

PF59082PF60142_PCT_SEQ_LIST.txt
SEQUENCE LISTING

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<120> Plants having increased yield-related traits and a method for making the same
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<170> PatentIn version 3.3
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<212> DNA
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 Cys Ser Arg Glu Ala Tyr Pro Asp Ser Lys Tyr Cys Glu Lys His Met
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 His Arg Gly Arg Asn Arg Ala Arg Lys Ser Leu Asp Gln Asn Gln Thr
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 165 170 175
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 Thr Asn Ser Thr Ser Gln Phe Asn Val Leu Ala Ser Ala Thr Asp His
 225 230 235 240
 Lys Asp Phe Arg Tyr Phe Gln Gly Ile Gly Glu Arg Val Gly Gly Val
 245 250 255
 Gly Glu Arg Thr Phe Phe Pro Glu Ala Ser Arg Ser Phe Gln Asp Ser
 260 265 270
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Tyr Ser Ser Ser Ser Ser Ser Gln His Leu His His Asp His Asp His
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340 345 350

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Pro His Leu Leu Phe Leu Ile Lys Arg Pro Phe Leu Phe Ser Ser Ser
35 40 45

Ser Ser Ser Ser Ser Ser Ser Ser Phe Phe Ser Pro Thr Leu Ser Pro
50 55 60

His Phe Gly Trp Asn Val Tyr Glu Met Gly Met Gly Arg Lys Ile Asp
65 70 75 80

Ala Glu Pro Gly Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys
85 90 95

Ser Lys Glu Ala Tyr Pro Asp Ser Lys Tyr Cys Glu Arg His Met His
100 105 110

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

Thr Pro Asn Leu Phe Leu Asp Ser Ser Ser Arg Arg Arg Arg Ser Gly
130 135 140

Tyr Met Asp Asp Phe Phe Ser Ile Glu Pro Ser Gly Ser Ile Lys Ser
145 150 155 160

Cys Ser Gly Ser Ala Met Glu Asp Asn Asp Asp Gly Ser Cys Arg Gly
165 170 175

Ile Asn Asn Glu Glu Lys Gln Pro Asp Arg His Cys Phe Ile Leu Gly
180 185 190

Thr Asp Leu Arg Thr Arg Glu Arg Pro Leu Met Leu Glu Glu Lys Leu
195 200 205

Lys Gln Arg Asp His Asp Asn Glu Glu Glu Gln Gly Ser Lys Arg Phe
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 Arg Lys Gly Gln Glu His Met Leu Ser Phe Ser Ser Ala Ser Gly Lys
 85 90 95
 Ser Asp Val Ser Pro Tyr Leu Gln Tyr Cys Arg Asn Ser Gly Tyr Gly
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 Leu Gly Gly Met Met Asn Thr Ser Asn Met His Gly Asn Leu Leu Thr
 115 120 125
 Gly Val Lys Gly Pro Phe Ser Leu Thr Gln Trp Ala Glu Leu Glu Gln
 130 135 140
 Gln Ala Leu Ile Tyr Lys Tyr Ile Thr Ala Asn Val Pro Val Pro Ser
 145 150 155 160
 Ser Leu Leu Leu Ser Leu Lys Lys Ser Phe Phe Pro Tyr Gly Ser Leu
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 Pro Pro Asn Ser Phe Gly Trp Gly Ser Phe His Leu Gly Phe Ser Gly
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 Gly Asn Met Asp Pro Glu Pro Gly Arg Cys Arg Arg Thr Asp Gly Lys
 195 200 205
 Lys Trp Arg Cys Ser Arg Asp Ala Val Pro Asp Gln Lys Tyr Cys Glu
 210 215 220
 Arg His Ile Asn Arg Gly Arg His Arg Ser Arg Lys Pro Val Glu Gly
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 Gln Asn Gly His Asn Thr Asn Ala Ala Ala Ala Ala Ser Ala Ala Ala
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 260 265 270
 Val Ala Met Arg Gly Ser Asp Asn Asn Asn Ser Leu Ala Ala Ala Val
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 Gly Thr Gln His His Thr Asn Asn Gln Ser Thr Asp Ser Leu Ala Asn
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PF59082PF60142_PCT_SEQ_LIST.txt

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325 330 335

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340 345 350

Ala Ser Tyr Ala Thr Ser Ser Lys Gly Phe Gly Ser Tyr Leu Asp Phe
355 360 365

Gly Asn Gln Ala Lys His Ala Gly Asn His Asn Asn Val Asp Ser Trp
370 375 380

Pro Glu Glu Leu Lys Ser Asp Trp Thr Gln Leu Ser Met Ser Ile Pro
385 390 395 400

Met Ala Pro Ser Ser Pro Val Gln Asp Lys Leu Ala Leu Ser Pro Leu
405 410 415

Arg Leu Ser Arg Glu Phe Asp Pro Ala Ile His Met Gly Leu Gly Val
420 425 430

Asn Thr Glu Phe Leu Asp Pro Gly Lys Lys Thr Asn Asn Trp Ile Pro
435 440 445

Ile Ser Trp Gly Asn Asn Asn Ser Met Gly Gly Pro Leu Gly Glu Val
450 455 460

Leu Asn Ser Thr Thr Asn Ser Pro Lys Phe Gly Ser Ser Pro Thr Gly
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Val Leu Gln Lys Ser Thr Phe Gly Ser Leu Ser Asn Ser Ser Ser Ala
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Arg Gly Arg Asn Arg Ser Arg Lys Pro Val Glu Thr Pro Thr Thr Val
180 185 190

Asn Ala Thr Ala Thr Ser Met Ala Ser Ser Val Ala Ala Ala Ala Thr
195 200 205

Thr Thr Thr Ala Thr Thr Thr Ser Thr Phe Ala Phe Gly Gly Gly Gly
210 215 220

Gly Ser Glu Glu Val Val Gly Gln Gly Gly Ser Phe Phe Phe Ser Gly
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245 250 255

Glu Met Lys Gln Glu Ser Asn Asn Met Asn Asn Lys Arg Pro Tyr Glu
260 265 270

Ser His Ile Gly Phe Ser Asn Asn Arg Ser Asp Gly Gly His Ile Leu
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290 295 300

Asn Ser Ser Ser Pro Met Ser Ser Ala Thr Cys Leu Ser Ile Ser Met
305 310 315 320

Pro Gly Asn Ser Ser Ser Asp Val Ser Leu Lys Leu Ser Thr Gly Asn
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Glu Glu Gly Ala Arg Ser Asn Asn Asn Gly Arg Asp Gln Gln Asn Met
340 345 350

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PF59082PF60142_PCT_SEQ_LIST.txt

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Met Gln Ala Leu Val Tyr Arg Tyr Ile Glu Ala Gly Leu Arg Val Pro
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50 55 60

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65 70 75 80

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

Met Ser Tyr Asp Asp Phe Ile Asn Glu Lys Glu Ala Ser Met Cys Val
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225 230 235 240

Phe Phe Pro Glu Val Ser Asp Lys Cys Leu Glu Ala Ala Lys Phe Ser
245 250 255

Ser Asn Arg Lys Asn Asp Ile Ile Ala Arg Ser Arg Glu Trp Lys Asn
260 265 270

Met Asn Val Asn Gly Gly Leu Phe His Gly Ile His Phe Ser Pro Asp
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Thr Val Leu Gln Glu Arg Gly Cys Phe Arg Leu Gln Gly Val Glu Thr
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 370 375 380

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gctacagatt tccagaacct ggtcaaagca ttttctgtgt cgggattagt cgttggttat   1380
ccatttggca aactgaacaa tgtagaggat gttgtcactg tgaatctttt cattgaggaa   1440
cttcgtaaga ccgaaaaact caaggatgtg aaatacacat attgggacga gcgattatca   1500
tcaaagaccg ttgaactgat gttgaagccc ttgaatttgc atcctgttca agagaagaca   1560
atgttggaca agttagccgc agtagttata cttcaggagt atttagatta cgcgaaacagg   1620
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<210> 12
<211> 548
<212> PRT
<213> Arabidopsis thaliana

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<400> 12

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20                                     25                                     30

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Gln Ile Gln Ser Gln Thr Ala Thr Ser Ala Ala Ala Ala Pro Leu Pro
35                                     40                                     45

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Leu Phe Val Pro Glu Pro Thr Ser Ser Ser Ser Phe Ser Cys Phe Ser
50                                     55                                     60

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Pro Asp Ser Ser Asn Ser Ser Ser Ser Ser Arg Phe Leu Lys Met Gly
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Asn Phe Phe Ser Trp Ala Gln Trp Gln Glu Leu Glu Leu Gln Ala Leu
85                                     90                                     95

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Ile Tyr Arg Tyr Met Leu Ala Gly Ala Ser Val Pro Gln Glu Leu Leu
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Leu Pro Ile Lys Lys Ser Leu Leu His Gln Ser Pro Met His Phe Leu
115                                    120                                    125

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PF59082PF60142_PCT_SEQ_LIST.txt

His His Pro Leu Gln His Ser Phe Pro His His Gln Pro Ser Trp Tyr
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Trp Gly Arg Gly Ala Met Asp Pro Glu Pro Gly Arg Cys Lys Arg Thr
145 150 155 160

Asp Gly Lys Lys Trp Arg Cys Ser Arg Asp Val Val Ala Gly His Lys
165 170 175

Tyr Cys Asp Arg His Ile His Arg Gly Arg Asn Arg Ser Arg Lys Pro
180 185 190

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

Ser Ser Phe Val Leu Gly Glu Glu Leu Gly His Gly Pro Asn Asn Asn
210 215 220

His Phe Phe Ser Ser Gly Ser Ser Gln Pro Leu His Leu Ser His Gln
225 230 235 240

Gln Ser Cys Ser Ser Glu Met Lys Gln Glu Ser Asn Asn Asn Lys Arg
245 250 255

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

His Ile Leu Arg His Phe Phe Asp Asp Trp Pro Arg Ser Ser Asp Ser
275 280 285

Thr Ser Ser Pro Met Ser Ser Ser Thr Cys His Leu Ser Ile Ser Met
290 295 300

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

Asn Glu Glu Glu Glu Glu Asn Met Arg Asn Asn Asn Asn Glu Arg Glu
325 330 335

Gln Met Asn Trp Trp Ser Asn Gly Gly Asn His His Asn Asn Met Gly
340 345 350

Gly Pro Leu Ala Glu Ala Leu Arg Ser Ala Ser Ser Thr Ser Ser Val
355 360 365

Leu His Gln Met Gly Ile Ser Thr Gln Glu Met Lys Tyr Val Lys Pro
370 375 380

Leu Ser Leu Leu Gly Asn Ala Leu Lys Thr Lys Val Ser Val Pro Gly
385 390 395 400

Arg Phe Leu Gly Leu Asp Val Gly Asp Lys Tyr Val Gly Leu Ala Ile

405

410

415

Ser Asp Pro Ser Asn Met Val Ala Ser Pro Leu Ser Val Leu Leu Arg
 420 425 430

Lys Lys Ser Asn Ile Asp Leu Met Ala Thr Asp Phe Gln Asn Leu Val
 435 440 445

Lys Ala Phe Ser Val Ser Gly Leu Val Val Gly Tyr Pro Phe Gly Lys
 450 455 460

Leu Asn Asn Val Glu Asp Val Val Thr Val Asn Leu Phe Ile Glu Glu
 465 470 475 480

Leu Arg Lys Thr Glu Lys Leu Lys Asp Val Lys Tyr Thr Tyr Trp Asp
 485 490 495

Glu Arg Leu Ser Ser Lys Thr Val Glu Leu Met Leu Lys Pro Leu Asn
 500 505 510

Leu His Pro Val Gln Glu Lys Thr Met Leu Asp Lys Leu Ala Ala Val
 515 520 525

Val Ile Leu Gln Glu Tyr Leu Asp Tyr Ala Asn Arg Tyr Val Asn Thr
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Glu Pro Ala Glu
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<210> 13
 <211> 1482
 <212> DNA
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 atgttttagta tttatgctga ttacaagaat ctgccgttgt ctatgtggat gacagtaact 660
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PF59082PF60142_PCT_SEQ_LIST.txt

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<210> 14
 <211> 493
 <212> PRT
 <213> Arabidopsis thaliana

<400> 14

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

Val Asp Lys Cys His Tyr Glu Leu Asp Val Glu Glu Arg Lys Glu Asp
 35 40 45

Phe Val Gly Gly Phe Gly Phe Gly Val Val Glu Asn Ser His Lys Asp
 50 55 60

Val Met Val Leu Pro His His His Tyr Tyr Pro Ser Tyr Ser Ser Pro
 65 70 75 80

Ser Ser Ser Ser Leu Cys Tyr Cys Ser Ala Gly Val Ser Asp Pro Met
 85 90 95

Phe Ser Val Ser Ser Asn Gln Ala Tyr Thr Ser Ser His Ser Gly Met
 100 105 110

Phe Thr Pro Ala Gly Ser Gly Ser Ala Ala Val Thr Val Ala Asp Pro
 115 120 125

Phe Phe Ser Leu Ser Ser Ser Gly Glu Met Arg Arg Ser Met Asn Glu
 130 135 140

PF59082PF60142_PCT_SEQ_LIST.txt

Asp Ala Gly Ala Ala Phe Ser Glu Ala Gln Trp His Glu Leu Glu Arg
 145 150 155 160
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 165 170 175
 Glu Leu Leu Thr Pro Phe Pro Lys Asn His Gln Ser Asn Thr Asn Pro
 180 185 190
 Asp Val Asp Thr Tyr Arg Ser Gly Met Phe Ser Ile Tyr Ala Asp Tyr
 195 200 205
 Lys Asn Leu Pro Leu Ser Met Trp Met Thr Val Thr Val Ala Val Ala
 210 215 220
 Thr Gly Gly Ser Leu Gln Leu Gly Ile Ala Ser Ser Ala Ser Asn Asn
 225 230 235 240
 Thr Ala Asp Leu Glu Pro Trp Arg Cys Lys Arg Thr Asp Gly Lys Lys
 245 250 255
 Trp Arg Cys Ser Arg Asn Val Ile Pro Asp Gln Lys Tyr Cys Glu Arg
 260 265 270
 His Thr His Lys Ser Arg Pro Arg Ser Arg Lys His Val Glu Ser Ser
 275 280 285
 His Gln Ser Ser His His Asn Asp Ile Arg Thr Ala Lys Asn Asp Thr
 290 295 300
 Ser Gln Leu Val Arg Thr Tyr Pro Gln Phe Tyr Gly Gln Pro Ile Ser
 305 310 315 320
 Gln Ile Pro Val Leu Ser Thr Leu Pro Ser Ala Ser Ser Pro Tyr Asp
 325 330 335
 His His Arg Gly Leu Arg Trp Phe Thr Lys Glu Asp Asp Ala Ile Gly
 340 345 350
 Thr Leu Asn Pro Glu Thr Gln Glu Ala Val Gln Leu Lys Val Gly Ser
 355 360 365
 Ser Arg Glu Leu Lys Arg Gly Phe Asp Tyr Asp Leu Asn Phe Arg Gln
 370 375 380
 Lys Glu Pro Ile Val Asp Gln Ser Phe Gly Ala Leu Gln Gly Leu Leu
 385 390 395 400
 Ser Leu Asn Gln Thr Pro Gln His Asn Gln Glu Thr Arg Gln Phe Val
 405 410 415

PF59082PF60142_PCT_SEQ_LIST.txt

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

Met Ala Gly Gly Gly Met Glu Glu Thr Glu Gly Thr Asn Gln His Gln
435 440 445

Trp Val Ser His Glu Gly Pro Ser Trp Leu Tyr Ser Thr Thr Pro Gly
450 455 460

Gly Pro Leu Ala Glu Ala Leu Cys Leu Gly Val Ser Asn Asn Pro Ser
465 470 475 480

Ser Ser Thr Thr Thr Ser Ser Cys Ser Arg Ser Ser Ser
485 490

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<211> 1608
<212> DNA
<213> Arabidopsis thaliana

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<210> 16
 <211> 535
 <212> PRT
 <213> Arabidopsis thaliana

<400> 16

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

Gly Phe Ile Gly Glu Asp Cys Leu Gln Arg Ser Leu Lys Leu Ala Arg
 35 40 45

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

Ala Ala Tyr Cys Lys Thr Met Ser Phe His Gln Gly Ile Pro Leu Met
 65 70 75 80

Arg Ser Ala Ser Pro Leu Ser Ser Asp Ser Arg Arg Gln Glu Gln Met
 85 90 95

Leu Ser Phe Ser Asp Lys Pro Asp Ala Leu Asp Phe Ser Lys Tyr Val
 100 105 110

Gly Leu Asp Asn Ser Ser Asn Asn Lys Asn Ser Leu Ser Pro Phe Leu
 115 120 125

His Gln Ile Pro Pro Pro Ser Tyr Phe Arg Ser Ser Gly Gly Tyr Gly
 130 135 140

Ser Gly Gly Met Met Met Asn Met Ser Met Gln Gly Asn Phe Thr Gly
 145 150 155 160

Val Lys Gly Pro Phe Thr Leu Thr Gln Trp Ala Glu Leu Glu Gln Gln
 165 170 175

Ala Leu Ile Tyr Lys Tyr Ile Thr Ala Asn Val Pro Val Pro Ser Ser
 180 185 190

Leu Leu Ile Ser Ile Lys Lys Ser Phe Tyr Pro Tyr Gly Ser Leu Pro
 195 200 205

PF59082PF60142_PCT_SEQ_LIST.txt

Pro Ser Ser Phe Gly Trp Gly Thr Phe His Leu Gly Phe Ala Gly Gly
210 215 220

Asn Met Asp Pro Glu Pro Gly Arg Cys Arg Arg Thr Asp Gly Lys Lys
225 230 235 240

Trp Arg Cys Ser Arg Asp Ala Val Pro Asp Gln Lys Tyr Cys Glu Arg
245 250 255

His Ile Asn Arg Gly Arg His Arg Ser Arg Lys Pro Val Glu Val Gln
260 265 270

Ser Gly Gln Asn Gln Thr Ala Ala Ala Ala Ser Lys Ala Val Thr Thr
275 280 285

Pro Gln Gln Pro Val Val Ala Gly Asn Thr Asn Arg Ser Asn Ala Arg
290 295 300

Ala Ser Ser Asn Arg Ser Leu Ala Ile Gly Ser Gln Tyr Ile Asn Pro
305 310 315 320

Ser Thr Glu Ser Leu Pro Asn Asn Arg Gly Val Ser Ile Tyr Pro Ser
325 330 335

Thr Val Asn Leu Gln Pro Lys Glu Ser Pro Val Ile His Gln Lys His
340 345 350

Arg Asn Asn Asn Asn Pro Phe Glu Phe Gly His Ile Ser Ser Asp Ser
355 360 365

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

Phe Ser Ser Asn Gln Glu Lys His Ser Gly Asn His Asn His Asn Ser
385 390 395 400

Trp Pro Glu Glu Leu Thr Ser Asp Trp Thr Gln Leu Ser Met Ser Ile
405 410 415

Pro Ile Ala Ser Ser Ser Pro Ser Ser Thr His Asn Asn Asn Asn Ala
420 425 430

Gln Glu Lys Thr Thr Leu Ser Pro Leu Arg Leu Ser Arg Glu Leu Asp
435 440 445

Leu Ser Ile Gln Thr Asp Glu Thr Thr Ile Glu Pro Thr Val Lys Lys
450 455 460

Val Asn Thr Trp Ile Pro Ile Ser Trp Gly Asn Ser Leu Gly Gly Pro
465 470 475 480

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Gly Glu Val Leu Asn Ser Thr Thr Asn Ser Pro Thr Phe Gly Ser
485 490 495

Ser Pro Thr Gly Val Leu Gln Lys Ser Thr Phe Cys Ser Leu Ser Asn
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Asn Ser Ser Val Ser Ser Pro Ile Ala Glu Asn Asn Arg His Asn Gly
515 520 525

Asp Tyr Phe His Tyr Thr Thr
530 535

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<211> 1098
<212> DNA
<213> Arabidopsis thaliana

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gaaagcagcc aggttttag 1098

<210> 18
<211> 365
<212> PRT
<213> Arabidopsis thaliana

<400> 18

PF59082PF60142_PCT_SEQ_LIST.txt

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Asp Ser Leu Phe Ser Leu Asn Gln Gln Gln Tyr Lys Glu Ser Ser Phe
20 25 30

Gly Phe Arg Asp Met Glu Ile His Pro His Pro Thr Pro Tyr Ala Gly
35 40 45

Asn Gly Leu Leu Gly Cys Tyr Tyr Tyr Tyr Pro Phe Thr Asn Ala Gln
50 55 60

Leu Lys Glu Leu Glu Arg Gln Ala Met Ile Tyr Lys Tyr Met Ile Ala
65 70 75 80

Ser Ile Pro Val Pro Phe Asp Leu Leu Val Ser Ser Pro Ser Ser Ala
85 90 95

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

Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys Ala Lys Glu Val Val
115 120 125

Ser Asn His Lys Tyr Cys Glu Lys His Leu His Arg Gly Arg Pro Arg
130 135 140

Ser Arg Lys His Val Glu Pro Pro Tyr Ser Arg Pro Asn Asn Asn Gly
145 150 155 160

Gly Ser Val Lys Asn Arg Asp Leu Lys Lys Leu Pro Gln Lys Leu Ser
165 170 175

Ser Ser Ser Ile Lys Asp Lys Thr Leu Glu Pro Met Glu Val Ser Ser
180 185 190

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

Leu Ala Thr Thr Glu Gln Glu Asn Lys Tyr Leu Asn Phe Ile Asp Val
210 215 220

Trp Ser Asp Gly Val Arg Ser Ser Glu Lys Gln Ser Thr Thr Ser Thr
225 230 235 240

Pro Val Ser Ser Ser Asn Gly Asn Leu Ser Leu Tyr Ser Leu Asp Leu
245 250 255

Ser Met Gly Gly Asn Asn Leu Met Gly Gln Asp Glu Met Gly Leu Ile
260 265 270

Gln Met Gly Leu Gly Val Ile Gly Ser Gly Ser Glu Asp His His Gly

275

280

285

Tyr Gly Pro Tyr Gly Val Thr Ser Ser Leu Glu Glu Met Ser Ser Trp
 290 295 300

Leu Ala Pro Met Ser Thr Thr Pro Gly Gly Pro Leu Ala Glu Ile Leu
 305 310 315 320

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

Leu Met Glu Thr Pro Thr Pro Ser Ser Ser Pro Ser Arg Val Met Lys
 340 345 350

Lys Met Thr Ser Ser Val Ser Asp Glu Ser Ser Gln Val
 355 360 365

<210> 19

<211> 1658

<212> DNA

<213> Aquilegia formosa x Aquilegia pubescens

<400> 19

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cagcaacaag aagaagaaca gcattgtttt attttaggta ctgatttcaa atctgacagg     1020
tttatgaaaa ctagtactac tactactgag aaagaagaat cacaacaacc acttcgccat     1080
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<210> 20

<211> 377

<212> PRT

<213> Aquilegia formosa x Aquilegia pubescens

<400> 20

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

Met Pro Ile Pro Pro Asp Leu Ile Phe Pro Ile Lys Arg Ser Leu Asp
 35 40 45

Ser Ser Arg Phe Phe Pro His Gln Pro Met Asp Trp Gly Cys Phe Gln
 50 55 60

Met Gly Tyr Gly Arg Lys Val Asp Pro Glu Pro Gly Arg Cys Arg Arg
 65 70 75 80

Thr Asp Gly Lys Lys Trp Arg Cys Ser Lys Glu Ala Tyr Pro Asp Ser
 85 90 95

Lys Tyr Cys Glu Arg His Met His Arg Gly Arg Asn Arg Ser Arg Lys
 100 105 110

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

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

Ser Ser Tyr Ser Leu Ser Ser Ser Leu Thr Ser Asp Lys Ser Gln Gln
 145 150 155 160

Glu His His His Pro Tyr His Asn Thr Pro Leu His Ser Phe Leu Asn
 165 170 175

Pro Ser Arg Thr Ser Cys Ser Ser Pro Arg Thr His Asn Ile Asp Phe

180

185

190

Ser Pro His Ser Asn Asn Asn Ala Asn Leu Val Leu Asp Ser Gly Ser
 195 200 205

Tyr Ser Asn Ser Tyr Glu Asp His Arg Asn Arg Tyr Val His Gly Leu
 210 215 220

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

Leu Arg Ser Val Pro Glu Ser Thr Leu Lys Asp Pro Trp Arg Leu Thr
 245 250 255

Pro Leu Arg Met Ser Ser Ser Thr His Asn Gln Pro Lys Asp Gly Asn
 260 265 270

Phe Ser Asp Leu Gln Arg Gly Tyr Ser Gln Phe Gln Leu Gln His Lys
 275 280 285

Gln Gln Gln Gln Gln Gln Glu Glu Glu Gln His Cys Phe Ile Leu Gly
 290 295 300

Thr Asp Phe Lys Ser Asp Arg Phe Met Lys Thr Ser Thr Thr Thr Thr
 305 310 315 320

Glu Lys Glu Glu Ser Gln Gln Pro Leu Arg His Phe Phe Asp Glu Trp
 325 330 335

Pro Pro Lys Ser Lys Asp Ser Trp Leu Gly Leu Glu Glu Asp Arg Ser
 340 345 350

Asp Gln Gly Ser His Ser Thr Thr Gln Leu Ser Ile Ser Ile Pro Met
 355 360 365

Ser Ser His Glu Phe Ser Val Ser Asn
 370 375

<210> 21
 <211> 1286
 <212> DNA
 <213> Brassica napus

<400> 21
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 caccaacaca atggcaagaa ctggagaatc aagccctaatt ttacaagtac atgggtctcag 120
 gagttcctgt cccacctgag ctcatcttct ccattagaag aagcttggac tcttccttgg 180
 tctctagact cctccctcac caatccattg ggtggggatg ctatcagatg gggttttggta 240
 gaaaaccaga tccagaacca ggaaggtgca gaagaacaga tggttaagaaa tggagatgct 300
 caagagaagc atacctgat tcaaagtact gtgaaaaaca catgcacaga ggaaggaacc 360

PF59082PF60142_PCT_SEQ_LIST.txt

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gtgccagaaa atctattgat cagaatcaga caactgctcc tttaacatca ccatctctct 420
ctttcccca caacaacaac ccaagcccta ccttgtcttc ttcctcctct acttattcag 480
ctgcttcttc atctccttcc attgatgctt acagtaatat caataggctt ggtgttggtta 540
gtagtaacag tagagggttac ttcaacaacc attcccttga ctatccttat cctttgtcct 600
cacctaaaca gcaacaacaa cagcaacaaa ctcttagtca tgtttctgct ttgtcacttc 660
atcaaaacac atctacacct cagctcaatg tctttgcctc tgcaactgac cacaagact 720
tcagatattt tcaagggatt ggggagagag ttggagttgg ggaaagaact tttttccag 780
aagcttctag aagctttcaa gattctccat accatcacca acaaccgtta gcaacggtag 840
tggaataatcc gtacgactgt actactgata ataagtttga tcatcatcat acatactcat 900
catcatctca acatcatcat catgaccaag atcatcgaca acaacaacaa tgttttgttt 960
tgggcgccga catgttcaac aaaccacaa gaactatctt ggaaaacaca tcgagacaag 1020
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cttcccagtc aagactcgac actggtagct gattgatgag gccagatagc atcagtgatg 1200
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<210> 22
 <211> 387
 <212> PRT
 <213> Brassica napus

<400> 22

Met Met Gly Leu Ser Gly Asn Gly Gly Arg Thr Ile Glu Arg Pro Pro
 1 5 10 15

Phe Thr Pro Thr Gln Trp Gln Glu Leu Glu Asn Gln Ala Leu Ile Tyr
 20 25 30

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

Ile Arg Arg Ser Leu Asp Ser Ser Leu Val Ser Arg Leu Leu Pro His
 50 55 60

Gln Ser Ile Gly Trp Gly Cys Tyr Gln Met Gly Phe Gly Arg Lys Pro
 65 70 75 80

Asp Pro Glu Pro Gly Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg
 85 90 95

Cys Ser Arg Glu Ala Tyr Pro Asp Ser Lys Tyr Cys Glu Lys His Met
 100 105 110

His Arg Gly Arg Asn Arg Ala Arg Lys Ser Ile Asp Gln Asn Gln Thr
 Seite 26

115

120

125

Thr Ala Pro Leu Thr Ser Pro Ser Leu Ser Phe Pro Asn Asn Asn Asn
 130 135 140
 Pro Ser Pro Thr Leu Ser Ser Ser Ser Ser Thr Tyr Ser Ala Ala Ser
 145 150 155 160
 Ser Ser Pro Ser Ile Asp Ala Tyr Ser Asn Ile Asn Arg Leu Gly Val
 165 170 175
 Gly Ser Ser Asn Ser Arg Gly Tyr Phe Asn Asn His Ser Leu Asp Tyr
 180 185 190
 Pro Tyr Pro Leu Ser Ser Pro Lys Gln Gln Gln Gln Gln Gln Thr
 195 200 205
 Leu Ser His Val Ser Ala Leu Ser Leu His Gln Asn Thr Ser Thr Pro
 210 215 220
 Gln Leu Asn Val Phe Ala Ser Ala Thr Asp His Lys Asp Phe Arg Tyr
 225 230 235 240
 Phe Gln Gly Ile Gly Glu Arg Val Gly Val Gly Glu Arg Thr Phe Phe
 245 250 255
 Pro Glu Ala Ser Arg Ser Phe Gln Asp Ser Pro Tyr His His Gln Gln
 260 265 270
 Pro Leu Ala Thr Val Val Asp Asn Pro Tyr Asp Cys Thr Thr Asp His
 275 280 285
 Lys Phe Asp His His His Thr Tyr Ser Ser Ser Ser Gln His His His
 290 295 300
 His Asp Gln Asp His Arg Gln Gln Gln Gln Cys Phe Val Leu Gly Ala
 305 310 315 320
 Asp Met Phe Asn Lys Pro Thr Arg Thr Ile Leu Glu Asn Thr Ser Arg
 325 330 335
 Gln Asp Tyr Leu Asn Gln Glu Glu Glu Glu Lys Asp Ser Ser Asp Thr
 340 345 350
 Lys Lys Ser Leu His His Phe Phe Gly Glu Glu Trp Thr Gln Asn Lys
 355 360 365
 Asn Ser Ser Asp Ser Trp Leu Asp Leu Ser Ser Gln Ser Arg Leu Asp
 370 375 380
 Thr Gly Ser
 385

PF59082PF60142_PCT_SEQ_LIST.txt

<210> 23
 <211> 1559
 <212> DNA
 <213> Hordeum vulgare

<400> 23
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 cgatgccctt tgcctccctg tcgccggcag ccgaccacca ccgctcctcc cccatcttcc 120
 ccttctgccg ctctccctt ctctactcgg taggggagga ggcgggcgcat cagcatcctc 180
 atcctcagca gcagcagcag cagcacgcga tgagcggcgc gcggtgggcg gcgaggccgg 240
 cgcccttcac ggcgggcgag tacgaggagc tggagcagca ggcgctcatc tacaagtacc 300
 tcgtcgccgg cgtccccgtc ccgcaggacc tcctcctccc catccgccgc ggcttcgaga 360
 ccctcgctc gcgcttctac caccaccacg cccttgggta cgggtcctac ttcgggaaga 420
 agctggatcc ggagccgggg cggtgccggc ggacggacgg caagaagtgg cggtgctcca 480
 aggaggccgc tcaggactcc aagtactgcg agcgccacat gcaccgcggc cgcaaccgtt 540
 caagaaagcc tgtggaaacg cagctcgctg ccagctccca ctcccagtcc cagcagcacg 600
 ccaccgccgc cttccacaac cactcgccgt atccggcgat cgccactggc ggtggctcct 660
 tcgccctggg gtctgctcag ctgcacatgg acactgctgc gccttacgcg acgaccgccg 720
 gtgctgccgg aaacaaagat ttcaggtatt ctgcctatgg agtgaggacg tcggcgatcg 780
 aggagcacia ccagttcatc accgcggcca tggacaccgc catggacaac tactcgtggc 840
 gcctgatgcc gtcccaggcc tcggcattct cgctctccag ctaccccatg ctgggcacgc 900
 tgagcgacct ggaccagagc gcgatctgct cgctggccaa gactgagagg gagccactgt 960
 ccttcttcgg cggcgggcgc gacttcgacg acgactcggc tgcggtgaag caggagaacc 1020
 agacgctgcg gcccttcttc gacgagtggc ccaaggacag ggactcgtgg ccggagctgc 1080
 aagaccacga cgccaacaac aacagcaacg ccttctcagc caccaagctg tccatctcca 1140
 tgccggtcac cagctccgac ttctctggca ccaccgccg ctcccgtcg cccaacggta 1200
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 gccgactgca gcttgcttgc tcattttgta tggatcgtcg tgcagcagga acgaaacact 1380
 actccttta tttcctttct ttaatttcac aacgtttttt ctgggttttg ccgtgtatcg 1440
 gccggaactg tactaccaag ttttctatag cctcgatggc catgcacgac atcgttgact 1500
 gtttcccgcg cacttactgt tgaaataatc ttccattttt ggcaaaaaaa aaaaaaaa 1559

<210> 24
 <211> 385
 <212> PRT
 <213> Hordeum vulgare

<400> 24

Met Ala Met Pro Phe Ala Ser Leu Ser Pro Ala Ala Asp His His Arg

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

PF59082PF60142_PCT_SEQ_LIST.txt

Ala Ile Cys Ser Leu Ala Lys Thr Glu Arg Glu Pro Leu Ser Phe Phe
290 295 300

Gly Gly Gly Gly Asp Phe Asp Asp Asp Ser Ala Ala Val Lys Gln Glu
305 310 315 320

Asn Gln Thr Leu Arg Pro Phe Phe Asp Glu Trp Pro Lys Asp Arg Asp
325 330 335

Ser Trp Pro Glu Leu Gln Asp His Asp Ala Asn Asn Asn Ser Asn Ala
340 345 350

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

Phe Ser Gly Thr Thr Ala Gly Ser Arg Ser Pro Asn Gly Ile Tyr Ser
370 375 380

Arg
385

<210> 25

<211> 1521

<212> DNA

<213> Lycopersicon esculentum

<400> 25

gatgataaga aacacacaaa tgacttaact ttgcaggttt caccgcactc gacactgcaa	60
aaaagataca tataaaaaaa aaggtccact caactctctg caaaaataaa aaaaattaaa	120
aacttttgtc caagacttaa ctttctcttc agaaataaat ttgccttcac attaatattt	180
tgttgttagt aacaaaaatc attctcaatc gaaacatgga cttcaatatg aagcaatgga	240
gtaatcaaca tgagtcagaa aatcaagaat caccaacaaa gttaccaaga cttcttcttg	300
acttccactc tgtttcttct gattctgctt ctgctgctgc tctaccattg tttgtatctg	360
aaccaacaac atcaacaaca acttgtacca aattaatgtc agattcagca accactgtca	420
ccaccaaatt tccaaggatt ggaagtgggt gtggttactt cagcttggct caatggcaag	480
aacttgaact acacagtttg atttttaggc attttgtagc tgggtgccct gttccttctg	540
aactacttca tcttgtaag aaaagtatta ttgcttctcc tcctcctcct cttcatatt	600
actttgtca tccatatcaa cagtatctc attatcaaca agctttgatg cagtcagggt	660
actggggtag agccgccatg gatccagaac caggaagggt taggaggact gatggcaaga	720
aatggagggt ctcaagggat gtagtggtg gccagaaata ctgcgagcgc cacgttcac	780
gtggccgcag ccgttcaaga aagcctgtgg aaattccac acctgccaac aatggcagta	840
aaaacaacaa cactgtttct catcatcaag ctttggaaa aatgactgga catgctcatg	900
ctggtggtgg tgctcctcag ttttctctt cgggacattc accttccact aatgctcctt	960
ttcatctcaa tcaaaggcca attaagggtc caccacaaga agtacttcaa aaagatgtat	1020

PF59082PF60142_PCT_SEQ_LIST.txt

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ctagacaaca acttcaagaa ggcgacaatg ctgcaaccag cctgtccatt tcgatgcccg 1140
gtgtaggggg taaccctcg tcagacttct cgttgaagct ttcaactggg aattactatg 1200
attcaggtac tcaagttagt aatgttgaac ggtctacatg ggggacgagt caccaccacg 1260
tagcctcaat ggggtggtcca cttgccgagg ccttaaggct atcaacaact aactcgtccc 1320
ctactagcgt gttgcatcaa ttggcacgag gtagcgcgct cgaggccagc tatattagca 1380
cttgatttct gcaagtgttc ttgttaaata ttttttctt ttggacttta ttgtttttta 1440
acttggttgt gttgttgttc attgttcttt attggtattg atatacctaa ctgtcacctg 1500
tacaaaaaaaa aaaaaaaaaa a 1521

<210> 26
<211> 389
<212> PRT
<213> Lycopersicon esculentum

<400> 26

Met Asp Phe Asn Met Lys Gln Trp Ser Asn Gln His Glu Ser Glu Asn
1 5 10 15

Gln Glu Ser Pro Thr Lys Leu Pro Arg Leu Leu Leu Asp Phe His Ser
20 25 30

Val Ser Ser Asp Ser Ala Ser Ala Ala Ala Leu Pro Leu Phe Val Ser
35 40 45

Glu Pro Thr Thr Ser Thr Thr Thr Cys Thr Lys Leu Met Ser Asp Ser
50 55 60

Ala Thr Thr Val Thr Thr Lys Phe Pro Arg Ile Gly Ser Gly Gly Gly
65 70 75 80

Tyr Phe Ser Leu Ala Gln Trp Gln Glu Leu Glu Leu His Ser Leu Ile
85 90 95

Phe Arg His Phe Val Ala Gly Ala Pro Val Pro Ser Glu Leu Leu His
100 105 110

Leu Val Lys Lys Ser Ile Ile Ala Ser Pro Pro Pro Pro Pro Ser Tyr
115 120 125

Tyr Phe Ala His Pro Tyr Gln Gln Tyr Pro His Tyr Gln Gln Ala Leu
130 135 140

Met Gln Ser Gly Tyr Trp Gly Arg Ala Ala Met Asp Pro Glu Pro Gly
145 150 155 160

Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys Ser Arg Asp Val
165 170 175

PF59082PF60142_PCT_SEQ_LIST.txt

Val Ala Gly Gln Lys Tyr Cys Glu Arg His Val His Arg Gly Arg Ser
180 185 190

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

Lys Asn Asn Asn Thr Val Ser His His Gln Ala Phe Gly Lys Met Thr
210 215 220

Gly His Ala His Ala Gly Gly Gly Ala Pro Gln Phe Ser Leu Ser Gly
225 230 235 240

His Ser Pro Ser Thr Asn Ala Pro Phe His Leu Asn Gln Arg Pro Ile
245 250 255

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

Gly Lys Ser Ser Ser Gly Gln Ile Leu Arg His Phe Phe Asp Asp Trp
275 280 285

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

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

Lys Leu Ser Thr Gly Asn Tyr Tyr Asp Ser Gly Thr Gln Val Ser Asn
325 330 335

Val Glu Arg Ser Thr Trp Gly Thr Ser His His His Val Ala Ser Met
340 345 350

Gly Gly Pro Leu Ala Glu Ala Leu Arg Ser Ser Thr Thr Asn Ser Ser
355 360 365

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

Ser Tyr Ile Ser Thr
385

<210> 27
<211> 1100
<212> DNA
<213> Medicago truncatula

<400> 27
atgatgagtg caagttcaag aaataggtca cttttcacac caaatcaatg gcaagaactt 60
gaacaacaag ccctagtttt taaatacatg gttactggaa cacctattcc accagatctc 120
atatactcta ttaagagaag tttagacact tcaatatctt caagaatctt tcctcatcca 180
Seite 32

PF59082PF60142_PCT_SEQ_LIST.txt

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ccaattgggt ggggatgttt tgaaatggga tttggcagaa aagtagaccc agagccaggg 240
aggtgcagaa gaacagatgg caagaaatgg agatgctcaa aggaagcata tccagactca 300
aagtactgtg aaagacacat gcacagaggt agaaaccgtt caagaaagcc tgtggaacta 360
gtagtttctt cttcaacaac aacaccaaca aataacacaa acacagcatc ttcttacagc 420
aacagaaaca tctccttgaa caacaacagc agcagcataa actcaccttc ttctttccct 480
ttctctactt catccatggc ttgtcatgat cagtcacaat ctttttcaca atcctaccaa 540
aactcttctt taaaccctta ctattactct caatcaatta cctctactaa cccacttgat 600
cattctcatt ttcaaactca agatgctact actcatcacc tcttttttga ctcaacatct 660
tattctcagg atgacaagga ctttaggtat gtacaagttc aaggaataag agatgggtact 720
gtggatgaga gaactttctt tccagaagct acagggttcac taggagctg ttatcatgat 780
tcatatcaac aacaactatc aatgaatccc tttaagtctt actcaagctc acagtttcag 840
aatatcaatg atgataattc aagacaacaa caagaacaac actgttttgt tttaggcact 900
gacatcaagt caacaagaac aacaacaag gacaaagaaa gtgagacaac tcagaaacca 960
cttcatcatt tctttggtga gtggacacca aagaacacag attcctggct agatcttgct 1020
tctaactcca gaattccaac aggttgatta tcatttatca tcattcctat gtttttgttt 1080
tttttttggt attattaata 1100

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<210> 28
<211> 348
<212> PRT
<213> Medicago truncatula
<400> 28

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

Trp Gln Glu Leu Glu Gln Gln Ala Leu Val Phe Lys Tyr Met Val Thr
          20          25          30

Gly Thr Pro Ile Pro Pro Asp Leu Ile Tyr Ser Ile Lys Arg Ser Leu
          35          40          45

Asp Thr Ser Ile Ser Ser Arg Ile Phe Pro His Pro Pro Ile Gly Trp
          50          55          60

Gly Cys Phe Glu Met Gly Phe Gly Arg Lys Val Asp Pro Glu Pro Gly
65          70          75          80

Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys Ser Lys Glu Ala
          85          90          95

Tyr Pro Asp Ser Lys Tyr Cys Glu Arg His Met His Arg Gly Arg Asn
          100          105          110

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PF59082PF60142_PCT_SEQ_LIST.txt

Arg Ser Arg Lys Pro Val Glu Leu Val Val Ser Ser Ser Thr Thr Thr
115 120 125

Pro Thr Asn Asn Thr Asn Thr Ala Ser Ser Tyr Ser Asn Arg Asn Ile
130 135 140

Ser Leu Asn Asn Asn Ser Ser Ser Ile Asn Ser Pro Ser Ser Phe Pro
145 150 155 160

Phe Ser Thr Ser Ser Met Ala Cys His Asp Gln Ser Gln Ser Phe Ser
165 170 175

Gln Ser Tyr Gln Asn Ser Ser Leu Asn Pro Tyr Tyr Tyr Ser Gln Ser
180 185 190

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

Ala Thr Thr His His Leu Phe Leu Asp Ser Thr Ser Tyr Ser Gln Asp
210 215 220

Asp Lys Asp Phe Arg Tyr Val Gln Val Gln Gly Ile Arg Asp Gly Thr
225 230 235 240

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

Cys Tyr His Asp Ser Tyr Gln Gln Gln Leu Ser Met Asn Pro Phe Lys
260 265 270

Ser Tyr Ser Ser Ser Gln Phe Gln Asn Ile Asn Asp Asp Asn Ser Arg
275 280 285

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

Thr Arg Thr Thr Asn Lys Asp Lys Glu Ser Glu Thr Thr Gln Lys Pro
305 310 315 320

Leu His His Phe Phe Gly Glu Trp Thr Pro Lys Asn Thr Asp Ser Trp
325 330 335

Leu Asp Leu Ala Ser Asn Ser Arg Ile Pro Thr Gly
340 345

<210> 29
<211> 1302
<212> DNA
<213> Medicago truncatula

<400> 29
atgcatatgt tgacaatgga agctaaacct cttcaacttg ttccctcttc acacaacagc 60
acaactggtg gtggaccca gatgaagatt gagaatggtg aagttgatga agagaaaagg 120
Seite 34

