccat gttcttcgtc ttcatttca tgttcacttc 540
aaagtgatat aacggatgac ccgtttcttg atttgccgga tctttatatg gacctcgggt 600
accggatttt taacacattg tcagagaaga ttactggtaa caatgaattc tggccagaag 660
atcatttctt gtggagctat agctaaaaat gtttttgtgc taaaataata ataattattat 720
attgttggtta cgtctagaaa cttaaatttt attatttgtg agattgaaat ctatattggt 780
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aaaaaaaa 847

<210> 234
<211> 205
<212> PRT

<213> H. annuus

<400> 234

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

Lys Pro Gly Asp Leu Asn Asp Glu Val Thr Lys Lys Thr Lys Lys Thr
20 25 30

Asp Ile Asp Gln Ile Asn His Pro Val Tyr Arg Gly Val Arg Lys Arg
35 40 45

Ser Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Lys Lys Lys Ser
50 55 60

Arg Ile Trp Leu Gly Thr Phe Asp Thr Pro Glu Met Ala Ala Arg Ala
65 70 75 80

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

Phe Pro Glu Leu Ala His Gln Leu Pro Lys Pro Ala Ser Asn Ser Pro
100 105 110

Arg Asp Ile Gln Ala Ala Ala Leu Lys Ala Ala Thr Leu Val Leu Arg
115 120 125

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

Gln Leu Pro Cys Ser Ser Ser Ser Ser Ser Cys Ser Leu Gln Ser Asp
145 150 155 160

Ile Thr Asp Asp Pro Phe Leu Asp Leu Pro Asp Leu Tyr Met Asp Leu
165 170 175

Gly Tyr Arg Ile Phe Asn Thr Leu Ser Glu Lys Ile Thr Gly Asn Asn
180 185 190

Glu Phe Trp Pro Glu Asp His Phe Leu Trp Ser Tyr Ser
195 200 205

<210> 235
 <211> 907
 <212> DNA
 <213> H. annuus

<400> 235	
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gtctccgata tcatccgttc ttacgcccgc ctcaaaaact cctcctctga tgtctggccc	120
gaattcaacc catatgaagc agaattcaac aactcatatg aagcagaatt caaccaatth	180
gtccaacaaa ccgattccga ttatcacaag cgacctcttc catattcagg tgggatgcat	240
gaaaccacca ggaaaaaaca gaggaagaat ctgtaccgtg ggatacggca gcgcccattg	300
gggaaatggg cggcgggagat tcgcatcct agaaaaggcg ttagggtttg gttgggtact	360
ttcaacacag cggaagaagc tgctagagct tacgacaaag aagctcgtaa aatccgagga	420
agaaaagcta aggttaatth tccaagcgat gaagaagaag agtatthta tgcaaaaac	480
cccaacctga ataactataa cgatattctt ctcggtttt ctgacgaaga agttatgggt	540
ccgcgttttg tgaaagaaaa cgagaagaag aagaagaaag ttgaagaagt tgtacagaag	600
gaagagaatg aggtgcagaa gctgtcggag gagctgatgg cgtatgagtc gtatatgaag	660

ttttatgata ttccgtatct tgaagggcag ccgtcggcgg tggctccggc gaatgcagac	720
ggtggtggtt cgattgagct ttggagcttt gatgatgtag cgtgatttgg aagtttacct	780
ttctgcgtgt tttttttagt ttaagtttaa ataattttgt gtttaataat gtaaattgct	840
gtgtttgaac ttctatatgt gttgggcata aaactaagaa gtttggtata aaaaaaaaaa	900
aaaaaaaa	907

Met Cys Gly Gly Ala Ile Val Ser Asp Leu Ile Arg Ser Ser Arg Arg
1 5 10 15

Ala Glu Phe Asn Asn Ser Tyr Glu Ala Glu Phe Asn Gln Phe Val Gln
35 40 45

Met His Glu Thr Thr Arg Lys Lys Gln Arg Lys Asn Leu Tyr Arg Gly
65 70 75 80

Arg Lys Gly Val Arg Val Trp Leu Gly Thr Phe Asn Thr Ala Glu Glu
100 105 110

Ala Ala Arg Ala Tyr Asp Lys Glu Ala Arg Lys Ile Arg Gly Arg Lys
115 120 125

Ala Lys Val Asn Phe Pro Ser Asp Glu Glu Glu Glu Tyr Phe Asn Arg
130 135 140

Lys Asn Pro Asn Leu Asn Asn Tyr Asn Asp Ile Leu Leu Gly Phe Ser
145 150 155 160

Asp Glu Glu Val Met Gly Pro Arg Leu Val Lys Glu Asn Glu Lys Lys
165 170 175

Lys Lys Lys Val Glu Glu Val Val Gln Lys Glu Glu Asn Glu Val Gln
180 185 190

Lys Leu Ser Glu Glu Leu Met Ala Tyr Glu Ser Tyr Met Lys Phe Tyr
195 200 205

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

Ala Asp Gly Gly Gly Ser Ile Glu Leu Trp Ser Phe Asp Asp Val Ala
225 230 235 240

<210> 237

<211> 806

<212> DNA

<213> H. annuus

<400> 237

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ggtgtcggtg ttttcgacca tcttctcctt ttccaatcac caaaaccaat ggaagccatc	180
atcacccggcg gcggagatgg gccgtgcaac cgtccgccgg agaaaaggaa gagtgatcaa	240
cggccgtaca aggggatacg catgaggaag tggggaaaat ggggtggcggg gattcgggag	300
ccgaataagc ggtccaggat ttggttgggg tcctattcga cgcccgtggc cgctgcacgg	360
gcgtacgaca cggccgtata ctacctacgg ggcccgcacgg ccagggtgaa ttttcccgaa	420
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atagagggtg gggccagagt ggatgcagag acgagttgta cgtcgttgct taggagtggt	540
acgcgtgtac ccgggtctgg gcttaaggcg tgttggtttc aggagaaacc cgacttgaat	600
atgaaacccg aaccgcagga gaatgatgga gattattggt gatggataca atacgaggat	660
gggttggttt ggtgggtcgg tcggtcgggg cagttggatg gaagatattt tctttctttt	720
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aaggaaaaaa aaaaaaaaaa aaaaaa	806

<210> 238
 <211> 157
 <212> PRT
 <213> H. annuus

<400> 238

Met	Glu	Ala	Ile	Ile	Thr	Gly	Gly	Gly	Asp	Gly	Pro	Cys	Asn	Arg	Pro
1				5					10					15	

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

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

Ser Arg Ile Trp Leu Gly Ser Tyr Ser Thr Pro Val Ala Ala Ala Arg
50 55 60

Ala Tyr Asp Thr Ala Val Tyr Tyr Leu Arg Gly Pro Thr Ala Arg Leu
65 70 75 80

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

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

Ala Glu Thr Ser Cys Thr Ser Leu Leu Arg Ser Gly Thr Arg Val Pro
115 120 125

Gly Ser Gly Leu Lys Ala Cys Trp Phe Gln Glu Lys Pro Asp Leu Asn
130 135 140

Met Lys Pro Glu Pro Glu Glu Asn Asp Gly Asp Tyr Trp
145 150 155

<210> 239

<211> 945

<212> DNA

<213> L. usitatissimum

<400> 239

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aaggggtgca tgcgtgggaa aggcggggccg gagaacgcac tatgcagcta caagggagtg	180
aggcaacgca cgtggggtaa atgggttgca gagatcaggg aaccaaccg cggcgctcgt	240
ctctggctcg gcaccttcga cacctccac gacgcgctt tggcctacga cactgccgct	300
cgtaagctct acggctctca cgccaagctc aacttgccca accacaacga cgtcgttcac	360
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agttatgata attacaatga gataggagtg gggaacgagt tctgggtcaa tttgcaggtg	540
aatttgccgt tgtttgatga atccatatgg gcggaggctg ccatgtcact ggactacttt	600
ccggtggtgg caatggacgg cgggcagttg gccggcggct gggatgctgc ttctgcttcc	660
gcgccact agtagtaatg aatacatagg tgcatgtaaa ttattataag gggaattaat	720
taatcaatta agattgtgtg tgctatgcaa ccattaatta gctgggtctgt attggattaa	780
gatatatcta aacaagtgtg taaataaagt gttaagtata agcactactg gtagcagcag	840
cttgtggttt aagctgctgg cttttctgtg tatcttgttt gtgaatacta atatactata	900
aaaatagata gttgctctta aaggccgaaa aaaaaaaaaa aaaaa	945

<210> 240
 <211> 211
 <212> PRT
 <213> L. usitatissimum

<400> 240

Met	Ser	Thr	Ser	Ser	Ser	Ser	Thr	Gly	Glu	Pro	Gly	Ser	Asn	Trp	Asn
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Pro His Met Lys Lys Ala Ala Gln Ala Ser Ser Arg Lys Gly Cys Met
20 25 30

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

Arg Gln Arg Thr Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro Asn
50 55 60

Arg Gly Ala Arg Leu Trp Leu Gly Thr Phe Asp Thr Ser His Asp Ala
65 70 75 80

Ala Leu Ala Tyr Asp Thr Ala Ala Arg Lys Leu Tyr Gly Pro His Ala
85 90 95

Lys Leu Asn Leu Pro Asn His Asn Asp Val Val His Val Pro Lys Gln
100 105 110

Asp Ser Gly Asp Ala Thr Thr Thr Thr Ser Ser Ser Phe Asp Met Pro
115 120 125

Ala Gly Tyr Tyr Asn Asn Tyr Ser Ser Asn Ser Ser Ser Glu Glu Gly
130 135 140

Ile Ser Ser Ser Ser Tyr Asp Asn Tyr Asn Glu Ile Gly Val Gly Asn
145 150 155 160

Glu Phe Trp Ser Asn Leu Gln Val Asn Leu Pro Leu Phe Asp Glu Ser
165 170 175

Ile Trp Ala Glu Ala Ala Met Ser Leu Asp Tyr Phe Pro Val Val Ala
180 185 190

Met Asp Gly Gly Gln Leu Ala Gly Gly Trp Asp Ala Ala Ser Ala Ser
195 200 205

Ala Pro Asn
210

<210> 241
<211> 1201
<212> DNA
<213> L. usitatissimum

<400> 241
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atgcgtggca aaggcggccc cgagaacgcc ctctgcacct acaaagggtgt ccgacagcgt 180
acttggggca aatgggtcgc cgagatccgc gagcccaacc gcgggggccc cctctggctc 240
ggcaccttcg acacctccca cgacgccgcc ttagcctacg acgccgccgc tcgtaagctc 300
tacgggcccg acgccaaact caatttgccc cacttccaca actccccaa caataccaat 360
cataataata tcgtcccca cgtggatgta cacgtgcctc tatcacttat ttctctgtgt 420
ggtcccaccc tttctccttc tttcacctct tcctcctcct ccaataatgg tcccactttc 480
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gctgcagcag cagcggacgc cagttgtaat tataattaca aggtaggagg aaacgaggtg 660
tggtctaatt tgaacgcaa tttgcccttg atggacgact ccatttgggt ggaggccgcc 720
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gcgcttccgc cgtccaatac caccctctgg tgcattctaat ttttaggaaca atatattaga 840
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 aagaatgaag ggtgggatag aaataaaagg gaaacatata tatatatagg gacgtgtata 960
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 a 1201

<210> 242
 <211> 259
 <212> PRT
 <213> L. usitatissimum

 <400> 242

Met Pro Asn Ala Thr Ser Ser Ser Thr Ser Asp His Cys Pro Lys Pro
 1 5 10 15

Arg Ala Ser Ser Gly Ser Ser Arg Lys Gly Cys Met Arg Gly Lys Gly
 20 25 30

Gly Pro Glu Asn Ala Leu Cys Thr Tyr Lys Gly Val Arg Gln Arg Thr
 35 40 45

Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro Asn Arg Gly Ala Arg
 50 55 60

Leu Trp Leu Gly Thr Phe Asp Thr Ser His Asp Ala Ala Leu Ala Tyr
 65 70 75 80

Asp Ala Ala Ala Arg Lys Leu Tyr Gly Pro Asp Ala Lys Leu Asn Leu
85 90 95

Pro His Phe His Asn Ser Pro Asn Asn Thr Asn His Asn Asn Ile Val
100 105 110

Pro His Val Asp Val His Val Pro Leu Ser Leu Ile Ser Ser Gly Gly
115 120 125

Pro Thr Leu Ser Pro Ser Phe Thr Ser Ser Ser Ser Ser Asn Asn Gly
130 135 140

Pro Thr Phe Thr Ser Asn Asn Ala Asp Val Gly Tyr Arg Gly Phe Asp
145 150 155 160

Leu Pro Leu His Gly Gly Asp Gly Gly Gln Trp Val Asp His Tyr Ser
165 170 175

Ser Ser Asp Trp Lys Asn Thr Asp Ser Ser Ala Ala Ala Ala Ala Ala
180 185 190

Asp Ala Ser Cys Asn Tyr Asn Tyr Lys Val Gly Gly Asn Glu Val Trp
195 200 205

Ser Asn Leu Asn Ala Asn Leu Pro Leu Met Asp Asp Ser Ile Trp Val
210 215 220

Glu Ala Ala Met Ser Leu Asp Tyr Phe Gln Val Ala Ala Met Gln Asp
225 230 235 240

Ser Asn Gly Trp Asp Thr Ala Ala Leu Pro Pro Ser Asn Thr Thr Pro
245 250 255

Trp Cys Ile

<210> 243
<211> 1162
<212> DNA
<213> L. usitatissimum

<400> 243
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agccccttcc ccagatcaac aacggcgggc gagaccggaa agagatgcat ttccggggag 180
tgaggaagcg cccgtggggc cgttacgcgg cggagatccg tgaccggggg aagaagacct 240
gggtctggct tggcacgttt gacactgcgg aggaagccgc cagagcttac gacaaagcgg 300
cgcgtagactt ccgtgggtcc aaggccaaga ccaacttccc atctcccaac gagatcgctt 360
cttccaaacc cggcggggtc accgccgttg ttgttccgac tgccgacagc ttogtcaatc 420
ggcagagccc cagccagagc agcaccgttg aatcgtctga tccaccggtg gcgagtgagt 480
tgactcgcca gatcgatttt ttcaggcctc tgctgtttgc cgccgcgcgc tccggcggtg 540
tcggcagtgt cggcggcatg gttggtaggt ttccgtttgt gtaccagcag cagcagccgc 600
aggggataat gactccggtg tggttcttcg acgggatggg gaagcctgag ttctgtgacag 660
ctcagcggtt cccggtccga ttcgaccggc tggattacaa cgggtggaaga gcgcacagcg 720
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ttcatttccc gaaaaataa ctttttttta atcgggtggt ttttcctatt atctaatttt	900
taccaacta attaagaaaa atttctgtaa ggttgagag atcacaggaa gaagaaaatt	960
acattaagta catgatcgac gaaggagatc tggaaattca aagggttaat taatgtaaat	1020
aagtcagttt ttttgcaacc catcgagat taagaagact aagtttgctc ttttgtctct	1080
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ttccaaaaaa aaaaaaaaaa aa	1162

<210> 244
 <211> 243
 <212> PRT
 <213> L. usitatissimum

<400> 244

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

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

Val	Trp	Leu	Gly	Thr	Phe	Asp	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala	Tyr
	50					55					60				

Asp	Lys	Ala	Ala	Arg	Asp	Phe	Arg	Gly	Ser	Lys	Ala	Lys	Thr	Asn	Phe
65					70				75					80	

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

Val Val Val Pro Thr Ala Asp Ser Phe Val Asn Arg Gln Ser Pro Ser
100 105 110

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

Thr Arg Gln Ile Asp Phe Phe Arg Pro Leu Pro Val Ala Ala Ala Ala
130 135 140

Ser Gly Gly Val Gly Ser Val Gly Gly Met Val Gly Arg Phe Pro Phe
145 150 155 160

Val Tyr Gln Gln Gln Gln Pro Gln Gly Ile Met Thr Pro Val Trp Phe
165 170 175

Phe Asp Gly Met Val Lys Pro Glu Phe Val Thr Ala Gln Arg Phe Pro
180 185 190

Val Arg Phe Asp Pro Val Asp Tyr Asn Gly Gly Arg Ala His Ser Glu
195 200 205

Ser Asp Ser Thr Ser Ser Val Val Leu Asp Cys Lys Pro Ser Ser Ser
210 215 220

Gly Gly Asn Gly Arg Val Leu Asp Leu Asp Leu Asn Leu Ala Pro Pro
225 230 235 240

Ala Glu Ala

<210> 245
<211> 975
<212> DNA
<213> T. aestivum

<400> 245

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cggccaaggg ttccaagaaa ggggtgcatgg cagggaaagg aggtccagag aattcaaact	180
gcgcttaccg cgggtgtgagg cagaggacgt ggggcaaagt ggttgctgag atccgtgagc	240
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aatggaagc acatgaagag taccaagatg gtgatgatgg gtttagtctt ttctcatatt	720
agggttttag ctatgagggg tgtagtcatg cggagcaata gggataactt tcattctagc	780
tgctaggaaa tacttcaaat tatctgcaac ccgaagcttt gtagtcactt atggttttca	840
tcttactgga gagaatagct ttataccata agtcaacggg tacaagaagt tgtcctgtgc	900
gttgagttca tgtactatgg taaaagttga gtccatattt aatgagctta ctctgtcgaa	960
aaaaaaaaa aaaaa	975

<210> 246

<211> 191
<212> PRT
<213> T. aestivum

<400> 246

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

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

Asn Arg Gly Asn Arg Leu Trp Leu Gly Ser Phe Pro Thr Ala Val Glu
35 40 45

Ala Ala Arg Ala Tyr Asp Asp Ala Ala Arg Ala Met Tyr Gly Ala Lys
50 55 60

Ala Arg Val Asn Phe Ser Glu Gln Ser Pro Asp Ala Ser Ser Gly Cys
65 70 75 80

Thr Leu Ala Pro Pro Leu Leu Met Ser Asn Gly Ala Thr Ala Ala Ser
85 90 95

His Pro Ser Asp Gly Lys Asp Glu Ser Glu Ser Ala Gly Thr Val Ala
100 105 110

His Lys Val Lys Lys Glu Val Ser Asn Asp Leu Arg Ser Thr His Glu
115 120 125

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

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

Asp Met Ile Ile Val Glu Leu Ser Ala Asp Val Lys Met Glu Ala His
 165 170 175

Glu Glu Tyr Gln Asp Gly Asp Asp Gly Phe Ser Leu Phe Ser Tyr
 180 185 190

<210> 247
 <211> 1334
 <212> DNA
 <213> T. aestivum

<400> 247
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 cgcggggctc ggccggcgtg gggggctcgg gctggacgac ggcgagggcg acttcgaggc 180
 cgacttcgag gagttcgagg ccgactccgg ggactccggc caggagctcg ggcgcggcg 240
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 caagaaggcc aaggtttaact ttccagagga accaacagtt cctcagaagc gccgtgcttg 600
 ccctgctgct cctaaagttt ccaagtcaag cgcagcacag gaacctaccg tcataccagc 660
 agtcaacaac cttgcccaacc caaatgcttt cgtctaccgc tctgctgact ttgcatcaaa 720

gcagccactt gttcagcctg ataacgtgcc atttgttcct gcaattaact ctgctgcacc	780
tggtgaagct cctgttatga atatgtactc tgaccagga agcaactcct ttggctgctc	840
tgacttgggc tgggagtatg acaccaagac tccagatata tcatccattg ctcccatttc	900
taccattgct gaaggagcag aaactgcact tctccagagt aacacctaca acccagcgg	960
gattgctgaa ggagctgaat ctgcgcctgt ccagaccaac acctacaact cagtgggtgcc	1020
tcctgtcatg gagaacaatg ctgttgattt tgaaccttgg atgaggtttc ttttgatga	1080
tggcgtggat gagccgattg atagccttct gaattttgat gtgcctcagg atgtcgttgg	1140
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tcaaaccct gtacatcagg acaaagggaa taagactatg ggagattggg aagcaccocg	1260
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gagtctcttt tgta	1334

<210> 248
 <211> 287
 <212> PRT
 <213> T. aestivum

<400> 248

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

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

Gly Thr Phe Asn Ser Ala Glu Glu Ala Ala Arg Ala Tyr Asp Val Glu
50 55 60

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

Pro Thr Val Pro Gln Lys Arg Arg Ala Cys Pro Ala Ala Pro Lys Val
85 90 95

Ser Lys Ser Ser Ala Ala Gln Glu Pro Thr Val Ile Pro Ala Val Asn
100 105 110

Asn Leu Ala Asn Pro Asn Ala Phe Val Tyr Pro Ser Ala Asp Phe Ala
115 120 125

Ser Lys Gln Pro Leu Val Gln Pro Asp Asn Val Pro Phe Val Pro Ala
130 135 140

Ile Asn Ser Ala Ala Pro Val Glu Ala Pro Val Met Asn Met Tyr Ser
145 150 155 160

Asp Gln Gly Ser Asn Ser Phe Gly Cys Ser Asp Leu Gly Trp Glu Tyr
165 170 175

Asp Thr Lys Thr Pro Asp Ile Ser Ser Ile Ala Pro Ile Ser Thr Ile
180 185 190

Ala Glu Gly Ala Glu Thr Ala Leu Leu Gln Ser Asn Thr Tyr Asn Pro
195 200 205

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

Tyr Asn Ser Val Val Pro Pro Val Met Glu Asn Asn Ala Val Asp Phe
 225 230 235 240

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

Asp Ser Leu Leu Asn Phe Asp Val Pro Gln Asp Val Val Gly Asn Met
 260 265 270

Asp Leu Trp Ser Phe Asp Asp Met Pro Ile Cys Gly Glu Ile Phe
 275 280 285

<210> 249
 <211> 1315
 <212> DNA
 <213> T. aestivum

<400> 249
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 tccggcagca gctcctggag gagccggcgc ggccggcgta ctgccggagc gcgagcttcg 180
 gcagcctggg ggcggaaccag tggagcgagt cgctcccgtt ccggcccaac gacgcgcgacg 240
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cagccgcggg ccagaagcgt ccgtctccgc agccggcgag ccccgactct cctcctccct	720
cctcaagcgc acccggtctg tcgaagcgga gaaagagagg cgaggccgcg gcagcgtcca	780
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cccagccgtg gctcgccacc ggcgccgtcc agcagctagt gagctgaagc ggcgaagcaa	900
ccactgatcg ttctcatgac cgacggttat tagttcttcc ttcatgtgtt gaacccacgg	960
agaaacagag catcaagatg agatcaatgg cgcgtaatgc gtcgctcgaa gaaaccttga	1020
tcagttggag gcaattacgc gccacgccgt cgtgaaattt gtgtggttcc gtgtgaaact	1080
tgtcgctaga gttagtggcg ttggcacagt agcaagtgtg cgcagtggaa ttctggaagc	1140
tggtttgtga gaggtggtga gagtgcaggt gcaaaacttg cacagacctt ctctctcca	1200
atggagaatc ttctttgttc aaccgttggt ttggtgctagc atcagtgagt ggttcctttc	1260
aaatttgcag gtttccatt gatatatagt ttaataacaa aaaaaaaaaa aaaaa	1315

<210> 250
 <211> 273
 <212> PRT
 <213> T. aestivum

<400> 250

Met	Leu	Leu	Leu	Asn	Pro	Ala	Ser	Glu	Ala	Ala	Ala	Ala	Ala	Ala	Leu
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Asp	Ser	Ile	Arg	Gln	Gln	Leu	Leu	Glu	Glu	Pro	Ala	Arg	Pro	Ala	Tyr
			20					25						30	

Cys Arg Ser Ala Ser Phe Gly Ser Leu Val Ala Asp Gln Trp Ser Glu
35 40 45

Ser Leu Pro Phe Arg Pro Asn Asp Ala Asp Asp Met Val Val Tyr Gly
50 55 60

Ala Leu Arg Asp Ala Phe Ser Cys Gly Trp Leu Pro Asp Gly Ser Phe
65 70 75 80

Ala Ala Val Lys Pro Glu Pro Leu Pro Ser Pro Gly Ser Tyr Asp Gly
85 90 95

Ser Cys Leu Gly Ser Phe Leu Ala Ser Pro Pro Glu Leu Asp Ala Pro
100 105 110

Trp Thr Glu Glu Glu Ala Glu Val Ala Ala Thr Ala Ser Arg Gly Lys
115 120 125

His Phe Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe Ala Ala Glu
130 135 140

Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu Gly Thr Phe
145 150 155 160

Asp Ser Ala Glu Asp Ala Ala Val Ala Tyr Asp Arg Ala Ala Tyr Arg
165 170 175

Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg Ile Gly Ser
180 185 190

Glu Ile Ala Ala Ala Ala Ala Ala Ala Gly Gln Lys Arg Pro Ser Pro
195 200 205

Gln Pro Ala Ser Pro Asp Ser Pro Pro Pro Ser Ser Ser Ala Pro Gly
 210 215 220

Ser Ser Lys Arg Arg Lys Arg Gly Glu Ala Ala Ala Ala Ser Met Ala
 225 230 235 240

Met Ala Leu Val Pro Pro Pro Pro Val Gln Ala Pro Val Gln Leu Thr
 245 250 255

Leu Pro Ala Gln Pro Trp Leu Ala Thr Gly Ala Val Gln Gln Leu Val
 260 265 270

Ser

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 <211> 1242
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 <213> Z. mays

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<210> 252

<211> 267

<212> PRT

<213> Z. mays

<400> 252

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Lys	Arg	Lys	Asn	Gln	Tyr	Arg	Gly	Ile	Arg	Gln	Arg	Pro	Trp	Gly	Lys
			20					25					30		

Trp Ala Ala Glu Ile Arg Asp Pro Gln Lys Gly Val Arg Val Trp Leu
35 40 45

Gly Thr Phe Asn Ser Pro Glu Glu Ala Ala Arg Ala Tyr Asp Ala Glu
50 55 60

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

Pro Ala Val Gly Gln Lys Cys Arg Ser Ser Ser Ala Ser Ala Lys Ala
85 90 95

Leu Lys Ser Cys Val Glu Gln Lys Pro Ile Val Lys Thr Asp Met Asn
100 105 110

Ile Leu Ala Asn Thr Asn Ala Pro Phe Tyr Gln Ser Val Asn Tyr Ala
115 120 125

Ser Asn Asn Pro Phe Val Pro Ala Met Asn Ser Thr Val Ser Phe Glu
130 135 140

Asp Pro Ile Met Asn Leu His Ser Asp Gln Gly Ser Asn Ser Leu Gly
145 150 155 160

Cys Ser Asp Leu Gly Trp Glu Asn Asp Thr Lys Thr Pro Asp Ile Thr
165 170 175

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

Val Asn Ser Asn Ser Asn Ser Ser Met Val Pro Pro Val Leu Glu Asn
195 200 205

Asn Ala Val Asp Leu Thr Asp Gly Leu Thr Asp Leu Glu Ser Tyr Met
210 215 220

Arg Phe Leu Met Asp Gly Gly Ala Ser Asp Ser Ile Asp Ser Leu Leu
225 230 235 240

Asn Leu Asp Gly Ser Gln Asp Leu Gly Ser Asn Met Asp Leu Trp Thr
245 250 255

Phe Asp Asp Met Pro Ile Ala Gly Asp Phe Phe
260 265

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<211> 1736
<212> DNA
<213> P. patents

<400> 253
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<211> 566
<212> PRT
<213> P. patents

<400> 254

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20 25 30

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

Trp Ser Ala Phe Lys Ser Glu Lys Arg Arg Gln Lys Glu His Asp Glu
50 55 60

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

Asp Gly Leu Val Cys Thr Ala Arg Arg Pro Trp Ile Ala Val Gly Met
85 90 95

Arg Asn Val Asp Tyr Lys Arg Ala Arg His Phe Glu Val Asp Leu Asn
100 105 110

Asp Phe Asn Gln Val Leu Glu Ile Asp Arg Glu Asn Met Ile Ala Arg
115 120 125

Cys Glu Pro Leu Val Asn Met Gly Gln Ile Thr Arg Met Thr Val Pro
130 135 140

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

Gly Gly Leu Ile Asn Gly Tyr Gly Ile Glu Gly Ser Ser His Ile Tyr
165 170 175

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

Gly Arg Leu Val Arg Ala Thr Ala Gly Asn Glu Phe Ser Asp Leu Phe
195 200 205

Tyr Ala Ile Pro Trp Ser Gln Gly Thr Leu Gly Leu Pro Val Ala Ala
210 215 220

Glu Ile Lys Leu Ile Glu Val Gly Pro Tyr Met Lys Val Thr Tyr Lys
225 230 235 240

Pro Ala Arg Gly Asp Leu Gln Glu Leu Ala Gln Ala Tyr Asn Asp Ser
245 250 255

Tyr Ile Pro Arg Asp Gly Asp Gln Asp Asn Pro Glu Lys Val Pro Asp
260 265 270

Phe Val Glu Thr Met Ile Tyr Ser Glu Thr Glu Gly Val Thr Met Thr
275 280 285

Gly Arg Tyr Ala Ser Lys Asp Glu Ala Lys Arg Lys Gly Asn Lys Ile
290 295 300

Asn Cys Gln Gly Trp Trp Tyr Lys Lys Trp Phe Tyr Gln His Ala Gln
305 310 315 320

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

Tyr Tyr Pro Arg His Thr Arg Cys Leu Tyr Trp Glu Gly Lys Leu Ile
340 345 350

Leu Pro Phe Ala Asp Gln Phe Trp Phe Arg Tyr Leu Phe Gly Trp Met
355 360 365

Met Pro Pro Lys Val Ser Phe Leu Lys Ala Thr Gln Gly Asp Ala Ile
370 375 380

Arg Asn Tyr Tyr His Glu Arg His Val Ile Gln Asp Met Leu Val Pro
385 390 395 400

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

Val Tyr Pro Ile Trp Leu Cys Pro His Arg Leu Phe Lys His Pro Met
420 425 430

Arg Thr Gln Ile Asn Pro Glu Pro Gly Phe Glu Tyr Ala Gly Arg Pro
435 440 445

Gly Asp Thr Pro Tyr Ala Gln Met Tyr Thr Asp Val Gly Val Tyr Tyr
450 455 460

Thr Pro Arg Cys Val Phe Lys Gly Glu Glu Phe Asp Gly Val Ala Ala
465 470 475 480

Val Lys Lys Met Glu Ala Trp Met Ile Glu Asn His Cys Phe Gln Pro
485 490 495

Gln Tyr Ala Val Ser Glu Leu Asn Glu Arg Asp Phe Trp Arg Met Phe
500 505 510

Asp Pro Thr Leu Tyr Gln Arg Cys Arg Asp Lys Tyr Lys Ala Val Gly
515 520 525

Thr Phe Met Ser Val Tyr Tyr Lys Cys Lys Lys Gly Arg Lys Thr Glu
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Lys Glu Val Ala Glu Glu Glu Ala Lys Val Thr Glu Ser Ala Tyr Ala
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Asp Val Glu Lys Pro Glu
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<211> 603
<212> DNA
<213> P. patents

<400> 255
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ccg	603

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 <211> 120
 <212> PRT
 <213> P. patents

<400> 256

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			20					25					30		

Arg	Phe	Glu	Ile	Lys	Lys	Trp	Asn	Ala	Val	Ala	Leu	Trp	Ala	Trp	Asp
		35					40					45			

Ile	Val	Val	Asp	Asn	Cys	Ala	Ile	Cys	Arg	Asn	His	Ile	Met	Asp	Leu
		50					55					60			

Cys	Ile	Glu	Cys	Gln	Ala	Asn	Gln	Ala	Ser	Ala	Thr	Ser	Glu	Glu	Cys
65					70					75				80	

Thr	Val	Ala	Trp	Gly	Val	Cys	Asn	His	Ala	Phe	His	Phe	His	Cys	Ile
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Ser Arg Trp Leu Lys Thr Arg Gln Val Cys Pro Leu Asp Asn Ser Glu
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Trp Glu Phe Gln Lys Tyr Gly Arg
115 120

<210> 257

<211> 1290

<212> DNA

<213> P. patents

<400> 257

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<210> 258

<211> 304

<212> PRT

<213> P. patents

<400> 258

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		20						25					30		

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

Cys	Gly	Asp	Ile	His	Gly	Gln	Phe	Tyr	Asp	Leu	Lys	Glu	Leu	Phe	Lys
	50					55					60				

Val Gly Gly Asp Cys Pro Lys Thr Asn Tyr Leu Phe Leu Gly Asp Phe
65 70 75 80

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

Leu Lys Val Arg Tyr Pro Asp Arg Ile Thr Leu Ile Arg Gly Asn His
100 105 110

Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly Phe Tyr Asp Glu Cys Leu
115 120 125

Arg Lys Tyr Gly Ser Ile Asn Val Trp Arg Tyr Cys Thr Asp Ile Phe
130 135 140

Asp Tyr Leu Ser Leu Ser Ala Leu Ile Asp Asn Arg Ile Phe Cys Val
145 150 155 160

His Gly Gly Leu Ser Pro Ser Ile Thr Thr Val Asp Gln Ile Arg Thr
165 170 175

Ile Asp Arg Lys Gln Glu Val Pro His Asp Gly Ala Met Cys Asp Leu
180 185 190

Leu Trp Ser Asp Pro Glu Glu Ile Glu Gly Trp Gly Leu Ser Pro Arg
195 200 205

Gly Ala Gly Tyr Leu Phe Gly Gly Asn Val Ala Thr Thr Phe Asn His
210 215 220

Thr Asn Lys Ile Asp Asn Ile Cys Arg Ala His Gln Leu Val Met Glu
225 230 235 240

Gly Tyr Lys Trp Met Phe Asn Asn Gln Val Val Thr Val Trp Ser Ala
245 250 255

Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Val Ala Ala Ile Leu Glu Leu
260 265 270

Asp Glu Asn Leu Asn Arg Lys Phe Thr Val Phe Glu Ala Ala Pro Pro
275 280 285

Glu Ala Arg Gly Val Pro Ser Lys Lys Pro Val Pro Asp Tyr Phe Leu
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<212> DNA
<213> B. napus

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 <212> PRT
 <213> B. napus

<400> 260

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 20 25 30

Ile Glu Glu Ser Asn Val Gln Pro Val Asn Ser Pro Val Thr Val Cys
 35 40 45

Gly Asp Ile His Gly Gln Phe His Asp Leu Met Lys Leu Phe Gln Thr
 50 55 60

Gly Gly His Val Pro Asp Thr Asn Tyr Ile Phe Met Gly Asp Phe Val
 65 70 75 80

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

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

Ser Arg Gln Leu Thr Gln Val Tyr Gly Phe Tyr Asp Glu Cys Gln Arg
115 120 125

Lys Tyr Gly Asn Ala Asn Ala Trp Arg Tyr Cys Thr Asp Val Phe Asp
130 135 140

Tyr Leu Thr Leu Ser Ala Ile Ile Asp Gly Thr Val Leu Cys Val His
145 150 155 160

Gly Gly Leu Ser Pro Asp Val Arg Thr Ile Asp Gln Ile Arg Leu Val
165 170 175

Asp Arg Asn Cys Glu Ile Pro His Glu Gly Pro Phe Cys Asp Leu Met
180 185 190

Trp Ser Asp Pro Glu Asp Ile Glu Thr Trp Ala Val Ser Pro Arg Gly
195 200 205

Ala Gly Trp Leu Phe Gly Ser Arg Val Thr Thr Glu Phe Asn His Ile
210 215 220

Asn Lys Leu Asp Leu Val Cys Arg Ala His Gln Leu Val Gln Glu Gly
225 230 235 240

Leu Lys Tyr Met Phe Gln Asp Lys Ser Leu Val Thr Val Trp Ser Ala
245 250 255

Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Val Ala Ser Ile Leu Ser Phe
260 265 270

Asp Asp Asn Met Glu Lys Ser Val Lys Tyr Phe Thr Glu Thr Glu Glu
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290 295 300

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<212>	PRT
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<400>	262

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20 25 30

Leu Val Glu Glu Ser Asn Val Gln Arg Val Asp Ala Pro Val Thr Leu
35 40 45

Cys Gly Asp Ile His Gly Gln Phe Tyr Asp Met Met Glu Leu Phe Lys
50 55 60

Val Gly Gly Asp Cys Pro Lys Thr Asn Tyr Leu Phe Leu Gly Asp Phe
65 70 75 80

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

Leu Lys Val Arg Tyr Pro Asp Arg Ile Thr Leu Ile Arg Gly Asn His
100 105 110

Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly Phe Tyr Asp Glu Cys Leu
115 120 125

Arg Lys Tyr Gly Ser Val Asn Val Trp Arg Tyr Cys Thr Asp Ile Phe
130 135 140

Asp Tyr Met Ser Leu Ser Ala Val Val Glu Asn Lys Ile Phe Cys Val
145 150 155 160

His Gly Gly Leu Ser Pro Ala Ile Ile Thr Leu Asp Gln Ile Arg Thr
165 170 175

Ile Asp Arg Lys Gln Glu Val Pro His Asp Gly Ala Met Cys Asp Leu
180 185 190

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

Arg Gly Ala Gly Phe Leu Phe Gly Gly Ser Val Val Ser Ser Phe Asn
210 215 220

His Thr Asn Asn Ile Asp Tyr Ile Ala Arg Ala His Gln Leu Val Met
225 230 235 240

Glu Gly Tyr Lys Trp Met Phe Asp Ser Gln Ile Val Thr Val Trp Ser
245 250 255

Ala Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Val Ala Ser Ile Leu Glu
260 265 270

Leu Asp Glu Asn Leu Asn Lys Glu Phe Arg Val Phe Glu Ala Ala Gln
275 280 285

Gln Asp Ser Arg Gly Pro Pro Ala Lys Lys Pro Ala Pro Asp Tyr Phe
290 295 300

Leu
305

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<213> B. napus

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gagatcttaa tggatgaaag caacgttcag cctgtgaaaa gccctgtgac aatctgcggt 180
gatattcatg gacagttcca tgatcttgct gagcttttcc gtattggcgg aatgtgcctt 240
gacaccaatt acctgtttat gggagattac gttgaccgtg gttattattc tgttgaaact 300
gttacgctgt tagtcgcctt aaagctgcga taccctcagc gaatcaccat tcttagagga 360
aaccatgaaa gtcgtcagat cactcagggt tatggatttt atgatgaatg totacgaaag 420
tatggcaatg caaatgtttg gaaaatcttt acagacctct ttgactattt cccactgaca 480
gccttggttg agtcagaaat attttgcctt catggtggat tgtctccatc tatcgagaca 540
cttgacaaca taaggaactt tgatcgagtt caagaagtgc cccatgaagg gcccatgtgt 600
gacttattat ggtctgatcc tgatgaccgt tgtggttggg gcatctctcc tcgtggtgct 660

ggatatacat ttggtcagga catatccgaa cagttcaacc actcaaacag cttaaagctg 720
 atcgccagag cccatcagct ggttatggat ggatacaact gggctcatga gcaaaagggtg 780
 gtaactatct tcagtcgacc aaactattgt taccgttgtg ggaacatggc ttcgattctt 840
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 gaaccagatg ttactcggag aacaccagac tatttcctgt ga 942

<210> 264
 <211> 313
 <212> PRT
 <213> B. napus

<400> 264

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

Gln Ile Ser Gln Leu Met Gln Cys Lys Pro Leu Ser Glu Gln Gln Val
 20 25 30

Arg Ala Leu Cys Glu Lys Ala Lys Glu Ile Leu Met Asp Glu Ser Asn
 35 40 45

Val Gln Pro Val Lys Ser Pro Val Thr Ile Cys Gly Asp Ile His Gly
 50 55 60

Gln Phe His Asp Leu Ala Glu Leu Phe Arg Ile Gly Gly Met Cys Pro
 65 70 75 80

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

Ser Val Glu Thr Val Thr Leu Leu Val Ala Leu Lys Leu Arg Tyr Pro
100 105 110

Gln Arg Ile Thr Ile Leu Arg Gly Asn His Glu Ser Arg Gln Ile Thr
115 120 125

Gln Val Tyr Gly Phe Tyr Asp Glu Cys Leu Arg Lys Tyr Gly Asn Ala
130 135 140

Asn Val Trp Lys Ile Phe Thr Asp Leu Phe Asp Tyr Phe Pro Leu Thr
145 150 155 160

Ala Leu Val Glu Ser Glu Ile Phe Cys Leu His Gly Gly Leu Ser Pro
165 170 175

Ser Ile Glu Thr Leu Asp Asn Ile Arg Asn Phe Asp Arg Val Gln Glu
180 185 190

Val Pro His Glu Gly Pro Met Cys Asp Leu Leu Trp Ser Asp Pro Asp
195 200 205

Asp Arg Cys Gly Trp Gly Ile Ser Pro Arg Gly Ala Gly Tyr Thr Phe
210 215 220

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

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

Glu Gln Lys Val Val Thr Ile Phe Ser Ala Pro Asn Tyr Cys Tyr Arg
260 265 270

Cys Gly Asn Met Ala Ser Ile Leu Glu Val Asp Asp Cys Arg Asn His
275 280 285

Thr Phe Ile Gln Phe Glu Pro Ala Pro Arg Arg Gly Glu Pro Asp Val
290 295 300

Thr Arg Arg Thr Pro Asp Tyr Phe Leu
305 310

<210> 265
<211> 921
<212> DNA
<213> B. napus

<400> 265
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aacgttcagc ccgtgaagtg tcctgtcacc gtctgcggcg atatccacgg acagttctat 180
gaccttatcg agctctttcg aatcgggtggg aatcctccgg atactaacta cctcttcatg 240
ggagactatg tagaccgtgg ctactattca gtagaaacag tttctctatt ggtggcactg 300
aaagtgcgat acagggatag gattacaatc ttgcgaggga atcacgagag tcggcagatt 360
actcaagtct atgggtttta tgatgaatgt ttgaggaagt atggaaatgc aaatgtctgg 420
aagtttttca cggacctttt cgattatctt cctcttactg ctctcataga gagtcagggtt 480
ttctgcttgc atggaggggt ttcaccttct ctggacaccc ttgataatat ccgaagcttg 540
gatcgtatac aagaggttcc acatgaagga ccaatgtgtg atttattatg gtctgatccc 600
gatgatcgat gtgggtgggg aatatctcca cgaggtgctg gttatacatt tggacaagac 660

atcgcaactc agtttaatca caacaatgga ctcagtctca tatcaagagc acatcaactt 720

gtcatggaag gctttaactg gtgtcaggac aaaaatgttg tgacggtggt tagtgcacca 780

aactattgct accggtgtgg aaacatggca gctattctag agataggaga gaacatggac 840

cagaacttcc tccagttcga tccagctcct cgtcaagtcg aaccagatac taccgcaag 900

accctgatt atttttgtg a 921

<210> 266

<211> 306

<212> PRT

<213> B. napus

<400> 266

Met Pro Pro Asn Gly Asp Leu Asp Arg Gln Ile Ser Gln Leu Met Glu
1 5 10 15

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

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

Val Thr Val Cys Gly Asp Ile His Gly Gln Phe Tyr Asp Leu Ile Glu
50 55 60

Leu Phe Arg Ile Gly Gly Asn Pro Pro Asp Thr Asn Tyr Leu Phe Met
65 70 75 80

Gly Asp Tyr Val Asp Arg Gly Tyr Tyr Ser Val Glu Thr Val Ser Leu
85 90 95

Leu Val Ala Leu Lys Val Arg Tyr Arg Asp Arg Ile Thr Ile Leu Arg
100 105 110

Gly Asn His Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly Phe Tyr Asp
115 120 125

Glu Cys Leu Arg Lys Tyr Gly Asn Ala Asn Val Trp Lys Phe Phe Thr
130 135 140

Asp Leu Phe Asp Tyr Leu Pro Leu Thr Ala Leu Ile Glu Ser Gln Val
145 150 155 160

Phe Cys Leu His Gly Gly Leu Ser Pro Ser Leu Asp Thr Leu Asp Asn
165 170 175

Ile Arg Ser Leu Asp Arg Ile Gln Glu Val Pro His Glu Gly Pro Met
180 185 190

Cys Asp Leu Leu Trp Ser Asp Pro Asp Asp Arg Cys Gly Trp Gly Ile
195 200 205

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

Phe Asn His Asn Asn Gly Leu Ser Leu Ile Ser Arg Ala His Gln Leu
225 230 235 240

Val Met Glu Gly Phe Asn Trp Cys Gln Asp Lys Asn Val Val Thr Val
245 250 255

Phe Ser Ala Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Met Ala Ala Ile
260 265 270

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

Ala Pro Arg Gln Val Glu Pro Asp Thr Thr Arg Lys Thr Pro Asp Tyr
290 295 300

Phe Leu
305

<210> 267
<211> 921
<212> DNA
<213> B. napus

<400> 267
atgccgccga acggagatct agaccgtcag atcgagcacc tgatggagtg caaaccttta 60
tcggaggagg atgtgaggac gctctgcgat caagctaagg ccatcctcgt cgaggaatgg 120
aacgtccagc ccgtgaaatg ccccgtcacc gtctgcggcg atatccacgg ccagttctat 180
gaccttatcg agctttttccg aatcggtggt aacgcccccg atacgaatta cctcttcatg 240
ggtgactatg tagaccgtgg ctactattca gtggaaacgg tttctttatt ggtggcattg 300
aaagtcagat acagggatag gattacaatc ttgcgaggga accacgagag tcgtcagatc 360
accaagtat atggtttttta tgacgagtgc ttgaggaagt acggaaacgc aaatgtgtgg 420
aagtatttca cagacctttt cgattatctt cctcttactg ctcttatcga gagtcagggtt 480
ttctgtttgc atggaggggt atcaccttct ctggatacac ttgataatat ccgaagcttg 540
gatcgtatac aagaggttcc acacgaagga ccaatgtgtg atttactatg gtctgatcca 600
gatgatcgat gcgggtgggg aatatctcca agaggtgctg gttatacatt tggacaggat 660

atagcaactc agtttaatca caacaatgga ctcagtctca tatcaagagc gcatcagctt	720
gtcatggaag gttttaactg gtgtcaggat aagaatgtgg tgacggtggt tagtgcacca	780
aactattgct accggtgtgg aaacatggca gcgattctag agataagtga gaacatggag	840
cagaacttcc ttcagtttga tccagctcca agacaagtcg aacctgatac tacccgtaag	900
accocctgatt attttttgtg a	921

<210>	268
<211>	306
<212>	PRT
<213>	B. napus
<400>	268

Met Pro Pro Asn Gly Asp Leu Asp Arg Gln Ile Glu His Leu Met Glu
1 5 10 15

Cys Lys Pro Leu Ser Glu Glu Asp Val Arg Thr Leu Cys Asp Gln Ala
20 25 30

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

Val Thr Val Cys Gly Asp Ile His Gly Gln Phe Tyr Asp Leu Ile Glu
50 55 60

Leu Phe Arg Ile Gly Gly Asn Ala Pro Asp Thr Asn Tyr Leu Phe Met
65 70 75 80

Gly Asp Tyr Val Asp Arg Gly Tyr Tyr Ser Val Glu Thr Val Ser Leu
85 90 95

Leu Val Ala Leu Lys Val Arg Tyr Arg Asp Arg Ile Thr Ile Leu Arg
100 105 110

Gly Asn His Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly Phe Tyr Asp
115 120 125

Glu Cys Leu Arg Lys Tyr Gly Asn Ala Asn Val Trp Lys Tyr Phe Thr
130 135 140

Asp Leu Phe Asp Tyr Leu Pro Leu Thr Ala Leu Ile Glu Ser Gln Val
145 150 155 160

Phe Cys Leu His Gly Gly Leu Ser Pro Ser Leu Asp Thr Leu Asp Asn
165 170 175

Ile Arg Ser Leu Asp Arg Ile Gln Glu Val Pro His Glu Gly Pro Met
180 185 190

Cys Asp Leu Leu Trp Ser Asp Pro Asp Asp Arg Cys Gly Trp Gly Ile
195 200 205

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

Phe Asn His Asn Asn Gly Leu Ser Leu Ile Ser Arg Ala His Gln Leu
225 230 235 240

Val Met Glu Gly Phe Asn Trp Cys Gln Asp Lys Asn Val Val Thr Val
245 250 255

Phe Ser Ala Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Met Ala Ala Ile
260 265 270

Leu Glu Ile Ser Glu Asn Met Glu Gln Asn Phe Leu Gln Phe Asp Pro
275 280 285

Ala Pro Arg Gln Val Glu Pro Asp Thr Thr Arg Lys Thr Pro Asp Tyr
290 295 300

Phe Leu
305

<210> 269
<211> 927
<212> DNA
<213> G. max

<400> 269
atgtcatcat cttcagacct ggacaggcaa atagagcagt tgaagagggtg tgagcctctt 60
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aacgttcaaa gggtcgacgc tcctgtcacc atatgtggtg atattcacgg tcagttttat 180
gacatgaagg agcttttcaa agtaggaggg gattgcccc aaactaacta tttattcctg 240
ggggattttg ttgatagagg gttttactcg gttgaaacgt ttctgcttct gctcgctctt 300
aaggtgaggt atccggatcg gataaacctc attaggggaa accatgaaag ccgtcagatc 360
accaggtgt atggattcta tgatgagtgc cttcgaaaat atggttcagt caatgtctgg 420
agatattgta ccgatatatt cgactactta agcttgtccg ctctaattga aaacaagatt 480
ttcagtgttc atgggtggtct ttctcctgcc atttcaacac tggatcagat acgaactatt 540
gatcgaagc aagaagtacc tcatgatggt gccatgtgtg accttctatg gtcagatcct 600
gaagatattg tggatagctg gggctcttagt ccccggtgtg ctggttactt atttggtggc 660

agtgttggtta cttcctttaa ccactccaat aacattgact atatatgtcg tgcacatcag 720
 ttggtaatgg aaggatataa atggatgttc aataaccaga tagttactgt ctggtcagct 780
 ccaaattatt gctacagatg tggcaatgta gctgcaattc tggagttgga tggaaatctt 840
 actaagcaat tccgggtggt tgaagctgct ccacaggaat caagaggaac acctgctaag 900
 aaaccagcac cagattactt tttatga 927

<210> 270
 <211> 308
 <212> PRT
 <213> G. max

<400> 270

Met Ser Ser Ser Ser Asp Leu Asp Arg Gln Ile Glu Gln Leu Lys Arg
 1 5 10 15

Cys Glu Pro Leu Lys Glu Ser Glu Val Lys Val Leu Cys Leu Lys Ala
 20 25 30

Met Glu Ile Leu Val Glu Glu Ser Asn Val Gln Arg Val Asp Ala Pro
 35 40 45

Val Thr Ile Cys Gly Asp Ile His Gly Gln Phe Tyr Asp Met Lys Glu
 50 55 60

Leu Phe Lys Val Gly Gly Asp Cys Pro Lys Thr Asn Tyr Leu Phe Leu
 65 70 75 80

Gly Asp Phe Val Asp Arg Gly Phe Tyr Ser Val Glu Thr Phe Leu Leu
 85 90 95

Leu Leu Ala Leu Lys Val Arg Tyr Pro Asp Arg Ile Thr Leu Ile Arg
100 105 110

Gly Asn His Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly Phe Tyr Asp
115 120 125

Glu Cys Leu Arg Lys Tyr Gly Ser Val Asn Val Trp Arg Tyr Cys Thr
130 135 140

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

Phe Ser Val His Gly Gly Leu Ser Pro Ala Ile Ser Thr Leu Asp Gln
165 170 175

Ile Arg Thr Ile Asp Arg Lys Gln Glu Val Pro His Asp Gly Ala Met
180 185 190

Cys Asp Leu Leu Trp Ser Asp Pro Glu Asp Ile Val Asp Ser Trp Gly
195 200 205

Leu Ser Pro Arg Gly Ala Gly Tyr Leu Phe Gly Gly Ser Val Val Thr
210 215 220

Ser Phe Asn His Ser Asn Asn Ile Asp Tyr Ile Cys Arg Ala His Gln
225 230 235 240

Leu Val Met Glu Gly Tyr Lys Trp Met Phe Asn Asn Gln Ile Val Thr
245 250 255

Val Trp Ser Ala Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Val Ala Ala
260 265 270