PF59082PF60142_PCT_SEQ_LIST.txt

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cgtgaacttg atcatcaagt ttttattttt aatcattttg cttataatct tcctcttcct 240
tattaccttt tgcaatttcc aagtaatatg tcagagtaca gtcgtcgtgg gtctgattat 300
gtgactatgg tggatcaaga accacatagg tgtagaagaa ctgacggaaa gaaatggagg 360
tgcggcaagg acacagtacc taatcagaag tattgtgaac gtcacatgca cagaggtcga 420
aatcgttcaa gaaagcttgt ggaaacatct caacttaact ctcctttgaa aacaaatcct 480
agtgggtgtg gcaagtcaca tgcaaaacta gtcccaaaca ttaaatcttc agtttcaaata 540
ccaaaccctt tgattattca tcacaatggc acattctcat acaatccgag gaccttctgc 600
gttgtagata cttcttctgt ttgtgatcgg tcgagacatg tcatagatta tggtgccact 660
gcagtgacaa cttcgggaag cacgacatcc gtttctttgg ataacagagt ttgtcctaac 720
gtatgcaagc aagatgagca gatcaagagg tgtatcaccg acaacgtggg tattaagaat 780
ggtcggaaag gaagcatatc ttgtgaaagt attggcatct ctactggaat aggcttttcc 840
ccaaagagtg ttcttccagt ttctggttgc aatgattcat acctcaacaa cagaaacaat 900
atattagaac ctgaaccgg tagatgccga agaacagatg gtaagaagtg gcgatgcaag 960
agtgcggttc ttccaggta gaagtattgt gcaacacata tgcataagagg tgctaaaagg 1020
cgttttacaa acctcgaatc tcctcctcct gccaccactg ttattcctaa aactactgat 1080
attagttcag ctgttaccat tgctcagttg cccgaccctt cggctccaat cgacatccag 1140
aaagcgaatt gttggtctcc gagcactaag ctttcaatgt cggttcaaga aagtgcgccc 1200
tttgttgatt gtaatgagaa aagtgttagc agcggtgaca cggatggtac tagtaccacc 1260
atcactgaca ccatgaatga gtgtagctat ctttctttct aa 1302

```

```

<210> 30
<211> 433
<212> PRT
<213> Medicago truncatula
<400> 30

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

```

```

Ser His Asn Ser Thr Thr Gly Gly Gly Pro Gln Met Lys Ile Glu Asn
20          25          30

```

```

Gly Glu Val Asp Glu Glu Lys Arg Val Val Val Gly Val Lys Glu Asp
35          40          45

```

```

Ile Glu Asn Lys Pro Leu Ile Thr Glu Ala Gln Arg Arg Glu Leu Asp
50          55          60

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His Gln Val Phe Ile Phe Asn His Phe Ala Tyr Asn Leu Pro Leu Pro
65          70          75          80

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PF59082PF60142_PCT_SEQ_LIST.txt

Tyr Tyr Leu Leu Gln Phe Pro Ser Asn Met Ser Glu Tyr Ser Arg Arg
 85 90 95
 Gly Ser Asp Tyr Val Thr Met Val Asp Gln Glu Pro His Arg Cys Arg
 100 105 110
 Arg Thr Asp Gly Lys Lys Trp Arg Cys Gly Lys Asp Thr Val Pro Asn
 115 120 125
 Gln Lys Tyr Cys Glu Arg His Met His Arg Gly Arg Asn Arg Ser Arg
 130 135 140
 Lys Leu Val Glu Thr Ser Gln Leu Asn Ser Pro Leu Lys Thr Asn Pro
 145 150 155 160
 Ser Gly Gly Gly Lys Ser His Ala Lys Leu Val Pro Asn Ile Lys Ser
 165 170 175
 Ser Val Ser Asn Pro Asn Pro Leu Ile Ile His His Asn Gly Thr Phe
 180 185 190
 Ser Tyr Asn Pro Arg Thr Phe Cys Val Val Asp Thr Ser Ser Val Cys
 195 200 205
 Asp Arg Ser Arg His Val Ile Asp Tyr Gly Ala Thr Ala Val Thr Thr
 210 215 220
 Ser Gly Ser Thr Thr Ser Val Ser Leu Asp Asn Arg Val Cys Pro Asn
 225 230 235 240
 Val Cys Lys Gln Asp Glu Gln Ile Lys Arg Cys Ile Thr Asp Asn Val
 245 250 255
 Gly Ile Lys Ser Gly Arg Lys Gly Ser Ile Ser Cys Glu Ser Ile Gly
 260 265 270
 Ile Ser Thr Gly Ile Gly Phe Ser Pro Lys Ser Val Leu Pro Val Ser
 275 280 285
 Gly Cys Asn Asp Ser Tyr Leu Asn Asn Arg Asn Asn Ile Leu Glu Pro
 290 295 300
 Glu Pro Gly Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys Lys
 305 310 315 320
 Ser Ala Val Leu Pro Gly Gln Lys Tyr Cys Ala Thr His Met His Arg
 325 330 335
 Gly Ala Lys Arg Arg Phe Thr Asn Leu Glu Ser Pro Pro Pro Ala Thr
 340 345 350
 Thr Val Ile Pro Lys Thr Thr Asp Ile Ser Ser Ala Val Thr Ile Ala
 Seite 36

355

360

365

Gln Leu Pro Asp Pro Ser Ala Pro Ile Asp Ile Gln Lys Ala Asn Cys
 370 375 380

Trp Ser Pro Ser Thr Lys Leu Ser Met Ser Val Gln Glu Ser Ala Pro
 385 390 395 400

Phe Val Asp Cys Asn Glu Lys Ser Val Ser Ser Gly Asp Thr Asp Gly
 405 410 415

Thr Ser Thr Thr Ile Thr Asp Thr Met Asn Glu Cys Ser Tyr Leu Ser
 420 425 430

Phe

<210> 31
 <211> 1185
 <212> DNA
 <213> Oryza sativa

<400> 31
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 gccgcgaccg cctccctcct ccccttctgc cgctccaccc cgctctccgc gggcggtggt 120
 ggcgtcgcga tgggggagga cgcgccgatg accgcgaggt ggccgccggc ggcggcggcg 180
 aggctgccgc cgttcaccgc ggcgcagtac gaggagctgg agcagcaggc gctcatatac 240
 aagtacctgg tggcaggcgt gcccgctccg ccgcatctcg tgctcccat ccgccgcgga 300
 ctcgactccc tcgccgccg cttctacaac catcccgccc ttggatatgg tccgtacttc 360
 ggcaagaagc tggaccaga gccagggcg tgccggcgta cggacggcaa gaaatggcgg 420
 tgctcgaagg aggccgcgcc ggattccaag tactgcgagc gccacatgca ccgcggccgc 480
 aaccgttcaa gaaagcctgt ggaaacgcag ctggtcgccc agtcccaacc gccctcatct 540
 gttgtcgggt ctgcggcggc gcccttctgt gctgcctcca atggcagcag cttccaaaac 600
 cactctcttt accctgctat tgccggcagc aatggcgggg gcggggggag gaacatgccc 660
 agctcatttg gtcggcggtt gggttctcag ctgcacatgg ataatgctgc cccttatgca 720
 gctgttggtg gtggaacagg caaagatctc aggtatactg cttatggcac aagatctttg 780
 gcggatgagc agagtcaact cattactgaa gctatcaaca catctattga aaatccatgg 840
 cggctgctgc catctcagaa ctcgccattt cccctttcaa gctattctca gctgggggca 900
 ctaagtgacc ttggtcagaa cacccccagc tcactttcaa aggttcagag gcagccactt 960
 tcgttctttg ggaacgacta tgcggctgtc gattctgtga agcaagagaa ccagacgctg 1020
 cgtcccttct ttgatgagtg gccaaaggga agggattcat ggtcagacct cgctgatgag 1080
 aatgctaatac tttcgtcatt ctcaggcacc caactgtcga tctccatacc aatggcatcc 1140
 tctgacttct cggcggccag ttctcgatca actaatggtg actga 1185

PF59082PF60142_PCT_SEQ_LIST.txt

<210> 32
 <211> 394
 <212> PRT
 <213> Oryza sativa

<400> 32

Met Ala Met Pro Tyr Ala Ser Leu Ser Pro Ala Val Ala Asp His Arg
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Ser Ser Pro Ala Ala Ala Thr Ala Ser Leu Leu Pro Phe Cys Arg Ser
 20 25 30

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

Pro Met Thr Ala Arg Trp Pro Pro Ala Ala Ala Ala Arg Leu Pro Pro
 50 55 60

Phe Thr Ala Ala Gln Tyr Glu Glu Leu Glu Gln Gln Ala Leu Ile Tyr
 65 70 75 80

Lys Tyr Leu Val Ala Gly Val Pro Val Pro Pro Asp Leu Val Leu Pro
 85 90 95

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

Ala Leu Gly Tyr Gly Pro Tyr Phe Gly Lys Lys Leu Asp Pro Glu Pro
 115 120 125

Gly Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys Ser Lys Glu
 130 135 140

Ala Ala Pro Asp Ser Lys Tyr Cys Glu Arg His Met His Arg Gly Arg
 145 150 155 160

Asn Arg Ser Arg Lys Pro Val Glu Thr Gln Leu Val Ala Gln Ser Gln
 165 170 175

Pro Pro Ser Ser Val Val Gly Ser Ala Ala Ala Pro Leu Ala Ala Ala
 180 185 190

Ser Asn Gly Ser Ser Phe Gln Asn His Ser Leu Tyr Pro Ala Ile Ala
 195 200 205

Gly Ser Asn Gly Gly Gly Gly Gly Arg Asn Met Pro Ser Ser Phe Gly
 210 215 220

Ser Ala Leu Gly Ser Gln Leu His Met Asp Asn Ala Ala Pro Tyr Ala
 225 230 235 240

Ala Val Gly Gly Gly Thr Gly Lys Asp Leu Arg Tyr Thr Ala Tyr Gly
 Seite 38

245

250

255

Thr Arg Ser Leu Ala Asp Glu Gln Ser Gln Leu Ile Thr Glu Ala Ile
 260 265 270

Asn Thr Ser Ile Glu Asn Pro Trp Arg Leu Leu Pro Ser Gln Asn Ser
 275 280 285

Pro Phe Pro Leu Ser Ser Tyr Ser Gln Leu Gly Ala Leu Ser Asp Leu
 290 295 300

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

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

Asn Gln Thr Leu Arg Pro Phe Phe Asp Glu Trp Pro Lys Gly Arg Asp
 340 345 350

Ser Trp Ser Asp Leu Ala Asp Glu Asn Ala Asn Leu Ser Ser Phe Ser
 355 360 365

Gly Thr Gln Leu Ser Ile Ser Ile Pro Met Ala Ser Ser Asp Phe Ser
 370 375 380

Ala Ala Ser Ser Arg Ser Thr Asn Gly Asp
 385 390

<210> 33
 <211> 1194
 <212> DNA
 <213> Oryza sativa

<400> 33
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 gcgtcgcagt ggcaggagct ggagcaccag gcgtcatct acaagtacat ggcgtccggg 120
 actcccatcc cctccgacct catcctcccc ctccgccgca gcttcctcct cgactccgcc 180
 ctgccacct ccccttcct cgccttcct cccaacctt cactggggtg gggttgcttt 240
 ggcatggggt ttgggcggaa ggcggaggac ccggagccag ggcgatgccg gcgtacggac 300
 ggcaagaagt ggcggtgctc caaggaggcg taccgggact ccaagtactg cgagaagcac 360
 atgcaccgtg gcaagaaccg ttcaagaaag cctgtggaaa tgccttggc cagccgccg 420
 ccgccgtcct cctccgccac ctccgccg cggaacacct ccgccggcgt cgcaccacc 480
 accaccacca cctcctcccc ggcgccctcc tacagccgcc cggcgccgca cgacgcggcg 540
 ccgtaccagg cgctctacgg cgggccctac gccgcggcca ccgcgcgcac cccgcgccg 600
 gcggcgtacc acgcgcaggt gagcccgtt cacctccagc tcgacaccac ccaccgcac 660
 ccgccgccgt cctactactc catggaccac aaggagtacg cgtacgggca cgccaccaag 720

PF59082PF60142_PCT_SEQ_LIST.txt

gaggtgcacg gcgagcacgc cttcttctcc gatggcaccg agagggagca ccaccacgcc 780
gccgccgggc acggccagtg gcagttcaag cagctcggca tggagcccaa gcagagcacc 840
acgcctctct tcccgggagc cggtacggc cacaccgagg cgtcgccgta cgccattgat 900
ctttcaaaag aggacgacga tgagaaagag aggcggcaac agcagcagca gcagcagcag 960
cagcactgct tcctcctggg cgccgacctc cgtctggaga agccggcggg ccacgaccac 1020
gcggcggcgg cgagaaacc tctccgccac ttcttcgacg agtggccgca tgagaagaac 1080
agcaagggct cctggatggg gctcgaaggc gagacgcagc tgtccatgtc catccccatg 1140
gccgccaacg acctcccgat caccaccacc tcccgctacc acaatgatga ttaa 1194

<210> 34
<211> 397
<212> PRT
<213> Oryza sativa

<400> 34

Met Met Met Met Ser Gly Arg Pro Ser Gly Gly Ala Gly Gly Gly Arg
1 5 10 15

Tyr Pro Phe Thr Ala Ser Gln Trp Gln Glu Leu Glu His Gln Ala Leu
20 25 30

Ile Tyr Lys Tyr Met Ala Ser Gly Thr Pro Ile Pro Ser Asp Leu Ile
35 40 45

Leu Pro Leu Arg Arg Ser Phe Leu Leu Asp Ser Ala Leu Ala Thr Ser
50 55 60

Pro Ser Leu Ala Phe Pro Pro Gln Pro Ser Leu Gly Trp Gly Cys Phe
65 70 75 80

Gly Met Gly Phe Gly Arg Lys Ala Glu Asp Pro Glu Pro Gly Arg Cys
85 90 95

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

Asp Ser Lys Tyr Cys Glu Lys His Met His Arg Gly Lys Asn Arg Ser
115 120 125

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

Ser Ala Thr Ser Ala Ala Ser Asn Thr Ser Ala Gly Val Ala Pro Thr
145 150 155 160

Thr Thr Thr Thr Ser Ser Pro Ala Pro Ser Tyr Ser Arg Pro Ala Pro
165 170 175

His Asp Ala Ala Pro Tyr Gln Ala Leu Tyr Gly Gly Pro Tyr Ala Ala

180

185

190

Ala Thr Ala Arg Thr Pro Ala Ala Ala Ala Tyr His Ala Gln Val Ser
 195 200 205

Pro Phe His Leu Gln Leu Asp Thr Thr His Pro His Pro Pro Pro Ser
 210 215 220

Tyr Tyr Ser Met Asp His Lys Glu Tyr Ala Tyr Gly His Ala Thr Lys
 225 230 235 240

Glu Val His Gly Glu His Ala Phe Phe Ser Asp Gly Thr Glu Arg Glu
 245 250 255

His His His Ala Ala Ala Gly His Gly Gln Trp Gln Phe Lys Gln Leu
 260 265 270

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

Tyr Gly His Thr Ala Ala Ser Pro Tyr Ala Ile Asp Leu Ser Lys Glu
 290 295 300

Asp Asp Asp Glu Lys Glu Arg Arg Gln Gln Gln Gln Gln Gln Gln
 305 310 315 320

Gln His Cys Phe Leu Leu Gly Ala Asp Leu Arg Leu Glu Lys Pro Ala
 325 330 335

Gly His Asp His Ala Ala Ala Ala Gln Lys Pro Leu Arg His Phe Phe
 340 345 350

Asp Glu Trp Pro His Glu Lys Asn Ser Lys Gly Ser Trp Met Gly Leu
 355 360 365

Glu Gly Glu Thr Gln Leu Ser Met Ser Ile Pro Met Ala Ala Asn Asp
 370 375 380

Leu Pro Ile Thr Thr Thr Ser Arg Tyr His Asn Asp Asp
 385 390 395

<210> 35
 <211> 1371
 <212> PRT
 <213> Oryza sativa

<400> 35

Ala Thr Gly Cys Ala Gly Gly Gly Thr Gly Cys Ala Ala Thr Gly Gly
 1 5 10 15

Cys Cys Ala Gly Gly Gly Thr Gly Ala Gly Gly Gly Gly Thr Cys Cys
 20 25 30

PF59082PF60142_PCT_SEQ_LIST.txt

Cys Thr Thr Cys Ala Cys Gly Cys Cys Gly Thr Cys Thr Cys Ala Gly
 35 40 45
 Thr Gly Gly Ala Thr Cys Gly Ala Gly Cys Thr Gly Gly Ala Gly Cys
 50 55 60
 Ala Cys Cys Ala Gly Gly Cys Gly Cys Thr Gly Ala Thr Ala Thr Ala
 65 70 75 80
 Cys Ala Ala Gly Thr Ala Cys Thr Thr Gly Gly Cys Thr Gly Cys Gly
 85 90 95
 Ala Ala Thr Ala Gly Cys Cys Cys Thr Gly Thr Ala Cys Cys Ala Cys
 100 105 110
 Ala Cys Ala Gly Cys Cys Thr Cys Cys Thr Cys Ala Thr Cys Cys Cys
 115 120 125
 Cys Ala Thr Cys Ala Gly Gly Ala Gly Gly Ala Gly Cys Cys Thr Cys
 130 135 140
 Ala Cys Ala Thr Cys Gly Cys Cys Cys Thr Ala Cys Thr Cys Ala Cys
 145 150 155 160
 Cys Thr Gly Cys Cys Thr Ala Cys Thr Thr Thr Gly Gly Cys Thr Cys
 165 170 175
 Ala Ala Gly Cys Ala Cys Ala Thr Thr Gly Gly Gly Ala Thr Gly Gly
 180 185 190
 Gly Gly Ala Thr Cys Thr Thr Thr Cys Cys Ala Gly Cys Thr Gly Gly
 195 200 205
 Gly Cys Thr Ala Cys Thr Cys Cys Gly Gly Cys Ala Gly Cys Gly Cys
 210 215 220
 Gly Gly Ala Thr Cys Cys Gly Gly Ala Gly Cys Cys Cys Gly Gly Cys
 225 230 235 240
 Cys Gly Gly Thr Gly Cys Cys Gly Cys Cys Gly Gly Ala Cys Gly Gly
 245 250 255
 Ala Cys Gly Gly Cys Ala Ala Gly Ala Ala Ala Thr Gly Gly Cys Gly
 260 265 270
 Gly Thr Gly Cys Thr Cys Gly Ala Gly Gly Gly Ala Thr Gly Cys Gly
 275 280 285
 Gly Thr Cys Gly Cys Cys Gly Ala Cys Cys Ala Gly Ala Ala Gly Thr
 290 295 300

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

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

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

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

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

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

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

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

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

Gly Thr Gly Gly Cys Gly Gly Ala Gly Cys Thr Gly Thr Thr Gly Cys
450 455 460

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

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

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

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

Thr Gly Cys Thr Cys Thr Cys Thr Gly Cys Ala Ala Thr Ala Thr Ala
530 535 540

Gly Cys Ala Gly Gly Gly Ala Thr Cys Thr Gly Gly Cys Ala Ala Ala
545 550 555 560

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

Gly Ala Ala Cys Ala Ala Gly Thr Gly Cys Ala Ala Gly Ala Cys Thr

580

585

590

Cys Ala Gly Ala Cys Ala Gly Thr Cys Thr Cys Thr Cys Gly Ala Thr
 595 600 605
 Gly Cys Thr Gly Ala Cys Thr Thr Cys Cys Ala Thr Thr Ala Gly Cys
 610 615 620
 Ala Cys Gly Ala Gly Ala Ala Ala Thr Ala Cys Gly Gly Gly Cys Ala
 625 630 635 640
 Gly Cys Cys Thr Gly Thr Thr Thr Cys Cys Gly Thr Thr Cys Thr Cys
 645 650 655
 Ala Ala Ala Ala Cys Ala Ala Cys Ala Thr Ala Ala Thr Cys Cys Thr
 660 665 670
 Thr Thr Thr Gly Ala Ala Gly Thr Gly Thr Cys Cys Ala Ala Cys Thr
 675 680 685
 Cys Ala Ala Gly Gly Cys Cys Ala Gly Ala Thr Thr Thr Thr Gly Gly
 690 695 700
 Cys Cys Thr Ala Gly Thr Ala Thr Cys Ala Cys Cys Thr Gly Ala Thr
 705 710 715 720
 Thr Cys Ala Cys Thr Gly Ala Thr Gly Ala Gly Thr Thr Cys Thr Cys
 725 730 735
 Cys Thr Cys Ala Thr Ala Gly Cys Thr Cys Cys Thr Thr Gly Gly Ala
 740 745 750
 Gly Ala Ala Cys Gly Thr Cys Ala Ala Thr Thr Thr Gly Cys Thr Cys
 755 760 765
 Ala Cys Thr Thr Cys Gly Cys Ala Gly Ala Gly Thr Cys Thr Gly Ala
 770 775 780
 Ala Thr Gly Ala Ala Cys Ala Ala Cys Ala Gly Ala Gly Thr Thr Cys
 785 790 795 800
 Ala Gly Thr Thr Thr Cys Cys Cys Thr Thr Cys Ala Ala Cys Ala Cys
 805 810 815
 Thr Thr Thr Gly Thr Gly Gly Ala Cys Thr Gly Gly Cys Cys Ala Ala
 820 825 830
 Gly Gly Ala Cys Ala Cys Cys Thr Gly Cys Ala Cys Ala Ala Gly Gly
 835 840 845
 Ala Gly Cys Thr Cys Thr Cys Gly Cys Ala Thr Gly Gly Cys Cys Thr
 850 855 860

Gly Ala Thr Gly Cys Thr Gly Ala Ala Gly Ala Cys Ala Thr Gly Cys
 865 870 875 880
 Ala Ala Gly Cys Thr Cys Ala Gly Ala Gly Ala Ala Gly Cys Cys Ala
 885 890 895
 Gly Cys Thr Cys Thr Cys Ala Ala Thr Ala Thr Cys Thr Gly Cys Thr
 900 905 910
 Cys Cys Ala Ala Thr Gly Gly Cys Gly Thr Cys Thr Thr Cys Thr Gly
 915 920 925
 Ala Cys Cys Thr Gly Thr Cys Ala Thr Cys Ala Gly Cys Cys Thr Cys
 930 935 940
 Ala Ala Cys Ala Thr Cys Thr Cys Cys Cys Ala Thr Cys Cys Ala Thr
 945 950 955 960
 Gly Ala Gly Ala Ala Gly Cys Thr Gly Ala Thr Gly Thr Thr Gly Thr
 965 970 975
 Cys Ala Cys Cys Ala Cys Thr Thr Ala Ala Ala Cys Thr Gly Ala Gly
 980 985 990
 Cys Cys Gly Thr Gly Ala Ala Thr Ala Thr Ala Gly Thr Cys Cys Thr
 995 1000 1005
 Ala Thr Thr Gly Gly Thr Cys Thr Cys Gly Gly Thr Thr Thr Thr
 1010 1015 1020
 Gly Cys Ala Gly Cys Ala Ala Ala Thr Ala Gly Ala Gly Ala Thr
 1025 1030 1035
 Gly Ala Gly Gly Thr Thr Ala Ala Cys Cys Ala Gly Gly Gly Ala
 1040 1045 1050
 Gly Ala Ala Gly Cys Ala Ala Ala Cys Thr Gly Gly Ala Thr Gly
 1055 1060 1065
 Cys Cys Thr Ala Thr Gly Thr Thr Cys Cys Gly Thr Gly Ala Thr
 1070 1075 1080
 Thr Cys Thr Thr Thr Gly Ala Thr Gly Gly Gly Cys Gly Gly Ala
 1085 1090 1095
 Cys Cys Ala Thr Thr Gly Gly Gly Ala Gly Ala Gly Gly Thr Thr
 1100 1105 1110
 Thr Thr Ala Ala Cys Cys Ala Ala Gly Ala Ala Thr Ala Ala Cys
 1115 1120 1125

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Ala Ala Cys Ala Thr Gly Gly Ala Ala Gly Cys Ala Ala Gly Gly
1130 1135 1140

Ala Ala Thr Thr Gly Cys Cys Thr Ala Thr Cys Gly Gly Ala Gly
1145 1150 1155

Thr Cys Thr Cys Thr Gly Ala Ala Thr Cys Thr Thr Thr Thr Ala
1160 1165 1170

Ala Ala Thr Gly Ala Thr Gly Gly Cys Thr Gly Gly Gly Ala Thr
1175 1180 1185

Thr Cys Ala Ala Gly Cys Thr Cys Ala Gly Gly Gly Thr Thr Thr
1190 1195 1200

Gly Ala Thr Thr Cys Ala Thr Cys Cys Cys Cys Ala Gly Thr Thr
1205 1210 1215

Gly Gly Thr Gly Thr Thr Cys Thr Gly Cys Ala Gly Ala Ala Gly
1220 1225 1230

Ala Cys Cys Ala Cys Cys Thr Thr Thr Gly Gly Ala Thr Cys Ala
1235 1240 1245

Gly Thr Ala Thr Cys Cys Ala Gly Thr Ala Gly Cys Ala Cys Cys
1250 1255 1260

Gly Gly Ala Ala Gly Cys Ala Gly Thr Cys Cys Thr Ala Gly Ala
1265 1270 1275

Cys Thr Gly Gly Ala Gly Ala Ala Thr Cys Ala Thr Ala Gly Thr
1280 1285 1290

Gly Thr Thr Thr Ala Thr Gly Ala Thr Gly Gly Cys Ala Ala Cys
1295 1300 1305

Ala Gly Thr Ala Ala Cys Cys Thr Gly Cys Gly Gly Gly Ala Thr
1310 1315 1320

Gly Ala Thr Cys Thr Cys Gly Gly Thr Thr Cys Ala Gly Thr Thr
1325 1330 1335

Gly Thr Thr Gly Thr Ala Ala Thr Cys Ala Thr Cys Cys Gly
1340 1345 1350

Ala Gly Cys Ala Thr Cys Cys Gly Cys Cys Thr Gly Gly Thr Gly
1355 1360 1365

Thr Gly Ala
1370

<210> 36

<211> 456

<212> PRT

<213> Oryza sativa

<400> 36

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

Asn Ser Pro Val Pro His Ser Leu Leu Ile Pro Ile Arg Arg Ser Leu
 35 40 45

Thr Ser Pro Tyr Ser Pro Ala Tyr Phe Gly Ser Ser Thr Leu Gly Trp
 50 55 60

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

Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys Ser Arg Asp Ala
 85 90 95

Val Ala Asp Gln Lys Tyr Cys Glu Arg His Met Asn Arg Gly Arg His
 100 105 110

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

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

Ala Pro Ala Ala His Ser Gly Gly Ala Val Ala Gly Leu Ala Ile Asn
 145 150 155 160

His Gln His Gln Gln Met Lys Asn Tyr Ala Ala Asn Thr Ala Asn Pro
 165 170 175

Cys Ser Leu Gln Tyr Ser Arg Asp Leu Ala Asn Lys His Asn Glu Ser
 180 185 190

Glu Gln Val Gln Asp Ser Asp Ser Leu Ser Met Leu Thr Ser Ile Ser
 195 200 205

Thr Arg Asn Thr Gly Ser Leu Phe Pro Phe Ser Lys Gln His Asn Pro
 210 215 220

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

Ser Leu Met Ser Ser Pro His Ser Ser Leu Glu Asn Val Asn Leu Leu
 245 250 255

PF59082PF60142_PCT_SEQ_LIST.txt

Thr Ser Gln Ser₂₆₀ Leu Asn Glu Gln₂₆₅ Gln Ser Ser Val Ser₂₇₀ Leu Gln His
Phe Val Asp₂₇₅ Trp Pro Arg Thr₂₈₀ Ala Gln Gly Ala₂₈₅ Leu Ala Trp Pro
Asp Ala₂₉₀ Glu Asp Met Gln₂₉₅ Ala Gln Arg Ser Gln₃₀₀ Leu Ser Ile Ser Ala
Pro Met Ala Ser Ser Asp₃₁₀ Leu Ser Ser Ala₃₁₅ Ser Thr Ser Pro Ile His₃₂₀
Glu Lys Leu Met₃₂₅ Leu Ser Pro Leu Lys₃₃₀ Leu Ser Arg Glu Tyr Ser₃₃₅ Pro
Ile Gly Leu Gly₃₄₀ Phe Ala Ala Asn₃₄₅ Arg Asp Glu Val Asn₃₅₀ Gln Gly Glu
Ala Asn Trp₃₅₅ Met Pro Met Phe Arg₃₆₀ Asp Ser Leu Met Gly₃₆₅ Gly Pro Leu
Gly Glu Val₃₇₀ Leu Thr Lys Asn₃₇₅ Asn Asn Met Glu Ala₃₈₀ Arg Asn Cys Leu
Ser Glu Ser Leu Asn₃₉₀ Leu Leu Asn Asp Gly₃₉₅ Trp Asp Ser Ser Ser Gly₄₀₀
Phe Asp Ser Ser₄₀₅ Pro Val Gly Val Leu₄₁₀ Gln Lys Thr Thr Phe Gly₄₁₅ Ser
Val ser ser₄₂₀ Ser Thr Gly Ser Ser Pro Arg Leu Glu Asn₄₃₀ His Ser Val
Tyr Asp Gly₄₃₅ Asn Ser Asn Leu Arg₄₄₀ Asp Asp Leu Gly₄₄₅ Ser Val Val Val
Asn His₄₅₀ Pro Ser Ile Arg₄₅₅ Leu Val

<210> 37
<211> 711
<212> DNA
<213> Oryza sativa

<400> 37
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cttgggctgg gtctcggctt gggcggcagc ggcagcgaca gcagtgggag cgacgcggaa 180
gcgctctgcg ccaccgtgcg ggaggcgcg ccgccgtcgg cgctgacgtt catgcagcgg 240
caggagctgg agcagcaggt gctcatctac cgctacttcg ccgccggcgc gcctgtgccg 300

PF59082PF60142_PCT_SEQ_LIST.txt

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ccggagccgg ggcggtgccg ggcacggac ggcaagaagt ggcggtgctc gcgcgacgtg 480
gtgccggggc acaagtattg cgagcggcac gtccaccgtg gccgcggccg ttcaagaaag 540
cctatggaag cctctgcagc agtcgctccc acatatctcc cggtcgggcc ggcactccac 600
accgtcgcca ccctcgccac cagcgcgcca tcgctgtcgc acctcggttt ctctccgcc 660
agcaaagtgc tcctcgcca caccaccacc ggcaccacgc gcgctacttg a 711

<210> 38
<211> 236
<212> PRT
<213> Oryza sativa

<400> 38

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

Met Ala Ala Pro Ser Pro Leu Val Leu Gly Leu Gly Leu Gly Leu Gly
35 40 45

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

Thr Val Arg Glu Ala Arg Pro Pro Ser Ala Leu Thr Phe Met Gln Arg
65 70 75 80

Gln Glu Leu Glu Gln Gln Val Leu Ile Tyr Arg Tyr Phe Ala Ala Gly
85 90 95

Ala Pro Val Pro Val His Leu Val Leu Pro Ile Trp Lys Ser Ile Ala
100 105 110

Ala Ala Ser Ser Phe Gly Pro Gln Ser Phe Pro Ser Leu Thr Gly Leu
115 120 125

Gly Ser Leu Cys Phe Asp Tyr Arg Ser Ser Met Glu Pro Glu Pro Gly
130 135 140

Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys Ser Arg Asp Val
145 150 155 160

Val Pro Gly His Lys Tyr Cys Glu Arg His Val His Arg Gly Arg Gly
165 170 175

Arg Ser Arg Lys Pro Met Glu Ala Ser Ala Ala Val Ala Pro Thr Tyr
180 185 190

PF59082PF60142_PCT_SEQ_LIST.txt

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

Ala Pro Ser Leu Ser His Leu Gly Phe Ser Ser Ala Ser Lys Val Leu
210 215 220

Leu Ala His Thr Thr Thr Gly Thr Thr Arg Ala Thr
225 230 235

<210> 39
<211> 1164
<212> DNA
<213> Oryza sativa

<400> 39
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cccttctgcc gtcctctccc tctctccgcg gtcggggagg aggcgcagca gcacatgatg 120
ggcgcgaggt gggcggcggc ggtggccagg ccgccgccct tcacggcggc gcagtacgag 180
gagctggagc agcaggcgct catatacaag tacctcgtcg ccggcggtgcc cgtcccggcg 240
gatctcctcc tccccatccg ccgtggcctc gactcactcg cctcgcgctt ctaccaccac 300
cctgtccttg gatacggttc ctacttcggc aagaagctgg acccggagcc cggacggtgc 360
cggcgtagcg acggcaagaa gtggcgggtgc tccaaggagg ccgcgccgga ctccaagtac 420
tgtgagcgac acatgcaccg cggccgcaac cgttcaagaa agcctgtgga agcgcagctc 480
gtcgcccccc actcgagcc ccccgccacg gcgccggccg ccgccgtcac ctccaccgcc 540
ttccagaacc actcgctgta cccggcgatt gctaattggcg gcggcgccaa cggaggcggt 600
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ctgcacatgg acaatgctgc gtcttactcg actgttgctg ctggtgccgg aaacaaagat 720
ttcaggtatt ctgcttatgg agtgagacca ttggcagatg agcacagccc actcatcact 780
ggagctatgg atacctctat tgacaattcg tggtgcttgc tgccttctca gacctccaca 840
ttttcagttt cgagctaccc tatgcttgga aatctgagtg agctggacca gaacaccatc 900
tgctcgctgc cgaaggtgga gaggagacca ttgtcattct tcgggagcga ctatgtgacc 960
gtcgactccg ggaagcagga gaaccagacg ctgcgccctt ttttcgacga gtggccaaag 1020
gcaagggact cctggcctga tctagctgat gacaacagcc ttgccacctt ctctgccact 1080
cagctctcga tctccattcc aatggcaacc tctgacttct cgaccaccag ctcacgatca 1140
cacaacggta tatactcccg atga 1164

<210> 40
<211> 387
<212> PRT
<213> Oryza sativa

<400> 40

Met Ala Met Pro Phe Ala Ser Leu Ser Pro Ala Ala Asp His Arg Pro
Seite 50

1 5 10 15
 Ser Phe Ile Phe₂₀ Pro Phe Cys Arg Ser₂₅ Ser Pro Leu Ser Ala₃₀ Val Gly
 Glu Glu Ala₃₅ Gln Gln His Met₄₀ Gly Ala Arg Trp Ala₄₅ Ala Ala Val
 Ala Arg₅₀ Pro Pro Pro Phe Thr₅₅ Ala Ala Gln Tyr₆₀ Glu Glu Leu Glu Gln
 Gln Ala Leu Ile Tyr₆₅ Lys₇₀ Tyr Leu Val Ala Gly₇₅ Val Pro Val Pro Ala₈₀
 Asp Leu Leu Leu₈₅ Pro Ile Arg Arg Gly₉₀ Leu Asp Ser Leu Ala Ser₉₅ Arg
 Phe Tyr His His₁₀₀ Pro Val Leu Gly Tyr₁₀₅ Gly Ser Tyr Phe Gly₁₁₀ Lys Lys
 Leu Asp Pro₁₁₅ Glu Pro Gly Arg Cys₁₂₀ Arg Arg Thr Asp Gly₁₂₅ Lys Lys Trp
 Arg Cys₁₃₀ Ser Lys Glu Ala Ala₁₃₅ Pro Asp Ser Lys Tyr₁₄₀ Cys Glu Arg His
 Met His Arg Gly Arg Asn₁₅₀ Arg Ser Arg Lys Pro Val Glu Ala Gln Leu₁₆₀
 Val Ala Pro His Ser₁₆₅ Gln Pro Pro Ala Thr₁₇₀ Ala Pro Ala Ala Ala₁₇₅ Val
 Thr Ser Thr Ala₁₈₀ Phe Gln Asn His Ser₁₈₅ Leu Tyr Pro Ala Ile₁₉₀ Ala Asn
 Gly Gly Gly₁₉₅ Ala Asn Gly Gly Gly₂₀₀ Gly Gly Gly Gly Gly₂₀₅ Gly Gly Gly Ser
 Ala Pro Gly Ser Phe Ala Leu₂₁₅ Gly Ser Asn Thr Gln₂₂₀ Leu His Met Asp
 Asn Ala Ala Ser Tyr Ser₂₃₀ Thr Val Ala Ala Gly₂₃₅ Ala Gly Asn Lys Asp₂₄₀
 Phe Arg Tyr Ser Ala₂₄₅ Tyr Gly Val Arg Pro₂₅₀ Leu Ala Asp Glu His₂₅₅ Ser
 Pro Leu Ile Thr₂₆₀ Gly Ala Met Asp Thr₂₆₅ Ser Ile Asp Asn Ser₂₇₀ Trp Cys
 Leu Leu Pro₂₇₅ Ser Gln Thr Ser Thr₂₈₀ Phe Ser Val Ser Ser₂₈₅ Tyr Pro Met

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Gly Asn Leu Ser Glu Leu Asp Gln Asn Thr Ile Cys Ser Leu Pro
290 295 300

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

Val Asp Ser Gly Lys Gln Glu Asn Gln Thr Leu Arg Pro Phe Phe Asp
325 330 335

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

Ser Leu Ala Thr Phe Ser Ala Thr Gln Leu Ser Ile Ser Ile Pro Met
355 360 365

Ala Thr Ser Asp Phe Ser Thr Thr Ser Ser Arg Ser His Asn Gly Ile
370 375 380

Tyr Ser Arg
385

<210> 41
<211> 1071
<212> DNA
<213> Oryza sativa

<400> 41
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aagtacctcg tcgccggtgt ccccggtccc ggcgatctcc tcctcccaat ccgccccac 180
tcctccgccg ccgccaccta ctcttcgcc aaccccgccg ccgcgccctt ctaccaccac 240
caccaccacc cctctctgag ctattatgcc tactatggca agaagcttga ccctgagccg 300
tggcgttgcc gccgcaccga cggcaagaag tggcggtgct ccaaggaggc gcaccccgac 360
tccaagtact gcgagcgcca catgcaccgt ggccgcaacc gttcaagaaa gcctgtggaa 420
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actcacgaca ccgatgcgcc tctcccgta ctactgtgg gtgctaaaac ccacggtctg 540
tcccttggtg gtgctggctc gtcgcagttc catgtcgacg caccatcgta cggcagcaag 600
tactctcttg gagctaaagc tgatgtgggt gaactgagct tcttctcagg agcatcagga 660
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tcggagatgg atgaggagag gtccaaccag acctccttct cgacaacca gctctcgatc 1020

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1071

<210> 42
 <211> 356
 <212> PRT
 <213> Oryza sativa

<400> 42

Met Leu Ser Ser Ser Pro Ser Ala Ala Ala Pro Gly Ile Gly Gly Tyr
 1 5 10 15

Gln Pro Gln Arg Gly Ala Ala Val Phe Thr Ala Ala Gln Trp Ala Glu
 20 25 30

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

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

Ala Thr Tyr Ser Phe Ala Asn Pro Ala Ala Ala Pro Phe Tyr His His
 65 70 75 80

His His His Pro Ser Leu Ser Tyr Tyr Ala Tyr Tyr Gly Lys Lys Leu
 85 90 95

Asp Pro Glu Pro Trp Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg
 100 105 110

Cys Ser Lys Glu Ala His Pro Asp Ser Lys Tyr Cys Glu Arg His Met
 115 120 125

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

Ala Pro Ala Pro Gln Ser Gln Pro Gln Leu Ser Asn Val Thr Thr Ala
 145 150 155 160

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

Thr His Gly Leu Ser Leu Gly Gly Ala Gly Ser Ser Gln Phe His Val
 180 185 190

Asp Ala Pro Ser Tyr Gly Ser Lys Tyr Ser Leu Gly Ala Lys Ala Asp
 195 200 205

Val Gly Glu Leu Ser Phe Phe Ser Gly Ala Ser Gly Asn Thr Arg Gly
 210 215 220

Phe Thr Ile Asp Ser Pro Thr Asp Ser Ser Trp His Ser Leu Pro Ser
 225 230 235 240

PF59082PF60142_PCT_SEQ_LIST.txt

Ser Val Pro Pro Tyr Pro Met Ser Lys Pro Arg Asp Ser Gly Leu Leu
245 250 255

Pro Gly Ala Tyr Ser Tyr Ser His Leu Glu Pro Ser Gln Glu Leu Gly
260 265 270

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

Gly Gly Gly Ala Gly Gly Met Leu Gly Asn Val Lys His Glu Asn Gln
290 295 300

Pro Leu Arg Pro Phe Phe Asp Glu Trp Pro Gly Arg Arg Asp Ser Trp
305 310 315 320

Ser Glu Met Asp Glu Glu Arg Ser Asn Gln Thr Ser Phe Ser Thr Thr
325 330 335

Gln Leu Ser Ile Ser Ile Pro Met Pro Arg Cys Gly Ser Pro Ile Gly
340 345 350

Pro Arg Leu Pro
355

<210> 43
<211> 1230
<212> DNA
<213> Oryza sativa

<400> 43
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catggcagat gtggtgagca gcaaggtgga ggaggaggag gagggaaga gcaagagcaa 120
gatgggttct tgggtgagaga ggcaagggca tccccaccat ctccatcttc ttcattcattt 180
cttgatcca caagctcttc ttgttctgga ggaggaggag gagggcagat gttgagcttc 240
tcctcccca atggaacagc agggttgggc ttgagctcag gaggaagcat gcaggggggc 300
ttggcaaggg tcagggggcc gttcaccca acacagtgga tggagctgga gcaccaggca 360
ctgatctaca agcacattgc tgcaaatgtt tctgtccctt ccagcttgct cctccccatc 420
aggagaagcc tccatccatg gggatgggga tcattccctc ctggctgtgc tgatgtagaa 480
cccagaagat gccgccgcac agacggcaag aagtggcggg gctccagaga tgctgttggg 540
gatcagaagt attgtgagcg acacataaac cgtggctgcc atcgttcaag aaagcatgtg 600
gaaggccgaa aggcgacact caccattgca gaaccatcca cggttattgc tgctggtgta 660
tcattctcgc gccacactgt ggctcggcag aagcaggatga aaggctcagc tgctactgtc 720
tctgatcctt tctcgagaca atccaacagg aaatttctgg agaaacagaa cgttgctgcac 780
caattgtctc ccatggattc atttgatttc tcatccacac aatcttctcc aaactatgac 840
aatgtagcat tgtcaccact gaagttgcac catgatcatg atgaatctta catcgggcat 900

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gcttctacag aaatcttaac tgaaaaatgg actgagaacc ccaacttaca ttgcccatct 1080
ggaatcctac aaatggctac taagttcaat tcaattttcca gcggcaacac agtaaatagt 1140
ggtggcaccg cagtggagaa tcttatcact gataatggat atcttactgc aagaatgatg 1200
aatcctcata ttgtcccaac acttctctaa 1230

<210> 44
<211> 409
<212> PRT
<213> Oryza sativa

<400> 44

Met Leu Ser Ser Cys Gly Gly His Gly His Gly Asn Pro Arg Ser Leu
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Gln Glu Glu His His Gly Arg Cys Gly Glu Gln Gln Gly Gly Gly Gly
20 25 30

Gly Gly Gly Gln Glu Gln Glu Gln Asp Gly Phe Leu Val Arg Glu Ala
35 40 45

Arg Ala Ser Pro Pro Ser Pro Ser Ser Ser Ser Phe Leu Gly Ser Thr
50 55 60

Ser Ser Ser Cys Ser Gly Gly Gly Gly Gly Gly Gln Met Leu Ser Phe
65 70 75 80

Ser Ser Pro Asn Gly Thr Ala Gly Leu Gly Leu Ser Ser Gly Gly Ser
85 90 95

Met Gln Gly Val Leu Ala Arg Val Arg Gly Pro Phe Thr Pro Thr Gln
100 105 110

Trp Met Glu Leu Glu His Gln Ala Leu Ile Tyr Lys His Ile Ala Ala
115 120 125

Asn Val Ser Val Pro Ser Ser Leu Leu Leu Pro Ile Arg Arg Ser Leu
130 135 140

His Pro Trp Gly Trp Gly Ser Phe Pro Pro Gly Cys Ala Asp Val Glu
145 150 155 160

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

Asp Ala Val Gly Asp Gln Lys Tyr Cys Glu Arg His Ile Asn Arg Gly
180 185 190

PF59082PF60142_PCT_SEQ_LIST.txt

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

Ile Ala Glu Pro Ser Thr Val Ile Ala Ala Gly Val Ser Ser Arg Gly
210 215 220

His Thr Val Ala Arg Gln Lys Gln Val Lys Gly Ser Ala Ala Thr Val
225 230 235 240

Ser Asp Pro Phe Ser Arg Gln Ser Asn Arg Lys Phe Leu Glu Lys Gln
245 250 255

Asn Val Val Asp Gln Leu Ser Pro Met Asp Ser Phe Asp Phe Ser Ser
260 265 270

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

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

Ser Ser Glu Lys Gly Ser Met Met Tyr Glu Ser Arg Leu Thr Val Ser
305 310 315 320

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

Asn Cys Gln Ser Ala Ser Thr Glu Ile Leu Thr Glu Lys Trp Thr Glu
340 345 350

Asn Pro Asn Leu His Cys Pro Ser Gly Ile Leu Gln Met Ala Thr Lys
355 360 365

Phe Asn Ser Ile Ser Ser Gly Asn Thr Val Asn Ser Gly Gly Thr Ala
370 375 380

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

Asn Pro His Ile Val Pro Thr Leu Leu
405

<210> 45
<211> 1293
<212> DNA
<213> Oryza sativa

<400> 45
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ggtgcccaga ttctaagctt ctctcctca ggtcacagcg gcaatggggtt ggattgtgga 120
agctcagatg tggcaagaat gcaggggggtt ttagcaaggg ttagggggcc attcacacca 180
acacaatgga tggagctgga gcaccaggct ctgatctaca agcacattgt ggcgaatgcg 240

PF59082PF60142_PCT_SEQ_LIST.txt

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ggctattctg ggagtgctga ctccgagccc gggagatgcc gtcgaaccga tggcaagaaa 420
tggcgggtgct cgagagacgc agttgtcgac caaaagtact gcgagcggca cataaaccgg 480
ggtcgccacc gttcaagaaa gcatgtggaa ggccaatcta gccatgccgc aaaagcaacg 540
gttcccccca tagcacaacc acccattggg gcatctaata gcaaattgtc aggcagccat 600
ggtgtgtcaa atgagctcac gaaaaccttg gctactaaca ggatgatggt ggataaagca 660
aatcttattg aacgctccca ggactacact aatcagcaac acaacatcct acagaacaac 720
acaaaagggtg ataattgggtc tgaagagatg tcctcacaag cagactatgc agtaatccct 780
gctgggtctc tcatgaacac accgcaatcg gcgaatttaa atccaattcc ccagcaacaa 840
cgctgtaagc agtcactctt tggcaaaggg atacagcatg atgacattca gctgtcgata 900
tccattcccg tggataactc cgacttacc actaactaca acaaggctca aatggaccat 960
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cccagcagca ctgttagtag tcctgcaggc agcctctgca atggcttgct cacttcaggc 1260
ctggtgaatg cccagactgt ccaaactg tga 1293

<210> 46
<211> 430
<212> PRT
<213> Oryza sativa

<400> 46

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

Ser Gly Asn Gly Leu Asp Cys Gly Ser Ser Asp Val Ala Arg Met Gln
35 40 45

Gly Val Leu Ala Arg Val Arg Gly Pro Phe Thr Pro Thr Gln Trp Met
50 55 60

Glu Leu Glu His Gln Ala Leu Ile Tyr Lys His Ile Val Ala Asn Ala
65 70 75 80

Pro Val Pro Ala Gly Leu Leu Leu Pro Ile Arg Arg Ser Leu His Pro
85 90 95

PF59082PF60142_PCT_SEQ_LIST.txt

Pro Val Phe Pro His Phe Ser Ser Gly Gly Ile Leu Gly Ser Ser
100 105 110

Leu Gly Trp Gly Ser Phe Gln Leu Gly Tyr Ser Gly Ser Ala Asp Ser
115 120 125

Glu Pro Gly Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys Ser
130 135 140

Arg Asp Ala Val Val Asp Gln Lys Tyr Cys Glu Arg His Ile Asn Arg
145 150 155 160

Gly Arg His Arg Ser Arg Lys His Val Glu Gly Gln Ser Ser His Ala
165 170 175

Ala Lys Ala Thr Val Pro Ala Ile Ala Gln Pro Pro Ile Gly Ala Ser
180 185 190

Asn Gly Lys Leu Ser Gly Ser His Gly Val Ser Asn Glu Leu Thr Lys
195 200 205

Thr Leu Ala Thr Asn Arg Met Met Leu Asp Lys Ala Asn Leu Ile Glu
210 215 220

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

Thr Lys Gly Asp Asn Trp Ser Glu Glu Met Ser Ser Gln Ala Asp Tyr
245 250 255

Ala Val Ile Pro Ala Gly Ser Leu Met Asn Thr Pro Gln Ser Ala Asn
260 265 270

Leu Asn Pro Ile Pro Gln Gln Gln Arg Cys Lys Gln Ser Leu Phe Gly
275 280 285

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

Asp Asn Ser Asp Leu Pro Thr Asn Tyr Asn Lys Ala Gln Met Asp His
305 310 315 320

Val Val Gly Gly Ser Ser Asn Gly Gly Asn Asn Thr Arg Ala Ser Trp
325 330 335

Ile Pro Gly Ser Trp Glu Ala Ser Ile Gly Gly Pro Leu Gly Glu Phe
340 345 350

Phe Thr Asn Thr Ser Ser Ala Ser Asp Asp Lys Gly Lys Ser Arg His
355 360 365

Pro Pro Ser Leu Asn Leu Leu Ala Asp Gly His Thr Thr Ser Pro Gln

370

Leu Gln Ser Pro Thr Gly Val Leu Gln Met Thr Ser Phe Ser Ser Val
385 390 395 400

Pro Ser Ser Thr Val Ser Ser Pro Ala Gly Ser Leu Cys Asn Gly Leu
405 410 415

Leu Thr Ser Gly Leu Val Asn Ala Gln Thr Val Gln Thr Leu
420 425 430

<210> 47
<211> 1281
<212> DNA
<213> Oryza sativa

<400> 47
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agcttcaccc aggtctgctgc tgcatacatc ctttccccct ttcttgatga acagaagatg 180
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gagcagaggt tcttgttgtc taggaccaag aggcctttca ctccctcaca gtggatggag 300
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gatggcaaga aatggcggtg ttcaaaggag gccatggccg accacaagta ttgtgagagg 540
cacatcaaca gaaaccgcca ccgttcaaga aagcctgtgg aaaaccaaag tagaaagact 600
gtgaaagaga caccgtgtgc tggctcattg ccatcttctg tcgggcaggg cagcttcaag 660
aaggcaaaag ttaatgaaat gaagccacgc agtatcagct attggacaga tagtttgaac 720
aggacaatgg cgaacaaaga gaaaggaaac aaagctgctg aagaaaacaa tggccactg 780
ctaaatttaa cgaatcaaca gccaacattg tccctgttct ctcagttgaa gcaacagaac 840
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gagtttcaga aaagcaaaga ttccaatgtc atgacagttc catcaacttt ctattcctcg 1080
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atctcaagtt cttgggagat gcctcaaggt ggacctctag gtgagatctt gacaaactcc 1200
aaaaatcctg acgattcaat catgaaacca gaagcaaggc catatgggtg gttactgaac 1260
ctcgaggatc atgcaatgtg a 1281

<210> 48
<211> 426
<212> PRT

<213> Oryza sativa

<400> 48

Met Phe Ala Asp Phe Ser Ala Ala Ala Met Glu Leu Gly Glu Val Leu
 1 5 10 15

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

Leu Ile Lys Arg Ala Ala Ala Gly Ser Phe Thr Gln Ala Ala Ala Ala
 35 40 45

Ser Tyr Pro Ser Pro Phe Leu Asp Glu Gln Lys Met Leu Arg Phe Ala
 50 55 60

Lys Ala Ala His Thr Leu Pro Ser Gly Leu Asp Phe Gly Arg Glu Asn
 65 70 75 80

Glu Gln Arg Phe Leu Leu Ser Arg Thr Lys Arg Pro Phe Thr Pro Ser
 85 90 95

Gln Trp Met Glu Leu Glu His Gln Ala Leu Ile Tyr Lys Tyr Leu Asn
 100 105 110

Ala Lys Ala Pro Ile Pro Ser Ser Leu Leu Ile Ser Ile Ser Lys Ser
 115 120 125

Phe Arg Ser Ser Ala Asn Arg Met Ser Trp Arg Pro Leu Tyr Gln Gly
 130 135 140

Phe Pro Asn Ala Asp Ser Asp Pro Glu Pro Gly Arg Cys Arg Arg Thr
 145 150 155 160

Asp Gly Lys Lys Trp Arg Cys Ser Lys Glu Ala Met Ala Asp His Lys
 165 170 175

Tyr Cys Glu Arg His Ile Asn Arg Asn Arg His Arg Ser Arg Lys Pro
 180 185 190

Val Glu Asn Gln Ser Arg Lys Thr Val Lys Glu Thr Pro Cys Ala Gly
 195 200 205

Ser Leu Pro Ser Ser Val Gly Gln Gly Ser Phe Lys Lys Ala Lys Val
 210 215 220

Asn Glu Met Lys Pro Arg Ser Ile Ser Tyr Trp Thr Asp Ser Leu Asn
 225 230 235 240

Arg Thr Met Ala Asn Lys Glu Lys Gly Asn Lys Ala Ala Glu Glu Asn
 245 250 255

Asn Gly Pro Leu Leu Asn Leu Thr Asn Gln Gln Pro Thr Leu Ser Leu
 Seite 60

260

265

270

Phe Ser Gln Leu Lys Gln Gln Asn Lys Pro Glu Lys Phe Asn Thr Ala
 275 280 285

Gly Asp Ser Glu Ser Ile Ser Ser Asn Thr Met Leu Lys Pro Trp Glu
 290 295 300

Ser Ser Asn Gln Gln Asn Asn Lys Ser Ile Pro Phe Thr Lys Met His
 305 310 315 320

Asp Arg Gly Cys Leu Gln Ser Val Leu Gln Asn Phe Ser Leu Pro Lys
 325 330 335

Asp Glu Lys Met Glu Phe Gln Lys Ser Lys Asp Ser Asn Val Met Thr
 340 345 350

Val Pro Ser Thr Phe Tyr Ser Ser Pro Glu Asp Pro Arg Val Ser Cys
 355 360 365

His Ala Pro Asn Met Ala Gln Met Gln Glu Asp Ser Ile Ser Ser Ser
 370 375 380

Trp Glu Met Pro Gln Gly Gly Pro Leu Gly Glu Ile Leu Thr Asn Ser
 385 390 395 400

Lys Asn Pro Asp Asp Ser Ile Met Lys Pro Glu Ala Arg Pro Tyr Gly
 405 410 415

Trp Leu Leu Asn Leu Glu Asp His Ala Met
 420 425

<210> 49
 <211> 894
 <212> DNA
 <213> Oryza sativa

<400> 49
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 ctgacccgaa tgccggagtg gtgaccatgg cagcaccccc gccgccggtg ggtcttgggc 240
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 ggaagagcgt cgcgtcctcc tccttcggcc cgcaccgctt cccttcctg gcagtgatgg 480
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<210> 50
 <211> 211
 <212> PRT
 <213> Oryza sativa

<400> 50

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

Pro Arg Leu Ser Gly Ala Asp Pro Asn Ala Gly Val Val Thr Met Ala
 20 25 30

Ala Pro Pro Pro Pro Val Gly Leu Gly Leu Gly Leu Gly Leu Gly Gly
 35 40 45

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

Lys Ala Thr Ala Leu Thr Phe Met Gln Gln Gln Glu Leu Glu His Gln
 65 70 75 80

Val Leu Ile Tyr Arg Tyr Phe Ala Ala Gly Ala Pro Val Pro Val His
 85 90 95

Leu Val Leu Pro Ile Trp Lys Ser Val Ala Ser Ser Ser Phe Gly Pro
 100 105 110

His Arg Phe Pro Ser Leu Ala Val Met Gly Leu Gly Asn Leu Cys Phe
 115 120 125

Asp Tyr Arg Ser Ser Met Glu Pro Asp Pro Gly Arg Cys Arg Arg Thr
 130 135 140

Asp Gly Lys Lys Trp Arg Cys Ser Arg Asp Val Val Pro Gly His Lys
 145 150 155 160

Tyr Cys Glu Arg His Val His Arg Gly Arg Gly Arg Ser Arg Lys Pro
 165 170 175

Val Glu Ala Ser Ala Ala Ala Thr Pro Ala Asn Asn Gly Gly Gly Gly
 180 185 190

Gly Ile Val Phe Ser Pro Thr Ser Val Leu Leu Ala His Gly Thr Ala
 195 200 205

Arg Ala Thr
210

<210> 51
<211> 1149
<212> DNA
<213> Oryza sativa

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<400> 51
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tgccgctcct cccctctctc cgcggtcggg gaggaggcgc agcagcacat gatgggcgcg      120
aggtagggcgg cggcggtggc caggccgccg cccttcacgg cggcgagta cgaggagctg      180
gagcagcagg cgctcatata caagtacctc gtcgccggcg tgcccgtccc ggcggatctc      240
ctcctcccca tccgccgtgg cctcgactca ctgcctcgc gcttctacca ccaccctgtc      300
cttgatacgt gttcctactt cggcaagaag ctggaccggg agcccgagc gtgccggcgt      360
acggacggca agaagtggcg gtgctccaag gaggccgcgc cggactccaa gtactgtgag      420
cgacacatgc accgcgggcc caaccgttca agaaagcctg tggagcgca gctcgtcggc      480
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aaccactcgc tgtaccggc gattgcta atggcgggcg ccaacggagg cggtaggtgt      600
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tattctgctt atggagttag accattggca gatgagcaca gccactcat cactggagct      780
atggatacct ctattgaaa ttcgtggtgc ttgctgcctt ctgagacctc cacattttca      840
gtttcgagct accctatgct tggaaatctg agtgagctgg accagaacac catctgctcg      900
ctgccgaagg tggagagggg gccattgtca ttcttcggga gcgactatgt gaccgtcgac      960
tccgggaagc aggagaacca gacgctgcgc ccctttttcg acgagtggcc aaaggcaagg     1020
gactcctggc ctgatctagc tgatgacaac agccttgcca cttctctcgc cactcagctc     1080
tcgatctcca ttccaatggc aacctctgac ttctcgacca ccagctcacg atcacacaac     1140
gatgagtga                                     1149

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<210> 52
<211> 382
<212> PRT
<213> Oryza sativa

<400> 52

Met Pro Phe Ala Ser Leu Ser Pro Ala Ala Asp His Arg Pro Ser Phe
1 5 10 15

Ile Phe Pro Phe Cys Arg Ser Ser Pro Leu Ser Ala Val Gly Glu Glu
20 25 30

Ala Gln Gln His Met Met Gly Ala Arg Trp Ala Ala Ala Val Ala Arg
35 40 45

PF59082PF60142_PCT_SEQ_LIST.txt

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

PF59082PF60142_PCT_SEQ_LIST.txt

Ser Gly Lys Gln Glu Asn Gln Thr Leu Arg Pro Phe Phe Asp Glu Trp
 325 330 335

Pro Lys Ala Arg Asp Ser Trp Pro Asp Leu Ala Asp Asp Asn Ser Leu
 340 345 350

Ala Thr Phe Ser Ala Thr Gln Leu Ser Ile Ser Ile Pro Met Ala Thr
 355 360 365

Ser Asp Phe Ser Thr Thr Ser Ser Arg Ser His Asn Asp Glu
 370 375 380

<210> 53
 <211> 1416
 <212> DNA
 <213> Oryza sativa

<400> 53
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 agcaaccctc ccgggggagg aggcggcgga ggtggagggg aggaggagga ggatagcagc 180
 ctggctgtcg gggaggcggc ggtcggggtg ggcgaggctg gtggaggagg aggaggaggg 240
 gagaaggcgg atcgagagga ggaggagggg aaggaggatg tggaggaggg cggcgtgtgt 300
 aaggatctgg tgctcgtcga ggacgccgtc cccgtcgagg atccggagga agccgcagca 360
 actgcagcac ttcaggaaga aatgaaagcg ctcgttgaat ccgtcccagt tgggtgctggg 420
 gcggcattca ccgcgatgca actacaggag cttgagcagc aatctcgtgt ctaccagtat 480
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 cgtggccgca agcgtcctgt acagcttggt gtcgaggatg acgagcctga ttctacctca 780
 gggtcgaaac cagcatctgg caaggccacc gaaggtggca agaagactga tgacaagagc 840
 tcaagtagca agaagcttgc agtggcagca ccagctgctg tggagtctac atgattgatg 900
 cagcatttag gagctgcata aagagcataa ctgtgctggc aattagagtt cgcttcttat 960
 tgtaatcctg aaaagactgt agtctggtct agctataacc tcatcaagca agaaaagtgt 1020
 ctgtggaaag aagccacaaa aactttcatt tagctgtcac tgaaattttc agtttaggtg 1080
 tatagtttga tttagctttg ccgtgccctc tgccttcagg cagatgagcg gcattattgg 1140
 ataaatcctc tctgactgac aatatcgcat tgtgactcaa gaagccgatg gaaggatctg 1200
 cgagactaga tacgaagcta tttgttggtg atcattttat atggcctgca caattgtgtg 1260
 attttgtcag ttgcataaca tgtggaagat ccataatttt atgcactatg gagattcaat 1320
 taccttcctg aatgtctgag cttcgacatg ttattggtta ttgtaactta aaagcaacct 1380

gagattcaat gtgaaagggt tttagattcc agcttc

1416

<210> 54
 <211> 269
 <212> PRT
 <213> Oryza sativa

<400> 54

Met Ala Ala Glu Gly Glu Ala Lys Lys Asp Ser Ala Ser Asn Pro Pro
 1 5 10 15

Gly Gly Gly Gly Gly Gly Gly Gly Gly Glu Glu Glu Glu Asp Ser Ser
 20 25 30

Leu Ala Val Gly Glu Ala Ala Val Gly Val Gly Glu Ala Gly Gly Gly
 35 40 45

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

Asp Val Glu Glu Gly Gly Val Cys Lys Asp Leu Val Leu Val Glu Asp
 65 70 75 80

Ala Val Pro Val Glu Asp Pro Glu Glu Ala Ala Ala Thr Ala Ala Leu
 85 90 95

Gln Glu Glu Met Lys Ala Leu Val Glu Ser Val Pro Val Gly Ala Gly
 100 105 110

Ala Ala Phe Thr Ala Met Gln Leu Gln Glu Leu Glu Gln Gln Ser Arg
 115 120 125

Val Tyr Gln Tyr Met Ala Ala Arg Val Pro Val Pro Thr His Leu Val
 130 135 140

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

Lys Tyr Pro Thr Leu Met Gly Leu Ala Thr Leu Cys Leu Asp Phe Gly
 165 170 175

Lys Asn Pro Glu Pro Glu Pro Gly Arg Cys Arg Arg Thr Asp Gly Lys
 180 185 190

Lys Trp Arg Cys Trp Arg Asn Ala Ile Ala Asn Glu Lys Tyr Cys Glu
 195 200 205

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

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

PF59082PF60142_PCT_SEQ_LIST.txt

Ala Thr Glu Gly Gly Lys Lys Thr Asp Asp Lys Ser Ser Ser Ser Lys
 245 250 255

Lys Leu Ala Val Ala Ala Pro Ala Ala Val Glu Ser Thr
 260 265

<210> 55
 <211> 1854
 <212> DNA
 <213> Populus tremuloides

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<400> 55
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gttaagtaag cgagaaagat cagcttcgtc tgctcaagat gattactgga ggacttcaaa      120
gatgccaaaa aatgatgatt tttctgtcac caaacaatg tcgttgcacc aaccacttc      180
tttactgaga tctaattaca tgctttctga tgattctcgc caacaagagc acatgatgag      240
cttctcttct ccaagaccag aaacgactcc atttctaagc aaagatggtg agttagtgga      300
gagaagcaca caaaaccaca ctgccttaag ctttcgttac catcagaaca cagcttcttc      360
ttatattaga agtgcagggt atgacaccgg aggcttgaat gcaggcatgc acgggcctct      420
tactgggggt agaggaccat ttactccatc tcagtggatg gagcttgaac atcaggcctt      480
gatctacaaa tacatcactg ctcggtgtgcc tgtgccttct aatttgatca ttctcttcaa      540
gaagtctgtc tacccttata gcttacctgg ctctcttact ggatccttcc ctcacaattc      600
attgggatgg agcgctttcc atcttggtta ccctggcaac aacactgatc cggagcctgg      660
aagggtgtcgt cggactgatg ggaagaaatg gcggtgtctc agggatgctg tagctgacca      720
aaagtattgt gaaaggcaca taaacagagg ccgccatcgt tcaagaaagc ctgtggaagg      780
ccagactggc catgctgcc a ctgggactgc cagttcaaag gtggtgccaa tgtcgaactc      840
gatgtcaaaa ttggcaataa ccagtgggtg tgcctccaac agcattgcga tgaccacgca      900
acaacagttc aaaattttgc agccggctgc tgccaacact tctgcagatg ttgatgtcaa      960
cagagcacia gatgcacaga gcatttctat gatgtcttcc accatcaacc ggaaatctga     1020
tgagtcctct ttctttgttc ctaaacaaga tatcttaatg gagcagtgtc ctcaaacaga     1080
gtttggattt gtctcctctg actctctcct caaccatcg cagaagagct cttacattaa     1140
ctctaagccc tacgagtctt ttctaaactt taatgacgaa gaaagccaag atcagcatcc     1200
ccttcgtcaa ttcatgatg agtggccgaa ggatcaatct aattgttctg tcattagctg     1260
gccagaagag ttgaaatctg actggaccca gctctccatg tcaatcccaa tggcctcatc     1320
agacttctca tcatcatcat cctcaccac acaagagaaa cttgccctct caccaatgag     1380
tttatcttgc gagtttgacc ctgtacaaat gggtttaagg gtgagcgttg accataatga     1440
atcaagccaa aagcaaacca actggatacc tatctcctgg gggacttcaa ttggtggccc     1500
tttaggagag gtcttgacca ccagcactag ccatgcggat tcctgcaaga gctcatcagc     1560
ccttagcctt ttgagagaag gttgtgatgg cagcccacag ttgggatctt ctccgacggg     1620
    
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PF59082PF60142_PCT_SEQ_LIST.txt

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 agctgagagc aagaaaaaca atgacactgc tagtctgtat gaggatgtgg gtggttcgat 1740
 aattgcaagt tcatcaccta ttccaccct gtaatcaagc gaactgtaag gatgaaacct 1800
 gtcaaggaaa tgtgaagaag cttggagttt ctatttatct gataaattcc tgta 1854

<210> 56
 <211> 607
 <212> PRT
 <213> Populus tremuloides
 <400> 56

Met Asp Phe Gly Val Leu Gly Leu Glu Gly Leu Val Gly Pro Glu Thr
 1 5 10 15

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

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

Gln Asp Asp Tyr Trp Arg Thr Ser Lys Met Pro Lys Asn Asp Asp Phe
 50 55 60

Ser Val Thr Lys Thr Met Ser Leu His Gln Pro Thr Ser Leu Leu Arg
 65 70 75 80

Ser Asn Tyr Met Leu Ser Asp Asp Ser Arg Gln Gln Glu His Met Met
 85 90 95

Ser Phe Ser Ser Pro Arg Pro Glu Thr Thr Pro Phe Leu Ser Lys Asp
 100 105 110

Gly Glu Leu Val Glu Arg Ser Thr Gln Asn His Thr Ala Leu Ser Phe
 115 120 125

Arg Tyr His Gln Asn Thr Ala Ser Ser Tyr Ile Arg Ser Ala Gly Tyr
 130 135 140

Asp Thr Gly Gly Leu Asn Ala Gly Met His Gly Pro Leu Thr Gly Val
 145 150 155 160

Arg Gly Pro Phe Thr Pro Ser Gln Trp Met Glu Leu Glu His Gln Ala
 165 170 175

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

Ile Ile Pro Leu Lys Lys Ser Val Tyr Pro Tyr Ser Leu Pro Gly Ser
 195 200 205

Ser Thr Gly Ser Phe Pro His Asn Ser Leu Gly Trp Ser Ala Phe His
 Seite 68

210

Leu Gly Tyr Pro Gly Asn Asn Thr Asp Pro Glu Pro Gly Arg Cys Arg
225 230 235 240

Arg Thr Asp Gly Lys Lys Trp Arg Cys Ser Arg Asp Ala Val Ala Asp
245 250 255

Gln Lys Tyr Cys Glu Arg His Ile Asn Arg Gly Arg His Arg Ser Arg
260 265 270

Lys Pro Val Glu Gly Gln Thr Gly His Ala Ala Thr Gly Thr Ala Ser
275 280 285

Ser Lys Val Val Pro Met Ser Asn Ser Met Ser Lys Leu Ala Ile Thr
290 295 300

Ser Gly Gly Ala Ser Asn Ser Ile Ala Met Thr Thr Gln Gln Gln Phe
305 310 315 320

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

Asn Arg Ala Gln Asp Ala Gln Ser Ile Ser Met Met Ser Ser Thr Ile
340 345 350

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

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

Ser Leu Leu Asn Pro Ser Gln Lys Ser Ser Tyr Ile Asn Ser Lys Pro
385 390 395 400

Tyr Glu Ser Phe Leu Asn Phe Asn Asp Glu Glu Ser Gln Asp Gln His
405 410 415

Pro Leu Arg Gln Phe Ile Asp Glu Trp Pro Lys Asp Gln Ser Asn Cys
420 425 430

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

Ser Met Ser Ile Pro Met Ala Ser Ser Asp Phe Ser Ser Ser Ser Ser
450 455 460

Ser Pro Thr Gln Glu Lys Leu Ala Leu Ser Pro Met Ser Leu Ser Cys
465 470 475 480

Glu Phe Asp Pro Val Gln Met Gly Leu Arg Val Ser Val Asp His Asn
485 490 495

PF59082PF60142_PCT_SEQ_LIST.txt

Glu Ser Ser Gln Lys Gln Thr Asn Trp Ile Pro Ile Ser Trp Gly Thr
500 505 510

Ser Ile Gly Gly Pro Leu Gly Glu Val Leu Thr Thr Ser Thr Ser His
515 520 525

Ala Asp Ser Cys Lys Ser Ser Ser Ala Leu Ser Leu Leu Arg Glu Gly
530 535 540

Cys Asp Gly Ser Pro Gln Leu Gly Ser Ser Pro Thr Gly Val Leu Gln
545 550 555 560

Lys Ser Thr Phe Cys Ser Leu Ser Asn Ser Ser Ser Gly Ser Ser Pro
565 570 575

Arg Ala Glu Ser Lys Lys Asn Asn Asp Thr Ala Ser Leu Tyr Glu Asp
580 585 590

Val Gly Gly Ser Ile Ile Ala Ser Ser Ser Pro Ile Pro Pro Leu
595 600 605

<210> 57
<211> 1848
<212> DNA
<213> Populus tremuloides

<400> 57
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attggccaaa accgagtcaa tgctgcttga ccagagaaac acttttcttc tgaaatctag 180
caacaactct ctcttcactg atggacagca gcagcagcag atgctcagct tctcctgtcc 240
caaatcagct tcttcagggg agagaagctc cccaaatgcc atgttgccat actttcacct 300
cacatcttct gcttgtaata gaaatacagg ctacaactct ggaatcttca atgctgccag 360
catgcatggg gttttgactg agactagatg gccattcact caattacaat ggatggagct 420
tgaacatcag gccttgatct acaaatacat gactgcaaat gtgcctatac catctaattct 480
gctcatcccc attaggaag ctcttgattc tgctgggttt tctagctttt ctggtggact 540
tttcaaacc agtgcatcgc aatgggggtac tttccatatg ggtttctcca gcaacactga 600
tccggagcca ggacggtgtc gaagaacaga tgggaagaaa tggcggtgct caagagacgc 660
agttgctgat cagaagtatt gtgagcggca catgaacagg ggtcgccatc gttcaagaaa 720
gcctgtggaa ggacaatcag gccattccgc tgcggccacc accactttaa agccaatggc 780
caatggcact tcctcttttg catcagcatc agtgggtggg cttcgcagcg ctgtgtccga 840
cagccacact attgtgcata atcagcagca acctgccagt tcttctaatac tttctgccac 900
caatacgtc agcaggggtgt tcctcgctac agagaatgta ggtgagagaa tgcaagatgc 960
atcgggctta tccatgctac catccagcat tgacctgaaa tccaaagaaa ctccattctt 1020

PF59082PF60142_PCT_SEQ_LIST.txt

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ctccgactcc ctctcaacc attcacagaa aagctcgtcc ttgatgagtt gcagaaattt 1140
tggttcgtct caggacctta ctgaccagga atctgtttca cagcactccc tccgccaatt 1200
tatggatgat tgtcctaaaa gtcattctga tcgctctgct gttgcttggc ctggacttga 1260
tctgcaatct gagagaaccc agctatcaat ttcaatcccc atggctcctg cagactttgt 1320
gtcatccact tcatcttcaa acaatgaaaa gatctctctc tccccgctga gattatcgcg 1380
tgaatttgat ccaataaaga tggggctggg agtgggagcc ggtagtgtcg ccaatgaacc 1440
aaaccaaagg caagcgaatt ggattcccat ttcttgggaa acttcaatgg gtgggtccact 1500
tgggggaggtt ttgcacaaca ccaataataa tgcaacagca gaatgcaaga atgaatcatc 1560
gctcaaccta atgacagaga gatgggacaa cagtcctcgg gtaggctcat ctctaccgg 1620
ggctttacaa aagtctgcct ttgcttctct ttcaaatagc agtgctggaa gcagcccaag 1680
agcagagaac aagaccattg aaggtggcaa tctctgcaat gaccttggat ctactatcgt 1740
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tgatgccaga ttatgaataa tttgtttttt aaagtcttca atcagtct 1848

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<210> 58
 <211> 605
 <212> PRT
 <213> Populus tremuloides

<400> 58

Met Asp Phe Gly Val Gln Val Gly Leu Asp Gly Leu Val Gly Ser Asp
 1 5 10 15

Thr Ser Asn Ser Gly Phe Ala Ser Leu Ala Ser Ser Asp Pro Glu Ala
 20 25 30

Lys Gln Lys Tyr Gly Ser Gly Phe Leu Lys Gln Glu Arg Ser Ala Ala
 35 40 45

Ala Asp Asp Asp Trp Arg Asn Ser Lys Leu Ala Lys Thr Glu Ser Met
 50 55 60

Leu Leu Asp Gln Arg Asn Thr Phe Leu Leu Lys Ser Ser Asn Asn Ser
 65 70 75 80

Leu Phe Thr Asp Gly Gln Gln Gln Gln Gln Met Leu Ser Phe Ser Cys
 85 90 95

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

Pro Tyr Phe His Leu Thr Ser Ser Ala Cys Asn Arg Asn Thr Gly Tyr
 115 120 125

PF59082PF60142_PCT_SEQ_LIST.txt

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

Thr Arg Trp Pro Phe Thr Gln Leu Gln Trp Met Glu Leu Glu His Gln
145 150 155 160

Ala Leu Ile Tyr Lys Tyr Met Thr Ala Asn Val Pro Ile Pro Ser Asn
165 170 175

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

Phe Ser Gly Gly Leu Phe Lys Pro Ser Ala Leu Gln Trp Gly Thr Phe
195 200 205

His Met Gly Phe Ser Ser Asn Thr Asp Pro Glu Pro Gly Arg Cys Arg
210 215 220

Arg Thr Asp Gly Lys Lys Trp Arg Cys Ser Arg Asp Ala Val Ala Asp
225 230 235 240

Gln Lys Tyr Cys Glu Arg His Met Asn Arg Gly Arg His Arg Ser Arg
245 250 255

Lys Pro Val Glu Gly Gln Ser Gly His Ser Ala Ala Ala Thr Thr Thr
260 265 270

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

Val Gly Leu Arg Ser Ala Val Ser Asp Ser His Thr Ile Val His Asn
290 295 300

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

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

Ala Ser Gly Leu Ser Met Leu Pro Ser Ser Ile Asp Leu Lys Ser Lys
340 345 350

Glu Thr Pro Phe Phe Ile Ser Lys Gln Gln Asn Ser Tyr Gly Glu Ser
355 360 365

Leu Gln Asn Glu Phe Ala Leu Val Thr Ser Asp Ser Leu Leu Asn His
370 375 380

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

Gln Asp Leu Thr Asp Gln Glu Ser Val Ser Gln His Ser Leu Arg Gln

405

410

415

Phe Met Asp Asp Cys Pro Lys Ser His Ser Asp Arg Ser Ala Val Ala
 420 425 430

Trp Pro Gly Leu Asp Leu Gln Ser Glu Arg Thr Gln Leu Ser Ile Ser
 435 440 445

Ile Pro Met Ala Pro Ala Asp Phe Val Ser Ser Thr Ser Ser Ser Asn
 450 455 460

Asn Glu Lys Ile Ser Leu Ser Pro Leu Arg Leu Ser Arg Glu Phe Asp
 465 470 475 480

Pro Ile Lys Met Gly Leu Gly Val Gly Ala Gly Ser Val Ala Asn Glu
 485 490 495

Pro Asn Gln Arg Gln Ala Asn Trp Ile Pro Ile Ser Trp Glu Thr Ser
 500 505 510

Met Gly Gly Pro Leu Gly Glu Val Leu His Asn Thr Asn Asn Asn Ala
 515 520 525

Thr Ala Glu Cys Lys Asn Glu Ser Ser Leu Asn Leu Met Thr Glu Arg
 530 535 540

Trp Asp Asn Ser Pro Arg Val Gly Ser Ser Pro Thr Gly Val Leu Gln
 545 550 555 560

Lys Ser Ala Phe Ala Ser Leu Ser Asn Ser Ser Ala Gly Ser Ser Pro
 565 570 575

Arg Ala Glu Asn Lys Thr Ile Glu Gly Gly Asn Leu Cys Asn Asp Leu
 580 585 590

Gly Ser Thr Ile Val His Ser Ser Ser Leu Pro Ala Leu
 595 600 605

<210> 59

<211> 1053

<212> DNA

<213> Populus tremuloides

<400> 59

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cttcctcac caacctattg ggtggggttg ttttcaggcg ggttttgga gaaaagcaga 180

cccagagcca ggaaggtgca gaagaacgga tggaaaaaaa tggaggtgct caaaggaagc 240

ataccagac tcaaaatatt gtgagaggca catgcacaga ggcagaagcc gttcaagaaa 300

gcctgtggaa ctacttcaa gtactactac aacagcaaca acaattcctt taacatcaat 360

PF59082PF60142_PCT_SEQ_LIST.txt

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caacagaaac ctctctaacc ccactatttc accctccagc tcctcttatt ctttctctca 420
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taacccttc ctttatcctc attcttcac cttctggacct cctgattctg gtttttcacc 540
tctaaatagc acccctcaca acctgttttt ggagtctgga tcttctcctc aagttgacaa 600
agagcacagg tattatcatg gaatgagggg ggatgtggat gagagagctt tctttccaga 660
tggttttagg agtgcaagag gtgttcaaga ttcataaac caattgacaa tgagttccta 720
caaaggttac tcaactgtcac agtttcaaac ctttgctgat acttctaaag aagagcagca 780
acaaccaggg cagcactgct ttgttttggg cactgatatt atcaagtcac cagcaacaag 840
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gtgggtcatc aatgcctttc ttgcctcaaa tga 1053

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<210> 60
 <211> 340
 <212> PRT
 <213> Populus tremuloides
 <400> 60

Met Leu Asn Thr Thr Ile Ser Arg Asn Arg Phe Pro Phe Thr Ala Thr
 1 5 10 15

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

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

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

Trp Gly Cys Phe Gln Ala Gly Phe Gly Arg Lys Ala Asp Pro Glu Pro
 65 70 75 80

Gly Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys Ser Lys Glu
 85 90 95

Ala Tyr Pro Asp Ser Lys Tyr Cys Glu Arg His Met His Arg Gly Arg
 100 105 110

Ser Arg Ser Arg Lys Pro Val Glu Leu Thr Ser Ser Thr Thr Thr Thr
 115 120 125

Ala Thr Thr Ile Pro Leu Thr Ser Ile Asn Arg Asn Leu Ser Asn Pro
 130 135 140

Thr Ile Ser Pro Ser Ser Ser Ser Tyr Ser Phe Ser His Pro Ser Ser
 Seite 74

145 150 155 160

Ala Glu Ser Glu Val Tyr Ala His Gln Asn Pro Ser His Gly Thr Phe
165 170 175

Leu Asn Pro Phe Leu Tyr Pro His Ser Ser Ser Ser Gly Pro Pro Asp
180 185 190

Ser Gly Phe Ser Pro Leu Asn Ser Thr Pro His Asn Leu Phe Leu Glu
195 200 205

Ser Gly Ser Ser Pro Gln Val Asp Lys Glu His Arg Tyr Tyr His Gly
210 215 220

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

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

Tyr Lys Gly Tyr Ser Leu Ser Gln Phe Gln Thr Phe Ala Asp Thr Ser
260 265 270

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

Asp Ile Ile Lys Ser Ser Ala Thr Arg Ser Ile Lys Leu Glu Lys Glu
290 295 300

Thr Glu Thr Leu Lys Pro Leu His His Phe Phe Asp Glu Trp Glu Pro
305 310 315 320

Lys Asp Ala Asp Ser Trp Leu Asp Leu Ala Ser Ser Ser Arg Pro His
325 330 335

Thr Ser Asp Asp
340

<210> 61
<211> 1265
<212> DNA
<213> Populus tremuloides

<400> 61
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atccccatcc ctcccgatct tcttttcacc atcaaaagaa gtggctgctt ggactcttca 180
ctctcttcaa agctcttttc ttgccaacct ccacattttt cctgggggctg ttttcagatg 240
ggtttgaggaa ggaaaataga tccagaaccg gggaggtgca ggagaactga tggaaagaaa 300
tgagatgct caaaagaagc ataccagat tctaagtact gtgagaaaca tatgcataga 360

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aatacagatt acagaagaaa caggaatggt tatgggctga aagaggaggt tgatgagcat 720
gctttcttct cagaaccttc aggttctatg agaagcttgt ccggttcac tttggatgat 780
gcttggcaac tcacccact cacaatgaac tcttctcctt ctaccaccaa ctcttcaaag 840
caaaggagct tgtctagttt acacaacgaa tattcttact tgcagcttca aagcctgagt 900
gatcccgata ccccaaaaca acaaaagcag tgtcaacata actatcttct gggaagtagt 960
gatgtagaca gtctagggcc cataaaaatg gagaaggaaa aatcccaaaa gactgttcac 1020
cgtttctttg atgaatggcc accaaaggat aaagattcat ggcttgattt ggatgacaaa 1080
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gactttcttc caatcttcag ttcaagaact aataatggtg gttgatttta ctctgggtggg 1200
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tcaga 1265

<210> 62
<211> 386
<212> PRT
<213> Populus tremuloides
<400> 62

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20 25 30

Ile Pro Ile Pro Pro Asp Leu Leu Phe Thr Ile Lys Arg Ser Gly Cys
35 40 45

Leu Asp Ser Ser Leu Ser Ser Lys Leu Phe Pro Cys Gln Pro Pro His
50 55 60

Phe Ser Trp Gly Cys Phe Gln Met Gly Leu Gly Arg Lys Ile Asp Pro
65 70 75 80

Glu Pro Gly Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys Ser
85 90 95

Lys Glu Ala Tyr Pro Asp Ser Lys Tyr Cys Glu Lys His Met His Arg
100 105 110

Gly Lys Asn Arg Ser Arg Lys Pro Val Glu Val Ala Thr Gln Ser Ile
Seite 76

115

120

125

Thr Ala Pro Thr Val Ser Ser Met Thr Arg Asn His Ser Asn Asn Ser
 130 135 140
 Leu Leu Thr Thr Ser Pro Thr Ser Leu Ser Leu Leu Ser Pro Lys Thr
 145 150 155 160
 His His Gln Asn His Leu His Tyr Pro Ala Pro Ala Gly Tyr His Ala
 165 170 175
 His Pro Asn His Gln Phe Leu Ser Ser Arg Pro Leu Gly Ile Gly
 180 185 190
 Leu Ser Pro His Glu Asn Pro Thr His Leu Leu Leu Asp Ser Gly Gly
 195 200 205
 Ser Ser Leu Ala Asn Thr Asp Tyr Arg Arg Asn Arg Asn Val Tyr Gly
 210 215 220
 Leu Lys Glu Glu Val Asp Glu His Ala Phe Phe Ser Glu Pro Ser Gly
 225 230 235 240
 Ser Met Arg Ser Leu Ser Gly Ser Ser Leu Asp Asp Ala Trp Gln Leu
 245 250 255
 Thr Pro Leu Thr Met Asn Ser Ser Pro Ser Thr Thr Asn Ser Ser Lys
 260 265 270
 Gln Arg Ser Leu Ser Ser Leu His Asn Glu Tyr Ser Tyr Leu Gln Leu
 275 280 285
 Gln Ser Leu Ser Asp Pro Asp Thr Pro Lys Gln Gln Lys Gln Cys Gln
 290 295 300
 His Asn Tyr Leu Leu Gly Ser Ser Asp Val Asp Ser Leu Gly Pro Ile
 305 310 315 320
 Lys Met Glu Lys Glu Lys Ser Gln Lys Thr Val His Arg Phe Phe Asp
 325 330 335
 Glu Trp Pro Pro Lys Asp Lys Asp Ser Trp Leu Asp Leu Asp Asp Lys
 340 345 350
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 Gly Gly
 385