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

Ala Ala Pro Gln Glu Ser Arg Gly Thr Pro Ala Lys Lys Pro Ala Pro
290 295 300

Asp Tyr Phe Leu
305

<210> 271
<211> 945
<212> DNA
<213> G. max

<400> 271
atgggcgccca attcgttgcc atcggcgga tcaaacttcg atctcgacga gcagatctcg 60
cagctcatgc aatgcaagcc actttccgag caccagggtta gagttttatg tgagaaggct 120
aaggagattt tgatggaaga aagtaatgtc cagcctgtga aaagccctgt gacaatttgt 180
ggtgatattc atgggcagtt tcatgacctt gctgaactat ttcgaattgg aggggaagtgt 240
ccagatacta attacttggt tatgggtgat tatgtggacc ggggttatta ttcagttgaa 300
actgtaacac ttcttggtgc actgaaagtg cgatatactc agcgaattac tattcttaga 360
ggaaaccatg aaagccgtca gatcactcaa gtatacggat tttacgatga atgcctcaga 420
aaatatggta atgctagtgt ttggaagatc tttacagacc ttttcgattt ctttcatttg 480
actgcattgg ttgagtctga aatattttgt ttgcatgggt ggctttcacc ttcaattgag 540
actcttgata acataaggaa cttcgatcgt gttcaagagg ttctcatga agggcccatg 600
tgcgatctgt tgtggtctga tccagatgat aggtgtggct ggggaatttc tctcgtggt 660

gctggatata catttgcca ggatatatcc gaacaattta atcacacaaa caagcttaag 720

ttaattgcta gagctcatca gctggttatg gatggattta actgggctca tgaacaaaag 780

gtggttacca tttttagtgc acctaactac tgttatcgat gtgggaacat ggcctccatt 840

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ggagaacctg atgtcacccg tagaacgcct gattacttct tatga 945

<210> 272

<211> 314

<212> PRT

<213> G. max

<400> 272

Met Gly Ala Asn Ser Leu Pro Ser Ala Glu Ser Asn Phe Asp Leu Asp

1 5 10 15

Glu Gln Ile Ser Gln Leu Met Gln Cys Lys Pro Leu Ser Glu His Gln

20 25 30

Val Arg Val Leu Cys Glu Lys Ala Lys Glu Ile Leu Met Glu Glu Ser

35 40 45

Asn Val Gln Pro Val Lys Ser Pro Val Thr Ile Cys Gly Asp Ile His

50 55 60

Gly Gln Phe His Asp Leu Ala Glu Leu Phe Arg Ile Gly Gly Lys Cys

65 70 75 80

Pro Asp Thr Asn Tyr Leu Phe Met Gly Asp Tyr Val Asp Arg Gly Tyr

85 90 95

Tyr Ser Val Glu Thr Val Thr Leu Leu Val Ser Leu Lys Val Arg Tyr
100 105 110

Pro Gln Arg Ile Thr Ile Leu Arg Gly Asn His Glu Ser Arg Gln Ile
115 120 125

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

Ala Ser Val Trp Lys Ile Phe Thr Asp Leu Phe Asp Phe Phe Pro Leu
145 150 155 160

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

Pro Ser Ile Glu Thr Leu Asp Asn Ile Arg Asn Phe Asp Arg Val Gln
180 185 190

Glu Val Pro His Glu Gly Pro Met Cys Asp Leu Leu Trp Ser Asp Pro
195 200 205

Asp Asp Arg Cys Gly Trp Gly Ile Ser Pro Arg Gly Ala Gly Tyr Thr
210 215 220

Phe Gly Gln Asp Ile Ser Glu Gln Phe Asn His Thr Asn Lys Leu Lys
225 230 235 240

Leu Ile Ala Arg Ala His Gln Leu Val Met Asp Gly Phe Asn Trp Ala
245 250 255

His Glu Gln Lys Val Val Thr Ile Phe Ser Ala Pro Asn Tyr Cys Tyr
260 265 270

Arg Cys Gly Asn Met Ala Ser Ile Leu Glu Val Asp Asp Ser Met Gly
275 280 285

His Thr Phe Ile Gln Phe Asp Pro Ala Pro Arg Arg Gly Glu Pro Asp
290 295 300

Val Thr Arg Arg Thr Pro Asp Tyr Phe Leu
305 310

<210> 273
<211> 921
<212> DNA
<213> G. max

<400> 273
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ccggaggccg aggtgaaggc gctgtgcatg caggcgaggg cgattctcgt cgaagagtgg 120
aacgttcagc cggatgaagtg ccccgctacc gtctgcggcg acattcacgg ccagttctac 180
gatctcatcg agctctttcg gataggagga aacgctcccg atactaatta cctctttatg 240
ggcgattatg tagatcgtgg gtactattca gtggagactg tcacgctttt ggtggccttg 300
aaagttcgtt atagagatag aattacaatc cttaggggaa atcatgagag ccgtcaaatc 360
actcaagtgt atggcttcta cgatgaatgc ttgagaaagt atggaaatgc caatgtcttg 420
aaattcttta ccgatttggt tgattattta cctctgaccg cccttattga gagtcagatt 480
ttctgtttgc atggaggtct ctcaccatct ttggatacac ttgataatat ccgtgccttg 540
gatcgcatatc aggaggttcc acacgaagga ccaatgtgtg acctcttggt gtctgatcca 600
gatgatcgct gtgggttgggg aatatctcca cgtggtgctg gatatacatt tggacaggat 660

atagctgctc agttcaatca taccaatggg ctatcgctga tatctagagc tcaccaactt	720
gtaatggaag gattcaattg gtgccaggac aagaatgtgg tgactgtttt tagtgcacct	780
aattactgtt accgatgtgg gaacatggct gccatactgg aaattggaga gaacatggat	840
cagaattttc tgcagtttga tccagctccc agacaaattg agcccgacac tacacgaaag	900
acgccagatt attttttgta a	921

<210> 274
 <211> 306
 <212> PRT
 <213> G. max

<400> 274

Met	Pro	Ser	His	Ala	Asp	Leu	Asp	Arg	Gln	Ile	Glu	His	Leu	Met	Glu
1				5					10					15	

Cys	Lys	Pro	Leu	Pro	Glu	Ala	Glu	Val	Lys	Ala	Leu	Cys	Asp	Gln	Ala
			20					25						30	

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

Val	Thr	Val	Cys	Gly	Asp	Ile	His	Gly	Gln	Phe	Tyr	Asp	Leu	Ile	Glu
	50						55					60			

Leu	Phe	Arg	Ile	Gly	Gly	Asn	Ala	Pro	Asp	Thr	Asn	Tyr	Leu	Phe	Met
65					70					75					80

Gly	Asp	Tyr	Val	Asp	Arg	Gly	Tyr	Tyr	Ser	Val	Glu	Thr	Val	Thr	Leu
				85						90					95

Leu Val Ala Leu Lys Val Arg Tyr Arg Asp Arg Ile Thr Ile Leu Arg
100 105 110

Gly Asn His Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly Phe Tyr Asp
115 120 125

Glu Cys Leu Arg Lys Tyr Gly Asn Ala Asn Val Trp Lys Phe Phe Thr
130 135 140

Asp Leu Phe Asp Tyr Leu Pro Leu Thr Ala Leu Ile Glu Ser Gln Ile
145 150 155 160

Phe Cys Leu His Gly Gly Leu Ser Pro Ser Leu Asp Thr Leu Asp Asn
165 170 175

Ile Arg Ala Leu Asp Arg Ile Gln Glu Val Pro His Glu Gly Pro Met
180 185 190

Cys Asp Leu Leu Trp Ser Asp Pro Asp Asp Arg Cys Gly Trp Gly Ile
195 200 205

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

Phe Asn His Thr Asn Gly Leu Ser Leu Ile Ser Arg Ala His Gln Leu
225 230 235 240

Val Met Glu Gly Phe Asn Trp Cys Gln Asp Lys Asn Val Val Thr Val
245 250 255

Phe Ser Ala Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Met Ala Ala Ile
260 265 270

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

Ala Pro Arg Gln Ile Glu Pro Asp Thr Thr Arg Lys Thr Pro Asp Tyr
290 295 300

Phe Leu
305

<210> 275
<211> 942
<212> DNA
<213> H. annuus

<400> 275
atgagcttcg attcgggtccc ttccagcacc catggcaacc ttgacgagca gattagtcag 60
cttatgcagt gcaagccctt atccgaacaa gatgttcggg ggctatgtga aaaggcaaag 120
gaaattctga tggacgaaag caatgtccag cccgtgaaaa gcccggttac aatctgtggt 180
gacatccatg gacaattcca tgatcttgca gagctatttc gcattggagg aaagtgcccg 240
gatacaaatt acttgttcat gggagactat gtggatcgtg ggtactactc tgttgaaact 300
gtgacactgc tggtttcctt gaaagtacgt tatcctcaaa gaattacat ttaagagga 360
aaccatgaga gtcgtcagat tactcaagtt tatggatttt acgatgagtg cctgaggaag 420
tatgggaatg caaatgtgtg gaagatcttt acagatcttt ttgattattt tccgctcaca 480
gcactggtcg agtccgagat tttttgtctt catggtgggt tgtccccttc cattgaaaca 540
ttggacaaca ttcggaactt tgaccgcgtg caagaagttc cgcacgaggg tcccatgtgt 600
gatcttttgt ggtccgaccc tgatgaccga tgtggttggg gtatttcacc tcggggagca 660

ggggtatacct ttggtcagga tatttctgag cagttcaacc atactaaca cctaaagctg 720
 attgcaagag ctcatcagct ggatcatgaa ggctacaact ggggtcatga tcaaaagggtg 780
 gttaccatat tcagtcgacc aaattattgc taccgctgtg gaaacatggc gtctattttg 840
 gaagttgacg attgcaaggg tcatacggtc atccagttcg agccggctcc tagaagggga 900
 gaacccgacg taaccaggag aacgcctgat tacttcctat ga 942

<210> 276
 <211> 313
 <212> PRT
 <213> H. annuus

<400> 276

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

Tyr Ile Ser Gln Leu Met Gln Cys Lys Pro Leu Ser Glu Pro Glu Val
 20 25 30

Lys Ser Leu Cys Asp Lys Ala Lys Glu Ile Leu Met Gln Glu Ser Asn
 35 40 45

Val Gln Pro Val Lys Ser Pro Val Thr Ile Cys Gly Asp Ile His Gly
 50 55 60

Gln Phe His Asp Leu Ala Glu Leu Phe Arg Ile Gly Gly Lys Cys Pro
 65 70 75 80

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

Ser Val Glu Thr Val Ser Leu Leu Val Ala Leu Lys Val Arg Tyr Pro
100 105 110

Gln Arg Leu Thr Ile Leu Arg Gly Asn His Glu Ser Arg Gln Ile Thr
115 120 125

Gln Val Tyr Gly Phe Tyr Asp Glu Cys Leu Arg Lys Tyr Gly Thr Ala
130 135 140

Asn Val Trp Lys Thr Phe Thr Asp Leu Phe Asp Tyr Leu Pro Leu Thr
145 150 155 160

Ala Leu Val Glu Ser Glu Ile Phe Cys Leu His Gly Gly Leu Ser Pro
165 170 175

Ser Ile Glu Thr Leu Asp Asn Ile Arg Asn Phe Asp Arg Val Gln Glu
180 185 190

Val Pro His Glu Gly Pro Met Cys Asp Leu Leu Trp Ser Asp Pro Asp
195 200 205

Asp Arg Cys Gly Trp Gly Ile Ser Pro Arg Gly Ala Gly Tyr Thr Phe
210 215 220

Gly Gln Asp Ile Ser Glu Gln Tyr Asn His Thr Asn Gly Leu Lys Leu
225 230 235 240

Ile Ala Arg Ala His Gln Leu Val Met Glu Gly Phe Asn Trp Gly His
245 250 255

Glu Arg Lys Val Val Thr Ile Phe Ser Ala Pro Asn Tyr Cys Tyr Arg
260 265 270

Cys Gly Asn Met Ala Ser Ile Leu Glu Val Asp Asp Cys Lys Gly His
275 280 285

Thr Phe Ile Gln Phe Glu Pro Ala Pro Arg Arg Gly Glu Pro Asp Val
290 295 300

Thr Arg Arg Thr Pro Asp Tyr Phe Leu
305 310

<210> 277
<211> 918
<212> DNA
<213> L. usitatissimum

<400> 277
atgtcagacc tagataggca gattgagcag cttagaagt gcgagccttt gaaagaatcg 60
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cgcgtaggacg cccctgtcac tatatgtgga gacattcatg gacagttcta tgacctgaag 180
gagcttttca aagtaggagg agattgccca aaaactaatt acttattttct tggagatttt 240
gttgatagag gattctactc gggtgagaca tttttgcttc tgcttgccct taaggtgcga 300
tatccagata gaataactct catcagagga aatcatgaga gccgtcagat aacacagggtg 360
tatggtttct atgatgagtg cctacgaaaa tacggctctg ttaatgtttg gagatattgc 420
actgacatat ttgattacct aagtttgtca gccctcattg agaacaaagt tttcagtgtc 480
cacggtggcc tttctcctgc gatatcaacc ttggatcaga tccgaaccat tgatcgaaag 540
caagaagtgc ctcatgatgg tgccatgtgt gacctaatgt ggtcagatcc tgaagatatt 600
gtggatggtt ggggtttgag cccacgtggt gcagggttcc tgtttggtgg cagcgtggtt 660

agttctttca accactcaaa taatatagac tacatttgtc gcgctcatca gttgggttatg	720
gaagggtaca aatggatggt taatgatcaa atcgttactg tttggtcggc tccaaactac	780
tgttacagat gtggtaatgt cgctgcaatc cttgagctgg atgagaacct caacaaacaa	840
tttcgtgtgt ttgatgctgc ccctcaggaa tcaagaggag cacctgcgaa aaaggcagcc	900
cctgattact ttttatga	918

<210>	278
<211>	305
<212>	PRT
<213>	L. usitatissimum
<400>	278

Met Ser Asp Leu Asp Arg Gln Ile Glu Gln Leu Lys Lys Cys Glu Pro
1 5 10 15

Leu Lys Glu Ser Glu Val Lys Ala Leu Cys Leu Lys Ala Met Glu Ile
20 25 30

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

Cys Gly Asp Ile His Gly Gln Phe Tyr Asp Leu Lys Glu Leu Phe Lys
50 55 60

Val Gly Gly Asp Cys Pro Lys Thr Asn Tyr Leu Phe Leu Gly Asp Phe
65 70 75 80

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

Leu Lys Val Arg Tyr Pro Asp Arg Ile Thr Leu Ile Arg Gly Asn His
100 105 110

Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly Phe Tyr Asp Glu Cys Leu
115 120 125

Arg Lys Tyr Gly Ser Val Asn Val Trp Arg Tyr Cys Thr Asp Ile Phe
130 135 140

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

His Gly Gly Leu Ser Pro Ala Ile Ser Thr Leu Asp Gln Ile Arg Thr
165 170 175

Ile Asp Arg Lys Gln Glu Val Pro His Asp Gly Ala Met Cys Asp Leu
180 185 190

Met Trp Ser Asp Pro Glu Asp Ile Val Asp Gly Trp Gly Leu Ser Pro
195 200 205

Arg Gly Ala Gly Phe Leu Phe Gly Gly Ser Val Val Ser Ser Phe Asn
210 215 220

His Ser Asn Asn Ile Asp Tyr Ile Cys Arg Ala His Gln Leu Val Met
225 230 235 240

Glu Gly Tyr Lys Trp Met Phe Asn Asp Gln Ile Val Thr Val Trp Ser
245 250 255

Ala Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Val Ala Ala Ile Leu Glu
260 265 270

Leu Asp Glu Asn Leu Asn Lys Gln Phe Arg Val Phe Asp Ala Ala Pro
275 280 285

Gln Glu Ser Arg Gly Ala Pro Ala Lys Lys Ala Ala Pro Asp Tyr Phe
290 295 300

Leu
305

<210> 279
<211> 912
<212> DNA
<213> L. usitatissimum

<400> 279
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gttaacagtc ctgtgactgt ttgtggagat atacatggtc agtttcatga tctaataaaa 180
cttttccaga ccggaggtca tgttccagag actaattata tatttatggg ggactttgtg 240
gaccgaggtt ataatagtct tgaagttttc tctatacttt tacttcttaa agcgaggtat 300
ccagctcata ttacgctttt gcgtgggaat catgagagcc gtcagctaac tcaggtttat 360
ggtttctatg acgagtgcc aacgaagtat gggaatacca atgcatggcg ctactgtaca 420
gatgttttcg attatctaac gctttcagct attatagatg gcactgtgct ttgtgttcac 480
ggtggtcttt ctctgatgt tcgaacaatt gatcagataa gagtaattga tcggaactgt 540
gaaattcctc atgaaggacc attctgtgat cttatgtgga gtgatccgga agagatagag 600
acatgggcgg ttagccccag aggagcaggt tggctttttg gatcaagggt cacttctgag 660

tttaaccaca ttaacaacct cgacctgggt tgtcggggcgc accaacttgt acaagaaggc	720
ctcaagtaca tgtttcaaga taaaggttta gtaactgtgt ggtctgcacc gaactactgt	780
taccgatgtg gtaatgtggc ttctatccta agcttcaatg agaatatgga gagagaagtg	840
aagttcttca ccgaaacgga ggagaacaat cagatgagag gaccaaggac tggagttcct	900
tattttcttat ga	912

<210>	280
<211>	303
<212>	PRT
<213>	L. usitatissimum
<400>	280

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

Leu Glu Asp Glu Leu Gln Leu Leu Cys Glu Tyr Val Lys Glu Ile Leu
20 25 30

Ile Glu Glu Ser Asn Val Gln Pro Val Asn Ser Pro Val Thr Val Cys
35 40 45

Gly Asp Ile His Gly Gln Phe His Asp Leu Met Lys Leu Phe Gln Thr
50 55 60

Gly Gly His Val Pro Glu Thr Asn Tyr Ile Phe Met Gly Asp Phe Val
65 70 75 80

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

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

Ser Arg Gln Leu Thr Gln Val Tyr Gly Phe Tyr Asp Glu Cys Gln Arg
115 120 125

Lys Tyr Gly Asn Thr Asn Ala Trp Arg Tyr Cys Thr Asp Val Phe Asp
130 135 140

Tyr Leu Thr Leu Ser Ala Ile Ile Asp Gly Thr Val Leu Cys Val His
145 150 155 160

Gly Gly Leu Ser Pro Asp Val Arg Thr Ile Asp Gln Ile Arg Val Ile
165 170 175

Asp Arg Asn Cys Glu Ile Pro His Glu Gly Pro Phe Cys Asp Leu Met
180 185 190

Trp Ser Asp Pro Glu Glu Ile Glu Thr Trp Ala Val Ser Pro Arg Gly
195 200 205

Ala Gly Trp Leu Phe Gly Ser Arg Val Thr Ser Glu Phe Asn His Ile
210 215 220

Asn Asn Leu Asp Leu Val Cys Arg Ala His Gln Leu Val Gln Glu Gly
225 230 235 240

Leu Lys Tyr Met Phe Gln Asp Lys Gly Leu Val Thr Val Trp Ser Ala
245 250 255

Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Val Ala Ser Ile Leu Ser Phe
260 265 270

Asn	Glu	Asn	Met	Glu	Arg	Glu	Val	Lys	Phe	Phe	Thr	Glu	Thr	Glu	Glu
	275						280					285			

Asn	Asn	Gln	Met	Arg	Gly	Pro	Arg	Thr	Gly	Val	Pro	Tyr	Phe	Leu
	290					295					300			

<210> 281
 <211> 942
 <212> DNA
 <213> L. usitatissimum

<400> 281	
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cttatgcagt gcaagccctt atccgaacaa gatgttcggg ggctatgtga aaaggcaaag	120
gaaattctga tggacgaaag caatgtccag cccgtgaaaa gcccggttac aatctgtggt	180
gacatccatg gacaattcca tgatcttgca gagctatttc gcattggagg aaagtgcccg	240
gatacaaatt acttgttcat gggagactat gtggatcgtg ggtactactc tgttgaaact	300
gtgacactgc tggtttcctt gaaagtacgt tatcctcaaa gaattacat ttttaagagga	360
aaccatgaga gtcgtcagat tactcaagtt tatggatttt acgatgagtg cctgaggaag	420
tatgggaatg caaatgtgtg gaagatcttt acagatcttt ttgattattt tccgctcaca	480
gcactggtcg agtccgagat tttttgtctt catggtgggt tgtccccttc cattgaaaca	540
ttggacaaca ttcggaactt tgaccgcgtg caagaagttc cgcacgaggg tcccatgtgt	600
gatcttttgt ggtccgaccc tgatgaccga tgtggttggg gtatttcacc tcggggagca	660
gggtatacct ttggtcagga tttttctgag cagttcaacc atactaaca cctaaagctg	720
attgcaagag ctcatcagct ggtcatggaa ggctacaact ggggtcatga tcaaaagggtg	780

gttaccatat tcagtgcacc aaattattgc taccgctgtg gaaacatggc gtctattttg 840

gaagttgacg attgcaaggg tcatacgttc atccagttcg agccggctcc tagaagggga 900

gaacccgacg taaccaggag aacgcctgat tacttcctat aa 942

<210> 282

<211> 313

<212> PRT

<213> L. usitatissimum

<400> 282

Met Ser Phe Asp Ser Val Pro Ser Ser Thr His Gly Asn Leu Asp Glu

1 5 10 15

Gln Ile Ser Gln Leu Met Gln Cys Lys Pro Leu Ser Glu Gln Asp Val

20 25 30

Arg Gly Leu Cys Glu Lys Ala Lys Glu Ile Leu Met Asp Glu Ser Asn

35 40 45

Val Gln Pro Val Lys Ser Pro Val Thr Ile Cys Gly Asp Ile His Gly

50 55 60

Gln Phe His Asp Leu Ala Glu Leu Phe Arg Ile Gly Gly Lys Cys Pro

65 70 75 80

Asp Thr Asn Tyr Leu Phe Met Gly Asp Tyr Val Asp Arg Gly Tyr Tyr

85 90 95

Ser Val Glu Thr Val Thr Leu Leu Val Ser Leu Lys Val Arg Tyr Pro

100 105 110

Gln Arg Ile Thr Ile Leu Arg Gly Asn His Glu Ser Arg Gln Ile Thr
115 120 125

Gln Val Tyr Gly Phe Tyr Asp Glu Cys Leu Arg Lys Tyr Gly Asn Ala
130 135 140

Asn Val Trp Lys Ile Phe Thr Asp Leu Phe Asp Tyr Phe Pro Leu Thr
145 150 155 160

Ala Leu Val Glu Ser Glu Ile Phe Cys Leu His Gly Gly Leu Ser Pro
165 170 175

Ser Ile Glu Thr Leu Asp Asn Ile Arg Asn Phe Asp Arg Val Gln Glu
180 185 190

Val Pro His Glu Gly Pro Met Cys Asp Leu Leu Trp Ser Asp Pro Asp
195 200 205

Asp Arg Cys Gly Trp Gly Ile Ser Pro Arg Gly Ala Gly Tyr Thr Phe
210 215 220

Gly Gln Asp Ile Ser Glu Gln Phe Asn His Thr Asn Asn Leu Lys Leu
225 230 235 240

Ile Ala Arg Ala His Gln Leu Val Met Glu Gly Tyr Asn Trp Gly His
245 250 255

Asp Gln Lys Val Val Thr Ile Phe Ser Ala Pro Asn Tyr Cys Tyr Arg
260 265 270

Cys Gly Asn Met Ala Ser Ile Leu Glu Val Asp Asp Cys Lys Gly His
275 280 285

Thr Phe Ile Gln Phe Glu Pro Ala Pro Arg Arg Gly Glu Pro Asp Val
 290 295 300

Thr Arg Arg Thr Pro Asp Tyr Phe Leu
 305 310

<210> 283
 <211> 924
 <212> DNA
 <213> T. aestivum

<400> 283
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 cacgatcttg cggaactgtt ccgaattggg ggaaagtgtc cggatacaaa ttacttgttt 240
 atgggagatt atgtagatcg tggctactat tctgtcgaaa ctgtcacgct gttggtgtcc 300
 ttgaaagttc gttatcctca gcgaatcacc attcttagag gaaacctga aagccgacag 360
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 tggaaaacct ttacggatct gtttgactac ttccccttga cagcattggg cgagtcagaa 480
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 tttgaccgca cccaagaagt tcctcatgaa gggcccatgt gtgatcttct gtggtctgac 600
 cccgatgatc gatgcggttg gggatatttct cctcgaggcg ctggatatac cttcggacag 660
 gatatatcag agcagttcaa tcataccaat aacttacgac ttattgctag agctcaccag 720
 ttggtgatgg agggattcaa ctgggctcat gagcaaaaag tggtcaccat atttagtgca 780

cctaattatt gctaccgctg tggaacatg gcatcaatct tggaagttga tgattgccgg 840

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agaacgccag actacttcct gtga 924

<210> 284

<211> 307

<212> PRT

<213> T. aestivum

<400> 284

Met Ser Ser Pro His Gly Gly Leu Asp Asp Gln Ile Glu Arg Leu Met

1 5 10 15

Gln Cys Lys Pro Leu Pro Glu Ala Glu Val Arg Ala Leu Cys Glu Lys

20 25 30

Ala Lys Glu Ile Leu Met Glu Glu Ser Asn Val Gln Pro Val Arg Ser

35 40 45

Pro Val Thr Ile Cys Gly Asp Ile His Gly Gln Phe His Asp Leu Ala

50 55 60

Glu Leu Phe Arg Ile Gly Gly Lys Cys Pro Asp Thr Asn Tyr Leu Phe

65 70 75 80

Met Gly Asp Tyr Val Asp Arg Gly Tyr Tyr Ser Val Glu Thr Val Thr

85 90 95

Leu Leu Val Ser Leu Lys Val Arg Tyr Pro Gln Arg Ile Thr Ile Leu

100 105 110

Arg Gly Asn His Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly Phe Tyr
115 120 125

Asp Glu Cys Leu Arg Lys Tyr Gly Asn Ala Thr Val Trp Lys Thr Phe
130 135 140

Thr Asp Leu Phe Asp Tyr Phe Pro Leu Thr Ala Leu Val Glu Ser Glu
145 150 155 160

Ile Phe Cys Leu His Gly Gly Leu Ser Pro Ser Ile Glu Thr Leu Asp
165 170 175

Asn Ile Arg Asn Phe Asp Arg Thr Gln Glu Val Pro His Glu Gly Pro
180 185 190

Met Cys Asp Leu Leu Trp Ser Asp Pro Asp Asp Arg Cys Gly Trp Gly
195 200 205

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

Gln Phe Asn His Thr Asn Asn Leu Arg Leu Ile Ala Arg Ala His Gln
225 230 235 240

Leu Val Met Glu Gly Phe Asn Trp Ala His Glu Gln Lys Val Val Thr
245 250 255

Ile Phe Ser Ala Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Met Ala Ser
260 265 270

Ile Leu Glu Val Asp Asp Cys Arg Glu His Thr Phe Ile Gln Phe Glu
275 280 285

Pro Ala Pro Arg Arg Gly Glu Pro Asp Val Thr Arg Arg Thr Pro Asp
 290 295 300

Tyr Phe Leu
 305

<210> 285
 <211> 921
 <212> DNA
 <213> Z. mays

<400> 285
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 aacgtgcagc ccgtgcgctg ccccgtcacc gtctgeggcg acatccacgg ccagttctat 180
 gacctcatcg agctcttccg catcggcggc gactctcccg acaccaacta cctcttcatg 240
 ggcgactacg tcgatcgtgg ctattattca gttgaaacgg tttctctggt agtggctttg 300
 aaagtccgtt acagagatag aattacaata cttcgaggaa atcatgagag cagacaaatc 360
 actcaagtgt acggcttcta tgatgaatgc ttaagaaaat atggaaatgc aaatgtatgg 420
 aagtatttta cagacttggt tgattatttg cctctcacag ctcttataga aaatcaggtc 480
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 gatcgcatac aggaggtacc tcatgaagga cccatgtgtg atcttttgtg gtctgacca 600
 gatgaccgat gtgggtgggg aatttcaccc agaggagcag gttacacatt tgggcaagac 660
 attgcacagc agttcaacca tacaaatggt ctctctctca tttcaagggc ccatcaactt 720
 gtaatggaag gatttaattg gtgccaggat aagaatgtag tcacagtctt cagtgcgcct 780

aattactgtt accgctgtgg taacatggct gctattcttg aaatcgggga aaacatggac 840
 cagaacttcc ttcaattcaa cccgcacct cggcaaattg agccagacac aactcgcaaa 900
 accccagact actttctgta a 921

<210> 286

<211> 306

<212> PRT

<213> Z. mays

<400> 286

Met Pro Ser His Gly Asp Leu Asp Arg Gln Ile Ala Gln Leu Arg Asp
 1 5 10 15

Cys Lys Tyr Leu Pro Glu Ala Glu Val Lys Val Leu Cys Glu Gln Ala
 20 25 30

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

Val Thr Val Cys Gly Asp Ile His Gly Gln Phe Tyr Asp Leu Ile Glu
 50 55 60

Leu Phe Arg Ile Gly Gly Asp Ser Pro Asp Thr Asn Tyr Leu Phe Met
 65 70 75 80

Gly Asp Tyr Val Asp Arg Gly Tyr Tyr Ser Val Glu Thr Val Ser Leu
 85 90 95

Leu Val Ala Leu Lys Val Arg Tyr Arg Asp Arg Ile Thr Ile Leu Arg
 100 105 110

Gly Asn His Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly Phe Tyr Asp
115 120 125

Glu Cys Leu Arg Lys Tyr Gly Asn Ala Asn Val Trp Lys Tyr Phe Thr
130 135 140

Asp Leu Phe Asp Tyr Leu Pro Leu Thr Ala Leu Ile Glu Asn Gln Val
145 150 155 160

Phe Cys Leu His Gly Gly Leu Ser Pro Ser Leu Asp Thr Leu Asp Asn
165 170 175

Ile Arg Ser Leu Asp Arg Ile Gln Glu Val Pro His Glu Gly Pro Met
180 185 190

Cys Asp Leu Leu Trp Ser Asp Pro Asp Asp Arg Cys Gly Trp Gly Ile
195 200 205

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

Phe Asn His Thr Asn Gly Leu Ser Leu Ile Ser Arg Ala His Gln Leu
225 230 235 240

Val Met Glu Gly Phe Asn Trp Cys Gln Asp Lys Asn Val Val Thr Val
245 250 255

Phe Ser Ala Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Met Ala Ala Ile
260 265 270

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

Ala Pro Arg Gln Ile Glu Pro Asp Thr Thr Arg Lys Thr Pro Asp Tyr
290 295 300

Phe Leu
305

<210> 287
<211> 1686
<212> DNA
<213> Escherichia coli

<400> 287
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gcgtttgtga atatggggga ggtaatgacc ttccgcaage tggaagaacg cagtcgcgcg 180
tttgccgctt atttgcaaca agggttgggg ctgaagaaag gcgatcgcgt tgcgttgatg 240
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gtcgtaaacg ttaaccgctt gtatacccg cgtgagcttg agcatcagct taacgatagc 360
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cccgaactgg tgccggaaga tttagctttt ctgcaatata ccggcgccac cactggtgtg 660
gcgaaaggcg cgatgctgac tcaccgcaat atgctggcga acctggaaca ggttaacgcg 720
acctatggc cgctgttgca tccgggcaaa gagctggtgg tgacggcgct gccgctgtat 780

cacatTTTTg ccctgaccat taactgcctg ctgtttatcg aactgggtgg gcagaacctg	840
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accgctatca cgggcggttaa caccttgttc aatgcgttgc tgaacaataa agagttccag	960
cagctggatt tctccagtct gcattcttcc gcaggcggtg ggatgccagt gcagcaagtg	1020
gtggcagagc gttgggtgaa actgaccgga cagtatctgc tggaaggcta tggccttacc	1080
gagtgtgcgc cgctggtcag cgtaaaccca tatgatattg attatcatag tggtagcatc	1140
ggtttgccgg tgccgtcgac ggaagccaaa ctgggtggatg atgatgataa tgaagtacca	1200
ccaggtcaac cgggtgagct ttgtgtcaaa ggaccgcagg tgatgctggg ttactggcag	1260
cgtcccgatg ctaccgatga aatcatcaaa aatggctggt tacacaccgg cgacatcgcg	1320
gtaatggatg aagaaggatt cctgcgcatt gtcgatcgta aaaaagacat gattctgggt	1380
tccggtttta acgtctatcc caacgagatt gaagatgtcg tcatgcagca tcttggcgta	1440
caggaagtcg cggctgttgg cgtaccttcc ggctccagtg gtgaagcggg gaaaatcttc	1500
gtagtgaaaa aagatccatc gcttaccgaa gagtcactgg tgactttttg ccgcgcgcag	1560
ctcacgggat acaaagtacc gaagctggtg gagtttcgtg atgagttacc gaaatctaac	1620
gtcggaaaaa ttttgcgacg agaattacgt gacgaagcgc gcggcaaagt ggacaataaa	1680
gcctaa	1686

<210> 288
 <211> 561
 <212> PRT
 <213> Escherichia coli

<400> 288

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

Val Ala Arg Tyr Ala Asp Gln Pro Ala Phe Val Asn Met Gly Glu Val
35 40 45

Met Thr Phe Arg Lys Leu Glu Glu Arg Ser Arg Ala Phe Ala Ala Tyr
50 55 60

Leu Gln Gln Gly Leu Gly Leu Lys Lys Gly Asp Arg Val Ala Leu Met
65 70 75 80

Met Pro Asn Leu Leu Gln Tyr Pro Val Ala Leu Phe Gly Ile Leu Arg
85 90 95

Ala Gly Met Ile Val Val Asn Val Asn Pro Leu Tyr Thr Pro Arg Glu
100 105 110

Leu Glu His Gln Leu Asn Asp Ser Gly Ala Ser Ala Ile Val Ile Val
115 120 125

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

Gln His Val Ile Leu Thr Arg Met Gly Asp Gln Leu Ser Thr Ala Lys
145 150 155 160

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

Lys Tyr His Leu Pro Asp Ala Ile Ser Phe Arg Ser Ala Leu His Asn
180 185 190

Gly Tyr Arg Met Gln Tyr Val Lys Pro Glu Leu Val Pro Glu Asp Leu
195 200 205

Ala Phe Leu Gln Tyr Thr Gly Gly Thr Thr Gly Val Ala Lys Gly Ala
210 215 220

Met Leu Thr His Arg Asn Met Leu Ala Asn Leu Glu Gln Val Asn Ala
225 230 235 240

Thr Tyr Gly Pro Leu Leu His Pro Gly Lys Glu Leu Val Val Thr Ala
245 250 255

Leu Pro Leu Tyr His Ile Phe Ala Leu Thr Ile Asn Cys Leu Leu Phe
260 265 270

Ile Glu Leu Gly Gly Gln Asn Leu Leu Ile Thr Asn Pro Arg Asp Ile
275 280 285

Pro Gly Leu Val Lys Glu Leu Ala Lys Tyr Pro Phe Thr Ala Ile Thr
290 295 300

Gly Val Asn Thr Leu Phe Asn Ala Leu Leu Asn Asn Lys Glu Phe Gln
305 310 315 320

Gln Leu Asp Phe Ser Ser Leu His Leu Ser Ala Gly Gly Gly Met Pro
325 330 335

Val Gln Gln Val Val Ala Glu Arg Trp Val Lys Leu Thr Gly Gln Tyr
340 345 350

Leu Leu Glu Gly Tyr Gly Leu Thr Glu Cys Ala Pro Leu Val Ser Val
355 360 365

Asn Pro Tyr Asp Ile Asp Tyr His Ser Gly Ser Ile Gly Leu Pro Val
370 375 380

Pro Ser Thr Glu Ala Lys Leu Val Asp Asp Asp Asp Asn Glu Val Pro
385 390 395 400

Pro Gly Gln Pro Gly Glu Leu Cys Val Lys Gly Pro Gln Val Met Leu
405 410 415

Gly Tyr Trp Gln Arg Pro Asp Ala Thr Asp Glu Ile Ile Lys Asn Gly
420 425 430

Trp Leu His Thr Gly Asp Ile Ala Val Met Asp Glu Glu Gly Phe Leu
435 440 445

Arg Ile Val Asp Arg Lys Lys Asp Met Ile Leu Val Ser Gly Phe Asn
450 455 460

Val Tyr Pro Asn Glu Ile Glu Asp Val Val Met Gln His Pro Gly Val
465 470 475 480

Gln Glu Val Ala Ala Val Gly Val Pro Ser Gly Ser Ser Gly Glu Ala
485 490 495

Val Lys Ile Phe Val Val Lys Lys Asp Pro Ser Leu Thr Glu Glu Ser
500 505 510

Leu Val Thr Phe Cys Arg Arg Gln Leu Thr Gly Tyr Lys Val Pro Lys
515 520 525

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

Leu Arg Arg Glu Leu Arg Asp Glu Ala Arg Gly Lys Val Asp Asn Lys
545 550 555 560

Ala

<210> 289

<211> 2235

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 289

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tctcaattac cactgaccag ctatcccagg tacaaaacat ttttaaagaa acaggcgggt 180

gccatttcga atccggataa tgaagctggt tttagctcga tttataggag ttctctttct 240

tctgaaaatc tagtgagctg tgtggataaa aacttaagaa ctgcatacga tcaattcatg 300

ttttctgcaa ggagatggcc tcaacgtgac tgtttagggt caaggccaat tgataaagcc 360

acaggcacct gggaggaaac attccgtttc gagtcgtact ccacggtatc taaaagatgt 420

cataatatcg gaagtggat attgtctttg gtaaacacga aaaggaaacg tcctttggaa 480

gccaatgatt ttgttggtgc tatcttatca cacaacaacc ctgaatggat cctaacagat 540

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acctccgagt acatattgaa ttttaaccgag gccccattc tgatTTTTgc aaaatcaa	660
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atatttgtct ttggagatcc tttaaagaca tttttagtgtg gcatcgttgg tgttgatggt 1920

gatgcagcgc aaccgatttt agctgcaaag caccagagg tgaaaacgtg gactaaggaa 1980

gtgctagtag aaaacttaaa tcgtaataaa aagctaagga aggaattttt aaacaaaatt 2040

aataaatgca ccgatgggct acaaggattc gaaaaattgc ataacatcaa agtcggactt 2100

gagcctttaa ctctcgagga tgatgttgtg acgccaactt ttaaaataaa gcgtgccaaa 2160

gcatcaaaat tcttcaaaga tacattagac caactatacg ccgaaggttc actagtcaag 2220

acagaaaagc tttag 2235

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<211> 744

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 290

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20 25 30

Asp Glu Tyr Ile Glu Glu Leu Tyr Ser Gln Leu Pro Leu Thr Ser Tyr

35 40 45

Pro Arg Tyr Lys Thr Phe Leu Lys Lys Gln Ala Val Ala Ile Ser Asn

50 55 60

Pro Asp Asn Glu Ala Gly Phe Ser Ser Ile Tyr Arg Ser Ser Leu Ser

65 70 75 80

Ser Glu Asn Leu Val Ser Cys Val Asp Lys Asn Leu Arg Thr Ala Tyr
85 90 95

Asp His Phe Met Phe Ser Ala Arg Arg Trp Pro Gln Arg Asp Cys Leu
100 105 110

Gly Ser Arg Pro Ile Asp Lys Ala Thr Gly Thr Trp Glu Glu Thr Phe
115 120 125

Arg Phe Glu Ser Tyr Ser Thr Val Ser Lys Arg Cys His Asn Ile Gly
130 135 140

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

Ala Asn Asp Phe Val Val Ala Ile Leu Ser His Asn Asn Pro Glu Trp
165 170 175

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

Leu Tyr Glu Thr Leu Gly Pro Asn Thr Ser Glu Tyr Ile Leu Asn Leu
195 200 205

Thr Glu Ala Pro Ile Leu Ile Phe Ala Lys Ser Asn Met Tyr His Val
210 215 220

Leu Lys Met Val Pro Asp Met Lys Phe Val Asn Thr Leu Val Cys Met
225 230 235 240

Asp Glu Leu Thr His Asp Glu Leu Arg Met Leu Asn Glu Ser Leu Leu
245 250 255

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

Glu Gln Val Glu Gln Val Gly Cys Phe Asn Lys Ile Pro Ala Ile Pro
275 280 285

Pro Thr Pro Asp Ser Leu Tyr Thr Ile Ser Phe Thr Ser Gly Thr Thr
290 295 300

Gly Leu Pro Lys Gly Val Glu Met Ser His Arg Asn Ile Ala Ser Gly
305 310 315 320

Ile Ala Phe Ala Phe Ser Thr Phe Arg Ile Pro Pro Asp Lys Arg Asn
325 330 335

Gln Gln Leu Tyr Asp Met Cys Phe Leu Pro Leu Ala His Ile Phe Glu
340 345 350

Arg Met Val Ile Ala Tyr Asp Leu Ala Ile Gly Phe Gly Ile Gly Phe
355 360 365

Leu His Lys Pro Asp Pro Thr Val Leu Val Glu Asp Leu Lys Ile Leu
370 375 380

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

Ala Gly Ile Lys Asn Ala Leu Asp Lys Ser Thr Val Gln Arg Asn Val
405 410 415

Ala Asn Thr Ile Leu Asp Ser Lys Ser Ala Arg Phe Thr Ala Arg Gly
420 425 430

Gly Pro Asp Lys Ser Ile Met Asn Phe Leu Val Tyr His Arg Val Leu
435 440 445

Ile Asp Lys Ile Arg Asp Ser Leu Gly Leu Ser Asn Asn Ser Phe Ile
450 455 460

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

Ser Ala Leu Asp Ile Gly Ile Arg Gln Gly Tyr Gly Leu Thr Glu Thr
485 490 495

Phe Ala Gly Val Cys Leu Ser Glu Pro Phe Glu Lys Asp Val Gly Ser
500 505 510

Cys Gly Ala Ile Gly Ile Ser Ala Glu Cys Arg Leu Lys Ser Val Pro
515 520 525

Glu Met Gly Tyr His Ala Asp Lys Asp Leu Lys Gly Glu Leu Gln Ile
530 535 540

Arg Gly Pro Gln Val Phe Glu Arg Tyr Phe Lys Asn Pro Asn Glu Thr
545 550 555 560

Ser Lys Ala Val Asp Gln Asp Gly Trp Phe Ser Thr Gly Asp Val Ala
565 570 575

Phe Ile Asp Gly Lys Gly Arg Ile Ser Val Ile Asp Arg Val Lys Asn
580 585 590

Phe Phe Lys Leu Ala His Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu
595 600 605

Asn Ile Tyr Leu Ser Ser Cys Pro Tyr Ile Thr Gln Ile Phe Val Phe
610 615 620

Gly Asp Pro Leu Lys Thr Phe Leu Val Gly Ile Val Gly Val Asp Val
625 630 635 640

Asp Ala Ala Gln Pro Ile Leu Ala Ala Lys His Pro Glu Val Lys Thr
645 650 655

Trp Thr Lys Glu Val Leu Val Glu Asn Leu Asn Arg Asn Lys Lys Leu
660 665 670

Arg Lys Glu Phe Leu Asn Lys Ile Asn Lys Cys Thr Asp Gly Leu Gln
675 680 685

Gly Phe Glu Lys Leu His Asn Ile Lys Val Gly Leu Glu Pro Leu Thr
690 695 700

Leu Glu Asp Asp Val Val Thr Pro Thr Phe Lys Ile Lys Arg Ala Lys
705 710 715 720

Ala Ser Lys Phe Phe Lys Asp Thr Leu Asp Gln Leu Tyr Ala Glu Gly
725 730 735

Ser Leu Val Lys Thr Glu Lys Leu
740

<210> 291
<211> 1557
<212> DNA
<213> G.max

<400> 291

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gttgaatccg ccgccgcccg cttagtcgcc gccggaatca aaccggcgga cgtcatcgct	180
ctcaccttcc ccaataccgt cgagtttggt gtcttgtttc tagccgtcat tcgagtgcgc	240
gccacagccg cgccgttaaa cgcggttac acagccgaag agtttgagtt ttacttgtcc	300
gactccgagt ccaagcttct tctaacaatca gcagaaggaa acaactcagc tcaagccgca	360
gcttcaaaac tcaacatcct tcacagcaca gcttcaataa cccaagccgg agacaaagaa	420
gccgagctga gcctctcatt aagccactcc gagtcagagt caattaactc ggttgagtca	480
ctcggaacg atccagatga cgtggcgctt ttcttcaca cctcgggcac cagagccga	540
cccaagggag tgcctttgac gcaacacaac ctgttctctt ccgtgaacaa cattaaatcg	600
gtgtaccgac tactgagtc cgactcgacg gtgatcgctt ttcttttatt ccacgtgcac	660
ggtttgatcg cggggctcct gagttcgctc ggcaccgggg cggcggtggc gctgccggca	720
gcggggagat tctccgcctc gtcattctgg aaggacatga ttaaatacag cgccacgtgg	780
tacacagcgg ttctacaat acaccagatc atactggacc gccactcgaa cagccccgaa	840
ccggtttacc cgcgcctccg gttcattcga agctgcagcg cgtcgctcgc accggctatt	900
ctgggtaaac ttgaggaggc cttcggtgcg ccagtgctgg aggcttacgc gatgacggaa	960
gcgtcgcat t gatggcttc gaaccctttg ccgcaagatg ggccccacaa ggccgggtcg	1020
gttgggaaac ccgtgggtca agaaatggtt atattggacg aaacgggtcg ggttcaagat	1080

gctgaagtta gtggagaggt ttgcattagg ggtcctaattg ttacgaaggg atataaaaat 1140

aacgtggatg ccaatacggc ggcgtttttg tttggttggg ttcacaccgg tgatgttggg 1200

tacttggatt ctgatgggta tttgcatctc gtgggtcggg tcaaggagct catcaaccga 1260

ggaggagaaa agatatcacc aatagaagtg gatgctgtcc ttctttcaca ccagacatt 1320

gctcaggcag ttgcttttgg agtgcctgat ccaaagtatg gggaggagat atactgtgct 1380

gtaatcccaa gagaaggatc agacattgat gatgcagagt tgctaagata ttgcaagaag 1440

aatcttgcac ctttcaaagt ccccaaaaag gtcttcatta ccgattcttt gcccaagact 1500

gccaccggaa agattttgcg tcgtcttgtg gcagaacact ttgtctctca aatttga 1557

<210> 292

<211> 518

<212> PRT

<213> G.max

<400> 292

Met Asp Thr Pro Met Thr Leu Thr Gly Leu Leu Arg Asp Val Ala Ala
1 5 10 15

Lys Phe Pro Ser Arg Arg Ala Ile Ser Val Ala Gly Lys Phe Asp Leu
20 25 30

Thr His Ser Arg Leu His Gln Leu Val Glu Ser Ala Ala Ala Arg Leu
35 40 45

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

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

Ala Thr Ala Ala Pro Leu Asn Ala Ala Tyr Thr Ala Glu Glu Phe Glu
85 90 95

Phe Tyr Leu Ser Asp Ser Glu Ser Lys Leu Leu Leu Thr Ser Ala Glu
100 105 110

Gly Asn Asn Ser Ala Gln Ala Ala Ala Ser Lys Leu Asn Ile Leu His
115 120 125

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

Leu Ser Leu Ser His Ser Glu Ser Glu Ser Ile Asn Ser Val Glu Ser
145 150 155 160

Leu Gly Asn Asp Pro Asp Asp Val Ala Leu Phe Leu His Thr Ser Gly
165 170 175

Thr Thr Ser Arg Pro Lys Gly Val Pro Leu Thr Gln His Asn Leu Phe
180 185 190

Ser Ser Val Asn Asn Ile Lys Ser Val Tyr Arg Leu Thr Glu Ser Asp
195 200 205

Ser Thr Val Ile Val Leu Pro Leu Phe His Val His Gly Leu Ile Ala
210 215 220

Gly Leu Leu Ser Ser Leu Gly Thr Gly Ala Ala Val Ala Leu Pro Ala
225 230 235 240

Ala Gly Arg Phe Ser Ala Ser Ser Phe Trp Lys Asp Met Ile Lys Tyr
245 250 255

Ser Ala Thr Trp Tyr Thr Ala Val Pro Thr Ile His Gln Ile Ile Leu
260 265 270

Asp Arg His Ser Asn Ser Pro Glu Pro Val Tyr Pro Arg Leu Arg Phe
275 280 285

Ile Arg Ser Cys Ser Ala Ser Leu Ala Pro Ala Ile Leu Gly Lys Leu
290 295 300

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

Ala Ser His Leu Met Ala Ser Asn Pro Leu Pro Gln Asp Gly Pro His
325 330 335

Lys Ala Gly Ser Val Gly Lys Pro Val Gly Gln Glu Met Val Ile Leu
340 345 350

Asp Glu Thr Gly Arg Val Gln Asp Ala Glu Val Ser Gly Glu Val Cys
355 360 365

Ile Arg Gly Pro Asn Val Thr Lys Gly Tyr Lys Asn Asn Val Asp Ala
370 375 380

Asn Thr Ala Ala Phe Leu Phe Gly Trp Phe His Thr Gly Asp Val Gly
385 390 395 400

Tyr Leu Asp Ser Asp Gly Tyr Leu His Leu Val Gly Arg Ile Lys Glu
405 410 415

Leu Ile Asn Arg Gly Gly Glu Lys Ile Ser Pro Ile Glu Val Asp Ala
420 425 430

Val Leu Leu Ser His Pro Asp Ile Ala Gln Ala Val Ala Phe Gly Val
435 440 445

Pro Asp Pro Lys Tyr Gly Glu Glu Ile Tyr Cys Ala Val Ile Pro Arg
450 455 460

Glu Gly Ser Asp Ile Asp Asp Ala Glu Leu Leu Arg Tyr Cys Lys Lys
465 470 475 480

Asn Leu Ala Ser Phe Lys Val Pro Lys Lys Val Phe Ile Thr Asp Ser
485 490 495

Leu Pro Lys Thr Ala Thr Gly Lys Ile Leu Arg Arg Leu Val Ala Glu
500 505 510

His Phe Val Ser Gln Ile
515

<210> 293

<211> 1416

<212> DNA

<213> G.max

<400> 293

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tctgatttac tccccaaaat caccgcagct gcaccctctc taccaatcgt tctcatggac	240
aacgacggcg ccaataataa caataacaat aataatatcg tggccactct tgatgagatg	300
gcgaagaagg aaccggtggc tcagcgcgtg aaagagcgcg tggagcagga cgacacggcc	360
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tcgatcgaga ggttcgcgc cacttacctc ccgctcgtgc cgccattct ggtggccatg	660
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<210> 294
<211> 471
<212> PRT
<213> G.max

<400> 294

Met Gly Ile Arg Lys Gly Asn Val Val Leu Ile Leu Ser Pro Asn Ser
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Ile His Phe Pro Val Val Cys Leu Ala Val Met Ser Leu Gly Ala Ile
20 25 30

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

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

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

Asn Asp Gly Ala Asn Asn Asn Asn Asn Asn Asn Ile Val Ala Thr
85 90 95

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

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

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

Met Val Gln Ile Val Leu Gly Arg Phe His Met Glu Glu Asn Glu Thr
145 150 155 160

Phe Ile Cys Thr Val Pro Met Phe His Ile Tyr Gly Leu Val Ala Phe
165 170 175

Ala Thr Gly Leu Leu Ala Ser Gly Ser Thr Ile Val Val Leu Ser Lys
180 185 190

Phe Glu Met His Asp Met Leu Ser Ser Ile Glu Arg Phe Arg Ala Thr
195 200 205

Tyr Leu Pro Leu Val Pro Pro Ile Leu Val Ala Met Leu Asn Asn Ala
210 215 220

Ala Ala Ile Lys Gly Lys Tyr Asp Ile Thr Ser Leu His Ser Val Leu
225 230 235 240

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

Lys Tyr Pro Asn Val Thr Ile Leu Gln Gly Tyr Gly Leu Thr Glu Ser
260 265 270

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

Gly Thr Ala Gly Leu Leu Ser Pro Ala Thr Gln Ala Met Ile Val Asp
290 295 300

Pro Glu Ser Gly Gln Ser Leu Pro Val Asn Arg Thr Gly Glu Leu Trp
305 310 315 320

Leu Arg Gly Pro Thr Ile Met Lys Gly Tyr Phe Ser Asn Glu Glu Ala
325 330 335

Thr Thr Ser Thr Leu Asp Ser Lys Gly Trp Leu Arg Thr Gly Asp Ile
340 345 350

Cys Tyr Ile Asp Asn Asp Gly Phe Ile Phe Ile Val Asp Arg Leu Lys
355 360 365

Glu Leu Ile Lys Tyr Lys Gly Tyr Gln Val Pro Pro Ala Glu Leu Glu
370 375 380

Ala Leu Leu Leu Thr His Pro Ala Ile Leu Asp Ala Ala Val Ile Pro
385 390 395 400

Tyr Pro Asp Lys Glu Ala Gly Gln His Pro Met Ala Tyr Val Val Arg
405 410 415

Lys Ala Gly Ser Ser Leu Ser Glu Thr Gln Val Met Asp Phe Val Ala
420 425 430

Gly Gln Val Ala Pro Tyr Lys Arg Ile Arg Lys Val Ala Phe Ile Ser
435 440 445

Ser Ile Pro Lys Asn Pro Ser Gly Lys Ile Leu Arg Lys Asp Leu Ile
450 455 460

Lys Leu Ala Thr Ser Lys Leu
465 470

<210> 295
<211> 1572
<212> DNA
<213> G.max

<400> 295
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aagaacatcg actcagtgtg ccgactcact gagtccgact cgacggtgat tgttcttct 660
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tccagcaacc ccgaaccggt ttaccgcgga ctccggttca tccgaagctg cagcgccctcg 900
ctcgcaccgg ttatactcgg taaactcgag gaggttttcg gtgcaccggt tttagaggcc 960
tatgcgatga cggaagcgtc gcatttgatg gcttcgaacc ctttgccaca agatggggcc 1020

cacaagtccg ggtcgggttg gaaacccgtg ggtcaggaaa tgggcatttt agacgaatcg	1080
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gagatatatt gtgctgtcat cccaagagaa ggatcaaacg ttgatgaggc agaggtgcta	1440
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<210> 296
 <211> 523
 <212> PRT
 <213> G.max