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 <212> DNA
 <213> Populus tremuloides

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 cagtctctta tctacaagta tatccaagct ggatttcctg taccttacca tcttgtttta 240
 cctatatgga aaagtgttac tgcttccctt ggtggtctca gttcaagctt gtaccagctc 300
 taccctagct ttatgggggtg taagtgtaac ccattatatt tggaatataa gaaaggaatg 360
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 aagcttgtgg aagctgcttc tcatagtaat gccagcacca acctctccat ttctctcctt 540
 ggaatcggtg gtgctagcgc ctacgagtac taatctctct ccaatatggt gtctctctcc 600
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<210> 64
 <211> 177
 <212> PRT
 <213> Populus tremuloides

<400> 64
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 20 25 30
 Gly Cys Lys Lys Pro Tyr Gly Phe Thr Ile Leu Gln Leu His Glu Leu
 35 40 45
 Glu Leu Gln Ser Leu Ile Tyr Lys Tyr Ile Gln Ala Gly Phe Pro Val
 50 55 60
 Pro Tyr His Leu Val Leu Pro Ile Trp Lys Ser Val Thr Ala Ser Leu
 65 70 75 80
 Gly Gly Leu Ser Ser Ser Leu Tyr Gln Leu Tyr Pro Ser Phe Met Gly
 85 90 95
 Cys Lys Cys Asn Pro Leu Tyr Leu Glu Tyr Lys Lys Gly Met Glu His
 100 105 110
 Glu Pro Gly Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys Ser
 115 120 125

PF59082PF60142_PCT_SEQ_LIST.txt

Lys Glu Val Leu Pro Asp Gln Lys Tyr Cys Asp Arg His Ile His Arg
130 135 140

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

Ala Ser Thr Asn Leu Ser Ile Ser Leu Pro Gly Ile Gly Ser Ala Ser
165 170 175

Ala

<210> 65
<211> 1154
<212> DNA
<213> Populus tremuloides

<400> 65
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gttcttatct ttaagtgttt aaatgcaggg ttacctgtcc ctccttcctt tctccttcct 180
attcgtgaaga gttttcagct tctttcccct ggtttcttgc acccatcaaa tttgagctac 240
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aatagaagcc gtaaccgttc aagaaagcct gtggaatcac aaactacctc tcagtccttg 420
tcaactgtgg catcagaaat tgcaactggg agcagcagca ttgggagcag agggatatcca 480
actaatcctg ggaccttagg tttgggaagt aatatgtcac gttggcagat ggagtctatg 540
ccttatggtg ttaatagtaa agactacagg tctctccatg gaccgaagcc tgaagcagat 600
gagaaaactt tcctaccaga agctttggga aatacaagaa gctttggaat gaactctact 660
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tgggcaaaat gcagggatat ggattcccat ctactgatc aaagatctaa caataactcg 960
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cattcccaa atggtgagac aggtttatct ggaacatact tttccgcaac ctagacgccc 1080
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cttgaaagga gcat 1154

<210> 66
<211> 347
<212> PRT
<213> Populus tremuloides

<400> 66

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

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Ser Ser Gly Ser Met Arg Arg Glu Asn Gln Ser Leu Gln Pro Leu Phe
275 280 285

Asp Glu Trp Pro Lys Cys Arg Asp Met Asp Ser His Leu Thr Asp Gln
290 295 300

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

Met Ala Pro Asn Pro Ala Ala Arg Ser Tyr His Ser Pro Asn Gly Glu
325 330 335

Thr Gly Leu Ser Gly Thr Tyr Phe Ser Ala Thr
340 345

<210> 67
<211> 1875
<212> DNA
<213> Populus tremuloides

<400> 67
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ctttaacgct aaaccctacg agtcttttct aaactttagt gatgaagaaa gccatgatca 1200
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PF59082PF60142_PCT_SEQ_LIST.txt

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<210> 68
<211> 555
<212> PRT
<213> Populus tremuloides
<400> 68

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20 25 30

Arg Gln Gln Glu His Met Leu Ser Phe Ser Ser Pro Lys Pro Glu Ala
35 40 45

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

Asn His Thr Ala Leu Ser Phe Pro Tyr Tyr Gln His Ala Pro Leu Ser
65 70 75 80

Ala Ser Arg Ser Ala Gly Tyr Gly Thr Gly Asn Leu Asn Ala Ser Met
85 90 95

Gln Gly Pro Phe Thr Gly Val Arg Gly Pro Phe Thr Pro Ser Gln Trp
100 105 110

Met Glu Leu Glu His Gln Ala Leu Ile Tyr Lys Tyr Ile Thr Ala Arg
115 120 125

Val Pro Val Pro Ser Asn Leu Ile Ile Pro Leu Lys Lys Ser Leu Asn
130 135 140

Pro Tyr Gly Leu Pro Phe Ser Ser Ala Gly Ser Phe Pro Pro Ser Ser
145 150 155 160

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Gly Trp Gly Thr Phe His Leu Gly Tyr Pro Gly Asn Asn Thr Asp
 165 170 175
 Gln Glu Pro Gly Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys
 180 185 190
 Ser Arg Asp Ala Val Ala Asp Gln Lys Tyr Cys Glu Arg His Ile Asn
 195 200 205
 Arg Gly Arg His Arg Ser Arg Lys Pro Val Glu Gly Gln Thr Gly His
 210 215 220
 Ala Ala Thr Gly Thr Ala Ser Ser Lys Val Val Pro Met Ser Asn Ser
 225 230 235 240
 Met Pro Thr Ser Ile Thr Thr Ser Gly Ala Thr Ser Asn Ser Ile Val
 245 250 255
 Ile Thr Gln Gln Gln Leu Lys Asn Phe Gln Pro Ala Ala Ala Ser Ile
 260 265 270
 Ser Ser Ala Asp Ala Arg Val Asn Gly Ala Gln Asp Ala Arg Arg Val
 275 280 285
 Ser Met Met Ser Ser Thr Ile Asn Arg Lys Ser Asp Glu Ser Thr Phe
 290 295 300
 Cys Ile Pro Arg Gln Asp Ile Leu Phe Glu Gln Cys Ser Gln Thr Glu
 305 310 315 320
 Phe Gly Leu Val Ser Tyr Asp Ser Leu Leu Asn Pro Ser Gln Lys Ser
 325 330 335
 Ser Tyr Phe Asn Ala Lys Pro Tyr Glu Ser Phe Leu Asn Phe Ser Asp
 340 345 350
 Glu Glu Ser His Asp Gln His Pro Leu Arg Gln Phe Ile Asp Asp Trp
 355 360 365
 Pro Lys Asp Gln Ser Asn Arg Ser Val Ile Ser Trp Pro Glu Glu Leu
 370 375 380
 Lys Ser Asp Cys Thr Gln Leu Ser Met Ser Ile Ser Met Val Ser Ser
 385 390 395 400
 Asp Phe Ser Ser Ser Ser Ser Ser Leu Leu Arg Glu Lys Leu Ala Phe
 405 410 415
 Ser Pro Leu Arg Leu Ser Arg Glu Phe Asp Pro Ile Gln Met Gly Leu
 420 425 430

PF59082PF60142_PCT_SEQ_LIST.txt

Arg Val Ser Gly Asp His Asn Glu Ser Ser Gln Lys Gln Ala Asn Trp
435 440 445

Ile Pro Ile Ser Trp Gly Thr Ser Ile Gly Gly Pro Leu Gly Glu Val
450 455 460

Leu Thr Thr Ser Ala Ser His Ala Asp Ser Cys Lys Ser Ser Ser Ala
465 470 475 480

Leu Asn Leu Leu Arg Glu Gly Trp Asp Gly Ser Pro Gln Leu Gly Ser
485 490 495

Ser Pro Thr Gly Val Leu Gln Lys Ser Thr Phe Gly Ser Leu Ser Asn
500 505 510

Ser Ser Ser Gly Ser Ser Pro Arg Ala Glu Ser Lys Lys Asn Asn Glu
515 520 525

Ser Ala Ser Leu Tyr Glu Asp Val Val Gly Ser Ile Ile Ala Ser Asp
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Pro Leu Phe His Pro Cys Asn Gln Glu Asn Gly
545 550 555

<210> 69
<211> 1715
<212> DNA
<213> Populus tremuloides

<400> 69
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cctcatgtta atcaccaccg tccaatgttt gacaatgggtc ccacatcatc atgtgataga 240
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aacaagaaga accgccataa tcctgctatt tgtccagaag ctctgttac cgtggccatt 780
tctaaacca caatcaaca cagcaacagt ggctctgcct ctcacgatca gttttttggg 840
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PF59082PF60142_PCT_SEQ_LIST.txt

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cagcattacc aaggagagtc tttgaatttg aactcatttg gaaattttta tgctagagaa 1140
gaccaacaaa gcaatcaata tagtctgttt cttgatgagg ctccaaggag ttttattgat 1200
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cagatccaaa tgggttttagg cctaataaaa tcagatcgaa atgaagaatg tggtaacact 1380
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acagtctctt ctccatctgg ggttttgcag aaaacacttg cctcattttc tgatagcagt 1560
ggtaatagca gtccaactct tgccagttca aggaccaaac ctgaaattgc catgctttgg 1620
ttaaatcaag gctaaatgtg ccactctcta gttagttaag ggcacacaag gccataaggg 1680
caatataaat ttttataagc ttgatataatt tttat 1715

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<210> 70
<211> 535
<212> PRT
<213> Populus tremuloides
<400> 70

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          20          25          30

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Leu His Gln Pro Ile Asp His His Gln Ser Phe Pro Ser Ser Thr Pro
          35          40          45

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Met Met Val Pro His Val Asn His His Arg Pro Met Phe Asp Asn Gly
          50          55          60

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Pro Thr Ser Ser Cys Asp Arg Asn Lys Ser Leu Met Asn Tyr Ile Ser
65          70          75          80

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Asp Arg Ile Tyr Arg Val Ala Ala Gly Gly Ala Thr Ser Gly Gly Ala
          85          90          95

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Val Gly Val Arg Asn Leu Gln Pro Phe Asp Ile Ser Glu Thr Ser Ile
          100          105          110

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Ser Thr Ala Ala Ser Ala Phe Arg Ser Pro Gly Gly Asn Met Ala Ala
          115          120          125

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Ser Leu Gly Phe Pro Phe Thr Asn Thr Gln Trp Lys Glu Leu Glu Arg
          130          135          140

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PF59082PF60142_PCT_SEQ_LIST.txt

Gln Ala Met Ile Tyr Asn Tyr Ile Thr Ala Ser Val Pro Val Pro Pro
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Gln Phe Leu Ile Pro Thr Pro Met Gly Asn Gly Leu Asn Val Arg Phe
165 170 175

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

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

Glu Arg His Met His Arg Gly Arg Pro Arg Ser Arg Lys His Val Glu
210 215 220

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

Ile Cys Pro Glu Ala Pro Val Thr Val Ala Ile Ser Lys Pro Thr Ile
245 250 255

Asn Asn Ser Asn Ser Gly Ser Ala Ser His Asp Gln Phe Phe Gly Pro
260 265 270

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

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

Lys Glu Pro Arg Ser Leu Asp Trp Met Leu Lys Gly Glu Ala Gly Pro
305 310 315 320

Ile Ala Lys Asn Asp Gln Gln Trp Pro His Leu Val His Lys Glu Ile
325 330 335

Glu Leu Ala Thr Glu Gly Ser Phe Asn Ser Ala Ser Val Leu Lys Gln
340 345 350

His Tyr Gln Gly Glu Ser Leu Asn Leu Asn Ser Phe Gly Asn Phe Asn
355 360 365

Ala Arg Glu Asp Gln Gln Ser Asn Gln Tyr Ser Leu Phe Leu Asp Glu
370 375 380

Ala Pro Arg Ser Phe Ile Asp Ala Trp Ser Asn Asp Ala Ile Ser Arg
385 390 395 400

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

PF59082PF60142_PCT_SEQ_LIST.txt

Ser Leu Ser Met Gly Ser Asn Arg Ser Thr Asp Asp Glu Met Gly Gln
420 425 430

Ile Gln Met Gly Leu Gly Leu Ile Lys Ser Asp Arg Asn Glu Glu Cys
435 440 445

Gly Asn Thr Ser Ser Ala Pro Gly Gly Pro Leu Ala Glu Val Leu Gln
450 455 460

Leu Arg Thr Ser Asn Thr Thr Gly Thr Asn Gln Ser Ser Ser Met Met
465 470 475 480

Glu Asn Gly Asp Ser Ile Ser Pro Pro Ala Thr Thr Val Ser Ser Pro
485 490 495

Ser Gly Val Leu Gln Lys Thr Leu Ala Ser Phe Ser Asp Ser Ser Gly
500 505 510

Asn Ser Ser Pro Thr Leu Ala Ser Ser Arg Thr Lys Pro Glu Ile Ala
515 520 525

Met Leu Trp Leu Asn Gln Gly
530 535

<210> 71
<211> 1053
<212> DNA
<213> Populus tremuloides

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aggctctgcct gttccacctg atcttgtgct ccctattcag aggagctttg aatccatttc 180
tcatagattc ttccaccatc ccaccatgag ctattgcact ttctatggca agaaggtgga 240
tccggaacca ggtcgatgca ggaggaccga cggcaagaag tggaggtgct ccaaagatgc 300
ctaccagac tccaagtact gtgagcgcca catgcaccgt ggccgcaacc gttcaagaaa 360
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ccagggcact gcttctggaa ctaaccaatc atattatcat atgaactcca ttccctacgg 540
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cttcttgtct gaagcctcag gaagcaacaa ggggcttcag atagactcac agctggacaa 660
tgcatggtct ttgatgcaat ccagagtctc atcattcccc acagagaaat caactgaaaa 720
ctcgatgttg caaagtaatc atccccagca ttcatTTTTT agtagtgatt tcaccaccag 780
ggaatctgtg aaacaggacg ggcagtctct tcgacccttc tttgatgagt ggcctaaaaa 840
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PF59082PF60142_PCT_SEQ_LIST.txt

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 acgagataac taagaggaca ctaagaattc acaaaacaaa gccaaaggtg gtcctggcca 1020
 aagattaaca catacttgtg ttaaattttt gtg 1053

<210> 72
 <211> 320
 <212> PRT
 <213> Populus tremuloides

<400> 72

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

Lys Tyr Met Val Ala Gly Leu Pro Val Pro Pro Asp Leu Val Leu Pro
 35 40 45

Ile Gln Arg Ser Phe Glu Ser Ile Ser His Arg Phe Phe His His Pro
 50 55 60

Thr Met Ser Tyr Cys Thr Phe Tyr Gly Lys Lys Val Asp Pro Glu Pro
 65 70 75 80

Gly Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys Ser Lys Asp
 85 90 95

Ala Tyr Pro Asp Ser Lys Tyr Cys Glu Arg His Met His Arg Gly Arg
 100 105 110

Asn Arg Ser Arg Lys Pro Val Glu Ser Gln Thr Met Thr Gln Ser Ser
 115 120 125

Ser Thr Val Thr Ser Leu Thr Val Thr Gly Ser Ser Ser Gly Thr Gly
 130 135 140

Ser Phe Gln Asn Leu Pro Leu His Thr Tyr Ser Asn Pro Gln Gly Thr
 145 150 155 160

Ala Ser Gly Thr Asn Gln Ser Tyr Tyr His Met Asn Ser Ile Pro Tyr
 165 170 175

Gly Ile Pro Thr Lys Asp Tyr Arg Tyr Leu Gln Glu Leu Thr Pro Glu
 180 185 190

Gly Gly Glu His Ser Phe Leu Ser Glu Ala Ser Gly Ser Asn Lys Gly
 195 200 205

Leu Gln Ile Asp Ser Gln Leu Asp Asn Ala Trp Ser Leu Met Gln Ser
 210 215 220

PF59082PF60142_PCT_SEQ_LIST.txt

Arg Val Ser Ser Phe Pro Thr Glu Lys Ser Thr Glu Asn Ser Met Leu
225 230 235 240

Gln Ser Asn His Pro Gln His Ser Phe Phe Ser Ser Asp Phe Thr Thr
245 250 255

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

Glu Trp Pro Lys Asn Arg Asp Ala Trp Ser Gly Leu Glu Asn Asp Ser
275 280 285

Ser Asn Gln Thr Ser Phe Ser Thr Thr Gln Leu Ser Ile Ser Ile Pro
290 295 300

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

<210> 73
<211> 1682
<212> DNA
<213> Populus tremuloides

<400> 73
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gatagacacg tgttcccaca gttaacagag actcagttgc atgagcttaa acagcaagct 180
ttgatattca agtacatagt agctggctct cgcgtgcctc ctgatcttgt agttcccatt 240
tggcatagtg ttgctagcag ctctcttggg tcatttagtg gtgctgatat ttataggcaa 300
ttcccaagct ttgtgggatt aagtcctcag ggatttgatt atagacaaat gatggatcca 360
gaacctggga gatgtagaag aactgatggg aagaaatgga ggtgtagcaa ggatgtagtt 420
gctggtcaga agtattgtga acgcatatg catagaggcc gtcaacgttc aagaaagctt 480
gtggaagctt ctcaaactgc tgctgcttct gaaaaacat cacctcaca ttcaagcaag 540
aattcagaca atccaaccac tcattcttct aatttagcca aagtaagttc acagataaaa 600
gccccacctc ttaataatac cccaccatt ttaaccactt gcaccacaag ttgcaattct 660
gacattgaaa tcaactggcat gagcttggcc actactgcta attctgactg caaaaacccc 720
tttacaacca tgactactag cattgttacc ggctacaaga aactgcaac aatgatcgct 780
agtgtgttc atgtgacat tacagccact ggtaacgact acaagagtag catcaactta 840
aagagacact acattgatga cagaaacagt aattgcagca actctgttac ttacaagggg 900
ataatcgaca gaaactgcag caacaaaaa ataaaaaatg ctggtagcaa tgtatctcaa 960
ggattgaact tctccccgaa gagtggttct caagttcaag gttgcggcgc ctcacacatt 1020
tacatgaatg atgtggaact tgaactggga aggtgtagaa gaacagatgg aaagaagtgg 1080
cgatgccgca gggatgttgt agctaatacag aagtattgag agatgcacat gcaccgaggt 1140

PF59082PF60142_PCT_SEQ_LIST.txt

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ttaaacaccg atctctgtat ttcgatccca acaagtcctc aactgatcat gaccaatgat	1320
gatacaagaa ctatcagcaa tagcagtgc actaccataa gcgacaccat gaggggcacc	1380
acaccaggac tggatatcaac acatgcaggt agtggggatc ccaaaagtcc tcctggtggt	1440
gacagagcca gggtattaaa gaaagctgaa gttatggagg cggcggtaga gatttacgag	1500
gaagtacaat ccggccgtgg ggtcagaagt tttatccaag gcagaagact tccaactttt	1560
ccctatgttt atatcacacc tctgctgtta atctgcaatt aattctagtc aaaccatgtg	1620
attaaagtta caagaggtgt aagagaagaa taacgtttta ttccatccta tgcagacaac	1680
tg	1682

<210> 74
 <211> 523
 <212> PRT
 <213> Populus tremuloides

<400> 74

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Leu	Gly	Ile	Gly	Ala	Gly	Asp	His	Gly	Asp	Asp	Asp	Gln	Asp	Asp	Arg
			20					25					30		

His	Val	Phe	Pro	Gln	Leu	Thr	Glu	Thr	Gln	Leu	His	Glu	Leu	Lys	Gln
		35					40					45			

Gln	Ala	Leu	Ile	Phe	Lys	Tyr	Ile	Val	Ala	Gly	Leu	Arg	Val	Pro	Pro
	50					55					60				

Asp	Leu	Val	Val	Pro	Ile	Trp	His	Ser	Val	Ala	Ser	Ser	Ser	Leu	Gly
65					70					75					80

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

Leu	Ser	Pro	Gln	Gly	Phe	Asp	Tyr	Arg	Gln	Met	Met	Asp	Pro	Glu	Pro
			100					105					110		

Gly	Arg	Cys	Arg	Arg	Thr	Asp	Gly	Lys	Lys	Trp	Arg	Cys	Ser	Lys	Asp
		115					120					125			

Val	Val	Ala	Gly	Gln	Lys	Tyr	Cys	Glu	Arg	His	Met	His	Arg	Gly	Arg
	130					135					140				

Gln	Arg	Ser	Arg	Lys	Leu	Val	Glu	Ala	Ser	Gln	Thr	Ala	Ala	Ala	Ser
145					150					155					160

Glu	Lys	Pro	Ser	Pro	His	Asn	Ser	Ser	Lys	Asn	Ser	Asp	Asn	Pro	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

165

170

175

Thr His Ser Ser Asn Leu Ala Lys Val Ser Ser Gln Ile Lys Ala Pro
 180 185 190
 Pro Leu Asn Asn Thr Pro Thr Ile Leu Thr Thr Cys Thr Thr Ser Cys
 195 200 205
 Asn Ser Asp Ile Glu Ile Thr Gly Met Ser Leu Ala Thr Thr Ala Asn
 210 215 220
 Ser Asp Cys Lys Asn Pro Phe Thr Thr Met Thr Thr Ser Ile Val Thr
 225 230 235 240
 Gly Tyr Lys Asn Thr Ala Thr Met Ile Ala Ser Ala Val His Ala Asp
 245 250 255
 Ile Thr Ala Thr Gly Asn Asp Tyr Lys Ser Ser Ile Asn Leu Lys Arg
 260 265 270
 His Tyr Ile Asp Asp Arg Asn Ser Asn Cys Ser Asn Ser Val Thr Tyr
 275 280 285
 Lys Gly Ile Ile Asp Arg Asn Cys Ser Asn Lys Lys Ile Lys Asn Ala
 290 295 300
 Gly Ser Asn Val Ser Gln Gly Leu Asn Phe Ser Pro Lys Ser Val Leu
 305 310 315 320
 Gln Val Gln Gly Cys Gly Ala Ser His Ile Tyr Met Asn Asp Val Glu
 325 330 335
 Leu Glu Leu Gly Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys
 340 345 350
 Arg Arg Asp Val Val Ala Asn Gln Lys Tyr Cys Glu Met His Met His
 355 360 365
 Arg Gly Ser Lys Gln His Leu Glu Ala Ser Lys Pro Ala Ala Ile Pro
 370 375 380
 Ala Thr Ile Pro Phe Val Pro Gly Asn Val His Ser Tyr Pro Ala Thr
 385 390 395 400
 Asn Leu Pro Ser Lys Ala Asp Arg Arg Ser Leu Asn Thr Asp Leu Cys
 405 410 415
 Ile Ser Ile Pro Thr Ser Pro Gln Leu Ile Met Thr Asn Asp Asp Thr
 420 425 430
 Arg Thr Ile Ser Asn Ser Ser Asp Thr Thr Ile Ser Asp Thr Met Arg
 435 440 445

PF59082PF60142_PCT_SEQ_LIST.txt

Gly Thr Thr Pro Gly Leu Val Ser Thr His Ala Gly Ser Gly Asp Pro
450 455 460

Lys Ser Pro Pro Gly Gly Asp Arg Ala Arg Leu Leu Lys Lys Ala Glu
465 470 475 480

Val Met Glu Ala Ala Val Glu Ile Tyr Glu Glu Val Gln Ser Gly Arg
485 490 495

Gly Val Arg Ser Phe Ile Gln Gly Arg Arg Leu Pro Thr Phe Pro Tyr
500 505 510

Val Tyr Ile Thr Pro Leu Leu Leu Ile Cys Asn
515 520

<210> 75
<211> 1812
<212> DNA
<213> Populus tremuloides

<400> 75
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cggatctggg ttcttgaagc aagagagacc tggcaacatc gatggtgatt ggaggagctc 120
taaattgtcg aaaactgagt caatgctgct tgagcagagt aacacttcac ttctgaaatc 180
tagctccaac tttctcttcg ctgatggaca gcagcagcag cagcagatgc tcagcttctc 240
ctatcccaga tcagctcctt cagcggagag aagctcccaa aatggcacat tgccctctgg 300
tatctacaat gctgccagca tgcattgggt tttgaccgag accagatggc cattcactca 360
atcacaatgg atggagcttg aacatcaggc cttgatctac aagtatatag cagcaaatgt 420
gcctatacca tctaactcgc tccttcccat tagaaaagct cttgattctg ctgggtttcc 480
tagcttttct gctggatttt tcaggcccaa tacattgcca tgggggtgctt tccatatggg 540
tttctccagc aacactgatc cggagccagg acggtgtcga aggacagatg gaaagaaatg 600
gcggtgctca agagatgcag ttgccgatca gaagtattgt gagcggcata tgaacagggg 660
ccgccatcgt tcaagaaagc ctgtggaagg ccaatcaggc cattccgctg cagccgccac 720
cactgtaaag ccagccaatg gcacttcgtc ttctacatca tcatcagtgg tggggcttcg 780
cagcactgtg tccgacagcc tcactattgc tcataatcag cagcaagcag ctagtccatc 840
taatctttct gcctctaata cgctcagcag gatgttcctt actaaagaga atgtagggtga 900
gagaacgcag gatgcgacag ccttgtccat gcttcgatcc aacatggatc ttaaattctaa 960
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ctccctccgc caattcatgg atgattggcc taaaagtcag tctgatcggt ctgctgtttc 1200
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PF59082PF60142_PCT_SEQ_LIST.txt

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tggtggtatt gccaacgaac caaaccaaag gcaagccaac tggattccca tttcttgggg 1440
aacttcaatg ggtggtccgc tcggggaggt cttgcacaac accaataaca atgcagcagc 1500
agagtgaag accacgtcat cgctgaacct gatgacctat agatgggaca acagtcctcg 1560
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ttttgaagtt gt 1812

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<210> 76
<211> 529
<212> PRT
<213> Populus tremuloides
<400> 76

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Met Leu Leu Glu Gln Ser Asn Thr Ser Leu Leu Lys Ser Ser Ser Asn
1 5 10 15

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Phe Leu Phe Ala Asp Gly Gln Gln Gln Gln Gln Met Leu Ser Phe
20 25 30

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Ser Tyr Pro Arg Ser Ala Pro Ser Ala Glu Arg Ser Ser Gln Asn Gly
35 40 45

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Thr Leu Pro Ser Gly Ile Tyr Asn Ala Ala Ser Met His Gly Val Leu
50 55 60

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Thr Glu Thr Arg Trp Pro Phe Thr Gln Ser Gln Trp Met Glu Leu Glu
65 70 75 80

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His Gln Ala Leu Ile Tyr Lys Tyr Ile Ala Ala Asn Val Pro Ile Pro
85 90 95

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

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Pro Ser Phe Ser Ala Gly Phe Phe Arg Pro Asn Thr Leu Pro Trp Gly
115 120 125

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Ala Phe His Met Gly Phe Ser Ser Asn Thr Asp Pro Glu Pro Gly Arg
130 135 140

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Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys Ser Arg Asp Ala Val
145 150 155 160

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PF59082PF60142_PCT_SEQ_LIST.txt

Ala Asp Gln Lys Tyr Cys Glu Arg His Met Asn Arg Gly Arg His Arg
165 170 175

Ser Arg Lys Pro Val Glu Gly Gln Ser Gly His Ser Ala Ala Ala Ala
180 185 190

Thr Thr Val Lys Pro Ala Asn Gly Thr Ser Ser Ser Thr Ser Ser Ser
195 200 205

Val Val Gly Leu Arg Ser Thr Val Ser Asp Ser Leu Thr Ile Ala His
210 215 220

Asn Gln Gln Gln Ala Ala Ser Pro Ser Asn Leu Ser Ala Ser Asn Thr
225 230 235 240

Leu Ser Arg Met Phe Leu Thr Lys Glu Asn Val Gly Glu Arg Thr Gln
245 250 255

Asp Ala Thr Ala Leu Ser Met Leu Arg Ser Asn Met Asp Leu Lys Ser
260 265 270

Lys Glu Thr Pro Phe Phe Ile Ser Lys Gln Gln Asn Ser Tyr Gly Glu
275 280 285

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

His Ser Gln Lys Ser Ser Ser Leu Met Ser Cys Arg Asn Phe Gly Ser
305 310 315 320

Ser Gln Asp Leu Thr Asp Gln Glu Ser Val Ser Gln His Ser Leu Arg
325 330 335

Gln Phe Met Asp Asp Trp Pro Lys Ser Gln Ser Asp Arg Ser Ala Val
340 345 350

Ser Trp Pro Glu Leu Asp Gln Gln Ser Glu Arg Thr Gln Leu Ser Ile
355 360 365

Ser Ile Pro Met Ala Pro Ala Asp Phe Met Ser Ser Thr Ser Ser Pro
370 375 380

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

Asp Pro Ile Gln Met Gly Leu Gly Val Gly Gly Gly Gly Gly Gly Ile
405 410 415

Ala Asn Glu Pro Asn Gln Arg Gln Ala Asn Trp Ile Pro Ile Ser Trp
420 425 430

Gly Thr Ser Met Gly Gly Pro Leu Gly Glu Val Leu His Asn Thr Asn

435

440

445

Asn Asn Ala Ala Ala Glu Cys Lys Thr Thr Ser Ser Leu Asn Leu Met
450 455 460

Thr Tyr Arg Trp Asp Asn Ser Pro Arg Ile Gly Ser Ser Pro Thr Gly
465 470 475 480

Val Leu Gln Lys Ser Ala Phe Ala Ser Leu Ser Asn Ser Ser Ala Gly
485 490 495

Ser Ser Pro Arg Ala Glu Asn Lys Thr Asn Glu Gly Gly Ser Leu Cys
500 505 510

Asn Asp Leu Leu Gly Ser Thr Ile Val His Ser Ser Ser Leu Pro Ala
515 520 525

Met

<210> 77
<211> 1017
<212> DNA
<213> Populus tremuloides

<400> 77
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tcagaggagt tttagtcca tttctcatag attcttccac catcccgcca tgggctattg 180
cactttctat gggaagaagg tggatccgga gccagggtcaa tgcaggagga ccgacggcaa 240
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cactgtgaca tcaactgactg taacaggaag cagcagtggg acaggagagct tccagaacct 420
tccactgctc acatatggta atccccaggg cactggttct ggacctaacc aatccatta 480
tcatatgaac tgcattcccc gtggaatccc aactaaagat tgcaggatc ttcaaggact 540
gaagactgag ggtggcgagc atagcttctt gtctgaacct tcaggatgca aaaggggtct 600
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<210> 78

<211> 310

<212> PRT

<213> Populus tremuloides

<400> 78

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

Pro Asp Leu Val Leu Pro Ile Gln Arg Ser Phe Glu Ser Ile Ser His
35 40 45

Arg Phe Phe His His Pro Ala Met Gly Tyr Cys Thr Phe Tyr Gly Lys
50 55 60

Lys Val Asp Pro Glu Pro Gly Gln Cys Arg Arg Thr Asp Gly Lys Lys
65 70 75 80

Trp Arg Cys Ser Lys Asp Ala Tyr Pro Gly Ser Lys Tyr Cys Glu Arg
85 90 95

His Met His Arg Gly Arg Asn Arg Ser Arg Lys Ala Val Glu Ser Gln
100 105 110

Thr Met Thr Gln Ser Ser Ser Thr Val Thr Ser Leu Thr Val Thr Gly
115 120 125

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

Gly Asn Pro Gln Gly Thr Gly Ser Gly Pro Asn Gln Ser His Tyr His
145 150 155 160

Met Asn Cys Ile Pro Arg Gly Ile Pro Thr Lys Asp Cys Arg Tyr Leu
165 170 175

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

Ser Gly Cys Lys Arg Gly Leu Gln Lys Asp Ser Gln Leu Asp Asn Ala
195 200 205

Trp Ser Leu Met Leu Ser Arg Gly Ser Ser Phe Pro Thr Glu Lys Ser
210 215 220

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

Ser Ser Asp Phe Thr Thr Gly Glu Pro Val Lys His Glu Gly Gln Ser
245 250 255

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Arg Pro Phe Phe Asp Glu Trp Pro Glu Asp Gln Asp Ile Trp Ser
260 265 270

Gly Leu Lys Asp Asn Arg Ser Asn Ser Thr Ser Phe Ser Thr Thr Lys
275 280 285

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

Arg Ser Pro Gln Glu Asn
305 310

<210> 79
<211> 1221
<212> DNA
<213> Populus tremuloides

<400> 79
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taacctgtca gcatttcctg attcaaacac agctgcaaac accagacttc ctaagatcat 180
ggggaattac tttagcctgg aacagtggca agagctagag ctgcaggctt tgatctacag 240
attcatgtta gccggtgcag ctattcctcc ggagctcctc caaccaatca agaaaacctt 300
tcttcattct caccctcctc catatttcct ccatcatcct cttcaattac attgctctta 360
ttatcagcca tcttgggtatt ggggaagagc agccatggat ccggagccag gtcggtgccg 420
gagaacagat gggaagaaat ggcggtgctc cagagacgtg gtggcagggc acaagtattg 480
cgagcgccac ttgcaccgtg gccgcaaccg ttcaagaaag cctgtggaaa atcccacacc 540
tacaatatcc actaacatca cttgcattgg tattggaggt gcgggtggta ccgcatcagc 600
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aagctcaatg aactctttta cctgcctctc cgtttcaatg cctggaaact caccagcatc 900
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cccagccccg atccctagag gcaatacaag caattgggct gctgcaggat ggggcacaaa 1020
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cactacaaa ctcatctccc acgaatgttc tgcaccagtt atgtcgcccc actgtttctg 1140
aaacttgatc tatttttaggt tagtttgtgg tgtagtaaca catgcatgca tacacacaca 1200
cacacacaca cacacacatc a 1221

<210> 80
<211> 377
<212> PRT

<213> Populus tremuloides

<400> 80

Met Asp Phe His Leu Lys Gln Trp Arg Asn Gln His Glu Glu Ser Gly
 1 5 10 15

Gln Gln Pro Ser Ala Lys Met Pro Lys Leu Leu Met Asp Pro His Gln
 20 25 30

Pro Gln Gln His Pro His Ser Ser Gly Ser Ala Ala Phe Pro Leu Phe
 35 40 45

Leu Pro Glu Pro Ser Cys Lys Asn Ser Asn Leu Ser Ala Phe Pro Asp
 50 55 60

Ser Asn Thr Ala Ala Asn Thr Arg Leu Pro Lys Ile Met Gly Asn Tyr
 65 70 75 80

Phe Ser Leu Glu Gln Trp Gln Glu Leu Glu Leu Gln Ala Leu Ile Tyr
 85 90 95

Arg Phe Met Leu Ala Gly Ala Ala Ile Pro Pro Glu Leu Leu Gln Pro
 100 105 110

Ile Lys Lys Thr Leu Leu His Ser His Pro Pro Pro Tyr Phe Leu His
 115 120 125

His Pro Leu Gln Leu His Cys Ser Tyr Tyr Gln Pro Ser Trp Tyr Trp
 130 135 140

Gly Arg Ala Ala Met Asp Pro Glu Pro Gly Arg Cys Arg Arg Thr Asp
 145 150 155 160

Gly Lys Lys Trp Arg Cys Ser Arg Asp Val Val Ala Gly His Lys Tyr
 165 170 175

Cys Glu Arg His Leu His Arg Gly Arg Asn Arg Ser Arg Lys Pro Val
 180 185 190

Glu Asn Pro Thr Pro Thr Ile Ser Thr Asn Ile Thr Cys Ile Gly Ile
 195 200 205

Gly Glu Leu Asp Gln Thr Thr Phe Ser Leu Phe Cys Phe Cys Phe Asn
 210 215 220

Leu Leu Ala His Pro Tyr Cys Ser Ser Lys Thr Glu Ser Lys Gly Leu
 225 230 235 240

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

Ile Leu Trp His Phe Phe Asp Asp Trp Pro Arg Ser Val Asp Glu Ser
 Seite 98

260

265

270

Asp Asn Met Asn Ala Gly Ser Ser Met Asn Ser Leu Thr Cys Leu Ser
 275 280 285

Val Ser Met Pro Gly Asn Ser Pro Ala Ser Asp Val Ser Leu Lys Leu
 290 295 300

Ser Thr Gly Asn Asn Ile Ala Glu Glu Glu Pro Glu Pro Val Pro Ala
 305 310 315 320

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

Thr Lys Ile Thr Asn Gln Val Val Thr Ser Met Gly Gly Pro Leu Ala
 340 345 350

Glu Ala Leu Arg Ser Ser Thr Thr Lys Leu Ile Ser His Glu Cys Ser
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Ala Pro Val Met Ser Pro His Cys Phe
 370 375

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 <211> 1280
 <212> DNA
 <213> Populus tremuloides

<400> 81
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 cctgtggaat tacacactca tgactccccg aggacattga ccaacaataa cactaacacc 420
 aacaatagca attactccac taatccacac ctgtttaatc aaaaacctta ctttccaagc 480
 catttattta tgtttcctag tgccatggcc ctttctgcca gctcatatga tcaaccagg 540
 agcttggaat ggctcttgaa aggcgagatt ttaccggtg ccagtaatta cagccaagaa 600
 tggcagcatt tgaagagaga cagcatcaag ggtaatggca aagtgtacaa cgtttatgga 660
 gaagagcagc cgctttgctc aaatacatat agaggtggcc attcattaca agctcagagg 720
 ctaaagtatc attgcagcgt gttatcaagt cccaaatcaa ctactttgga aagggtttta 780
 agtcctagcc tgaccaaga acaagagaca aggcaattca ttgatgcttg gtcaactaat 840
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<210> 82
 <211> 513
 <212> PRT
 <213> Populus tremuloides

<400> 82

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Ile Gly Leu Gly Leu Arg Met Gln Asp Asn Leu Glu Ser Cys Ser Gly
 20 25 30

Ser Ser Lys Arg Ser Val Thr Ala Met Ser Cys Asp His Glu Pro Ala
 35 40 45

Ala His Glu Leu Ser Ser Ser Cys Ser Gly Gly Gly Gly Gly Ser
 50 55 60

Gly Pro Leu Phe Tyr Ser Thr Ser Asn His Val Thr Cys Leu Gly Asp
 65 70 75 80

Ile Lys Asp Val Val Ala Ser Val Ser Ala Ser Gly Thr Gly Thr Pro
 85 90 95

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

Asp Ser Ser Pro Phe Thr Phe Asn Ser Ser Gly Glu Met Thr Pro Ser
 115 120 125

Val Asn Glu Arg Val Leu Phe Thr Ala Ala Gln Trp Gln Glu Leu Glu
 130 135 140

Arg Gln Thr Thr Ile Tyr Lys Tyr Met Met Ala Ser Val Pro Val Pro
 145 150 155 160

Pro Glu Leu Leu Ile Pro Ile Thr Lys Asn Gln Ser Asn Val Leu Pro
 165 170 175

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

Ser Asp Ala Glu Pro Trp Arg Cys Lys Arg Thr Asp Gly Lys Lys Trp

195

200

205

Arg Cys Ser Arg Asp Val Ala Pro Asp Gln Lys Tyr Cys Glu Arg His
 210 215 220

Ser His Lys Ser Arg Pro Arg Ser Arg Lys Pro Val Glu Leu His Thr
 225 230 235 240

His Asp Ser Pro Arg Thr Leu Thr Asn Asn Thr Asn Thr Asn Asn
 245 250 255

Ser Asn Tyr Ser Thr Asn Pro His Leu Phe Asn Gln Lys Pro Tyr Phe
 260 265 270

Pro Ser His Leu Phe Met Phe Pro Ser Ala Met Ala Pro Ser Ala Ser
 275 280 285

Ser Tyr Asp Gln Pro Arg Ser Leu Glu Trp Leu Leu Lys Gly Glu Ile
 290 295 300

Leu Pro Val Ala Ser Asn Tyr Ser Gln Glu Trp Gln His Leu Lys Arg
 305 310 315 320

Asp Ser Ile Lys Gly Asn Gly Lys Val Tyr Asn Val Tyr Gly Glu Glu
 325 330 335

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

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

Thr Leu Glu Arg Ala Leu Ser Pro Ser Leu Thr Gln Glu Gln Glu Thr
 370 375 380

Arg His Phe Ile Asp Ala Trp Ser Thr Asn Ser Gly Arg Asp Asp Ile
 385 390 395 400

Gly Gly Ile Gly Lys Lys Ser Tyr Val Ser Ser Ser Glu Lys Leu Val
 405 410 415

Leu Pro His Ser Ala Leu Thr Leu Ser Met Ser Pro Gly Thr Gly Ser
 420 425 430

Glu Thr Asn Asn Glu Gly Asn Gly Ser Ala Gln Leu Ser Ser Phe Gly
 435 440 445

Ile Met Gly Leu Ser Asp Arg Asp His Gln Ser Ala Ser Gly Leu Arg
 450 455 460

Pro Gln Trp Met Met Ser His Gly Gly Ser Trp Ile Val Ser Pro Pro
 465 470 475 480

Gly Gly Pro Leu Ala Glu Ala Leu Cys Leu Gly Ile Ser Ser Asn Ala
 485 490 495

Lys Thr Ala Ser Asn Leu Pro Ser Pro Cys Ser Ser Ser Cys Gly Pro
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Asn

<210> 83
 <211> 1623
 <212> DNA
 <213> Saccharum officinarum

<400> 83
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 cgccatcacc gcgccatcgc ccaggggcag cggcgacctg ggtcttctca agcgagcagc 180
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 aagcgagcag gctttcctgc tgtccaggac caagaggcca tttactccct cgcagtggat 360
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 cagcctgctc atttcaatca gcaagagctt cagatcatcc aatagagtga gctggaggcc 480
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 gaagaaggca aaagttaatg actccaagcc aggcactgtc agctggttga cagatagttt 780
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 caaaccagat aagttaggtc ccacactgga aaatgagtca aactcagaca caatactgaa 960
 agcctggggg ggcaaccagc ctagccacaa gagcatttcc tccacacagc accatgatgc 1020
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 accatgattc ctcaatccat ggagagcttg acatagatgt ctaccatgg aagcaaacaa 1380
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PF59082PF60142_PCT_SEQ_LIST.txt

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acc 1623

<210> 84
<211> 426
<212> PRT
<213> Saccharum officinarum

<400> 84

Met Ser Ala Glu Phe Cys Ala Ala Ala Gly Met Glu Leu Gly Val Gly
1 5 10 15

Asp Val Met Gly Leu Gln Gln Gly Ile Ala Ile Thr Ala Pro Ser Pro
20 25 30

Arg Gly Ser Gly Asp Leu Gly Leu Leu Lys Arg Ala Ala Leu Thr Gln
35 40 45

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

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

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

Arg Pro Phe Thr Pro Ser Gln Trp Met Glu Leu Glu His Gln Ala Leu
100 105 110

Ile Tyr Lys Tyr Leu Asn Ala Lys Ala Pro Ile Pro Ser Ser Leu Leu
115 120 125

Ile Ser Ile Ser Lys Ser Phe Arg Ser Ser Asn Arg Val Ser Trp Arg
130 135 140

Pro Leu Tyr Gln Gly Tyr Thr Asn Ala Asp Ser Asp Pro Glu Pro Gly
145 150 155 160

Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys Ser Lys Glu Ala
165 170 175