<400> 296

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His	Val	Ala	Ala	Lys	Phe	Pro	Ser	Arg	Arg	Ala	Ile	Ser	Val	Ala	Ala
			20					25					30		

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

Ala	Ala	Gln	Leu	Val	Ser	Ala	Gly	Val	Lys	Pro	Gly	Asp	Val	Val	Ala
		50				55					60				

Leu Thr Phe Pro Asn Thr Ile Glu Phe Val Val Met Phe Leu Ala Val
65 70 75 80

Ile Arg Ala Arg Ala Thr Ala Ala Pro Leu Asn Ser Ala Tyr Thr Ala
85 90 95

Glu Glu Phe Glu Phe Tyr Leu Ser Asp Ser Glu Ser Lys Leu Leu Leu
100 105 110

Thr Ser Pro Glu Gly Asn Lys Pro Ala Gln Ala Ala Ala Ser Lys Leu
115 120 125

Cys Ile Pro His Ala Thr Ala Ser Ile Thr Lys Ala Glu Asn Glu Glu
130 135 140

Ala Glu Leu Ser Leu Ser Leu Leu Asn His Pro Glu Leu Asn Ser Val
145 150 155 160

Asn Ser Val Glu Ser Leu Val Asn Asp Pro Asp Asp Val Ala Leu Phe
165 170 175

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

Gln Tyr Asn Leu Leu Ser Ser Val Lys Asn Ile Asp Ser Val Tyr Arg
195 200 205

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

His Gly Leu Ile Ala Gly Leu Leu Ser Ser Leu Gly Ala Gly Ala Ala
225 230 235 240

Val Ala Leu Pro Ala Ala Gly Arg Phe Ser Ala Ser Ala Phe Trp Lys
245 250 255

Asp Met Ile Lys Tyr Ser Ala Thr Trp Tyr Thr Ala Val Pro Thr Ile
260 265 270

His Gln Ile Ile Leu Asp Arg His Ser Ser Asn Pro Glu Pro Val Tyr
275 280 285

Pro Arg Leu Arg Phe Ile Arg Ser Cys Ser Ala Ser Leu Ala Pro Val
290 295 300

Ile Leu Gly Lys Leu Glu Glu Ala Phe Gly Ala Pro Val Leu Glu Ala
305 310 315 320

Tyr Ala Met Thr Glu Ala Ser His Leu Met Ala Ser Asn Pro Leu Pro
325 330 335

Gln Asp Gly Ala His Lys Ser Gly Ser Val Gly Lys Pro Val Gly Gln
340 345 350

Glu Met Gly Ile Leu Asp Glu Ser Gly Arg Val Gln Glu Ala Gly Ile
355 360 365

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

Asn Asn Val Ala Ala Asn Thr Ala Ser Phe Leu Phe Asp Trp Phe His
385 390 395 400

Thr Gly Asp Ile Gly Tyr Phe Asp Ser Asp Gly Tyr Leu His Leu Val
405 410 415

Gly Arg Ile Lys Glu Leu Ile Asn Arg Gly Gly Glu Lys Ile Ser Pro
420 425 430

Ile Glu Val Asp Ala Val Leu Leu Ser His Pro Glu Ile Ala Gln Ala
435 440 445

Val Ala Phe Gly Val Pro Asp Ala Lys Tyr Gly Glu Glu Ile Tyr Cys
450 455 460

Ala Val Ile Pro Arg Glu Gly Ser Asn Val Asp Glu Ala Glu Val Leu
465 470 475 480

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

Phe Ile Thr Asp Ser Leu Pro Lys Thr Ala Thr Gly Lys Ile Leu Arg
500 505 510

Arg Leu Val Ala Glu His Phe Val Ser Gln Ile
515 520

<210> 297

<211> 1329

<212> DNA

<213> Z.mays

<400> 297

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cttccgagga acctcaggtg cgttgatcatc ggctcgaatg	agtacaagag cctctcctcc	180
gccggcggtg tagcgccgtc cccgccggtg gcggtgaagc	agtccgacac ggccggccgta	240
ctgtactcgt cgggcaccac gggtcgggtc aaggccgccc	cgggtctcgca ccgcaacctc	300
atcgcggtga tcagcgcgca caggaacaac cgggttatag	cggagaagga ggctgccgag	360
gccggcgagg agccgctccc gcctacggtg acgctgttcc	ccctcccact cttccacgta	420
ttcgggttca tgatgctgct gaggtcgggtg gccatggggg	agactgccgt cctcatggac	480
cgattcgact tcacgcagc gctgcgcgcc atcgagcgg	accgcgtcac gctgctgccc	540
gcggcgcccc cgggtgctggt ggccatgac aagtccgagg	aggcgcgccg ttgcgacctc	600
tcctccctcc tcttcatcgg catcggcggc gcgcccctcg	gccgcgaggt cgcgagcgc	660
ttcgccgcca tcttcccaa catagaactc attcagggt	acggtctgac ggagacatct	720
ggttctgtgg cttcgacggt cgggccagat gaggcgaag	cgtacgggtc ggtcgggaag	780
ctggcatcgc acttgaggc gaagatcgtc gatccctcca	ccggcgaggc gcttgggcca	840
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gacgaggcta ctgcagcaac agtggattca gaaggctggt	tgaaaaccgg tgacctatgc	960
tacttcaacg aggatgggtt actctacatt gttgatcgg	tgaaagagtt gataaagtac	1020
aagggatatc aggtacctc tgccgaactg gagcatatcc	tgaattctca tctgatatc	1080
atggacgcag cagttattcc ttatccagac gaagacgccg	ggcaactccc aatggctttt	1140
atagtgagga aaccagggtc aaaccttacc gagcaacaag	tcatggattt cgtggctaaa	1200
caggtcgcac cctacaagaa agttcgtcga gtggcctttg	tttctgcaat ccccaaatcg	1260
cctgctggga agatcttgcg gcgggagctt gtagagcagg	ccgtgtccat gggtaacctc	1320

aagctttga

1329

<210> 298

<211> 442

<212> PRT

<213> Z.mays

<400> 298

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Glu Glu Tyr Thr His Met Val Ala Leu Ser Arg Pro Val Val Ala Leu
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Ala Ala Pro Glu Val Ala Ala Lys Leu Pro Arg Asn Leu Arg Cys Val
35 40 45

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

Ala Pro Ser Pro Pro Val Ala Val Lys Gln Ser Asp Thr Ala Ala Val
65 70 75 80

Leu Tyr Ser Ser Gly Thr Thr Gly Arg Val Lys Ala Ala Ala Val Ser
85 90 95

His Arg Asn Leu Ile Ala Val Ile Ser Ala His Arg Asn Asn Arg Val
100 105 110

Ile Ala Glu Lys Glu Ala Ala Glu Ala Gly Glu Glu Pro Leu Pro Pro
115 120 125

Thr Val Thr Leu Phe Pro Leu Pro Leu Phe His Val Phe Gly Phe Met
130 135 140

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

Arg Phe Asp Phe Ile Ala Ala Leu Arg Ala Ile Glu Arg Tyr Arg Val
165 170 175

Thr Leu Leu Pro Ala Ala Pro Pro Val Leu Val Ala Met Ile Lys Ser
180 185 190

Glu Glu Ala Arg Arg Cys Asp Leu Ser Ser Leu Leu Phe Ile Gly Ile
195 200 205

Gly Gly Ala Pro Leu Gly Arg Glu Val Ala Glu Arg Phe Ala Ala Ile
210 215 220

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

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

Ser Val Gly Lys Leu Ala Ser His Leu Glu Ala Lys Ile Val Asp Pro
260 265 270

Ser Thr Gly Glu Ala Leu Gly Pro Gly Gln Arg Gly Glu Leu Trp Val
275 280 285

Arg Gly Pro Val Val Met Lys Gly Tyr Val Gly Asp Asp Glu Ala Thr
290 295 300

Ala Ala Thr Val Asp Ser Glu Gly Trp Leu Lys Thr Gly Asp Leu Cys
305 310 315 320

Tyr Phe Asn Glu Asp Gly Leu Leu Tyr Ile Val Asp Arg Leu Lys Glu
325 330 335

Leu Ile Lys Tyr Lys Gly Tyr Gln Val Pro Pro Ala Glu Leu Glu His
340 345 350

Ile Leu Asn Ser His Pro Asp Ile Met Asp Ala Ala Val Ile Pro Tyr
355 360 365

Pro Asp Glu Asp Ala Gly Gln Leu Pro Met Ala Phe Ile Val Arg Lys
370 375 380

Pro Gly Ser Asn Leu Thr Glu Gln Gln Val Met Asp Phe Val Ala Lys
385 390 395 400

Gln Val Ala Pro Tyr Lys Lys Val Arg Arg Val Ala Phe Val Ser Ala
405 410 415

Ile Pro Lys Ser Pro Ala Gly Lys Ile Leu Arg Arg Glu Leu Val Glu
420 425 430

Gln Ala Val Ser Met Gly Thr Ser Lys Leu
435 440

<210> 299

<211> 1668

<212> DNA

<213> Z.mays

<400> 299

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cgcgccgacg tgtgcccctc cgctctcgcg ctggctgact ccgccaccgg ccaatccctc	180
accttcgccg cctttcgctc cgccgtcctc accacggccg tcgccctctc ctgcgcgcgc	240
ggcgtccggc gcggcgacgt cgtcctcttc ttgcceccca actgcttctt ctaccccgtc	300
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cctcgggagg tcgctaaaca ggccaccgac tcgcggggcca agctcgcaat cacggtctct	420
gaactccttc caaaaatcgt ggacctcggc ttccccacca tcttgctcga cggcggcggc	480
gacggcgacg cggccagtgc cgccgcctcc aagcctcagg gagccagcgt gacgctttac	540
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gaggggcca acgtcttctt ctgcttcttg cccatgttcc acatcttcgg cttgtccgtc	780
atcacgttcg cgcagatgca gcgtggcaat tccgtcgtcg tgatgtcgcg gtttgacatg	840
gactctgtga tggccgcggt gcagcggcac cgtgtcactc acctcttctg cgtgcgcgcg	900
gtcatgatag cgctcgccaa gctcgggagc gttgggaaat atgacctcag ctgctcagg	960
ttcatcggct ctggcgcagc accgctcggc aaggacgtga tggagggagt ggccaagaat	1020
ttccagaag ctgtgattgc ccagggttac ggaatgactg aaacttggtg gatcatatct	1080
ttagagtacc cagaaaaagg acaaattcgt caatttggtt caactggagc acttgtctca	1140
ggagttgaag caaaaattgt tgatgtagaa acattgatat gtctgccacc aaatcaacta	1200

ggagaaattt gtgttcgagg accgaacata atgcaagggt atttcaacaa tgtgcaagct 1260
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 gttatcccgt tccccgatgc tgaagctggt gaagttccta ttgcttacgt cgtaagggtcc 1500
 tctgagagtt ctttgactga agttgatgtc cagaaattta ttgaaaagca ggtcgcatac 1560
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 <212> PRT
 <213> Z.mays

<400> 300

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Tyr Arg Ser Pro Arg Pro Ala Val Arg Ile Glu Ser Asp Thr Gly Leu
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Ser Leu Asn Asp Leu Leu Phe Arg Arg Ala Asp Val Cys Pro Ser Ala
 35 40 45

Leu Ala Leu Val Asp Ser Ala Thr Gly Gln Ser Leu Thr Phe Ala Ala
 50 55 60

Phe Arg Ser Ala Val Leu Thr Thr Ala Val Ala Leu Ser Ser Arg Ala
 65 70 75 80

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

Leu Tyr Pro Val Cys Phe Phe Ala Val Thr Ala Leu Gly Ala Val Ala
100 105 110

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

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

Lys Ile Val Asp Leu Gly Phe Pro Thr Ile Leu Leu Asp Gly Gly Gly
145 150 155 160

Asp Gly Asp Ala Ala Ser Ala Ala Ala Ser Lys Pro Gln Gly Ala Ser
165 170 175

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

Arg Arg Pro Pro Thr Lys Gln Ser Asp Thr Thr Ala Leu Met Tyr Ser
195 200 205

Ser Gly Thr Thr Gly Ala Ser Lys Gly Val Ile Leu Thr His Arg Asn
210 215 220

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

Glu Gly Pro Asn Val Phe Leu Cys Phe Leu Pro Met Phe His Ile Phe
245 250 255

Gly Leu Ser Val Ile Thr Phe Ala Gln Met Gln Arg Gly Asn Ser Val
260 265 270

Val Val Met Ser Arg Phe Asp Met Asp Ser Val Met Ala Ala Val Gln
275 280 285

Arg His Arg Val Thr His Leu Phe Cys Val Pro Pro Val Met Ile Ala
290 295 300

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

Phe Ile Gly Ser Gly Ala Ala Pro Leu Gly Lys Asp Val Met Glu Gly
325 330 335

Val Ala Lys Asn Phe Pro Glu Ala Val Ile Ala Gln Gly Tyr Gly Met
340 345 350

Thr Glu Thr Cys Gly Ile Ile Ser Leu Glu Tyr Pro Glu Lys Gly Gln
355 360 365

Ile Arg Gln Phe Gly Ser Thr Gly Ala Leu Val Ser Gly Val Glu Ala
370 375 380

Lys Ile Val Asp Val Glu Thr Leu Ile Cys Leu Pro Pro Asn Gln Leu
385 390 395 400

Gly Glu Ile Cys Val Arg Gly Pro Asn Ile Met Gln Gly Tyr Phe Asn
405 410 415

Asn Val Gln Ala Thr Glu Phe Thr Ile Lys Gln Gly Trp Leu His Thr
420 425 430

Gly Asp Ile Gly Tyr Phe Asp Glu Gly Gly Gln Leu Phe Val Val Asp
435 440 445

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

Glu Leu Glu Gly Leu Leu Leu Ser His Pro Glu Ile Leu Asp Ala Val
465 470 475 480

Val Ile Pro Phe Pro Asp Ala Glu Ala Gly Glu Val Pro Ile Ala Tyr
485 490 495

Val Val Arg Ser Ser Glu Ser Ser Leu Thr Glu Val Asp Val Gln Lys
500 505 510

Phe Ile Glu Lys Gln Val Ala Tyr Tyr Lys Lys Leu Arg Arg Val Thr
515 520 525

Phe Val Asp Ser Val Pro Lys Ser Ala Ser Gly Lys Ile Leu Arg Arg
530 535 540

Glu Leu Ile Ser Lys Val Arg Ser Ser Lys Leu
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<210> 301

<211> 1749

<212> PRT

<213> Z.mays

<400> 301

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Cys Gly Gly Gly Gly Cys Cys Gly Gly Thr Gly Ala Gly Cys Gly Gly
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Gly Thr Thr Cys Gly Cys Gly Gly Cys Gly Cys Cys Gly Gly Ala Gly
35 40 45

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Thr Gly Thr Thr Gly Thr Gly Ala Ala Cys Thr Gly Cys Gly Thr Cys

325

330

335

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

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

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

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

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

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

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

Thr Thr Gly Gly Cys Ala Ala Gly Ala Ala Gly Ala Ala Gly Ala Cys
450 455 460

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

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

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

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

Cys Thr Ala Cys Ala Gly Cys Ala Thr Gly Cys Thr Cys Thr Gly Gly
530 535 540

Gly Ala Ala Ala Gly Gly Gly Ala Gly Cys Thr Ala Thr Ala Gly Ala
545 550 555 560

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

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

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

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

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

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

Thr Ala Cys Thr Thr Cys Cys Ala Gly Cys Cys Cys Ala Ala Ala Gly

660

665

670

Gly Gly Cys Gly Thr Cys Gly Thr Gly Thr Thr Gly Cys Ala Thr Cys
675 680 685

Ala Cys Cys Gly Cys Gly Gly Thr Gly Cys Thr Thr Ala Thr Cys Thr
690 695 700

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

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

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

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

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

Ala Thr Gly Gly Thr Thr Gly Gly Thr Gly Cys Thr Ala Cys Ala Cys
785 790 795 800

Thr Thr Gly Gly Gly Cys Gly Cys Thr Gly Gly Cys Ala Gly Cys Gly
805 810 815

Thr Thr Cys Thr Gly Cys Gly Gly Ala Ala Cys Ala Ala Gly Cys Ala
820 825 830

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

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

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

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

Cys Thr Thr Cys Thr Gly Thr Gly Cys Cys Gly Cys Ala Cys Cys Thr
900 905 910

Gly Thr Cys Gly Thr Cys Cys Thr Thr Ala Ala Cys Ala Ala Cys Cys
915 920 925

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

Ala Ala Gly Cys Gly Ala Gly Ala Cys Cys Thr Thr Cys Cys Thr Gly
945 950 955 960

Cys Cys Gly Cys Thr Gly Cys Cys Cys Cys Gly Cys Gly Thr Cys Gly
965 970 975

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

Cys Gly Gly Ala Gly Cys Cys Gly Cys Cys Cys Cys Gly Ala Cys Gly

995

1000

1005

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

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Cys Ala Cys Ala Cys Gly Thr Ala Cys Gly Gly Cys Cys Thr Gly
1055 1060 1065

Thr Cys Ala Gly Ala Gly Ala Cys Gly Thr Ala Cys Gly Gly Thr
1070 1075 1080

Cys Cys Cys Thr Cys Gly Ala Cys Gly Gly Thr Gly Thr Gly Cys
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Gly Cys Gly Thr Gly Gly Ala Ala Gly Cys Cys Cys Gly Ala Gly
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Thr Gly Gly Gly Ala Cys Gly Ala Gly Cys Thr Gly Cys Cys Gly
1115 1120 1125

Cys Thr Gly Gly Ala Gly Gly Ala Gly Cys Gly Gly Thr Cys Cys
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Cys Gly Gly Cys Thr Gly Cys Ala Cys Thr Gly Cys Cys Gly Ala
1145 1150 1155

Cys Ala Gly Gly Gly Cys Gly Thr Cys Ala Gly Gly Thr Ala Cys
1160 1165 1170

Ala Thr Cys Gly Cys Gly Ala Thr Gly Gly Ala Gly Gly Gly Cys
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Cys Thr Gly Gly Ala Cys Gly Thr Cys Gly Thr Gly Gly Ala Cys
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Cys Cys Cys Ala Ala Gly Ala Cys Gly Ala Thr Gly Gly Cys Gly
1205 1210 1215

Cys Cys Cys Gly Thr Cys Cys Cys Gly Gly Cys Cys Gly Ala Cys
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Gly Ala Gly Ala Thr Cys Gly Thr Gly Cys Thr Gly Cys Gly Gly
1250 1255 1260

Gly Gly Cys Ala Ala Cys Gly Cys Cys Gly Thr Gly Ala Thr Gly
1265 1270 1275

Ala Ala Gly Gly Gly Gly Thr Ala Cys Cys Thr Cys Ala Ala Gly
1280 1285 1290

Ala Ala Cys Cys Cys Cys Gly Gly Gly Gly Cys Gly Ala Ala Cys
1295 1300 1305

Gly Cys Gly Gly Ala Gly Gly Cys Gly Thr Thr Cys Gly Cys Gly

1310

1315

1320

Gly Gly Cys Gly Gly Gly Thr Gly Gly Thr Ala Cys Cys Ala Cys
1325 1330 1335

Thr Cys Gly Gly Gly Cys Gly Ala Cys Cys Thr Cys Gly Gly Cys
1340 1345 1350

Gly Thr Gly Ala Ala Gly Cys Ala Cys Cys Cys Cys Gly Ala Cys
1355 1360 1365

Gly Gly Gly Thr Ala Cys Gly Thr Cys Gly Ala Gly Gly Thr Gly
1370 1375 1380

Ala Gly Gly Gly Ala Cys Cys Gly Gly Ala Thr Gly Ala Ala Gly
1385 1390 1395

Gly Ala Cys Gly Thr Gly Ala Thr Cys Ala Thr Cys Thr Cys Cys
1400 1405 1410

Gly Gly Ala Gly Gly Gly Gly Ala Gly Ala Ala Cys Ala Thr Cys
1415 1420 1425

Ala Gly Cys Ala Gly Cys Cys Thr Gly Gly Ala Gly Gly Thr Cys
1430 1435 1440

Gly Ala Gly Ala Ala Gly Gly Thr Gly Cys Thr Gly Thr Gly Cys
1445 1450 1455

Gly Cys Gly Cys Ala Cys Cys Cys Gly Gly Cys Ala Gly Thr Gly
1460 1465 1470

Thr Thr Cys Gly Ala Gly Gly Thr Ala Thr Cys Gly Gly Thr Gly
1475 1480 1485

Gly Thr Cys Gly Cys Cys Ala Gly Gly Gly Cys Cys Gly Ala Cys
1490 1495 1500

Gly Ala Gly Cys Gly Gly Thr Gly Gly Gly Gly Cys Gly Ala Gly
1505 1510 1515

Thr Cys Gly Cys Cys Gly Thr Gly Cys Gly Cys Gly Thr Thr Cys
1520 1525 1530

Gly Thr Gly Ala Cys Gly Cys Thr Cys Ala Ala Gly Gly Ala Cys
1535 1540 1545

Gly Gly Ala Gly Cys Ala Gly Cys Ala Gly Cys Cys Gly Ala Cys
1550 1555 1560

Gly Gly Gly Thr Cys Gly Gly Ala Cys Gly Ala Gly Gly Cys Gly
1565 1570 1575

Gly Cys Gly Cys Thr Gly Gly Cys Cys Ala Ala Cys Gly Ala Cys
1580 1585 1590

Ala Thr Cys Ala Thr Gly Cys Gly Cys Thr Thr Cys Thr Gly Cys
1595 1600 1605

Cys Gly Gly Gly Ala Gly Ala Gly Gly Ala Thr Gly Cys Cys Gly
1610 1615 1620

Gly Gly Gly Thr Ala Cys Thr Gly Gly Gly Thr Gly Cys Cys Cys

1625

1630

1635

Ala Ala Gly Thr Cys Gly Gly Thr Cys Ala Thr Cys Thr Thr Cys
1640 1645 1650

Gly Gly Gly Cys Cys Gly Cys Thr Gly Cys Cys Cys Ala Ala Gly
1655 1660 1665

Ala Cys Gly Gly Cys Cys Ala Cys Gly Gly Gly Gly Ala Ala Gly
1670 1675 1680

Ala Thr Cys Ala Ala Gly Ala Ala Gly Cys Ala Cys Gly Ala Gly
1685 1690 1695

Cys Thr Gly Ala Gly Gly Gly Cys Cys Ala Gly Gly Gly Cys Cys
1700 1705 1710

Ala Ala Ala Gly Ala Gly Cys Thr Cys Gly Gly Cys Cys Cys Thr
1715 1720 1725

Gly Thr Gly Ala Ala Gly Ala Ala Gly Ala Gly Cys Ala Gly Gly
1730 1735 1740

Ala Thr Gly Thr Gly Ala
1745

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<211> 582

<212> PRT

<213> Z.mays

<400> 302

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Arg Asp Ile Asp Asp Leu Pro Arg Asn Asp Ala Asn Tyr Thr Ala Leu
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Thr Pro Leu Trp Phe Leu Glu Arg Ala Ala Leu Ala His Pro Gly Arg
35 40 45

Ala Ser Val Val His Gly Pro Val Arg Tyr Thr Trp Ala Asp Thr Tyr
50 55 60

Arg Arg Cys Arg Arg Leu Ala Ser Ala Leu Ala Arg Leu Ser Val Gly
65 70 75 80

His Gly Ser Thr Val Ala Val Ile Ala Pro Asn Val Pro Ala Val Tyr
85 90 95

Glu Ala His Phe Gly Val Pro Met Ser Gly Ala Val Val Asn Cys Val
100 105 110

Asn Ile Arg Leu Asn Ala Glu Thr Ile Ala Phe Leu Leu Glu His Ser
115 120 125

Val Ala Glu Val Val Met Val Asp Gln Glu Phe Phe Thr Leu Ala Glu
130 135 140

Glu Ser Leu Lys Ile Ile Gly Lys Lys Lys Thr Ser Ala Phe Arg Arg
145 150 155 160

Pro Pro Ile Leu Ile Val Ile Gly Asp Pro Thr Cys Asp Pro Lys Ser
165 170 175

Leu Gln His Ala Leu Gly Lys Gly Ala Ile Glu Tyr Glu Glu Phe Leu
180 185 190

Lys Thr Gly Asp Pro Glu Phe Ser Trp Lys Pro Pro Lys Asp Glu Trp
195 200 205

Gln Ser Ile Ala Leu Gly Tyr Thr Ser Gly Thr Thr Ser Ser Pro Lys
210 215 220

Gly Val Val Leu His His Arg Gly Ala Tyr Leu Met Ala Leu Ser Val
225 230 235 240

Ala Ile Val Trp Gly Met Pro Glu Gly Ala Val Tyr Leu Trp Thr Leu
245 250 255

Pro Met Phe His Cys Asn Gly Trp Cys Tyr Thr Trp Ala Leu Ala Ala
260 265 270

Phe Cys Gly Thr Ser Ile Cys Leu Arg Gln Val Ser Thr Lys Ala Ile
275 280 285

Tyr Glu Gly Ile Thr Lys Gln Gly Val Thr His Phe Cys Ala Ala Pro
290 295 300

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

Pro Leu Pro Arg Val Val Asn Val Asn Val Ala Gly Ala Ala Pro Thr
325 330 335

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

Thr Tyr Gly Leu Ser Glu Thr Tyr Gly Pro Ser Thr Val Cys Ala Trp
355 360 365

Lys Pro Glu Trp Asp Glu Leu Pro Leu Glu Glu Arg Ser Arg Leu His
370 375 380

Cys Arg Gln Gly Val Arg Tyr Ile Ala Met Glu Gly Leu Asp Val Val
385 390 395 400

Asp Pro Lys Thr Met Ala Pro Val Pro Ala Asp Gly Lys Ser Tyr Gly
405 410 415

Glu Ile Val Leu Arg Gly Asn Ala Val Met Lys Gly Tyr Leu Lys Asn
420 425 430

Pro Gly Ala Asn Ala Glu Ala Phe Ala Gly Gly Trp Tyr His Ser Gly
435 440 445

Asp Leu Gly Val Lys His Pro Asp Gly Tyr Val Glu Val Arg Asp Arg
450 455 460

Met Lys Asp Val Ile Ile Ser Gly Gly Glu Asn Ile Ser Ser Leu Glu
465 470 475 480

Val Glu Lys Val Leu Cys Ala His Pro Ala Val Phe Glu Val Ser Val
485 490 495

Val Ala Arg Ala Asp Glu Arg Trp Gly Glu Ser Pro Cys Ala Phe Val
500 505 510

Thr Leu Lys Asp Gly Ala Ala Ala Asp Gly Ser Asp Glu Ala Ala Leu
515 520 525

Ala Asn Asp Ile Met Arg Phe Cys Arg Glu Arg Met Pro Gly Tyr Trp
530 535 540

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

Lys Ile Lys Lys His Glu Leu Arg Ala Arg Ala Lys Glu Leu Gly Pro
565 570 575

Val Lys Lys Ser Arg Met
580

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<400> 303
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gaggattctt tgaggattat cgcagataaa aagaaaggca cttttgaaca gccacttcta 180
atagttattg gtgacgcaac ttgcgatcca acaaccctcc aagacgcttt gagaaaagga 240
gccatcgatt atgaggcatt cttggaaagt ggagatcctg aatttgcttg gagaccacca 300
caggatgaat ggaagagtat cgcgctaggt tatacttctg ggacaacttc taacccaaag 360
gggtgtggtat tgcacacag gggggcttac ctaatgtcac tgagtgggtgc tttgatatgg 420

ggaatgaacg aaggcgctgt ttacttgtgg actttgcaa tgttccattg caacggttgg	480
tgctatacat ggacacttgc tgctctctgc gggacaagca tatgtcttcg tcaggtttca	540
gcgaaggcca tcttctcagc tatagccaac gagggcgtga ctcaacttctg tggggcaccg	600
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gcgctggcg gggacatcat gcggttctgc cgcgagaagc tgcccggtta ctgggtgcc	1320
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<210> 304

<211> 476

<212> PRT

<213> Z.mays

<400> 304

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20 25 30

Asp Gln Glu Phe Phe Thr Leu Ala Glu Asp Ser Leu Arg Ile Ile Ala
35 40 45

Asp Lys Lys Lys Gly Thr Phe Glu Gln Pro Leu Leu Ile Val Ile Gly
50 55 60

Asp Ala Thr Cys Asp Pro Thr Thr Leu Gln Asp Ala Leu Arg Lys Gly
65 70 75 80

Ala Ile Asp Tyr Glu Ala Phe Leu Glu Ser Gly Asp Pro Glu Phe Ala
85 90 95

Trp Arg Pro Pro Gln Asp Glu Trp Lys Ser Ile Ala Leu Gly Tyr Thr
100 105 110

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

Ala Tyr Leu Met Ser Leu Ser Gly Ala Leu Ile Trp Gly Met Asn Glu
130 135 140

Gly Ala Val Tyr Leu Trp Thr Leu Pro Met Phe His Cys Asn Gly Trp
145 150 155 160

Cys Tyr Thr Trp Thr Leu Ala Ala Leu Cys Gly Thr Ser Ile Cys Leu
165 170 175

Arg Gln Val Ser Ala Lys Ala Ile Phe Ser Ala Ile Ala Asn Glu Gly
180 185 190

Val Thr His Phe Cys Gly Ala Pro Val Val Leu Asn Thr Ile Ile Asn
195 200 205

Ala Pro Pro Ala Asp Thr Ile Leu Pro Leu Pro Arg Val Val Asn Val
210 215 220

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

Lys Leu Gly Phe Arg Ile Thr His Thr Tyr Gly Leu Ser Glu Thr Tyr
245 250 255

Gly Pro Ser Thr Val Cys Ala Trp Lys Pro Glu Trp Asp Arg Leu Pro
260 265 270

Ala Asp Glu Arg Ala Arg Leu His Ala Arg Gln Gly Val Arg Tyr Val
275 280 285

Gly Leu Glu Gly Leu Asp Val Val Asp Pro Lys Thr Met Thr Pro Val
290 295 300

Pro Ala Asp Gly Thr Thr Met Gly Glu Ile Val Met Arg Gly Asn Gly
305 310 315 320

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

Glu Asn Gly Trp Phe His Ser Gly Asp Leu Gly Val Arg His Gly Asp
340 345 350

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

Gly Glu Asn Ile Ser Ser Leu Glu Val Glu Lys Ala Val Tyr Leu His
370 375 380

Pro Ala Val Leu Glu Ala Ser Val Val Ala Arg Ala Asp Glu Arg Trp
385 390 395 400

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

Ser Asp Glu Ala Ala Leu Ala Arg Asp Ile Met Arg Phe Cys Arg Glu
420 425 430

Lys Leu Pro Gly Tyr Trp Val Pro Lys Ser Val Val Phe Gly Pro Leu
435 440 445

Pro Lys Thr Ala Thr Gly Lys Ile Lys Lys His Glu Leu Arg Ala Lys
450 455 460

Ala Lys Glu Leu Gly Pro Val Gly Lys Ser Arg Met
465 470 475

<210> 305
<211> 1689
<212> DNA
<213> G.max

<400> 305

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gttgtgagat caaacggctt tgatctaact gaagaggctg taaaagagtt tatagctaaa 1560

caggtagtgt ttacaaaag actgcacaaa gtttattttg ttcatgctat tcccaagtct 1620

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acgccttga 1689

<210> 306

<211> 562

<212> PRT

<213> G.max

<400> 306

Met Ile Thr Leu Ala Pro Ser Leu Asp Thr Pro Lys Thr Asp Gln Asn

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Gln Val Ser Asp Pro Gln Thr Ser His Val Phe Lys Ser Lys Leu Pro

20 25 30

Asp Ile Pro Ile Ser Asn His Leu Pro Leu His Ser Tyr Cys Phe Gln

35 40 45

Asn Leu Ser Gln Phe Ala His Arg Pro Cys Leu Ile Val Gly Pro Ala

50 55 60

Ser Lys Thr Phe Thr Tyr Ala Asp Thr His Leu Ile Ser Ser Lys Ile

65 70 75 80

Ala Ala Gly Leu Ser Asn Leu Gly Ile Leu Lys Gly Asp Val Val Met
85 90 95

Ile Leu Leu Gln Asn Ser Ala Asp Phe Val Phe Ser Phe Leu Ala Ile
100 105 110

Ser Met Ile Gly Ala Val Ala Thr Thr Ala Asn Pro Phe Tyr Thr Ala
115 120 125

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

Thr Gln Ala Met Tyr Val Asp Lys Leu Arg Asn His Asp Gly Ala Lys
145 150 155 160

Leu Gly Glu Asp Phe Lys Val Val Thr Val Asp Asp Pro Pro Glu Asn
165 170 175

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

Glu Val Glu Ile His Pro Asp Asp Ala Val Ala Met Pro Phe Ser Ser
195 200 205

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

Thr Thr Ser Val Ala Gln Gln Val Asp Gly Glu Asn Pro Asn Leu Tyr
225 230 235 240

Leu Thr Thr Glu Asp Val Leu Leu Cys Val Leu Pro Leu Phe His Ile
245 250 255

Phe Ser Leu Asn Ser Val Leu Leu Cys Ala Leu Arg Ala Gly Ser Ala
260 265 270

Val Leu Leu Met Gln Lys Phe Glu Ile Gly Thr Leu Leu Glu Leu Ile
275 280 285

Gln Arg His Arg Val Ser Val Ala Met Val Val Pro Pro Leu Val Leu
290 295 300

Ala Leu Ala Lys Asn Pro Met Val Ala Asp Phe Asp Leu Ser Ser Ile
305 310 315 320

Arg Leu Val Leu Ser Gly Ala Ala Pro Leu Gly Lys Glu Leu Glu Glu
325 330 335

Ala Leu Arg Asn Arg Met Pro Gln Ala Val Leu Gly Gln Gly Tyr Gly
340 345 350

Met Thr Glu Ala Gly Pro Val Leu Ser Met Cys Leu Gly Phe Ala Lys
355 360 365

Gln Pro Phe Gln Thr Lys Ser Gly Ser Cys Gly Thr Val Val Arg Asn
370 375 380

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

Asn Gln Pro Gly Glu Ile Cys Ile Arg Gly Gln Gln Ile Met Lys Gly
405 410 415

Tyr Leu Asn Asp Glu Ala Ala Thr Ala Ser Thr Ile Asp Ser Glu Gly
420 425 430

Trp Leu His Thr Gly Asp Val Gly Tyr Val Asp Asp Asp Asp Glu Ile
435 440 445

Phe Ile Val Asp Arg Val Lys Glu Leu Ile Lys Tyr Lys Gly Phe Gln
450 455 460

Val Pro Pro Ala Glu Leu Glu Gly Leu Leu Val Ser His Pro Ser Ile
465 470 475 480

Ala Asp Ala Ala Val Val Pro Gln Lys Asp Val Ala Ala Gly Glu Val
485 490 495

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

Ala Val Lys Glu Phe Ile Ala Lys Gln Val Val Phe Tyr Lys Arg Leu
515 520 525

His Lys Val Tyr Phe Val His Ala Ile Pro Lys Ser Pro Ser Gly Lys
530 535 540

Ile Leu Arg Lys Asp Leu Arg Ala Lys Leu Glu Thr Ala Ala Thr Gln
545 550 555 560

Thr Pro

<210> 307
<211> 1644
<212> DNA
<213> G.max

<400> 307

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<210> 308
 <211> 547
 <212> PRT
 <213> G.max

<400> 308

Met	Ala	Asp	Asp	Gly	Ser	Arg	Arg	Glu	Leu	Ile	Phe	Arg	Ser	Lys	Leu
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Pro	Asp	Ile	Tyr	Ile	Pro	Lys	His	Met	Pro	Leu	His	Ser	Tyr	Cys	Phe
				20				25					30		

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

Thr	Gly	Asp	Val	Tyr	Ser	Tyr	His	Glu	Val	Asp	Ser	Thr	Ala	Arg	Lys
								50			55			60	

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

Met Ile Leu Leu Pro Asn Cys Pro Glu Phe Val Phe Ser Phe Leu Gly
85 90 95

Ala Ser His Arg Gly Ala Met Ala Thr Ala Ala Asn Pro Phe Phe Thr
100 105 110

Pro Ala Glu Ile Ala Lys Gln Ala His Ala Ser Asn Ala Lys Leu Leu
115 120 125

Ile Thr Gln Ala Ser Tyr Tyr Asp Lys Val Lys Asp Leu Arg Asp Ile
130 135 140

Lys Leu Val Phe Val Asp Ser Cys Pro Pro His Thr Glu Glu Lys Gln
145 150 155 160

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

Asp Val Asp Val Asp Ile Lys Pro Asp Asp Val Val Ala Leu Pro Tyr
180 185 190

Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Met Leu Ser His Lys
195 200 205

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

Leu Tyr Tyr His Cys His Asp Thr Ile Leu Cys Val Leu Pro Leu Phe
225 230 235 240

His Ile Tyr Ser Leu Asn Ser Val Leu Leu Cys Gly Leu Arg Ala Lys
245 250 255

Ala Thr Ile Leu Leu Met Pro Lys Phe Asp Ile Asn Ser Leu Leu Ala
260 265 270

Leu Ile His Lys His Lys Val Thr Ile Ala Pro Val Val Pro Pro Ile
275 280 285

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

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

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

Tyr Gly Met Thr Glu Ala Gly Pro Val Leu Thr Met Ser Leu Ala Phe
340 345 350

Ala Lys Glu Pro Ile Asp Val Lys Pro Gly Ala Cys Gly Thr Val Val
355 360 365

Arg Asn Ala Glu Met Lys Ile Val Asp Pro Glu Thr Gly His Ser Leu
370 375 380

Pro Arg Asn Gln Ser Gly Glu Ile Cys Ile Arg Gly Asp Gln Ile Met
385 390 395 400

Lys Gly Tyr Leu Asn Asp Gly Glu Ala Thr Glu Arg Thr Ile Asp Lys
405 410 415

Asp Gly Trp Leu His Thr Gly Asp Ile Gly Tyr Ile Asp Asp Asp Asp
420 425 430

Glu Leu Phe Ile Val Asp Arg Leu Lys Glu Leu Ile Lys Tyr Lys Gly
435 440 445

Phe Gln Val Ala Pro Ala Glu Leu Glu Ala Leu Leu Leu Thr His Pro
450 455 460

Lys Ile Ser Asp Ala Ala Val Val Pro Met Lys Asp Glu Ala Ala Gly
465 470 475 480

Glu Val Pro Val Ala Phe Val Val Ile Ser Asn Gly Tyr Thr Asp Thr
485 490 495

Thr Glu Asp Glu Ile Lys Gln Phe Ile Ser Lys Gln Val Val Phe Tyr
500 505 510

Lys Arg Ile Asn Arg Val Phe Phe Ile Asp Ala Ile Pro Lys Ser Pro
515 520 525

Ser Gly Lys Ile Leu Arg Lys Asp Leu Arg Ala Lys Ile Ala Ala Ser
530 535 540

Val Pro Lys
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<210> 309
<211> 1638
<212> DNA
<213> G.max

<400> 309

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<210> 310
 <211> 546
 <212> PRT
 <213> G.max

<400> 310

Met	Ala	Pro	Ser	Pro	Gln	Glu	Ile	Ile	Phe	Arg	Ser	Pro	Leu	Pro	Asp
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Ile	Pro	Ile	Pro	Thr	His	Leu	Pro	Leu	Tyr	Ser	Tyr	Cys	Phe	Gln	Asn
			20					25					30		

Leu	Ser	Lys	Phe	His	Asp	Arg	Pro	Cys	Leu	Ile	Asp	Gly	Asp	Thr	Gly
		35						40					45		

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

Ser Gly Leu His Lys Ile Gly Ile Arg Gln Gly Asp Val Ile Met Leu
65 70 75 80

Val Leu Arg Asn Cys Pro Gln Phe Ala Leu Ala Phe Leu Gly Ala Thr
85 90 95

His Arg Gly Ala Val Val Thr Thr Ala Asn Pro Phe Tyr Thr Pro Ala
100 105 110

Glu Leu Ala Lys Gln Ala Thr Ala Thr Lys Thr Arg Leu Val Ile Thr
115 120 125

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

Asp Val Met Val Met Cys Ile Asp Asp Asp Phe Ser Tyr Glu Asn Asp
145 150 155 160

Gly Val Leu His Phe Ser Thr Leu Ser Asn Ala Asp Glu Thr Glu Ala
165 170 175

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

Ser Gly Thr Ser Gly Leu Pro Lys Gly Val Met Leu Ser His Glu Asn
195 200 205

Leu Val Thr Thr Ile Ser Gln Leu Val Asp Gly Glu Asn Pro His Gln
210 215 220

Tyr Thr His Ser Glu Asp Val Leu Leu Cys Val Leu Pro Met Phe His
225 230 235 240

Ile Tyr Ala Leu Asn Ser Ile Leu Leu Cys Gly Ile Arg Ser Gly Ala
245 250 255

Ala Val Leu Ile Val Gln Lys Phe Glu Ile Thr Thr Leu Phe Glu Leu
260 265 270

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

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

Ile Arg Ala Val Val Thr Gly Ala Ala Pro Leu Gly Gly Glu Leu Gln
305 310 315 320

Glu Ala Val Lys Ala Arg Leu Pro His Ala Thr Phe Gly Gln Gly Tyr
325 330 335

Gly Met Thr Glu Ala Gly Pro Leu Ala Ile Ser Met Ala Phe Ala Lys
340 345 350

Glu Pro Ser Lys Ile Lys Pro Gly Ala Cys Gly Thr Val Val Arg Asn
355 360 365

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

Asn Lys Ser Gly Glu Ile Cys Ile Arg Gly Ala Lys Val Met Lys Gly
385 390 395 400

Tyr Leu Asn Asp Pro Glu Ala Thr Glu Arg Thr Ile Asp Arg Glu Gly
405 410 415

Trp Leu His Thr Gly Asp Ile Gly Phe Ile Asp Asp Asp Asn Glu Leu
420 425 430

Phe Ile Val Asp Arg Leu Lys Glu Leu Ile Lys Tyr Lys Gly Phe Gln
435 440 445

Val Ala Pro Ala Glu Leu Glu Ala Leu Leu Ile Ala His Pro Asn Ile
450 455 460

Ser Asp Ala Ala Val Val Gly Met Lys Asp Glu Ala Ala Gly Glu Ile
465 470 475 480

Pro Val Ala Phe Val Val Arg Ser Asn Gly Ser Glu Ile Thr Glu Asp
485 490 495

Glu Ile Lys Thr Tyr Ile Ser Gln Gln Val Val Phe Tyr Lys Arg Ile
500 505 510

Gly Arg Val Phe Phe Thr Asp Ser Ile Pro Lys Ala Pro Ser Gly Lys
515 520 525

Ile Leu Arg Lys Val Leu Thr Ala Arg Leu Asn Glu Gly Leu Val Val
530 535 540

Ala Asn
545

<210> 311
<211> 2076
<212> DNA
<213> Z.mays

<400> 311
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gtgaaggagt ctggtgggct gaaagaaaaa ttgtttcata ctgcatacaa tgccaagaga	1140
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gcagatgtca tggaattcct gaggatatgc tttggtggtg aagttcttga aggctatgga	1320
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acatctgatg atcaacctta tcctcgtgga gaaatttgtg ttagaggacc tataatattc	1500
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<210> 312
 <211> 691
 <212> PRT
 <213> Z.mays

 <400> 312

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

Thr Gly Arg Trp Asn Val Tyr Arg Ser Ala Arg Ser Pro Leu Arg Leu
50 55 60

Ile Ser Arg Phe Pro Asp Thr Pro Asp Ile Gly Thr Leu His Asp Asn
65 70 75 80

Phe Thr Tyr Ala Val Glu Thr Phe Thr Asp Cys Lys Tyr Leu Gly Thr
85 90 95

Arg Ile Arg Ala Asp Gly Thr Ile Gly Asp Tyr Lys Trp Met Thr Tyr
100 105 110

Gly Glu Ala Ser Thr Ser Arg Thr Ala Val Gly Ser Gly Leu Ile Tyr
115 120 125

His Gly Val Arg Glu Gly Ala Cys Ile Gly Leu Tyr Phe Val Asn Arg
130 135 140

Pro Glu Trp Ile Ile Val Asp His Ala Cys Ser Ala Tyr Ser Tyr Val
145 150 155 160

Ser Val Pro Leu Tyr Asp Thr Leu Gly Pro Asp Ala Val Gln Phe Ile
165 170 175

Val Asn His Ala Ala Val Glu Val Ile Phe Cys Val Pro Gln Thr Leu
180 185 190

Ser Thr Leu Leu Ser Phe Ile Ala Gln Met Pro Cys Val Arg Leu Ile
195 200 205

Val Val Val Gly Gly Asp Asp Ala Asn Leu Pro Ser Thr Pro Val Thr
210 215 220

Thr Gly Val Gln Ile Ile Thr Tyr Ser Arg Leu Leu Ile Gln Gly Lys
225 230 235 240

Ala Ser Pro Gln Pro Phe Cys Leu Pro Lys Pro Glu Asp Val Ala Thr
245 250 255

Ile Cys Tyr Thr Ser Gly Thr Thr Gly Thr Pro Lys Gly Ala Val Leu
260 265 270

Ser His Gly Asn Leu Ile Ala Asn Val Ala Gly Ser Ser Leu Asn Ile
275 280 285

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

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

Ile Gly Phe Tyr Gln Gly Asp Asn Leu Lys Leu Met Asp Asp Leu Ala
325 330 335

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

Ile Tyr Thr Ala Ile Thr Asn Ala Val Lys Glu Ser Gly Gly Leu Lys
355 360 365

Glu Lys Leu Phe His Thr Ala Tyr Asn Ala Lys Arg Gln Ala Ile Leu
370 375 380

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

Ile Lys Ala Arg Leu Gly Gly Arg Val Arg Leu Met Ser Ser Gly Ala
405 410 415

Ser Pro Leu Ser Ala Asp Val Met Glu Phe Leu Arg Ile Cys Phe Gly
420 425 430

Gly Glu Val Leu Glu Gly Tyr Gly Met Thr Glu Thr Ser Cys Ile Ile
435 440 445

Ser Ala Met Asp Ile Gly Asp Arg Ser Ile Gly His Val Gly Ser Pro
450 455 460

Thr Ala Ser Cys Glu Val Lys Leu Val Asp Val Pro Glu Met Asn Tyr
465 470 475 480

Thr Ser Asp Asp Gln Pro Tyr Pro Arg Gly Glu Ile Cys Val Arg Gly
485 490 495

Pro Ile Ile Phe Gln Gly Tyr Tyr Lys Asp Glu Val Gln Thr Lys Glu
500 505 510

Val Ile Asp Glu Asp Gly Trp Leu His Thr Gly Asp Ile Gly Leu Trp
515 520 525

Leu Pro Gly Gly Arg Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile Phe
530 535 540

Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu Asn Val
545 550 555 560

Tyr Ala Lys Cys Lys Phe Ile Ala Gln Cys Phe Ile Tyr Gly Asp Ser
565 570 575

Phe Asn Ser Ser Leu Val Gly Ile Val Ala Val Glu Pro Glu Val Met
580 585 590

Lys Ala Trp Ala Ala Ser Glu Gly Ile Gln Cys Glu Asp Leu Arg Gln
595 600 605

Leu Cys Ala Asp Pro Arg Ala Arg Ala Ala Val Leu Ala Asp Met Asp
610 615 620

Ser Val Gly Lys Glu Ala Gln Leu Arg Gly Phe Glu Phe Ala Lys Ala
625 630 635 640

Val Arg Leu Val Ala Glu Pro Phe Thr Val Asp Asn Gly Leu Leu Thr
645 650 655

Pro Thr Phe Lys Val Lys Arg Gln Gln Ala Lys Thr Tyr Phe Ala Lys
660 665 670

Glu Ile Ser Asp Met Tyr Ala Glu Leu Arg Glu Ala Glu Ala Pro Arg
675 680 685

Ser Lys Leu
690

<210> 313
<211> 1995
<212> DNA
<213> Z.mays

<400> 313
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tgggtcatca gtatgcaggc ctgcaatgcc catggcatct actgtgtgcc actatatgac 420
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gttgaggaaa agaagatcgg agagatgctc aagacatttc ccaatgcgac caaatatctg 540
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ggcttgtcca tctactcatg ggaagagttt ctgcaactgg gaggtaaaga gaagtttgaa 660
cttccacca aggaaaagga tgacatatgt acaataatgt acaccagtgg aacaactgg 720
gatcctaagg gagtactaat ctgacaag agcattgtta ccattgtttc agcagtagat 780
gagttcctca acaactcaaa cgagcagctt aacatggatg acgtttacat ttctatctt 840

ccgcttgctc atatatattga ccgggtgatt gaagaggtgt tcattcgtca tgggtgcttca	900
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acagtttttt gtgctgttcc acgtgttcta gacagaattt atggaggatt gcaagataaa	1020
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gaccgcaaga agaacatctt caagctctca caggagagat acgttgcggt tgagaatctg	1620
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agggctgttc atctggaccc cgcaccgttc gacatggagc gcgaccttat cccccgacg	1920
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aatagcatga agtag	1995

<211> 664
<212> PRT
<213> Z.mays

<400> 314

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

Cys Ala Ala Gly Gly Asn Ala Ala Ser Pro Pro Ala Val Pro Gly Leu
35 40 45

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

Asn Lys Met Leu Gly Arg Arg Glu Ile Val His Gly Lys Ala Gly Ser
65 70 75 80

Tyr Thr Trp Leu Thr Tyr Lys Gln Val Tyr Asp Thr Val Leu Asp Val
85 90 95

Gly Ser Ala Ile Arg Ser Cys Gly Val Gly Lys Gly Gly Arg Cys Gly
100 105 110

Ile Tyr Gly Ala Asn Ser Pro Glu Trp Val Ile Ser Met Gln Ala Cys
115 120 125

Asn Ala His Gly Ile Tyr Cys Val Pro Leu Tyr Asp Thr Leu Gly Ala
130 135 140

Gly Ala Val Glu Phe Val Leu Cys His Ala Glu Val Gln Ile Ala Phe
145 150 155 160

Val Glu Glu Lys Lys Ile Gly Glu Met Leu Lys Thr Phe Pro Asn Ala
165 170 175

Thr Lys Tyr Leu Lys Thr Leu Val Ser Phe Gly Lys Val Asp Pro Gly
180 185 190

His Lys Glu Lys Val Glu Gln Asn Gly Leu Ser Ile Tyr Ser Trp Glu
195 200 205

Glu Phe Leu Gln Leu Gly Gly Lys Glu Lys Phe Glu Leu Pro Pro Lys
210 215 220

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

Asp Pro Lys Gly Val Leu Ile Ser Asn Lys Ser Ile Val Thr Ile Val
245 250 255

Ser Ala Val Asp Glu Phe Leu Asn Asn Ser Asn Glu Gln Leu Asn Met
260 265 270

Asp Asp Val Tyr Ile Ser Tyr Leu Pro Leu Ala His Ile Phe Asp Arg
275 280 285

Val Ile Glu Glu Val Phe Ile Arg His Gly Ala Ser Ile Gly Phe Trp
290 295 300

Arg Gly Asp Val Lys Leu Leu Val Glu Asp Ile Gly Glu Leu Lys Pro
305 310 315 320

Thr Val Phe Cys Ala Val Pro Arg Val Leu Asp Arg Ile Tyr Gly Gly
325 330 335

Leu Gln Asp Lys Ile Thr Ala Gly Gly Phe Leu Lys Lys Thr Leu Phe
340 345 350

Asn Val Ala Tyr Lys Tyr Lys Gln Gly Asn Met Leu Lys Gly Asn Lys
355 360 365

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

Lys Arg Gly Leu Gly Gly Arg Val Arg Leu Ile Leu Ser Gly Ala Ala
385 390 395 400

Pro Leu Ser Arg His Val Glu Glu Tyr Leu Arg Val Val Thr Cys Ser
405 410 415

His Val Leu Gln Gly Tyr Gly Leu Thr Glu Thr Cys Ala Gly Ser Phe
420 425 430

Val Ser Leu Pro Asn Asn Met Ser Met Leu Gly Thr Val Gly Pro Pro
435 440 445

Val Pro Tyr Val Glu Val Arg Leu Glu Ser Val Pro Glu Met Gly Tyr
450 455 460

Asp Ala Leu Ser Ser Glu Thr Pro Arg Gly Glu Ile Cys Ile Arg Gly
465 470 475 480

Asp Thr Leu Phe Ser Gly Tyr Tyr Lys Arg Glu Asp Leu Thr Lys Glu
485 490 495

Val Leu Val Asp Gly Trp Phe His Thr Gly Asp Ile Gly Glu Trp Gln
500 505 510

Ser Asp Gly Ser Met Lys Ile Ile Asp Arg Lys Lys Asn Ile Phe Lys
515 520 525

Leu Ser Gln Gly Glu Tyr Val Ala Val Glu Asn Leu Glu Asn Ile Phe
530 535 540

Gly Gln Thr Pro Ala Val Asp Ser Ile Trp Val Tyr Gly Asn Ser Phe
545 550 555 560

Glu Ser Ser Leu Val Ala Val Val Asn Pro Asn Thr Gln Ala Leu Glu
565 570 575

Arg Trp Ala Glu Ser Asn Gly Val Thr Gly Glu Phe Ala Thr Ile Cys
580 585 590

Glu Asp Pro Arg Ala Arg Glu Phe Ile Leu Gly Glu Leu Thr Lys Met
595 600 605

Gly Lys Glu Lys Lys Leu Lys Gly Phe Glu Leu Ile Arg Ala Val His
610 615 620

Leu Asp Pro Ala Pro Phe Asp Met Glu Arg Asp Leu Ile Thr Pro Thr
625 630 635 640

Tyr Lys Lys Lys Arg Pro Gln Leu Leu Lys His Tyr Gln Thr Ile Ile
645 650 655

Asp Gly Met Tyr Asn Ser Met Lys

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<210> 315

<211> 2181

<212> DNA

<213> Z.mays

<400> 315

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cgagctaatz tgggtggaga ggaaggattt gccatgcgaa acagtagggt ttctctctta 240