Met Ala Asp His Lys Tyr Cys Glu Arg His Ile Asn Arg Asn Arg His
180 185 190

Arg Ser Arg Lys Pro Val Glu Asn Gln Pro Lys Lys Thr Thr Lys Glu
195 200 205

Val Pro Ala Ala Ala Ser Ser Leu Pro Cys Ala Gly Pro Gln Gly Cys
210 215 220

PF59082PF60142_PCT_SEQ_LIST.txt

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

Trp Thr Asp Ser Leu Asn Arg Thr Met Leu Ser Arg Glu Lys Ala Asn
 245 250 255

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

Pro Thr Leu Ser Leu Leu Ser Gln Leu Lys Gln Gln Asn Lys Pro Asp
 275 280 285

Lys Leu Gly Pro Thr Leu Glu Asn Glu Ser Asn Ser Asp Thr Ile Leu
 290 295 300

Lys Ala Trp Gly Gly Asn Gln Pro Ser His Lys Ser Ile Ser Ser Thr
 305 310 315 320

Gln His His Asp Ala Glu Ser Leu Gln Ser Val Leu Gln Asn Phe Ser
 325 330 335

Leu Ala Gln Asn Glu Lys Met Glu Ser Glu Lys Asn Lys Tyr Ser Asp
 340 345 350

Ser Met Leu Val Ser Ser Thr Phe Tyr Ser Ala Asp Gly Pro Arg Ser
 355 360 365

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

Ser Ser Trp Glu Met Pro Gln Gly Gly Pro Leu Gly Glu Ile Leu Thr
 385 390 395 400

Asn Ser Lys Asn Ser Glu Asp Leu Ser Lys Cys Glu Ser Arg Ser Tyr
 405 410 415

Gly Trp Leu Leu Asn Leu Asp His Ala Pro
 420 425

<210> 85
 <211> 1515
 <212> DNA
 <213> Vitis vinifera

<400> 85
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 Seite 104

PF59082PF60142_PCT_SEQ_LIST.txt

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 <211> 356
 <212> PRT
 <213> Vitis vinifera

<400> 86

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 20 25 30

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

Ser Ser Leu Ser Ser Arg Leu Phe Pro His Gln Pro Ile Gly Trp Gly
 50 55 60

Cys Phe Gln Met Gly Phe Gly Arg Lys Ala Asp Pro Glu Pro Gly Arg
 65 70 75 80

PF59082PF60142_PCT_SEQ_LIST.txt

Cys Arg Arg Thr Asp₈₅ Gly Lys Lys Trp Arg₉₀ Cys Ser Lys Glu Ala₉₅ Tyr
 Pro Asp Ser Lys₁₀₀ Tyr Cys Glu Arg His₁₀₅ Met His Arg Gly Lys₁₁₀ Asn Arg
 Ser Arg Lys₁₁₅ Pro Val Glu Val Ile₁₂₀ Ser Ala Thr Asn Pro₁₂₅ Ser Pro Thr
 Ile Ser₁₃₀ Ser Ile Asn Ser Asn₁₃₅ Pro Ser Ser Thr Thr₁₄₀ Thr Asn Ser Tyr
 Ser₁₄₅ Leu Ser Pro Leu Ser₁₅₀ Pro Leu Ser Ser Ser₁₅₅ Met Thr Ser Glu Thr₁₆₀
 Ser His Pro His His₁₆₅ His Ser Tyr His Asn₁₇₀ Thr Ser Leu Tyr Pro₁₇₅ Phe
 Leu Tyr Pro His₁₈₀ Pro Ser Ser Ser Arg₁₈₅ Pro Pro Gly Ser Cys₁₉₀ Leu Ser
 Pro Gln Ala₁₉₅ Thr Ser Ser Tyr Ser₂₀₀ Thr His His Leu Phe₂₀₅ Leu Asp Ser
 Gly Ser₂₁₀ Tyr Ser Gln Ala Asp₂₁₅ Arg Asp Tyr Arg Gly₂₂₀ Val Asp Glu Arg
 Ala₂₂₅ Phe Phe Pro Glu Ala₂₃₀ Ser Gly Thr Val Arg₂₃₅ Gly Leu His Asp Ser₂₄₀
 Tyr Thr Pro Leu Thr₂₄₅ Met Ser Ser Ser Lys₂₅₀ Gly Tyr Ser His Phe₂₅₅ Gln
 Tyr Gln Ser Pro₂₆₀ Ala Asp Asn Pro Lys₂₆₅ Gln Gln Gln Glu Gln₂₇₀ Gln Glu
 Gln Gln His₂₇₅ Cys Phe Val Leu Gly₂₈₀ Thr Asp Phe Lys Ser₂₈₅ Ser Arg Pro
 Ile Lys₂₉₀ Val Glu Arg Asp Asp₂₉₅ Glu Ala Gln Lys Pro₃₀₀ Leu His His Phe
 Phe₃₀₅ Gly Glu Trp Pro Leu₃₁₀ Lys Asn Arg Asp Ser₃₁₅ Trp Leu Asp Leu Glu₃₂₀
 Glu Asp Pro Pro Thr₃₂₅ His Ala Ser Phe Ser₃₃₀ Thr Thr Gln Leu Ser₃₃₅ Ile
 Ser Ile Pro Met₃₄₀ Ser Ser His Lys Leu₃₄₅ Leu Ala Ser Asp Ser₃₅₀ Arg Ile

Gln Thr Gly Thr
355

<210> 87
<211> 945
<212> DNA
<213> Zea mays

<400> 87
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<210> 88
<211> 269
<212> PRT
<213> Zea mays

<400> 88

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20 25 30

Gly Glu Val Ala Gln Glu Ala Ala Val Gln Gly Thr Gly Gln Glu Gln
35 40 45

Glu Arg Asp Lys Ala Asp Arg Glu Val Gln Gly Gly Ala Gly Glu Lys
50 55 60

Asp Asp Gly Ala Cys Arg Asp Leu Val Leu Val Glu Asp Pro Glu Val
65 70 75 80

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Ala Val Glu Asp₈₅ Pro Glu Glu Ala₉₀ Ala Ala Thr Ala Ala Leu Gln₉₅
 Glu Glu Met Lys₁₀₀ Ala Leu Val Ala₁₀₅ Ile Pro Asp Gly₁₁₀ Ala Gly Ala
 Ala Phe Thr₁₁₅ Ala Met Gln Leu₁₂₀ Glu Leu Glu Gln₁₂₅ Gln Ser Arg Val
 Tyr Gln₁₃₀ Tyr Met Ala Ala Arg₁₃₅ Val Pro Val Pro Thr₁₄₀ His Leu Val Phe
 Pro Val Trp Lys Ser₁₅₀ Val Thr Gly Ala Ser₁₅₅ Ser Glu Gly Ala Gln Lys₁₆₀
 Tyr Pro Thr Leu₁₆₅ Met Gly Leu Ala Thr₁₇₀ Leu Cys Leu Asp Phe Gly₁₇₅ Lys
 Asn Pro Glu₁₈₀ Pro Glu Pro Gly Arg₁₈₅ Cys Arg Arg Thr Asp Gly₁₉₀ Lys Lys
 Trp Arg Cys₁₉₅ Trp Arg Asn Thr₂₀₀ Ile Pro Asn Glu Lys Tyr₂₀₅ Cys Glu Arg
 His Met₂₁₀ His Arg Gly Arg₂₁₅ Lys Arg Pro Val Gln₂₂₀ Val Phe Leu Glu Asp
 Asp Glu Pro Asp Ser₂₃₀ Ala Ser Gly Ser Lys₂₃₅ Pro Ala Ala Pro Gly Lys₂₄₀
 Ala Thr Glu Gly₂₄₅ Ala Lys Lys Ala Asp₂₅₀ Asp Lys Ser Pro Ser₂₅₅ Ser Lys
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<210> 89
 <211> 1372
 <212> DNA
 <213> Zea mays

<400> 89
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PF59082PF60142_PCT_SEQ_LIST.txt

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<210> 90
 <211> 318
 <212> PRT
 <213> Zea mays

<400> 90

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          20          25          30

Ser Gly Ala Pro Val Pro His Asp Leu Val Leu Pro Leu Arg Leu Ala
          35          40          45

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

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

Arg Lys Ala Glu Asp Pro Glu Pro Gly Arg Cys Arg Arg Thr Asp Gly
          85          90          95

Lys Lys Trp Arg Cys Ser Arg Glu Ala His Gly Asp Ser Lys Tyr Cys
          100          105          110

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PF59082PF60142_PCT_SEQ_LIST.txt

Glu Lys His Ile His Arg Gly Lys Ser Arg Ser Arg Lys Pro Val Glu
115 120 125

Val Thr Ser Pro Ala Ala Tyr Arg Pro Ser Ala Phe Ser Ile Ser Pro
130 135 140

Pro Arg Ala Ala Asp Ala Pro Pro Pro Pro Pro Gly Leu Gly His Pro
145 150 155 160

Gln Gln Gln His Leu Arg His Gly Ala Leu Ser Pro Ala Gly Arg Ala
165 170 175

His Ala Ala Gly Ala Leu Gln Leu His Leu Asp Ser Ser Leu His Ala
180 185 190

Ala Ser Pro Pro Pro Ser Tyr His Arg Tyr Ala His Ser His Ala His
195 200 205

Tyr Thr Pro Pro Pro Pro Pro Ser Leu Tyr Asp Tyr Gly Gln Ser Lys
210 215 220

Glu Leu Arg Glu Ala Ala Glu Leu Arg Arg Arg His Phe His Ala Leu
225 230 235 240

Gly Ala Asp Leu Ser Leu Asp Lys Pro Leu Ala Asp Ala Gly Ala Ala
245 250 255

Glu Lys Pro Leu Arg Arg Phe Phe Asp Glu Trp Pro Arg Glu Arg Gly
260 265 270

Asp Thr Arg Pro Ser Trp Ala Gly Ala Glu Asp Ala Thr Gln Leu Ser
275 280 285

Ile Ser Ile Pro Ala Ala Ser Pro Ser Ser Asp His Ala Ala Ser Ala
290 295 300

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305 310 315

<210> 91
<211> 1099
<212> DNA
<213> Zea mays

<400> 91
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caccagccgc tgccactgcc gcagcgcggg gcggcggccg cggctctcac cgccgcgcag 180
tgggcgggagc tggagcagca ggcgctcatc tacaagtacc tcatggccgg cgtccccgtc 240
ccgcccgatc tcttcgccc cgccccccac gccgcccgtt tctccttcgc cagccccgcc 300
gcgtcgccct tctaccatca ccaccaccac caccggtccc tgagttacta cgcctactac 360

PF59082PF60142_PCT_SEQ_LIST.txt

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tgctccaagg aggcgcaccc cgactccaag tactgcgagc gccacatgca ccgtggccgc 480
aaccgttcaa gaaagcctgt ggaatccaag accgcctcct cgccgccccca gctgtccacc 540
gtcgtcacca ccaccaccac ccgggaggcc gccgccgca cggccctcga gtccctcgcg 600
ggggcggggg gtaaggctca cggcctgtcc ctggcgggcg gggctggctc gtcgcacctc 660
agcgtcgacg cttcgaacac tcactttcgc tatggcagca agtaccctct tggagctaaa 720
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cagcggggcc ggcgctggtg ggttgctggg gagcgtgaag caggagaacc agccgctgag 960
gcccttcttc gacgagtggc ctgggacgcg ggactcgtgg tcggagatgg acgacgcgag 1020
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tgattgagaa cgaagctcg 1099

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<210> 92
 <211> 321
 <212> PRT
 <213> Zea mays

<400> 92

Met Leu Ser Ser Ala Ser Ser Ala Gly Ala Ala Met Gly Met Gly Gly
 1 5 10 15

Gly Tyr Gln His Gln Pro Leu Pro Leu Pro Gln Arg Gly Ala Ala Ala
 20 25 30

Ala Val Phe Thr Ala Ala Gln Trp Ala Glu Leu Glu Gln Gln Ala Leu
 35 40 45

Ile Tyr Lys Tyr Leu Met Ala Gly Val Pro Val Pro Pro Asp Leu Leu
 50 55 60

Arg Pro Ala Pro His Ala Ala Ala Phe Ser Phe Ala Ser Pro Ala Ala
 65 70 75 80

Ser Pro Phe Tyr His His His His His His Pro Ser Leu Ser Tyr Tyr
 85 90 95

Ala Tyr Tyr Gly Lys Lys Leu Asp Pro Glu Pro Trp Arg Cys Arg Arg
 100 105 110

Thr Asp Gly Lys Lys Trp Arg Cys Ser Lys Glu Ala His Pro Asp Ser
 115 120 125

Lys Tyr Cys Glu Arg His Met His Arg Gly Arg Asn Arg Ser Arg Lys
 130 135 140

PF59082PF60142_PCT_SEQ_LIST.txt

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

Val Thr Thr Thr Thr Thr Arg Glu Ala Ala Ala Ala Thr Pro Leu Glu
165 170 175

Ser Leu Ala Gly Ala Gly Gly Lys Ala His Gly Leu Ser Leu Gly Gly
180 185 190

Gly Ala Gly Ser Ser His Leu Ser Val Asp Ala Ser Asn Thr His Phe
195 200 205

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

Leu Ser Phe Phe Ser Gly Ala Pro Gly Asn Ser Arg Gly Phe Thr Ile
225 230 235 240

Asp Ser Pro Ala Asp Asn Ser Trp His Ser Leu Pro Ser Asn Val Pro
245 250 255

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

Pro Pro Val Val Val Gln Gln Gln Arg Gly Arg Arg Trp Trp Val Ala
275 280 285

Gly Glu Arg Glu Ala Gly Glu Pro Ala Ala Glu Ala Leu Leu Arg Arg
290 295 300

Val Ala Trp Asp Ala Gly Leu Val Val Gly Asp Gly Arg Arg Glu Val
305 310 315 320

Gln

<210> 93
<211> 1328
<212> DNA
<213> Zea mays

<400> 93
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ccgccaccgg gccatcgtcc ggagacagcg acctgggtct tctcaagcga gcaggcctcg 180
cccaggcagc cacctcctac ccctcccctt tcctcgacca acagaagatg ctcaggttct 240
ccaaggcggc ggcggtcac acgtcgccct caggcctaga tttcggagga ggcccaagcg 300
agcaggcttt cctgctgtcc aggaccaagc ggccgttcac cccgtcgcag tggatggagc 360
tggagcacca ggctctcata tacaagtatc tcaatgccaa ggcccccata ccttcagcc 420

PF59082PF60142_PCT_SEQ_LIST.txt

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accaaggcta cgcaaacgca gactccgacc cagaacctgg gaggtgccgg cggacagacg 540
gaaagaagtg gcggtgctct aaggaggcga tgcctgatca caagtactgc gagcgccaca 600
tcaataggaa ccgccaccgt tcaagaaagc ctgtggaaaa ccaacctaga aagaccagca 660
aggaggtgcc taccgctgct gctggctcgt tgccgtgtgc cgggccacaa ggtagcttga 720
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acaaaccaga taagttaggt cccacaccgg aaaatgagcc gaactcggac acaatgttga 960
aagcctgggg tggcagccac cacaagaaca tttcctccac acagcgccat gacgctgaat 1020
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gattcctc 1328

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<210> 94
 <211> 430
 <212> PRT
 <213> Zea mays

<400> 94

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

Leu Gly Val Gly Asp Val Met Gly Leu Gln Gln Gly Ile Ala Ala Ala
 20 25 30

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

Gly Leu Ala Gln Ala Ala Thr Ser Tyr Pro Ser Pro Phe Leu Asp Gln
 50 55 60

Gln Lys Met Leu Arg Phe Ser Lys Ala Ala Ala Ala His Thr Ser Pro
 65 70 75 80

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

Ser Arg Thr Lys Arg Pro Phe Thr Pro Ser Gln Trp Met Glu Leu Glu
 100 105 110

PF59082PF60142_PCT_SEQ_LIST.txt

His Gln Ala Leu Ile Tyr Lys Tyr Leu Asn Ala Lys Ala Pro Ile Pro
115 120 125

Ser Ser Leu Leu Val Ser Ile Ser Lys Ser Phe Arg Ser Ser Asn Arg
130 135 140

Val Ser Trp Arg Pro Leu Tyr Gln Gly Tyr Ala Asn Ala Asp Ser Asp
145 150 155 160

Pro Glu Pro Gly Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys
165 170 175

Ser Lys Glu Ala Met Pro Asp His Lys Tyr Cys Glu Arg His Ile Asn
180 185 190

Arg Asn Arg His Arg Ser Arg Lys Pro Val Glu Asn Gln Pro Arg Lys
195 200 205

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

Gly Pro Gln Gly Ser Leu Lys Lys Ala Lys Val Asn Asp Ser Lys Pro
225 230 235 240

Gly Thr Gly Ser Tyr Trp Thr Asp Ser Leu Asn Arg Thr Met Leu Ser
245 250 255

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

Ser Thr Lys Asn Ser Gln Pro Thr Leu Ser Leu Leu Thr Gln Leu Lys
275 280 285

Gln Gln Asn Lys Pro Asp Lys Leu Gly Pro Thr Pro Glu Asn Glu Pro
290 295 300

Asn Ser Asp Thr Met Leu Lys Ala Trp Gly Gly Ser His His Lys Asn
305 310 315 320

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

Gln Asn Phe Ser Leu Ala Gln Asn Asp Arg Leu Glu Ser Glu Lys Asn
340 345 350

Arg Tyr Ser Asp Ser Val Leu Val Ser Ser Ala Phe Tyr Ser Ala Asp
355 360 365

Gly Pro Gln Thr Thr Cys Leu Thr Pro Asn Met Thr Gln Val Gln Gln
370 375 380

Asp Cys Ile Ser Ser Ser Trp Glu Met Pro Gln Gly Gly Pro Leu Gly

385 390 395 400

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

Ser Arg Ser Tyr Gly Trp Leu Leu Asn Leu Asp His Ala Pro
420 425 430

<210> 95
<211> 1440
<212> DNA
<213> Zea mays

<400> 95
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ttccccgcgc ctccgcccgt acgtcccgtt cccggtcggc cggccgggtcc aaagggaggg 120
gaggaggagg ggcgcgggag tcggggcccg caccgatgct gagctcggca tcctcggccg 180
cgggggcggc catggggatg ggcggcggcg ggtacgcgca ccagcccccg ccacagcgcg 240
cggtcttcac cgccgcgcag tgggcgggagc tggagcagca ggcgctcatc tacaagtacc 300
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ccgccttctc cttcgccggc cccgccgccc cgtcgccctt ctaccaccaa caccaccgt 420
ccctgagcta ctacgcctac tacggcaaga agctggaccc ggagccgtgg cggtgccgcc 480
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agcgccacat gcaccgtggc cgcaaccgtt caagaaagcc tgtggaatcc aagaccgcct 600
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ctctcgagcc cttgcagcg gcggggggca aggtccacgg cctgtccctc ggcgggcgcg 720
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cgccgcgggc cggcaggacc tccttctcct cctccaccac ccagctctcc atctccatcc 1260
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aatcatgctt gaccgaaact tgttttctgc aggcgactga cgaggaaccg tcgatcgggc 1380
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<210> 96
<211> 382
<212> PRT

<213> Zea mays

<400> 96

Met Leu Ser Ser Ala Ser Ser Ala Ala Gly Ala Ala Met Gly Met Gly
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Gly Gly Gly Tyr Ala His Gln Pro Pro Pro Gln Arg Ala Val Phe Thr
 20 25 30

Ala Ala Gln Trp Ala Glu Leu Glu Gln Gln Ala Leu Ile Tyr Lys Tyr
 35 40 45

Leu Met Ala Gly Val Pro Val Pro Pro Asp Leu Leu Leu Pro Val Arg
 50 55 60

Pro Gly Pro Ala Ala Ala Phe Ser Phe Ala Gly Pro Ala Ala Ala Ser
 65 70 75 80

Pro Phe Tyr His Gln His His Pro Ser Leu Ser Tyr Tyr Ala Tyr Tyr
 85 90 95

Gly Lys Lys Leu Asp Pro Glu Pro Trp Arg Cys Arg Arg Thr Asp Gly
 100 105 110

Lys Lys Trp Arg Cys Ser Lys Glu Ala His Pro Asp Ser Lys Tyr Cys
 115 120 125

Glu Arg His Met His Arg Gly Arg Asn Arg Ser Arg Lys Pro Val Glu
 130 135 140

Ser Lys Thr Ala Ser Ser Ser Ser Pro Ala His Pro Ser Pro Pro Gln
 145 150 155 160

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

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

Ser His Leu Gly Val Asp Ala Ser Asn Ala His Tyr Arg Tyr Gly Ser
 195 200 205

Asn Arg Tyr Pro Leu Gly Ala Lys Pro Asp Gly Gly Glu Leu Ser Phe
 210 215 220

Phe Ser Gly Ala Ser Ser Gly Asn Asn Ser Arg Gly Gly Phe Thr Ile
 225 230 235 240

Asp Ser Pro Ser Asp Asn Asn Ser Trp His Ser Ala Leu Ala Ser Ser
 245 250 255

Val Pro Pro Phe Thr Leu Ser Thr Lys Ser Gly Asp Ser Gly Leu Leu
 Seite 116

260

265

270

Pro Gly Ala Tyr Ala Ser Tyr Ser Gln Ser His Ser His Met Glu Pro
 275 280 285

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

Glu Arg Gln Gln Pro Phe Ser Gly Gly Met Leu Gly Asn Val Lys Gln
 305 310 315 320

Glu Asn Gln Asn Gln Pro Leu Arg Pro Phe Phe Asp Glu Trp Pro Gly
 325 330 335

Thr Arg Ala Asp Ser Trp Pro Pro Glu Met Asp Gly Ala Pro Arg Ala
 340 345 350

Gly Arg Thr Ser Phe Ser Ser Ser Thr Thr Gln Leu Ser Ile Ser Ile
 355 360 365

Pro Met Pro Arg Cys Glu Leu His Leu Arg Asn Gln Asn Ser
 370 375 380

<210> 97
 <211> 1388
 <212> DNA
 <213> Zea mays

<400> 97
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 actccctcgc taccgcgttc tacggccaac ccacactcgg gtacggaccg tacctgggga 360
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PF59082PF60142_PCT_SEQ_LIST.txt

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tcgacgagtg gcccaaggcg cgggactcct ggccgggcct ctccgacgag accgccagcc 1140
tcgcctcgtc cccccggcg acccagctgt cgatgtccat acccatggcg tcctccgact 1200
tctccgtggc cagctcccag tcgcccaacg atgactaatg gtgcgtggat cgtcgcgttc 1260
tggccctttg tctatctccc ctccagtcct ccaccaccg cgcagtagta gctgcggaag 1320
cagcccatgc tcctgtatat ttgtcgggtca ttttccgtgt cagatctgtg taccaaacca 1380
agcggcgg 1388
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<210> 98
 <211> 408
 <212> PRT
 <213> Zea mays

<400> 98

Met Ala Met Pro Tyr Ala Ser Leu Ser Pro Ala Gly Ala Ala Asp His
 1 5 10 15

Arg Ser Ser Thr Ala Thr Ala Ser Leu Val Pro Phe Cys Arg Ser Thr
 20 25 30

Pro Leu Ser Ala Gly Gly Gly Leu Gly Glu Glu Asp Ala Gln Ala Ser
 35 40 45

Ala Arg Trp Pro Ala Ala Arg Pro Val Val Pro Phe Thr Pro Ala Gln
 50 55 60

Tyr Gln Glu Leu Glu Gln Gln Ala Leu Ile Tyr Lys Tyr Leu Val Ala
 65 70 75 80

Gly Val Pro Val Pro Pro Asp Leu Val Val Pro Ile Arg Arg Gly Leu
 85 90 95

Asp Ser Leu Ala Thr Arg Phe Tyr Gly Gln Pro Thr Leu Gly Tyr Gly
 100 105 110

Pro Tyr Leu Gly Arg Lys Leu Asp Pro Glu Pro Gly Arg Cys Arg Arg
 115 120 125

Thr Asp Gly Lys Lys Trp Arg Cys Ser Lys Glu Ala Ala Pro Asp Ser
 130 135 140

Lys Tyr Cys Glu Arg His Met His Arg Gly Arg Asn Arg Ser Arg Lys
 145 150 155 160

Pro Val Glu Thr Gln Leu Ala Pro Gln Ser Gln Pro Pro Ala Ala Ala
 165 170 175

Ala Val Ser Ala Ala Pro Pro Leu Ala Ala Ala Ala Ala Ala Thr
 Seite 118

180

185

190

Asn Gly Ser Gly Phe Gln Asn His Ser Leu Tyr Pro Ala Ile Ala Gly
 195 200 205

Ser Thr Gly Gly Gly Gly Gly Val Gly Gly Ser Gly Asn Ile Ser Ser
 210 215 220

Pro Phe Ser Ser Ser Met Gly Gly Ser Ser Gln Leu His Met Asp Ser
 225 230 235 240

Val Ala Ser Tyr Ser Tyr Ala Ala Leu Gly Gly Gly Thr Ala Lys Asp
 245 250 255

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

Gln Leu Ile Ala Glu Ala Ile Asp Ser Ser Ile Glu Ser Gln Arg Arg
 275 280 285

Leu Pro Ser Ser Ser Phe Pro Leu Ser Ser Tyr Pro His Leu Gly Ala
 290 295 300

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

Met Glu Lys Gln Gln Pro Pro Ser Ser Phe Leu Gly Asn Asp Thr Gly
 325 330 335

Ala Gly Met Ala Met Gly Ser Ala Ser Ala Lys Gln Glu Gly Gln Thr
 340 345 350

Leu Arg His Phe Phe Asp Glu Trp Pro Lys Ala Arg Asp Ser Trp Pro
 355 360 365

Gly Leu Ser Asp Glu Thr Ala Ser Leu Ala Ser Ser Pro Pro Ala Thr
 370 375 380

Gln Leu Ser Met Ser Ile Pro Met Ala Ser Ser Asp Phe Ser Val Ala
 385 390 395 400

Ser Ser Gln Ser Pro Asn Asp Asp
 405

<210> 99
 <211> 1506
 <212> DNA
 <213> Zea mays

<400> 99
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cagccatcac ctccgccgct ctccaccatg aatcccatcc accagcacga catcgtaccc 120

PF59082PF60142_PCT_SEQ_LIST.txt

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tgttttagag ttgttatatg ttcacgtcat gttgcctttc attttcggtt tcattcagat 1440
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gtgggt 1506

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<210> 100
 <211> 369
 <212> PRT
 <213> Zea mays
 <400> 100

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

Pro Pro Pro Pro Ser Cys Pro Phe His Gly Ser Ala Thr Ala Thr Arg
 20 25 30

Ser Gly Gly Ala Gln Met Leu Ser Phe Ser Ser Asn Gly Val Ala Gly
 35 40 45

Leu Gly Leu Cys Ser Gly Ala Ser Lys Met Gln Gly Val Leu Ser Arg
 Seite 120

50

Val Arg Arg Pro Phe Thr Pro Thr Gln Trp Met Glu Leu Glu His Gln
65 70 75 80

Ala Leu Ile Tyr Lys His Phe Ala Val Asn Ala Pro Val Pro Ser Ser
85 90 95

Leu Leu Leu Pro Ile Lys Arg Ser Leu Asn Pro Trp Ser Ser Leu Gly
100 105 110

Ser Ser Ser Leu Gly Trp Ala Pro Phe Arg Ser Gly Ser Ala Asp Ala
115 120 125

Glu Pro Gly Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp Arg Cys Ser
130 135 140

Arg Asp Ala Val Gly Asp Gln Lys Tyr Cys Glu Arg Tyr Ile Lys Arg
145 150 155 160

Gly Cys His Arg Ser Arg Lys His Val Glu Gly Arg Lys Ala Thr Pro
165 170 175

Thr Thr Ala Asp Pro Thr Met Ala Val Ser Gly Gly Ser Leu Leu His
180 185 190

Ser His Ala Val Ala Trp Gln Gln Gln Gly Lys Ser Ser Ala Ala Asn
195 200 205

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

Gln Asn Leu Gly Asp Gln Phe Ser Val Ser Thr Ser Met Asp Ser Phe
225 230 235 240

Asp Phe Ser Ser Ser His Ser Ser Pro Asn Gln Ala Lys Val Ala Phe
245 250 255

Ser Pro Val Ala Met Gln His Glu His Asp Gln Leu Tyr Leu Val His
260 265 270

Gly Ala Gly Ser Ser Ala Glu Asn Val Asn Lys Ser Gln Asp Gly Gln
275 280 285

Leu Leu Val Ser Arg Glu Thr Ile Asp Asp Gly Pro Leu Gly Glu Val
290 295 300

Phe Lys Gly Lys Ser Cys Gln Ser Ala Ser Ala Asp Ile Leu Thr Asp
305 310 315 320

His Trp Thr Ser Thr Arg Asp Leu Arg Pro Pro Thr Gly Val Leu Gln
325 330 335

PF59082PF60142_PCT_SEQ_LIST.txt

Met Ser Ser Ser Asn Thr Val Pro Ala Glu Asn His Thr Ser Asn Ser
340 345 350

Ser Tyr Leu Met Ala Arg Met Ala Asn Ser Gln Thr Val Pro Thr Leu
355 360 365

His

<210> 101
<211> 1350
<212> DNA
<213> Zea mays

<400> 101
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cacgacgcca cgccgtctcc gtaccacgcg ctgtatggag gcggcggcgg cggcggcggt 660
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gcgcagcatg tgagcccctt ccacctccac ctcgagacca cccaccgca cccgccgccg 780
ccctacaact actccgccga ccagagggac tacgcgtacg ggcacgcggc cgccaaggag 840
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gcggggcagt ggcagttcag gcagctcggg gtggagacga agccggggcc cagccgctg 960
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aaggccgggt cgtggatggg gctcgacggc gagacgcagc tctccatgtc catccccatg 1260
gccgctaccg acctccccgt cacctccgcg ttccgtaacg acgagtgatg ccacatcaaa 1320
cctggcgctg gaaactcgga acgtatggtg 1350

<210> 102
<211> 400

<212> PRT
 <213> Zea mays

<400> 102

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20      25      30

Leu Ile Tyr Lys Cys Leu Ala Ser Gly Lys Pro Ile Pro Ser Tyr Leu
35      40      45

Met Pro Pro Leu Arg Arg Ile Leu Asp Ser Ala Leu Ala Thr Ser Pro
50      55      60

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

Met Gly Phe Thr Arg Lys Ala Asp Glu Asp Pro Glu Pro Gly Arg Cys
85      90      95

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

Asp Ser Lys Tyr Cys Glu Lys His Met His Arg Gly Lys Asn Arg Ser
115     120     125

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

Pro Ala Ala Ala Thr Thr Ala Thr Ala Thr Ser Ser Pro Ala Pro Ser
145     150     155     160

Tyr His Arg Pro Ala His Asp Ala Thr Pro Ser Pro Tyr His Ala Leu
165     170     175

Tyr Gly Gly Gly Gly Gly Gly Gly Gly Ser Pro Tyr Ser Ala Ser Ala
180     185     190

Arg Pro Gly Ala Thr Gly Gly Gly Gly Ala Tyr His His Ala Gln His
195     200     205

Val Ser Pro Phe His Leu His Leu Glu Thr Thr His Pro His Pro Pro
210     215     220

Pro Pro Tyr Asn Tyr Ser Ala Asp Gln Arg Asp Tyr Ala Tyr Gly His
225     230     235     240

Ala Ala Ala Lys Glu Val Gly Glu His Ala Phe Phe Ser Asp Gly Ala
245     250     255

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PF59082PF60142_PCT_SEQ_LIST.txt

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

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

Lys Asp Asp Asp Glu Gln Glu Glu Arg Arg Arg Gln His Cys Phe Val
305 310 315 320

Leu Gly Ala Asp Leu Arg Leu Glu Arg Pro Ser Ser Gly His Gly His
325 330 335

Gly His Gly His Asp His Asp Asp Ala Ala Ala Ala Gln Lys Pro Leu
340 345 350

Arg Pro Phe Phe Asp Glu Trp Pro His Gln Lys Gly Asp Lys Ala Gly
355 360 365

Ser Trp Met Gly Leu Asp Gly Glu Thr Gln Leu Ser Met Ser Ile Pro
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<210> 103
<211> 1028
<212> DNA
<213> Zea mays

<400> 103
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PF59082PF60142_PCT_SEQ_LIST.txt

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<210> 104
 <211> 273
 <212> PRT
 <213> Zea mays

<400> 104

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

Pro Met Ala Gln Gly Glu Ala Val Gln Glu Ala Gly Ala Gln Ala Thr
 35 40 45

Gly Gln Glu Pro Glu Gly Glu Lys Ala Asn Arg Asp Gly Glu Gly Ser
 50 55 60

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

Asp Pro Glu Val Leu Ala Val Glu Asp Pro Glu Glu Ala Ala Ala Thr
 85 90 95

Ala Ala Leu Gln Glu Glu Met Lys Ala Leu Val Ala Ser Val Pro Asp
 100 105 110

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

Gln Ser Arg Val Tyr Gln Tyr Met Ala Ala Arg Val Pro Val Pro Thr
 130 135 140

His Leu Val Phe Pro Val Trp Lys Ser Val Thr Gly Ala Ser Ser Glu
 145 150 155 160

Gly Ala Gln Lys Tyr Pro Thr Leu Leu Gly Leu Ala Thr Leu Cys Leu
 165 170 175

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

Asp Gly Lys Lys Trp Arg Cys Trp Arg Asn Thr Ile Pro Asn Glu Lys
 195 200 205

PF59082PF60142_PCT_SEQ_LIST.txt

Tyr Cys Glu Arg Arg Met His Arg Gly Arg Lys Arg Pro Val Gln Val
210 215 220

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

Gly Lys Ala Thr Glu Gly Ala Lys Lys Val Gly Asp Lys Ser Pro Gly
245 250 255

Ser Lys Lys Leu Ala Val Ala Ala Ala Ala Ala Ala Ala Gln Ser
260 265 270

Thr

<210> 105
<211> 1374
<212> DNA
<213> Zea mays

<400> 105
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1374

<210> 106
 <211> 374
 <212> PRT
 <213> Zea mays

<400> 106

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

PF59082PF60142_PCT_SEQ_LIST.txt

Ser Asp Glu His Ser Thr Leu Leu Ser Gly Gly Met Asp Pro Ser Met
245 250 255

Met Asp Asn Ser Trp Arg Leu Leu Pro Ser Gln Asn Asn Thr Phe Gln
260 265 270

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

Thr Ile Ala Ser Leu Pro Lys Thr Gln Arg Glu Pro Leu Ser Phe Phe
290 295 300

Gly Ser Asp Phe Val Thr Ala Ala Lys Gln Glu Asn Gln Thr Leu Arg
305 310 315 320

Pro Phe Phe Asp Glu Trp Pro Lys Ser Arg Asp Ser Trp Pro Glu Leu
325 330 335

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

Ile Pro Met Ala Thr Ser Asp Phe Ser Asn Thr Ser Ser Arg Ser Pro
355 360 365

Gly Gly Ile Pro Ser Arg
370

<210> 107
<211> 1172
<212> DNA
<213> Zea mays

<400> 107
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cgcagcagca gcagcagcag caccgtatga gcggcagggtg ggcagcgagg ccgccggcgc 180
tcttcacagc ggcgcagtac gaggagctgg agcaccaggc gctcatatac aagtacctcg 240
tcgccggcgt gcccgtcccc ccggacctcc tcctccccct acgccgaggc ttcgtctacc 300
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agtactgcga gcgccacatg caccgcggcc gcaaccgttc aagaaagcct gtggaagcgc 480
agctcgtgcc cccgccgcac gccagccgc agcagcaggc ccccgcgccc accgctggct 540
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PF59082PF60142_PCT_SEQ_LIST.txt

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<210> 108
 <211> 380
 <212> PRT
 <213> Zea mays

<400> 108

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

Ser Gly Arg Trp Ala Ala Arg Pro Pro Ala Leu Phe Thr Ala Ala Gln
 50 55 60

Tyr Glu Glu Leu Glu His Gln Ala Leu Ile Tyr Lys Tyr Leu Val Ala
 65 70 75 80

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

Val Tyr His Gln Pro Ala Leu Gly Tyr Gly Pro Tyr Phe Gly Lys Lys
 100 105 110

Val Asp Pro Glu Pro Gly Arg Cys Arg Arg Thr Asp Gly Lys Lys Trp
 115 120 125

Arg Cys Ser Lys Glu Ala Ala Pro Asp Ser Lys Tyr Cys Glu Arg His
 130 135 140

Met His Arg Gly Arg Asn Arg Ser Arg Lys Pro Val Glu Ala Gln Leu
 145 150 155 160

Val Pro Pro Pro His Ala Gln Pro Gln Gln Gln Ala Pro Ala Pro Thr
 165 170 175

Ala Gly Phe Gln Ser His Pro Met Tyr Pro Ser Ile Leu Ala Gly Asn
 180 185 190

PF59082PF60142_PCT_SEQ_LIST.txt

Gly Gly Gly Gly Gly Gly Val Gly Gly Gly Ala Gly Gly Gly Thr Phe
195 200 205

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

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

Gly Val Lys Ser Leu Ser Asp Glu His Ser Gln Leu Leu Pro Gly Gly
245 250 255

Gly Gly Gly Met Asp Ala Ser Met Asp Asn Ser Trp Arg Leu Leu Pro
260 265 270

Ser Gln Thr Ala Ala Thr Phe Gln Ala Thr Ser Tyr Pro Leu Phe Gly
275 280 285

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

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

Gln Glu Asn Gln Thr Leu Arg Pro Phe Phe Asp Glu Trp Pro Lys Ser
325 330 335

Arg Asp Ser Trp Pro Glu Leu Asn Glu Asp Asn Ser Leu Gly Ser Ser
340 345 350

Ala Thr Gln Leu Ser Thr Ser Ile Pro Met Ala Pro Ser Asp Phe Asn
355 360 365

Thr Ser Ser Arg Ser Pro Asn Gly Ile Pro Ser Arg
370 375 380

<210> 109
<211> 1154
<212> DNA
<213> Zea mays

<400> 109
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gcgctcatct tcaagtacat ggcctcgggc gcgcccgatc cgcacgacct cgtcctaccg 180
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ccgtcgctgg cgtactgggg ctgctacggc gcggggggcg cggttcgctcg ccgcaaggcg 300
gcggaggaca cggagccggg gcggtgccgg cggacggacg gcaagaagtg gcggtgctcc 360
agggaggccc acggcgactc caagtactgc gagaagcaca ttcaccgcgg gaagagccgt 420

PF59082PF60142_PCT_SEQ_LIST.txt

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atggcgggcg acgacgcgac gcagctttcc atctccatcc ccgcggcttc gccctccgac      960
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ctgcttctgc ctct                                     1154
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<210> 110
 <211> 321
 <212> PRT
 <213> Zea mays

<400> 110

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Ser Gly Ala Pro Val Pro His Asp Leu Val Leu Pro Leu Arg Leu Ala
 35 40 45

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

Pro Ser Leu Ala Tyr Trp Gly Cys Tyr Gly Ala Gly Ala Pro Phe Val
 65 70 75 80

Gly Arg Lys Ala Ala Glu Asp Thr Glu Pro Gly Arg Cys Arg Arg Thr
 85 90 95

Asp Gly Lys Lys Trp Arg Cys Ser Arg Glu Ala His Gly Asp Ser Lys
 100 105 110

Tyr Cys Glu Lys His Ile His Arg Gly Lys Ser Arg Ser Arg Lys Pro
 115 120 125

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

PF59082PF60142_PCT_SEQ_LIST.txt

Pro Ser Ala Ile Ser Thr Ile Ser Pro Pro Arg Ala Ala Asp Ala Pro
 145 150 155 160

Pro Pro Ser Leu Ala Tyr Pro Gln Gln His Leu Leu His Gly Ala Ser
 165 170 175

Ser Ser Ala Ala Ala Arg Ala Pro Ala Gly Ala Leu Gln Leu His Leu
 180 185 190

Asp Ala Ser Leu His Ala Ala Ala Ala Ser Pro Ser Pro Pro Pro Ser
 195 200 205

Tyr His Arg Tyr Ala His Tyr Thr Pro Pro Ala Ser Ser Leu Phe Pro
 210 215 220

Gly Gly Gly Tyr Gly Tyr Asp Tyr Asp Tyr Gly Gln Ser Lys Glu Leu
 225 230 235 240

Arg Arg Arg His Phe His Ala Leu Gly Ala Asp Leu Ser Leu Asp Lys
 245 250 255

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

Arg Phe Phe Asp Glu Trp Pro Arg Glu Ser Gly Asp Met Ala Ala Asp
 275 280 285

Asp Ala Thr Gln Leu Ser Ile Ser Ile Pro Ala Ala Ser Pro Ser Asp
 290 295 300

Leu Ala Ala Thr Ser Ala Ser Ala Ala Ala Ala Arg Phe His Asn Gly
 305 310 315 320

Glu

<210> 111
 <211> 1516
 <212> DNA
 <213> Zea mays

<400> 111
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PF59082PF60142_PCT_SEQ_LIST.txt

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tgggagatgc cgacgaacgg atggaaagaa gtggcggtgc tccaaggaag caatggctga 600
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<210> 112
 <211> 427
 <212> PRT
 <213> Zea mays
 <400> 112

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

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

Thr Gln Ala Ala Ala Ala Ala Pro Tyr Pro Ser Pro Phe Leu Asp Gly
 50 55 60

Glu Lys Met Leu Arg Phe Ser Lys Ala Ala His Thr Ser His Ser Gly
 65 70 75 80

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

PF59082PF60142_PCT_SEQ_LIST.txt

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

PF59082PF60142_PCT_SEQ_LIST.txt

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

Ser Ser Ser Trp Glu Met Pro Gln Gly Gly Pro Leu Gly Glu Ile Leu
385 390 395 400

Thr Asn Ser Lys Asn Ser Lys Asp Leu Ser Lys Cys Lys Pro Arg Ser
405 410 415

Tyr Gly Trp Leu Leu Asn Leu Asp His Ala Pro
420 425

<210> 113
<211> 1139
<212> DNA
<213> Zea mays

<400> 113
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agcagctcgg gacgatggag gcgacgaagc cgtgccccac cccacgccg ctgctccccg 840
ccgccgggta cggcgctcgt caggccaagg aagacgagga ggaggaaacg cggcggcagc 900
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<210> 114
<211> 363
<212> PRT
<213> Zea mays