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aaatactctc gacggaggtg tcttggcacg aggaagctaa tcaagaggga atttgtggaa 360

tcttctgatg gtaggaagtt tgagaaactg caccttggtg aatacgaatz ggatacgtac 420

gccgaggcat ttaaccgcgc atgtaatttt gcttctggac ttgtcaagat gggccacgac 480

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ctggtgacgg cggcgcttaa gctgaagagg gagcagataa aggccaaatt caaagacgat	2160

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2181

<210> 316

<211> 726

<212> PRT

<213> Z.mays

<400> 316

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

Met Met Phe Gly Lys Lys Thr Lys Gln Arg Ala Val Arg Ala Asn Val
50 55 60

Gly Gly Glu Glu Gly Phe Ala Met Arg Asn Ser Arg Phe Ser Ser Leu
65 70 75 80

Val Glu Val Pro Trp Glu Gly Ala Thr Thr Met Ser Ala Leu Phe Glu
85 90 95

Met Ala Ser Lys Lys Tyr Ser Arg Arg Arg Cys Leu Gly Thr Arg Lys
100 105 110

Leu Ile Lys Arg Glu Phe Val Glu Ser Ser Asp Gly Arg Lys Phe Glu
115 120 125

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

Asn Arg Ala Cys Asn Phe Ala Ser Gly Leu Val Lys Met Gly His Asp
145 150 155 160

Leu Asp Ser His Ala Ala Ile Phe Ser Asp Thr Arg Ala Glu Trp Ile
165 170 175

Ile Ala Ala Gln Gly Cys Phe Arg Gln Asn Leu Thr Val Val Thr Ile
180 185 190

Tyr Ala Ser Leu Gly Glu Asp Ala Leu Val His Ser Leu Asn Glu Thr
195 200 205

Gln Val Ser Thr Leu Ile Cys Asp Ser Lys Gln Leu Lys Lys Ile Pro
210 215 220

Ala Ile Ser Ser Lys Leu Gln Ser Leu Arg His Ile Ile Tyr Ile Glu
225 230 235 240

Asp Glu Pro Val Glu Ala Glu Thr Leu Asn Gln Val Lys His Leu Thr
245 250 255

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

Asp Ala Arg Leu Pro Ser Ser Ser Asp Thr Ala Val Ile Met Tyr Thr
275 280 285

Ser Gly Ser Thr Gly Leu Pro Lys Gly Val Met Ile Thr His Gly Asn
290 295 300

Met Val Ala Thr Thr Ala Ala Val Met Thr Ile Val Pro Lys Leu Gly
305 310 315 320

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

Leu Ala Gly Glu Thr Val Met Leu Ala Ser Gly Thr Ala Ile Gly Tyr
340 345 350

Gly Ser Thr Leu Thr Met Thr Asp Thr Ser Asn Lys Ile Lys Lys Gly
355 360 365

Thr Lys Gly Asp Val Ser Val Leu Asn Pro Thr Leu Ile Ile Ser Val
370 375 380

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

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

Asn Leu Ala Ser Ile Glu Gly Ser Trp Phe Gly Ser Trp Ala Pro Glu
420 425 430

Arg Met Ile Trp Asp Thr Ile Ile Tyr Lys Pro Ile Arg Ala Met Leu
435 440 445

Gly Gly Arg Val Arg Phe Val Leu Cys Gly Gly Ala Pro Leu Ser Gly
450 455 460

Asp Thr Gln Arg Phe Met Asn Ile Cys Leu Gly Val Pro Val Gly Gln
465 470 475 480

Gly Tyr Gly Leu Thr Glu Thr Cys Ala Gly Ala Ala Phe Thr Glu Trp
485 490 495

Asp Asp Thr Ser Val Gly Arg Val Gly Pro Pro Leu Pro Cys Cys Tyr
500 505 510

Val Lys Leu Val Ser Trp Glu Glu Gly Gly Tyr Lys Ile Ser Asp Tyr
515 520 525

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

Gly Tyr Phe Ser Asn Glu Ala Lys Thr Asn Glu Val Tyr Lys Val Asp
545 550 555 560

Glu Arg Gly Ile Arg Trp Phe Tyr Thr Gly Asp Ile Gly Gln Phe His
565 570 575

Pro Asp Gly Cys Leu Glu Ile Ile Asp Arg Lys Lys Asp Ile Val Lys
580 585 590

Leu Gln His Gly Glu Tyr Val Ser Leu Gly Lys Val Glu Ser Ala Leu
595 600 605

Ala Thr Ser Ser Tyr Val Glu Ser Ile Met Val Tyr Ala Asp Pro Phe
610 615 620

His Asn Tyr Cys Val Ala Leu Val Val Pro Val Arg Gln Ala Leu Glu
625 630 635 640

Lys Trp Ala Gln Asn Ser Gly Ile Asn Cys Glu Gly Phe Glu Glu Leu
645 650 655

Cys Gln Asn Gly Gln Ala Val Lys Glu Val Gln Gln Ser Leu Ser Lys
660 665 670

Ala Ala Lys Ala Ala Arg Leu Glu Arg Phe Glu Val Pro Ala Lys Ile
675 680 685

Glu Leu Leu Pro Glu Pro Trp Thr Pro Glu Ser Gly Leu Val Thr Ala
690 695 700

Ala Leu Lys Leu Lys Arg Glu Gln Ile Lys Ala Lys Phe Lys Asp Asp
705 710 715 720

Leu Asp Lys Leu Tyr His
725

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<211> 954
<212> DNA
<213> E.coli

<400> 317
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gaacgccaca ttgccgcgcc aaacgaaacc gtttcaacca tgggctttga agcggcgaca 180
cgcgcaattg agatggcggg cattgagaaa gaccagattg gcttgatcgt tgtggcaacg 240
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aaaggttgcc cggcatttga cgttgcagca gcctgcgcag gtttcaccta tgcattaagc	360
gtagccgatc aatacgtgaa atctggggcg gtgaagtatg ctctggtcgt cggttccgat	420
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gcgggcgctg cggtgctggc tgcctctgaa gagccgggaa tcatttccac ccatctgcat	540
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<210> 318
 <211> 317
 <212> PRT
 <213> E.coli

<400> 318

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			20					25					30		

Ile	Val	Thr	Arg	Thr	Gly	Ile	Arg	Glu	Arg	His	Ile	Ala	Ala	Pro	Asn
		35					40					45			

Glu Thr Val Ser Thr Met Gly Phe Glu Ala Ala Thr Arg Ala Ile Glu
50 55 60

Met Ala Gly Ile Glu Lys Asp Gln Ile Gly Leu Ile Val Val Ala Thr
65 70 75 80

Thr Ser Ala Thr His Ala Phe Pro Ser Ala Ala Cys Gln Ile Gln Ser
85 90 95

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

Ala Gly Phe Thr Tyr Ala Leu Ser Val Ala Asp Gln Tyr Val Lys Ser
115 120 125

Gly Ala Val Lys Tyr Ala Leu Val Val Gly Ser Asp Val Leu Ala Arg
130 135 140

Thr Cys Asp Pro Thr Asp Arg Gly Thr Ile Ile Ile Phe Gly Asp Gly
145 150 155 160

Ala Gly Ala Ala Val Leu Ala Ala Ser Glu Glu Pro Gly Ile Ile Ser
165 170 175

Thr His Leu His Ala Asp Gly Ser Tyr Gly Glu Leu Leu Thr Leu Pro
180 185 190

Asn Ala Asp Arg Val Asn Pro Glu Asn Ser Ile His Leu Thr Met Ala
195 200 205

Gly Asn Glu Val Phe Lys Val Ala Val Thr Glu Leu Ala His Ile Val
210 215 220

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

Leu Val Pro His Gln Ala Asn Leu Arg Ile Ile Ser Ala Thr Ala Lys
 245 250 255

Lys Leu Gly Met Ser Met Asp Asn Val Val Val Thr Leu Asp Arg His
 260 265 270

Gly Asn Thr Ser Ala Ala Ser Val Pro Cys Ala Leu Asp Glu Ala Val
 275 280 285

Arg Asp Gly Arg Ile Lys Pro Gly Gln Leu Val Leu Leu Glu Ala Phe
 290 295 300

Gly Gly Gly Phe Thr Trp Gly Ser Ala Leu Val Arg Phe
 305 310 315

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 <211> 960
 <212> DNA
 <213> E.coli

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 catcgtctgc gtgaaaaaag cgtagaactg acacgtaaaa tcttcgccga tctcggtgca 180
 tggcagattg cgcaactggc acgccatcca cagcgtcctt ataccttggg ttacgttcgc 240
 ctggcatttg atgaatttga cgaactggct ggcgaccgcg cgtatgcaga cgataaagct 300

atcgtcgggtg gtatcgcccg tctcgatggt cgtccgggtga tgatcattgg tcatcaaaaa	360
ggtcgtgaaa ccaaagaaaa aattcgccgt aactttggta tgccagcgcc agaaggttac	420
cgcaaagcac tgcgtctgat gcaaattggct gaacgcttta agatgcctat catcaccttt	480
atcgacaccc cgggggctta tcctggcgtg ggcgcagaag agcgtgggtca gtctgaagcc	540
attgcacgca acctgcgtga aatgtctcgc ctcggcgtac cggtagtttg tacggttatc	600
ggtgaagggtg gttctggcgg tgcgctggcg attggcgtgg gcgataaagt gaatatgctg	660
caatacagca cctattccgt tatctcgccg gaaggttgtg cgtccattct gtggaagagc	720
gccgacaaag cgccgctggc ggctgaagcg atgggtatca ttgctccgcg tctgaaagaa	780
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gcgatggcgg catcgttgaa agcgcaactg ctggcggatc tggccgatct cgacgtgtta	900
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<210> 320
 <211> 319
 <212> PRT
 <213> E.coli

<400> 320

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

Asp	Ile	Asn	Ile	Asp	Glu	Glu	Val	His	Arg	Leu	Arg	Glu	Lys	Ser	Val
					35			40				45			

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

Gln Leu Ala Arg His Pro Gln Arg Pro Tyr Thr Leu Asp Tyr Val Arg
65 70 75 80

Leu Ala Phe Asp Glu Phe Asp Glu Leu Ala Gly Asp Arg Ala Tyr Ala
85 90 95

Asp Asp Lys Ala Ile Val Gly Gly Ile Ala Arg Leu Asp Gly Arg Pro
100 105 110

Val Met Ile Ile Gly His Gln Lys Gly Arg Glu Thr Lys Glu Lys Ile
115 120 125

Arg Arg Asn Phe Gly Met Pro Ala Pro Glu Gly Tyr Arg Lys Ala Leu
130 135 140

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

Ile Asp Thr Pro Gly Ala Tyr Pro Gly Val Gly Ala Glu Glu Arg Gly
165 170 175

Gln Ser Glu Ala Ile Ala Arg Asn Leu Arg Glu Met Ser Arg Leu Gly
180 185 190

Val Pro Val Val Cys Thr Val Ile Gly Glu Gly Gly Ser Gly Gly Ala
195 200 205

Leu Ala Ile Gly Val Gly Asp Lys Val Asn Met Leu Gln Tyr Ser Thr
210 215 220

Tyr Ser Val Ile Ser Pro Glu Gly Cys Ala Ser Ile Leu Trp Lys Ser
 225 230 235 240

Ala Asp Lys Ala Pro Leu Ala Ala Glu Ala Met Gly Ile Ile Ala Pro
 245 250 255

Arg Leu Lys Glu Leu Lys Leu Ile Asp Ser Ile Ile Pro Glu Pro Leu
 260 265 270

Gly Gly Ala His Arg Asn Pro Glu Ala Met Ala Ala Ser Leu Lys Ala
 275 280 285

Gln Leu Leu Ala Asp Leu Ala Asp Leu Asp Val Leu Ser Thr Glu Asp
 290 295 300

Leu Lys Asn Arg Arg Tyr Gln Arg Leu Met Ser Tyr Gly Tyr Ala
 305 310 315

<210> 321
 <211> 1350
 <212> DNA
 <213> E.coli

<400> 321
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 cacgtattac tggcagatga aacggctctgt attggccctg ctccgtcagt aaaaagttat 180
 ctgaacatcc cggcaatcat cagcgccgct gaaatcacgc gcgcagtagc aatccatccg 240
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gcggcgatga aaaaagcggg cgtcccttgc gtaccggggtt ctgacggccc gctgggogac	420
gatatggata aaaaccgtgc cattgctaaa cgcattgggtt atccgggtgat tatcaaagcc	480
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gagaaatacc tggaaaatcc tcgccacgtc gagattcagg tactggctga cggtcagggc	660
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gaagaagcgc cagcaccggg cattaccccg gaactgcgtc gctacatcgg cgaacggttc	780
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<210> 322
 <211> 449
 <212> PRT
 <213> E.coli

<400> 322

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

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

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

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

Gly Tyr Gly Phe Leu Ser Glu Asn Ala Asn Phe Ala Glu Gln Val Glu
85 90 95

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

Met Gly Asp Lys Val Ser Ala Ile Ala Ala Met Lys Lys Ala Gly Val
115 120 125

Pro Cys Val Pro Gly Ser Asp Gly Pro Leu Gly Asp Asp Met Asp Lys
130 135 140

Asn Arg Ala Ile Ala Lys Arg Ile Gly Tyr Pro Val Ile Ile Lys Ala
145 150 155 160

Ser Gly Gly Gly Gly Gly Arg Gly Met Arg Val Val Arg Gly Asp Ala
165 170 175

Glu Leu Ala Gln Ser Ile Ser Met Thr Arg Ala Glu Ala Lys Ala Ala
180 185 190

Phe Ser Asn Asp Met Val Tyr Met Glu Lys Tyr Leu Glu Asn Pro Arg
195 200 205

His Val Glu Ile Gln Val Leu Ala Asp Gly Gln Gly Asn Ala Ile Tyr
210 215 220

Leu Ala Glu Arg Asp Cys Ser Met Gln Arg Arg His Gln Lys Val Val
225 230 235 240

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

Gly Glu Arg Cys Ala Lys Ala Cys Val Asp Ile Gly Tyr Arg Gly Ala
260 265 270

Gly Thr Phe Glu Phe Leu Phe Glu Asn Gly Glu Phe Tyr Phe Ile Glu
275 280 285

Met Asn Thr Arg Ile Gln Val Glu His Pro Val Thr Glu Met Ile Thr
290 295 300

Gly Val Asp Leu Ile Lys Glu Gln Leu Arg Ile Ala Ala Gly Gln Pro
305 310 315 320

Leu Ser Ile Lys Gln Glu Glu Val His Val Arg Gly His Ala Val Glu
325 330 335

Cys Arg Ile Asn Ala Glu Asp Pro Asn Thr Phe Leu Pro Ser Pro Gly
 340 345 350

Lys Ile Thr Arg Phe His Ala Pro Gly Gly Phe Gly Val Arg Trp Glu
 355 360 365

Ser His Ile Tyr Ala Gly Tyr Thr Val Pro Pro Tyr Tyr Asp Ser Met
 370 375 380

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

Arg Met Lys Asn Ala Leu Gln Glu Leu Ile Ile Asp Gly Ile Lys Thr
 405 410 415

Asn Val Asp Leu Gln Ile Arg Ile Met Asn Asp Glu Asn Phe Gln His
 420 425 430

Gly Gly Thr Asn Ile His Tyr Leu Glu Lys Lys Leu Gly Leu Gln Glu
 435 440 445

Lys

<210> 323

<211> 1608

<212> DNA

<213> B.napus

<400> 323

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gtttactcaa ccatcgacaa ggatgcattg catgtcaaat tggctgatga agctgtttgt	360
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gtaccaggga gtgatggact attaaagagc acagaagaag gagtcaagct cgccaatgag	660
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gctaataaac cgtcagagtt tgtgaaactg ctgcaggcag caaagagtga ggccgcggct	780
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ttcaagaacg gaaaagttga cactgcattc atccccaagc atgaagagga attagcagag 1560

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<211> 535

<212> PRT

<213> B.napus

<400> 324

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

Thr Leu Lys Val Ser Arg Lys Asn Val Asn Arg Arg Cys Gly Gly Gly
50 55 60

Ala Leu Gly Ala Thr Cys Ser Gly Asp Lys Ile Leu Val Ala Asn Arg
65 70 75 80

Gly Glu Ile Ala Val Arg Val Ile Arg Thr Ala His Glu Met Gly Ile
85 90 95

Pro Cys Val Ala Val Tyr Ser Thr Ile Asp Lys Asp Ala Leu His Val
100 105 110

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

Ser Tyr Leu Val Ile Pro Asn Val Leu Ser Ala Ala Ile Ser Arg Gly
130 135 140

Cys Thr Met Leu His Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala Leu
145 150 155 160

Phe Val Glu Met Cys Arg Glu His Arg Ile Asn Phe Ile Gly Pro Asn
165 170 175

Pro Asp Ser Ile Arg Val Met Gly Asp Lys Ser Thr Ala Arg Glu Thr
180 185 190

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

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

Val Met Ile Lys Ala Thr Ala Gly Gly Gly Gly Arg Gly Met Arg Leu
225 230 235 240

Ala Asn Glu Pro Ser Glu Phe Val Lys Leu Leu Gln Ala Ala Lys Ser
245 250 255

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

Val Gln Asn Pro Arg His Ile Glu Phe Gln Ile Leu Ala Asp Lys Phe
275 280 285

Gly Asn Val Val His Phe Gly Glu Arg Asp Cys Ser Ile Gln Arg Arg
290 295 300

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

Leu Arg Lys Ala Met Gly Asp Ala Ala Val Ala Ala Ala Ala Ser Ile
325 330 335

Gly Tyr Ile Gly Val Gly Thr Val Glu Phe Leu Leu Asp Glu Arg Gly
340 345 350

Ser Phe Tyr Phe Met Glu Met Asn Thr Arg Ile Gln Val Glu His Pro
355 360 365

Val Thr Glu Met Ile Tyr Ser Val Asp Leu Ile Glu Glu Gln Ile Arg
370 375 380

Val Ala Met Gly Glu Lys Leu Arg Tyr Thr Gln Asp Glu Ile Val Leu
385 390 395 400

Arg Gly His Ser Ile Glu Cys Arg Ile Asn Ala Glu Asp Pro Phe Lys
405 410 415

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

Gly Pro Phe Val Arg Met Asp Ser His Val Tyr Pro Asp Tyr Val Val
435 440 445

Pro Pro Ser Tyr Asp Ser Leu Leu Gly Lys Leu Ile Val Trp Ala Pro
450 455 460

Thr Arg Glu Arg Ala Ile Glu Arg Met Lys Arg Ala Leu Asn Asp Thr
465 470 475 480

Ile Ile Thr Gly Val Pro Thr Thr Ile Glu Tyr His Lys Leu Ile Leu
485 490 495

Glu Val Glu Asp Phe Lys Asn Gly Lys Val Asp Thr Ala Phe Ile Pro
500 505 510

Lys His Glu Glu Glu Leu Ala Glu Pro His Glu Ile Val Leu Val Lys
515 520 525

Asp Leu Thr Asn Ala Ala Ala
530 535

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<211> 2199
<212> DNA
<213> G.max

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gcaggtgtgc ctcttgatcc tggatatcac ggatatgac aagatattga aaaaatgaag	540
ttggaagctg atagaattgg atatccagtc ctaattaagc caactcatgg tggaggtgga	600
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<210> 326
 <211> 732
 <212> PRT
 <213> G.max

<400> 326

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		20					25				30				

Asn	Lys	His	Arg	Ile	Glu	Lys	Ile	Leu	Val	Ala	Asn	Arg	Gly	Glu	Ile
	35						40				45				

Ala Cys Arg Ile Thr Arg Thr Ala Arg Arg Leu Gly Ile Gln Thr Val
50 55 60

Ala Val Tyr Ser Asp Ala Asp Arg Asp Ser Leu His Val Ala Thr Ala
65 70 75 80

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

Asn Gly Ala Ser Ile Val Asp Ala Ala Ile Arg Ser Gly Ala Gln Ala
100 105 110

Ile His Pro Gly Tyr Gly Phe Leu Ser Glu Ser Ala Asp Phe Ala Lys
115 120 125

Leu Cys Glu Glu Ser Gly Leu Thr Phe Ile Gly Pro Pro Ala Ser Ala
130 135 140

Ile Arg Asp Met Gly Asp Lys Ser Ala Ser Lys Arg Ile Met Gly Ala
145 150 155 160

Ala Gly Val Pro Leu Val Pro Gly Tyr His Gly Tyr Asp Gln Asp Ile
165 170 175

Glu Lys Met Lys Leu Glu Ala Asp Arg Ile Gly Tyr Pro Val Leu Ile
180 185 190

Lys Pro Thr His Gly Gly Gly Gly Lys Gly Met Arg Ile Val His Thr
195 200 205

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

Ala Ser Phe Gly Val Asn Thr Ile Leu Leu Glu Lys Tyr Ile Thr Arg
225 230 235 240

Pro Arg His Ile Glu Val Gln Ile Phe Gly Asp Lys His Gly Asn Val
245 250 255

Leu His Leu Tyr Glu Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys
260 265 270

Ile Ile Glu Glu Ala Pro Ala Pro Asn Ile Ser Ala Asp Phe Arg Ala
275 280 285

Gln Leu Gly Val Ala Ala Val Ser Ala Ala Lys Ala Val Asn Tyr Tyr
290 295 300

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

Tyr Phe Met Glu Met Asn Thr Arg Leu Gln Val Glu His Pro Val Thr
325 330 335

Glu Met Ile Val Gly Gln Asp Leu Val Glu Trp Gln Ile Leu Val Ala
340 345 350

Asn Gly Glu Ala Leu Pro Leu Ser Gln Ser Gln Val Pro Leu Ser Gly
355 360 365

His Ala Phe Glu Ala Arg Ile Tyr Ala Glu Asn Val Gln Lys Gly Phe
370 375 380

Leu Pro Ala Thr Gly Val Leu His His Tyr His Val Pro Val Ser Ser
385 390 395 400

Ala Val Arg Val Glu Thr Gly Val Lys Glu Gly Asp Lys Val Ser Met
405 410 415

His Tyr Asp Pro Met Ile Ala Lys Leu Val Val Trp Gly Glu Asn Arg
420 425 430

Ala Ala Ala Leu Val Lys Leu Lys Asp Ser Leu Ser Lys Phe Gln Val
435 440 445

Ala Gly Leu Pro Thr Asn Val Asn Phe Leu Gln Lys Leu Ala Asn His
450 455 460

Arg Ala Phe Ala Asn Gly Asn Val Glu Thr His Phe Ile Asp Asn Tyr
465 470 475 480

Lys Glu Asp Leu Phe Val Asp Ala Asn Asn Ser Val Ser Val Lys Glu
485 490 495

Ala Tyr Glu Ala Ala Arg Leu Asn Ala Ser Leu Val Ala Ala Cys Leu
500 505 510

Ile Glu Lys Glu His Phe Ile Leu Ala Arg Asn Pro Pro Gly Leu Leu
515 520 525

Pro Ile Trp Tyr Ser Ser Pro Pro Phe Arg Ile His His Gln Ala Lys
530 535 540

Arg Arg Met Glu Leu Glu Trp Asp Asn Glu Tyr Gly Ser Gly Ser Ser
545 550 555 560

Lys Ile Met Lys Leu Thr Ile Thr Tyr Gln Pro Asp Gly Arg Tyr Leu
565 570 575

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

Tyr Val Lys Asp Asn Tyr Phe Arg Val Glu Ala Ala Gly Val Ile Asn
595 600 605

Asp Val Asn Val Ala Val Tyr Ser Lys Asp Gln Ile Arg His Ile His
610 615 620

Ile Trp Gln Gly Ser Cys His His Tyr Phe Arg Glu Lys Leu Gly Leu
625 630 635 640

Glu Leu Ser Glu Asp Glu Glu Ser Gln His Lys Pro Lys Val Glu Thr
645 650 655

Ser Ala Asn Pro Gln Gly Thr Val Val Ala Pro Met Ala Gly Leu Val
660 665 670

Val Lys Val Leu Val Glu Asn Lys Thr Arg Val Glu Glu Gly Gln Pro
675 680 685

Val Leu Val Leu Glu Ala Met Lys Met Glu His Val Val Lys Ala Pro
690 695 700

Ser Ser Gly Tyr Val His Gly Leu Gln Leu Met Val Gly Glu Gln Val
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Ser Asp Gly Ser Val Leu Phe Ser Val Lys Asp Gln
725 730

<210> 327
<211> 1620
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<213> G.max

<400> 327
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gcatttggca atgatggggg ttatttggag aagtacattc aaaaccaag gcacattgag 840
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gttggaacgg ttgagttcct tttggatgaa agaggttcct tttactttat ggagatgaac	1080
actcgtatcc aggttgagca tccggtgaca gaaatgattt cctcaacgga tttgatagaa	1140
gagcaaattc gtgtagctat gggagaaaaa cttcgataca aacaggagga tattgtcctc	1200
agaggacatt ctattgaatg ccgtatcaat gcagaagatg cttttaaggg atttagacca	1260
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catgtttatc ctgattatgt ggttcctcca agctatgatt cccttcttgg aaagctgatt	1380
gtatgggctc caactagaga aaaagcaatt gaacgcatga aaagggcact tgatgatact	1440
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ttcagaaatg gcaaggttga tactgctttt attccaaaac acgaggaaga gttggcaatg	1560
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<210> 328
 <211> 539
 <212> PRT
 <213> G.max

<400> 328

Met	Glu	Val	Thr	Leu	Ser	Ala	Cys	Lys	Ser	Val	Ser	Ser	Pro	Ser	Val
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Pro	Val	Ala	Gly	Leu	Phe	Ala	Gly	Asn	Gly	Gly	Ile	Lys	Ser	Ser	Gln
			20					25					30		

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

Gly Gln Val Ser His Leu Arg Lys Gln Arg Gln Thr Arg His Cys Gly
50 55 60

Ala Leu His Ala Thr Cys Ser Gly Asp Lys Ile Leu Ile Ala Asn Arg
65 70 75 80

Gly Glu Ile Ala Val Arg Val Ile Arg Thr Ala His Glu Leu Gly Ile
85 90 95

Pro Cys Val Ala Val Tyr Ser Thr Ile Asp Lys Asp Ala Leu His Val
100 105 110

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

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

Cys Thr Met Leu His Pro Gly Tyr Gly Phe Leu Ala Glu Asn Ala Val
145 150 155 160

Phe Val Glu Met Cys Arg Glu His Gly Ile Asn Phe Ile Gly Pro Asn
165 170 175

Pro Asp Ser Ile Arg Val Met Gly Asp Lys Ala Thr Ala Arg Glu Thr
180 185 190

Met Lys Lys Ala Gly Val Pro Thr Val Pro Gly Ser Asp Gly Leu Leu
195 200 205

Gln Ser Thr Glu Glu Ala Ile Arg Leu Ala Asn Glu Ile Gly Phe Pro
210 215 220

Val Met Ile Lys Ala Thr Ala Gly Gly Gly Gly Arg Gly Met Arg Leu
225 230 235 240

Ala Lys Glu Pro Ala Glu Phe Val Lys Phe Leu Gln Gln Ala Lys Ser
245 250 255

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

Ile Gln Asn Pro Arg His Ile Glu Phe Gln Val Leu Ala Asp Lys Tyr
275 280 285

Gly Asn Val Val His Phe Gly Glu Arg Asp Cys Ser Ile Gln Arg Arg
290 295 300

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

Leu Arg Lys Ala Met Gly Asp Ala Ala Val Ala Ala Ala Ala Ser Ile
325 330 335

Gly Tyr Ile Gly Val Gly Thr Val Glu Phe Leu Leu Asp Glu Arg Gly
340 345 350

Ser Phe Tyr Phe Met Glu Met Asn Thr Arg Ile Gln Val Glu His Pro
355 360 365

Val Thr Glu Met Ile Ser Ser Thr Asp Leu Ile Glu Glu Gln Ile Arg
370 375 380

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

Arg Gly His Ser Ile Glu Cys Arg Ile Asn Ala Glu Asp Ala Phe Lys
405 410 415

Gly Phe Arg Pro Gly Pro Gly Arg Ile Thr Ala Tyr Leu Pro Ser Gly
420 425 430

Gly Pro Phe Val Arg Met Asp Ser His Val Tyr Pro Asp Tyr Val Val
435 440 445

Pro Pro Ser Tyr Asp Ser Leu Leu Gly Lys Leu Ile Val Trp Ala Pro
450 455 460

Thr Arg Glu Lys Ala Ile Glu Arg Met Lys Arg Ala Leu Asp Asp Thr
465 470 475 480

Ile Ile Thr Gly Val Pro Thr Thr Ile Asp Tyr His Lys Leu Ile Leu
485 490 495

Asp Ile Glu Asp Phe Arg Asn Gly Lys Val Asp Thr Ala Phe Ile Pro
500 505 510

Lys His Glu Glu Glu Leu Ala Met Pro Pro Gln Lys Met Val Leu Ala
515 520 525

Asn Arg Val Asn Glu Leu Ala Gly Ser Thr Ala
530 535

<210> 329
<211> 471
<212> DNA
<213> E.coli

<400> 329
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ttccctgtga tgcaacaagc ttacgttgca ccaatgatgc agcagccagc tcaatctaac 180
gcagccgctc cggcgaccgt tccttccatg gaagcgccag cagcagcgga aatcagtggg 240
cacatcgtag gttccccgat ggttggtact ttctaccgca cccaagccc ggacgcaaaa 300
gcgttcacg aagtgggtca gaaagtcaac gtgggagata ccctgtgcat cgttgaagcc 360
atgaaaatga tgaaccagat cgaagcggac aaatccggtc ccgtgaaagc aattctgggc 420
gaaagtggac aaccggtaga atttgacgag ccgctgggtc tcacgagta a 471

<210> 330
<211> 156
<212> PRT
<213> E.coli

<400> 330

Met Asp Ile Arg Lys Ile Lys Lys Leu Ile Glu Leu Val Glu Glu Ser
1 5 10 15

Gly Ile Ser Glu Leu Glu Ile Ser Glu Gly Glu Glu Ser Val Arg Ile
20 25 30

Ser Arg Ala Ala Pro Ala Ala Ser Phe Pro Val Met Gln Gln Ala Tyr
35 40 45

Ala Ala Pro Met Met Gln Gln Pro Ala Gln Ser Asn Ala Ala Ala Pro
50 55 60

Ala Thr Val Pro Ser Met Glu Ala Pro Ala Ala Ala Glu Ile Ser Gly
65 70 75 80

His Ile Val Arg Ser Pro Met Val Gly Thr Phe Tyr Arg Thr Pro Ser
85 90 95

Pro Asp Ala Lys Ala Phe Ile Glu Val Gly Gln Lys Val Asn Val Gly
100 105 110

Asp Thr Leu Cys Ile Val Glu Ala Met Lys Met Met Asn Gln Ile Glu
115 120 125

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

Pro Val Glu Phe Asp Glu Pro Leu Val Val Ile Glu
145 150 155

<210> 331
<211> 849
<212> DNA
<213> B.napus

<400> 331
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ctctccgcca agcctaagct ccgcttttctc tccaagccta gtcgtggtag ctaccctgtg 180
gtcaaagccc aatctaacaa gggttggtagt ggtgcgtcat caaatgcttc agctcctaca 240

aaaactgatg agccagaatc agatgaagga aaggatagaa actcttcttc ttcgactgat	300
ttagctacag aagagtctat ctctgagttc cttacccaag tcacaactct tgtcaagctt	360
gtggattcga gagacattgt cgagttgcag ttgaaacaac tgcactgtga acttgtcatt	420
cgaaagaagg aagctttgcc acaacccgag tccccccctg cgcaatatgt tatgatgcag	480
caaccaaacc aatcatctta tgtgcaatca gtggctcctc ctctcctcc ttctgcacct	540
gctgcatcac ctgcaccttc tgctccagct tctttgcctt caccatctcc acctgctcca	600
gctaaatcat cgcttcctac tgttaaaagc cctatggctg gcacattcta ccgtagtcca	660
ggacctggtg aaccaccctt tatcaagggt ggagacaaag tgcagaaggg acaagttcta	720
tgcacggtt aagccatgaa attgatgaat gaaatagagt ctgaccaaac gggaaccgta	780
gtggatatcg ttgcagaaga tggcaagcct gttagcctcg acactcctct gtttgtgggt	840
caaccgtag	849

<210> 332
 <211> 282
 <212> PRT
 <213> B.napus

<400> 332

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

Thr	Gln	Thr	Ser	Ser	His	Leu	Pro	Leu	Pro	Thr	Thr	Arg	Ser	Arg	Leu
			20					25					30		

Phe	Pro	Arg	Arg	Val	Ser	Phe	His	Leu	Ser	Ala	Lys	Pro	Lys	Leu	Arg
			35					40				45			

Phe Leu Ser Lys Pro Ser Arg Gly Ser Tyr Pro Val Val Lys Ala Gln
50 55 60

Ser Asn Lys Val Gly Ser Gly Ala Ser Ser Asn Ala Ser Ala Pro Thr
65 70 75 80

Lys Thr Asp Glu Pro Glu Ser Asp Glu Gly Lys Asp Arg Asn Ser Ser
85 90 95

Ser Ser Thr Asp Leu Ala Thr Glu Glu Ser Ile Ser Glu Phe Leu Thr
100 105 110

Gln Val Thr Thr Leu Val Lys Leu Val Asp Ser Arg Asp Ile Val Glu
115 120 125

Leu Gln Leu Lys Gln Leu Asp Cys Glu Leu Val Ile Arg Lys Lys Glu
130 135 140

Ala Leu Pro Gln Pro Glu Ser Pro Pro Ala Gln Tyr Val Met Met Gln
145 150 155 160

Gln Pro Asn Gln Ser Ser Tyr Val Gln Ser Val Ala Pro Pro Pro Pro
165 170 175

Pro Ser Ala Pro Ala Ala Ser Pro Ala Pro Ser Ala Pro Ala Ser Leu
180 185 190

Pro Ser Pro Ser Pro Pro Ala Pro Ala Lys Ser Ser Leu Pro Thr Val
195 200 205

Lys Ser Pro Met Ala Gly Thr Phe Tyr Arg Ser Pro Gly Pro Gly Glu
210 215 220

Pro Pro Phe Ile Lys Val Gly Asp Lys Val Gln Lys Gly Gln Val Leu
225 230 235 240

Cys Ile Val Glu Ala Met Lys Leu Met Asn Glu Ile Glu Ser Asp Gln
245 250 255

Thr Gly Thr Val Val Asp Ile Val Ala Glu Asp Gly Lys Pro Val Ser
260 265 270

Leu Asp Thr Pro Leu Phe Val Val Gln Pro
275 280

<210> 333
<211> 759
<212> DNA
<213> B.napus

<400> 333
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tctcagaatc aatctacaat ctggaggttg cgtgcgacaa ccaacgaggt tgtctctaac 180
tctaccccag tgactaacgg tgggtgcttg aacgggaacg tgaagagcaa tgttcctgaa 240
tccgctaaac tctctaactt tatggctaaa gtttcaggtc ttcttaagct tgtggattca 300
agagatatag tggaacttga acttaagcag ctcgactgtg agattgttat tcgaaagaag 360
gaagcttttag ctgcaccacc agctccagtc tatcactcta tgcctcctcc aatggcaggc 420
tttccaatgg ctccatctca tccagttgct cctcctcctt tttctcctag tccctcctca 480
gccctgaaa cagcaaaacc agtaaccca ccttcctctt cacatcctcc actcaagagt 540

cctatggctg gtactttcta cagatctcct ggtcctgggtg aacctccttt tgtcaaggtt	600
ggagataagg tgcagaaggg tcaagttggt tgcattattg aagctatgaa actgatgaat	660
gagattgagg ctgagaaatc aggaaccatc actgaactac tagctgaaga tggaaaaccg	720
gtagcggtg acacgcctct gtttaccatc gtgccttga	759

<210> 334
 <211> 252
 <212> PRT
 <213> B.napus

<400> 334

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

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

Arg	Leu	Arg	Ala	Thr	Thr	Asn	Glu	Val	Val	Ser	Asn	Ser	Thr	Pro	Val
	50					55					60				

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

Ser	Ala	Lys	Leu	Ser	Asn	Phe	Met	Ala	Lys	Val	Ser	Gly	Leu	Leu	Lys
			85						90					95	

Leu	Val	Asp	Ser	Arg	Asp	Ile	Val	Glu	Leu	Glu	Leu	Lys	Gln	Leu	Asp
			100					105					110		

Cys Glu Ile Val Ile Arg Lys Lys Glu Ala Leu Ala Ala Pro Pro Ala
115 120 125

Pro Val Tyr His Ser Met Pro Pro Pro Met Ala Gly Phe Pro Met Ala
130 135 140

Pro Ser His Pro Val Ala Pro Pro Pro Phe Ser Pro Ser Pro Ser Ser
145 150 155 160

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

Pro Leu Lys Ser Pro Met Ala Gly Thr Phe Tyr Arg Ser Pro Gly Pro
180 185 190

Gly Glu Pro Pro Phe Val Lys Val Gly Asp Lys Val Gln Lys Gly Gln
195 200 205

Val Val Cys Ile Ile Glu Ala Met Lys Leu Met Asn Glu Ile Glu Ala
210 215 220

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

Val Ser Val Asp Thr Pro Leu Phe Thr Ile Val Pro
245 250

<210> 335

<211> 1242

<212> DNA

<213> E.coli

<400> 335

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ttcgatacta gcgcctatgc aacgaaatth gctggcttag taaaggattt taactgtgag	180
gacattatct cgcgcaaaga acagcgcaag atggatgcct tcattcaata tggaattgtc	240
gctggcgctt aggccatgca ggattctggc ctgaaataa cggaagagaa cgcaaccgcg	300
attggtgccg caattggctc cgggattggc ggcctcggac tgatcgaaga aaaccacaca	360
tctctgatga acggtggtcc acgtaagatc agcccattct tcgttccgtc aacgattgtg	420
aacatggtgg caggtcatct gactatcatg tatggcctgc gtggcccgag catctctatc	480
gcgactgcct gtacttccgg cgtgcacaac attggccatg ctgcgcgtat tatcgcgat	540
ggcgatgctg acgtgatggt tgcaggtggc gcagagaaag ccagtaagcc gctgggctt	600
ggtggttttg gcgcggcacg tgcattatct acccgcaatg ataaccgcga agcggcgagc	660
cgcctgtggg ataaagagcg tgatggtttc gtactgggcg atggtgccgg tatgctggta	720
cttgaagagt acgaacacgc gaaaaaacgc ggtgcgaaaa ttacgctga actcgctggc	780
tttggtatga gcagcgatgc ttatcatatg acgtcaccgc cagaaaatgg cgcaggcgca	840
gctctggcga tggcaaatgc tctgcgtgat gcaggcattg aagcgagtca gattggctac	900
gttaacgcgc acggtacttc tacgccggct ggcgataaag ctgaagcgca ggcggtgaaa	960
accatcttcg gtgaagctgc aagccgtgtg ttggtaagct ccacgaaatc tatgaccggt	1020
cacctgttag gtgcggcggg tgcagtagaa tctatctact ccatcctggc gctgcgcgat	1080
caggctgttc cgccaaccat caacctgat aaccggatg aaggttgca tctggatttc	1140
gtaccgcacg aagcgcgtca ggtagcgga atggaataca ctctgtgtaa ctcttcggc	1200

ttcgggtggca ctaatggttc ttgatcttt aaaaagatct aa

1242

<210> 336

<211> 413

<212> PRT

<213> E.coli

<400> 336

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

Ser Gly Ile Ser Leu Ile Asp His Phe Asp Thr Ser Ala Tyr Ala Thr
35 40 45

Lys Phe Ala Gly Leu Val Lys Asp Phe Asn Cys Glu Asp Ile Ile Ser
50 55 60

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

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

Asn Ala Thr Arg Ile Gly Ala Ala Ile Gly Ser Gly Ile Gly Gly Leu
100 105 110

Gly Leu Ile Glu Glu Asn His Thr Ser Leu Met Asn Gly Gly Pro Arg
115 120 125

Lys Ile Ser Pro Phe Phe Val Pro Ser Thr Ile Val Asn Met Val Ala
130 135 140

Gly His Leu Thr Ile Met Tyr Gly Leu Arg Gly Pro Ser Ile Ser Ile
145 150 155 160

Ala Thr Ala Cys Thr Ser Gly Val His Asn Ile Gly His Ala Ala Arg
165 170 175

Ile Ile Ala Tyr Gly Asp Ala Asp Val Met Val Ala Gly Gly Ala Glu
180 185 190

Lys Ala Ser Thr Pro Leu Gly Val Gly Gly Phe Gly Ala Ala Arg Ala
195 200 205

Leu Ser Thr Arg Asn Asp Asn Pro Gln Ala Ala Ser Arg Pro Trp Asp
210 215 220

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

Leu Glu Glu Tyr Glu His Ala Lys Lys Arg Gly Ala Lys Ile Tyr Ala
245 250 255

Glu Leu Val Gly Phe Gly Met Ser Ser Asp Ala Tyr His Met Thr Ser
260 265 270

Pro Pro Glu Asn Gly Ala Gly Ala Ala Leu Ala Met Ala Asn Ala Leu
275 280 285

Arg Asp Ala Gly Ile Glu Ala Ser Gln Ile Gly Tyr Val Asn Ala His
290 295 300

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

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

Ser Met Thr Gly His Leu Leu Gly Ala Ala Gly Ala Val Glu Ser Ile
 340 345 350

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

Leu Asp Asn Pro Asp Glu Gly Cys Asp Leu Asp Phe Val Pro His Glu
 370 375 380

Ala Arg Gln Val Ser Gly Met Glu Tyr Thr Leu Cys Asn Ser Phe Gly
 385 390 395 400

Phe Gly Gly Thr Asn Gly Ser Leu Ile Phe Lys Lys Ile
 405 410

<210> 337
 <211> 1221
 <212> DNA
 <213> G.max

<400> 337
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 ggaggtcaga tacgtgattt ctcttcagaa ggctacattg atggcaagaa tgaccggcgc 180

cttgacaatt gctggaggta ttgcattggt gcaggcaaga gggcccttga tgatgccaac	240
cttggaagc aagtccttga cactatggac aaaacaagaa taggagttct ggtgggatca	300
ggaatgggag gtataacggc tttctcgaat ggtgtggaag ctcttgtaca aaagggatat	360
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gttggtggaa ctgaggctgc aatcatgcct agtggctctg gaggcctcat tgcttgcagg	600
gctttgtctc acagaaacga agacccaag aaggcttcaa gaccatggga caaagatcgt	660
gatggttttg tgatgggtga aggctctggt gtgctggtaa tggagagctt ggagagtga	720
acaaaaaggg gagccaaaat aatagcagaa tatttggggg gtgccataac gtgtgatgct	780
catcacatga ctgatccaag agctgatggt ctggagttt catcttgcac aagcaagagt	840
ttagaagatg ctggagtttc tcctgaagag gtgaactatg tgaatgctca tgccacgtca	900
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gaattgaaaa tgaatgcaac taagtcaatg attggtcatg gtcttggggc tgctggtggt	1020
ttggaagcca tagcaactat caaagccata acaactggct ggttgcaccc aagcattaac	1080
ctagataact tggaggctag tggtacaatt gacactgtcc ctaacgttaa gaagaagcat	1140
gaagttaatg ttggtatatc caactcattt ggattcgggtg gacacaattc agtagttgtc	1200
tttgcccat tcaggccatg a	1221

<210> 338
 <211> 406
 <212> PRT
 <213> G.max

<400> 338

Met Gly Leu Val Ser Val Phe Gly Ser Asp Val Asp Ala Phe Tyr Asn
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Lys Leu Leu Glu Gly Glu Ser Gly Ile Ser Leu Ile Asp Arg Phe Asp
20 25 30

Ala Ser Asn Phe Ser Val Arg Phe Gly Gly Gln Ile Arg Asp Phe Ser
35 40 45

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

Trp Arg Tyr Cys Ile Val Ala Gly Lys Arg Ala Leu Asp Asp Ala Asn
65 70 75 80

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

Leu Val Gly Ser Gly Met Gly Gly Ile Thr Ala Phe Ser Asn Gly Val
100 105 110

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

Pro Tyr Ser Ile Thr Asn Met Gly Ser Ala Leu Leu Ala Ile Asp Thr
130 135 140

Gly Leu Met Gly Pro Asn Tyr Ser Ile Ser Thr Ala Cys Ala Thr Ala
145 150 155 160

Asn Tyr Cys Phe Cys Ala Ala Ala Asn His Ile Arg Lys Gly Glu Ala
165 170 175

Asp Ile Met Val Val Gly Gly Thr Glu Ala Ala Ile Met Pro Ser Gly
180 185 190

Leu Gly Gly Phe Ile Ala Cys Arg Ala Leu Ser His Arg Asn Glu Asp
195 200 205

Pro Lys Lys Ala Ser Arg Pro Trp Asp Lys Asp Arg Asp Gly Phe Val
210 215 220

Met Gly Glu Gly Ser Gly Val Leu Val Met Glu Ser Leu Glu Ser Ala
225 230 235 240

Thr Lys Arg Gly Ala Lys Ile Ile Ala Glu Tyr Leu Gly Gly Ala Ile
245 250 255

Thr Cys Asp Ala His His Met Thr Asp Pro Arg Ala Asp Gly Leu Gly
260 265 270

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

Glu Glu Val Asn Tyr Val Asn Ala His Ala Thr Ser Thr Leu Ala Gly
290 295 300

Asp Leu Ala Glu Val Asn Ala Ile Lys Lys Val Phe Lys Asp Thr Ser
305 310 315 320

Glu Leu Lys Met Asn Ala Thr Lys Ser Met Ile Gly His Gly Leu Gly
325 330 335

Ala Ala Gly Gly Leu Glu Ala Ile Ala Thr Ile Lys Ala Ile Thr Thr
340 345 350

Gly Trp Leu His Pro Ser Ile Asn Leu Asp Asn Leu Glu Ala Ser Val
355 360 365

Thr Ile Asp Thr Val Pro Asn Val Lys Lys Lys His Glu Val Asn Val
370 375 380

Gly Ile Ser Asn Ser Phe Gly Phe Gly Gly His Asn Ser Val Val Val
385 390 395 400

Phe Ala Pro Phe Arg Pro
405

<210> 339
<211> 1386
<212> DNA
<213> Zea mays

<400> 339
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tgcacgtca gtggcaagaa ggctctcgag gctgccggta ttgccacgg ctccaagccc 420

atggaaaaga ttgacaaaac ccgggctggt gtgcttgtgg gcactggtat gggtaggcctc	480
acggtgtttt ctgatggtgt tcagaatctc attgagaagg gctacagaaa aataactcct	540
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aatgatgacc ctaaaacagc atccaggcct tgggacaagg atcgtgatgg ttttgtcatg	840
ggtgaaggag ctggagtcct ggtcatggag agcctagagc atgcaattaa acgtgatgca	900
ccaataattg cggagtattt aggaggtgct gtgaactgtg atgcttacca tatgactgac	960
ccgagatctg atggctcttg tgtttcatct tgcataagc aaagtctcga agatgctggt	1020
gtggctcctg aggaggtcaa ctatattaat gctcatgcaa catcaaccct tgctggtgat	1080
ctggcagagg tgaatgcat caagcaagtc ttcaaggacc catctgggat caaaataaat	1140
gcaaccaagt ccatgatagg acattgcctt ggtgcagcag gtggtttgga agccattgct	1200
actgtcaaag cgataactac tggatgggtg catccaagca taaaccaatt taaccagag	1260
gaagcggttg aattcgacac agtaccta atgtaaaaagc agcatgaagt gaacgttggc	1320
atctcaaatt cttttggatt tggaggtcac aattctgtcg tagtatttgc gccatttaag	1380
ccataa	1386

<210> 340
 <211> 461
 <212> PRT
 <213> Zea mays

<400> 340

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

Pro Arg Ala Arg Arg Asn Leu Pro Met Arg Leu Ser Val Arg Ala Ser
20 25 30

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

Val Val Ile Thr Gly Met Gly Leu Val Ser Val Phe Gly Asn Asp Val
50 55 60

Asp Ala Tyr Tyr Asp Arg Leu Leu Ala Gly Glu Ser Gly Ile Gly Pro
65 70 75 80

Ile Asp Arg Phe Asp Ala Ser Lys Phe Pro Thr Arg Phe Ala Gly Gln
85 90 95

Ile Arg Gly Phe Ser Ser Glu Gly Tyr Ile Asp Gly Lys Asn Asp Arg
100 105 110

Arg Leu Asp Asp Cys Leu Arg Tyr Cys Ile Val Ser Gly Lys Lys Ala
115 120 125

Leu Glu Ala Ala Gly Ile Ala His Gly Ser Lys Pro Met Glu Lys Ile
130 135 140

Asp Lys Thr Arg Ala Gly Val Leu Val Gly Thr Gly Met Gly Gly Leu
145 150 155 160

Thr Val Phe Ser Asp Gly Val Gln Asn Leu Ile Glu Lys Gly Tyr Arg
165 170 175

Lys Ile Thr Pro Phe Phe Ile Pro Tyr Ala Ile Thr Asn Met Gly Ser
180 185 190

Ala Leu Leu Gly Met Asp Ile Gly Phe Met Gly Pro Asn Tyr Ser Ile
195 200 205

Ser Thr Ala Cys Ala Thr Ser Asn Tyr Cys Phe Tyr Ala Ala Ala Asn
210 215 220

His Ile Arg Arg Gly Glu Ala Asp Ile Met Ile Ala Gly Gly Thr Glu
225 230 235 240

Ala Ala Ile Ile Pro Ile Gly Val Gly Gly Phe Val Ala Cys Arg Ala
245 250 255

Leu Ser Gln Arg Asn Asp Asp Pro Lys Thr Ala Ser Arg Pro Trp Asp
260 265 270

Lys Asp Arg Asp Gly Phe Val Met Gly Glu Gly Ala Gly Val Leu Val
275 280 285

Met Glu Ser Leu Glu His Ala Ile Lys Arg Asp Ala Pro Ile Ile Ala
290 295 300

Glu Tyr Leu Gly Gly Ala Val Asn Cys Asp Ala Tyr His Met Thr Asp
305 310 315 320

Pro Arg Ser Asp Gly Leu Gly Val Ser Ser Cys Ile Lys Gln Ser Leu
325 330 335

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

Ala Thr Ser Thr Leu Ala Gly Asp Leu Ala Glu Val Asn Ala Ile Lys
355 360 365

Gln Val Phe Lys Asp Pro Ser Gly Ile Lys Ile Asn Ala Thr Lys Ser
370 375 380

Met Ile Gly His Cys Leu Gly Ala Ala Gly Gly Leu Glu Ala Ile Ala
385 390 395 400

Thr Val Lys Ala Ile Thr Thr Gly Trp Val His Pro Ser Ile Asn Gln
405 410 415

Phe Asn Pro Glu Glu Ala Val Glu Phe Asp Thr Val Pro Asn Val Lys
420 425 430

Lys Gln His Glu Val Asn Val Gly Ile Ser Asn Ser Phe Gly Phe Gly
435 440 445

Gly His Asn Ser Val Val Val Phe Ala Pro Phe Lys Pro
450 455 460

<210> 341
<211> 1221
<212> DNA
<213> G.max

<400> 341
atgggcctcg cgtcggtgtt cggtaacgac gtggagggtt actacgagaa gctcctcgcc 60
ggcgagagcg gcatcaccgc catcgaccgc ttcgacgcct ccaagttccc caccggtttc 120

ggcggccaga tccgcggctt ctctgccgag ggctacatcg acggcaagaa cgaccgccgc	180
ctcgacgact gcctccgcta ctgcattgtc gccggcaaaa aggccctcga aaacgccgac	240
cttgcccccg acaaccactc caagattgat aaggagcgtg ctggtgttct tgtaggctcc	300
ggaatgggag gtttaacggt gttttctgac ggtgttcagg ctctgattga gaaggggcac	360
aggaagataa cgccgttttt tattccgtat gccattacta acatgggttc ggctttgctt	420
gggatagacc ttgggttcat ggggtcccaac tactctatat ccacggcttg tgctacctcc	480
aactattgct tttatgctgc ggcgaaccat attcggagag gggaggctga tttgatgatt	540
gccggtggga ctgaggctgc cattattcca attgggttag ggggttttgt tgcttgacgg	600
gcgctttctc agaggaatga tgaccctaaa accgcttcca ggccatggga taaggaacgt	660
gatggctttg ttatgggtga aggtgctgga gttttggtaa tggagagctt ggagcatgct	720
atgaagcgag gcgcacctat tattgctgaa ttttgggag gagctgttaa ctgtgatgct	780
tatcacatga ctgatccaag gtctgatgga cttggtgtgt ctacatgcat tcagagcagc	840
cttgaagatg ccggtgtgtc accagaggag gtcaactaca taaatgcaca tgcaacttcc	900
actcttgctg gagacttggc agagatcaat gctattaaaa aggttttcaa ggacattct	960
ggaatcaaaa ttaatgcaac caagtctatg atagggcact gccttggtgc agctgggggt	1020
ttggaagcca ttgccacagt gaaagccata acaacaggat ggctgcatcc aacaatcaat	1080
caatttaacc cagaacctgc agttgatttt gatacagtgg caaatgtcaa gcagcagcat	1140
gaaatcaacg ttgccatttc aaattcattt ggattcgggtg gacacaactc tgtggtagca	1200
ttttctgctt tcaggccttg a	1221

<210> 342

<211> 406

<212> PRT

<213> G.max

<400> 342

Met Gly Leu Ala Ser Val Phe Gly Asn Asp Val Glu Gly Tyr Tyr Glu
1 5 10 15

Lys Leu Leu Ala Gly Glu Ser Gly Ile Thr Ala Ile Asp Arg Phe Asp
20 25 30

Ala Ser Lys Phe Pro Thr Arg Phe Gly Gly Gln Ile Arg Gly Phe Ser
35 40 45

Ala Glu Gly Tyr Ile Asp Gly Lys Asn Asp Arg Arg Leu Asp Asp Cys
50 55 60

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

Leu Ala Pro Asp Asn His Ser Lys Ile Asp Lys Glu Arg Ala Gly Val
85 90 95

Leu Val Gly Ser Gly Met Gly Gly Leu Thr Val Phe Ser Asp Gly Val
100 105 110

Gln Ala Leu Ile Glu Lys Gly His Arg Lys Ile Thr Pro Phe Phe Ile
115 120 125

Pro Tyr Ala Ile Thr Asn Met Gly Ser Ala Leu Leu Gly Ile Asp Leu
130 135 140

Gly Phe Met Gly Pro Asn Tyr Ser Ile Ser Thr Ala Cys Ala Thr Ser
145 150 155 160

Asn Tyr Cys Phe Tyr Ala Ala Ala Asn His Ile Arg Arg Gly Glu Ala
165 170 175

Asp Leu Met Ile Ala Gly Gly Thr Glu Ala Ala Ile Ile Pro Ile Gly
180 185 190

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

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

Met Gly Glu Gly Ala Gly Val Leu Val Met Glu Ser Leu Glu His Ala
225 230 235 240

Met Lys Arg Gly Ala Pro Ile Ile Ala Glu Tyr Leu Gly Gly Ala Val
245 250 255

Asn Cys Asp Ala Tyr His Met Thr Asp Pro Arg Ser Asp Gly Leu Gly
260 265 270

Val Ser Thr Cys Ile Gln Ser Ser Leu Glu Asp Ala Gly Val Ser Pro
275 280 285

Glu Glu Val Asn Tyr Ile Asn Ala His Ala Thr Ser Thr Leu Ala Gly
290 295 300

Asp Leu Ala Glu Ile Asn Ala Ile Lys Lys Val Phe Lys Asp Thr Ser
305 310 315 320

Gly Ile Lys Ile Asn Ala Thr Lys Ser Met Ile Gly His Cys Leu Gly
325 330 335

Ala Ala Gly Gly Leu Glu Ala Ile Ala Thr Val Lys Ala Ile Thr Thr
340 345 350

Gly Trp Leu His Pro Thr Ile Asn Gln Phe Asn Pro Glu Pro Ala Val
355 360 365

Asp Phe Asp Thr Val Ala Asn Val Lys Gln Gln His Glu Ile Asn Val
370 375 380

Ala Ile Ser Asn Ser Phe Gly Phe Gly Gly His Asn Ser Val Val Ala
385 390 395 400

Phe Ser Ala Phe Arg Pro
405

<210> 343
<211> 735
<212> DNA
<213> E.coli

<400> 343
atgaattttg aaggaaaaat cgcactggta accggtgcaa gccgcggaat tggccgcgca 60
attgctgaaa cgctcgcagc ccgtggcgcg aaagttattg gcaactgcgac cagtgaaaat 120
ggcgctcagg cgatcagtga ttatttaggt gccaacggca aaggtctgat gttgaatgtg 180
accgacccgg catctatcga atctgttctg gaaaaaattc gcgcagaatt tgggtgaagtg 240
gatatcctgg tcaataatgc cggatatcact cgtgataacc tgttaatgcg aatgaaagat 300
gaagagtgga acgatattat cgaaaccaac ctttcatctg ttttccgtct gtcaaaagcg 360

gtaatgcgcg ctatgatgaa aaagcgtcat ggtcgtatta tcactatcgg ttctgtgggt 420

ggtaccatgg gaaatggcgg tcaggccaac tacgctgcgg cgaaagcggg cttgatcggc 480

ttcagtaa at cactggcgcg cgaagttgcg tcacgcggta ttactgtaaa cgttgttgct 540

ccgggcttta ttgaaacgga catgacacgt gcgctgagcg atgaccagcg tgcgggtatc 600

ctggcgcagg ttcttgcggg tcgcctcggc ggcgcacagg aaatcgccaa cgcggttgca 660

ttcttggcat ccgacgaagc agcttacatc acgggtgaaa ctttgcattgt gaacggcggg 720

atgtacatgg tctaa 735

<210> 344

<211> 244

<212> PRT

<213> E.coli

<400> 344

Met Asn Phe Glu Gly Lys Ile Ala Leu Val Thr Gly Ala Ser Arg Gly

1 5 10 15

Ile Gly Arg Ala Ile Ala Glu Thr Leu Ala Ala Arg Gly Ala Lys Val

20 25 30

Ile Gly Thr Ala Thr Ser Glu Asn Gly Ala Gln Ala Ile Ser Asp Tyr

35 40 45

Leu Gly Ala Asn Gly Lys Gly Leu Met Leu Asn Val Thr Asp Pro Ala

50 55 60

Ser Ile Glu Ser Val Leu Glu Lys Ile Arg Ala Glu Phe Gly Glu Val

65 70 75 80

Asp Ile Leu Val Asn Asn Ala Gly Ile Thr Arg Asp Asn Leu Leu Met
85 90 95

Arg Met Lys Asp Glu Glu Trp Asn Asp Ile Ile Glu Thr Asn Leu Ser
100 105 110

Ser Val Phe Arg Leu Ser Lys Ala Val Met Arg Ala Met Met Lys Lys
115 120 125

Arg His Gly Arg Ile Ile Thr Ile Gly Ser Val Val Gly Thr Met Gly
130 135 140

Asn Gly Gly Gln Ala Asn Tyr Ala Ala Ala Lys Ala Gly Leu Ile Gly
145 150 155 160

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

Asn Val Val Ala Pro Gly Phe Ile Glu Thr Asp Met Thr Arg Ala Leu
180 185 190

Ser Asp Asp Gln Arg Ala Gly Ile Leu Ala Gln Val Pro Ala Gly Arg
195 200 205

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

Asp Glu Ala Ala Tyr Ile Thr Gly Glu Thr Leu His Val Asn Gly Gly
225 230 235 240

Met Tyr Met Val

<210> 345
<211> 744
<212> DNA
<213> Synechocystis PCC6803

<400> 345
atgacggcat taacggcaca ggtggcattg gtaacggggg catcccgggg tattggtaaa 60
gcgacggctt tggcctggc cgccacgggc atgaaagtgg tagtgaacta tgctcaatcc 120
agtacggccg ccgatgctgt ggtagcggaa attattgcca acgggggaga ggcatcgcc 180
gtgcaggcca atgtggctaa tgctgacgaa gtggatcaac tgattaaaac cacgctggat 240
aaatttagtc gcatcgatgt gttagtgaac aatgctggca ttaccaggga tacgctgttg 300
ttgagaatga aactggaaga ttggcaagcg gtcattgact tgaatttaac cgggggtgtt 360
ctttgcacca aagcgggtgc taagttaatg ctcaagcaaa aaagtgggcg tatcattaac 420
atcacttctg tagcgggcat gatggggaat ccggggcaag ctaactacag cgccgctaag 480
gctggggtaa ttggttttac taaaaccgtt gccaaagagt tggccagtcg gggggtaact 540
gtcaatgccg tagctcctgg ttctattgcc acggatatga cggaaaatct caatgcagag 600
ccaattttgc aatttattcc cctggctcgc tatggtcaac cggaggaagt ggcgggcacc 660
atccgttttt tagccacaga tccagcagcg gcctatatca cgggacaaac atttaatgtg 720
gatggcggca tggtaatgtt ctaa 744

<210> 346
<211> 247
<212> PRT
<213> Synechocystis PCC6803

<400> 346

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

Gly Ile Gly Lys Ala Thr Ala Leu Ala Leu Ala Ala Thr Gly Met Lys
20 25 30

Val Val Val Asn Tyr Ala Gln Ser Ser Thr Ala Ala Asp Ala Val Val
35 40 45

Ala Glu Ile Ile Ala Asn Gly Gly Glu Ala Ile Ala Val Gln Ala Asn
50 55 60

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

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

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

Asp Leu Asn Leu Thr Gly Val Phe Leu Cys Thr Lys Ala Val Ser Lys
115 120 125

Leu Met Leu Lys Gln Lys Ser Gly Arg Ile Ile Asn Ile Thr Ser Val
130 135 140

Ala Gly Met Met Gly Asn Pro Gly Gln Ala Asn Tyr Ser Ala Ala Lys
145 150 155 160

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

Arg Gly Val Thr Val Asn Ala Val Ala Pro Gly Phe Ile Ala Thr Asp
180 185 190

Met Thr Glu Asn Leu Asn Ala Glu Pro Ile Leu Gln Phe Ile Pro Leu
195 200 205

Ala Arg Tyr Gly Gln Pro Glu Glu Val Ala Gly Thr Ile Arg Phe Leu
210 215 220

Ala Thr Asp Pro Ala Ala Ala Tyr Ile Thr Gly Gln Thr Phe Asn Val
225 230 235 240

Asp Gly Gly Met Val Met Phe
245

<210> 347
<211> 762
<212> DNA
<213> B.napus

<400> 347
atgacagctc ttgtaaccgg tggaaccaag ggaattgggt atgcatagtg ggaggaactt 60
gctggttttg gtgcaagagt tcacacgtgt gctagagacc aaactctgct tgatgaatgt 120
ttaagtgaat ggaaagagaa agggtttcaa gtcactgggt cagtctgtga tgtatcctct 180
cgacctcaga gagatgagtt gatgaagacg gtctcttctc tattcagtggt caaactcaac 240
atccttatca acaatgttgg tacccttggt tcaaagccga ctacagagtt tacagcacia 300
gatttctcag gtcaaatagc taccaatttg gattctgctt atcacttctc tcaattggcc 360
catcctttac ttaaggcatc tggatttggt agcattgtgt tcatgtcttc agtatgtggg 420

gttgatcag ccggtaccgt atccatatac agcttaacaa aaggaggcat gaatcaattg 480

gcaagaaact tggcatgtga atgggcaagt gatggcataa gggctaactc tgtagctcct 540

tggatgacaa aaactcctct tgcccaagat cgtcttgatg acgagaaatt cgcggaggct 600

atcttctcaa gaactccatt aggtcgtgcg tgtgagccgc gtgagggttgc ctcgttgggt 660

acctttcttt gtctccctgc agcttcttat ataacaggac aaaccatttg tattgatgga 720

ggtttcactg ttaatggctt ctctacaag ccagaggttt ga 762

<210> 348

<211> 253

<212> PRT

<213> B.napus

<400> 348

Met Thr Ala Leu Val Thr Gly Gly Thr Lys Gly Ile Gly Tyr Ala Ile

1 5 10 15

Val Glu Glu Leu Ala Gly Phe Gly Ala Arg Val His Thr Cys Ala Arg

20 25 30

Asp Gln Thr Leu Leu Asp Glu Cys Leu Ser Glu Trp Lys Glu Lys Gly

35 40 45

Phe Gln Val Thr Gly Ser Val Cys Asp Val Ser Ser Arg Pro Gln Arg

50 55 60

Asp Glu Leu Met Lys Thr Val Ser Ser Leu Phe Ser Gly Lys Leu Asn

65 70 75 80

Ile Leu Ile Asn Asn Val Gly Thr Leu Val Ser Lys Pro Thr Thr Glu

85 90 95

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

Ala Tyr His Phe Ser Gln Leu Ala His Pro Leu Leu Lys Ala Ser Gly
115 120 125

Phe Gly Ser Ile Val Phe Met Ser Ser Val Cys Gly Val Val Ser Ala
130 135 140

Gly Thr Val Ser Ile Tyr Ser Leu Thr Lys Gly Gly Met Asn Gln Leu
145 150 155 160

Ala Arg Asn Leu Ala Cys Glu Trp Ala Ser Asp Gly Ile Arg Ala Asn
165 170 175

Ser Val Ala Pro Trp Met Thr Lys Thr Pro Leu Ala Gln Asp Arg Leu
180 185 190

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

Arg Ala Cys Glu Pro Arg Glu Val Ala Ser Leu Val Thr Phe Leu Cys
210 215 220

Leu Pro Ala Ala Ser Tyr Ile Thr Gly Gln Thr Ile Cys Ile Asp Gly
225 230 235 240

Gly Phe Thr Val Asn Gly Phe Ser Tyr Lys Pro Glu Val
245 250

<210> 349
<211> 732
<212> DNA
<213> B.napus

<400> 349
atgtttgggt atgcatagt agaagagtta gctagttttg gagctagaat ccatgtatgc 60

gacatatcta aaactttgct caatcaaagt ttaagcgaat gggaaaagaa agggtttcaa 120

gtgagtggct cagtctgtga tgtaacctct cgtcctgagg gagaaacttt gatacaaaaa 180

gtctcctcgc tgtttgatgg caagctcaac atttttgtga acaatgtggg agtgcttcgc 240

ggaaagccaa caacagaata tggagcagac gatttcgctt tccatatctc aacaaacttg 300

gaatctgctt accatttttg ccagctttca catcctctcc taaaggcttc aggctatgga 360

agcattgtct tcttgtcctc tgttgcaggg gttgtatcca cgagcggcgg atcaatttat 420

agtctaacca aaggagcttt aaatcagcta gctagaaatt tggcatgtga atgggcagaa 480

gacagcatac gagccaacgc tgttgcacct aatatcatca agactccgct ggccctacct 540

tatcttgagg acgtcggggt caggggaagga ctgttcggta gaactccact tggtcgagct 600

ggagagccgc atgaagttgc atcagttgtg gtcttcttgt gtcttcttgc agcttcttat 660

attactggtc agaccatttg tgttgatgga ggcctaacga ttaacggttt ctcataccaa 720

ccacacgctt ga 732

<210> 350
<211> 243
<212> PRT
<213> B.napus

<400> 350

Met Phe Gly Tyr Ala Ile Val Glu Glu Leu Ala Ser Phe Gly Ala Arg
1 5 10 15

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

Glu Trp Glu Lys Lys Gly Phe Gln Val Ser Gly Ser Val Cys Asp Val
35 40 45

Thr Ser Arg Pro Glu Gly Glu Thr Leu Ile Gln Lys Val Ser Ser Leu
50 55 60

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

Gly Lys Pro Thr Thr Glu Tyr Gly Ala Asp Asp Phe Ala Phe His Ile
85 90 95

Ser Thr Asn Leu Glu Ser Ala Tyr His Phe Cys Gln Leu Ser His Pro
100 105 110

Leu Leu Lys Ala Ser Gly Tyr Gly Ser Ile Val Phe Leu Ser Ser Val
115 120 125

Ala Gly Val Val Ser Thr Ser Gly Gly Ser Ile Tyr Ser Leu Thr Lys
130 135 140

Gly Ala Leu Asn Gln Leu Ala Arg Asn Leu Ala Cys Glu Trp Ala Glu
145 150 155 160

Asp Ser Ile Arg Ala Asn Ala Val Ala Pro Asn Ile Ile Lys Thr Pro
165 170 175

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

Gly Arg Thr Pro Leu Gly Arg Ala Gly Glu Pro His Glu Val Ala Ser
195 200 205

Val Val Val Phe Leu Cys Leu Pro Ala Ala Ser Tyr Ile Thr Gly Gln
210 215 220

Thr Ile Cys Val Asp Gly Gly Leu Thr Ile Asn Gly Phe Ser Tyr Gln
225 230 235 240

Pro His Ala

<210> 351
<211> 711
<212> DNA
<213> B.napus

<400> 351
atggtcgcag tccaagacga tctcggagac aaagttctca aaactctggt agccaactcg 60
gaggagtcag cttgtttcat ccacggtgac gtcacacaag aagacgacat cagtaacgct 120
gttgacttcg ccgtcaagcg tttcgggaca cttgacatac tcatcaacaa cgcaggagta 180
agcgaagcac cgtgtccgga catccgcaac aacagtttaa ccgagttcga gatggtcttc 240
aacgtcaacg tgaaaggagc tttcctaggg atgaaacatg cggcgcgtgt gatgatcccc 300
gccaagaaaag gctcgatagt ctctttatgc agcgttggcg gcgttgtcgg aggcgttggt 360
ccgcacgctt acgtcggctc caagcacgcg gttctagggt tgactaggag cgttgcggcg 420
gagctaggac agcatgggat acgcgtgaac tgcgtttctc cttacgcggt tttgactaac 480

ctcgcgttgg ctcatTTGCC tgaggatgag aggaaggaag gcgtggTcgc Tggtttcagg 540

agtttcgccg ctgcgaacgc gaatctgaaa ggtgttgagt tgacggttga tgacgtggcg 600

aacgcggttt tgtttctggc gagtgaTgag tcgcggtatg tgagtggaga taatctgatg 660

gttgatggTg ggttcacttg cactaaccac tcctttaaag tttttagatg a 711

<210> 352

<211> 236

<212> PRT

<213> B.napus

<400> 352

Met Val Asp Val Gln Asp Asp Leu Gly Asp Lys Val Leu Lys Thr Leu

1 5 10 15

Leu Ala Asn Ser Glu Glu Ser Ala Cys Phe Ile His Gly Asp Val Thr

20 25 30

Gln Glu Asp Asp Ile Ser Asn Ala Val Asp Phe Ala Val Lys Arg Phe

35 40 45

Gly Thr Leu Asp Ile Leu Ile Asn Asn Ala Gly Val Ser Glu Ala Pro

50 55 60

Cys Pro Asp Ile Arg Asn Asn Ser Leu Thr Glu Phe Glu Met Val Phe

65 70 75 80

Asn Val Asn Val Lys Gly Ala Phe Leu Gly Met Lys His Ala Ala Arg

85 90 95

Val Met Ile Pro Ala Lys Lys Gly Ser Ile Val Ser Leu Cys Ser Val

100 105 110

Gly Gly Val Val Gly Gly Val Gly Pro His Ala Tyr Val Gly Ser Lys
115 120 125

His Ala Val Leu Gly Leu Thr Arg Ser Val Ala Ala Glu Leu Gly Gln
130 135 140

His Gly Ile Arg Val Asn Cys Val Ser Pro Tyr Ala Val Leu Thr Asn
145 150 155 160

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

Ala Gly Phe Arg Ser Phe Ala Ala Ala Asn Ala Asn Leu Lys Gly Val
180 185 190

Glu Leu Thr Val Asp Asp Val Ala Asn Ala Val Leu Phe Leu Ala Ser
195 200 205

Asp Glu Ser Arg Tyr Val Ser Gly Asp Asn Leu Met Val Asp Gly Gly
210 215 220

Phe Thr Cys Thr Asn His Ser Phe Lys Val Phe Arg
225 230 235

<210> 353
<211> 963
<212> DNA
<213> G.max

<400> 353

atggcttcca ttgccgatc caactgcgtc gctctccgaa cgcgcaactt cggcgctcc

ggtaaccgga aaatcggcca gatccgcca tggtctccga ttctcacgaa tctccgtccc	120
gtttccggtc ttcgtcaccg atcgaatact ccgttttagct cctccggtgt gagagcacag	180
gttgctactc tggaggaagc aggaaccgga gcaactcaga aagtggaagc gccggttgca	240
gtggtgaccg gagcttccag aggcattggc aaagcgattg cactgtcatt aggtaaagca	300
ggttgcaagg ttctgggtcaa ctatgcaagg tcatccaagg aagctgagga ggtttccaag	360
gagattgagg agtttgggtg tcaagctctt acatttgggtg gagatgtttc taacgaggct	420
gatgtggagt ctatgattaa aactgcagtt gatgcttggg gaacagttga tgtattaata	480
aacaatgcag gaataacaag agatggttta ttaatgagaa tgaagaaatc tcaatggcag	540
gatgttattg atctaaatct cactggtggt tttctttgca cacaggctgc tgctaagatt	600
atgatgaaga aaaagaaggg aaggatcgtc aatattgcat cagttggttg tttggttggc	660
aatgttggac aagccaatta tagtgctgca aaagcaggag taattggcct gacaaaaact	720
gttgcggaagg aatatgctag tagaaacatc actgttaatg cagttgctcc agggtttatt	780
gcatctgaca tgactgcca gctaggacaa gacattgaga aaaagatttt ggagacaatc	840
ccattaggaa gatatggcca gccagaggaa gttgctggac tggttgaatt ottggctctt	900
aatcaagctg ccagttacat cactgggcag gttttcacca ttgatggagg tatggtgatg	960
taa	963

<210> 354
 <211> 320
 <212> PRT
 <213> G.max

<400> 354

Met	Ala	Ser	Ile	Ala	Gly	Ser	Asn	Cys	Val	Ala	Leu	Arg	Thr	Ala	Asn
1				5							10				15

Phe Gly Ala Ser Gly Asn Arg Lys Ile Gly Gln Ile Arg Gln Trp Ser
20 25 30

Pro Ile Leu Thr Asn Leu Arg Pro Val Ser Gly Leu Arg His Arg Ser
35 40 45

Asn Thr Pro Phe Ser Ser Ser Gly Val Arg Ala Gln Val Ala Thr Leu
50 55 60

Glu Glu Ala Gly Thr Gly Ala Thr Gln Lys Val Glu Ala Pro Val Ala
65 70 75 80

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

Leu Gly Lys Ala Gly Cys Lys Val Leu Val Asn Tyr Ala Arg Ser Ser
100 105 110

Lys Glu Ala Glu Glu Val Ser Lys Glu Ile Glu Glu Phe Gly Gly Gln
115 120 125

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

Met Ile Lys Thr Ala Val Asp Ala Trp Gly Thr Val Asp Val Leu Ile
145 150 155 160

Asn Asn Ala Gly Ile Thr Arg Asp Gly Leu Leu Met Arg Met Lys Lys
165 170 175

Ser Gln Trp Gln Asp Val Ile Asp Leu Asn Leu Thr Gly Val Phe Leu
180 185 190

Cys Thr Gln Ala Ala Ala Lys Ile Met Met Lys Lys Lys Lys Gly Arg
195 200 205

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

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

Val Ala Lys Glu Tyr Ala Ser Arg Asn Ile Thr Val Asn Ala Val Ala
245 250 255

Pro Gly Phe Ile Ala Ser Asp Met Thr Ala Lys Leu Gly Gln Asp Ile
260 265 270

Glu Lys Lys Ile Leu Glu Thr Ile Pro Leu Gly Arg Tyr Gly Gln Pro
275 280 285

Glu Glu Val Ala Gly Leu Val Glu Phe Leu Ala Leu Asn Gln Ala Ala
290 295 300

Ser Tyr Ile Thr Gly Gln Val Phe Thr Ile Asp Gly Gly Met Val Met
305 310 315 320

<210> 355

<211> 828

<212> DNA

<213> G.max

<400> 355

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gtagtgatcg ctgacatcca agacgaactg ggacattccg ttgctcagtc catagggcca	180
tcaacatggt gttatgtcca ttgcgatgtc accgatgaga accaaataaa aaatgccgtc	240
caaaaagccg tagatgctta tgggaagcta gacatcatgt tcaacaacgc cggcattggt	300
gatcccaaca agaaccgaat cattgacaac gataaggcag atttcgaacg tgtcctaagc	360
gtcaatgtca cgggtgtttt ccttgggatg aagcatgcgg cgcaggcgat gatcccagca	420
cgcagtggta gcatcatctc tacggccagc ataagctcct acgttggtgg tgcagcctcg	480
catgcttact gttgtgctaa gcatgctgtg gttggtctaa ctaaaaatgc agcagttgag	540
cctggacagt tcggaataag ggtgaattgt ttgtcacctt acgctcttgc tacacctttg	600
gccaccaagt ttgttgagc taatgatgag gagcttgaga ctatcatgaa ctcaactggct	660
aatctcaagg gtgtcactct taaagctgag gatgtggcta atgccgcact ttattttgct	720
agtgatgatt ccaggtacgt cagtgggcaa aatttgctca tagatggagg cttcagcatt	780
gttaatcctt cttttcacat gtttcagtac ccggactcgg agtcttga	828

<210> 356
 <211> 275
 <212> PRT
 <213> G.max

<400> 356

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

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

Val Phe Ala Gln Gln Gly Ala Lys Val Val Ile Ala Asp Ile Gln Asp
35 40 45

Glu Leu Gly His Ser Val Ala Gln Ser Ile Gly Pro Ser Thr Cys Cys
50 55 60

Tyr Val His Cys Asp Val Thr Asp Glu Asn Gln Ile Lys Asn Ala Val
65 70 75 80

Gln Lys Ala Val Asp Ala Tyr Gly Lys Leu Asp Ile Met Phe Asn Asn
85 90 95

Ala Gly Ile Val Asp Pro Asn Lys Asn Arg Ile Ile Asp Asn Asp Lys
100 105 110

Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu
115 120 125

Gly Met Lys His Ala Ala Gln Ala Met Ile Pro Ala Arg Ser Gly Ser
130 135 140

Ile Ile Ser Thr Ala Ser Ile Ser Ser Tyr Val Gly Gly Ala Ala Ser
145 150 155 160

His Ala Tyr Cys Cys Ala Lys His Ala Val Val Gly Leu Thr Lys Asn
165 170 175

Ala Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser
180 185 190

Pro Tyr Ala Leu Ala Thr Pro Leu Ala Thr Lys Phe Val Gly Ala Asn
195 200 205

Asp Glu Glu Leu Glu Thr Ile Met Asn Ser Leu Ala Asn Leu Lys Gly
210 215 220

Val Thr Leu Lys Ala Glu Asp Val Ala Asn Ala Ala Leu Tyr Phe Ala
225 230 235 240

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

Gly Phe Ser Ile Val Asn Pro Ser Phe His Met Phe Gln Tyr Pro Asp
260 265 270

Ser Glu Ser
275

<210> 357
<211> 783
<212> DNA
<213> G.max

<400> 357
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gacgatttgg gtctctctat ttgcaaacac ttggaatccg cttcctatgt tcaactgcgac 180
gtgacaaacg aaaccgacgt tgaaaactgc gtgaacacca ccgtttccaa acacggcaaa 240
ctagatatca tgttcaacaa cgctggcata accggtgtga acaaaaccag catcctcgac 300
aacacaaagt cagagtttga ggaagtgatc aacgttaacc tagttggtgt ctttctggga 360

acaaagcacg ccgcaagggg aatgatccct gctagaagag gaagcatagt taacactgca 420
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 gtggtggggc tcacaaagaa cactgcggtg gagcttggag catttggtgt tagggttaac 540
 tgcgtgtcac cctacgtggt tgccacgccc ttggctaaga atttttttaa gcttgatgat 600
 gacggagttc aggggattta ttcaaacctt aagggtactg atcttgtgcc taatgatgta 660
 gccgaagctg ctttgtacct ggcaagtgat gagtccaagt atgttagtgg gcacaatctt 720
 gtggttgatg gaggcttcac tgtggtcaat agtgggtttt gtgtccttgg gcaatcttcg 780
 tga 783

<210> 358
 <211> 260
 <212> PRT
 <213> G.max

<400> 358

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

Ser Gly Ile Gly Glu Ala Thr Ala Arg Leu Phe Ser Lys His Gly Ala
 20 25 30

His Val Val Ile Ala Asp Ile Gln Asp Asp Leu Gly Leu Ser Ile Cys
 35 40 45

Lys His Leu Glu Ser Ala Ser Tyr Val His Cys Asp Val Thr Asn Glu
 50 55 60

Thr Asp Val Glu Asn Cys Val Asn Thr Thr Val Ser Lys His Gly Lys
 65 70 75 80

Leu Asp Ile Met Phe Asn Asn Ala Gly Ile Thr Gly Val Asn Lys Thr
85 90 95

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

Asn Leu Val Gly Val Phe Leu Gly Thr Lys His Ala Ala Arg Val Met
115 120 125

Ile Pro Ala Arg Arg Gly Ser Ile Val Asn Thr Ala Ser Val Cys Gly
130 135 140

Ser Ile Gly Gly Val Ala Ser His Ala Tyr Thr Ser Ser Lys His Ala
145 150 155 160

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

Val Arg Val Asn Cys Val Ser Pro Tyr Val Val Ala Thr Pro Leu Ala
180 185 190

Lys Asn Phe Phe Lys Leu Asp Asp Asp Gly Val Gln Gly Ile Tyr Ser
195 200 205

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

Leu Tyr Leu Ala Ser Asp Glu Ser Lys Tyr Val Ser Gly His Asn Leu
225 230 235 240

Val Val Asp Gly Gly Phe Thr Val Val Asn Ser Gly Phe Cys Val Leu
245 250 255

Gly Gln Ser Ser
260

<210> 359
<211> 885
<212> DNA
<213> G.max

<400> 359
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ctccaggga aggtggcggtt ggtgacagga ggtgactcag gaattggcag agcggtttgc 180
ctgtgttttcg caaaagaggg tgcaaccgtg gcctttacat acgtaaaggg ccatgaggac 240
agggataaag atgatactct gaagatgctg cttgaagcta agacaagtgg tgcagacaat 300
ccattggcaa tagcagcgga tattggcttt gatgagaact gcaaacaggt cattgacctt 360
gttgtcaaag aatatggccg ccttgatgtt ctggtcaaca atgcagctga gcagcatttg 420
acaaactctg ttgaggaaat cacacaacag cagcttgaga gagtcttcgg aaccaacatc 480
ttttctcagt tctttttggt caagcatgct ctgaagcaca tgaaagaagg gagctgcac 540
ataaactcta cttcagttaa tgcatacaat gggaatccag aagcgttgga ctacactgct 600
accaagggag caattgtggc cttcaccaga ggtctttctc agcagctagc gagtagggga 660
attaggggtga atgggtgtggc acctggccca gtttgagcgc caatacaacc agcttcaaag 720
cctgctgaga tgattcagaa cttgggggtgt gaggtgccaa tgaaccgcgt ggctcagcct 780
tgtgagattg caccatgtta tttgttcttg gcaacttgtc aggactcttc ctactttact 840

ggccaagtcc tccatccaaa tgggtgggatg gtcgtcaacg cttga

885

<210> 360

<211> 294

<212> PRT

<213> G.max

<400> 360

Met Ala Ser Asn Lys Glu Ser Lys Phe Pro Ala Gln Ser Gln Lys Thr
1 5 10 15

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

Pro Asp His Lys Ala Ala Asn Lys Leu Gln Gly Lys Val Ala Leu Val
35 40 45

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

Lys Glu Gly Ala Thr Val Ala Phe Thr Tyr Val Lys Gly His Glu Asp
65 70 75 80

Arg Asp Lys Asp Asp Thr Leu Lys Met Leu Leu Glu Ala Lys Thr Ser
85 90 95

Gly Ala Asp Asn Pro Leu Ala Ile Ala Ala Asp Ile Gly Phe Asp Glu
100 105 110

Asn Cys Lys Gln Val Ile Asp Leu Val Val Lys Glu Tyr Gly Arg Leu
115 120 125

Asp Val Leu Val Asn Asn Ala Ala Glu Gln His Leu Thr Asn Ser Val
130 135 140

Glu Glu Ile Thr Gln Gln Gln Leu Glu Arg Val Phe Gly Thr Asn Ile
145 150 155 160

Phe Ser Gln Phe Phe Leu Val Lys His Ala Leu Lys His Met Lys Glu
165 170 175

Gly Ser Cys Ile Ile Asn Ser Thr Ser Val Asn Ala Tyr Asn Gly Asn
180 185 190

Pro Glu Ala Leu Asp Tyr Thr Ala Thr Lys Gly Ala Ile Val Ala Phe
195 200 205

Thr Arg Gly Leu Ser Gln Gln Leu Ala Ser Arg Gly Ile Arg Val Asn
210 215 220

Gly Val Ala Pro Gly Pro Val Trp Thr Pro Ile Gln Pro Ala Ser Lys
225 230 235 240

Pro Ala Glu Met Ile Gln Asn Leu Gly Cys Glu Val Pro Met Asn Arg
245 250 255

Val Ala Gln Pro Cys Glu Ile Ala Pro Cys Tyr Leu Phe Leu Ala Thr
260 265 270

Cys Gln Asp Ser Ser Tyr Phe Thr Gly Gln Val Leu His Pro Asn Gly
275 280 285

Gly Met Val Val Asn Ala
290

<210> 361
<211> 804
<212> DNA
<213> G.max

<400> 361
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ctcgtcaccg gtggatccaa aggaatcgga tatgctatcg tggaggagtt ggcacagctt 120

ggagccactg tgcacacttg cgctcggaac gaagctgaac tcaatgaatc cttaaataaa 180

tggaacacaa aaggatacag agtaactggg tccgtctgtg acgtggcggt tcgtgcagaa 240

agacaagacc tcatagctag agtctccaat gaggtttaatg gcaaaactca tacccttgta 300

aacaacgtgg gaacaaacgt accgaaacat acccttgatg ttacggagga agacttctca 360

tttctgataa atacaaatct tgaatctgct taccacetaa gccagcttgc acatcctctc 420

ctgaaagctt cagaggctgc aaacatcatt tttatatcct ccattgctgg tgtgctatca 480

ataggtatag gatccactta tgggtgcaaa aaaggagcaa tgaaccaact gactaaaaat 540

ttggcatgtg agtgggcaaa agacaatata aggactaatt gcgttgccac agggccaatc 600

aaaaccctc tcggtgacaa gcatttttaa aatgaaaaac ttcttaatgc tttcatttcg 660

caaaccccc ttggacggat tggagaagca gaggaagtgt cttcattggg ggcattcctc 720

tgcttacctg cagcctctta cataacagga cagaccattt gtgttgatgg tggattaaca 780

gtgaatgggt tctatataaa ttga 804

<210> 362
<211> 267
<212> PRT
<213> G.max

<400> 362

Met Ala Glu Ala Ser Ile Gly Ser Lys Ser Ser Arg Trp Ser Leu Gln
1 5 10 15

Gly Met Thr Ala Leu Val Thr Gly Gly Ser Lys Gly Ile Gly Tyr Ala
20 25 30

Ile Val Glu Glu Leu Ala Gln Leu Gly Ala Thr Val His Thr Cys Ala
35 40 45

Arg Asn Glu Ala Glu Leu Asn Glu Ser Leu Asn Glu Trp Asn Thr Lys
50 55 60

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

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

Asn Ile Leu Val Asn Asn Val Gly Thr Asn Val Pro Lys His Thr Leu
100 105 110

Asp Val Thr Glu Glu Asp Phe Ser Phe Leu Ile Asn Thr Asn Leu Glu
115 120 125

Ser Ala Tyr His Leu Ser Gln Leu Ala His Pro Leu Leu Lys Ala Ser
130 135 140

Glu Ala Ala Asn Ile Ile Phe Ile Ser Ser Ile Ala Gly Val Leu Ser
145 150 155 160

Ile Gly Ile Gly Ser Thr Tyr Gly Ala Thr Lys Gly Ala Met Asn Gln
165 170 175

Leu Thr Lys Asn Leu Ala Cys Glu Trp Ala Lys Asp Asn Ile Arg Thr
180 185 190

Asn Cys Val Ala Pro Gly Pro Ile Lys Thr Pro Leu Gly Asp Lys His
195 200 205

Phe Lys Asn Glu Lys Leu Leu Asn Ala Phe Ile Ser Gln Thr Pro Leu
210 215 220

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

Cys Leu Pro Ala Ala Ser Tyr Ile Thr Gly Gln Thr Ile Cys Val Asp
245 250 255

Gly Gly Leu Thr Val Asn Gly Leu Tyr Ile Asn
260 265

<210> 363
<211> 819
<212> DNA
<213> G.max

<400> 363
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gctctcgtca ccggcggcac ccgtgggatc gggcacgcca tagtgagtga cttggccgcg 120
tttggcgctg ctgtgcacac ttgctccagg acccaaacag agctcaacaa atgcttataa 180
gagtggcaga gtctgggctt tcaggtaact gggtcggtgt gtgacgtgtc ctcaccatcc 240

cagagagaga agctcattga ggaagtcact tccatcttga atggcaagct taacatctat 300
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 tcacagctta tgacagttaa tttagactcc tcattccatc tgtgccaaact tgcataatcct 420
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 aacctggcct gtgaatgggc caaagacaac ataaggagca actgtgttgt accatgggca 600
 accagaaccc cacttgtaga acatttgctg agagaccaa agtttgtgga tgatattatg 660
 tctcgaactc cgattaaacg tatagcagaa cccgaagaag tgtcatcggt ggtgactgtc 720
 ctttgcttgc ctgctgcttc ttacatcact ggacagggtta tttgtgttga tggaggatta 780
 acggtgaatg gatgtcaacc cagcatgaga attacctga 819

<210> 364
 <211> 272
 <212> PRT
 <213> G.max

<400> 364

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

Asn Gly Thr Thr Ala Leu Val Thr Gly Gly Thr Arg Gly Ile Gly His
 20 25 30

Ala Ile Val Ser Asp Leu Ala Ala Phe Gly Ala Ala Val His Thr Cys
 35 40 45

Ser Arg Thr Gln Thr Glu Leu Asn Lys Cys Leu Gln Glu Trp Gln Ser
 50 55 60

Leu Gly Phe Gln Val Thr Gly Ser Val Cys Asp Val Ser Ser Pro Ser
65 70 75 80

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

Leu Asn Ile Tyr Val Asn Asn Val Gly Thr Asn Phe Arg Lys Pro Thr
100 105 110

Ile Glu Tyr Thr Ala Glu Glu Tyr Ser Gln Leu Met Thr Val Asn Leu
115 120 125

Asp Ser Ser Phe His Leu Cys Gln Leu Ala Tyr Pro Leu Leu Lys Ala
130 135 140

Ser Glu Asn Gly Ser Ile Val Phe Ile Ser Ser Val Ala Gly Val Val
145 150 155 160

Ser Leu Gly Thr Gly Ala Val Tyr Ala Ala Ser Lys Ala Ala Ile Asn
165 170 175

Gln Leu Thr Lys Asn Leu Ala Cys Glu Trp Ala Lys Asp Asn Ile Arg
180 185 190

Ser Asn Cys Val Val Pro Trp Ala Thr Arg Thr Pro Leu Val Glu His
195 200 205

Leu Leu Arg Asp Gln Lys Phe Val Asp Asp Ile Met Ser Arg Thr Pro
210 215 220

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

Leu Cys Leu Pro Ala Ala Ser Tyr Ile Thr Gly Gln Val Ile Cys Val
245 250 255

Asp Gly Gly Leu Thr Val Asn Gly Cys Gln Pro Ser Met Arg Ile Thr
260 265 270

<210> 365

<211> 843

<212> DNA

<213> G.max

<400> 365

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catggtgcta aaatatgtat agctgatgtg caagacaacc ttggaaagca ggtctgtcag 180

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aatgccgga tttctggatc accttggttcc gatatccgca atgcagactt atcagaattc 360

gataaggtgt ttagtgtaaa tacgaaggga gtgttccacg ggatgaaaca cgctgctcga 420

attatgatcc cgaagaagaa gggctcaatc atttctttat gcagtgtagc aagtgccata 480

ggtggcttag gaccgcatgc atacacaggg tccaagtatg ctgtattggg gctcaciaag 540

aatgttgtag ctgaattggg gaaacatgct ataagagtga actgtgtgtc accttatggt 600

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gtcagttttc gtgattttac tgggagaatg gccaaactgc agggggtaga attaactact 720

cacgatgtgg ctaatgctgt gctcttcctt gcaagtgatg atgctaaata tataagtgga 780

gagaatctca tggttgatgg aggcttcaca agtgcaaata actcactcca agttttttaga 840

tga 843

<210> 366

<211> 280

<212> PRT

<213> G.max

<400> 366

Met Ser Thr Thr Gly Thr Val Leu Ala Ser Thr Pro Thr Gln Arg Leu

1 5 10 15

Leu Gly Lys Val Ala Leu Val Thr Gly Gly Ala Ser Gly Ile Gly Glu

20 25 30

Ser Ile Val Arg Leu Phe His Ile His Gly Ala Lys Ile Cys Ile Ala

35 40 45

Asp Val Gln Asp Asn Leu Gly Lys Gln Val Cys Gln Ser Leu Gly Asp

50 55 60

Glu Ala Asn Val Val Phe Val His Cys Asp Val Thr Val Glu Asp Asp

65 70 75 80

Val Ser His Ala Val Asp Phe Thr Val Gly Lys Phe Gly Thr Leu His

85 90 95

Ile Ile Val Asn Asn Ala Gly Ile Ser Gly Ser Pro Cys Ser Asp Ile

100 105 110

Arg Asn Ala Asp Leu Ser Glu Phe Asp Lys Val Phe Ser Val Asn Thr
115 120 125

Lys Gly Val Phe His Gly Met Lys His Ala Ala Arg Ile Met Ile Pro
130 135 140

Lys Lys Lys Gly Ser Ile Ile Ser Leu Cys Ser Val Ala Ser Ala Ile
145 150 155 160

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

Gly Leu Thr Lys Asn Val Ala Ala Glu Leu Gly Lys His Ala Ile Arg
180 185 190

Val Asn Cys Val Ser Pro Tyr Gly Val Ala Thr Gly Leu Ala Leu Ala
195 200 205

His Leu Pro Glu Asp Glu Arg Thr Asp Asp Ala Leu Val Ser Phe Arg
210 215 220

Asp Phe Thr Gly Arg Met Ala Asn Leu Gln Gly Val Glu Leu Thr Thr
225 230 235 240

His Asp Val Ala Asn Ala Val Leu Phe Leu Ala Ser Asp Asp Ala Lys
245 250 255

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

Asn His Ser Leu Gln Val Phe Arg
275 280

<210> 367
<211> 849
<212> DNA
<213> G.max

<400> 367
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atggtcaccg gcgcctcctc cggcctcggc cgcgacttct gcctcgacct cggtcgggct 120

ggctgtcggg tcgtcgtggc ggcccgcaga gtcgaccgcc tcgagtcctt gtgcgacgaa 180

attaacagca tggccgccgg agacggtggc cgaagccgcc gcgcgctcgc cgttgaactc 240

gatgtcgtg ccgatgaccc cgcgctcgac aaatacgtgc agaaggcgtg ggaggcgttt 300

ggtcacattg atgctcttat caacaacgct ggtgtcagag ggaatgtcaa atcacctttg 360

gaattgtctg aggaggaatg gaaccatgcy ttcagaacaa acttaactgg gacatggttg 420

gtctcaaaat atgtatgcaa acgcatgcyt gatgcacaaa gaaaaggatc aatcattaat 480

attgcttcaa ttgctggttt gaaccgtggt caattgcctg gaggtgctgc atattcatcc 540

tcaaaagcag gcgtcaatat gctaacaagg gtcatggcat tagaattggg ggcacacaaa 600

atcagagtga attccatatc acctggactt ttcaaacttg aaatcactga aaaactaatg 660

gagaaaaatt ggttgaataa tgtggccatg aaaacagtac ccttgagaaa atttggcact 720

tctgatccag cattaacatc gctggctcgt tatttaattc acgattcttc tgagtatgtg 780

tcaggcaaca attttgttgt ggatgctgga gccaccttac caggtgtgcc tatttattcc 840

tccctatga 849

<210> 368
<211> 282
<212> PRT

<213> G.max

<400> 368

Met Ala Thr Gln Leu Ser Asp Arg Leu Glu Pro Trp His Thr Leu Ala
1 5 10 15

Gly Lys Val Val Met Val Thr Gly Ala Ser Ser Gly Leu Gly Arg Asp
20 25 30

Phe Cys Leu Asp Leu Gly Arg Ala Gly Cys Arg Val Val Val Ala Ala
35 40 45

Arg Arg Val Asp Arg Leu Glu Ser Leu Cys Asp Glu Ile Asn Ser Met
50 55 60

Ala Ala Gly Asp Gly Gly Arg Ser Arg Arg Ala Val Ala Val Glu Leu
65 70 75 80

Asp Val Ala Ala Asp Asp Pro Ala Val Asp Lys Tyr Val Gln Lys Ala
85 90 95

Trp Glu Ala Phe Gly His Ile Asp Ala Leu Ile Asn Asn Ala Gly Val
100 105 110

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

His Ala Phe Arg Thr Asn Leu Thr Gly Thr Trp Leu Val Ser Lys Tyr
130 135 140

Val Cys Lys Arg Met Arg Asp Ala Gln Arg Lys Gly Ser Ile Ile Asn
145 150 155 160

Ile Ala Ser Ile Ala Gly Leu Asn Arg Gly Gln Leu Pro Gly Gly Ala
165 170 175

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

Ala Leu Glu Leu Gly Ala His Lys Ile Arg Val Asn Ser Ile Ser Pro
195 200 205

Gly Leu Phe Lys Ser Glu Ile Thr Glu Lys Leu Met Glu Lys Asn Trp
210 215 220

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

Ser Asp Pro Ala Leu Thr Ser Leu Ala Arg Tyr Leu Ile His Asp Ser
245 250 255

Ser Glu Tyr Val Ser Gly Asn Asn Phe Val Val Asp Ala Gly Ala Thr
260 265 270

Leu Pro Gly Val Pro Ile Tyr Ser Ser Leu
275 280

<210> 369

<211> 849

<212> DNA

<213> G.max

<400> 369

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gctggctgct gtgtcgtcgc ggcagctcgt cgcctcgatc gcctcacttc cctctgccac	180
gaaatcaacc accgatggcc ctccaacgtc ggaatccacc gcgcgggtggc ggtggagctt	240
gatgtcgccg ccgatggccc cgccatcgac agggctgtgc agaaggcctg ggacgccttt	300
ggccgcgttg attccttgat taacaacgct ggtgtcagag gaagtgttaa atcacccttg	360
aaattgtctg aagaggaatg ggatcatgtc ttcaagacta acctaactgg ttgttggttg	420
gtgtcaaaat atgtatgcaa acgcatgtgt gatatccagc ttaagggatc aattattaat	480
atttcttcag tttctggttt aaatcgggg caattgcctg gagctgctgc atatgcatct	540
tcgaaggcag gggtaaacad gctgactaag gtcatggcta tggaattggg gatgcacaaa	600
attagagtaa attccatatc ccctggaatt ttcaaactctg aaataactga aaatttatta	660
caaaaagatt ggctgaatga tgtggtcagg aaaataatgc ctttgagaag attaggtact	720
tcagatccag cattaacatc tctagctcgt tatcttattc atgattcttc tgagtacgtc	780
acgggcaaca attttattgt cgattatgga ggcaccttac caggtgtacc aatttattct	840
tctctgtga	849

<210> 370
 <211> 282
 <212> PRT
 <213> G.max

<400> 370

Met	Asn	Ala	Ile	Ala	Ala	Glu	Gln	Val	Leu	Glu	Pro	Trp	His	Lys	Leu
1				5					10					15	

Asp	Asp	Lys	Val	Val	Leu	Val	Thr	Gly	Ala	Ser	Ser	Gly	Leu	Gly	Arg
			20					25					30		