<400> 114

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20 25 30

Cys Leu Ala Ser Gly Lys Pro Ile Pro Ser Tyr Leu Met Pro Pro Leu
35 40 45

Arg Arg Ile Leu Asp Ser Ala Leu Ala Thr Ser Pro Ser Leu Ala Ala
50 55 60

Phe Gln Pro Gln Pro Ser Leu Gly Trp Gly Gly Cys Phe Gly Met Gly
65 70 75 80

Phe Ser Arg Lys Pro Ala Asp Glu Asp Pro Glu Pro Gly Arg Cys Arg
85 90 95

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

Ser Lys Tyr Cys Glu Lys His Met His Arg Gly Lys Asn Arg Ser Arg
115 120 125

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

Ala Ala Thr Thr Ser Thr Ser Pro Ala Pro Ser Tyr His Arg Pro Ala
145 150 155 160

Pro Ala Ala His Asp Ala Val Pro Tyr His Ala Pro Tyr Gly Ala Ala
165 170 175

Tyr His His Thr Gln Thr Gln Val Met Ser Pro Phe His Leu His Leu
180 185 190

Glu Thr Thr His Pro His Pro Pro Pro Pro Pro Tyr Tyr Tyr Ala
195 200 205

Asp Gln Arg Asp Tyr Ala Tyr Gly Lys Glu Val Gly Glu Arg Ala Phe
210 215 220

Phe Ser Asp Gly Ala Gly Glu Arg Asp Arg Gln Gln Gln Ala Ala Gly
225 230 235 240

Gln Trp Gln Phe Lys Gln Leu Gly Thr Met Glu Ala Thr Lys Pro Cys
245 250 255

Pro Thr Pro Thr Pro Leu Leu Pro Ala Ala Gly Tyr Gly Val Gly Gln
260 265 270

Ala Lys Glu Asp Glu Glu Glu Glu Thr Arg Arg Gln Gln Gln Gln His

275

280

285

Cys Phe Val Leu Gly Ala Asp Leu Arg Leu Ala Glu Arg Pro Ser Gly
 290 295 300

Ala His Asp Asp Ala Ala Gln Lys Pro Leu Arg His Phe Phe Asp Glu
 305 310 315 320

Trp Pro His Glu Lys Gly Ser Lys Ala Gly Trp Trp Ile Gly Gly Leu
 325 330 335

Asp Gly Glu Thr Thr Gln Leu Ser Met Ser Ile Pro Met Ala Ala Ala
 340 345 350

Ala Asp Leu Pro Val Thr Ser Arg Tyr Arg Thr
 355 360

<210> 115
 <211> 39
 <212> PRT
 <213> Artificial sequence

<220>
 <223> QLQ domain

<400> 115

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

Ile Phe Ser Ile Arg Arg Ser
 35

<210> 116
 <211> 44
 <212> PRT
 <213> Artificial sequence

<220>
 <223> WRC domain

<400> 116

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

His Arg Gly Arg Asn Arg Ala Arg Lys Ser Leu Asp
 35 40

<210> 117
 <211> 2194

<212> DNA
 <213> Oryza sativa

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 catccaccta ctttagtggc aatcgggcta aataaaaaag agtcgctaca ctagtttcgt 180
 tttccttagt aattaagtgg gaaaatgaaa tcattattgc ttagaatata cgttcacatc 240
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 aaaaaatctt tctagctgaa ctcaatgggt aaagagagag atttttttta aaaaaataga 360
 atgaagatat tctgaacgta ttggcaaaga tttaaacata taattatata attttatagt 420
 ttgtgcattc gtcatatcgc acatcattaa ggacatgtct tactccatcc caatttttat 480
 ttagtaatta aagacaattg acttattttt attatttatc ttttttcgat tagatgcaag 540
 gtacttacgc acacactttg tgctcatgtg catgtgtgag tgcacctcct caatacacgt 600
 tcaactagca acacatctct aatatcactc gcctatttaa tacatttagg tagcaatatc 660
 tgaattcaag cactccacca tcaccagacc acttttaata atatctaaaa taaaaaaat 720
 aattttacag aatagcatga aaagtatgaa acgaactatt taggtttttc acatacaaaa 780
 aaaaaaagaa ttttgctcgt gcgcgagcgc caatctccca tattgggcac acaggcaaca 840
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 cgaccgcctt ctcgatccat atcttccggt cgagttcttg gtcgatctct tccctcctcc 1140
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 aagctgtaat cgggatagtt atactgcttg ttcttatgat tcatttcctt tgtgcagttc 2160
 ttggtgtagc ttgccacttt caccagcaaa gttc 2194

<210> 118
 <211> 58
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: prm10010

<400> 118
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<210> 119
 <211> 52
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: prm10011

<400> 119
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<210> 120
 <211> 785
 <212> DNA
 <213> Oryza sativa

<400> 120
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 agctagagaa aaagagtttg agagagatct aagagatgtc agggggtttgg gtgttcaaga 120
 acgggggtggg gagattgggtg gagaagcagc aggcgacggc ggggacggcg gtggcgggag 180
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 cctccgtcca catgtacgac atcgtcgtca agaaccgcga ctccttccgc gtcgtcgacg 420
 cctaaattga cctatgtata ggctcgcgtg catgcaagggt agacgaccat ccaccttgca 480
 tgcattgcagg ctatcattct ctcttcgtct ccgtcttcgt ctttcatctt tgttgtgggtg 540
 tgtgtgaatt tattatactt cttatgactg tgtgtgtgac tgtgtgagag ttcatggaga 600
 gtgatgagta gtggatatac tatgtgtcgt cgctgatcga tttggtttat taccttgtgg 660
 gtgggtatta attatcagca gtgtgttata tcaattgctt acttgtatgt gtatcatgta 720
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 ttgtg 785

<210> 121
 <211> 109
 <212> PRT
 <213> Oryza sativa

<400> 121

Met Ser Gly Val Trp Val Phe Lys Asn Gly Val Val Arg Leu Val Glu
 1 5 10 15

Lys Gln Gln Ala Thr Ala Gly Thr Ala Val Ala Gly Gly Arg Arg Lys
 20 25 30

Ala Leu Val His Thr Pro Ser Gly Gln Val Val Ser Ser Tyr Ala Ala
 35 40 45

Leu Glu Ala Arg Leu Thr Ala Leu Gly Trp Glu Arg Tyr Tyr Glu Asp
 50 55 60

Pro Ser Leu Phe Gln Phe His Lys Arg Gly Ser Leu Asp Leu Ile Ser
 65 70 75 80

Leu Pro Ala Asp Phe Ser Ala Phe Ser Ser Val His Met Tyr Asp Ile
 85 90 95

Val Val Lys Asn Arg Asp Ser Phe Arg Val Val Asp Ala
 100 105

<210> 122
 <211> 53
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: prm09129

<400> 122
 ggggacaagt ttgtacaaaa aagcaggctt aaacaatgtc aggggttttg gtg 53

<210> 123
 <211> 50
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: prm09988

<400> 123
 ggggaccact ttgtacaaga aagctggggtt gtcgcatagg tcaatttagg 50

<210> 124
 <211> 2194
 <212> DNA
 <213> Oryza sativa

<400> 124
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aaatataaaa tgagacctta tatatgtagc gctgataact agaactatgc aagaaaaact 120

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ttgtgcattc gtcatatcgc acatcattaa ggacatgtct tactccatcc caatttttat	480
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gtacttacgc acacactttg tgctcatgtg catgtgtgag tgcacctcct caatacacgt	600
tcaactagca acacatctct aatatcactc gcctatttaa tacatttagg tagcaatatc	660
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aattttacag aatagcatga aaagtatgaa acgaactatt taggtttttc acatacaaaa	780
aaaaaaagaa ttttgctcgt gcgcgagcgc caatctccca tattgggcac acaggcaaca	840
acagagtggc tgcccacaga acaaccaca aaaaacgatg atctaacgga ggacagcaag	900
tccgcaacaa ctttttaaca gcaggctttg cggccaggag agaggaggag aggcaaagaa	960
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gtaataaagt acggttggtt ggtcctcgat tctggtagtg atgcttctcg atttgacgaa	1500
gctatccttt gtttattccc tattgaacaa aaataatcca actttgaaga cgggtcccgtt	1560
gatgagattg aatgattgat tcttaagcct gtccaaaatt tcgcagctgg cttgtttaga	1620
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atttctgatc tccattttta attatatgaa atgaactgta gcataagcag tattcatttg	1920
gattattttt tttattagct ctcaccctt cattattctg agctgaaagt ctggcatgaa	1980
ctgtcctcaa ttttgttttc aaattcacat cgattatcta tgcattatcc tcttgtatct	2040
acctgtagaa gtttcttttt gggtattcct tgactgcttg attacagaaa gaaatttatg	2100
aagctgtaat cgggatagtt atactgcttg ttcttatgat tcatttcctt tgtgcagttc	2160
ttggtgtagc ttgccacttt caccagcaaa gttc	2194

<210> 125
 <211> 1130
 <212> DNA
 <213> Oryza sativa

<400> 125
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 caggattaga aaaacgggac gacaaatagt aatggaaaaa caaaaaaaaa caaggaaaca 180
 catggcaata taaatggaga aatcacaaga ggaacagaat ccgggcaata cgctgcgaaa 240
 gtactcgtag gtaaaaaaaaa gaggcgcatt catgtgtgga cagcgtgcag cagaagcagg 300
 gatttgaaac cactcaaadc caccactgca aaccttcaaa cgaggccatg gtttgaagca 360
 tagaaagcac aggtaagaag cacaacgccc tcgctctcca cctcccacc caatcgcgac 420
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 ctcttctc ctctcttctc cctcctctc tccccctc tcacaagaga gagagcgcca 1020
 gactctcccc aggtgaggtg agaccagtct ttttgctcga ttcgacgcgc ctttcacgcc 1080
 gcctcgcgcg gatctgaccg cttccctcgg ctttctcgca ggattcagcc 1130

<210> 126
 <211> 321
 <212> DNA
 <213> Oryza sativa

<400> 126
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 gcgctggagc ggaggctggg ggcgctgggg tgggagcgct actacgagga ccgcccacc 180
 ctgcagctcc acaggcgca cggcagcgcc gacctcatct ccatcccccg cgacttctcc 240
 cgcttccgct ccaccacat gtacgacgtc gtcgtcaaga accgcgacca cttcaagggt 300
 gatgtgatgg aaaagaactg a 321

<210> 127
 <211> 106
 <212> PRT

<213> Oryza sativa

<400> 127

Met Ala Gly Gly Gly Val Trp Val Phe Arg Asn Asn Gly Val Met Glu
 1 5 10 15

Leu Glu Glu Gln Ala Thr Ser Arg Lys Ala Leu Val His Val Ala Thr
 20 25 30

Ser Glu Val Ile Arg Ser Thr Glu Ala Leu Glu Arg Arg Leu Gly Ala
 35 40 45

Leu Gly Trp Glu Arg Tyr Tyr Glu Asp Arg Ala Thr Leu Gln Leu His
 50 55 60

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

Arg Phe Arg Ser Thr His Met Tyr Asp Val Val Val Lys Asn Arg Asp
 85 90 95

His Phe Lys Val Asp Val Met Glu Lys Asn
 100 105

<210> 128

<211> 318

<212> DNA

<213> Oryza sativa

<400> 128

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 gcgctgggagc ggaggctggg ggcgctgggg tgggagcgct actacgagga ccgcgccacc 180
 ctgcagctcc acaggcgga cggcagcgcc gacctcatct ccatcccccg cgacttctcc 240
 cgcttcgct ccaccacat gtacgacgtc gtcgtcaaga accgcgacca cttcaaggtc 300
 gtcgacctcc acacctag 318

<210> 129

<211> 105

<212> PRT

<213> Oryza sativa

<400> 129

Met Ala Gly Gly Gly Val Trp Val Phe Arg Asn Asn Gly Val Met Glu
 1 5 10 15

Leu Glu Glu Gln Ala Thr Ser Arg Lys Ala Leu Val His Val Ala Thr
 20 25 30

Ser Glu Val Ile Arg Ser Thr Glu Ala Leu Glu Arg Arg Leu Gly Ala
 35 40 45

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Gly Trp Glu Arg Tyr Tyr Glu Asp Arg Ala Thr Leu Gln Leu His
50 55 60

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

Arg Phe Arg Ser Thr His Met Tyr Asp Val Val Val Lys Asn Arg Asp
85 90 95

His Phe Lys Val Val Asp Leu His Thr
100 105

<210> 130
<211> 672
<212> DNA
<213> Arabidopsis thaliana

<400> 130
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tcttcaagaa cggagtgata agacttgtgg agaaccctaa ccagtcagga tccgacacac 120
agaaccgaag gaaagtgatg gtctatttac cgacaggaga agtgggtctca tcttactcga 180
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tccgagactc ccattgattc ttcttttgtg tgttggtgtg tgtgttgtgt tcggttgttt 420
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<210> 131
<211> 110
<212> PRT
<213> Arabidopsis thaliana

<400> 131
Met Ser Gly Val Trp Val Phe Lys Asn Gly Val Ile Arg Leu Val Glu
1 5 10 15

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

Val Tyr Leu Pro Thr Gly Glu Val Val Ser Ser Tyr Ser Thr Leu Glu
35 40 45

Gln Ile Leu Gln Ser Leu Gly Trp Glu Arg Tyr Phe Gly Gly Gly Asp
50 55 60

PF59082PF60142_PCT_SEQ_LIST.txt

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

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

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

<210> 132
<211> 442
<212> DNA
<213> Oryza sativa

<400> 132
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gcggcggcgg cggcggcggc ggcggtggcg gcggcggcat ccggcgcaag gcgctgctgc 180
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tccagttcca caagcgctcg tcggtggacc tgatctcgct gcccaaggac ttctcccagt 360
tcggctccgt ccacatgtac gacatcgctg tcaagaaccg cgacgccttc cgagtcatcg 420
acgtctaata acccaagtgt ct 442

<210> 133
<211> 127
<212> PRT
<213> Oryza sativa

<400> 133
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Asn Pro Pro Ala Ser Ala Asn Ser Gly Gly Gly Gly Gly Gly Gly Gly
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Gly Gly Gly Gly Gly Gly Ile Arg Arg Lys Ala Leu Leu His Met Pro
35 40 45

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

Ala Leu Gly Trp Glu Arg Tyr Tyr Ser Gly Gly Gly Gly Ala Ala Ala
65 70 75 80

Ala Ala Ala Met Met Leu Gln Phe His Lys Arg Ser Ser Val Asp Leu
85 90 95

Ile Ser Leu Pro Lys Asp Phe Ser Gln Phe Gly Ser Val His Met Tyr
Seite 145

100

105

110

Asp Ile Val Val Lys Asn Arg Asp Ala Phe Arg Val Ile Asp Val
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 <213> Arabidopsis thaliana

<400> 134
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<210> 135
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 <212> PRT
 <213> Arabidopsis thaliana

<400> 135
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 20 25 30
 Asn Val Leu Val Tyr Leu Pro Thr Gly Glu Ala Val Ser Ser Tyr Ser
 35 40 45
 Ser Leu Glu Gln Ile Leu Arg Ser Leu Gly Trp Glu Arg Tyr Phe Ser
 50 55 60
 Gly Asp Ser Asp Leu Ile Gln Tyr His Lys Arg Ser Ser Ile Asp Leu
 65 70 75 80
 Ile Ser Leu Pro Arg Asp Phe Ser Lys Phe Asn Ser Val Tyr Met Tyr
 85 90 95
 Asp Ile Val Val Lys Asn Pro Asn Ser Phe His Val Arg Asp Phe Asn
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<210> 136
 <211> 546
 <212> DNA
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<400> 136
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<210> 137
 <211> 181
 <212> PRT
 <213> Arabidopsis thaliana

<400> 137

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

Phe Phe Lys Tyr Ile Ile Thr Ser Thr Met Ser Gly Val Trp Val Phe
 50 55 60

Asn Lys Asn Gly Val Met Arg Leu Val Glu Asn Pro Tyr Asn Gln Ser
 65 70 75 80

Ala Gly Asp Ser Ser Glu Ser Ser Ser Ser Gly Gly Asn Gln Gln Gln
 85 90 95

Arg Met Arg Arg Lys Ile Leu Val His Leu Pro Ser Ser Glu Val Val
 100 105 110

Ser Ser Tyr Gly Ser Leu Glu Lys Ile Leu Lys Asn Leu Gly Trp Glu
 115 120 125

Arg Tyr Tyr Ser Gly Asp Asn Thr Asp His Leu Leu Gln Phe His Lys
 130 135 140

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

Asn Ser Ile His Met Tyr Asp Ile Val Val Lys Asn Pro Asn Val Phe
 165 170 175

His Val Arg Asp Met
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<212> DNA
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<210> 139
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<212> PRT
<213> Oryza sativa

<400> 139

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Gly Lys Val Leu Val His Val Pro Ser Ser Glu Val Val Thr Ser Tyr
35 40 45

Glu Val Leu Glu Arg Arg Leu Arg Glu Leu Gly Trp Glu Arg Tyr Leu
50 55 60

Asn Asp Pro Cys Leu Leu Gln Phe His Gln Arg Ser Thr Val His Leu
65 70 75 80

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Ile Ser Val Pro Arg Asp Phe Ser Arg Leu Lys Leu Val His Met Tyr
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Asp Val Val Val Lys Thr Arg Asn Val Phe Glu Val
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cgcgactcct tccgcgtcgt cgacgcctaa 330

<210> 141
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<212> PRT
<213> Oryza sativa

<400> 141
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20 25 30

Ala Leu Val His Thr Pro Ser Gly Gln Val Val Ser Ser Tyr Ala Ala
35 40 45

Leu Glu Ala Arg Leu Thr Ala Leu Gly Trp Glu Arg Tyr Tyr Glu Asp
50 55 60

Pro Ser Leu Phe Gln Phe His Lys Arg Gly Ser Leu Asp Leu Ile Ser
65 70 75 80

Leu Pro Ala Asp Phe Ser Ala Phe Ser Ser Val His Met Tyr Asp Ile
85 90 95

Val Val Lys Asn Arg Asp Ser Phe Arg Val Val Asp Ala
100 105

<210> 142
<211> 333
<212> DNA
<213> Sinapis alba

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<210> 143
<211> 110
<212> PRT
<213> Sinapis alba

<400> 143

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20 25 30

Val Tyr Leu Pro Thr Gly Glu Val Ile Ser Ser Tyr Ser Thr Leu Glu
35 40 45

Gln Ile Leu Arg Ser Leu Gly Trp Glu Arg Tyr Phe Gly Gly Gly Asp
50 55 60

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

Leu Pro Lys Asp Phe Thr Lys Phe Ser Ser Val Tyr Met Tyr Asp Ile
85 90 95

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

<210> 144
<211> 369
<212> DNA
<213> Oryza sativa

<400> 144

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<210> 145

<211> 122
 <212> PRT
 <213> Oryza sativa

<400> 145

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 20 25 30

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

Ser Tyr Glu Val Leu Glu Arg Arg Leu Arg Glu Leu Gly Trp Glu Arg
 50 55 60

Tyr Leu Thr Asp Pro Cys Leu Leu Gln Phe His Gln Arg Ser Thr Val
 65 70 75 80

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

Met Tyr Asp Ile Val Val Lys Thr Arg Asn Val Phe Glu Val Arg Asp
 100 105 110

Ala Ala Ala Pro Ala Val Ser Pro Ala Thr
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<210> 146
 <211> 1098
 <212> DNA
 <213> Oryza sativa

<400> 146

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agaacccccg cagcgaggaa tcgtcgtcgg cgggggacgg cggcggaggc gggcggcgga	300
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ggctgcggga gctcgggtgg gagaggtacc tcaccgacct gtgcctcctg cagttccacc	420
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<210> 147
<211> 122
<212> PRT
<213> Oryza sativa

<400> 147

Met Ala Gly Val Trp Val Phe Lys Asp Gly Ile Val Arg Arg Val Glu
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Asn Pro Gly Ser Glu Glu Ser Ser Ser Ala Gly Asp Gly Gly Gly Gly
20 25 30

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

Ser Tyr Glu Val Leu Glu Arg Arg Leu Arg Glu Leu Gly Trp Glu Arg
50 55 60

Tyr Leu Thr Asp Pro Cys Leu Leu Gln Phe His Gln Arg Ser Thr Val
65 70 75 80

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

Met Tyr Asp Ile Val Val Lys Thr Arg Asn Val Phe Glu Val Arg Asp
100 105 110

Ala Ala Ala Pro Ala Val Ser Pro Ala Thr
115 120

<210> 148
<211> 934
<212> DNA
<213> Oryza sativa

<400> 148

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<210> 149
 <211> 124
 <212> PRT
 <213> Oryza sativa

<400> 149

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			20					25					30		

Ser	Gly	Gly	Asn	Gln	Gln	Gln	Arg	Met	Arg	Arg	Lys	Ile	Leu	Val	His
		35					40					45			

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

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

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

Pro	Arg	Asp	Phe	Ser	Lys	Phe	Asn	Ser	Ile	His	Met	Tyr	Asp	Ile	Val
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Val	Lys	Asn	Pro	Asn	Val	Phe	His	Val	Arg	Asp	Met
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<210> 150
 <211> 357
 <212> DNA
 <213> Oryza sativa

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<210> 151
 <211> 118
 <212> PRT
 <213> Oryza sativa

<400> 151

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 20 25 30

Gly Lys Val Leu Val His Val Pro Ser Ser Glu Val Val Thr Ser Tyr
 35 40 45

Glu Val Leu Glu Arg Arg Leu Arg Glu Leu Gly Trp Glu Arg Tyr Leu
 50 55 60

Asn Asp Pro Cys Leu Leu Gln Phe His Gln Arg Ser Thr Val His Leu
 65 70 75 80

Ile Ser Val Pro Arg Asp Phe Ser Arg Leu Lys Leu Val His Met Tyr
 85 90 95

Asp Val Val Val Lys Thr Arg Asn Val Phe Glu Val Arg Asp Ala Ala
 100 105 110

Thr Thr Ala Ala Pro Pro
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<210> 152
 <211> 309
 <212> DNA
 <213> Nicotiana tabacum

<400> 152

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<210> 153
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 <212> PRT
 <213> Nicotiana tabacum

<400> 153

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 20 25 30

Asn Glu Val Ile Thr Ser Tyr Ala Val Leu Glu Arg Lys Leu His Ser
 35 40 45

Leu Gly Trp Glu Arg Tyr Tyr Asp Asp Leu Asp Leu Leu Gln Tyr His
 50 55 60

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

Phe Glu Val Arg Asp Ile
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<210> 154
 <211> 2415
 <212> DNA
 <213> Arabidopsis thaliana

<400> 154

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<210> 155
 <211> 804
 <212> PRT
 <213> Arabidopsis thaliana
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Met Ser Gly Val Trp Val Phe Asn Asn Gly Val Ile Arg Leu Val Glu
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Asn Pro Asn Gln Ser Gly Gly Val Ser Thr Gln Ser His Gly Arg Arg
 20 25 30

PF59082PF60142_PCT_SEQ_LIST.txt

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

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Pro Lys Ala Lys Ala Asp Met Ser Asn Glu Thr Ser Ser Ser Ser
 305 310 315 320
 Lys Tyr Met Glu Thr Ser Glu Ser Leu Thr Gly Thr Met Asn Lys Met
 325 330 335
 Ser Leu Ile Gly Glu Thr Glu Asn Ser Ser Asp Ile Lys Ile Arg Gly
 340 345 350
 Pro Lys Ser Gln Ser Lys His Lys Pro Glu Glu Trp Met Leu Leu Asp
 355 360 365
 Lys Glu Ser Asp Ala Leu Ser Gln Leu Asn Leu Ala Ile Val Gly His
 370 375 380
 Val Asp Ser Gly Lys Ser Thr Leu Ser Gly Arg Leu Leu His Leu Leu
 385 390 395 400
 Gly Arg Ile Ser Gln Lys Gln Met His Lys Tyr Glu Lys Glu Ala Lys
 405 410 415
 Leu Gln Gly Lys Gly Ser Phe Ala Tyr Ala Trp Ala Leu Asp Glu Ser
 420 425 430
 Ala Glu Glu Arg Glu Arg Gly Ile Thr Met Thr Val Ala Val Ala Tyr
 435 440 445
 Phe Asn Ser Lys Arg His His Val Val Leu Leu Asp Ser Pro Gly His
 450 455 460
 Lys Asp Phe Val Pro Asn Met Ile Ala Gly Ala Thr Gln Ala Asp Ala
 465 470 475 480
 Ala Ile Leu Val Ile Asp Ala Ser Val Gly Ala Phe Glu Ala Gly Phe
 485 490 495
 Asp Asn Leu Lys Gly Gln Thr Arg Glu His Ala Arg Val Leu Arg Gly
 500 505 510
 Phe Gly Val Glu Gln Val Ile Val Ala Ile Asn Lys Met Asp Ile Val
 515 520 525
 Gly Tyr Ser Lys Glu Arg Phe Asp Leu Ile Lys Gln His Val Gly Ser
 530 535 540
 Phe Leu Gln Ser Cys Arg Phe Lys Asp Ser Ser Leu Thr Trp Ile Pro
 545 550 555 560
 Leu Ser Ala Met Glu Asn Gln Asn Leu Val Ala Ala Pro Ser Asp Asn
 565 570 575

Arg Leu Ser Ser Trp Tyr Gln Gly Pro Cys Leu Leu Asp Ala Val Asp
580 585 590

Ser Val Lys Ser Pro Asp Arg Asp Val Ser Lys Pro Leu Leu Met Pro
595 600 605

Ile Cys Asp Ala Val Arg Ser Thr Ser Gln Gly Gln Val Ser Ala Cys
610 615 620

Gly Lys Leu Glu Ala Gly Ala Val Arg Pro Gly Ser Lys Val Met Val
625 630 635 640

Met Pro Ser Gly Asp Gln Gly Thr Ile Arg Ser Leu Glu Arg Asp Ser
645 650 655

Gln Ala Cys Thr Ile Ala Arg Ala Gly Asp Asn Val Ala Leu Ala Leu
660 665 670

Gln Gly Ile Asp Ala Asn Gln Val Met Ala Gly Asp Val Leu Cys His
675 680 685

Pro Asp Phe Pro Val Ser Val Ala Thr His Leu Glu Leu Met Val Leu
690 695 700

Val Leu Glu Gly Ala Thr Pro Ile Leu Leu Gly Ser Gln Leu Glu Phe
705 710 715 720

His Val His His Ala Lys Glu Ala Ala Thr Val Val Lys Leu Val Ala
725 730 735

Met Leu Asp Pro Lys Thr Gly Gln Pro Thr Lys Lys Ser Pro Arg Cys
740 745 750

Leu Thr Ala Lys Gln Ser Ala Met Leu Glu Val Ser Leu Gln Asn Pro
755 760 765

Val Cys Val Glu Thr Phe Ser Glu Ser Arg Ala Leu Gly Arg Val Phe
770 775 780

Leu Arg Ser Ser Gly Arg Thr Val Ala Met Gly Lys Val Thr Arg Ile
785 790 795 800

Ile Gln Asp Ser

<210> 156
<211> 852
<212> DNA
<213> Oryza sativa

<400> 156
gcaccaccac cattgctgag ctccaaagct tctagctgtg atcaagcaaa gaagaattga 60
aaaaaacat atatatatta tatatatggc aggggtgtgg gtgtttgagg atgggatggt 120
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PF59082PF60142_PCT_SEQ_LIST.txt

gaggagggca gatagcgagg cgccgtcgag agggcgcggt gtcggtggtg gaggtggggg 180
 agggaaggtg cttgtgcacg tgccgagcag cgaggtggtg acgagctacg aggttctgga 240
 gaggcggctg cgggagctcg ggtgggagag gtacctcaac gaccctgcc tcctccagtt 300
 ccaccagcgc tccaccgtcc acctcatctc cgtgccccgc gacttctccc gcctcaagct 360
 cgtccacatg tacgacgtcg tcgtcaagac ccgcaacgtc ttcgaggtcc gtgacgccgc 420
 caccactgct tccccgcat gatcgcatcg atgtctatgc tttgatcatc atcgatatga 480
 ccttcctcga ctccgggctc aggccagaca cgccgcatg ggcctacaa tcgtatgtgt 540
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 gtacaggtat aacgtatgcg tatatacgta cgtgtgcatg cgatcgggtg tgtgtgatat 660
 atattaaaat aagcgtggct ggtttaattg caagtgaagt tttagttatt taattatacg 720
 agagccatga gcacgtgtgt agctagcttt ggagtcttgt actttgtggt ttggagccat 780
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 attagttttg tc 852

<210> 157
 <211> 118
 <212> PRT
 <213> Oryza sativa

<400> 157

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

Ser Glu Ala Pro Ser Arg Gly Arg Gly Val Gly Gly Gly Gly Gly Gly
 20 25 30

Gly Lys Val Leu Val His Val Pro Ser Ser Glu Val Val Thr Ser Tyr
 35 40 45

Glu Val Leu Glu Arg Arg Leu Arg Glu Leu Gly Trp Glu Arg Tyr Leu
 50 55 60

Asn Asp Pro Cys Leu Leu Gln Phe His Gln Arg Ser Thr Val His Leu
 65 70 75 80

Ile Ser Val Pro Arg Asp Phe Ser Arg Leu Lys Leu Val His Met Tyr
 85 90 95

Asp Val Val Val Lys Thr Arg Asn Val Phe Glu Val Arg Asp Ala Ala
 100 105 110

Thr Thr Ala Ser Pro Pro
 115

<210> 158
 <211> 306

<212> DNA
 <213> Oryza sativa

<400> 158
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 gaggaccgcg ccgtggtgca gctccaccgc cgcgacggcg gcgccgacct catctccctc 120
 ccccgcgact tcgcccgtt ccgctccacc cacatgtacg acgtcgtcct caagaaccgc 180
 gaccattca agggaggaag cgcagaggag agggcgtggc tccgtcggct gtcggcgacc 240
 tcgacggcgg cgggaggtgg ccccggtgc ggtggcgcta aggatcggag tggcagccgg 300
 tggtag 306

<210> 159
 <211> 101
 <212> PRT
 <213> Oryza sativa

<400> 159
 Met Gly Ser Leu Gln Ala Leu Glu Arg Arg Leu Ala Gly Leu Gly Trp
 1 5 10 15
 Glu Arg Tyr Tyr Glu Asp Arg Ala Val Val Gln Leu His Arg Arg Asp
 20 25 30
 Gly Gly Ala Asp Leu Ile Ser Leu Pro Arg Asp Phe Ala Arg Phe Arg
 35 40 45
 Ser Thr His Met Tyr Asp Val Val Leu Lys Asn Arg Asp His Phe Lys
 50 55 60
 Gly Gly Ser Ala Glu Glu Arg Ala Trp Leu Arg Arg Leu Ser Ala Thr
 65 70 75 80
 Ser Thr Ala Ala Gly Gly Gly Pro Gly Cys Gly Gly Ala Lys Asp Arg
 85 90 95
 Ser Gly Ser Arg Trp
 100

<210> 160
 <211> 371
 <212> DNA
 <213> Vitis vinifera

<400> 160
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 gggagtcgtt cgaacaaaag gagccgcat ttccgggcac agccaccgcc ccaggtgcac 120
 gtccacggct tctggtgtac ctcccagaga atcaggtgat tcgaagctac acggaactgg 180
 agcagcgact gaaccaactg ggggtggagtc ggtaccacaa ctaccagcat cccagcctgg 240
 tccagttcca caagtccgac aactcttctc acctcctgtc cctccccaaa agctttgcca 300
 acttcaagtc ttttcacttt tacgatatcg tcgtcaagaa tcgatctttc tttgaagtcc 360

gcgaggcctg a

371

<210> 161
 <211> 123
 <212> PRT
 <213> Vitis vinifera

<400> 161

Met Ser Gly Val Trp Val Phe Asp Lys Asn Gly Val Ala Arg Leu Val
 1 5 10 15

Thr Asn Pro Thr Arg Glu Ser Phe Glu Gln Lys Glu Pro Pro Phe Pro
 20 25 30

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

Pro Glu Asn Gln Val Ile Arg Ser Tyr Thr Glu Leu Glu Gln Arg Leu
 50 55 60

Asn Gln Leu Gly Trp Ser Arg Tyr His Asn Tyr Gln His Pro Ser Leu
 65 70 75 80

Val Gln Phe His Lys Ser Asp Asn Ser Ser His Leu Leu Ser Leu Pro
 85 90 95

Lys Ser Phe Ala Asn Phe Lys Ser Phe His Phe Tyr Asp Ile Val Val
 100 105 110

Lys Asn Arg Ser Phe Phe Glu Val Arg Glu Ala
 115 120

<210> 162
 <211> 5
 <212> PRT
 <213> Artificial sequence

<220>
 <223> motif 1

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

<400> 162

Gly Val Trp Val Phe
 1 5

<210> 163
 <211> 7
 <212> PRT
 <213> Artificial sequence

<220>

<223> motif 2

<220>

<221> VARIANT

<222> (4)..(4)

<223> /replace = "Ser"

<220>

<221> VARIANT

<222> (7)..(7)

<223> /replace = "Phe"

<400> 163

Leu Gly Trp Glu Arg Tyr Tyr
1 5

<210> 164

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> motif 3

<220>

<221> VARIANT

<222> (1)..(1)

<223> /replace = "His"

<220>

<221> VARIANT

<222> (3)..(3)

<223> /replace = "Ile"

<220>

<221> VARIANT

<222> (5)..(5)

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

<220>

<221> VARIANT

<222> (7)..(7)

<223> /replace = "Lys" /replace = "Ala"

<220>

<221> VARIANT

<222> (8)..(8)

<223> /replace = "Asp"

<400> 164

Asp Leu Leu Ser Ile Pro Arg Ser Phe
1 5

<210> 165

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> motif 4

<220>

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

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

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

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

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

<400> 165

His Phe Tyr Asp Val Val Val Lys Asn Arg
 1 5 10

<210> 166
 <211> 2578
 <212> DNA
 <213> Artificial sequence

<220>
 <223> GOS2-RAA1-like expression cassette

<400> 166
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 aaatataaaa tgagacctta tatatgtagc gctgataact agaactatgc aagaaaaact 120
 catccaccta ctttagtggc aatcgggcta aataaaaaag agtcgctaca ctagtttcgt 180
 tttccttagt aattaagtgg gaaaatgaaa tcattattgc ttagaatata cgttcacatc 240
 tctgtcatga agttaatta ttcgaggtag ccataattgt catcaaactc ttcttgaata 300
 aaaaaatctt tctagctgaa ctcaatgggt aaagagagag atttttttta aaaaaataga 360
 atgaagatat tctgaacgta ttggcaaaga tttaaacata taattatata attttatagt 420
 ttgtgcattc gtcatatcgc acatcattaa ggacatgtct tactccatcc caatttttat 480
 ttagtaatta aagacaattg acttattttt attatttatc ttttttcgat tagatgcaag 540
 gtacttacgc acacactttg tgctcatgtg catgtgtgag tgcacctcct caatacacgt 600
 tcaactagca acacatctct aatatcactc gcctatttta tacatttagg tagcaatatc 660
 tgaattcaag cactccacca tcaccagacc acttttaata atatctaaaa taaaaaaat 720
 aatttttacag aatagcatga aaagtatgaa acgaactatt taggtttttc acatacaaaa 780
 aaaaaaagaa ttttgctcgt gcgcgagcgc caatctccca tattgggcac acaggcaaca 840
 acagagtggc tgcccacaga acaaccaca aaaaacgatg atctaacgga ggacagcaag 900

PF59082PF60142_PCT_SEQ_LIST.txt

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ggaggcatcc	aagccaagaa	gagggagagc	accaaggaca	cgcgactagc	agaagccgag	1080
cgaccgcctt	cttcgatcca	tatcttccgg	tcgagttctt	ggtcgatctc	ttccctcctc	1140
cacctcctcc	tcacagggta	tgtgcccttc	ggttggttctt	ggattttattg	ttctagggttg	1200
tgtagtacgg	gcgttgatgt	taggaaaggg	gatctgtatc	tgtgatgatt	cctggttcttg	1260
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ggttttcaat	cgtctggaga	gctctatgga	aatgaaatgg	tttaggggtac	ggaatcttgc	1380
gattttgtga	gtaccttttg	tttgaggtaa	aatcagagca	ccggtgattt	tgcttggtgt	1440
aataaaagta	cggttgtttg	gtcctcgatt	ctggtagtga	tgcttctcga	tttgacgaag	1500
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acatgtacga	catcgtcgtc	aagaaccgcg	actccttccg	cgtcgtcgac	gcctaaat	2578

<210> 167
 <211> 1515
 <212> DNA
 <213> Artificial sequence

<220>
 <223> HMGP-RAA1-like combination

<400> 167	
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tactccagta	cattatggaa
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gtatcagcaa	gagagaggca
cacaagttgt	agcagtagca
	120

PF59082PF60142_PCT_SEQ_LIST.txt

caggattaga	aaaacgggac	gacaaatagt	aatggaaaaa	caaaaaaaaa	caaggaaaca	180
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tagaaagcac	aggtagaag	cacaacgccc	tcgctctcca	ccctcccacc	caatcgcgac	420
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gccgctcttc	caccaggtc	cctctcgtaa	tccataatgg	cgtgtgtacc	ctcggctggt	660
tgtacgtggg	cggtttacc	tgggggtgtg	ggtggatgac	gggtgggccc	ggaggaggctc	720
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gaaaattcaa	attaggaggt	ggggggcggg	gcccttgag	aataagcgga	atcgcagata	840
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gactctcccc	aggtgaggtg	agaccagtct	ttttgctcga	ttcgacgcgc	ctttcacgcc	1080
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<210> 168
 <211> 353
 <212> DNA
 <213> Oryza sativa

<400> 168						
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tcgaattact	tcagtatcga	ggcgttctc	gtgctcgtct	tcctcaccat	gtcattgctc	180
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gtctgcctgc	tcacctgct	ggttggtgctg	gccttcatgc	caacggatgt	gcggagcatg	300
gcttctctt	acttgtaaat	acatctccta	ggggaattta	ttttgtttt	tga	353

<210> 169
 <211> 105
 <212> PRT
 <213> Oryza sativa

<400> 169

Met Glu Gly Val Gly Ala Arg Gln Arg Arg Asn Pro Leu Ile Pro Arg
 1 5 10 15

Pro Asn Gly Ser Lys Arg His Leu Gln His Gln His Gln Pro Asn Ala
 20 25 30

Ala Glu Lys Lys Thr Ala Ala Thr Ser Asn Tyr Phe Ser Ile Glu Ala
 35 40 45

Phe Leu Val Leu Val Phe Leu Thr Met Ser Leu Leu Ile Leu Pro Leu
 50 55 60

Val Leu Pro Pro Leu Pro Pro Pro Pro Ser Leu Leu Leu Leu Leu Pro
 65 70 75 80

Val Cys Leu Leu Ile Leu Leu Val Val Leu Ala Phe Met Pro Thr Asp
 85 90 95

Val Arg Ser Met Ala Ser Ser Tyr Leu
 100 105

<210> 170
 <211> 56
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: prm08170

<400> 170
 ggggacaagt ttgtacaaaa aagcaggctt aaacaatgga aggtgtaggt gctagg 56

<210> 171
 <211> 51
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: prm08171

<400> 171
 ggggaccact ttgtacaaga aagctgggtc aaaaacaaaa ataaattccc c 51

<210> 172
 <211> 2193
 <212> DNA
 <213> Oryza sativa

<400> 172
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aaatataaaa tgagacctta tatatgtagc gctgataact agaactatgc aagaaaaact 120

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tctgtcatga agttaatta ttcgaggtag ccataattgt catcaaactc ttcttgaata	300
aaaaaatctt tctagctgaa ctcaatgggt aaagagagag atttttttta aaaaaataga	360
atgaagatat tctgaacgta ttggcaaaga tttaaacata taattatata attttatagt	420
ttgtgcattc gtcatatcgc acatcattaa ggacatgtct tactccatcc caatttttat	480
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gtacttacgc acacactttg tgctcatgtg catgtgtgag tgcacctcct caatacacgt	600
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aattttacag aatagcatga aaagtatgaa acgaactatt taggtttttc acatacaaaa	780
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tccgcaacaa ctttttaaca gcaggctttg cggccaggag agaggaggag aggcaagaa	960
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tgtagtacgg gcgttgatgt taggaaaggg gatctgtatc tgtgatgatt cctgttcttg	1260
gatttgggat agaggggttc ttgatgttgc atgttatcgg ttcggtttga ttagtagtat	1320
ggttttcaat cgtctggaga gctctatgga aatgaaatgg tttagggtac ggaatcttgc	1380
gattttgtga gtaccttttg tttgaggtaa aatcagagca ccggtgattt tgcttggtgt	1440
aataaaaagta cggttgtttg gtcctcgatt ctggtagtga tgcttctcga tttgacgaag	1500
ctatcctttg tttattccct attgaacaaa aataatccaa ctttgaagac ggtcccgttg	1560
atgagattga atgattgatt cttaagcctg tccaaaattt cgcagctggc ttgttttagat	1620
acagtagtcc ccatcacgaa attcatggaa acagttataa tcctcaggaa caggggattc	1680
cctgttcttc cgatttgctt tagtcccaga attttttttc ccaaatatct taaaaagtca	1740
ctttctggtt cagttcaatg aattgattgc taaaaataat gcttttatag cgttatccta	1800
gctgtagttc agttaatagg taatacccct atagtttagt caggagaaga acttatccga	1860
tttctgatct ccatttttaa ttatatgaaa tgaactgtag cataagcagt attcatttgg	1920
attatttttt ttattagctc tcacccttc attattctga gctgaaagtc tggcatgaac	1980
tgtcctcaat tttgttttca aattcacatc gattatctat gcattatcct cttgtatcta	2040
cctgtagaag tttctttttg gttattcctt gactgcttga ttacagaaag aaatttatga	2100
agctgtaatc gggatagtta tactgcttgt tcttatgatt catttccttt gtgcagttct	2160
tggtgtagct tgccactttc accagcaaag ttc	2193

<210> 173
 <211> 3
 <212> PRT
 <213> Artificial sequence

<220>
 <223> conserved motif 1a

<400> 173

Tyr Phe Ser
 1

<210> 174
 <211> 3
 <212> PRT
 <213> Artificial sequence

<220>
 <223> conserved motif 1b

<400> 174

Tyr Phe Thr
 1

<210> 175
 <211> 3
 <212> PRT
 <213> Artificial sequence

<220>
 <223> conserved motif 1c

<400> 175

Tyr Phe Gly
 1

<210> 176
 <211> 3
 <212> PRT
 <213> Artificial sequence

<220>
 <223> conserved motif 1d

<400> 176

Tyr Leu Gly
 1

<210> 177
 <211> 7
 <212> PRT
 <213> Artificial sequence

<220>
 <223> conserved motif 2

<220>
 <221> VARIANT

<222> (1)..(1)
 <223> /replace = "Ala" /replace = "Ile"

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

<400> 177

Val Leu Ala Phe Met Pro Thr
 1 5

<210> 178
 <211> 3
 <212> PRT
 <213> Artificial sequence

<220>
 <223> conserved motif 3

<220>
 <221> VARIANT
 <222> (1)..(1)
 <223> /replace = "Ala" conserved motif 1aIle"