Asp Phe Cys Ile Asp Leu Ala Lys Ala Gly Cys Cys Val Val Ala Ala
35 40 45

Ala Arg Arg Leu Asp Arg Leu Thr Ser Leu Cys His Glu Ile Asn His
50 55 60

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

Asp Val Ala Ala Asp Gly Pro Ala Ile Asp Arg Ala Val Gln Lys Ala
85 90 95

Trp Asp Ala Phe Gly Arg Val Asp Ser Leu Ile Asn Asn Ala Gly Val
100 105 110

Arg Gly Ser Val Lys Ser Pro Leu Lys Leu Ser Glu Glu Glu Trp Asp
115 120 125

His Val Phe Lys Thr Asn Leu Thr Gly Cys Trp Leu Val Ser Lys Tyr
130 135 140

Val Cys Lys Arg Met Cys Asp Ile Gln Leu Lys Gly Ser Ile Ile Asn
145 150 155 160

Ile Ser Ser Val Ser Gly Leu Asn Arg Gly Gln Leu Pro Gly Ala Ala
165 170 175

Ala Tyr Ala Ser Ser Lys Ala Gly Val Asn Met Leu Thr Lys Val Met
180 185 190

Ala Met Glu Leu Gly Met His Lys Ile Arg Val Asn Ser Ile Ser Pro
195 200 205

Gly Ile Phe Lys Ser Glu Ile Thr Glu Asn Leu Leu Gln Lys Asp Trp
210 215 220

Leu Asn Asp Val Val Arg Lys Ile Met Pro Leu Arg Arg Leu Gly Thr
225 230 235 240

Ser Asp Pro Ala Leu Thr Ser Leu Ala Arg Tyr Leu Ile His Asp Ser
245 250 255

Ser Glu Tyr Val Thr Gly Asn Asn Phe Ile Val Asp Tyr Gly Gly Thr
260 265 270

Leu Pro Gly Val Pro Ile Tyr Ser Ser Leu
275 280

<210> 371
<211> 798
<212> DNA
<213> G.max

<400> 371
atggcttcta gttcagaatc tcaatctcag tctaaaccgc tccaagaccg agttgcaatc 60
gtcaccgggt cgtcccgcg aatcggccga gaaatcgcg ttcacctcgc ctcaactcggc 120
gcgcgactcg tcgtcaacta cacctccaac tcggcccaag ccgactcagt cgcggcgcag 180
atcaacgccg gttccgccac cacgacaccg cgcgccgtcg tgggtccaagc cgacgtgtcc 240
gatccggctc aggtgaagtc gctcttcgac tcggccgagc gcgccttcga ctgcgccgatc 300
cacatccttg tcaactcggc gggcgtgatc gacggcacgt atccctccgt cgccgacacc 360

accgtggagt ccttcgaccg cacttttcgcg gtgaacgcgc gtggcgccctt cgcgtgcgcc 420

agggaggccg cgaaccgcct caagcgcggc ggcggagggc ggatcattct actgacgaca 480

tcgcaggtgg tggcgctgag gccgggggtac ggggcgtacg cggcgtcgaa ggcggcggtg 540

gaggcaatgg tgaagatcct ggcgaaggaa ctgaaaggga cgcagataac ggcgaattgc 600

gttgcgccgg gaccgattgc gacggagatg ttcttcgagg gtaagacgga ggaggtggtg 660

aatcggatcg tgcaagagag tcccttgggg aggctcgggtg agaccaaaga cgtggcaccc 720

gttgtgggat tcttggccac tgatgcttct gaatgggtca acggtcaaat tgttcgtgtc 780

aacggtggct atatttga 798

<210> 372

<211> 265

<212> PRT

<213> G.max

<400> 372

Met Ala Ser Ser Ser Glu Ser Gln Ser Gln Ser Lys Pro Leu Gln Asp

1 5 10 15

Arg Val Ala Ile Val Thr Gly Ser Ser Arg Gly Ile Gly Arg Glu Ile

20 25 30

Ala Leu His Leu Ala Ser Leu Gly Ala Arg Leu Val Val Asn Tyr Thr

35 40 45

Ser Asn Ser Ala Gln Ala Asp Ser Val Ala Ala Gln Ile Asn Ala Gly

50 55 60

Ser Ala Thr Thr Thr Pro Arg Ala Val Val Val Gln Ala Asp Val Ser

65 70 75 80

Asp Pro Ala Gln Val Lys Ser Leu Phe Asp Ser Ala Glu Arg Ala Phe
85 90 95

Asp Ser Pro Ile His Ile Leu Val Asn Ser Ala Gly Val Ile Asp Gly
100 105 110

Thr Tyr Pro Ser Val Ala Asp Thr Thr Val Glu Ser Phe Asp Arg Thr
115 120 125

Phe Ala Val Asn Ala Arg Gly Ala Phe Ala Cys Ala Arg Glu Ala Ala
130 135 140

Asn Arg Leu Lys Arg Gly Gly Gly Gly Arg Ile Ile Leu Leu Thr Thr
145 150 155 160

Ser Gln Val Val Ala Leu Arg Pro Gly Tyr Gly Ala Tyr Ala Ala Ser
165 170 175

Lys Ala Ala Val Glu Ala Met Val Lys Ile Leu Ala Lys Glu Leu Lys
180 185 190

Gly Thr Gln Ile Thr Ala Asn Cys Val Ala Pro Gly Pro Ile Ala Thr
195 200 205

Glu Met Phe Phe Glu Gly Lys Thr Glu Glu Val Val Asn Arg Ile Val
210 215 220

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

Val Val Gly Phe Leu Ala Thr Asp Ala Ser Glu Trp Val Asn Gly Gln
245 250 255

Ile Val Arg Val Asn Gly Gly Tyr Ile
260 265

<210> 373
<211> 795
<212> DNA
<213> G.max

<400> 373
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ctagtccacag gaggcacccg aggcataagg catgccattg ttgaagagtt agctgagttt 120
ggagcaactg ttcatatatg tgcacgtaat caagatgata tagataaatg tttagaagag 180
tggaaaagca agggacttaa tgtgactggg tcagtatgtg atttactatg ttctgaccaa 240
cgtaaaagat taatggaaat tgttggtctc atctttcatg gaaagctcaa tattctagtg 300
aacaatgctg ctacaaatat acaaagaag ataacagatt acacagcaga ggatatatca 360
gccataatgg gcaccaatth tgagtccgtt taccatttgt gtcaagttgc acaccactt 420
ctaaaagatt ctgggaatgg gagcatagta tttatttctt ccgtagcagg tttaaaagct 480
cttcctgtgt tctctgttta tgcagcctct aaaggagcca tgaatcaatt caccaaaaac 540
ttggcattgg aatgggcaaa ggataatatt cgtgcaaag ctgttgcccc tggacctgtt 600
aagactaaac ttttgagtg tatcgtgaat tcttcggaag ggaatgagtc tataaatgga 660
gtagtgtctc aaacatttgt tggtcgcatg ggagaaacta aagagatatc agcattagtt 720
gcttttcttt gccttcgggc tgcatacatc atcactggac aggttatatg tgtagatggg 780
ggtttcacaa cttga 795

<210> 374
<211> 264
<212> PRT
<213> G.max

<400> 374

Met Ala Glu Thr Lys Trp Val Met Lys Asp Lys Arg Trp Ser Leu His
1 5 10 15

Gly Met Thr Ala Leu Val Thr Gly Gly Thr Arg Gly Ile Gly His Ala
20 25 30

Ile Val Glu Glu Leu Ala Glu Phe Gly Ala Thr Val His Ile Cys Ala
35 40 45

Arg Asn Gln Asp Asp Ile Asp Lys Cys Leu Glu Glu Trp Lys Ser Lys
50 55 60

Gly Leu Asn Val Thr Gly Ser Val Cys Asp Leu Leu Cys Ser Asp Gln
65 70 75 80

Arg Lys Arg Leu Met Glu Ile Val Gly Ser Ile Phe His Gly Lys Leu
85 90 95

Asn Ile Leu Val Asn Asn Ala Ala Thr Asn Ile Thr Lys Lys Ile Thr
100 105 110

Asp Tyr Thr Ala Glu Asp Ile Ser Ala Ile Met Gly Thr Asn Phe Glu
115 120 125

Ser Val Tyr His Leu Cys Gln Val Ala His Pro Leu Leu Lys Asp Ser
130 135 140

Gly Asn Gly Ser Ile Val Phe Ile Ser Ser Val Ala Gly Leu Lys Ala
 145 150 155 160

Leu Pro Val Phe Ser Val Tyr Ala Ala Ser Lys Gly Ala Met Asn Gln
 165 170 175

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

Asn Ala Val Ala Pro Gly Pro Val Lys Thr Lys Leu Leu Glu Cys Ile
 195 200 205

Val Asn Ser Ser Glu Gly Asn Glu Ser Ile Asn Gly Val Val Ser Gln
 210 215 220

Thr Phe Val Gly Arg Met Gly Glu Thr Lys Glu Ile Ser Ala Leu Val
 225 230 235 240

Ala Phe Leu Cys Leu Pro Ala Ala Ser Tyr Ile Thr Gly Gln Val Ile
 245 250 255

Cys Val Asp Gly Gly Phe Thr Thr
 260

<210> 375

<211> 816

<212> DNA

<213> G.max

<400> 375

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ctcgttactg gaggaacgcg tggaattggg cacgctgtgg tggaggaact agcggagttt	120
ggtgccacag tgtacacttg ttcgaggaat gaagaagagc tgaatgcatg cttgaaggag	180
tggaaagaga agggattttc ggtttctggg ttggtttgtg atgcgtcttc tccaccccat	240
agagagaacc tcattcaaca agtggcctct gctttcaacg gcaagctcaa catacttgta	300
aacaatgttg gaacaaatgt gaggaagccg acaattgagt atacagccga agaataattca	360
aaattgatgg caactaactt ggactccaca taccatttgt gccaaacttg atactctctt	420
cttaaagcat ctggaaatgg aagtattgtg tccatttcct ctgttgcaag tcagacaagc	480
gtaggttctg gagccattta cgcagcaact aaagctgcta ttgatcagct taccaaatat	540
tttgcttgtg aatgggcaaa agacaatata aggagcaacg gtgttgacc ctggtatacc	600
ataacttcac ttgtggaacc tttgcttgcg aacaaacagc ttgttagtga gataatatct	660
cgaacgccga taaagcggat ggcagaaaca catgaagttt catccttggg gaactttcctt	720
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gctaatggat ttcaaccag catgagaatt tcttga	816

<210> 376
 <211> 271
 <212> PRT
 <213> G.max

<400> 376

Met	Ala	Asn	Pro	Glu	Gly	Ser	Ser	Arg	Gly	Ser	Arg	Trp	Ser	Leu	Lys
1			5					10						15	

Gly	Thr	Thr	Ala	Leu	Val	Thr	Gly	Gly	Thr	Arg	Gly	Ile	Gly	His	Ala
			20					25					30		

Val Val Glu Glu Leu Ala Glu Phe Gly Ala Thr Val Tyr Thr Cys Ser
35 40 45

Arg Asn Glu Glu Glu Leu Asn Ala Cys Leu Lys Glu Trp Lys Glu Lys
50 55 60

Gly Phe Ser Val Ser Gly Leu Val Cys Asp Ala Ser Ser Pro Pro His
65 70 75 80

Arg Glu Asn Leu Ile Gln Gln Val Ala Ser Ala Phe Asn Gly Lys Leu
85 90 95

Asn Ile Leu Val Asn Asn Val Gly Thr Asn Val Arg Lys Pro Thr Ile
100 105 110

Glu Tyr Thr Ala Glu Glu Tyr Ser Lys Leu Met Ala Thr Asn Leu Asp
115 120 125

Ser Thr Tyr His Leu Cys Gln Leu Ala Tyr Pro Leu Leu Lys Ala Ser
130 135 140

Gly Asn Gly Ser Ile Val Ser Ile Ser Ser Val Ala Ser Gln Thr Ser
145 150 155 160

Val Gly Ser Gly Ala Ile Tyr Ala Ala Thr Lys Ala Ala Ile Asp Gln
165 170 175

Leu Thr Lys Tyr Phe Ala Cys Glu Trp Ala Lys Asp Asn Ile Arg Ser
180 185 190

Asn Gly Val Ala Pro Trp Tyr Thr Ile Thr Ser Leu Val Glu Pro Leu
195 200 205

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

Lys Arg Met Ala Glu Thr His Glu Val Ser Ser Leu Val Thr Phe Leu
225 230 235 240

Cys Leu Pro Ala Ala Ser Tyr Ile Thr Gly Gln Ile Val Ser Val Asp
245 250 255

Gly Gly Phe Thr Ala Asn Gly Phe Gln Pro Ser Met Arg Ile Ser
260 265 270

<210> 377
<211> 771
<212> DNA
<213> H.vulgare

<400> 377
atgagcaggg aggagaggtg gaggcctggcc ggcgcgacgc gctcgtcacc ggcggcagaa 60
agggatcggc cagcgatcg tggaggagct ggcggggcac ggggcgcggg tgcacacgtg 120
cgccaggagc cggcggacgt ggaggagtgc cgccgccggt gggaggccaa ggggcttccg 180
gtcaccgtct ccgtctgcga cgtctccctg cgcgcccaca gggagcagct cgtggagacg 240
gtcaagcaag tcttcggcgg caagctcgac atactggtga acaacgcggc acagattctt 300
gccaaggcgg ccgtggagtg gacatcggag gactactcgc acctcatggc gaccaatcta 360
gagtcgtgct tccacctcag ccagctcgcg cacccttgc tcctcaacgc ctccatcgct 420
ggaggtagca tcgtcaacat atcctccctt gggggcacac ttggtttcac gggccttgcg 480
ctttacagta tgacaaaagg aggaataaac cagcttaciaa ggagccttgc tactgaatgg 540

gcccagaaca agatccgggt gaattgcgtc gccccgggcg cgaccaagag tgacatgtta 600

agcagtctcc cactggagat tagagagaac gagttggcga ggactccaat gcggcgggca 660

ggcgagccag cggaggtggc tgcaatggtg tcgttcctct gcatgccggc ggcatacttc 720

gtcaccggcc aggtcatcgc cgtcgacggt ggtcggacaa ttagtgcttg a 771

<210> 378

<211> 256

<212> PRT

<213> H.vulgare

<400> 378

Met Ser Arg Glu Glu Arg Trp Ser Leu Ala Gly Ala Thr Arg Ser Ser

1 5 10 15

Pro Ala Ala Glu Arg Asp Arg Pro Arg Asp Arg Gly Gly Ala Gly Gly

20 25 30

Ala Arg Gly Ala Gly Ala His Val Arg Gln Glu Pro Ala Asp Val Glu

35 40 45

Glu Cys Arg Arg Arg Trp Glu Ala Lys Gly Leu Pro Val Thr Val Ser

50 55 60

Val Cys Asp Val Ser Leu Arg Ala His Arg Glu Gln Leu Val Glu Thr

65 70 75 80

Val Lys Gln Val Phe Gly Gly Lys Leu Asp Ile Leu Val Asn Asn Ala

85 90 95

Ala Gln Ile Leu Ala Lys Ala Ala Val Glu Trp Thr Ser Glu Glu Tyr

100 105 110

Ser His Leu Met Ala Thr Asn Leu Glu Ser Cys Phe His Leu Ser Gln
115 120 125

Leu Ala His Pro Leu Leu Leu Asn Ala Ser Ile Ala Gly Gly Ser Ile
130 135 140

Val Asn Ile Ser Ser Leu Gly Gly Thr Leu Gly Phe Thr Gly Leu Ala
145 150 155 160

Leu Tyr Ser Met Thr Lys Gly Gly Ile Asn Gln Leu Thr Arg Ser Leu
165 170 175

Ala Thr Glu Trp Ala Gln Asn Lys Ile Arg Val Asn Cys Val Ala Pro
180 185 190

Gly Ala Thr Lys Ser Asp Met Leu Ser Ser Leu Pro Leu Glu Ile Arg
195 200 205

Glu Asn Glu Leu Ala Arg Thr Pro Met Arg Arg Ala Gly Glu Pro Ala
210 215 220

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

Val Thr Gly Gln Val Ile Ala Val Asp Gly Gly Arg Thr Ile Ser Ala
245 250 255

<210> 379

<211> 972

<212> DNA

<213> L.usitatissimum

<400> 379

atggctgcta gtaccggatc caccgccgtc gcattcaaat ccgccggggt cgtcgctgcc	60
tcctccggcg aaaggggcat taaccagttc cgccactggg ctctgttcc cgccagcctc	120
cacttctccc gcgctggcct ccgctgcaga tcgagaagct cggatcctc ttccggtgtg	180
agagctcagg ttgctgcagt tgaaccagta agcagtgagt cagttaagaa ggtggaatct	240
ccagtcgtta ttgtaactgg agcttccaga ggaatcggga aagcgattgc attgtcgttg	300
gggaaagcag gttgcaaggt tctggttaac tatgcaaggt catccaagga ggctgaggaa	360
gtctccaaag agattgaagc ttccggtggg caagctgtaa cctttgggtg tgatgtctct	420
aaagaagagg atgtggaggc catgatgaaa actgctattg atgcttttgg aacagttgac	480
atactgataa acaatgcagg gatcacaagg gacactttgt tgatgcggat gaagaaacag	540
cagtggcagg atgttattga cctcaatctt actggtgtct tcctttgtac acaggctgca	600
gccaagatca tgatgaagaa aagaaaggga aggattatca atatcgcttc agttgttggt	660
ttggttggtg acattgggca agctaactac agtgctgcaa aggctggagt cattggcttc	720
acaaagagtg ttgcgaagga atattcaagc agaaatatca acgtcaatgc tgtcgctcct	780
ggattcattg catctgacat gactgccaa cttggggatg acattgaaaa gaaaatattg	840
gagacaattc ctttagggcg gtacggtcag ccggaagagg tggccggatt ggtggaattc	900
ctcgctctga acccagctgc tggctacatg accgggcagg tgcttaccat cgacggagga	960
atggtgatgt ga	972

<210> 380

<211> 323

<212> PRT

<213> L.usitatissimum

<400> 380

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

Phe Val Ala Ala Ser Ser Gly Glu Arg Gly Ile Asn Gln Phe Arg His
20 25 30

Trp Ser Pro Val Pro Ala Ser Leu His Phe Ser Arg Ala Gly Leu Arg
35 40 45

Cys Arg Ser Arg Ser Ser Val Ser Ser Ser Gly Val Arg Ala Gln Val
50 55 60

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

Pro Val Val Ile Val Thr Gly Ala Ser Arg Gly Ile Gly Lys Ala Ile
85 90 95

Ala Leu Ser Leu Gly Lys Ala Gly Cys Lys Val Leu Val Asn Tyr Ala
100 105 110

Arg Ser Ser Lys Glu Ala Glu Glu Val Ser Lys Glu Ile Glu Ala Ser
115 120 125

Gly Gly Gln Ala Val Thr Phe Gly Gly Asp Val Ser Lys Glu Glu Asp
130 135 140

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

Ile Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Thr Leu Leu Met Arg
165 170 175

Met Lys Lys Gln Gln Trp Gln Asp Val Ile Asp Leu Asn Leu Thr Gly
180 185 190

Val Phe Leu Cys Thr Gln Ala Ala Ala Lys Ile Met Met Lys Lys Arg
195 200 205

Lys Gly Arg Ile Ile Asn Ile Ala Ser Val Val Gly Leu Val Gly Asn
210 215 220

Ile Gly Gln Ala Asn Tyr Ser Ala Ala Lys Ala Gly Val Ile Gly Phe
225 230 235 240

Thr Lys Ser Val Ala Lys Glu Tyr Ser Ser Arg Asn Ile Asn Val Asn
245 250 255

Ala Val Ala Pro Gly Phe Ile Ala Ser Asp Met Thr Ala Lys Leu Gly
260 265 270

Asp Asp Ile Glu Lys Lys Ile Leu Glu Thr Ile Pro Leu Gly Arg Tyr
275 280 285

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

Pro Ala Ala Gly Tyr Met Thr Gly Gln Val Leu Thr Ile Asp Gly Gly
305 310 315 320

Met Val Met

<210> 381
<211> 762
<212> DNA
<213> O.sativa

<400> 381
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ggcatcggtc tcgccatcgc cgagcgcctc ggctcagagg gcgccgccgt cgtcatctcc 120
tcccgaaga agaagaacgt cgacgaggcg gtcgtggggc tcagggcgaa ggggatcacc 180
gtcgtcgggg tggctcgcca tgtctccatc ccggagcagc gcaagaacct catcgacacg 240
gcggtcaaga attttgggca tatcgacata gttgtctcca atgctgctgc caatccttcc 300
gtagataaca tattagaaat gaaagagcct atccttgaca aactatggga tattaatggt 360
aaggcatcta ttcttcttct tcaggatgct gctgcatatt tgcggaaggg atcatccgtg 420
atattgattt cttcaattac tggctataat ccagaaccag cattgtcgat gtatgctggt 480
acaaaaactg ccctgcttgg tctcaciaag gctcttgctg ctgagatggg gccaaatact 540
cgtgttaact gtatagcccc tggttttggt cctacaaatt ttgctcgttt cctcacaact 600
aatgacacca ttaaaaatga gcttattgac aggagcacac ttaagagatt ggggtactgtg 660
gaagacatgg ctgcagccgc agctttcttg gcatcagacg atgcatcatt cattacagct 720
gaaactattg ctgttgctgc aggaactcga tctaggctgt ag 762

<210> 382
<211> 253
<212> PRT
<213> O.sativa

<400> 382

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

Ala Ser Thr Gln Gly Ile Gly Leu Ala Ile Ala Glu Arg Leu Gly Leu
20 25 30

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

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

Val Cys His Val Ser Ile Pro Glu Gln Arg Lys Asn Leu Ile Asp Thr
65 70 75 80

Ala Val Lys Asn Phe Gly His Ile Asp Ile Val Val Ser Asn Ala Ala
85 90 95

Ala Asn Pro Ser Val Asp Asn Ile Leu Glu Met Lys Glu Pro Ile Leu
100 105 110

Asp Lys Leu Trp Asp Ile Asn Val Lys Ala Ser Ile Leu Leu Leu Gln
115 120 125

Asp Ala Ala Ala Tyr Leu Arg Lys Gly Ser Ser Val Ile Leu Ile Ser
130 135 140

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

Thr Lys Thr Ala Leu Leu Gly Leu Thr Lys Ala Leu Ala Ala Glu Met
165 170 175

Gly Pro Asn Thr Arg Val Asn Cys Ile Ala Pro Gly Phe Val Pro Thr
180 185 190

Asn Phe Ala Arg Phe Leu Thr Thr Asn Asp Thr Ile Lys Asn Glu Leu
195 200 205

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

Ala Ala Ala Ala Phe Leu Ala Ser Asp Asp Ala Ser Phe Ile Thr Ala
225 230 235 240

Glu Thr Ile Ala Val Ala Ala Gly Thr Arg Ser Arg Leu
245 250

<210> 383
<211> 963
<212> DNA
<213> Z.mays

<400> 383
atggccaccg ccgccgccac cgcagcagca gcagcagtct cctccccggc tgcgcgtgga 60
gcagccgggg ccgccgccgc ctcccgccgg gggttcgtca cgtttggtgg aggcgccgcc 120
cgcttctctc ccacgctgcg gtccggccgt gggttctctg gtgtgcaaac ccatgttgc 180
gctgttgaac aagcagttgt aaaagatgct accaagctgg aagctccagt tggtgttgtt 240
acaggtgcat ctagagggat tggtaaggca actgctctag cccttggaag agcaggatgc 300
aaggttctgg taaactatgc ccggtcctcg aaagaggctg aagaggtctc caaagagatt 360
gaagcatctg gtggtgaggc tatcaccttc ggaggagatg tttcaaaaga agctgatgta 420

gagtctatga tgaaagcagc tctagataaa tggggaacaa tagatgtgct ggtaaataat	480
gcaggtttag ggattacacg agacacattg ttgatgagga tgaagaaatc tcagtggcaa	540
gacgtaattg atctgaatct tactggcgtc ttcctttgta cacaggctgc aacaaaagta	600
atgatgaaaa agagaaaggg aaaaattatc aacattgcat ctgtagttgg tcttactggc	660
aatgttggcc aagctaatta tagcgcagcc aaggctggag tgattggttt cacaaaaaca	720
gttgccaggg agtatgcaag cagaaatatc aatgtcaatg ctattgcacc agggttcatt	780
gcatctgata tgactgccga acttgagaa gagcttgaga agaaaatctt gtcaaccatt	840
ccgttaggta gatatggcca accagaggaa gttgcagggg tggtcgagtt cctggccctt	900
aaccccgag ctagctatat gactggacag gtgcttaca ttgacggagg gatggtaatg	960
taa	963

<210> 384
 <211> 320
 <212> PRT
 <213> Z.mays

<400> 384

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

Ala	Ala	Arg	Gly	Ala	Ala	Gly	Ala	Ala	Ala	Ala	Ser	Arg	Arg	Gly	Phe
			20					25						30	

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

Gly	Arg	Gly	Phe	Ser	Gly	Val	Gln	Thr	His	Val	Ala	Ala	Val	Glu	Gln
	50						55						60		

Ala Val Val Lys Asp Ala Thr Lys Leu Glu Ala Pro Val Val Val Val
65 70 75 80

Thr Gly Ala Ser Arg Gly Ile Gly Lys Ala Thr Ala Leu Ala Leu Gly
85 90 95

Lys Ala Gly Cys Lys Val Leu Val Asn Tyr Ala Arg Ser Ser Lys Glu
100 105 110

Ala Glu Glu Val Ser Lys Glu Ile Glu Ala Ser Gly Gly Glu Ala Ile
115 120 125

Thr Phe Gly Gly Asp Val Ser Lys Glu Ala Asp Val Glu Ser Met Met
130 135 140

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

Ala Gly Leu Gly Ile Thr Arg Asp Thr Leu Leu Met Arg Met Lys Lys
165 170 175

Ser Gln Trp Gln Asp Val Ile Asp Leu Asn Leu Thr Gly Val Phe Leu
180 185 190

Cys Thr Gln Ala Ala Thr Lys Val Met Met Lys Lys Arg Lys Gly Lys
195 200 205

Ile Ile Asn Ile Ala Ser Val Val Gly Leu Thr Gly Asn Val Gly Gln
210 215 220

Ala Asn Tyr Ser Ala Ala Lys Ala Gly Val Ile Gly Phe Thr Lys Thr
 225 230 235 240

Val Ala Arg Glu Tyr Ala Ser Arg Asn Ile Asn Val Asn Ala Ile Ala
 245 250 255

Pro Gly Phe Ile Ala Ser Asp Met Thr Ala Glu Leu Gly Glu Glu Leu
 260 265 270

Glu Lys Lys Ile Leu Ser Thr Ile Pro Leu Gly Arg Tyr Gly Gln Pro
 275 280 285

Glu Glu Val Ala Gly Leu Val Glu Phe Leu Ala Leu Asn Pro Ala Ala
 290 295 300

Ser Tyr Met Thr Gly Gln Val Leu Thr Ile Asp Gly Gly Met Val Met
 305 310 315 320

<210> 385
 <211> 738
 <212> DNA
 <213> Z.mays

<400> 385
 atggcagcag cagagcgcga ccgcgagcga tggatcctgc ccggcgcgac ggcgctggtc 60
 accggcggga gcaaggggat cgggcacgcg atcgtggagg agctggcggc gctgggcgcg 120
 cgcgtcaca cgtgctcccg caacgccgcg gagctggagg agtgccgccg gaggtgggca 180
 gagaagggcg gcggcctgct gcagcaggtg accgtctccg tctgcgacgt cgccgtgcgc 240
 gccgacaggg aggcgctcat ggccaccgtc agggatgtct tcggcggcaa gctggacatc 300
 ctcgtgaata acgcggcgca ggtggtcttc aagccggcgg tggagtgcac cggggaggag 360

tacacgcgga tcatggcgac caacctggag tcttgcttcc acctcagcca gctcgcgcac 420

ccgctgctcc gcgacgcctc cctcgccggc ggcgggagcg tcgtgcacat ctctccacc 480

gcgggcctcc tcggctttcg aggggcggtg ctttacagca ctgcgaaagg aggagtgaac 540

cagctcacga ggagcctggc tgctgagtgg gcctgtgaca agattcgtgt caactcggtc 600

gcgccaggaa tcgtcatgac tgacatggtt aagaacgcag caagctcgga ggccgtcgag 660

caagaaactt cacggattcc gctgcggcgg gccggcgagc cggcagaggt ggcgtccgtg 720

gtgtcgtttc tgtgcatg 738

<210> 386

<211> 246

<212> PRT

<213> Z.mays

<400> 386

Met Ala Ala Ala Glu Arg Asp Arg Glu Arg Trp Ile Leu Pro Gly Ala

1 5 10 15

Thr Ala Leu Val Thr Gly Gly Ser Lys Gly Ile Gly His Ala Ile Val

20 25 30

Glu Glu Leu Ala Ala Leu Gly Ala Arg Val His Thr Cys Ser Arg Asn

35 40 45

Ala Ala Glu Leu Glu Glu Cys Arg Arg Arg Trp Ala Glu Lys Gly Gly

50 55 60

Gly Leu Leu Gln Gln Val Thr Val Ser Val Cys Asp Val Ala Val Arg

65 70 75 80

Ala Asp Arg Glu Ala Leu Met Ala Thr Val Arg Asp Val Phe Gly Gly
85 90 95

Lys Leu Asp Ile Leu Val Asn Asn Ala Ala Gln Val Val Phe Lys Pro
100 105 110

Ala Val Glu Cys Thr Gly Glu Glu Tyr Thr Arg Ile Met Ala Thr Asn
115 120 125

Leu Glu Ser Cys Phe His Leu Ser Gln Leu Ala His Pro Leu Leu Arg
130 135 140

Asp Ala Ser Leu Ala Gly Gly Gly Ser Val Val His Ile Ser Ser Thr
145 150 155 160

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

Gly Gly Val Asn Gln Leu Thr Arg Ser Leu Ala Ala Glu Trp Ala Cys
180 185 190

Asp Lys Ile Arg Val Asn Ser Val Ala Pro Gly Ile Val Met Thr Asp
195 200 205

Met Val Lys Asn Ala Ala Ser Ser Glu Ala Val Glu Gln Glu Thr Ser
210 215 220

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

Val Ser Phe Leu Cys Met
245

<210> 387
<211> 774
<212> DNA
<213> Z.mays

<400> 387
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gtcaccggcg gcagcaaggg cattgggcac gcgatcgctg aggagctcgc cgggttcggc 120
gcccgggtgc acacgtgctc gcgcaacgcg gcggagctgg aggagtgcg gcggagatgg 180
gacgagaagg ggctgcaggt gaccgtgtcc gcctgcgacg tgcgggcgcg cgccgaccgc 240
gagcgctctg tggccaccgt gggggccacc ttcggcggca ggctcgatat cctcgtgaac 300
aacgcggggc agtcctgtt caagcggacg gccgagtga cgggcgagga ctactcccg 360
atcatggcga ccaacctgga gtcgtgcttc cacctcagcc agctcgcgca cccgctcctc 420
cgcctcgcca gcggcggcgg gggcggcagc gtcgtgcacg tctcctccgt cgctggcttc 480
gtcgggctcc cggcgctcgc cgtctactcc atgtccaagg gcgccctgaa ccagctcacg 540
cgcagcctcg ccgccgagtg ggccggcgac ggcacccgcg tcaactgcgt cgcgcggggg 600
ggcatcagaa ccgacatcag cagcgataag acgatagacc cagagctggc gaagagggag 660
atggcgcggg tgcccatggg gaggatcggc gagccggagg aggtggcgtc catggtggcc 720
ttcctctgca tgccggcggc gtctacatg accggccaag tcctctgcat cgat 774

<210> 388
<211> 258
<212> PRT
<213> Z.mays

<400> 388

Met Val Ala Ala Gly Arg Asn Arg Ala Glu Arg Trp Asn Leu Ala Gly
1 5 10 15

Ala Thr Ala Leu Val Thr Gly Gly Ser Lys Gly Ile Gly His Ala Ile
20 25 30

Val Glu Glu Leu Ala Gly Phe Gly Ala Arg Val His Thr Cys Ser Arg
35 40 45

Asn Ala Ala Glu Leu Glu Glu Cys Arg Arg Arg Trp Asp Glu Lys Gly
50 55 60

Leu Gln Val Thr Val Ser Ala Cys Asp Val Ser Ala Arg Ala Asp Arg
65 70 75 80

Glu Arg Leu Val Ala Thr Val Gly Ala Thr Phe Gly Gly Arg Leu Asp
85 90 95

Ile Leu Val Asn Asn Ala Gly Gln Ser Leu Phe Lys Arg Thr Ala Glu
100 105 110

Cys Thr Gly Glu Asp Tyr Ser Arg Ile Met Ala Thr Asn Leu Glu Ser
115 120 125

Cys Phe His Leu Ser Gln Leu Ala His Pro Leu Leu Arg Leu Ala Ser
130 135 140

Gly Gly Gly Gly Gly Ser Val Val His Val Ser Ser Val Ala Gly Phe
145 150 155 160

Val Gly Leu Pro Ala Leu Ala Val Tyr Ser Met Ser Lys Gly Ala Leu
165 170 175

Asn Gln Leu Thr Arg Ser Leu Ala Ala Glu Trp Ala Gly Asp Gly Ile
180 185 190

Arg Val Asn Cys Val Ala Pro Gly Gly Ile Arg Thr Asp Ile Ser Ser
195 200 205

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

Pro Met Gly Arg Ile Gly Glu Pro Glu Glu Val Ala Ser Met Val Ala
225 230 235 240

Phe Leu Cys Met Pro Ala Ala Ser Tyr Met Thr Gly Gln Val Ile Cys
245 250 255

Ile Asp

<210> 389
<211> 963
<212> DNA
<213> Z.mays

<400> 389
atggccaccg ccgccgccac cgcagcagca gcagcagtct cctccccggc tgcgcgtgga 60
gcagccgggg ccgccgccgc ctcccgccgg gggttcgtca cgtttggtgg aggcgccgcc 120
cgcttctctc ccacgctgcg gtccggccgt gggttctctg gtgtgcaaac ccatgttgct 180
gctgttgaac aagcagttgt aaaagatgct accaagctgg aagctccagt tgttgttggt 240
acaggtgcat ctagagggat tggttaaggca actgctctag cccttggaag agcaggatgc 300

aaggttctgg taaactatgc ccggtcctcg aaagaggctg aagaggtctc caaagagatt	360
gaagcatctg gtggtgaggc tatcaccttc ggaggagatg tttcaaaaga agctgatgta	420
gagtctatga tgaaagcagc tctagataaa tggggaacaa tagatgtgct ggtaaataat	480
gcaggtttag ggattacacg agacacattg ttgatgagga tgaagaaatc tcagtggcaa	540
gacgtaattg atctgaatct tactggcgtc ttcctttgta cacaggctgc aacaaaagta	600
atgatgaaaa agagaaaggg aaaaattatc aacattgcat ctgtagttgg tcttactggc	660
aatgttggcc aagctaatta tagcgcagcc aaggctggag tgattggttt cacaaaaaca	720
gttgccaggg agtatgcaag cagaaatatc aatgtcaatg ctattgcacc agggttcatt	780
gcatctgata tgactgccga acttgagaa gagcttgaga agaaaatctt gtcaaccatt	840
ccgttaggta gatatggcca accagaggaa gttgcagggg tggtcgagtt cctggccctt	900
aacccgcag ctagctatat gactggacag gtgcttaca ttgacggagg gatggtaatg	960
taa	963

<210> 390
 <211> 318
 <212> PRT
 <213> Z.mays

<400> 390

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

Ala	Ala	Arg	Gly	Ala	Ala	Gly	Ala	Ala	Ala	Ala	Ser	Arg	Arg	Gly	Phe
			20				25					30			

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

Gly Arg Gly Phe Ser Gly Val Gln Thr His Val Ala Ala Val Glu Gln
50 55 60

Ala Val Val Lys Asp Ala Thr Lys Leu Glu Ala Pro Val Val Val Val
65 70 75 80

Thr Gly Ala Ser Arg Gly Ile Gly Lys Ala Thr Ala Leu Ala Leu Gly
85 90 95

Lys Ala Gly Cys Lys Val Leu Val Asn Tyr Ala Arg Ser Ser Lys Glu
100 105 110

Ala Glu Glu Val Ser Lys Glu Ile Glu Ala Ser Gly Gly Glu Ala Ile
115 120 125

Thr Phe Gly Gly Asp Val Ser Lys Glu Ala Asp Val Glu Ser Met Met
130 135 140

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

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

Trp Gln Asp Val Ile Asp Leu Asn Leu Thr Gly Val Phe Leu Cys Thr
180 185 190

Gln Ala Ala Thr Lys Val Met Met Lys Lys Arg Lys Gly Lys Ile Ile
195 200 205

Asn Ile Ala Ser Val Val Gly Leu Thr Gly Asn Val Gly Gln Ala Asn
210 215 220

Tyr Ser Ala Ala Lys Ala Gly Val Ile Gly Phe Thr Lys Thr Val Ala
225 230 235 240

Arg Glu Tyr Ala Ser Arg Asn Ile Asn Val Asn Ala Ile Ala Pro Gly
245 250 255

Phe Ile Ala Ser Asp Met Thr Ala Glu Leu Gly Glu Glu Leu Glu Lys
260 265 270

Lys Ile Leu Ser Thr Ile Pro Leu Gly Arg Tyr Gly Gln Pro Glu Glu
275 280 285

Val Ala Gly Leu Val Glu Phe Leu Ala Leu Asn Pro Ala Ala Ser Tyr
290 295 300

Met Thr Gly Gln Val Leu Thr Ile Asp Gly Gly Met Val Met
305 310 315

<210> 391
<211> 762
<212> DNA
<213> Z.mays

<400> 391
atggatgtca agtgccggcg tctggagggg aaggtggcca tcgtgacggc gtccacgatg 60
gggatcggcc tcgccatcgc cgagcgcctc ggtctggagg gcgccgccgt ggatcatctcc 120
tcccgaagc agaagaacgt taacgaggcg gtggaggggc tcagggccaa gggatatcacc 180
gcggttggtg ccgtctgcc cgtctccgac gcacagcagc gcaagagcct catcgagacg 240

gccgtcaaga gctttgggca catagatatc cttgtctcca atgctgccgc aaatccttct 300
 gtagatagca tacttgaaat gaaagagtct gttctcgata agctgtggga tattaacgtc 360
 aaggcttcta tccttcttat tcaggatgct gctcctcacc tacggaagg gtcattctgtg 420
 attattattt cttcaattgc tggttacaat ccagaacaag gattgacaat gtatgggtgc 480
 acaaagactg ctctctttgg tctcacgaag gctcttgctg gtgagatggg acccgatact 540
 cgtgttaact gtgtagcccc tggttttggt cctacacggt ttgctagttt cctcacagaa 600
 aatgagacca ttaggaaaga gcttaacgag aggaccaagc ttaagagatt ggggtactgtg 660
 gaagacatgg ctgcggctgc ggcttttctg gcgtctgacg acgcatcata cattacggct 720
 gaaaccattg ttgttgctgg aggggtgcag tctaggctgt ga 762

<210> 392
 <211> 253
 <212> PRT
 <213> Z.mays

<400> 392

Met Asp Val Lys Cys Arg Arg Leu Glu Gly Lys Val Ala Ile Val Thr
 1 5 10 15

Ala Ser Thr Met Gly Ile Gly Leu Ala Ile Ala Glu Arg Leu Gly Leu
 20 25 30

Glu Gly Ala Ala Val Val Ile Ser Ser Arg Lys Gln Lys Asn Val Asn
 35 40 45

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

Val Cys His Val Ser Asp Ala Gln Gln Arg Lys Ser Leu Ile Glu Thr
65 70 75 80

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

Ala Asn Pro Ser Val Asp Ser Ile Leu Glu Met Lys Glu Ser Val Leu
100 105 110

Asp Lys Leu Trp Asp Ile Asn Val Lys Ala Ser Ile Leu Leu Ile Gln
115 120 125

Asp Ala Ala Pro His Leu Arg Lys Gly Ser Ser Val Ile Ile Ile Ser
130 135 140

Ser Ile Ala Gly Tyr Asn Pro Glu Gln Gly Leu Thr Met Tyr Gly Val
145 150 155 160

Thr Lys Thr Ala Leu Phe Gly Leu Thr Lys Ala Leu Ala Gly Glu Met
165 170 175

Gly Pro Asp Thr Arg Val Asn Cys Val Ala Pro Gly Phe Val Pro Thr
180 185 190

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

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

Ala Ala Ala Ala Phe Leu Ala Ser Asp Asp Ala Ser Tyr Ile Thr Ala
225 230 235 240

Glu Thr Ile Val Val Ala Gly Gly Val Gln Ser Arg Leu
245 250

<210> 393
<211> 822
<212> DNA
<213> Z.mays

<400> 393
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ggcaagacag ccctcgtcac cggcggcacc cgcggcacgc ggcgtgcggt agtggaggag 120
ctggcggcgc tgggggcggc cgtgcacaca tgctcccga aggcggagga gctcggcgag 180
cgcatcaagg agtgggaggc caggggattc agcggtaccg ggtccgtctg cgacctctcc 240
gagagggacc agcgggagcg gttgctccgc gaggttgccg accgcttcgg cggcaagctc 300
aacatcctcg taaacaatgt aggaacaaac ataaggaaac caactactga gtttactgca 360
gaggaatact cgtttctgat ggctactaat cttgaatctg catatcactt gtgccaaatt 420
gcacatcctc ttttgaaatt atctgggtca ggcagcatta tattcatatc atctgttgc 480
ggagcgatag gaatctttag tggaactata tatgctatga ctaaagggtgc cattaaccag 540
ctaaccaaga atttagcttg tgaatgggct aaggacaaca taagagcaa ctctgtcgct 600
ccgtggtaca tcaccacttc acttacggaa ggaattttgg caaataagaa ctttgaggaa 660
caagttgtga gtcgaactcc gcttggacgt gtcggagaac ctggagaagt atcggcactt 720
gttgcttttc tttgcatgcc gggttccact tatattagcg gccagacgat tgcggtcgac 780
ggaggtatga ctgtgaacgg gttttaccct cccaagccct ag 822

<210> 394

<211> 273
<212> PRT
<213> Z.mays

<400> 394

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

Trp Ala Leu His Gly Lys Thr Ala Leu Val Thr Gly Gly Thr Arg Gly
20 25 30

Ile Gly Arg Ala Val Val Glu Glu Leu Ala Ala Leu Gly Ala Ala Val
35 40 45

His Thr Cys Ser Arg Lys Ala Glu Glu Leu Gly Glu Arg Ile Lys Glu
50 55 60

Trp Glu Ala Arg Gly Phe Ser Val Thr Gly Ser Val Cys Asp Leu Ser
65 70 75 80

Glu Arg Asp Gln Arg Glu Arg Leu Leu Arg Glu Val Ala Asp Arg Phe
85 90 95

Gly Gly Lys Leu Asn Ile Leu Val Asn Asn Val Gly Thr Asn Ile Arg
100 105 110

Lys Pro Thr Thr Glu Phe Thr Ala Glu Glu Tyr Ser Phe Leu Met Ala
115 120 125

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

Leu Lys Leu Ser Gly Ser Gly Ser Ile Ile Phe Ile Ser Ser Val Ala
145 150 155 160

Gly Ala Ile Gly Ile Phe Ser Gly Thr Ile Tyr Ala Met Thr Lys Gly
165 170 175

Ala Ile Asn Gln Leu Thr Lys Asn Leu Ala Cys Glu Trp Ala Lys Asp
180 185 190

Asn Ile Arg Ala Asn Ser Val Ala Pro Trp Tyr Ile Thr Thr Ser Leu
195 200 205

Thr Glu Gly Ile Leu Ala Asn Lys Asn Phe Glu Glu Gln Val Val Ser
210 215 220

Arg Thr Pro Leu Gly Arg Val Gly Glu Pro Gly Glu Val Ser Ala Leu
225 230 235 240

Val Ala Phe Leu Cys Met Pro Gly Ser Thr Tyr Ile Ser Gly Gln Thr
245 250 255

Ile Ala Val Asp Gly Gly Met Thr Val Asn Gly Phe Tyr Pro Pro Lys
260 265 270

Pro

<210> 395

<211> 762

<212> DNA

<213> Z.mays

<400> 395

atggatgtca aatgccggcg tctggagggg aaggtggccg tcgtgacggc gtccacgcag	60
gggatcggcc tcgccatcgc cgagcgcctc ggcctggagg gcgccgccgt cgtcgtctcc	120
tcccgcaagc agaagaacgt ggacgaggcc gtggaggggc tcaaggccaa ggggatcacc	180
gtggtgggcg ccgtctgcc a cgtatccgac gcacagcaac gcaagaacct cgtcgagacg	240
gccgtcaaga actttgggca cattgatatt cttgtctcca acgctgctgc aaatcctact	300
gtgaatgtca tacttgaaat gaaagagggt gttctcgata agttgtggga tattaacgtc	360
aaggcttcta ttcttcttat tcaggatgct gctccccacc tacgagcaag gtcattctgtg	420
atccttattt cttcaattgc tggttacaat cctgagcacg gattgacaat gtatggtgtt	480
acaaagaccg ctctctttgg tctcaciaag gctcttgctg gtgagatggg acccgatatt	540
cgtgttaact gtatagcccc tggttttgtt ccgacacggt ttgctagttt cttcgtagac	600
aacgagacca ttaggaaaaa gcttaacgag aggactatgc ttaagagatt gggttccgtg	660
gaagatatgg cggcagctgc cgcattcctg gcattctgac atgcatcatt catcacagct	720
gaaaccattg ttgttgctgg aggggtgccg tcgagattgt ag	762

<210> 396
 <211> 253
 <212> PRT
 <213> Z.mays

<400> 396

Met	Asp	Val	Lys	Cys	Arg	Arg	Leu	Glu	Gly	Lys	Val	Ala	Val	Val	Thr
1				5					10					15	

Ala	Ser	Thr	Gln	Gly	Ile	Gly	Leu	Ala	Ile	Ala	Glu	Arg	Leu	Gly	Leu
			20				25					30			

Glu Gly Ala Ala Val Val Val Ser Ser Arg Lys Gln Lys Asn Val Asp
35 40 45

Glu Ala Val Glu Gly Leu Lys Ala Lys Gly Ile Thr Val Val Gly Ala
50 55 60

Val Cys His Val Ser Asp Ala Gln Gln Arg Lys Asn Leu Val Glu Thr
65 70 75 80

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

Ala Asn Pro Thr Val Asn Val Ile Leu Glu Met Lys Glu Val Val Leu
100 105 110

Asp Lys Leu Trp Asp Ile Asn Val Lys Ala Ser Ile Leu Leu Ile Gln
115 120 125

Asp Ala Ala Pro His Leu Arg Ala Arg Ser Ser Val Ile Leu Ile Ser
130 135 140

Ser Ile Ala Gly Tyr Asn Pro Glu His Gly Leu Thr Met Tyr Gly Val
145 150 155 160

Thr Lys Thr Ala Leu Phe Gly Leu Thr Lys Ala Leu Ala Gly Glu Met
165 170 175

Gly Pro Asp Ile Arg Val Asn Cys Ile Ala Pro Gly Phe Val Pro Thr
180 185 190

Arg Phe Ala Ser Phe Phe Val Asp Asn Glu Thr Ile Arg Lys Lys Leu
195 200 205

Asn Glu Arg Thr Met Leu Lys Arg Leu Gly Ser Val Glu Asp Met Ala
 210 215 220

Ala Ala Ala Ala Phe Leu Ala Ser Asp Asp Ala Ser Phe Ile Thr Ala
 225 230 235 240

Glu Thr Ile Val Val Ala Gly Gly Val Pro Ser Arg Leu
 245 250

<210> 397
 <211> 1089
 <212> DNA
 <213> Synechocystis PCC6803

<400> 397
 atggttctag catcttcccg tcccccttcc cccaccaatt ccccggcga tcgccagggg 60
 actttgcaag cctgggtaac aggtctcagt cagcgcatta ttgacggcga tcgcctaacc 120
 cggaagaag cttacagtt ggcggcgatc gagggggaag agaatttct tttgctctgt 180
 gaagcagcca atcgattcg ggaagcctgc tgtggcaatg tggtaggatc gtgtagcatc 240
 atcaatgta aatccggtaa ctgctcgga aactgcggct tttgctcca gtctagtcac 300
 catcccgacc ccaattcccc catttacggt ctgaaaacgg aagcagaaat tttagaacag 360
 gccagggcgg cagcggcggc gggagctaaa cgcttttgct tagttagtca gggtcggggc 420
 cccaaatacc atagcccaa ggatcgagaa tttgagcaga tcctggccac agtgcgggca 480
 attatccagg aaaccaacat caagccctgt tgcgcgttgg gggaagtgc cccggaacag 540
 gccagcaat tgaaggaagc tggggtgact cggtataacc ataacttga agcatccgct 600
 acctattacg acaaaattgt cagcaccac acctggcaag accgggtaga tacggtgaaa 660

aaccttaagg cagcgggcat tcaagcttgc actggcggca ttttaggcat gggagaaacc 720
 tgggaagacc gcattgatct agctttggct ctgcgggaac tggaagtgga atccgtgccc 780
 ctgaatctac tcaatccccg ccccggtact cctttggggg aacaacaaaa gttaaattccc 840
 tacgatgccc tcaaggcgat cgccattttc cggtttattt tgccccaaca aattattcgc 900
 tatgctgggg gccgggaagc ggtgatggga gaattacagg atttagggct aaaagcgggc 960
 attaacgcta tgctagtggg ccattattta actaccctgg gccagcctcc cgaacgggat 1020
 caaaaattat tggcatccct tggcctcgaa gggggagagg cccctatccc cgggtgaatac 1080
 caatcctga 1089

<210> 398
 <211> 362
 <212> PRT
 <213> Synechocystis PCC6803

<400> 398

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

Asp Arg Gln Gly Thr Leu Gln Ala Trp Leu Thr Gly Leu Ser Gln Arg
 20 25 30

Ile Ile Asp Gly Asp Arg Leu Thr Arg Glu Glu Ala Leu Gln Leu Ala
 35 40 45

Ala Ile Glu Gly Glu Glu Asn Ile Leu Leu Leu Cys Glu Ala Ala Asn
 50 55 60

Arg Ile Arg Glu Ala Cys Cys Gly Asn Val Val Asp Leu Cys Ser Ile
 65 70 75 80

Ile Asn Val Lys Ser Gly Asn Cys Ser Glu Asn Cys Gly Phe Cys Ser
85 90 95

Gln Ser Ser His His Pro Asp Pro Asn Ser Pro Ile Tyr Gly Leu Lys
100 105 110

Thr Glu Ala Glu Ile Leu Glu Gln Ala Arg Ala Ala Ala Ala Gly
115 120 125

Ala Lys Arg Phe Cys Leu Val Ser Gln Gly Arg Gly Pro Lys Tyr His
130 135 140

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

Ile Ile Gln Glu Thr Asn Ile Lys Pro Cys Cys Ala Leu Gly Glu Val
165 170 175

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

Asn His Asn Leu Glu Ala Ser Ala Thr Tyr Tyr Asp Lys Ile Val Ser
195 200 205

Thr His Thr Trp Gln Asp Arg Val Asp Thr Val Lys Asn Leu Lys Ala
210 215 220

Ala Gly Ile Gln Ala Cys Thr Gly Gly Ile Leu Gly Met Gly Glu Thr
225 230 235 240

Trp Glu Asp Arg Ile Asp Leu Ala Leu Ala Leu Arg Glu Leu Glu Val
245 250 255

Glu Ser Val Pro Leu Asn Leu Leu Asn Pro Arg Pro Gly Thr Pro Leu
260 265 270

Gly Glu Gln Gln Lys Leu Asn Pro Tyr Asp Ala Leu Lys Ala Ile Ala
275 280 285

Ile Phe Arg Phe Ile Leu Pro Gln Gln Ile Ile Arg Tyr Ala Gly Gly
290 295 300

Arg Glu Ala Val Met Gly Glu Leu Gln Asp Leu Gly Leu Lys Ala Gly
305 310 315 320

Ile Asn Ala Met Leu Val Gly His Tyr Leu Thr Thr Leu Gly Gln Pro
325 330 335

Pro Glu Arg Asp Gln Lys Leu Leu Ala Ser Leu Gly Leu Glu Gly Gly
340 345 350

Glu Ala Pro Ile Pro Gly Glu Tyr Gln Ser
355 360

<210> 399

<211> 915

<212> DNA

<213> B.napus

<400> 399

atgatgcttg ctcgattcgt atttcgatct cagctcagac cttctctctc cgccccgacaa 60

tctgcttctt actcctctgc ttccgcagcc tcagctgaag ccgaaagaac gatccgtgaa 120

gggccgagaa atgactggag caaagatgaa atcaaagccg tctatgactc tcccgttctt	180
gacctcctct tccatggagc acaggttcat aggcattgtc ataacttcag ggaagtgcag	240
caatgtactc tcctctccat aaagactgga ggggtgcagtg aggactgttc ttattgtcct	300
cagtcctcca gatatgacac tggagtcaag gcccaaagac tcatgtccaa ggacgctgtc	360
attgttgctg ctaagaaggc aaaagaagct ggaagcacac gggtttgcat ggggtgctgcg	420
tggagagata caataggacg gaaaacaaat ttcaaccaga tacttgacta catcaaagaa	480
ataagaggca tggggatgga gggttgctgc acattgggca tgattgagaa gcagcaagcg	540
ttagagctaa agaaggccgg actcactgct tataaccaca atcttgatac atcaagagag	600
tactacccaa acgtcatcac tacgagaagt tatgacgacg gacttgaaac tcttgagcat	660
gttcgtgaag ctggaatcaa tgtctgttca ggaggaatca tagggcttgg agaggcagag	720
gaggacagag taggtttatt acacacattg gcaacacttc cttctcaccg tgagagtgtt	780
cccatcaacg ctctgctagc agtgaaaggc actcctcttg aagaccagaa gccggttgag	840
atatgggaga tgatcaggat gattgcaaca gcaaggatcg tgatgccaaa agcaatgggtg	900
aggctatctg cttag	915

<210> 400
 <211> 304
 <212> PRT
 <213> B.napus

<400> 400

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

Ser	Ala	Arg	Gln	Ser	Ala	Ser	Tyr	Ser	Ser	Ala	Ser	Ala	Ala	Ser	Ala
			20					25					30		

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

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

His Gly Ala Gln Val His Arg His Val His Asn Phe Arg Glu Val Gln
65 70 75 80

Gln Cys Thr Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys
85 90 95

Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Asp Thr Gly Val Lys Ala Gln
100 105 110

Arg Leu Met Ser Lys Asp Ala Val Ile Val Ala Ala Lys Lys Ala Lys
115 120 125

Glu Ala Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Asp Thr
130 135 140

Ile Gly Arg Lys Thr Asn Phe Asn Gln Ile Leu Asp Tyr Ile Lys Glu
145 150 155 160

Ile Arg Gly Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu
165 170 175

Lys Gln Gln Ala Leu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn
180 185 190

His Asn Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Val Ile Thr Thr
195 200 205

Arg Ser Tyr Asp Asp Arg Leu Glu Thr Leu Glu His Val Arg Glu Ala
210 215 220

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

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

Pro Glu Ser Val Pro Ile Asn Ala Leu Leu Ala Val Lys Gly Thr Pro
260 265 270

Leu Glu Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile
275 280 285

Ala Thr Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu Ser Ala
290 295 300

<210> 401
<211> 1119
<212> DNA
<213> Z.mays

<400> 401
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aacgactgga gccggcccga gatccaggcc gtctacgact caccgctcct cgacctctc 180
tttcacgggg ctcaggtcca cagaaatgtc cataaattca gagaagtgca gcaatgcaca 240

cttctttcaa tcaagactgg tggatgcagt gaagattggt cttactgtcc tcagtcatca	300
agatacaaca ctggattgaa ggcccaaaaa ttgatgaaca aatatgctgt cttggaagca	360
gcaaaaaagg caaaagagtc tgggagcacc cgtttttgca tgggagctgc atggagagaa	420
accattggca ggaaatcaaa cttcaaccag attcttgaat atgtcaagga aataaggggt	480
atgggcatgg aggtctgttg cacactaggc atgatagaga aacaacaagc tgaagaactc	540
aagaaggctg gacttacagc atataatcat aacctagata catcaagaga gtattatccc	600
aacattatta ccacaagatc atatgatgat agactgcaga ctcttgagca tgtccgtgaa	660
gctggaataa gcatctgctc aggtggaatc attggtcttg gtgaagcaga ggaggaccgg	720
gtagggttgt tgcataccct agctaccttg cctacacacc cagagagcgt tcctattaat	780
gcattggttg ctgtaaaagg cacacctctt gaggaccaga agcctgtaga gatctgggaa	840
atgatccgca tgatcgccac tgctcggatc acgatgcaa aggcaatggg gaggctttca	900
gcaggccgag tacggttctc gatgccagaa caagcgtgtg gcttcctcgc tggggccaac	960
tccatctttg ccggcgagaa acttctcaca accgcaaaca acgactttga tgcggaccag	1020
gcgatgttca agatccttgg cctgatcccc aaggctcaa gctttggcga ggaagaggcg	1080
tctgcggcgg ctcccacaga atccgagagg tctgagtag	1119

<210> 402
 <211> 372
 <212> PRT
 <213> Z.mays

<400> 402

Met	Ala	Leu	Met	Leu	Leu	Ala	Arg	Asn	Leu	Arg	Ser	Arg	Leu	Arg	Pro
1			5					10					15		

Pro Leu Ala Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu
20 25 30

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

Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
50 55 60

Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr
65 70 75 80

Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys
85 90 95

Pro Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met
100 105 110

Asn Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly
115 120 125

Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg
130 135 140

Lys Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly
145 150 155 160

Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu Lys Gln Gln
165 170 175

Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu
180 185 190

Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Ser Tyr
195 200 205

Asp Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser
210 215 220

Ile Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg
225 230 235 240

Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser
245 250 255

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

Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr Ala
275 280 285

Arg Ile Thr Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val
290 295 300

Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn
305 310 315 320

Ser Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe
325 330 335

Asp Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala
340 345 350

Pro Ser Phe Gly Glu Glu Glu Ala Ser Ala Ala Ala Pro Thr Glu Ser
355 360 365

Glu Arg Ser Glu
370

<210> 403
<211> 674
<212> DNA
<213> Artificial

<220>
<223> Artificial

<400> 403
caaatttaca cattgccact aaacgtctaa acccttgtaa ttgttttttg ttttactatg 60
tgtgttatgt atttgatttg cgataaattt ttatatattgg tactaaattt ataacacctt 120
ttatgctaac gtttgccaac acttagcaat ttgcaagttg attaattgat tctaaattat 180
ttttgtcttc taaatacata tactaatcaa ctggaaatgt aaatatttgc taatatttct 240
actataggag aattaaagtg agtgaatatg gtaccacaag gtttggagat ttaattgttg 300
caatgctgca tggatggcat atacaccaa cattcaataa ttcttgagga taataatggt 360
accacacaag atttgaggtg catgaacgtc acgtggacaa aaggtttagt aatttttcaa 420
gacaacaatg ttaccacaca caagttttga ggtgcatgca tggatgcct gtggaaagtt 480
taaaaatatt ttggaaatga ttgcatgga agccatgtgt aaaaccatga catccacttg 540
gaggatgcaa taatgaagaa aactacaaat ttacatgcaa ctagttatgc atgtagtcta 600
tataatgagg attttgcaat actttcattc atacacactc actaagtttt acacgattat 660
aatttcttca tagc 674

<210> 404
<211> 695
<212> DNA
<213> Artificial

<220>
<223> Artificial

<400> 404
ctagactgca gcaaatttac acattgccac taaacgtcta aacccttgta atttgttttt 60
gttttactat gtgtgttatg tatttgattt gcgataaatt tttatatattg gtactaaatt 120
tataacacct tttatgctaa cgtttgccaa cacttagcaa tttgcaagtt gattaattga 180
ttctaaatta tttttgtctt ctaaatacat atactaatca actggaaatg taaatatttg 240
ctaataatttc tactatagga gaattaaagt gagtgaatat ggtaccacaa ggtttggaga 300
tttaattgtt gcaatgctgc atggatggca tatacaccaa acattcaata attcttgagg 360
ataataatgg taccacacaa gatttgaggt gcatgaacgt cacgtggaca aaaggtttag 420
taatttttca agacaacaat gttaccacac acaagttttg aggtgcatgc atggatgccc 480
tgtggaaagt ttaaaaatat tttggaaatg atttgcatgg aagccatgtg taaaaccatg 540
acatccactt ggaggatgca ataatgaaga aaactacaaa tttacatgca actagttatg 600
catgtagtct atataatgag gattttgcaa tactttcatt catacacact cactaagttt 660
tacacgatta taatttcttc ataccattaa ttaag 695

<210> 405
<211> 1112
<212> DNA
<213> Artificial

<220>
<223> Artificial

<400> 405

ggatccctga aagcgacgtt ggatgttaac atctacaaat tgccttttct tatcgaccat	60
gtacgtaagc gcttacgttt ttggtggacc cttgaggaaa ctggtagctg ttgtgggcct	120
gtggtctcaa gatggatcat taatttccac cttcacctac gatggggggc atcgcaccgg	180
tgagtaatat tgtacggcta agagcgaatt tggcctgtag gatccctgaa agcgacgttg	240
gatgttaaca tctacaaatt gccttttctt atcgaccatg tacgtaagcg cttacgtttt	300
tggtggaccc ttgaggaaac tggtagctgt tgtgggcctg tgggtctcaag atggatcatt	360
aatttccacc ttcacctacg atggggggca tcgcaccggt gagtaatatt gtacggctaa	420
gagcgaattt ggctgtagg atccctgaaa gcgacgttgg atgttaacat ctacaaattg	480
ccttttctta tcgaccatgt acgtaagcgc ttacgttttt ggtggaccct tgaggaaact	540
ggtagctgtt gtgggcctgt ggtctcaaga tggatcatta atttccacct tcacctacga	600
tggggggcat cgcaccggtg agtaatattg tacggctaag agcgaatttg gcctgtagga	660
tccgcgagct ggtcaatccc attgcttttg aagcagctca acattgatct ctttctcgat	720
cgagggagat ttttcaaata agtgcgcaag acgtgacgta agtatccgag tcagttttta	780
tttttctact aatttggtcg tttatttcgg cgtgtaggac atggcaaccg ggctgaatt	840
tcgcgggtat tctgtttcta ttccaacttt ttcttgatcc gcagccatta acgacttttg	900
aatagatacg ctgacacgcc aagcctcgct agtcaaaagt gtaccaaaca acgctttaca	960
gcaagaacgg aatgcgcgtg acgctcgcgg tgacgccatt tcgccttttc agaaatggat	1020
aaatagcctt gcttcctatt atatcttccc aaattaccaa tacattacac tagcatctga	1080
atttcataac caatctcgat acaccaaata ga	1112

<210> 406

<211> 986

<212> DNA

<213> Artificial

<220>

<223> Artificial

<400> 406

ctagaattcg aatccaaaa ttacggatat gaatataggc atatccgtat ccgaattatc	60
cgtttgacag ctagcaacga ttgtacaatt gcttctttaa aaaaggaaga aagaaagaaa	120
gaaaagaatc aacatcagcg ttaacaaacg gcccggttac ggcccaaacg gtcatataga	180
gtaacggcgt taagcgttga aagactccta tcgaaatacg taaccgcaaa cgtgtcatag	240
tcagatcccc tcttccttca ccgcctcaaa cacaaaaata atcttctaca gcctatatat	300
acaaccccc cttctatctc tcctttctca caattcatca tctttcttct tctaccccca	360
attttaagaa atcctctctt ctctcttca ttttcaaggt aaatctctct ctctctctct	420
ctctctgtta ttcttgttt taattaggta tgtattattg ctagtttggt aatctgctta	480
tcttatgtat gccttatgtg aatatcttta tcttgttcat ctcacccgtt tagaagctat	540
aaatttggtg atttgactgt gtatctacac gtgggttatgt ttatatctaa tcagatatga	600
atttcttcat attggtgcgt ttgtgtgtac caatccgaaa tcgttgattt ttttcattta	660
atcgtgtagc taattgtacg tatacatatg gatctacgta tcaattgttc atctgtttgt	720
gtttgtatgt atacagatct gaaaacatca cttctctcat ctgattgtgt tgttacatac	780
atagatatag atctgttata tcattttttt tattaattgt gtatatatat atgtgcatag	840
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agatctggac tttttggagt tgttgacttg attgtatttg tgtgtgtata tgtgtgttct	960
gatcttgata tgttatgtat gtgcag	986

<210> 407
<211> 102
<212> DNA
<213> Arabidopsis thaliana

<400> 407
atgcagaggt ttttctccgc cagatcgatt ctcggttacg ccgtcaagac gcggaggagg 60

tctttctctt ctcgttcttc gtctctcctt tgctcttcca tg 102

<210> 408
<211> 34
<212> PRT
<213> Arabidopsis thaliana

<400> 408

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

Thr Arg Arg Arg Ser Phe Ser Ser Arg Ser Ser Ser Leu Leu Cys Ser
20 25 30

Ser Met

<210> 409
<211> 102
<212> DNA
<213> Arabidopsis thaliana

<400> 409
atgcagaggt ttttctccgc cagatcgatt ctcggttacg ccgtcaagac gcggaggagg 60

tctttctctt ctcgttcttc ggaattccag ctgaccacca tg 102

<210> 410

<211> 34
<212> PRT
<213> Arabidopsis thaliana

<400> 410

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

Thr Arg Arg Arg Ser Phe Ser Ser Arg Ser Ser Glu Phe Gln Leu Thr
20 25 30

Thr Met

<210> 411
<211> 419
<212> DNA
<213> Spinacia oleracea

<400> 411
gcataaactt atcttcatag ttgccactcc aatttgctcc ttgaatctcc tccacccaat 60
acataatcca ctctccatc acccacttca ctactaaatc aaacttaact ctgtttttct 120
ctctcctcct ttcatttctt attcttccaa tcatcgtact cgcgatgac caccgctgtc 180
accgcccgtg tttctttccc ctctaccaa accacctctc tctccgcccg aagctcctcc 240
gtcatttccc ctgacaaaat cagctacaaa aaggtgattc ccaatttcac tgtgtttttt 300
attaataatt tggtattttg atgatgagat gattaatttg ggtgctgcag gttcctttgt 360
actacaggaa tgtatctgca actgggaaaa tgggacccat cagggccag atcgccctct 419

<210> 412
<211> 59
<212> PRT

<213> Spinacia oleracea

<400> 412

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

Thr Ser Leu Ser Ala Arg Ser Ser Ser Val Ile Ser Pro Asp Lys Ile
20 25 30

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

Lys Met Gly Pro Ile Arg Ala Gln Ile Ala Ser
50 55

<210> 413

<211> 900

<212> DNA

<213> Escherichia coli

<400> 413

atggactttc cgcagcaact cgaagcctgc gttaagcagg ccaaccaggc gctgagccgt 60

tttatcgccc cactgccctt tcagaacact cccgtggctg aaaccatgca gtatggcgca 120

ttattaggtg gtaagcgcct gcgaccttc ctggtttatg ccaccggtca tatgttcggc 180

gtagcacaa acacgctgga cgcacccgct gccgccgttg agtgtatcca cgcttactca 240

ttaattcatg atgatttacc ggcaatggat gatgacgata tgcgtcgcgg ttgccaacc 300

tgccatgtga agtttggcga agcaaacgcg attctcgctg gcgacgcttt acaaacgctg 360

gcgttctcga ttttaagcga tgccgatatg ccggaagtgt cggaccgcga cagaatttcg 420

atgatttctg aactggcgag cgccagtggg attgccggaa tgtgcggtgg tcaggcatta 480

gatttagacg cggaaggcaa acacgtacct ctggacgcgc ttgagcgtat tcatcgtcat 540

aaaaccggcg cattgattcg cgccgccgtt cgccttggtg cattaagcgc cggagataaa 600

ggacgtcgtg ctctgccggt actcgacaag tatgcagaga gcatcggcct tgccttccag 660

gttcaggatg acatcctgga tgtggtggga gatactgcaa cgttgggaaa acgccagggt 720

gccgaccagc aacttggtaa aagtacctac cctgcacttc tgggtcttga gcaagcccgg 780

aagaaagccc gggatctgat cgacgatgcc cgtcagtcgc tgaaacaact ggctgaacag 840

tcactcgata cctcggcact ggaagcgcta gcggactaca tcatccagcg taataaataa 900

<210> 414

<211> 299

<212> PRT

<213> Escherichia coli

<400> 414

Met Asp Phe Pro Gln Gln Leu Glu Ala Cys Val Lys Gln Ala Asn Gln

1 5 10 15

Ala Leu Ser Arg Phe Ile Ala Pro Leu Pro Phe Gln Asn Thr Pro Val

20 25 30

Val Glu Thr Met Gln Tyr Gly Ala Leu Leu Gly Gly Lys Arg Leu Arg

35 40 45

Pro Phe Leu Val Tyr Ala Thr Gly His Met Phe Gly Val Ser Thr Asn

50 55 60

Thr Leu Asp Ala Pro Ala Ala Ala Val Glu Cys Ile His Ala Tyr Ser

65 70 75 80

Leu Ile His Asp Asp Leu Pro Ala Met Asp Asp Asp Asp Leu Arg Arg
85 90 95

Gly Leu Pro Thr Cys His Val Lys Phe Gly Glu Ala Asn Ala Ile Leu
100 105 110

Ala Gly Asp Ala Leu Gln Thr Leu Ala Phe Ser Ile Leu Ser Asp Ala
115 120 125

Asp Met Pro Glu Val Ser Asp Arg Asp Arg Ile Ser Met Ile Ser Glu
130 135 140

Leu Ala Ser Ala Ser Gly Ile Ala Gly Met Cys Gly Gly Gln Ala Leu
145 150 155 160

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

Ile His Arg His Lys Thr Gly Ala Leu Ile Arg Ala Ala Val Arg Leu
180 185 190

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

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

Ile Leu Asp Val Val Gly Asp Thr Ala Thr Leu Gly Lys Arg Gln Gly
225 230 235 240

Ala Asp Gln Gln Leu Gly Lys Ser Thr Tyr Pro Ala Leu Leu Gly Leu
245 250 255

Glu Gln Ala Arg Lys Lys Ala Arg Asp Leu Ile Asp Asp Ala Arg Gln
260 265 270

Ser Leu Lys Gln Leu Ala Glu Gln Ser Leu Asp Thr Ser Ala Leu Glu
275 280 285

Ala Leu Ala Asp Tyr Ile Ile Gln Arg Asn Lys
290 295

<210> 415
<211> 1059
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 415
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gaggaattga acgcatcgct tttggcttac ggtatgccta aggaagcatg tgactggtat 120
gccactcat tgaactacaa cactccaggc ggtaagctaa atagagggtt gtccgttgtg 180
gacacgtatg ctattctctc caacaagacc gttgaacaat tggggcaaga agaatacgaa 240
aaggttgcca ttctaggttg gtgcattgag ttgttgcagg cttacttctt ggtcgccgat 300
gatatgatgg acaagtccat taccagaaga ggccaacat gttggtacaa ggttcttgaa 360
gttggggaaa ttgccatcaa tgacgcattc atgttagagg ctgctatcta caagcttttg 420
aaatctcact tcagaaacga aaaatactac atagatatca ccgaattggt ccatgagggtc 480
accttccaaa ccgaattggg ccaattgatg gacttaatca ctgcacctga agacaaagtc 540
gacttgagta agttctccct aaagaagcac tccttcatag ttactttcaa gactgcttac 600
tattctttct acttgctgt cgcatggcc atgtacgttg ccggtatcac ggatgaaaag 660

gatttgaaac aagccagaga tgtcttgatt ccattgggtg aatacttcca aattcaagat 720

gactacttag actgcttcgg taccccagaa cagatcggtg agatcggtac agatatccaa 780

gataacaaat gttcttgggt aatcaacaag gcattggaac ttgcttcgc agaacaaaga 840

aagacttttag acgaaaatta cggtaagaag gactcagtcg cagaagccaa atgcaaaaag 900

attttcaatg acttgaaaat tgaacagcta taccacgaat atgaagagtc tattgccaag 960

gatttgaagg ccaaatttc tcaggtcgat gagtctcgtg gcttcaaagc tgatgtctta 1020

actgcgttct tgaacaaagt ttacaagaga agcaaatag 1059

<210> 416

<211> 352

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 416

Met Ala Ser Glu Lys Glu Ile Arg Arg Glu Arg Phe Leu Asn Val Phe

1 5 10 15

Pro Lys Leu Val Glu Glu Leu Asn Ala Ser Leu Leu Ala Tyr Gly Met

20 25 30

Pro Lys Glu Ala Cys Asp Trp Tyr Ala His Ser Leu Asn Tyr Asn Thr

35 40 45

Pro Gly Gly Lys Leu Asn Arg Gly Leu Ser Val Val Asp Thr Tyr Ala

50 55 60

Ile Leu Ser Asn Lys Thr Val Glu Gln Leu Gly Gln Glu Glu Tyr Glu

65 70 75 80

Lys Val Ala Ile Leu Gly Trp Cys Ile Glu Leu Leu Gln Ala Tyr Phe
85 90 95

Leu Val Ala Asp Asp Met Met Asp Lys Ser Ile Thr Arg Arg Gly Gln
100 105 110

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

Ala Phe Met Leu Glu Ala Ala Ile Tyr Lys Leu Leu Lys Ser His Phe
130 135 140

Arg Asn Glu Lys Tyr Tyr Ile Asp Ile Thr Glu Leu Phe His Glu Val
145 150 155 160

Thr Phe Gln Thr Glu Leu Gly Gln Leu Met Asp Leu Ile Thr Ala Pro
165 170 175

Glu Asp Lys Val Asp Leu Ser Lys Phe Ser Leu Lys Lys His Ser Phe
180 185 190

Ile Val Thr Phe Lys Thr Ala Tyr Tyr Ser Phe Tyr Leu Pro Val Ala
195 200 205

Leu Ala Met Tyr Val Ala Gly Ile Thr Asp Glu Lys Asp Leu Lys Gln
210 215 220

Ala Arg Asp Val Leu Ile Pro Leu Gly Glu Tyr Phe Gln Ile Gln Asp
225 230 235 240

Asp Tyr Leu Asp Cys Phe Gly Thr Pro Glu Gln Ile Gly Lys Ile Gly
245 250 255

Thr Asp Ile Gln Asp Asn Lys Cys Ser Trp Val Ile Asn Lys Ala Leu
260 265 270

Glu Leu Ala Ser Ala Glu Gln Arg Lys Thr Leu Asp Glu Asn Tyr Gly
275 280 285

Lys Lys Asp Ser Val Ala Glu Ala Lys Cys Lys Lys Ile Phe Asn Asp
290 295 300

Leu Lys Ile Glu Gln Leu Tyr His Glu Tyr Glu Glu Ser Ile Ala Lys
305 310 315 320

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

Ala Asp Val Leu Thr Ala Phe Leu Asn Lys Val Tyr Lys Arg Ser Lys
340 345 350

<210> 417
<211> 885
<212> DNA
<213> Brassica napus

<400> 417
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ctccgggagc cgctcaagat ccacgaggcg atgcgctact ccctcctcgc cggcggcaaa 120
cgcgtcaggc ccgtcctctg catcgccgcc tgcgagctcg tcggcgggga agagtcocctc 180
gccatgccgg cggcctgcgc cgtcgagatg atccacacca tgctcgtgat ccacgacgac 240
ttgccgtgca tggacaacga cgacctccgc cgcgggaagc cgacgaacca caaggtttac 300

ggcgaggacg tggcggctct ggccggagac gcgcttctct ccttcgcctt cgagcatttg 360

gcgtcggcga cgagctccga agtttctccg gcgagagtgg tccgagccgt cggagagttg 420

gcgaaagcta taggaaccga agggctggtg gcgggacagg tggcggatat aagcagcgaa 480

ggattagagt taaacgacgt cggattggat catttagagt ttattcattt gcataaaacg 540

gcggcgttgc ttgaggcttc agccgttttg ggcgggatcg tcggtggagg gagcgacgag 600

gagatcgaga ggctgaggaa gttcgcgagg tgtatcggtc tgttgtttca ggtggttgat 660

gatatcctgg acgtgaccaa gtcgtctcag gagctgggga aaaccgccgg gaaagatttg 720

atcgctgata agctgacgta tccgaagctc atggggtttg agaaatcgag agagttcgct 780

gagaagttga atagagaggc gcgtgatcag cttttggggt ttgattccga caaggttgct 840

cctttgttgg ctttggttaa ttacattgcc aatagacaga actga 885

<210> 418

<211> 294

<212> PRT

<213> Brassica napus

<400> 418

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

Ser Ala Val Pro Leu Arg Glu Pro Leu Lys Ile His Glu Ala Met Arg
20 25 30

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

Ala Ala Cys Glu Leu Val Gly Gly Glu Glu Ser Leu Ala Met Pro Ala
50 55 60

Ala Cys Ala Val Glu Met Ile His Thr Met Ser Leu Ile His Asp Asp
65 70 75 80

Leu Pro Cys Met Asp Asn Asp Asp Leu Arg Arg Gly Lys Pro Thr Asn
85 90 95

His Lys Val Tyr Gly Glu Asp Val Ala Val Leu Ala Gly Asp Ala Leu
100 105 110

Leu Ser Phe Ala Phe Glu His Leu Ala Ser Ala Thr Ser Ser Glu Val
115 120 125

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

Gly Thr Glu Gly Leu Val Ala Gly Gln Val Ala Asp Ile Ser Ser Glu
145 150 155 160

Gly Leu Glu Leu Asn Asp Val Gly Leu Asp His Leu Glu Phe Ile His
165 170 175

Leu His Lys Thr Ala Ala Leu Leu Glu Ala Ser Ala Val Leu Gly Gly
180 185 190

Ile Val Gly Gly Gly Ser Asp Glu Glu Ile Glu Arg Leu Arg Lys Phe
195 200 205

Ala Arg Cys Ile Gly Leu Leu Phe Gln Val Val Asp Asp Ile Leu Asp
210 215 220

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

Ile Ala Asp Lys Leu Thr Tyr Pro Lys Leu Met Gly Leu Glu Lys Ser
 245 250 255

Arg Glu Phe Ala Glu Lys Leu Asn Arg Glu Ala Arg Asp Gln Leu Leu
 260 265 270

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

Ile Ala Asn Arg Gln Asn
 290

<210> 419
 <211> 822
 <212> DNA
 <213> B.napus

<400> 419
 atgctattaa gcgcttcagc gactcctctc cgatttggtg ggcattgttc cgagaaaccc 60
 tgtcgtatgc gcatgaaaca agcaattcga tcatcatcgt ccaataactt cgatctgagg 120
 acgtattgga caaccctaataaacggagatc aaccagaagc tggacgaagc gataccagtc 180
 aagtaccctg cagggatcta tgaggcgatg agatactcag tctcgtctaa aggcgcgaag 240
 cgtgcccctc ctgtaatgtg cgtggccgcc tgcgagctct tcggtggcga tcgactcgcc 300
 gctttcccca ccgcatgtgc ccttgaaatg gtccacgcgg cttcgtctgat tcacgatgac 360
 ctcccctgta tggacgatga tctgtgccgc agaggaaagc catctaacca cactgtcttc 420
 ggcgctgaca tggccattct ggctggtgat gccctcttcc cactcggctt ccagcacatt 480

gtctctctca cccctcctca ccttggtccc cgatccacca tcctccgtct catctccgag 540

attgcccgca ccgtcggctc caccggcatg gctgcagggc agtacgttga cctogaagga 600

ggcccccttc ctatttcctt tgctcaggag aagaaattcg gagccatggg ggagtgtca 660

gccgtctgtg gaggtctctt ggggtggtgcc actgacgatg agcttcagag tctcagattg 720

tacggcagag ctgttgggat gctgtatcag gtggtggatg acatcagaga cgacgacaag 780

aagagctatg cgggagtctt tggttcagag agggcaatgg aa 822

<210> 420

<211> 274

<212> PRT

<213> B.napus

<400> 420

Met Leu Leu Ser Ala Ser Ala Thr Pro Leu Arg Phe Gly Gly His Val

1 5 10 15

Pro Glu Lys Pro Cys Arg Met Arg Met Lys Gln Ala Ile Arg Ser Ser

20 25 30

Ser Ser Asn Asn Phe Asp Leu Arg Thr Tyr Trp Thr Thr Leu Ile Thr

35 40 45

Glu Ile Asn Gln Lys Leu Asp Glu Ala Ile Pro Val Lys Tyr Pro Ala

50 55 60

Gly Ile Tyr Glu Ala Met Arg Tyr Ser Val Leu Ala Lys Gly Ala Lys

65 70 75 80

Arg Ala Pro Pro Val Met Cys Val Ala Ala Cys Glu Leu Phe Gly Gly

85 90 95

Asp Arg Leu Ala Ala Phe Pro Thr Ala Cys Ala Leu Glu Met Val His
100 105 110

Ala Ala Ser Leu Ile His Asp Asp Leu Pro Cys Met Asp Asp Asp Pro
115 120 125

Val Arg Arg Gly Lys Pro Ser Asn His Thr Val Phe Gly Ala Asp Met
130 135 140

Ala Ile Leu Ala Gly Asp Ala Leu Phe Pro Leu Gly Phe Gln His Ile
145 150 155 160

Val Ser Leu Thr Pro Pro His Leu Val Pro Arg Ser Thr Ile Leu Arg
165 170 175

Leu Ile Ser Glu Ile Ala Arg Thr Val Gly Ser Thr Gly Met Ala Ala
180 185 190

Gly Gln Tyr Val Asp Leu Glu Gly Gly Pro Phe Pro Ile Ser Phe Ala
195 200 205

Gln Glu Lys Lys Phe Gly Ala Met Gly Glu Cys Ser Ala Val Cys Gly
210 215 220

Gly Leu Leu Gly Gly Ala Thr Asp Asp Glu Leu Gln Ser Leu Arg Leu
225 230 235 240

Tyr Gly Arg Ala Val Gly Met Leu Tyr Gln Val Val Asp Asp Ile Arg
245 250 255

Asp Asp Asp Lys Lys Ser Tyr Ala Gly Val Phe Gly Ser Glu Arg Ala
260 265 270

Met Glu

<210> 421
<211> 1029
<212> DNA
<213> Glycine max

<400> 421
atggcagatc tcaagtccac attcttgaac gtctattctg ttctcaaate tgaactcctc 60
cacgaccctg cttttgagtt ctccgatgat gctcgtaatt gggtcgaccg gatgctggac 120
tacaatgtgc cgggaggaaa gttgaaccgg ggactgtcag taattgatag ctacagattg 180
ttaaaagaag gacaggcatt aaatgatgac gaaatttttc atgccagtgc tcttggttgg 240
tgtattgaat ggcttcaggc atattttctt gttcttgatg acattatgga taactctcac 300
acacgccgtg gtcagccatg ctggttttaga gtgccaagg ttggaatgat tgcagccaat 360
gatggagttc tactaagaaa ccatattcca cgtatcctta aaaagcactt caggggaaag 420
ccatattacg ttgatcttct tgatttggtt aatgagggtg agttccagac tgcttcagga 480
cagatgatag atctgatcac cacactggaa ggagaaaaag acctgtctaa atacacatta 540
aactgcatc gacgtattgt tcagtacaag actgcatatt attcctttta ccttcgggtt 600
gcatgtgcat tgctcatggc gggtgaggat cttgacaaaa atgttgatgt aaagaacatt 660
cttggtgaga tgggaacata ctttcaagta caggatgatt atttggttgg ctttggtgat 720
cctcaaacia ttggaaagat aggtacagat attgaagatt tcaagtgtc ttggttaatt 780
gtgaaagcct tggaacttag taatgaacia caaaagaaag ttctacaaga gaactatggt 840

aagccagatc cagaaaatgt tgctaaagta aaggccctgt acaatgagct taatcttcag	900
gggtgtatttg aggagtacga gagtgggagc tatgcgaagc ttgtatcctc cattgaagct	960
catcctatca aagcagttca agctgtattg aagtcctttt tggctaaaat ttacaaaagg	1020
cagaagtag	1029

<210> 422
 <211> 342
 <212> PRT
 <213> Glycine max

<400> 422

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

Ser	Glu	Leu	Leu	His	Asp	Pro	Ala	Phe	Glu	Phe	Ser	Asp	Asp	Ala	Arg
		20						25					30		

Asn	Trp	Val	Asp	Arg	Met	Leu	Asp	Tyr	Asn	Val	Pro	Gly	Gly	Lys	Leu
		35					40						45		

Asn	Arg	Gly	Leu	Ser	Val	Ile	Asp	Ser	Tyr	Arg	Leu	Leu	Lys	Glu	Gly
	50						55				60				

Gln	Ala	Leu	Asn	Asp	Asp	Glu	Ile	Phe	His	Ala	Ser	Ala	Leu	Gly	Trp
65					70					75				80	

Cys	Ile	Glu	Trp	Leu	Gln	Ala	Tyr	Phe	Leu	Val	Leu	Asp	Asp	Ile	Met
				85					90					95	

Asp	Asn	Ser	His	Thr	Arg	Arg	Gly	Gln	Pro	Cys	Trp	Phe	Arg	Val	Pro
			100					105						110	

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

Ile Pro Arg Ile Leu Lys Lys His Phe Arg Gly Lys Pro Tyr Tyr Val
130 135 140

Asp Leu Leu Asp Leu Phe Asn Glu Val Glu Phe Gln Thr Ala Ser Gly
145 150 155 160

Gln Met Ile Asp Leu Ile Thr Thr Leu Glu Gly Glu Lys Asp Leu Ser
165 170 175

Lys Tyr Thr Leu Thr Leu His Arg Arg Ile Val Gln Tyr Lys Thr Ala
180 185 190

Tyr Tyr Ser Phe Tyr Leu Pro Val Ala Cys Ala Leu Leu Met Ala Gly
195 200 205

Glu Asp Leu Asp Lys Asn Val Asp Val Lys Asn Ile Leu Val Glu Met
210 215 220

Gly Thr Tyr Phe Gln Val Gln Asp Asp Tyr Leu Asp Cys Phe Gly Asp
225 230 235 240

Pro Gln Thr Ile Gly Lys Ile Gly Thr Asp Ile Glu Asp Phe Lys Cys
245 250 255

Ser Trp Leu Ile Val Lys Ala Leu Glu Leu Ser Asn Glu Gln Gln Lys
260 265 270

Lys Val Leu Gln Glu Asn Tyr Gly Lys Pro Asp Pro Glu Asn Val Ala
275 280 285

Lys Val Lys Ala Leu Tyr Asn Glu Leu Asn Leu Gln Gly Val Phe Glu
290 295 300

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

His Pro Ile Lys Ala Val Gln Ala Val Leu Lys Ser Phe Leu Ala Lys
325 330 335

Ile Tyr Lys Arg Gln Lys
340

<210> 423
<211> 741
<212> DNA
<213> G.max

<400> 423
atgtgcatct ctgcacgcga actctctagt ggcagccgcc ttgccgcctt tcccactgcc 60
tgtgcccttg aaatggttca tgcagcttca ttgatacacg atgatcttcc ctgcatggat 120
gactccccct cacgccgtgg tcagccttca aaccatacca tctatggtgt tgacatggca 180
attcttgccg gcgatgcact ctttccccct ggatttcgac acattgtttc aaaaactcca 240
tcagaccttg tgcctgagtc gcacctcctt cgtgtgattg ccgagatagc ccgctctgta 300
ggatccactg gaatggctgc agggcagttc ctggaccttg aaggaggacc caatgcagtt 360
ggatttatac aagaaaaaaa gtttggtgaa atgggggagt cttctgcagt gtgtggagga 420
ttcttggtcg gagctgaaga tgatgagata gagagactga ggaggtatgg gagagctgtt 480

ggggtattgt atgcagttgt ggatgatatt atagaagaga gattgaaagt tgagggagat 540
 ggtgacagga aaaacaaggg taagagttat gcagaggttt atggagttga aaaggcaata 600
 gaaaaagctg aagagctcag agcaaaggct aaagaagaat tggatggatt tgagaagcat 660
 ggggaacggg tctttcctct ctacagtttt gtggattatg cttttgatag aagtttcagt 720
 gttgatgatg ccagtggata a 741

<210> 424
 <211> 222
 <212> PRT
 <213> G.max

<400> 424

Met Val His Ala Ala Ser Leu Ile His Asp Asp Leu Pro Cys Met Asp
 1 5 10 15

Asp Ser Pro Ser Arg Arg Gly Gln Pro Ser Asn His Thr Ile Tyr Gly
 20 25 30

Val Asp Met Ala Ile Leu Ala Gly Asp Ala Leu Phe Pro Leu Gly Phe
 35 40 45

Arg His Ile Val Ser Gln Thr Pro Ser Asp Leu Val Pro Glu Ser His
 50 55 60

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

Met Ala Ala Gly Gln Phe Leu Asp Leu Glu Gly Gly Pro Asn Ala Val
 85 90 95

Gly Phe Ile Gln Glu Lys Lys Phe Gly Glu Met Gly Glu Ser Ser Ala
100 105 110

Val Cys Gly Gly Phe Leu Ala Gly Ala Glu Asp Asp Glu Ile Glu Arg
115 120 125

Leu Arg Arg Tyr Gly Arg Ala Val Gly Val Leu Tyr Ala Val Val Asp
130 135 140

Asp Ile Ile Glu Glu Arg Leu Lys Val Glu Gly Asp Gly Asp Arg Lys
145 150 155 160

Asn Lys Gly Lys Ser Tyr Ala Glu Val Tyr Gly Val Glu Lys Ala Ile
165 170 175

Glu Lys Ala Glu Glu Leu Arg Ala Lys Ala Lys Glu Glu Leu Asp Gly
180 185 190

Phe Glu Lys His Gly Glu Arg Val Phe Pro Leu Tyr Ser Phe Val Asp
195 200 205

Tyr Ala Phe Asp Arg Ser Phe Ser Val Asp Asp Ala Ser Gly
210 215 220

<210> 425
<211> 786
<212> DNA
<213> G.max

<400> 425
atgcggtact cgctcctcgc cggcggcaag cgcgtgaggc cggttttgtg cgtggcggcc 60
tgcgagctcg tcggcggcga ggaggccacg gcgatgcccg ccgcctgcgc catcgagatg 120

atccacacca tgctgctcat ccacgatgac ctcccctgca tggacaacga cgacctccgc	180
cgcggttaagc ccaccaacca caaggtcttc ggcgaggacg tggcggtcct cgccggcgac	240
gcgctcctcg ccttcgcgtt cgagcacgtg gcagcgcca cggagggagt gtcgccgtca	300
cgcgtggttc gagcgattgg ggaattagcg aagtcgatcg gtacggaagg gcttgtggcg	360
ggacaagtgg tggatataga ttcggagggg gtggcgaatg tggggctgga gacgctggaa	420
ttcattcacg tgcacaaaac ggcggcggtt ctggaagctg cggttgtgtt gggggcaata	480
gtgggaggtg ggagcgacga ggaggttgag aaattaagga agttcgctag gtgcattggg	540
ttgttgtttc aggttgtgga cgacattctg gatgttacga agtcgtcgga ggaattgggg	600
aagacggcgg ggaaggattt ggtggctgat aaggttactt atcccaagct attggggata	660
gataagtcaa aggaatttgc tcaagaattg ttaaaggatg ccaaggaaca attgtctggc	720
ttcgatcctc caaaggcggc tcccttgttt gcattaacca attacattgc ttataggcaa	780
aattaa	786

<210> 426
 <211> 261
 <212> PRT
 <213> G.max

<400> 426

Met	Arg	Tyr	Ser	Leu	Leu	Ala	Gly	Gly	Lys	Arg	Val	Arg	Pro	Val	Leu
1				5					10					15	

Cys	Val	Ala	Ala	Cys	Glu	Leu	Val	Gly	Gly	Glu	Glu	Ala	Thr	Ala	Met
				20				25					30		

Pro	Ala	Ala	Cys	Ala	Ile	Glu	Met	Ile	His	Thr	Met	Ser	Leu	Ile	His
				35				40					45		

Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Leu Arg Arg Gly Lys Pro
50 55 60

Thr Asn His Lys Val Phe Gly Glu Asp Val Ala Val Leu Ala Gly Asp
65 70 75 80

Ala Leu Leu Ala Phe Ala Phe Glu His Val Ala Ala Ser Thr Glu Gly
85 90 95

Val Ser Pro Ser Arg Val Val Arg Ala Ile Gly Glu Leu Ala Lys Ser
100 105 110

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

Glu Gly Val Ala Asn Val Gly Leu Glu Thr Leu Glu Phe Ile His Val
130 135 140

His Lys Thr Ala Ala Leu Leu Glu Ala Ala Val Val Leu Gly Ala Ile
145 150 155 160

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

Arg Cys Ile Gly Leu Leu Phe Gln Val Val Asp Asp Ile Leu Asp Val
180 185 190

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

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

Glu Phe Ala Gln Glu Leu Leu Lys Asp Ala Lys Glu Gln Leu Ser Gly
 225 230 235 240

Phe Asp Pro Pro Lys Ala Ala Pro Leu Phe Ala Leu Thr Asn Tyr Ile
 245 250 255

Ala Tyr Arg Gln Asn
 260

<210> 427
 <211> 486
 <212> DNA
 <213> T.aestivum

<400> 427
 atgattcaca ctgcgagttt aatacatgat gatgtcatag atgatatgtgg aatgcgcaga 60
 gggaaagaaa ccattcatca gctgtacgga acacggatag cgggtgcttgc tggcgatttt 120
 atgtttgcac aatcttcttg gtttctcgca aacctagaga acattgaggt tataaagctc 180
 atcagccagg tgatcaagga ctttgctagt ggggagataa agcagcaatc gaccctgttc 240
 gactgcgacg tcaccctgga cgactacctg ctcaagagct actacaagac tgccctccctg 300
 ctcgcttcaa gcacgaggtc cgcggccata ttcagcgggg tgagcacgcg cgtatgcgag 360
 cagatgtacg agtacggcag gaacctgggg ctgtcggttc aggtggtgga cgacatcctc 420
 gacttcacgc agtcggcggc gagctgggca agccggcggg gagcgacctg gccaaagggga 480
 acctga 486

<210> 428

<211> 161
<212> PRT
<213> T.aestivum

<400> 428

Met Ile His Thr Ala Ser Leu Ile His Asp Asp Val Ile Asp Asp Ser
1 5 10 15

Gly Met Arg Arg Gly Lys Glu Thr Ile His Gln Leu Tyr Gly Thr Arg
20 25 30

Ile Ala Val Leu Ala Gly Asp Phe Met Phe Ala Gln Ser Ser Trp Phe
35 40 45

Leu Ala Asn Leu Glu Asn Ile Glu Val Ile Lys Leu Ile Ser Gln Val
50 55 60

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

Asp Cys Asp Val Thr Leu Asp Asp Tyr Leu Leu Lys Ser Tyr Tyr Lys
85 90 95

Thr Ala Ser Leu Leu Ala Ser Ser Thr Arg Ser Ala Ala Ile Phe Ser
100 105 110

Gly Val Ser Thr Ala Val Cys Glu Gln Met Tyr Glu Tyr Gly Arg Asn
115 120 125

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

Ser Ala Ala Ser Trp Ala Ser Arg Arg Gly Ala Thr Trp Pro Arg Gly
 145 150 155 160

Thr

<210> 429
 <211> 606
 <212> DNA
 <213> T.aestivum

<400> 429
 atgtttcttg cctccactct cggttggtgc attgaatggc ttcaagcctt ctctcttgtg 60
 ctcgatgata tcatggacga ctcccacact cgacgtgggc agccttggtg gtttaggggtg 120
 tctcagggtg gcttgattgc tgtaaattgat gggattctcc ttcgcaacca tatttcgaga 180
 atgcttcggc tccactttaa gaagaagcct tactatgccg atctccttga tttattcaac 240
 gaggttgagt tcaagacagc ttctggtcaa atgctggatc ttattacaac ccacgaggga 300
 gaaaaagatc taacgaaata taacattgga gtccaccgcc gaattgttca attcaagaca 360
 gcctactatt cattttatct gccggttgca tgtgcgctgc tactctctgg ggagagtttg 420
 gagaactacg gggctgtaga gaacatactt gtcgagatgg gaacttactt ccaagttcag 480
 gatgattatc tagactgtta tggatgatcct gaatttattg gcaagattgg caccgacatt 540
 gaagattaca agtgctcctg gctaggtgtc caagctcttg agcgggctga tgagagccaa 600
 aagtga 606

<210> 430
 <211> 201
 <212> PRT
 <213> T.aestivum

<400> 430

Met Phe Leu Ala Ser Thr Leu Gly Trp Cys Ile Glu Trp Leu Gln Ala
1 5 10 15

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

Gly Gln Pro Cys Trp Phe Arg Val Ser Gln Val Gly Leu Ile Ala Val
35 40 45

Asn Asp Gly Ile Leu Leu Arg Asn His Ile Ser Arg Met Leu Arg Leu
50 55 60

His Phe Lys Lys Lys Pro Tyr Tyr Ala Asp Leu Leu Asp Leu Phe Asn
65 70 75 80

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

Thr His Glu Gly Glu Lys Asp Leu Thr Lys Tyr Asn Ile Gly Val His
100 105 110

Arg Arg Ile Val Gln Phe Lys Thr Ala Tyr Tyr Ser Phe Tyr Leu Pro
115 120 125

Val Ala Cys Ala Leu Leu Leu Ser Gly Glu Ser Leu Glu Asn Tyr Gly
130 135 140

Ala Val Glu Asn Ile Leu Val Glu Met Gly Thr Tyr Phe Gln Val Gln
145 150 155 160

Asp Asp Tyr Leu Asp Cys Tyr Gly Asp Pro Glu Phe Ile Gly Lys Ile
165 170 175

Gly Thr Asp Ile Glu Asp Tyr Lys Cys Ser Trp Leu Gly Val Gln Ala
180 185 190

Leu Glu Arg Ala Asp Glu Ser Gln Lys
195 200

<210> 431
<211> 738
<212> DNA
<213> Zea mays

<400> 431
atgattcaca ctgcgagttt aatacatgat gatgtcatag atgatatgtgg gatgagaaga 60
gggaaggaaa ctattcacca actatatggt acacgtgtgg ctgtacttgc tggtgatttt 120
atgtttgcac aatcttcttg gtttcttgca aacctagaaa atattgaagt tataaaattg 180
atcagtcagg tcatcaagga ctttgcaagc ggcgagataa aacaagcttc cactcttttt 240
gattgtgaca tcacacttga cgactacctt ctcaagagct actacaagac tgcattcttg 300
attgcagcca gcacaaaatc agcttccata ttcagtggcg tcagcaccac tatttgtgaa 360
aaaatgtatg catatggcag gaatcttggc ctatccttcc aggttgtcga tgacatcctg 420
gatttcaccc agtcagccga acaacttggc aaaccagcag caagtgactt ggcaaagggg 480
aacctgactg ctccagtcatt cttcgctttg caaagtgaac cagagctaag ggagatcatt 540
gattctgagt tcagtgacac ggattcggtta gctactgcaa tagagctcgt tcatagaagt 600
ggtgggatac ggagggcaca tgagcttgca agagagaagg gtgacttggc aatccaaaat 660
ctgcagtgcc ttccaagaag tgacttcaga agtgcccttg agaagatggg ggaatacaat 720

<210> 432

<211> 245

<212> PRT

<213> Zea mays

<400> 432

Met Ile His Thr Ala Ser Leu Ile His Asp Asp Val Ile Asp Asp Ser
1 5 10 15

Gly Met Arg Arg Gly Lys Glu Thr Ile His Gln Leu Tyr Gly Thr Arg
20 25 30

Val Ala Val Leu Ala Gly Asp Phe Met Phe Ala Gln Ser Ser Trp Phe
35 40 45

Leu Ala Asn Leu Glu Asn Ile Glu Val Ile Lys Leu Ile Ser Gln Val
50 55 60

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

Asp Cys Asp Ile Thr Leu Asp Asp Tyr Leu Leu Lys Ser Tyr Tyr Lys
85 90 95

Thr Ala Ser Leu Ile Ala Ala Ser Thr Lys Ser Ala Ser Ile Phe Ser
100 105 110

Gly Val Ser Thr Thr Ile Cys Glu Lys Met Tyr Ala Tyr Gly Arg Asn
115 120 125

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

Ser Ala Glu Gln Leu Gly Lys Pro Ala Ala Ser Asp Leu Ala Lys Gly
145 150 155 160

Asn Leu Thr Ala Pro Val Ile Phe Ala Leu Gln Ser Glu Pro Glu Leu
165 170 175

Arg Glu Ile Ile Asp Ser Glu Phe Ser Asp Thr Asp Ser Leu Ala Thr
180 185 190

Ala Ile Glu Leu Val His Arg Ser Gly Gly Ile Arg Arg Ala His Glu
195 200 205

Leu Ala Arg Glu Lys Gly Asp Leu Ala Ile Gln Asn Leu Gln Cys Leu
210 215 220

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

Leu Glu Arg Ile Glu
245

<210> 433
<211> 1053
<212> DNA
<213> Z.mays

<400> 433
atggcggcgg gcgggaatgg cgccggcggg gacaccaggg cggccttcgc gcggatctac 60
aagacgctca aggaggagct gctcaccgac ccggccttcg agttcaccga ggagtcacgc 120

cagtggatcg accgcatggt tgactacaat gtactcggag gcaagtgtaa ccgtgggctc	180
tctgtggtcg acagctacaa gctgctcaag ggcgctgatg ctctgggcga ggaggaaacg	240
ttccttgctt gcaccctcgg ctggtgcatt gaatggcttc aggccttctt tcttgctt	300
gatgatatca tggatgactc tcacactcgt cgcggccagc cttgctgggt cagggcgcct	360
caggttggct taattgctgc gaatgacggg atcatccttc gcaaccatat ctacaggatc	420
cttcggcgcc actttaaggg caaaccttac tatgctgatc tccttgattt gttcaatgag	480
gttgagttca agacagcttc aggtcagctg ctggacctta tcactacca tgagggagaa	540
aaagatctaa caaagtataa cataacagtt cacggtcgaa ttgttcaata caagacagcc	600
tattattcat tttatctgcc ggttgcatgt gccctgctgc tctctggcga gaatttggac	660
aattatggtg atgtagagaa catccttggt gaaatgggaa catactttca agtccaggat	720
gactatctgg attgttatgg tgatcctgaa tttatcgga agattggaac ggacattgaa	780
gattacaagt gctcatggct agttgtgcaa gcccttgagc gtgctgatga gagccaaaag	840
cgcattctat ttgaaaatta tggcaagaaa gatccagcct gtgtggcaaa agtgaagaac	900
ctctacaaag aacttgacct agaggcggta tttcaggagt acgagaatga gagctacaag	960
aagctgattg cagacattga agcccagcca agcattgcgg ttcagaaagt gctgaaatcc	1020
ttcttgaca agatctacaa gaggcagaag tag	1053

<210> 434
 <211> 350
 <212> PRT
 <213> Z.mays

<400> 434

Met	Ala	Ala	Gly	Gly	Asn	Gly	Ala	Gly	Gly	Asp	Thr	Arg	Ala	Ala	Phe
1				5					10					15	

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

Phe Glu Phe Thr Glu Glu Ser Arg Gln Trp Ile Asp Arg Met Val Asp
35 40 45

Tyr Asn Val Leu Gly Gly Lys Cys Asn Arg Gly Leu Ser Val Val Asp
50 55 60

Ser Tyr Lys Leu Leu Lys Gly Ala Asp Ala Leu Gly Glu Glu Glu Thr
65 70 75 80

Phe Leu Ala Cys Thr Leu Gly Trp Cys Ile Glu Trp Leu Gln Ala Phe
85 90 95

Phe Leu Val Leu Asp Asp Ile Met Asp Asp Ser His Thr Arg Arg Gly
100 105 110

Gln Pro Cys Trp Phe Arg Val Pro Gln Val Gly Leu Ile Ala Ala Asn
115 120 125

Asp Gly Ile Ile Leu Arg Asn His Ile Ser Arg Ile Leu Arg Arg His
130 135 140

Phe Lys Gly Lys Pro Tyr Tyr Ala Asp Leu Leu Asp Leu Phe Asn Glu
145 150 155 160

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

His Glu Gly Glu Lys Asp Leu Thr Lys Tyr Asn Ile Thr Val His Gly
180 185 190

Arg Ile Val Gln Tyr Lys Thr Ala Tyr Tyr Ser Phe Tyr Leu Pro Val
195 200 205

Ala Cys Ala Leu Leu Leu Ser Gly Glu Asn Leu Asp Asn Tyr Gly Asp
210 215 220

Val Glu Asn Ile Leu Val Glu Met Gly Thr Tyr Phe Gln Val Gln Asp
225 230 235 240

Asp Tyr Leu Asp Cys Tyr Gly Asp Pro Glu Phe Ile Gly Lys Ile Gly
245 250 255

Thr Asp Ile Glu Asp Tyr Lys Cys Ser Trp Leu Val Val Gln Ala Leu
260 265 270

Glu Arg Ala Asp Glu Ser Gln Lys Arg Ile Leu Phe Glu Asn Tyr Gly
275 280 285

Lys Lys Asp Pro Ala Cys Val Ala Lys Val Lys Asn Leu Tyr Lys Glu
290 295 300

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

Lys Leu Ile Ala Asp Ile Glu Ala Gln Pro Ser Ile Ala Val Gln Lys
325 330 335

Val Leu Lys Ser Phe Leu His Lys Ile Tyr Lys Arg Gln Lys
340 345 350

<210> 435
<211> 1327
<212> DNA
<213> synthetic

<400> 435
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gtcggcgcta gtaccatccg taagaggttc gagactatct tccaggatgg cgatcactgg 120

ggaaacttcg aagagtctag gggcctggct ccatctgtga aggcagagga cggcttctct 180

ggctctaagg gctactcttt cggcccacag ttcggctttc tcctgtctaa cgctaagacc 240

ggcctttgga agctgttcca ctgctacatt gctgcaggag cttggttgag gaacgctgtg 300

tgcgtgttct acttgggtgct gaggggactc caagcagttg aggatgatct gaccatcccc 360

tacgatctga aggttgagct gctcaggaac ctgcacaaga agatcttcga tagggacttc 420

cacttccttt gcggcaacaa cgactacaag ctgctcaccg gtaagctgtc tttcacctgg 480

ttctctcctt cttgggggtca accagacacc gaagaggtga tcaccgagat caccgagcgt 540

atgggagaag gcatggtcaa gtacctgaac accgagatca tcagtcgcga ggattacaac 600

gagtactgcc acttctctgc tgggttgatg ggtttgggtc tgaccaggat cttctacacc 660

gctggaatgg aacagttcac ccagattac ctgtctaacg caatgggcct cttcctccag 720

aagaccaacg tgatcagga ttacctggag aacatcaacg ctcagcctac ttctaggctg 780

aggtggccaa aagaggtgtg gtcaaagtac gctgataagc ctgaggcttt catggacgag 840

accaactaca agcagggatt gcactgcctg aacgagatgg ttaccgatgc actttcacac 900

gggctggatt gccttcacta catggctgca ctccaggatc agccaaacct gaggttttgc 960

gctaccttcc agatcaccgc actgggtaca cttgcaatgt gctacaacaa cgtcgagggtg 1020

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aggcctagtg ccgtgactat cacctctcag accatgatcc caagcatctg gcgcttcgag	1200
tctaagaggg ggttcacag gatcagcggc taccacctca agtcccctta caggccaatg	1260
ctgatcatga tcgtcctgct cttggtggct atactgttcg gcgtgatggt ctagactaat	1320
cagttag	1327

<210> 436
 <211> 436
 <212> PRT
 <213> synthetic

 <400> 436

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

Phe	Gln	Asp	Gly	Asp	His	Trp	Gly	Asn	Phe	Glu	Glu	Ser	Arg	Gly	Leu
		35					40					45			

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

Ser	Phe	Gly	Pro	Gln	Phe	Gly	Phe	Leu	Leu	Ser	Asn	Ala	Lys	Thr	Gly
65					70					75				80	

Leu	Trp	Lys	Leu	Phe	His	Cys	Tyr	Ile	Ala	Ala	Gly	Ala	Trp	Leu	Arg
				85					90					95	