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

<400> 178

Ser Tyr Leu
 1

<210> 179
 <211> 178
 <212> PRT
 <213> Oryza sativa

<400> 179

Met Tyr Leu Leu Ser Pro Arg Asn Gly Asp Glu Glu Asp Glu Gln Glu
 1 5 10 15

Glu Ile Gln Glu Leu Ile Ser Asp Asp Glu Pro Pro Asn Leu Lys Leu
 20 25 30

Ala Ser Cys Ala Thr Ala Ala Ser Ser Ser Ser Ser Gly Ser Asp
 35 40 45

Met Glu Lys Gly Arg Gly Lys Ala Cys Gly Gly Gly Ser Thr Ala Pro
 50 55 60

Pro Pro Pro Pro Pro Ser Ser Ser Gly Lys Ser Gly Gly Gly Gly Gly
 65 70 75 80

Ser Asn Ile Arg Glu Ala Ala Ala Ser Gly Gly Gly Gly Gly Val Trp
 85 90 95

PF59082PF60142_PCT_SEQ_LIST.txt

Gly Lys Tyr Phe Ser Val Glu Ser Leu Leu Leu Leu Val Cys Val Thr
100 105 110

Ala Ser Leu Val Ile Leu Pro Leu Val Leu Pro Pro Leu Pro Pro Pro
115 120 125

Pro Ser Met Leu Met Leu Val Pro Val Ala Met Leu Val Leu Leu Leu
130 135 140

Ala Leu Ala Phe Met Pro Thr Thr Thr Ser Ser Ser Ser Ala Gly
145 150 155 160

Gly Gly Gly Gly Gly Gly Arg Asn Gly Ala Thr Thr Gly His Ala Pro
165 170 175

Tyr Leu

<210> 180
<211> 126
<212> PRT
<213> Oryza sativa

<400> 180

Met Leu Leu Glu His Leu Met Ile Thr Met Glu Glu Gln Met Phe Arg
1 5 10 15

Glu Gln Gln Met Gln Arg Gly Gly Arg His His Gln His His Thr Thr
20 25 30

Arg Glu Gln Glu Gln Gln Gln Lys Gln Gln Gln Arg Arg Arg Leu Met
35 40 45

Asn Asn Ala Thr Asn Gly Gly Gly Gly Asp Gly Gly Ser Arg Cys Tyr
50 55 60

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

Leu Val Leu Pro Leu Ile Leu Pro Pro Leu Pro Pro Pro Pro Thr Leu
85 90 95

Leu Leu Leu Leu Pro Val Cys Leu Leu Ala Leu Leu Val Val Leu Ala
100 105 110

Phe Met Pro Thr Asp Met Arg Thr Met Ala Ser Ser Tyr Leu
115 120 125

<210> 181
<211> 105
<212> PRT
<213> Zea mays

<220>
 <221> UNSURE
 <222> (65)..(75)
 <223> Xaa can be any naturally occuring amino acid

<400> 181

```

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

<210> 182
 <211> 110
 <212> PRT
 <213> Triticum aestivum

<400> 182

```

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


<210> 183
 <211> 110
 <212> PRT
 <213> Hordeum vulgare

<400> 183

```

Met Asp Ser Gln Phe Gly Ala Met Asp Arg Gly Gly Ser Arg Gln Arg
1          5          10          15

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

Gln Gln Arg Ala Asn Ala Ala Asp Lys Lys Val Val Ile Pro Asn Tyr
          35          40          45

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

Leu Ile Leu Pro Leu Val Leu Pro Pro Leu Pro Pro Pro Pro Ser Leu
65          70          75          80

Leu Leu Leu Leu Pro Val Cys Leu Leu Ile Leu Leu Met Val Leu Ala
          85          90          95

Phe Met Pro Thr Asp Val Arg Ser Met Ala Thr Ser Tyr Leu
          100          105          110
    
```

<210> 184
 <211> 99
 <212> PRT
 <213> Saccharum officinarum

<220>
 <221> UNSURE
 <222> (62)..(62)
 <223> Xaa can be any naturally occuring amino acid

<400> 184

```

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

His Leu Gln Gln Arg Gln Gln Glu Ala Asp Phe Leu Asp Lys Lys Val
          20          25          30

Ile Ala Ser Thr Tyr Phe Ser Ile Glu Ala Phe Leu Val Leu Ala Cys
          35          40          45

Leu Thr Val Ser Leu Leu Ile Leu Pro Leu Val Leu Pro Xaa Leu Pro
          50          55          60

Ala Pro Ala Ser Leu Leu Leu Trp Leu Pro Val Trp Leu Leu Glu Leu
65          70          75          80
    
```

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Ile Val Leu Ala Phe Met Pro Thr Asp Val Arg Ser Met Ala Ser
85 90 95

Ser Tyr Leu

<210> 185
<211> 99
<212> PRT
<213> Saccharum officinarum

<400> 185

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

His Leu Gln Gln Arg Gln Gln Glu Ala Asp Phe Leu Asp Lys Lys Val
20 25 30

Ile Ala Ser Thr Tyr Phe Ser Ile Glu Ala Phe Leu Val Leu Ala Cys
35 40 45

Leu Thr Val Ser Leu Leu Ile Leu Pro Leu Val Leu Pro Pro Leu Pro
50 55 60

Pro Pro Pro Ser Leu Leu Leu Trp Leu Pro Val Cys Leu Leu Ile Leu
65 70 75 80

Leu Ile Val Leu Ala Phe Met Pro Thr Asp Val Arg Ser Met Ala Ser
85 90 95

Ser Tyr Leu

<210> 186
<211> 107
<212> PRT
<213> Sorghum bicolor

<400> 186

Met Ala Ser Arg Ser Ser Ala Leu Glu Gly Gly Gly Ala Ala Ile Gln
1 5 10 15

Arg Arg Asn Asn Ala Val Lys Arg His Leu Gln Gln Arg Gln Gln Glu
20 25 30

Ala Asp Phe His Asp Lys Lys Val Ile Ala Ser Thr Tyr Phe Ser Ile
35 40 45

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

Pro Leu Val Leu Pro Pro Leu Pro Pro Pro Ser Leu Leu Leu Trp
65 70 75 80

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Pro Val Cys Leu Leu Val Leu Leu Val Val Leu Ala Phe Met Pro
85 90 95

Thr Asp Val Arg Ser Val Ala Ala Ser Tyr Leu
100 105

<210> 187
<211> 130
<212> PRT
<213> Arabidopsis thaliana

<400> 187

Met Ile Arg Glu Ile Ser Asn Leu Gln Lys Asp Ile Ile Asn Ile Gln
1 5 10 15

Asp Ser Tyr Ser Asn Asn Arg Val Met Asp Val Gly Arg Asn Asn Arg
20 25 30

Lys Asn Met Ser Phe Arg Ser Ser Pro Glu Lys Ser Lys Gln Glu Leu
35 40 45

Arg Arg Ser Phe Ser Ala Gln Lys Arg Met Met Ile Pro Ala Asn Tyr
50 55 60

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

Leu Ile Leu Pro Leu Val Leu Pro Pro Leu Pro Pro Pro Pro Phe Met
85 90 95

Leu Leu Leu Val Pro Ile Gly Ile Met Val Leu Leu Val Val Leu Ala
100 105 110

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

Phe Met
130

<210> 188
<211> 135
<212> PRT
<213> Arabidopsis thaliana

<400> 188

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

Glu His Tyr Ser Leu Asn Asn Asn Met Asp Val Arg Gly Asp His Asn
20 25 30

Arg Lys Asn Thr Ser Phe Arg Gly Ser Ala Pro Ala Pro Ile Met Gly
Seite 175

35

40

45

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

Leu Ile Ser Ala Ser Tyr Phe Ser Leu Glu Ser Met Val Val Leu Val
 65 70 75 80

Gly Leu Thr Ala Ser Leu Leu Ile Leu Pro Leu Ile Leu Pro Pro Leu
 85 90 95

Pro Pro Pro Pro Phe Met Leu Leu Leu Ile Pro Ile Gly Ile Met Val
 100 105 110

Leu Leu Met Val Leu Ala Phe Met Pro Ser Ser Asn Ser Lys His Val
 115 120 125

Ser Ser Ser Ser Thr Phe Met
 130 135

<210> 189
 <211> 139
 <212> PRT
 <213> Vitis vinifera

<400> 189

Met Ser Ile Glu Gln Pro Glu Ala Asp Ser Arg Leu Ser Glu Gly Pro
 1 5 10 15

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

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

Pro Pro Met Ala Glu Gly Lys Lys Met Glu Tyr Asn Arg Thr Pro Leu
 50 55 60

Ser Arg Glu Asn Ser Arg Arg Leu Ile Pro Ala Ser Tyr Phe Ser Leu
 65 70 75 80

Glu Ser Leu Leu Leu Leu Ile Cys Leu Thr Ala Ser Leu Leu Ile Leu
 85 90 95

Pro Leu Ile Leu Pro Pro Leu Pro Pro Pro Phe Met Leu Leu Leu
 100 105 110

Leu Pro Ile Gly Ile Leu Ala Val Leu Met Ile Leu Ala Phe Met Pro
 115 120 125

Ser Asn Val Arg Asp Leu Thr Tyr Thr Tyr Val
 130 135

PF59082PF60142_PCT_SEQ_LIST.txt

<210> 190
 <211> 126
 <212> PRT
 <213> Citrus reticulata

<220>
 <221> UNSURE
 <222> (103)..(103)
 <223> Xaa can be any naturally occuring amino acid
 <400> 190

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Met Asn Ser Asp Asn Ser Glu Ser Arg Gln Arg Leu Ser Lys Gly Ile
 1          5          10          15

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

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

Arg Ser Tyr Ser Gln Gly Ala Ser Arg Lys Leu Phe Ser Ala Ser Tyr
 50          55          60

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

Leu Ile Leu Pro Leu Val Leu Pro Pro Leu Pro Pro Pro Pro Phe Leu
      85          90          95

Leu Leu Leu Val Pro Ile Xaa Ile Leu Ala Val Leu Leu Val Leu Ala
100          105          110

Phe Met Pro Ser Asn Val Arg Asp Ile Thr Ser Thr Tyr Val
115          120          125
```

<210> 191
 <211> 118
 <212> PRT
 <213> Lycopersicon esculentum

<400> 191

```
Met Asn Met Asp Met Glu Ser Ser Glu Ala Lys Leu Arg Ser Ser Lys
 1          5          10          15

Gly Phe Ile Asn Leu Glu Glu His Gln Gln Tyr Phe Asn Asn Ile Met
      20          25          30

Glu Gly Asn Lys Met Glu His Lys Arg Ser Phe Thr Gln Gly His Gly
      35          40          45

Lys Lys Met Leu Ser Met Asn Tyr Phe Ser Leu Glu Ser Ile Ile Leu
50          55          60
```

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Leu Gly Leu Thr Ala Ser Leu Leu Leu Leu Pro Leu Met Leu Pro
65 70 75 80

Pro Leu Pro Pro Pro Phe Met Leu Leu Leu Val Pro Ile Phe Ile
85 90 95

Leu Val Val Leu Met Ile Leu Ala Phe Met Pro Ser Asn Val Arg Asn
100 105 110

Val Thr Cys Ser Tyr Leu
115

<210> 192
<211> 87
<212> PRT
<213> Lycopersicon esculentum
<400> 192

Met Glu Gly Asn Lys Met Glu His Lys Arg Ser Phe Thr Gln Gly His
1 5 10 15

Gly Lys Lys Met Leu Ser Met Asn Tyr Phe Ser Leu Glu Ser Ile Ile
20 25 30

Leu Leu Leu Gly Leu Thr Ala Ser Leu Leu Leu Leu Pro Leu Met Leu
35 40 45

Pro Pro Leu Pro Pro Pro Pro Phe Met Leu Leu Leu Val Pro Ile Phe
50 55 60

Ile Leu Val Val Leu Met Ile Leu Ala Phe Met Pro Ser Asn Val Arg
65 70 75 80

Asn Val Thr Cys Ser Tyr Leu
85

<210> 193
<211> 106
<212> PRT
<213> Arabidopsis thaliana
<400> 193

Met Asp Val Gly Arg Asn Asn Arg Lys Asn Met Ser Phe Arg Ser Ser
1 5 10 15

Pro Glu Lys Ser Lys Gln Glu Leu Arg Arg Ser Phe Ser Ala Gln Lys
20 25 30

Arg Met Met Ile Pro Ala Asn Tyr Phe Ser Leu Glu Ser Leu Phe Leu
35 40 45

Leu Val Gly Leu Thr Ala Ser Leu Leu Ile Leu Pro Leu Val Leu Pro
50 55 60

PF59082PF60142_PCT_SEQ_LIST.txt

Pro Leu Pro Pro Pro Pro Phe Met Leu Leu Leu Val Pro Ile Gly Ile
65 70 75 80

Met Val Leu Leu Val Val Leu Ala Phe Met Pro Ser Ser His Ser Asn
85 90 95

Ala Asn Thr Asp Val Thr Cys Asn Phe Met
100 105

<210> 194
<211> 537
<212> PRT
<213> Oryza sativa

<400> 194

Ala Thr Gly Thr Ala Cys Thr Thr Gly Thr Thr Gly Ala Gly Cys Cys
1 5 10 15

Cys Ala Ala Gly Ala Ala Ala Thr Gly Gly Cys Gly Ala Cys Gly Ala
20 25 30

Gly Gly Ala Gly Gly Ala Cys Gly Ala Ala Cys Ala Gly Gly Ala Gly
35 40 45

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

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

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

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

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

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

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

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

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

Cys Cys Gly Cys Cys Gly Cys Cys Gly Cys Cys Gly Cys Cys Gly Thr
Seite 179

195

200

205

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

Cys Gly Gly Cys Gly Gly Cys Gly Gly Cys Gly Gly Cys Gly Gly Cys
 225 230 235 240

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

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

Cys Gly Gly Cys Gly Gly Cys Gly Gly Cys Gly Thr Gly Thr Gly Gly
 275 280 285

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

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

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

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

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

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

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

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

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

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

Cys Gly Ala Cys Gly Ala Cys Gly Ala Cys Gly Thr Cys Gly Thr Cys
 450 455 460

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

Gly Gly Cys Gly Gly Cys Gly Gly Cys Gly Gly Cys Gly Gly Cys Gly
485 490 495

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

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

Thr Ala Cys Thr Thr Gly Thr Ala Gly
530 535

<210>	195
<211>	538
<212>	DNA
<213>	Zea mays

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<220>
<221> misc_feature
<222> (177)..(208)
<223> n is a, c, g, or t
```

```
<220>
<221> misc_feature
<222> (493)..(493)
<223> n is a, c, g, or t
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<400>	195						
ttcacattac	actcatgact	cgtcttagga	cgaatcctgc	agctgcaaaa	cacagaaaat		60
ctggccaaga	cctattttatc	tattttacagg	taagaggagg	ccatgctgcg	cacatctgtc		120
ggcatgaagg	ccagtacaac	cagcaagacg	agcaggcaga	ccggcagcca	cagcagnnnn		180
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnncc	agcggcagta	tcagcagcga	gacggtgagg		240
caggcgagca	cgaggaatgc	cccgatgctg	aagtaggtgg	acgcgatgac	cttcttgtcg		300
aggaaatccg	cctcctgctg	acgctgctgc	agatgccgct	tcacggcatt	cctcctttgt		360
attgccgccc	ctccttccat	cgcgctagat	cggcttgcca	tgtgttcttt	ggtgtaggcg		420
gaggtggaga	ccagtcgcag	tgagtggttg	ccaaagtaag	caagaagtga	aaggcggtgt		480
agaaccgcct	tgngttttct	gaacgttttg	taatcagatc	tgagctcggg	tggtcgaa		538