Asn Ala Val Cys Val Phe Tyr Leu Val Leu Arg Gly Leu Gln Ala Val
100 105 110

Glu Asp Asp Leu Thr Ile Pro Tyr Asp Leu Lys Val Glu Leu Leu Arg
115 120 125

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

Asn Asn Asp Tyr Lys Leu Leu Thr Gly Lys Leu Ser Phe Thr Trp Phe
145 150 155 160

Ser Pro Ser Trp Gly Gln Pro Asp Thr Glu Glu Val Ile Thr Glu Ile
165 170 175

Thr Glu Arg Met Gly Glu Gly Met Val Lys Tyr Leu Asn Thr Glu Ile
180 185 190

Ile Ser Arg Glu Asp Tyr Asn Glu Tyr Cys His Phe Ser Ala Gly Leu
195 200 205

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

Phe Thr Pro Asp Tyr Leu Ser Asn Ala Met Gly Leu Phe Leu Gln Lys
225 230 235 240

Thr Asn Val Ile Arg Asp Tyr Leu Glu Asn Ile Asn Ala Gln Pro Thr
245 250 255

Ser Arg Leu Arg Trp Pro Lys Glu Val Trp Ser Lys Tyr Ala Asp Lys
260 265 270

Pro Glu Ala Phe Met Asp Glu Thr Asn Tyr Lys Gln Gly Leu His Cys
275 280 285

Leu Asn Glu Met Val Thr Asp Ala Leu Ser His Gly Leu Asp Cys Leu
290 295 300

His Tyr Met Ala Ala Leu Gln Asp Gln Pro Asn Leu Arg Phe Cys Ala
305 310 315 320

Thr Phe Gln Ile Thr Ala Leu Gly Thr Leu Ala Met Cys Tyr Asn Asn
325 330 335

Val Glu Val Phe Arg Gly Ser Val Arg Met Arg Arg Gly Leu Thr Ala
340 345 350

Lys Asn Pro Arg Cys Glu Glu His Gly Arg Cys Leu Trp Arg Val Tyr
355 360 365

Asp Ser Pro Ala Asn Cys Cys Gln Asp Gln Asp Arg Pro Ser Ala Val
370 375 380

Thr Ile Thr Ser Gln Thr Met Ile Pro Ser Ile Trp Arg Phe Glu Ser
385 390 395 400

Lys Arg Gly Phe His Arg Ile Ser Gly Tyr His Leu Lys Ser Pro Tyr
405 410 415

Arg Pro Met Leu Ile Met Ile Val Leu Leu Leu Val Ala Ile Leu Phe
420 425 430

Gly Val Met Phe

435

<210> 437

<211> 1327

<212> DNA

<213> synthetic

<400> 437

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ggaaacttcg aagagtctag gggcctggct ccatctgtga aggcagagga cggcttctct	180
ggctctaagg gctactcttt cggcccacag ttcggctttc tcctgtctaa cgctaagacc	240
ggcctttgga agctgttcca ctgctacatt gctgcaggag cttggttgag gaacgctgtg	300
tgcgtgttct acttggtgct gaggggactc gacaccgttg aggatgatct gaccatcccc	360
tacgatctga aggttgagct gctcaggaac ctgcacaaga agatcttcga tagggacttc	420
cacttcctt gcggcaacaa cgactacaag ctgctcaccg gtaagctgtc tttcacctgg	480
ttctctcctt cttgggtca accagacacc gaagaggtga tcaccgagat caccgagcgt	540
atgggagaag gcatggtcaa gtacctgaac accgagatca tcagtcgcga ggattacaac	600
gagtactgcc acttctctgc tgggttggtc ggtttgggtc tgaccaggat cttctacacc	660
gctggaatgg aacagttcac cccagattac ctgtctaacg caatgggcct ctctctccag	720
aagaccaaca ttatcagga ttacctggag gacatcaacg ctcagcctac ttctaggctg	780
ttctggccaa aagaggtgtg gtcaaagtac gctgataagc ctgaggcttt catggacgag	840
accaactaca agcagggatt gcactgcctg aacgagatgg ttaccgatgc actttcacac	900

gggctggatt gccttcacta catggctgca ctccaggatc agccaaacct gaggttttgc 960
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 cacggaaggt gtttgtggag agtgtacgat agccctgcaa actgctgtca ggatcaggat 1140
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 tctaagaggg ggttcacag gatcagcggc taccacctca agtcccctta caggccaatg 1260
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 cagttag 1327

<210> 438
 <211> 436
 <212> PRT
 <213> synthetic

<400> 438

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

Phe Gln Asp Gly Asp His Trp Gly Asn Phe Glu Glu Ser Arg Gly Leu
 35 40 45

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

Ser Phe Gly Pro Gln Phe Gly Phe Leu Leu Ser Asn Ala Lys Thr Gly
 65 70 75 80

Leu Trp Lys Leu Phe His Cys Tyr Ile Ala Ala Gly Ala Trp Leu Arg
85 90 95

Asn Ala Val Cys Val Phe Tyr Leu Val Leu Arg Gly Leu Asp Thr Val
100 105 110

Glu Asp Asp Leu Thr Ile Pro Tyr Asp Leu Lys Val Glu Leu Leu Arg
115 120 125

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

Asn Asn Asp Tyr Lys Leu Leu Thr Gly Lys Leu Ser Phe Thr Trp Phe
145 150 155 160

Ser Pro Ser Trp Gly Gln Pro Asp Thr Glu Glu Val Ile Thr Glu Ile
165 170 175

Thr Glu Arg Met Gly Glu Gly Met Val Lys Tyr Leu Asn Thr Glu Ile
180 185 190

Ile Ser Arg Glu Asp Tyr Asn Glu Tyr Cys His Phe Ser Ala Gly Leu
195 200 205

Val Gly Leu Gly Leu Thr Arg Ile Phe Tyr Thr Ala Gly Met Glu Gln
210 215 220

Phe Thr Pro Asp Tyr Leu Ser Asn Ala Met Gly Leu Phe Leu Gln Lys
225 230 235 240

Thr Asn Ile Ile Arg Asp Tyr Leu Glu Asp Ile Asn Ala Gln Pro Thr
245 250 255

Ser Arg Leu Phe Trp Pro Lys Glu Val Trp Ser Lys Tyr Ala Asp Lys
260 265 270

Pro Glu Ala Phe Met Asp Glu Thr Asn Tyr Lys Gln Gly Leu His Cys
275 280 285

Leu Asn Glu Met Val Thr Asp Ala Leu Ser His Gly Leu Asp Cys Leu
290 295 300

His Tyr Met Ala Ala Leu Gln Asp Gln Pro Asn Leu Arg Phe Cys Ala
305 310 315 320

Thr Phe Gln Ile Thr Ala Leu Gly Thr Leu Ala Met Cys Tyr Asn Asn
325 330 335

Val Glu Val Phe Arg Gly Ser Val Arg Met Arg Arg Gly Leu Thr Ala
340 345 350

Lys Asn Pro Arg Cys Glu Glu His Gly Arg Cys Leu Trp Arg Val Tyr
355 360 365

Asp Ser Pro Ala Asn Cys Cys Gln Asp Gln Asp Arg Pro Ser Ala Val
370 375 380

Thr Ile Thr Ser Gln Thr Met Ile Pro Ser Ile Trp Arg Phe Glu Ser
385 390 395 400

Lys Arg Gly Phe His Arg Ile Ser Gly Tyr His Leu Lys Ser Pro Tyr
405 410 415

Arg Pro Met Leu Ile Met Ile Val Leu Leu Leu Val Ala Ile Leu Phe
420 425 430

Gly Val Met Phe
435

<210> 439
<211> 1072
<212> DNA
<213> B.napus

<400> 439
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tattcaatgc tccacaaggt ttctcggagc ttctctctcg ttattcagca actaggtacc 180
gacctccgta acgctgtgtg tgtgttctac ttggttctcc gagctcttga tactgtcgag 240
gatgacacaa gcataccaac tgatgagaag ctgcccattc tgattgcctt ccaccgtcac 300
atctacgata ctgactggca ctattcatgt ggcacgaagg agtacaaggt totgatggac 360
caatttcacc atgttgctgc agcttttctg gaacttgaaa aagggtatca agaggctatc 420
gaggaaatta ctaaaagaat ggggtgcagga atggccaagt ttatctgcca agaggtagaa 480
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aattcaatgg gtttatttct tcagaaaaca aacattatca gagattatct tgaggacatt 660
aatgaaatac caaagtcccg catgttttgg cctcgcaaga tttggggcaa atatgctggc 720
aagctcgagg acttgaaata cgagaagaac tcaagcaatg cagtgcagtg cttgaatgaa 780

atggtcacca atgctttgac gcatattgaa gattgcctca aatacatggc tgccttgcg 840

gacctttcta tttttcgggtt ctgtgctatc cctcagatca tggcgattgg aacacttgcg 900

ctatgctata acaatgtgca agtatttaga ggcgttgtga aattgaggcg aggtcttact 960

gctaaagtga ttgatcggac aaagacaatg gctgatgtct atggcgctt ctatgatttt 1020

tcttgatgc tgaaaacaaa gggtgacaag aacgatccac atgctagtaa ga 1072

<210> 440

<211> 357

<212> PRT

<213> B.napus

<400> 440

Met Gly Ser Leu Gly Thr Phe Leu Arg Tyr Pro Asp Asp Val Tyr Pro
1 5 10 15

Leu Leu Lys Met Lys Arg Ala Ile Glu Lys Ala Glu Lys Gln Ile Pro
20 25 30

Pro Glu Pro His Trp Gly Phe Cys Tyr Ser Met Leu His Lys Val Ser
35 40 45

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

Ala Val Cys Val Phe Tyr Leu Val Leu Arg Ala Leu Asp Thr Val Glu
65 70 75 80

Asp Asp Thr Ser Ile Pro Thr Asp Glu Lys Leu Pro Ile Leu Ile Ala
85 90 95

Phe His Arg His Ile Tyr Asp Thr Asp Trp His Tyr Ser Cys Gly Thr
100 105 110

Lys Glu Tyr Lys Val Leu Met Asp Gln Phe His His Val Ala Ala Ala
115 120 125

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

Lys Arg Met Gly Ala Gly Met Ala Lys Phe Ile Cys Gln Glu Val Glu
145 150 155 160

Thr Val Asp Asp Tyr Asp Glu Tyr Cys His Tyr Val Ala Gly Leu Val
165 170 175

Gly Leu Gly Leu Ser Lys Leu Phe Leu Ala Ser Gly Ser Glu Val Leu
180 185 190

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

Lys Thr Asn Ile Ile Arg Asp Tyr Leu Glu Asp Ile Asn Glu Ile Pro
210 215 220

Lys Ser Arg Met Phe Trp Pro Arg Lys Ile Trp Gly Lys Tyr Ala Gly
225 230 235 240

Lys Leu Glu Asp Leu Lys Tyr Glu Lys Asn Ser Ser Asn Ala Val Gln
245 250 255

Cys Leu Asn Glu Met Val Thr Asn Ala Leu Thr His Ile Glu Asp Cys
260 265 270

Leu Lys Tyr Met Ala Ala Leu Arg Asp Pro Ser Ile Phe Arg Phe Cys
275 280 285

Ala Ile Pro Gln Ile Met Ala Ile Gly Thr Leu Ala Leu Cys Tyr Asn
290 295 300

Asn Val Gln Val Phe Arg Gly Val Val Lys Leu Arg Arg Gly Leu Thr
305 310 315 320

Ala Lys Val Ile Asp Arg Thr Lys Thr Met Ala Asp Val Tyr Gly Ala
325 330 335

Phe Tyr Asp Phe Ser Cys Met Leu Lys Thr Lys Val Asp Lys Asn Asp
340 345 350

Pro His Ala Ser Lys
355

<210> 441
<211> 1242
<212> DNA
<213> G.max

<400> 441
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tacacaatgc tccacaaggt ttctcgaagt ttcgccctcg tcattcagca actcggcacc 180
gagcttcgca acgccgtttg catattttat ttggttctgc gagctctcga caccgttgag 240
gatgatacta gcatagaaac agatgtcaag gtgccaatac tgatagcctt tcaccgtcat 300

atztatgatc gtgattggca cttttcatgt ggcacaaagg agtacaaagt tctaattggac	360
cagtttcatc atgtttcaac tgcttttctg gaacttggaa agaactacca ggaagcaatt	420
gaggacatta ccaaaagaat ggggtgctgga atggccaaat ttatttgcaa ggaggtagaa	480
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atccccaagt cacgcatgtt ttggccacga cagatttgga gtgaatatgt taacaaactt	720
gaggatttga aatatgagga gaactctgtt aaggcagtgc aatgcttaaa tgacatggtc	780
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tacaacaaca ttgaggtctt cagaggtgta gttaaaatga ggcgaggttt aactgccaaa	960
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gaagctatac agaaaacttg cagagaatct ggtctcttaa gtaaaaggaa atottacatt	1140
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atcatttttg cttatctgtc tgctaaccac cataatagct ag	1242

<210> 442
 <211> 413
 <212> PRT
 <213> G.max

<400> 442

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

Pro Glu Pro His Trp Ala Phe Cys Tyr Thr Met Leu His Lys Val Ser
35 40 45

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

Ala Val Cys Ile Phe Tyr Leu Val Leu Arg Ala Leu Asp Thr Val Glu
65 70 75 80

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

Phe His Arg His Ile Tyr Asp Arg Asp Trp His Phe Ser Cys Gly Thr
100 105 110

Lys Glu Tyr Lys Val Leu Met Asp Gln Phe His His Val Ser Thr Ala
115 120 125

Phe Leu Glu Leu Gly Lys Asn Tyr Gln Glu Ala Ile Glu Asp Ile Thr
130 135 140

Lys Arg Met Gly Ala Gly Met Ala Lys Phe Ile Cys Lys Glu Val Glu
145 150 155 160

Thr Ile Asp Asp Tyr Asp Glu Tyr Cys His Tyr Val Ala Gly Leu Val
165 170 175

Gly Leu Gly Leu Ser Lys Leu Phe His Ala Ser Gly Ser Glu Asp Leu
180 185 190

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

Asn Ile Ile Arg Asp Tyr Leu Glu Asp Ile Asn Glu Ile Pro Lys Ser
210 215 220

Arg Met Phe Trp Pro Arg Gln Ile Trp Ser Glu Tyr Val Asn Lys Leu
225 230 235 240

Glu Asp Leu Lys Tyr Glu Glu Asn Ser Val Lys Ala Val Gln Cys Leu
245 250 255

Asn Asp Met Val Thr Asn Ala Leu Met His Ala Glu Asp Cys Leu Lys
260 265 270

Tyr Met Ala Ala Leu Arg Asp Pro Pro Ile Phe Arg Phe Cys Ala Ile
275 280 285

Pro Gln Ile Met Ala Ile Gly Thr Leu Ala Leu Cys Tyr Asn Asn Ile
290 295 300

Glu Val Phe Arg Gly Val Val Lys Met Arg Arg Gly Leu Thr Ala Lys
305 310 315 320

Val Ile Asp Arg Thr Lys Thr Met Ala Asp Val Tyr Gly Ala Phe Phe
325 330 335

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

Ala Thr Lys Thr Leu Ser Arg Leu Glu Ala Ile Gln Lys Thr Cys Arg
 355 360 365

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

Ser Gly Tyr Gly Ser Thr Met Ile Val Ile Leu Val Ile Met Val Ser
 385 390 395 400

Ile Ile Phe Ala Tyr Leu Ser Ala Asn His His Asn Ser
 405 410

<210> 443
 <211> 1206
 <212> DNA
 <213> Z.mays

<400> 443
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 cagaaggtgt cccgtagctt cgctctcgtc atccagcagc tcggaccgga actccgcaat 180
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 gtatccactg ccttcctgga gcttggtgaa ggttaccaaagggaataga agaagtcact 420
 aggcgaatgg gtgcaggaat ggcaaaatct atatgcaaag aggttgaaac tgttgatgac 480
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tatgctgctg ggacggaaga tctggctcta gattcactgt caaattcaat gggcctat	600
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cgcatgttct ggcctcgaga gatatggagt aaatatgcag ataaacttga ggacttcaaa	720
tatgaggaga actccaaaaa agcagtacaa tgcttgaaca atatggtgac tgatgcactg	780
attcatgctg aagagtgcct tcagtacatg tcagccttga aggatcctgc ctttttcogt	840
ttttgtgcaa taccacagat aatggcaatt ggaacatgtg ctctttgcta caataacgtg	900
catgtcttca gaggagtgtg gaagatgaga cgtgggtctca cggcacgaat aattgacgag	960
acaaactcaa tgacagatgt ctatactgct ttctatgagt tttcttcatt gatagagtca	1020
aagattgatg acagtgatcc aaatgctgct ctaacacaga gacgtgtgga ttcaataaag	1080
caaacttgca agtcatctgg tttggtaaag caaagggggt accatttgga gaagtcacct	1140
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ttctag	1206

<210> 444
 <211> 401
 <212> PRT
 <213> Z.mays

<400> 444

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

Arg	Val	Ala	Ala	Gly	Gln	Ile	Lys	Arg	Gln	Ile	Pro	Pro	Glu	Glu	His
		20						25					30		

Trp	Ala	Phe	Ala	Tyr	Ser	Met	Leu	Gln	Lys	Val	Ser	Arg	Ser	Phe	Ala
		35					40					45			

Leu Val Ile Gln Gln Leu Gly Pro Glu Leu Arg Asn Ala Val Cys Ile
50 55 60

Phe Tyr Leu Val Leu Arg Ala Leu Asp Thr Val Glu Asp Asp Thr Ser
65 70 75 80

Ile Pro Thr Glu Val Lys Val Pro Ile Leu Gln Glu Phe Tyr Arg His
85 90 95

Ile Tyr Asn Arg Asp Trp His Tyr Ser Cys Gly Thr Asn His Tyr Lys
100 105 110

Met Leu Met Asp Lys Phe Arg His Val Ser Thr Ala Phe Leu Glu Leu
115 120 125

Gly Glu Gly Tyr Gln Lys Ala Ile Glu Glu Val Thr Arg Arg Met Gly
130 135 140

Ala Gly Met Ala Lys Phe Ile Cys Lys Glu Val Glu Thr Val Asp Asp
145 150 155 160

Tyr Asp Glu Tyr Cys His Tyr Val Ala Gly Leu Val Gly Tyr Gly Leu
165 170 175

Ser Arg Leu Phe Tyr Ala Ala Gly Thr Glu Asp Leu Ala Leu Asp Ser
180 185 190

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

Asp Tyr Leu Glu Asp Ile Asn Glu Ile Pro Lys Ser Arg Met Phe Trp
210 215 220

Pro Arg Glu Ile Trp Ser Lys Tyr Ala Asp Lys Leu Glu Asp Phe Lys
225 230 235 240

Tyr Glu Glu Asn Ser Lys Lys Ala Val Gln Cys Leu Asn Asn Met Val
245 250 255

Thr Asp Ala Leu Ile His Ala Glu Glu Cys Leu Gln Tyr Met Ser Ala
260 265 270

Leu Lys Asp Pro Ala Ile Phe Arg Phe Cys Ala Ile Pro Gln Ile Met
275 280 285

Ala Ile Gly Thr Cys Ala Leu Cys Tyr Asn Asn Val His Val Phe Arg
290 295 300

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

Thr Asn Ser Met Thr Asp Val Tyr Thr Ala Phe Tyr Glu Phe Ser Ser
325 330 335

Leu Ile Glu Ser Lys Ile Asp Asp Ser Asp Pro Asn Ala Ala Leu Thr
340 345 350

Gln Arg Arg Val Asp Ser Ile Lys Gln Thr Cys Lys Ser Ser Gly Leu
355 360 365

Val Lys Gln Arg Gly Tyr His Leu Glu Lys Ser Pro Tyr Arg Pro Met
370 375 380

Leu	Ile	Met	Ile	Val	Leu	Leu	Leu	Val	Ala	Ile	Leu	Phe	Gly	Val	Met
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Phe

<210> 445

<211> 1491

<212> DNA

<213> *S.cerevisiae*

<400> 445

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ggtaagaaag ttcttatcgt agaacgtgac tgggctatgc ctgatagaat tgttggtgaa	180
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ccagaccatg ttccaactgt cggttcttcg tttgtcggta tgtctttggt caatgctaag	720
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gaagaacgtg gtttcttggg attaccaatg gctttatttg aaggtattat gattttgatc	1440
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<210> 446
 <211> 496
 <212> PRT
 <213> S.cerevisiae

<400> 446

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

Val	Ala	Thr	Gly	Leu	Ala	Arg	Lys	Gly	Lys	Lys	Val	Leu	Ile	Val	Glu
			35					40					45		

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

Gly Gly Val Arg Ala Leu Arg Ser Leu Gly Met Ile Gln Ser Ile Asn
65 70 75 80

Asn Ile Glu Ala Tyr Pro Val Thr Gly Tyr Thr Val Phe Phe Asn Gly
85 90 95

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

Glu Lys Leu Lys Asp Leu Val Lys Asp Gly Asn Asp Lys Val Leu Glu
115 120 125

Asp Ser Thr Ile His Ile Lys Asp Tyr Glu Asp Asp Glu Arg Glu Arg
130 135 140

Gly Val Ala Phe Val His Gly Arg Phe Leu Asn Asn Leu Arg Asn Ile
145 150 155 160

Thr Ala Gln Glu Pro Asn Val Thr Arg Val Gln Gly Asn Cys Ile Glu
165 170 175

Ile Leu Lys Asp Glu Lys Asn Glu Val Val Gly Ala Lys Val Asp Ile
180 185 190

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

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

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

Asn Pro Ala Pro Met His Gly His Val Ile Leu Gly Ser Asp His Met
245 250 255

Pro Ile Leu Val Tyr Gln Ile Ser Pro Glu Glu Thr Arg Ile Leu Cys
260 265 270

Ala Tyr Asn Ser Pro Lys Val Pro Ala Asp Ile Lys Ser Trp Met Ile
275 280 285

Lys Asp Val Gln Pro Phe Ile Pro Lys Ser Leu Arg Pro Ser Phe Asp
290 295 300

Glu Ala Val Ser Gln Gly Lys Phe Arg Ala Met Pro Asn Ser Tyr Leu
305 310 315 320

Pro Ala Arg Gln Asn Asp Val Thr Gly Met Cys Val Ile Gly Asp Ala
325 330 335

Leu Asn Met Arg His Pro Leu Thr Gly Gly Gly Met Thr Val Gly Leu
340 345 350

His Asp Val Val Leu Leu Ile Lys Lys Ile Gly Asp Leu Asp Phe Ser
355 360 365

Asp Arg Glu Lys Val Leu Asp Glu Leu Leu Asp Tyr His Phe Glu Arg
370 375 380

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

Leu Phe Ala Ala Asp Ser Asp Asn Leu Lys Ala Leu Gln Lys Gly Cys
 405 410 415

Phe Lys Tyr Phe Gln Arg Gly Gly Asp Cys Val Asn Lys Pro Val Glu
 420 425 430

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

Phe Ala Val Ala Phe Tyr Thr Ile Tyr Leu Asn Met Glu Glu Arg Gly
 450 455 460

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

<210> 447
 <211> 1539
 <212> DNA
 <213> B.napus

<400> 447
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 ggtggtcctg acgtcatcat cgtcggagct ggtgttggcg gctcagctct cgcctatgct 180

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gattgttttg agggaataga cgcacagaaa gccaccggct tgacacttta caaggatgga	360
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aatgtgcgac tagaagaagg gacggtgaga tctttgatag aagaaaaagg agtaatcaaa	540
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<210> 448

<211> 512

<212> PRT

<213> B.napus

<400> 448

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Thr Tyr His Val Thr Asn Arg Arg Lys Lys Ala Thr Lys Leu Ala Asp
20 25 30

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

Gly Ala Gly Val Gly Gly Ser Ala Leu Ala Tyr Ala Leu Ala Lys Asp
50 55 60

Gly Arg Arg Val His Val Ile Glu Arg Asp Met Arg Glu Pro Glu Arg
65 70 75 80

Met Met Gly Glu Phe Met Gln Pro Gly Gly Arg Leu Phe Leu Ser Lys
85 90 95

Leu Asp Leu Gln Asp Cys Leu Glu Gly Ile Asp Ala Gln Lys Ala Thr
100 105 110

Gly Leu Thr Leu Tyr Lys Asp Gly Lys Glu Ala Ala Ser Pro Phe Pro
115 120 125

Val Glu Asp Asn Asn Phe Pro Tyr Glu Pro Ser Ala Arg Met Phe Tyr
130 135 140

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

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

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

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

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

Val Gly Tyr Val Ser Lys Asn Cys Arg Leu Glu Glu Pro Glu Lys Leu
225 230 235 240

His Leu Ile Met Ala Lys Pro Ser Phe Thr Met Leu Tyr Gln Ile Ser
245 250 255

Ser Thr Asp Val Arg Cys Gly Phe Glu Leu Phe Ser Asn Tyr Phe Pro
260 265 270

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

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

Glu Gly Ala Lys Ile Lys Val Thr Pro Ala Lys Arg Met Ser Ala Thr
305 310 315 320

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

Arg His Pro Ala Ile Ala Ser Gly Met Met Val Leu Leu Ser Asp Ile
340 345 350

Leu Ile Leu Arg Arg Leu Leu Lys Pro Leu Arg Asn Leu Gly Asp Ala
355 360 365

Asn Lys Val Ser Glu Val Ile Lys Cys Phe Tyr Val Ile Arg Lys Met
370 375 380

Ser Ala Thr Val Asn Thr Leu Gly Asn Ala Phe Ser Gln Val Leu Val
385 390 395 400

Ala Ser Thr Asp Gln Ala Lys Glu Ala Met Arg Gln Gly Cys Phe Asp
405 410 415

Tyr Leu Ser Ser Gly Gly Phe Arg Thr Ser Gly Met Met Ala Leu Leu
420 425 430

Gly Gly Met Asn Pro Arg Pro Leu Ser Leu Ile Phe His Leu Cys Gly
435 440 445

Ile Thr Leu Ser Ser Ile Gly Gln Leu Leu Ser Pro Phe Pro Ser Pro
450 455 460

Leu Gly Ile Trp His Ser Leu Arg Leu Phe Gly Leu Ser Ile Lys Met
 465 470 475 480

Leu Val Pro His Leu Lys Ala Glu Gly Val Ser Gln Met Leu Ser Pro
 485 490 495

Ala Tyr Ala Ala Ala Tyr Arg Lys Ser Tyr Met Ala Ala Thr Ala Leu
 500 505 510

<210> 449
 <211> 1590
 <212> DNA
 <213> Z.mays

<400> 449
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 gggacggacg tcatcatcgt cggcgccggg gtagctggat ctgcgctggc atacacgctc 240
 ggaaaggatg gccgtcgggt gcatgtcatc gagagggatc tgacagaacc tgacagaatt 300
 gtgggcgagc tgttgcaacc tgggggttac ttgaaattaa ttgagctggg cctccaagat 360
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ttggccaatc cttctccaat cttatttttac ccaattagca gcacagaggt gcgctgtttg	840
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gataagggaa gcatacggac aatgccaaac aggagcatgc cagcggctcc acatccgacc	1020
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gatcaagcta ggaatgagat gcgccaggct tgttttgatt acttgagcct cggaggcgtc	1320
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cgggccgcac ctacgggaga aaaggcatga	1590

<210> 450
 <211> 529
 <212> PRT
 <213> Z.mays

<400> 450

Met	Ala	Ala	Thr	Ala	Ala	Ala	Ala	Gly	Val	Glu	Phe	Pro	Leu	Ile	Gly
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20 25 30

Arg Arg Arg Arg Arg Pro Trp His Gln Ala Pro Leu Val Glu Gly Lys
35 40 45

Pro Ala Pro Glu Ala Gly Cys Ala Val Ser Asp Gly Gly Thr Asp Val
50 55 60

Ile Ile Val Gly Ala Gly Val Ala Gly Ser Ala Leu Ala Tyr Thr Leu
65 70 75 80

Gly Lys Asp Gly Arg Arg Val His Val Ile Glu Arg Asp Leu Thr Glu
85 90 95

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

Leu Ile Glu Leu Gly Leu Gln Asp Cys Val Glu Glu Ile Asp Ala Gln
115 120 125

Arg Val Leu Gly Tyr Ala Leu Phe Lys Asp Gly Arg Asn Thr Lys Leu
130 135 140

Ala Tyr Pro Leu Glu Lys Phe His Ser Asp Val Ala Gly Arg Ser Phe
145 150 155 160

His Asn Gly Arg Phe Ile Gln Arg Met Arg Gln Lys Ala Ala Ser Leu
165 170 175

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

Asn Gly Thr Val Lys Gly Val Gln Tyr Lys Thr Lys Ser Gly Glu Glu
195 200 205

Leu Lys Ala Tyr Ala Pro Leu Thr Ile Val Cys Asp Gly Cys Phe Ser
210 215 220

Asn Leu Arg Arg Ala Leu Cys Ser Pro Lys Val Asp Val Pro Ser Cys
225 230 235 240

Phe Val Gly Leu Val Leu Glu Asn Cys Gln Leu Pro His Pro Asn His
245 250 255

Gly His Val Ile Leu Ala Asn Pro Ser Pro Ile Leu Phe Tyr Pro Ile
260 265 270

Ser Ser Thr Glu Val Arg Cys Leu Val Asp Val Pro Gly Gln Lys Val
275 280 285

Pro Ser Ile Ala Thr Gly Glu Met Ala Asn Tyr Leu Lys Thr Val Val
290 295 300

Ala Pro Gln Ile Pro Pro Glu Ile Tyr Asp Ser Phe Ile Ala Ala Ile
305 310 315 320

Asp Lys Gly Ser Ile Arg Thr Met Pro Asn Arg Ser Met Pro Ala Ala
325 330 335

Pro His Pro Thr Pro Gly Ala Leu Leu Met Gly Asp Ala Phe Asn Met
340 345 350

Arg His Pro Leu Thr Gly Gly Gly Met Thr Val Ala Leu Ser Asp Ile
355 360 365

Val Val Leu Arg Asn Leu Leu Lys Pro Leu Arg Asn Leu His Asp Ala
370 375 380

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

Val Ala Ser Thr Ile Asn Thr Leu Ala Gly Ala Leu Tyr Lys Val Phe
405 410 415

Ser Ala Ser Pro Asp Gln Ala Arg Asn Glu Met Arg Gln Ala Cys Phe
420 425 430

Asp Tyr Leu Ser Leu Gly Gly Val Phe Ser Asn Gly Pro Ile Ala Leu
435 440 445

Leu Ser Gly Leu Asn Pro Arg Pro Leu Ser Leu Val Ala His Phe Phe
450 455 460

Ala Val Ala Ile Tyr Gly Val Gly Arg Leu Met Leu Pro Leu Pro Ser
465 470 475 480

Pro Lys Arg Met Trp Ile Gly Ala Arg Leu Ile Ser Gly Ala Cys Gly
485 490 495

Ile Ile Leu Pro Ile Ile Lys Ala Glu Gly Val Arg Gln Met Phe Phe
500 505 510

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

Ala

<210> 451
<211> 674
<212> DNA
<213> Vicia faba

<400> 451
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ttatgctaac gtttgccaac acttagcaat ttgcaagttg attaattgat tctaaattat 180
ttttgtcttc taaatacata tactaatcaa ctggaaatgt aaatatttgc taatatttct 240
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caatgctgca tggatggcat atacaccaa cattcaataa ttcttgagga taataatggg 360
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gacaacaatg ttaccacaca caagttttga ggtgcatgca tggatgccct gtggaaagtt 480
taaaaatatt ttggaaatga tttgcatgga agccatgtgt aaaaccatga catccacttg 540
gaggatgcaa taatgaagaa aactacaaat ttacatgcaa ctagttatgc atgtagtcta 600
tataatgagg attttgcaat actttcattc atacacactc actaagtttt acacgattat 660
aatttcttca tagc 674

<210> 452
<211> 695
<212> DNA

<213> Vicia faba

<400> 452

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ttctaaatta tttttgtctt ctaaatacat atactaatca actggaaatg taaatatttg	240
ctaataatttc tactatagga gaattaaagt gagtgaatat ggtaccacaa ggtttggaga	300
tttaattggt gcaatgctgc atggatggca tatacaccaa acattcaata attcttgagg	360
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<210> 453

<211> 1112

<212> DNA

<213> Artificial

<220>

<223> Artificial

<400> 453

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<210> 454

<211> 986

<212> DNA

<213> *Petroselinum crispum*

<400> 454

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gaaaagaatc aacatcagcg ttaacaaacg gccccgttac ggcccaaacg gtcatataga	180
gtaacggcgt taagcgttga aagactccta tcgaaatacg taaccgcaaa cgtgtcatag	240
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atagatatag atctgttata tcattttttt tattaattgt gtatatatat atgtgcatag	840
atctggatta catgattgtg attatttaca tgattttgtt atttacgtat gtatatatgt	900
agatctggac tttttggagt tgttgacttg attgtatttg tgtgtgtata tgtgtgttct	960
gatcttgata tgttatgtat gtgcag	986

<210> 455

<211> 102

<212> DNA

<213> Arabidopsis thaliana

<400> 455

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<210> 456
<211> 34
<212> PRT
<213> Arabidopsis thaliana

<400> 456

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

Thr Arg Arg Arg Ser Phe Ser Ser Arg Ser Ser Ser Leu Leu Cys Ser
20 25 30

Ser Met

<210> 457
<211> 102
<212> DNA
<213> Arabidopsis thaliana

<400> 457
atgcagaggt ttttctccgc cagatcgatt ctcggttacg ccgtcaagac gcggaggagg 60

tcttttctctt ctcggttcttc ggaattccag ctgaccacca tg 102

<210> 458
<211> 34
<212> PRT
<213> Arabidopsis thaliana

<400> 458

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

Thr Arg Arg Arg Ser Phe Ser Ser Arg Ser Ser Glu Phe Gln Leu Thr
 20 25 30

Thr Met

<210> 459

<211> 419

<212> DNA

<213> Spinacia oleracea

<400> 459

gcataaactt atcttcatag ttgccactcc aatttgctcc ttgaatctcc tccacccaat 60

acataatcca ctctccatc acccattca ctactaaatc aaacttaact ctgtttttct 120

ctctctcct ttcatctt attcttccaa tcatcgctact ccgccatgac caccgctgtc 180

accgccgctg tttctttccc ctctacaaa accacctctc tctccgcccg aagctcctcc 240

gtcatttccc ctgacaaaat cagctacaaa aaggtgattc ccaatttcac tgtgtttttt 300

attaataatt tggtattttg atgatgagat gattaatttg ggtgctgcag gttcctttgt 360

actacaggaa tgtatctgca actgggaaaa tgggacccat cagggcccag atcgctct 419

<210> 460

<211> 59

<212> PRT

<213> Spinacia oleracea

<400> 460

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

Thr Ser Leu Ser Ala Arg Ser Ser Ser Val Ile Ser Pro Asp Lys Ile

20

25

30

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

Lys Met Gly Pro Ile Arg Ala Gln Ile Ala Ser
50 55

<210> 461
<211> 12
<212> PRT
<213> Motif

<400> 461

Asp Arg Ile Val Gly Glu Leu Met Gln Pro Gly Gly
1 5 10

<210> 462
<211> 17
<212> PRT
<213> Motif

<220>
<221> misc_feature
<222> (3)..(4)
<223> Xaa can be any naturally occurring amino acid

<400> 462

Gly Asp Xaa Xaa Asn Met Arg His Pro Leu Thr Gly Gly Gly Met Thr
1 5 10 15

Val

<210> 463
<211> 406
<212> PRT
<213> Physcomitrella patens

<400> 463

Met Gly Ile Ile Gly Ala Ile Leu Lys Asn Pro Glu Asp Leu His His
1 5 10 15

Leu Leu Lys Leu Lys Met Ala Ser Ala Ala Ala Asn Arg Ala Ile Pro
20 25 30

Ser Asp Pro Asn Leu Ala Phe Cys Tyr Gln Met Leu Arg Arg Val Ser
35 40 45

Gly Ser Phe Ser Ile Val Ile Leu Gln Leu Glu Pro Gly Leu Arg Asn
50 55 60

Ala Val Cys Val Phe Tyr Leu Val Leu Arg Gly Leu Gln Ala Val Glu
65 70 75 80

Asp Asp Leu Thr Ile Pro Tyr Asp Leu Lys Val Glu Leu Leu Arg Asn
85 90 95

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

Asn Asp Tyr Lys Leu Leu Met Asp Lys Phe Tyr Leu Val Ile Leu Ala
115 120 125

Phe Leu Gly Leu Thr Thr Gly Tyr Gln Glu Val Ile Thr Glu Ile Thr
130 135 140

Glu Arg Met Gly Glu Gly Met Val Lys Tyr Leu Asn Thr Glu Ile Ile
145 150 155 160

Ser Arg Glu Asp Tyr Asn Glu Tyr Cys His Phe Ser Ala Gly Leu Met
165 170 175

Gly Leu Gly Leu Thr Arg Ile Phe Tyr Thr Ala Gly Met Glu Gln Phe
180 185 190

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

Asn Val Ile Arg Asp Tyr Leu Glu Asn Ile Asn Ala Gln Pro Thr Ser
210 215 220

Arg Leu Arg Trp Pro Lys Glu Val Trp Ser Lys Tyr Ala Asp Lys Pro
225 230 235 240

Glu Ala Phe Met Asp Glu Thr Asn Tyr Lys Gln Gly Leu His Cys Leu
245 250 255

Asn Glu Met Val Thr Asp Ala Leu Ser His Gly Leu Asp Cys Leu His
260 265 270

Tyr Met Ala Ala Leu Gln Asp Gln Pro Asn Leu Arg Phe Cys Ala Thr
275 280 285

Phe Gln Ile Thr Ala Leu Gly Thr Leu Ala Met Cys Tyr Asn Asn Val
290 295 300

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

Ile Leu Asp Val Lys Asn Met Val Asp Val Tyr Gly Ala Phe Tyr Asp
325 330 335

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

Val Thr Thr His Lys Phe Val Asp Asp Ile Arg Ser Ile Cys Arg Phe
355 360 365

Glu Ile Lys Asn Arg Arg Ala Phe Thr Ile Glu Ser Lys Phe Gly His
370 375 380

Glu Thr Phe Leu Val Val Ala Leu Phe Val Ile Leu Val Ile Met Leu
385 390 395 400

Leu Ile Val Thr Lys Gln
405

<210> 464

<211> 413

<212> PRT

<213> Glycine max

<400> 464

Met Gly Ser Leu Gly Ala Ile Leu Lys His Pro Asp Asp Phe Tyr Pro
1 5 10 15

Leu Leu Lys Leu Lys Met Ala Ala Arg Asn Ala Glu Lys Gln Ile Pro
20 25 30

Pro Glu Pro His Trp Ala Phe Cys Tyr Thr Met Leu His Lys Val Ser
35 40 45

Arg Ser Phe Ala Leu Val Ile Gln Gln Leu Gly Ile Glu Leu Arg Asn
50 55 60

Ala Val Cys Ile Phe Tyr Leu Val Leu Arg Ala Leu Asp Thr Val Glu
65 70 75 80

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

Phe His Arg His Ile Tyr Asp Arg Asp Trp His Phe Ser Cys Gly Thr
100 105 110

Lys Glu Tyr Lys Val Leu Met Asp Gln Phe His His Val Ser Thr Ala
115 120 125

Phe Leu Glu Leu Gly Lys Asn Tyr Gln Glu Ala Ile Glu Asp Ile Thr
130 135 140

Lys Arg Met Gly Ala Gly Met Ala Lys Phe Ile Cys Lys Glu Val Glu
145 150 155 160

Thr Ile Asp Asp Tyr Asp Glu Tyr Cys His Tyr Val Ala Gly Leu Val
165 170 175

Gly Leu Gly Leu Ser Lys Leu Phe His Ala Ser Gly Ser Glu Asp Leu
180 185 190

Ala Pro Asp Asp Leu Ser Asn Ser Met Gly Leu Phe Leu Gln Lys Thr

195

200

205

Asn Ile Ile Arg Asp Tyr Leu Glu Asp Ile Asn Glu Ile Pro Lys Ser
210 215 220

Arg Met Phe Trp Pro Arg Gln Ile Trp Ser Glu Tyr Val Asn Lys Leu
225 230 235 240

Glu Asp Leu Lys Tyr Glu Glu Asn Ser Val Lys Ala Val Gln Cys Leu
245 250 255

Asn Asp Met Val Thr Asn Ala Leu Met His Pro Glu Asp Cys Leu Lys
260 265 270

Tyr Met Ala Ala Leu Arg Asp Pro Pro Ile Phe Arg Phe Cys Ala Ile
275 280 285

Pro Gln Ile Met Ala Ile Gly Thr Leu Ala Leu Cys Tyr Asn Asn Ile
290 295 300

Glu Val Phe Arg Gly Val Val Lys Met Arg Arg Gly Leu Thr Ala Lys
305 310 315 320

Val Ile Asp Arg Thr Lys Thr Met Ala Asp Val Tyr Gly Ala Phe Phe
325 330 335

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

Ala Thr Lys Thr Leu Ser Arg Leu Glu Ala Ile Gln Lys Thr Cys Arg
355 360 365

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

Ser Gly Tyr Gly Ser Thr Met Ile Val Ile Leu Val Ile Met Val Ser
385 390 395 400

Ile Ile Phe Ala Tyr Leu Ser Ala Asn His His Asn Ser
405 410

<210> 465
<211> 413
<212> PRT
<213> Lotus corniculatus

<400> 465

Met Gly Ser Leu Gly Ala Ile Val Lys His Pro Asp Asp Leu Tyr Pro
1 5 10 15

Leu Leu Lys Leu Lys Met Ala Ala Arg His Ala Glu Lys Gln Ile Pro
20 25 30

Ser Glu Pro His Trp Gly Phe Cys Tyr Ser Met Leu His Lys Val Ser
35 40 45

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

Ala Val Cys Ile Phe Tyr Leu Val Leu Arg Ala Leu Asp Thr Val Glu
65 70 75 80

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

Phe His Arg His Ile Tyr Asp Arg Asp Trp His Phe Ser Cys Gly Thr
100 105 110

Lys Glu Tyr Lys Val Leu Met Gly Gln Phe His Leu Val Ser Thr Ala
115 120 125

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

Asp Arg Met Gly Ala Gly Met Ala Lys Phe Ile Cys Lys Glu Val Glu
145 150 155 160

Thr Ile Asp Asp Tyr Asp Glu Tyr Cys His Tyr Val Ala Gly Leu Val
165 170 175

Gly Leu Gly Leu Ser Lys Leu Phe His Ala Ser Gly Lys Glu Asn Leu
180 185 190

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

Asn Ile Ile Arg Asp Tyr Leu Glu Asp Ile Asn Glu Ile Pro Lys Ser
210 215 220

Arg Met Phe Trp Pro Arg Gln Ile Trp Ser Lys Tyr Val Asn Lys Leu
225 230 235 240

Glu Asp Leu Lys Tyr Glu Glu Asn Ser Val Lys Ala Val Gln Cys Leu
245 250 255

Asn Asp Met Val Thr Asn Ala Leu Met His Ala Glu Asp Cys Leu Lys
260 265 270

Tyr Met Ser Asp Leu Arg Asp Asp Ser Ile Phe Arg Phe Cys Ala Ile
275 280 285

Pro Gln Ile Met Ala Ile Gly Thr Leu Ala Ile Cys Tyr Asn Asn Val
290 295 300

Glu Val Phe Arg Gly Val Val Lys Met Arg Arg Gly Leu Thr Ala Lys
305 310 315 320

Val Ile Asp Arg Thr Lys Thr Ile Ala Asp Val Tyr Gly Ala Phe Phe
325 330 335

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

Ala Thr Lys Thr Leu Ser Arg Leu Val Ala Ile Gln Lys Thr Cys Arg
355 360 365

Glu Ser Gly Leu Leu Asn Lys Arg Lys Ser Tyr Ile Leu Arg Lys Glu
370 375 380

Asn Gly Tyr Gly Ser Thr Leu Ile Ile Ile Leu Val Leu Leu Phe Ser
385 390 395 400

Ile Met Phe Ala Tyr Ser Ser Ala Thr Arg His Ser Asn
405 410

<210> 466

<211> 401

<212> PRT

<213> Zea mays

<400> 466

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

Arg Val Ala Ala Gly Gln Ile Lys Arg Gln Ile Pro Pro Glu Glu His
20 25 30

Trp Ala Phe Ala Tyr Ser Met Leu Gln Lys Val Ser Arg Ser Phe Ala
35 40 45

Leu Val Ile Gln Gln Leu Gly Pro Glu Leu Arg Asn Ala Val Cys Ile
50 55 60

Phe Tyr Leu Val Leu Arg Ala Leu Asp Thr Val Glu Asp Asp Thr Ser
65 70 75 80

Ile Pro Thr Glu Val Lys Val Pro Ile Leu Gln Glu Phe Tyr Arg His
85 90 95

Ile Tyr Asn Arg Asp Trp His Tyr Ser Cys Gly Thr Asn His Tyr Lys
100 105 110

Met Leu Met Asp Lys Phe Arg His Val Ser Thr Ala Phe Leu Glu Leu
115 120 125

Gly Glu Gly Tyr Gln Lys Ala Ile Glu Glu Val Thr Arg Arg Met Gly
130 135 140

Ala Gly Met Ala Lys Phe Ile Cys Lys Glu Val Glu Thr Val Asp Asp

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

Thr Asn Ser Met Thr Asp Val Tyr Thr Ala Phe Tyr Glu Phe Ser Ser
325 330 335

Leu Ile Glu Ser Lys Ile Asp Asp Ser Asp Pro Asn Ala Ala Leu Thr
340 345 350

Gln Arg Arg Val Asp Ser Ile Lys Gln Thr Cys Lys Ser Ser Gly Leu
355 360 365

Val Lys Gln Arg Gly Tyr His Leu Glu Lys Ser Pro Tyr Arg Pro Met
370 375 380

Leu Ile Met Ile Val Leu Leu Leu Val Ala Ile Leu Phe Gly Val Met
385 390 395 400

Phe

<210> 467
<211> 410
<212> PRT
<213> Oryza sativa

<400> 467

Met Gly Val Val Gly Ala Leu Leu Gly Pro Glu Ala Glu Ala Leu Val
1 5 10 15

Arg Leu Arg Ala Ala Ala Trp Arg Leu Arg Arg Glu Val Ala Ala Ala
20 25 30

Thr Asp Asp Asp Glu His Trp Ala Phe Ala Tyr Ser Met Leu His Arg
35 40 45

Val Ser Arg Ser Phe Ala Ile Val Ile Gln Gln Leu Gly Pro Asp Leu
50 55 60

Arg Asn Ala Val Cys Val Phe Tyr Leu Val Leu Arg Ala Leu Asp Thr
65 70 75 80

Val Glu Asp Asp Thr Ser Ile Pro Thr Glu Ile Lys Val Pro Ile Leu
85 90 95

Gln Glu Phe His Arg His Ile Tyr Asn Arg Asp Trp His Phe Ser Cys
100 105 110

Gly Thr Lys Asp Cys Lys Ile Leu Met Asp Lys Phe His Tyr Val Leu
115 120 125

Thr Ala Phe Leu Glu Leu Gly Ser Gly Tyr Gln Glu Ala Ile Glu Glu
130 135 140

Ile Thr Arg Arg Met Gly Ala Gly Met Ala Lys Phe Ile Cys Lys Glu
145 150 155 160

Val Glu Thr Val Asp Asp Tyr Asp Glu Tyr Cys His Tyr Val Ala Gly
165 170 175

Leu Val Gly Ile Gly Leu Ser Arg Leu Phe His Ala Ala Gly Leu Glu
180 185 190

Asp Leu Ala Pro Glu Ser Leu Ser Asn Ser Met Gly Leu Phe Leu Gln
195 200 205

Lys Val Asn Ile Thr Arg Asp Tyr Leu Glu Asp Ile Asn Glu Ile Pro
210 215 220

Lys Ser Arg Met Phe Trp Pro Arg Glu Ile Trp Ser Lys Tyr Val Asp
225 230 235 240

Lys Leu Glu Asp Leu Lys Tyr Glu Asn Asn Ser Val Lys Ala Val Lys
245 250 255

Cys Leu Asn Glu Met Val Thr Asn Gly Leu Ile His Thr Glu Asp Cys
260 265 270

Leu Arg Tyr Met Ser Ala Leu Lys Asp Ile Thr Ile Leu Arg Phe Cys
275 280 285

Ala Ile Pro Gln Val Met Ala Leu Ala Thr Tyr Ala Leu Cys Tyr Asn
290 295 300

Asn Val Asn Val Phe Arg Gly Val Val Lys Leu Arg Arg Gly Leu Thr
305 310 315 320

Ala Arg Ile Ile Asn Glu Thr Asn Ser Met Ala Asp Val Tyr Thr Ala
325 330 335

Phe Tyr Glu Phe Ser Ser Leu Leu Ala Glu Lys Ile Asp Asp Asn Asp
340 345 350

Pro Asn Ala Ser Leu Thr Arg Lys Arg Val Asn Ala Ile Lys Glu Thr
355 360 365

Cys Lys Ser Ser Gly Leu Leu Lys Ile Arg Gly Tyr Asp Leu Asp Arg
370 375 380

Pro Lys Arg Asn Pro Ala Met Ile Met Met Leu Leu Leu Leu Leu Val
385 390 395 400

Ala Ile Phe Leu Gly Ala Leu Tyr Arg Arg
405 410

<210> 468
<211> 444
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 468

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

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

Gln Ser Thr Ser Pro Tyr Leu Leu His Cys Phe Glu Leu Leu Asn Leu
35 40 45

Thr Ser Arg Ser Phe Ala Ala Val Ile Arg Glu Leu His Pro Glu Leu
50 55 60

Arg Asn Cys Val Thr Leu Phe Tyr Leu Ile Leu Arg Ala Leu Asp Thr
65 70 75 80

Ile Glu Asp Asp Met Ser Ile Glu His Asp Leu Lys Ile Asp Leu Leu
85 90 95

Arg His Phe His Glu Lys Leu Leu Leu Thr Lys Trp Ser Phe Asp Gly

100

105

110

Asn Ala Pro Asp Val Lys Asp Arg Ala Val Leu Thr Asp Phe Glu Ser
115 120 125

Ile Leu Ile Glu Phe His Lys Leu Lys Pro Glu Tyr Gln Glu Val Ile
130 135 140

Lys Glu Ile Thr Glu Lys Met Gly Asn Gly Met Ala Asp Tyr Ile Leu
145 150 155 160

Asp Glu Asn Tyr Asn Leu Asn Gly Leu Gln Thr Val His Asp Tyr Asp
165 170 175

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

Leu Ile Val Ile Ala Lys Phe Ala Asn Glu Ser Leu Tyr Ser Asn Glu
195 200 205

Gln Leu Tyr Glu Ser Met Gly Leu Phe Leu Gln Lys Thr Asn Ile Ile
210 215 220

Arg Asp Tyr Asn Glu Asp Leu Val Asp Gly Arg Ser Phe Trp Pro Lys
225 230 235 240

Glu Ile Trp Ser Gln Tyr Ala Pro Gln Leu Lys Asp Phe Met Lys Pro
245 250 255

Glu Asn Glu Gln Leu Gly Leu Asp Cys Ile Asn His Leu Val Leu Asn
260 265 270

Ala Leu Ser His Val Ile Asp Val Leu Thr Tyr Leu Ala Gly Ile His
275 280 285

Glu Gln Ser Thr Phe Gln Phe Cys Ala Ile Pro Gln Val Met Ala Ile
290 295 300

Ala Thr Leu Ala Leu Val Phe Asn Asn Arg Glu Val Leu His Gly Asn
305 310 315 320

Val Lys Ile Arg Lys Gly Thr Thr Cys Tyr Leu Ile Leu Lys Ser Arg
325 330 335

Thr Leu Arg Gly Cys Val Glu Ile Phe Asp Tyr Tyr Leu Arg Asp Ile
340 345 350

Lys Ser Lys Leu Ala Val Gln Asp Pro Asn Phe Leu Lys Leu Asn Ile
355 360 365

Gln Ile Ser Lys Ile Glu Gln Phe Met Glu Glu Met Tyr Gln Asp Lys
370 375 380

Leu Pro Pro Asn Val Lys Pro Asn Glu Thr Pro Ile Phe Leu Lys Val
385 390 395 400

Lys Glu Arg Ser Arg Tyr Asp Asp Glu Leu Val Pro Thr Gln Gln Glu
405 410 415

Glu Glu Tyr Lys Phe Asn Met Val Leu Ser Ile Ile Leu Ser Val Leu
420 425 430

Leu Gly Phe Tyr Tyr Ile Tyr Thr Leu His Arg Ala