```
<210> 196
<211> 578
<212> DNA
<213> Vitis vinifera
```

<400>	196						
tactttgaac	cggttggaac	ttggtgaccg	gtaaaggaga	aatttaaagt	agtattgagc		60
agcctgaagc	agattcaaga	ctgtctgaag	gacctttgat	caatctgcaa	gatcgatatt		120
tgagtggcat	catggaagcg	agaggaagga	ggaactctgc	tcctctgcaa	gttgagagga		180
aaaaccctac	tcctcctatg	gccgaaggaa	agaagatgga	atataataga	actcccctct		240
cacgagagaa	cagcaggaga	ctgatccag	caagctat	ttt cagcttgag	tcattgcttt		300

PF59082PF60142_PCT_SEQ_LIST.txt

tgctcatctg tctcacggct tcattgctga tccttcccct gatactacca ccattgccac	360
cccctccttt catgctgctt ctgctcccca ttggcattct agcagtgcctt atgatcttgg	420
ctttcatgcc ttctaattgc agagatttga cttatacata tgtgtaaattg gtgggtgttca	480
aaagtgcacc tcttctcatc atacaatttt tgttatttgg cttgatattc agatgaaaat	540
cagttatttt atttcttgat taaaaaaaaa aaaaaaaa	578

<210> 197
 <211> 704
 <212> DNA
 <213> Citrus reticulata

<220>
 <221> misc_feature
 <222> (619)..(619)
 <223> n is a, c, g, or t

<400> 197	
agggtttctt caaagatagg tagccatttg cacatttgaa tctgcttggt ggatattgtc	60
aaggaggctg ttggaattag gccacatttc agaatctgggt ttcattcctgg atcgctgggc	120
atttgaaggc attttgtgat catcgctgtt taaaatttgg ccgcatatta gaatctgggt	180
tctcatcggg tttccgtaca ttacatttga ccacatttgg atatctgggt tgagctgcat	240
tttagccttc gtatttaaaa ggacttgatc taatctgggg tcttggtgag ccggggcaac	300
tgatcatagt aaatgaattc tgataattct gagtcgagac agagactatc aaagggcatt	360
ataaacttgc aagatcgata tccgaccagc attatggatc gtgggtgtaag aaaaattgca	420
actcctccgg tcgagaagag gaaagttgag tatcaccgaa gttactcgca aggggcatcc	480
agaaaactgt tttcggcaag ctatttcacc ctggaatcat tgcttttgct cgtatgtctg	540
acggcctcat tgctgatcct gccattgggt cttccgccct tgccgcccc gccattcctg	600
ctgcttctgg ttctatang tattctagcc gtgcttttgg tcttggcatt catgccttct	660
aatgtaagag atataacttc cacgtacgtg taaatggtgt tgct	704

<210> 198
 <211> 382
 <212> DNA
 <213> Lycopersicon esculentum

<400> 198	
gaaaaaaaaatg tatttaataca ttatgtaaaa aacaagtga tctactttga tattttcttc	60
taaattaaac cacacaatta aagatatgag caagtcacat tcctaacatt agaaggcata	120
aaagctaaga tcataagaac aacaagaatg aaaattggga ctaacaacaa cataaaagggt	180
ggtggtggca atggtggaag catcaatggc aaaagtaaca aagatgctgt aagaccaagt	240
aacaaaataa ttgactctaa gctaaaataa ttcatgaca acattttctt gccatgtcct	300
tgtgtaaattg atctcttatg ctccatctta ttgccttcca taatgttggt gaaatattgt	360
tgatgttcct ccaaattaat aa	382

PF59082PF60142_PCT_SEQ_LIST.txt

<210> 199
<211> 624
<212> DNA
<213> Lycopersicon esculentum

<400> 199
tttgttaaag attggcacat tttcaagttc agtattcatt cgatttttga tatctacata 60
aaaaaaaaagt gtcctggtac tactcaatat tcctcagaac gacttcatat tcagggtctcg 120
aattcaaaac ctcacatcaa gattccttagg aaatttcaag attggttgaa aaactcatat 180
ccttctctaa gtttcaagat tggttccaaa ttaaaactcg agacttctga gtaagagcgt 240
acgactagta atgaacatgg acatggaatc atcagaggca aaattgagat catcaaaagg 300
gtttattaat ttggagggaac atcaacaata tttcaacaac attatggaag gcaataagat 360
ggagcataag agatcattta cacaaggaca tggcaagaaa atgttgtcaa tgaattatatt 420
tagcttagag tcaattatatt tgttacttgg tcttacagca tctttgttac ttttgccatt 480
gatgcttcca ccattgccac caccaccttt tatgttgttg ttagtcccaa ttttcattct 540
tggtgttctt atgatcttag cttttatgcc ttctaattgtt aggaatgtga cttgctcata 600
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<213> Medicago sativa

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

Tyr Ser Ser Ser Ser Ser Gly Ile Ala Asn Ser Lys Arg
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<212> PRT
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<400> 202

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Val Leu Pro Leu Val Met Pro Pro Leu Pro Pro Pro Pro Leu Leu Leu
35 40 45

Leu Leu Val Pro Val Phe Ile Met Leu Leu Leu Phe Phe Ile Ala Phe
50 55 60

Ser Pro Ser Lys Lys Val Pro Asn Lys Ala Ser Phe Val Ser
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cgtgactgat ctccacgcac accaaagaac acaacacgtg gcaacccgat ctagcgcgat	180
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 <211> 1104
 <212> DNA
 <213> Oryza sativa

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 <212> PRT
 <213> Oryza sativa

<400> 213
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 Gly Lys Asp Lys Gln Thr His Arg Ala Ala Thr Ala Ala Lys Glu Ala
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 115 120 125
 Ser Leu Asn Arg Glu Asn Ser Pro Ser Ser Pro Asn Gly Leu Ser Ala
 130 135 140
 Thr Ser Ser Ser Ser Ser Arg Thr Val Ser Arg Pro Ser His Arg Ala
 145 150 155 160
 Ala Ser Arg Ile Arg Lys Ala Asp Glu Gly Ala Asn Ala Gly Ala Val
 165 170 175
 Asn Val Arg Arg Asp Ser Ser Gly Asp Thr Arg Arg Asn Ser Asp Arg
 180 185 190
 Asp Val Asp Asp Phe Leu Leu Val Glu Gln Ala Ala Arg Asp Ser Thr
 195 200 205
 Glu Gly Phe Ile Ser Gly Phe Leu Ala Arg Tyr Arg Ser Asn His Gln
 210 215 220
 Gly Leu Leu Ser Ser Leu Asp Asp Ser Ile Glu Asp Ala Asn Gly Tyr
 225 230 235 240
 Trp Arg Phe Asn Met Glu Gly Ser Glu Glu Leu Glu Asn Tyr Phe Ile
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 Phe Asn Asp Arg Tyr Arg Gly Met Arg Met Asp Ile Asp Gly Met Ser
 260 265 270
 Tyr Glu Glu Leu Leu Ala Leu Gly Asp Arg Ile Gly Thr Val Ser Thr
 275 280 285
 Gly Leu Ser Glu Asp Ala Leu Ser Lys Cys Leu Asp Arg Ser Met Tyr
 290 295 300
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 305 310 315 320
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 325 330 335

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 <212> DNA
 <213> Oryza sativa

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 gcttccccgaa taaggaaggc agatgaagggt gcaaatgcag gagctgtaaa tgtacgcaga 540
 gacagcagtg gagataccag gaggaattca gatagggatg tcgatgattt cttgctagtt 600
 gagcaggcag caagagatag cactgaagga ttcatatctg gattccttggc aagatacaga 660
 agtaatcatc agggactact ttcattctttg gacgacagca tagaggatgc aaatgggtac 720
 tggcgccttca atatggaagg aagtgaagag cttgagaact acttcatatt caatgatcgg 780
 tacagaggga tgagaatgga cattgacggc atgtcttatg aggaattgct agcattggga 840
 gatagaattg gcaccgtaag cactggcctt tcagaagacg cgctgtccaa gtgtctagac 900
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 atatgccagg caagaatatt cagatggtga 990

<210> 215
 <211> 329
 <212> PRT
 <213> Oryza sativa

<400> 215
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Lys Gly Gly Ser Ile Leu Leu Phe Arg Glu Asp Ser Ala Arg His Lys
 20 25 30

Ala Thr Asn Cys Cys Thr Arg His Gly Cys Ser Ser Lys His Leu Ala
 35 40 45

Gly Lys Asp Lys Gln Thr His Arg Ala Ala Thr Ala Ala Lys Glu Ala
 Seite 192

50

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

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

Ser Ser Tyr Ser Glu Asn Asp Asn Arg Pro Arg Glu Thr Pro Gly Arg
100 105 110

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

Ser Leu Asn Arg Glu Asn Ser Pro Ser Ser Pro Asn Gly Leu Ser Ala
130 135 140

Thr Ser Ser Ser Ser Ser Arg Thr Val Ser Arg Pro Ser His Arg Ala
145 150 155 160

Ala Ser Arg Ile Arg Lys Ala Asp Glu Gly Ala Asn Ala Gly Ala Val
165 170 175

Asn Val Arg Arg Asp Ser Ser Gly Asp Thr Arg Arg Asn Ser Asp Arg
180 185 190

Asp Val Asp Asp Phe Leu Leu Val Glu Gln Ala Ala Arg Asp Ser Thr
195 200 205

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

Gly Leu Leu Ser Ser Leu Asp Asp Ser Ile Glu Asp Ala Asn Gly Tyr
225 230 235 240

Trp Arg Phe Asn Met Glu Gly Ser Glu Glu Leu Glu Asn Tyr Phe Ile
245 250 255

Phe Asn Asp Arg Tyr Arg Gly Met Arg Met Asp Ile Asp Gly Met Ser
260 265 270

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

Gly Leu Ser Glu Asp Ala Leu Ser Lys Cys Leu Asp Arg Ser Met Tyr
290 295 300

Met Ala Thr Thr Ser Gly Thr His Glu Asp Cys Glu Arg Lys Cys Ser
305 310 315 320

Ile Cys Gln Ala Arg Ile Phe Arg Trp
325

PF59082PF60142_PCT_SEQ_LIST.txt

<210> 216
<211> 1743
<212> DNA
<213> Oryza sativa

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ggaatcacca caagactcaa tccgatgaaa accaggctgt ctgataatca ggagagacca      180
agatacctac gtgactcatt cagatcttca acctcaatgg ccattcatgg aagctcttcc      240
aaagtccgc ttaggaaatt cggtgacgaa aaacgaaggc aaacgttggt ggcaggggta      300
gacattgctg aaagtagcag cagaaatgct gggggcaaac atctggaggg tagtaataag      360
agaatcgttg tcgatgatag gagttcagat gttctgcata ctgaaacaga aggccttggt      420
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gatatttctg aacatgcagt tgaatccttg gtaaggagtg ctgctccaag ttctagaacc      540
cgtagacaga aggacaaaga attgaatttg ggtcaatcag gagtttgctc ttcgtcatgt      600
actaacaggc ctactatc aagatatgct cctgccgatg tgaagcgacc gtgtaatcat      660
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gaagaagttg gacggctggg atgtgagcat cagtaccatg tgtgctgcat tcaccagtgg     1680
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taa                                                                    1743

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<210> 217
 <211> 580
 <212> PRT
 <213> Oryza sativa

<400> 217

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 1 5 10 15

Arg Arg Gly Gly Gly Phe Ser Ser Arg Asn Gln Ser Thr Glu Glu Arg
 20 25 30

Thr Ile Gln Asn Tyr Asp Gly Pro Gly Ile Thr Thr Arg Leu Asn Pro
 35 40 45

Met Lys Thr Arg Leu Ser Asp Asn Gln Glu Arg Pro Arg Tyr Leu Arg
 50 55 60

Asp Ser Phe Arg Ser Ser Thr Ser Met Ala Ile His Gly Ser Ser Ser
 65 70 75 80

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

Leu Ala Gly Val Asp Ile Ala Glu Ser Ser Ser Arg Asn Ala Gly Gly
 100 105 110

Lys His Leu Glu Gly Ser Asn Lys Arg Ile Val Val Asp Asp Arg Ser
 115 120 125

Ser Asp Val Leu His Thr Glu Thr Glu Gly Leu Ala Thr Glu Gln Asp
 130 135 140

Gln Leu Ile Ala Pro Asn Ala Gly Val Ser Asp Ser Ala Ser Ser Ser
 145 150 155 160

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

Ser Ser Arg Thr Arg Arg Gln Lys Asp Lys Glu Leu Asn Leu Gly Gln
 180 185 190

Ser Gly Val Cys Ser Ser Ser Cys Thr Asn Arg Pro Thr Ile Ser Arg
 195 200 205

Tyr Ala Pro Ala Asp Val Lys Arg Pro Cys Asn His Ala Ser Gly Val
 210 215 220

Gln Gln His Gly His Asn Asn Leu Asp Cys Thr Ser Val Pro Asn Phe
 225 230 235 240

Leu Pro Ser Gly Cys Ser Ser Gly Ser Val Tyr Ser Arg Arg Phe Asp
 245 250 255

PF59082PF60142_PCT_SEQ_LIST.txt

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

Gly Leu Ser Gly Thr Ala Ser Leu Asp Asp Ser Pro Pro Ala Tyr Pro
275 280 285

Ala Ile Ala Gly Pro Arg Ile Arg Thr Thr Thr Thr Glu Arg Ala Ser
290 295 300

Gln Gln Asn Ala Leu Arg Ser Arg Arg Asn Phe Gln Asp Ser Ala Val
305 310 315 320

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

Glu Glu Arg Glu Asp Gly Met Ile Ser Gln Arg Asp Ser Ser Ile Gly
340 345 350

Asn Gln Gln Ser Asp Gln Val His Ser Ser Ser Glu Glu Ala Ser Thr
355 360 365

Glu Ser Ser Ser Arg Pro Phe Ser Ala Glu Leu Pro His Ala Ile Tyr
370 375 380

Ser Ser Arg Gly Glu Gly Ser Asn Ala Phe Thr Ala Arg Arg Arg Arg
385 390 395 400

Ser Ser Ser Leu Tyr Glu Glu Arg Pro Pro Gln Thr Phe His Asp Leu
405 410 415

Phe Arg Glu Arg Asn Gly Arg Arg His Ile Ser Ile Glu Gly Ile Ala
420 425 430

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

Tyr Glu Gln Leu Met Val Leu Glu Thr Asn Ile Leu Leu Gly Ala Phe
450 455 460

Thr Ser His Asp Gln His Ser Asp Met Arg Met Asp Ile Asp Asn Met
465 470 475 480

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

Thr Ala Leu Ser Glu Glu Gln Phe Val Lys Cys Leu Arg Arg Ser Ile
500 505 510

Tyr Ile Pro Val Ala Thr Lys Ala Asn Ala Gln Val Val Asp Asp Ile
515 520 525

PF59082PF60142_PCT_SEQ_LIST.txt

Lys Cys Ser Ile Cys Gln Glu Glu Tyr Ile Glu Gly Glu Glu Val Gly
530 535 540

Arg Leu Gly Cys Glu His Gln Tyr His Val Cys Cys Ile His Gln Trp
545 550 555 560

Leu Arg Gln Lys Asn Trp Cys Pro Ile Cys Lys Ala Ser Ala Glu Pro
565 570 575

Ser Thr Val Ser
580

<210> 218
<211> 2130
<212> DNA
<213> Oryza sativa

<400> 218
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PF59082PF60142_PCT_SEQ_LIST.txt

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ccatgctgta ttgcccagga agaatatgcc gaaggtgagg acatgggcag actagactgt 2040
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<210> 219
<211> 709
<212> PRT
<213> Oryza sativa

<400> 219

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20 25 30

Pro Ser Asn Pro Thr Ala Asp Glu Gln Asn Leu Leu Pro Asn Thr Leu
35 40 45

Glu Asp Asp Asp Tyr Pro His Tyr Leu Leu Gly Ser His Glu Val Glu
50 55 60

Met Pro Asn Gly Ser Val Ile Gly Gln Gln Asn Thr Ser Leu Asn Leu
65 70 75 80

Trp Asp Ser Ala Gly Ser Ser Ser Met Gly Cys Val Ala Asp His Asp
85 90 95

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

Arg Ala Pro Leu Ile Ile Gly Gly Arg Arg His Glu Gly Ser Ser Ser
115 120 125

Leu Pro Ser Gln Ser Leu Asn Leu Asp Leu Asn Leu Asn Gln Ala Asp
130 135 140

PF59082PF60142_PCT_SEQ_LIST.txt

Gln Phe Asp Ser Glu Asp Val Asp Met Ile Gln Ser Asn Gly Gln Pro
145 150 155 160

Gly Ile Asn Ala Phe Pro Leu Asn Arg Gly Leu Ser Ile Pro Glu His
165 170 175

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

Val Ala Ser Phe Ser Asp Gly Met Thr Gly Gln Glu Val Asn Leu Phe
195 200 205

Gly Gly His Arg Ser Ser Cys Lys Arg Lys Asn Ile Asp Gly Ser Leu
210 215 220

Ala Glu Ser Ser Ala Asn Gly Ser Ser Arg Asn Asn Gln Arg Asn Asn
225 230 235 240

Ile Ile Leu Glu Pro Ser Pro Ser Ser His Glu Ser Thr Ser Gly Leu
245 250 255

Thr Ala Pro Ala Pro Thr Asn His Val Phe Ser Tyr Ser Pro Val Glu
260 265 270

Gln Leu Asn Gln Asn Thr Asn Met Ser Ala Asn Ala Met Leu Ser Asp
275 280 285

His Tyr Ser Leu Tyr Gly Asp His Glu Arg Glu Arg Phe Leu Arg Asn
290 295 300

Thr Arg Met Arg Thr Ser Pro Asn Glu Tyr Asp Gln Ser Ser Ser Asn
305 310 315 320

Leu Leu Pro Glu Gly Ser Leu Arg Cys Ser Val Tyr Gln Pro Thr Gln
325 330 335

Gln Gln Ser Leu Phe Ile Pro Val Gln Pro Arg Ala Ser Ser Ser Ser
340 345 350

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

Gln Asn Leu His Arg Ala Pro Ser Ser Gly Asn Phe Gly Ser Arg Ile
370 375 380

Gly Ile Phe Pro Ser Ser Ala Asp Thr Thr Asn Gln Leu Ser Ser Gln
385 390 395 400

Asp Pro Asn Arg Ser Ser Val Arg Gly Asn Phe Pro Glu Pro Leu Leu
405 410 415

Leu Gly Ser Ser Leu Phe Pro Ser Asp Ser Ala Glu Leu Leu Ser Met
420 425 430

Pro Gly Gly Arg Ser Asn Gln Gln Asn Ser Ser Ser Thr Ile Arg Thr
435 440 445

Ala Val Asn Ile Gly Ala Gln Gln Ile Ala Gly Leu Asn Ala Ser Gln
450 455 460

Pro Thr Ser Ser Ser Arg Gly Ser Val Asp Ile Val Arg Arg Ser Leu
465 470 475 480

Gln Ala Ala Ser Val Pro Gln Ser Arg Gly Ser Ser Ile Thr Ser Gln
485 490 495

Gln Gln Arg Gly His Ser Ser Thr Ser His Glu Ile Arg Ser His Gln
500 505 510

Pro Gly Ser Ser Ser Arg Ala Asn Gln Gln His Tyr Val Arg Ala Val
515 520 525

Pro His Ser Val Asp Arg Gln Asn Ser Asn Tyr Leu Asp Leu Gln Ser
530 535 540

Phe Met Gln Ser Ile Ala Ala Ser Arg Asp Gly Ile Arg Thr Val Ser
545 550 555 560

Glu Ser Ala Asn Gln Leu Val His Leu Arg Asn Val Val Glu Gln Ile
565 570 575

Arg Gln Gly Arg Gly Gly Arg Phe Glu Asp Pro Asn Phe Glu Arg Ala
580 585 590

Leu Phe Ala Arg Arg Ala Ser Leu Ile Asp Arg His Arg Asp Met Arg
595 600 605

Leu Asp Val Asp Asn Met Ser Tyr Glu Glu Leu Leu Ala Leu Gly Glu
610 615 620

Arg Ile Gly Tyr Val Asn Thr Gly Leu Ser Glu Asp Lys Ile Arg Thr
625 630 635 640

Gly Leu Lys Gln Trp Lys Tyr Val Ser Ile Pro Ile Glu Glu Pro Leu
645 650 655

Thr Gly Val Glu Pro Cys Cys Ile Cys Gln Glu Glu Tyr Ala Glu Gly
660 665 670

Glu Asp Met Gly Arg Leu Asp Cys Gly His Asp Phe His Thr Ala Cys
675 680 685

Ile Lys Gln Trp Leu Val Ile Lys Asn Leu Cys Pro Ile Cys Lys Lys

690

PF59082PF60142_PCT_SEQ_LIST.txt
695 700Thr Gly Leu Gly Thr
705<210> 220
<211> 1506
<212> DNA
<213> Oryza sativa

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cgtcataatt ttaataatat ttcatgggaa cctagaccag tccattctac ttcgaatggt      660
tcccaaagta catcaatgaa aaggaatgga ccatcctttt ctacgcgaat gagaactatg      720
ccttcaggtg cctctggaat gcactctgga gaaatgcctt acactatggg aagcagcaac      780
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<210> 221
<211> 501
<212> PRT

<213> Oryza sativa

<400> 221

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Phe Val His Ala Gly Asn Asp Ala Ala Leu Lys Ile Gly Pro Ser Tyr
 35 40 45

His Gly Asn Val Ala Ile Arg Ser Asn Asp Leu Pro Ser Ser Ser Arg
 50 55 60

Val Ala Gln Tyr Ser Gly His Arg Val Lys Asn Thr Gly Thr Leu His
 65 70 75 80

Asn Ser Tyr Val His Tyr Pro Ala Gly Ser Ser Gly Gly His Val Ser
 85 90 95

Tyr Asn Pro Gln Thr Glu Pro Val Ile Thr Tyr Pro His Arg Ser Glu
 100 105 110

Gly Glu Phe Ala Arg Gly Ser Ser Gln Ile Asp Asn Arg Thr Ala Ala
 115 120 125

Val Lys Arg Lys Asn Pro Val Ile Tyr Pro Glu Tyr Ser Ile Asn Gly
 130 135 140

Asp Gly Tyr Cys Ala Gly Ser Ser Ser Ser Thr Gln Phe Ser Asn Tyr
 145 150 155 160

Pro Gln Pro Ala Pro Phe Ser Glu Ser Leu His Arg Gln Met Pro Pro
 165 170 175

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

Gly Ser Gln Arg Asn Val Arg Ala Arg His Asn Phe Asn Asn Ile Ser
 195 200 205

Leu Glu Pro Arg Pro Val His Ser Thr Ser Asn Val Ser Gln Ser Thr
 210 215 220

Ser Met Lys Arg Asn Gly Pro Ser Phe Ser Thr Arg Met Arg Thr Met
 225 230 235 240

Pro Ser Gly Ala Ser Gly Met His Ser Gly Glu Met Pro Tyr Thr Met
 245 250 255

Gly Ser Ser Asn Ser Ser Val Pro Val Pro Thr Leu Gln Gly Ser Ser
 Seite 202

260

265

270

Ser Ser Ala Ile Phe Ala Ser Gly Val Phe Ala Pro Arg His Val His
 275 280 285

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

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

Ala Thr Ser Ala Thr Thr Ser Thr Pro Met Arg Ala Ser Gln Pro Leu
 325 330 335

Pro Val Arg Ala Val Ala Ser Ser Arg His Ala Arg Asn Val Leu Ile
 340 345 350

Gly His Ala Asn Ser Gly Arg Asn Arg Arg Ala Arg Ser Ser Tyr Tyr
 355 360 365

Gly Ile Gln Pro Leu Met Ile Asp Ala Gln Gln Leu Ile Met Met Gln
 370 375 380

Gln Phe Ala Leu Arg Glu Ser Arg Glu Ala Gln Asp Pro His Arg Ala
 385 390 395 400

Met Arg Leu Asp Ile Asp Asn Met Ser Tyr Glu Asp Leu Leu Ala Leu
 405 410 415

Gly Glu Ser Ile Gly Asn Val Cys Thr Gly Leu Val Asp Glu Lys Ile
 420 425 430

Ser Gly Cys Val Arg Glu Val Ile Tyr Cys Ser Ser Asp Glu Gln Gln
 435 440 445

Asn Asp Gln Asp Asp Gly Lys Cys Ala Ile Cys Leu Glu Glu Tyr Lys
 450 455 460

Asp Asn Ser Leu Leu Gly Ile Leu Lys Cys Asn His Asp Phe His Thr
 465 470 475 480

Asp Cys Val Lys Lys Trp Leu Lys Glu Lys Asn Ser Cys Pro Ile Cys
 485 490 495

Lys Ser Ala Ala Ala
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<210> 222
 <211> 1095
 <212> DNA
 <213> Oryza sativa

<400> 222

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acggcggcgg cgatgggctc cggccgccgc ggggaggcgg agcggcgcca cagagagagg 540
ccggccgctc ctcgagctcg aagggtgacc atgcgtgagc acatatcctc gtcgctcatg 600
gactcgccgc cgttccccga catgccgtc ctcaacgccg acctgctacc accaccaccc 660
tccggccgcc accgccatgg ataccgccac cccacgtcg gcgccgccga ggaagagatc 720
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tggcgactcg acgttgacaa catgacatat gaggagctgc tggatcttga agacagaatt 840
gggtatgtaa gcacaggggt gcatgacgat gaaatcgctc gcagccttag gatggtcaag 900
tattcagcat tcaaccccaa gcattttgca acagaagtag aaaggaattg cagtatttgt 960
caggaagaat ttgaagcaaa tgaggaaaca gggaggctga tctgtggcca cagctatcat 1020
gtgcaatgca taaagcagt gctttctagg aagaacacct gccctgtctg caaaactgtt 1080
gtatcgaaga catga 1095

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<210> 223
 <211> 364
 <212> PRT
 <213> Oryza sativa
 <400> 223

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

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PF59082PF60142_PCT_SEQ_LIST.txt

Arg Arg Lys Val Gln Glu Arg Arg Ser Ala Arg Gly Gly Gly Gly Gly
100 105 110

Gly Gly Gly Gly Val Ala Pro Pro Gly Pro Ala Pro Ala Ala Ala Gly
115 120 125

Asp Val Trp Cys Thr Cys Ala Pro Gly Ile Pro Phe Ala Ala Glu Ala
130 135 140

Ser Ser Val Asp Cys Val Val Val Ala Arg His His His Ala His His
145 150 155 160

Thr Ala Ala Ala Met Gly Ser Gly Arg Arg Gly Glu Ala Glu Arg Arg
165 170 175

His Arg Glu Arg Pro Ala Ala Pro Arg Ala Arg Arg Val Thr Met Arg
180 185 190

Glu His Ile Ser Ser Ser Leu Met Asp Ser Pro Pro Phe Pro Asp Met
195 200 205

Pro Leu Leu Asn Ala Asp Leu Leu Pro Pro Pro Pro Ser Gly Arg His
210 215 220

Arg His Gly Tyr Arg His Pro His Val Gly Ala Ala Glu Glu Glu Ile
225 230 235 240

Met Met Leu Arg Thr Arg Leu Leu Trp Gly Arg Phe Gly Met His Asp
245 250 255

Gln His Gln Asp Trp Arg Leu Asp Val Asp Asn Met Thr Tyr Glu Glu
260 265 270

Leu Leu Asp Leu Glu Asp Arg Ile Gly Tyr Val Ser Thr Gly Leu His
275 280 285

Asp Asp Glu Ile Ala Arg Ser Leu Arg Met Val Lys Tyr Ser Ala Phe
290 295 300

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

Gln Glu Glu Phe Glu Ala Asn Glu Glu Thr Gly Arg Leu Ile Cys Gly
325 330 335

His Ser Tyr His Val Gln Cys Ile Lys Gln Trp Leu Ser Arg Lys Asn
340 345 350

Thr Cys Pro Val Cys Lys Thr Val Val Ser Lys Thr
355 360

PF59082PF60142_PCT_SEQ_LIST.txt

<210> 224
<211> 1602
<212> DNA
<213> Oryza sativa

<400> 224
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aacggagctg gatcgtctgg ctatgtgggt aacacaatga gatcgaatga tcttccgtct 180
tcaagttatg ctggccaagc ttatggtcag cagaatagag ccccatcca tgcttcatat 240
tctggtcatg cacctgctgg aagctctagt ggtagctatg caccatacaa tactcaacat 300
atgcctgctt caagctatcc acacggatcc gaggataatt tcattccaag ttcccatgtg 360
gatggcagaa gggttgcatt gaagagaaga aatcccatca ttcctctac agatggattc 420
gggtgttgaa attattatgc tggcagttct tccaatactc agttctctcg gcccatgcct 480
ccaaatccta ttccacctcc tgaatcctgt gttcgaatgc cctcacactt gggttcgaac 540
cactggaatg atcaccgcta tgttaatcat gaaggatctc agaggaatgt gaggggaaga 600
catgatcata gtactatcca tttggaacaa agtccagctg cagcttgccc gtcaagcagc 660
atcaatgtgc caccatacca tccaaatgca aatggtcctt ttggaagtgc accagtacaa 720
cgtgacagag ctcttttatc tgtgcatcca agaattcttc ctccagggcc tgatggtagt 780
agcatagcat tcagagagag gccatactat cctgctccac agagcaccaa cataagtga 840
cctgtgcaa cgcttcctat ttcttgtgac agtgcacat ttgctcatgg tgggtacgcc 900
cctagatcag ctcatcgtaa caacttacgc acttatcctc ctccagcttt tgcattcttct 960
tccaaccctg gagcagtctc ccatgagcca gctattccta gctatccacc tgctgcccct 1020
agctatccac ctgcaacctc tgcagcatca tcaagtgtcc agccatttca tgctgaagct 1080
gctgcacatt tgaggcatcc aaggcatgta tctgtagggg gcagtggtag tgcaaggagt 1140
agaaggatga gggattccta tcatggtttt catcatttga tgattgaaga caataacttg 1200
ggaagatcag cagctgagcg gtttatgatg ctggatcagt tagttatcca tgaatcaaga 1260
gaagcattcg atcctcactg ggacatgaga ctggacattg atgacatgag ctatgaggag 1320
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tctggctgtg tgatggaggt agcctgctgc agcagtagtc atttgcagga tgatcaggac 1440
aatgaaagat gtgtaatctg cctggaggaa tacaagcatg aggacacact tgggaggctg 1500
aaatgcggcc acgggtttca ctgcaattgc atcaagaagt ggctgcaggt gaagaacacc 1560
tgcccagttt gcaaagctgc tgccgcagat gaaggcagct ga 1602

<210> 225
<211> 533
<212> PRT
<213> Oryza sativa

<400> 225

Met Ala Gly His Gln Tyr Asn Asn Ser Gln Met Ser Arg Met Asp His

1 5 10 15
 Met Asp Arg Leu₂₀ Asn Asn Glu Pro Pro₂₅ Pro Phe Gly Gln Lys₃₀ Leu Phe
 Met His Pro₃₅ Arg Ser Asp Pro Ala₄₀ Asn Gly Ala Gly Ser₄₅ Ser Gly Tyr
 Val Gly₅₀ Asn Thr Met Arg Ser₅₅ Asn Asp Leu Pro Ser₆₀ Ser Ser Tyr Ala
 Gly Gln Ala Tyr Gly Gln₇₀ Gln Asn Arg Ala Pro₇₅ Ile His Ala Ser Tyr₈₀
 Ser Gly His Ala Pro₈₅ Ala Gly Ser Ser Ser₉₀ Gly Ser Tyr Ala Pro₉₅ Tyr
 Asn Thr Gln His₁₀₀ Met Pro Ala Ser Ser₁₀₅ Tyr Pro His Gly Ser₁₁₀ Glu Asp
 Asn Phe Ile₁₁₅ Pro Ser Ser His Val₁₂₀ Asp Gly Arg Arg Val₁₂₅ Ala Leu Lys
 Arg Arg₁₃₀ Asn Pro Ile Ile His₁₃₅ Pro Thr Asp Gly Phe₁₄₀ Gly Val Gly Asn
 Tyr Tyr Ala Gly Ser Ser₁₅₀ Ser Asn Thr Gln Phe₁₅₅ Ser Arg Pro Met Pro₁₆₀
 Pro Asn Pro Ile Pro₁₆₅ Pro Pro Glu Ser Cys₁₇₀ Val Arg Met Pro Ser₁₇₅ His
 Leu Gly Ser Asn₁₈₀ His Trp Asn Asp His₁₈₅ Arg Tyr Val Asn His₁₉₀ Glu Gly
 Ser Gln Arg₁₉₅ Asn Val Arg Gly Arg₂₀₀ His Asp His Ser Thr₂₀₅ Ile His Leu
 Glu Gln Ser Pro Ala Ala Ala₂₁₅ Cys Pro Ser Ser Ser₂₂₀ Ile Asn Val Pro
 Pro Tyr His Pro Asn Ala₂₃₀ Asn Gly Pro Phe Gly₂₃₅ Ser Ala Pro Val Gln₂₄₀
 Arg Asp Arg Ala Pro₂₄₅ Leu Ser Val His Pro₂₅₀ Arg Ile Leu Pro Pro₂₅₅ Gly
 Pro Asp Gly Ser₂₆₀ Ser Ile Ala Phe Arg₂₆₅ Glu Arg Pro Tyr Tyr₂₇₀ Pro Ala
 Pro Gln Ser Thr Asn Ile Ser Ala₂₈₀ Pro Val Pro Thr Leu₂₈₅ Pro Ile Ser

PF59082PF60142_PCT_SEQ_LIST.txt

Cys Asp Ser Ala Pro Phe Ala His Gly Gly Tyr Ala Pro Arg Ser Ala
 290 295 300
 His Arg Asn Asn Leu Arg Thr Tyr Pro Pro Pro Ala Phe Ala Ser Ser
 305 310 315 320
 Ser Asn Pro Gly Ala Val Ser His Glu Pro Ala Ile Pro Ser Tyr Pro
 325 330 335
 Pro Ala Ala Pro Ser Tyr Pro Pro Ala Thr Ser Ala Ala Ser Ser Ser
 340 345 350
 Val Gln Pro Phe His Ala Glu Ala Ala Ala His Leu Arg His Pro Arg
 355 360 365
 His Val Ser Val Gly Gly Ser Gly Ser Ala Arg Ser Arg Arg Met Arg
 370 375 380
 Asp Ser Tyr His Gly Phe His His Leu Met Ile Glu Asp Asn Asn Leu
 385 390 395 400
 Gly Arg Ser Ala Ala Glu Arg Phe Met Met Leu Asp Gln Leu Val Ile
 405 410 415
 His Glu Ser Arg Glu Ala Phe Asp Pro His Trp Asp Met Arg Leu Asp
 420 425 430
 Ile Asp Asp Met Ser Tyr Glu Glu Leu Leu Ala Leu Glu Glu Arg Ile
 435 440 445
 Gly His Val Asn Thr Gly Leu Ala Asp Glu Lys Ile Ser Gly Cys Val
 450 455 460
 Met Glu Val Ala Cys Cys Ser Ser Ser His Leu Gln Asp Asp Gln Asp
 465 470 475 480
 Asn Glu Arg Cys Val Ile Cys Leu Glu Glu Tyr Lys His Glu Asp Thr
 485 490 495
 Leu Gly Arg Leu Lys Cys Gly His Gly Phe His Cys Asn Cys Ile Lys
 500 505 510
 Lys Trp Leu Gln Val Lys Asn Thr Cys Pro Val Cys Lys Ala Ala Ala
 515 520 525
 Ala Asp Glu Gly Ser
 530

<210> 226
 <211> 1503
 <212> DNA

<213> Oryza sativa

<400> 226

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gctgttggag ttccaggaaa tactgatttc cggagtcact atgagagcat taatcttcag      180
caccagcatg ttcagaatcc ataccacat gtgggtgttg cttcaagttc tgtgttccca      240
tctactatgt acaaccctg catatcaaca acagcagtgg acagatatgt tcctcctatt      300
caaagttttg gattgggcaa tccactacta ctgcctttat atcatcaact tgctcaagga      360
tccatggatg agaacggcag cagtggcaat ttttgtgaca gcgtcaggga atttatcaag      420
aggaaaaatg cattacttgt ggggtggccat cttttgttta atagttttgc aagctcaagc      480
tcatctgctt atgtgcctcc aaatccttta cataggtcat ggaacgcttc atttgaagca      540
aatatcctac ccagcactgg agtttccaat ccaccagagt actcttctgc agattcactg      600
aacaattcca attcgatggc ttcacatcca gaattggtgc atcatggcaa ttatgtattt      660
ccagctgggtc acatgagcca atacaatgca tggattgcac aggcaagcag aactgggtgga      720
gtaccacagt gggaacatgg caatgcagcg gctaatcctc caggtggatt tgttcattct      780
ggaaccatag acatgcaaaa tggaggtctt cagggatacc aagctggccc ttttgccaat      840
tattatgggc ctctgcccc a tttccaccaa aatcctctga atagcatgca gcctcctgct      900
ctatttaatc atatccaaat gcaagtacct catcaacatt gcctcagtaa caatttattg      960
catcaccctt ctggcaatgg cctccccttg gatccaagaa ttctggcaat ttcatccaat     1020
tctgggcata cttttgggcc tacagctcag ccatctttag caaaccaagt taatgctggg     1080
agttcgagaa ttcagccata tgagaatgct ccgttcgtgg atctttcgag attgtatgaa     1140
gcaggagtta ttgatgaaca tagagatatg cggcttgatg tagacagcat gacttatgag     1200
gagctttag cgttggagga gcggattgga aatgttaata gtggttttac agaaagctac     1260
attgaggaaa atttgaagtc aagttcttat gtcccggacg ctgattgcat gcctgatcag     1320
tcttctgtgg agaaggatgc ttgcataatc tgccaggagg aatatgaggc taaagaactc     1380
gttgaaccc ttggttgtgg tcacaagtac catgcatgtg gcataaaagg gtggctgatg     1440
gtgaagaacc tgtgccccat ctgcaaaaca acagctttgc cagctgatag aagaaacgga     1500
tga                                                                    1503

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<210> 227

<211> 500

<212> PRT

<213> Oryza sativa

<400> 227

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Met Leu Gln Arg Asn Met Val Trp Thr His Gln Val Ala Ser Pro Glu
1           5           10           15

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Asn Gln Val Gln Pro Glu Ser Phe Tyr His Gly Gly Ala Gly Ser Asn
          20           25           30

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PF59082PF60142_PCT_SEQ_LIST.txt

Leu Ser Asn₃₅ Leu Ser Val Gln₄₀ Val Ala Val Gly Val Pro Gly Asn Thr
 Asp Phe₅₀ Arg Ser His Tyr Gln₅₅ Ser Ile Asn Leu Gln₆₀ His Gln His Val
 Gln₆₅ Asn Pro Tyr Pro His₇₀ Val Gly Val Ala Ser₇₅ Ser Ser Val Phe Pro₈₀
 Ser Thr Met Tyr Asn₈₅ Pro Cys Ile Ser Thr₉₀ Thr Ala Val Asp Arg Tyr₉₅
 Val Pro Pro Ile₁₀₀ Gln Ser Phe Gly Leu₁₀₅ Gly Asn Pro Leu Leu₁₁₀ Leu Pro
 Leu Tyr His₁₁₅ Gln Leu Ala Gln Gly₁₂₀ Ser Met Asp Glu Asn₁₂₅ Gly Ser Ser
 Gly Asn₁₃₀ Phe Cys Asp Ser Val₁₃₅ Arg Glu Phe Ile Lys₁₄₀ Arg Lys Asn Ala
 Leu₁₄₅ Leu Val Gly Gly His₁₅₀ His Phe Val Asn Ser₁₅₅ Phe Ala Ser Ser Ser₁₆₀
 Ser Ser Ala Tyr Val₁₆₅ Pro Pro Asn Pro Leu₁₇₀ His Arg Ser Trp Asn₁₇₅ Ala
 Ser Phe Glu Ala₁₈₀ Asn Ile Leu Pro Ser₁₈₅ Thr Gly Val Ser Asn₁₉₀ Pro Pro
 Glu Tyr Ser₁₉₅ Ser Ala Asp Ser Leu₂₀₀ Asn Asn Ser Asn Ser₂₀₅ Met Ala Ser
 His Pro₂₁₀ Glu Leu Val His His₂₁₅ Gly Asn Tyr Val Phe₂₂₀ Pro Ala Gly His
 Met₂₂₅ Ser Gln Tyr Asn Ala₂₃₀ Trp Ile Ala Gln Ala₂₃₅ Ser Arg Thr Gly Gly₂₄₀
 Val Pro Gln Trp Glu₂₄₅ His Gly Asn Ala Ala₂₅₀ Ala Asn Pro Pro Gly₂₅₅ Gly
 Phe Val His Ser₂₆₀ Gly Thr Ile Asp Met₂₆₅ Pro Asn Gly Gly Leu₂₇₀ Gln Gly
 Tyr Gln Ala₂₇₅ Gly Pro Phe Ala Asn₂₈₀ Tyr Tyr Gly Pro Leu₂₈₅ Pro His Phe
 His Gln₂₉₀ Asn Pro Leu Asn Ser₂₉₅ Met Gln His Pro Ala₃₀₀ Leu Phe Asn His

PF59082PF60142_PCT_SEQ_LIST.txt

Ile Gln Met Gln Val Pro His Gln His Cys Leu Ser Asn Asn Leu Leu
305 310 315 320

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

Ile Ser Ser Asn Ser Gly His Thr Phe Gly Pro Thr Ala Gln Pro Ser
340 345 350

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

Asn Ala Pro Phe Val Asp Leu Ser Arg Leu Tyr Glu Ala Gly Val Ile
370 375 380

Asp Glu His Arg Asp Met Arg Leu Asp Val Asp Ser Met Thr Tyr Glu
385 390 395 400

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

Thr Glu Ser Tyr Ile Glu Glu Asn Leu Lys Ser Ser Ser Tyr Val Pro
420 425 430

Asp Ala Asp Cys Met Pro Asp Gln Ser Ser Val Glu Lys Asp Ala Cys
435 440 445

Ile Ile Cys Gln Glu Glu Tyr Glu Ala Lys Glu Leu Val Gly Thr Leu
450 455 460

Gly Cys Gly His Lys Tyr His Ala Met Cys Ile Lys Gly Trp Leu Met
465 470 475 480

Val Lys Asn Leu Cys Pro Ile Cys Lys Thr Thr Ala Leu Pro Ala Asp
485 490 495

Arg Arg Asn Gly
500

<210> 228
<211> 918
<212> DNA
<213> Oryza sativa

<400> 228
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cccaccgccg cagctccacc cgatgactcc gcggcggcgg cggcggcggg gagacggccc 120
ttcaccagcc tcaccagga ggaggccgac ctgcacctcg cccgcgtcct ccaggagcag 180
gagcgggcgt acatgatgct cagcgcgcac cacggcggcg actacgcggc ctccgatggt 240
gggagctacg agtttgacga ggaaggggag gggagcgatt ttgaggacga ggatggggac 300

PF59082PF60142_PCT_SEQ_LIST.txt

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ggggacggcg acggggaggg gctggatgag gacgaggagg tggccgacgc agacgcagac 360
gccgccggtg acccggtga gttggacccc gcgcggtacg aggacgacga ggccttcgcg 420
cgggcgctgc aggacgccga ggagcgcgag gtcgccggcc gcctcatggc gctcgcgggc 480
ctcagtgatt ggcgagtgat ggacatgat gatgacgatg ttgatgatga tgatgatgag 540
gatgatgatg atgatgatga tgatgaagat gaagacgggg atgatccaca ggatgcatgg 600
gaagatgttg atccagatga atattcttat gaggagctgg ttgcattggg tgaagtagtt 660
ggtacggaaa gcagaggcct ctctgctgat acacttgctt cattaccttc aataacttat 720
cgagcacaag ataagcaaga cggcaacatg gaacaatgtg ttatttgccg tgtggaattt 780
gaggaaggtg aatcattggt tgcacttcct tgcaagcatt cataccattc tgaatgcata 840
aaccaatggc tgcaattaa taaggtatgc cctatgtgca gtgctgaagt tcctacttca 900
caggacaccc gggcatga 918

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<210> 229
 <211> 305
 <212> PRT
 <213> Oryza sativa

<400> 229

Met Asp Ala Ala Lys Asp Thr Thr Ala Ala Ala Asp Gln Asn Pro
 1 5 10 15

Thr Pro Asn Pro Pro Thr Ala Ala Ala Pro Pro Asp Asp Ser Ala Ala
 20 25 30

Ala Ala Ala Ala Gly Arg Arg Pro Phe Thr Ser Leu Thr Gln Glu Glu
 35 40 45

Ala Asp Leu Ala Leu Ala Arg Val Leu Gln Glu Gln Glu Arg Ala Tyr
 50 55 60

Met Met Leu Ser Ala His His Gly Gly Asp Tyr Ala Ala Ser Asp Gly
 65 70 75 80

Gly Ser Tyr Glu Phe Asp Glu Glu Gly Glu Gly Ser Asp Phe Glu Asp
 85 90 95

Glu Asp Gly Asp Gly Asp Gly Asp Gly Glu Ala Leu Asp Glu Asp Glu
 100 105 110

Glu Val Ala Asp Ala Asp Ala Asp Ala Ala Gly Asp Pro Ala Glu Leu
 115 120 125

Asp Pro Ala Arg Tyr Glu Asp Asp Glu Ala Phe Ala Arg Ala Leu Gln
 130 135 140

Asp Ala Glu Glu Arg Glu Val Ala Gly Arg Leu Met Ala Leu Ala Gly
 145 150 155 160

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Ser Asp Trp Arg Val Met Asp His Asp Asp Asp Asp Val Asp Asp
165 170 175

Asp Asp Asp Glu Asp Asp Asp Asp Asp Asp Asp Asp Glu Asp Glu Asp
180 185 190

Gly Asp Asp Pro Gln Asp Ala Trp Glu Asp Val Asp Pro Asp Glu Tyr
195 200 205

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

Arg Gly Leu Ser Ala Asp Thr Leu Ala Ser Leu Pro Ser Ile Thr Tyr
225 230 235 240

Arg Ala Gln Asp Lys Gln Asp Gly Asn Met Glu Gln Cys Val Ile Cys
245 250 255

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

His Ser Tyr His Ser Glu Cys Ile Asn Gln Trp Leu Gln Leu Asn Lys
275 280 285

Val Cys Pro Met Cys Ser Ala Glu Val Pro Thr Ser Gln Asp Thr Arg
290 295 300

Ala
305

<210> 230
<211> 770
<212> DNA
<213> Zea mays

<220>
<221> misc_feature
<222> (502)..(514)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (544)..(562)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (634)..(667)
<223> n is a, c, g, or t

<400> 230
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agtttggatt tcaattcttg ctgacggcag tcttgcaaac tgggcaaattg ttcttctgcg 120
agagccactg cttgatgcag tacacatggt agctatggcc acagtctagc cttcccatct 180

PF59082PF60142_PCT_SEQ_LIST.txt

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cttcatttgt ttcaaattct tcttggcaaa tgctgcattt tctttccatt tctgttgcca 240
accgtaagga actgaaggat ggggtgcttga ccttccgaag gttgagagta atctcgtcgt 300
cacgtaaccc tgtgttgaca tatccaattt tgtctccaag ctcgagcaac tcctcgtatg 360
tcatgttatc aacgtcaagg cgccaatcct ggtagcggtc atacatgttc attcctccca 420
gtaacactct tgtctgaaac atccttatct cttcctcgag tcctccggcg ctctaccgtg 480
agccgcgggt cccctgacat gnnnnnnnnn nnnngagatc ggcgccgaat aaggcgacat 540
cgcnnnnnnn nnnnnnnnnn nngtccatga aggacgagga tatctgctcc tgcacggtca 600
ccctccggga caagcacggc ctctctctgt gggnnnnnnn nnnnnnnnnn nnnnnnnnnn 660
nnnnnnncaa catctggtgg cgcgccacca cgcagttcac ggaggacgcc tccgccgcga 720
agggtatgcc ggggtgcgcac cacacgtcgg cgccgatccc accggtgacg 770

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<210> 231
 <211> 123
 <212> PRT
 <213> Zea mays

<400> 231

Met Phe Gln Thr Arg Val Leu Leu Gly Gly Met Asn Met Tyr Asp Arg
 1 5 10 15

Tyr Gln Asp Trp Arg Leu Asp Val Asp Asn Met Thr Tyr Glu Glu Leu
 20 25 30

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

Asp Glu Ile Thr Arg Asn Leu Arg Lys Val Lys His Pro Ser Phe Ser
 50 55 60

Ser Leu Arg Phe Ala Thr Glu Met Glu Arg Lys Cys Ser Ile Cys Gln
 65 70 75 80

Glu Glu Phe Glu Thr Asn Glu Glu Met Gly Arg Leu Asp Cys Gly His
 85 90 95

Ser Tyr His Val Tyr Cys Ile Lys Gln Trp Leu Ser Gln Lys Asn Ile
 100 105 110

Cys Pro Val Cys Lys Thr Ala Val Ser Lys Asn
 115 120

<210> 232
 <211> 814
 <212> DNA
 <213> Zea mays

<220>
 <221> misc_feature
 <222> (759)..(759)

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

<400> 232
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taatggagat tcggaatgca cttgaaatga tccatagagg ggagaatgta aggcttgagt 120
ctatcttcta tggcgggtgtt gacattcacg atagacacag ggacatgcgc cttgacattg 180
acaatatgtc ctatgaggag ctattagcac tcgaggaaag aataggaaat gttggcactg 240
gcctcagtga ggaagctgtg ataaggttgc tcaaacaag gaaattttca tcttggacac 300
taaaagcatc tttggaccct gaaccatgtt gtatctgcca ggaggagtac gctgatggag 360
acgacctcgg gaggctggac tgcgggcacg acttcacgc tggctgcatc aagcaatggc 420
tgggtggtgaa gaacgtgtgc cccatctgca agagcaccgc attgaagaag acctgaaacc 480
cgaacaaagg ctctgtgtcag agacaccccc ccatgtttct atgttcactc gatcgttcgc 540
gagatccttt gccgattcgt attgctacgt tttttttggg cgggaaaatt ttgccagaca 600
cctgcatgct attgggaaag gaaaagagag agaaaaagag agagagagag aggatgcggt 660
tgcggtcctc tgtaaactgc tgctgcagta aataatccct ggaatatgtc tccctgcatc 720
caaccaaata tttagtagct gttatagtgg acgccgtang attaaaacct ggaagagagc 780
ctgttggtgctg ttgccacaa aaaaaaaaaa aaaa 814

<210> 233
<211> 137
<212> PRT
<213> Zea mays

<400> 233

Met Glu Ile Arg Asn Ala Leu Glu Met Ile His Arg Gly Glu Asn Val
1 5 10 15

Arg Leu Glu Ser Ile Phe Tyr Gly Gly Val Asp Ile His Asp Arg His
20 25 30

Arg Asp Met Arg Leu Asp Ile Asp Asn Met Ser Tyr Glu Glu Leu Leu
35 40 45

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

Ala Val Ile Arg Leu Leu Lys Gln Arg Lys Phe Ser Ser Trp Thr Leu
65 70 75 80

Lys Ala Ser Leu Asp Pro Glu Pro Cys Cys Ile Cys Gln Glu Glu Tyr
85 90 95

Ala Asp Gly Asp Asp Leu Gly Arg Leu Asp Cys Gly His Asp Phe His
100 105 110

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

PF59082PF60142_PCT_SEQ_LIST.txt

Cys Lys Ser Thr Ala Leu Lys Lys Thr
130 135

<210> 234
<211> 2276
<212> DNA
<213> Hordeum vulgare

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PF59082PF60142_PCT_SEQ_LIST.txt

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<210> 235
 <211> 582
 <212> PRT
 <213> Hordeum vulgare

<400> 235

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Arg Arg Gly Ser Gly Ile Asn Arg Ser Pro Glu Glu Thr Ile Ser Gln
 20 25 30

Asn Thr Glu Val Gln Gly Arg Thr Ser Arg Val Asn Pro Met Lys Thr
 35 40 45

Arg Leu Val Asp Asn Gln Glu Arg Pro Arg Tyr Leu His Gly Ser Tyr
 50 55 60

Lys Tyr Ala Ser Ser Asn Val Met Ser Gly Ser Ser Ser Lys Phe Pro
 65 70 75 80

Lys Lys Phe Pro Leu Arg Lys Phe Gly Glu Glu Lys Arg Arg Gln Thr
 85 90 95

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

Val Gly Cys Leu Glu Gly Ser Lys Lys Thr Ile Val Glu Asn Gln Gly
 115 120 125

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

Glu Leu Ile Ala Pro Asp Pro Glu Val Ser His Ser Ala Gly Ser Ser
 145 150 155 160

Gly Ile Pro Ala His Thr Asp Gly Ser Leu Ile Arg Ser Ala Ser Leu
 165 170 175

PF59082PF60142_PCT_SEQ_LIST.txt

Ser Ser Glu Thr His Arg Gln Lys Asn Lys Glu Leu Asn Leu Gly Arg
180 185 190

Pro Gly Tyr Ser Cys Ser Ser Ser Phe Ser Asn Gln Pro Thr Ile Pro
195 200 205

Arg Ile Pro Thr Val Gly Ala Lys Pro Ser Tyr Gly Leu Val Ser Gly
210 215 220

Glu Gln Arg Arg Val Pro Arg Gly Leu Lys Asn Leu Gly Cys Thr Ser
225 230 235 240

Val Ser Asp Val Leu Pro Ser Gly Cys Ser Ser Asp Ser Val Tyr Arg
245 250 255

Met Ser Phe Asp Ala Met Arg Lys Arg Ala Ser Asp Gly Asp Gly Ser
260 265 270

Ser Arg Ser Arg Phe Ile Ser Gly Pro Ser Ser Leu Gly His Ser His
275 280 285

Thr Ile Tyr Pro Ser Ile Ser Gly Pro Arg Ile Arg Thr Thr Glu Glu
290 295 300

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

Ser Ala Val Ser Val Arg Thr Arg Arg Thr Ser Pro Arg Asp Thr Arg
325 330 335

Phe Arg Met Ser Glu Glu Thr Glu Asp Ser Val Leu His Leu Asn Glu
340 345 350

Ser Asn Ala Gly Asn Gln Gln Ser Val Gly Ala Asp Phe Ser Val Glu
355 360 365

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

His Ala Ile Tyr Ser Ser Ser Arg Gln Gly Ser Ser Thr Arg Thr Ala
385 390 395 400

Arg Arg Thr Ser Thr Ser Arg Phe Glu Gln Ser Pro Pro Gln Thr Phe
405 410 415

Arg Ser Leu Ala Arg Glu Arg Gly Gly His Arg Arg Ile Asn Met Glu
420 425 430

Gly Ile Ala Glu Val Leu Leu Val Leu Glu Arg Ile Glu Gln Glu Ala
435 440 445

PF59082PF60142_PCT_SEQ_LIST.txt

Glu Leu Thr Tyr Glu Gln Leu Arg Val Leu Glu Thr Asn Leu Leu Leu
450 455 460

Gly Ala Phe Thr Ser His Asp His His Ser Asp Met Arg Met Asp Ile
465 470 475 480

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

Phe Val Ser Thr Ala Leu Ser Glu Glu Gln Phe Ala Lys Cys Ile Arg
500 505 510

Arg Arg Leu Tyr Arg Pro Val Ala Ala Lys Gly Asn Lys Thr Ala Ile
515 520 525

Asp Asp Ile Lys Cys Ser Ile Cys Gln Glu Glu Phe Val Lys Gly Glu
530 535 540

Glu Val Gly Arg Leu Arg Cys Glu His Gln Tyr His Val Cys Cys Ile
545 550 555 560

Arg Gln Trp Leu Leu Gln Lys Asn Trp Cys Pro Val Cys Lys Ala Pro
565 570 575

Ala Leu Pro Ser Met Asn
580

<210> 236
<211> 2688
<212> DNA
<213> Hordeum vulgare

<400> 236
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PF59082PF60142_PCT_SEQ_LIST.txt

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<210> 237
 <211> 653
 <212> PRT
 <213> Hordeum vulgare

<400> 237

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

Tyr Trp Asn Ser Met Leu Gly Ala Ala Glu Ser Gln Asn Leu Gln Gly
 35 40 45

Tyr Glu Met Asn Arg Gly Asp Gly Ala Ile Pro Tyr Gly Gly Glu Gly
 50 55 60

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

Ser Ser Gly Asn Ala Leu Asn Ile Gly Gly Gly Leu Arg Ile Gly Glu
 85 90 95

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

Asn Leu Asn Ala Ser Gly His Asp Leu Phe Gly Gln Ser Ser Asn Ala
 115 120 125

Asn Ala Thr Ser Gln Ala Ser Gln Gln Asn Ala Gly Cys Ser Arg Ala
 130 135 140

Asp Thr Thr Ala Gln Ala Thr Glu Leu Arg Leu His Pro Tyr Arg Thr
 145 150 155 160

Phe Gly Leu Asp Asp Glu Gln Pro Glu Pro Phe Pro Ser Leu Asn Ala
 165 170 175

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

Gln Arg Pro Gly Ser Ser Leu Asp Gly Arg Arg Leu Ala Cys Lys Arg
 195 200 205

Lys Asn Ile Glu Gly Val His Gly Gln Phe Ser Ala Gly Ala Ser Thr
 210 215 220

Ser Phe Ser His Arg Asn Asp Asn Ala Phe His Ser Val Pro Ser Ser
 225 230 235 240

Ser Phe Asn Pro Ala Pro Gly Pro Asn Val Ser Ser His Asn Phe Leu
 245 250 255

Leu Ala Pro Ser Ser Ile Glu Glu Gln Leu Pro Asn Tyr Gly Thr Thr
 260 265 270

PF59082PF60142_PCT_SEQ_LIST.txt

Thr Gly Met Ser Ser Val Ser Tyr Asn Pro Pro Ser Gly Gly Asn Asn
275 280 285

Ser Ser Gly Asn Ser Gln Arg Ser Phe Arg Ala Arg Thr Thr Thr Ala
290 295 300

Gln Gln Val Ser Pro Tyr Gly Val Trp Pro Ser Ser Gly Ser Ile Arg
305 310 315 320

His Pro Gly Ser Tyr Tyr His Gln Ala Pro Ala Phe Gln Ser Ala Phe
325 330 335

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

Tyr Gln His Pro Gly Asn Val Val Pro Gly Ile Pro Gln Thr Ala Gln
355 360 365

Arg Phe Ala Gly Arg Ala Ala Ala Ser Ser Ser Arg Ala Gly Ser Leu
370 375 380

Asp Asn Ile Ile Leu Gly Arg Glu Asp Val Arg Asn Leu Val Val Pro
385 390 395 400

Ser Phe Pro Asn Ala Ala Pro His Ser Ala Leu Asn Met Arg His Leu
405 410 415

Val Pro Glu Leu Ser Asn Trp Asn Pro Asp Ile Pro Gly Ala Thr Ile
420 425 430

Pro Gly Asn Val Ser Ser Val Ser Arg Ala Asn Ala Thr Ser Thr Ile
435 440 445

Ser Arg Pro Ala Gly Ser Thr Ser Ile Ala His Gln Asn Leu His Arg
450 455 460

Arg His Pro Arg Asn Leu Ser Glu Glu Ile Gly Arg Leu Ser Gly Ala
465 470 475 480

Leu Arg Ser Gln Gln His Pro Arg Leu Arg Ser Gly Phe Leu Leu Glu
485 490 495

Arg Gln Gly Asp Gly Val Trp Gly Val Pro Leu Pro Met Arg Asn Ser
500 505 510

Arg Glu Gly Arg Arg Leu Met Glu Ile Arg Asn Ala Leu Glu Met Ile
515 520 525

Gln Arg Gly Glu Asn Val Arg Phe Glu Ser Ile Phe Tyr Gly Gly Val
530 535 540

PF59082PF60142_PCT_SEQ_LIST.txt

Glu Ile His Asp Arg His Arg Asp Met Arg Leu Asp Ile Asp Asn Met
545 550 555 560

Ser Tyr Glu Glu Leu Leu Ala Leu Glu Glu Arg Ile Gly Asn Val Ser
565 570 575

Thr Gly Leu Thr Glu Asn Asp Val Met Lys Leu Leu Lys Gln Arg Lys
580 585 590

Phe Ser Ser Trp Arg Leu Ser Ser Met Glu Phe Glu Pro Cys Cys Ile
595 600 605

Cys Gln Glu Asp Tyr Val Glu Gly Asp Asp Leu Gly Thr Leu His Cys
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Gly His Asp Phe His Ala Ser Cys Ile Ser Gln Trp Leu Val Val Lys
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Asn Leu Cys Pro Ile Cys Lys Ser Thr Ala Leu Lys Thr
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<210> 238
<211> 1586
<212> DNA
<213> Hordeum vulgare

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PF59082PF60142_PCT_SEQ_LIST.txt

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<210> 239
 <211> 374
 <212> PRT
 <213> Hordeum vulgare

<400> 239

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Thr	Asp	Lys	Gly	Arg	Pro	Thr	Pro	Ser	His	Arg	Glu	Ala	Ala	Ala	Thr
	50					55					60				

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65				70						75				80	

Lys	Lys	Pro	Pro	Gln	Gly	Ser	Ser	Asn	Pro	Ala	Glu	Pro	Cys	Ser	Glu
				85				90						95	

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

Leu	Ala	Arg	Glu	Met	Ser	Ser	Ser	Ser	Ser	Ser	Gly	Gly	Phe	Ser	
	130				135					140					

Ala	Ser	Ser	Ser	Gly	Gly	Gly	Ala	Thr	Arg	Ser	Ser	Ala	Val	Ser	Arg
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Pro	Thr	Arg	Arg	Ala	Ala	Ser	Arg	Ile	Arg	Lys	Ala	Asp	Glu	Gly	Glu
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165

170

175

Asn Ala Gly Gly Ala Arg Arg Ala Pro Arg Arg Asp Thr Gly Gly Gly
 180 185 190

Val Gly Ala Arg Arg Asn Ser Asp Asp Pro Val Met Val Gly Gln Arg
 195 200 205

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

Ala Arg Tyr Arg Gly Ser Leu Gln Gly Gly Ser Ser Leu Gln Asp Gly
 225 230 235 240

Thr Glu Asp Ser Ser Gly Tyr Trp Arg Phe Asp Val Glu Gly Ser Glu
 245 250 255

Glu Leu Glu Asn Tyr Phe Met Leu Ser Asp Arg His Arg Ala Met Arg
 260 265 270

Met Asp Ile Asp Gly Met Ser Tyr Glu Glu Leu Leu Ala Leu Gly Asp
 275 280 285

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

Cys Leu Lys Arg Ser Leu Tyr Thr Pro Thr Ala Pro Glu Thr His Leu
 305 310 315 320

Asp Cys Asp Arg Lys Cys Ser Ile Cys Gln Glu Glu Tyr Ser Gly Gly
 325 330 335

Glu Glu Val Gly Asn Met Ala Cys Lys His Tyr Tyr His Ile Thr Cys
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Ile Gln His Trp Leu Arg Gln Lys Asn Trp Cys Pro Ile Cys Lys Ser
 355 360 365

Val Ala Ala Lys Thr Val
 370

<210> 240

<211> 1564

<212> DNA

<213> Lycopersicon esculentum

<400> 240

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PF59082PF60142_PCT_SEQ_LIST.txt

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aaaacaactt ctcccctcat gaaccttttg gtctgttgta tagcttcttc tgttatcatt 1440
acaagcaaga aaattcttta cagagtgttt ctatcctcta cttatgtgat tactgaaagt 1500
gatggttctg ttgtttgagt gccaatccaa tgtggatgga ttgaaacgag tggtacacaa 1560
agta 1564

```

```

<210> 241
<211> 387
<212> PRT
<213> Lycopersicon esculentum
<400> 241

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```

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

```

```

Tyr Arg Lys Pro Arg Thr Gln Asn Gln Gln Glu Thr Gln Asp Met Asp
20 25 30

```

```

Pro Val Ser Ser Ser Ser Arg Ser Thr Lys Pro Thr Ile Ser Ser Leu
35 40 45

```

```

Leu Leu Ala Pro Phe Ser Pro Thr Ser Pro Ile His Glu Asn Ser Thr
50 55 60

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PF59082PF60142_PCT_SEQ_LIST.txt

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

PF59082PF60142_PCT_SEQ_LIST.txt

Arg Gln Cys Thr Ile Cys Gln Glu Glu Tyr Glu Ala Glu Asp Glu Met
340 345 350

Gly Lys Leu Asp Cys Gly His Phe Tyr His Ile Arg Cys Ile Lys Gln
355 360 365

Trp Leu Ser Gln Lys Asn Ser Cys Pro Val Cys Lys Ser Ala Ala Met
370 375 380

Ser Asn Ser
385

<210> 242
<211> 2609
<212> DNA
<213> Lycopersicon esculentum

<400> 242
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atgtttttgga ggtctgctta gcggtgaagt ttgagacact gctgtcacta caatactatc 120
tttgtctttt ggagattgtg aatatagagt tataggccta atgcaagggc aacggagtgct 180
aatcggatcc ctgccagaaa ctttgggttt tactcatggt tcaacatcga gtgatggtgg 240
tatagatcag cagatatgtt ggaataattt gcgaaatcct gcacaaaatc ggctaccaga 300
ttatatggta ctttctaagt agacaacat accatttctt agtcatgcaa accaagaaag 360
gcagagtgtg attggatgga atttaggaga atccagctcc tccaatacac aaaatagtgt 420
tagtcgtagt gaaaatacta caatgagtgc ccgtcctggg ctttctcact tctctgctga 480
acagcattat gggctttcca atattctttc attgggtgat gttgaaataa atttgaataa 540
ccagtttagct aacaacactt tattttctca agcttctacg tctagcactg ttccaaatga 600
actaagtaga agtgctggac atgaggggag tgatggcgat gaagatgatg atgatgactg 660
cgaagtgatg gagtgcaccc caacattcaa gtctaattga cctggaaaag aacggatgtc 720
aaccgccagt acttcttctg atccccttgc tgggacttct gcaactaatg ggtttctgag 780
ggatgaaagt gatggcagac caggctgtac actggatggt cgacgcatgg cttgtaagag 840
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aaacagctta tggcgttcta tacctgctcc aaataatctg actgcaggtg ctaatagctc 960
tgcatcaaca gaaagtagaa gaaacatcaa tttgccagcg cagataaatc caagacttgg 1020
gctcactatg ggtggcacca ctatggaagg tccggttgca ttgcctgctt caaggagagc 1080
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cgcatagagg ctgccttcta atcagtcttt ggattcgagg tctgtttctg ctgcagataa 1260
tgtaagtccc cgaagccagc cagttgtggg gccggttcct tctctgagac gaaatgcaca 1320
gaggtgggat tcatctagtt caagagctgg cagtccatca agttattctg tttttcttga 1380
gaggaattct gcagcctatg aacaaccaag ctcaagaagt gtgccagaa acatttcgca 1440

PF59082PF60142_PCT_SEQ_LIST.txt

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gggttttagct ggtggaaata tttccattgc tggaaatggt gcatcttctt ctcgagtggt 1560
tcctagctca gtagcccctt cctcttctcc tggttgggtg gaacaaagaa atcctcagca 1620
atatcctcga cgactctcag aatatgttcg tagatctatg ttgtcttcag ctgtcagtga 1680
acctggaagt cacaatggta acactccgcc acatttgagt tctgctacct cacaggagat 1740
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gagacaactc gatggtgcaa tgggagttcc atattcctgg aggactttgg ctgctgccgg 1860
tgaaggaaga ggcaggctag tttccgagat tcgcaatgtg ttggatctaa tgcgcagggg 1920
agagagctta agatttgagg acgttatgat cctcgatcag tcagggttct ttgggatggt 1980
ggatattcag gatcgccatc gtgatatgcg tcttgatggt gataacatgt cctatgagga 2040
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ttgtggccat gattttcatg ccgactgctg taaacaatgg ctcatgcaga agaatttgtg 2280
cccaatttgc aaaacaacag gactcaatac ttcaggaaaa caatgatcca tggaagtttg 2340
atgtaccagt tggaccatgg aaggttgaca caaagcgtgt ctacgcgttt ggtccatgag 2400
ttcattctga gtgagaaaga tctatgtatt tttctcatta attttattct gacctctgct 2460
tagagggagt tatttttagag atagaagaag cactagctac aattagggtc attaggcaag 2520
agttatacat tatttggttg tttggaaatt tacattctta ctttccaatt tattgatacc 2580
tttgaatatt ttgaaaaaaa aaaaaaaaaa 2609

```

```

<210> 243
<211> 721
<212> PRT
<213> Lycopersicon esculentum
<400> 243

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Met Gln Gly Gln Arg Ser Ala Ile Gly Ser Leu Pro Glu Thr Leu Gly
1 5 10 15

Phe Thr His Gly Ser Thr Ser Ser Asp Gly Gly Ile Asp Gln Gln Ile
20 25 30

Cys Trp Asn Asn Leu Arg Asn Pro Ala Gln Asn Arg Leu Pro Asp Tyr
35 40 45

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

Gln Glu Arg Gln Ser Val Ile Gly Trp Asn Leu Gly Glu Ser Ser Ser
65 70 75 80

PF59082PF60142_PCT_SEQ_LIST.txt

Ser Asn Thr Gln Asn Ser Val Ser Arg Ser Glu Asn Thr Thr Met Ser
85 90 95

Ala Arg Pro Gly Pro Ser His Phe Ser Ala Glu Gln His Tyr Gly Ser
100 105 110

Ser Asn Ile Leu Ser Leu Gly Asp Val Glu Ile Asn Leu Asn Asn Gln
115 120 125

Leu Ala Asn Asn Thr Leu Phe Ser Gln Ala Ser Thr Ser Ser Thr Val
130 135 140

Pro Asn Glu Leu Ser Arg Ser Ala Gly His Glu Gly Arg Asp Gly Asp
145 150 155 160

Glu Asp Asp Asp Asp Asp Cys Glu Val Met Glu Cys Thr Pro Thr Phe
165 170 175

Lys Ser Asn Gly Pro Gly Lys Glu Arg Met Ser Thr Ala Ser Thr Ser
180 185 190

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

Glu Ser Asp Gly Arg Pro Gly Cys Thr Leu Asp Gly Arg Arg Met Ala
210 215 220

Cys Lys Arg Lys Ala Val Glu Gly His Leu Gly Gln Ser Ser Gly Ser
225 230 235 240

Gly Ser Pro Asp Tyr Leu Leu Asn Ser Leu Trp Arg Ser Ile Pro Ala
245 250 255

Pro Asn Asn Leu Thr Ala Gly Ala Asn Ser Ser Ala Ser Thr Glu Ser
260 265 270

Arg Arg Asn Ile Asn Leu Pro Ala Gln Ile Asn Pro Arg Leu Gly Leu
275 280 285

Thr Met Gly Gly Thr Thr Met Glu Gly Pro Val Ala Leu Pro Ala Ser
290 295 300

Arg Arg Ala Glu Ser Tyr Arg Arg Asn Phe Arg Leu Arg Ile Asn Gly
305 310 315 320

Ser His Gln Gln Val Pro Ile Pro Gly Asn Thr Phe Pro Thr Val Gly
325 330 335

Asn Asp Arg Asn Val Thr Met Ser Asp Trp Asp Ala Leu Arg Leu Pro
340 345 350

Ser Asn Gln Ser Leu Asp Ser Arg Ser Val Ser Ala Ala Asp Asn Val

355

360

365

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

PF59082PF60142_PCT_SEQ_LIST.txt

Gly Leu Thr Glu Glu Thr Ile Leu Asn Arg Leu Lys Gln Arg Lys His
645 650 655

Val Ser Ile Arg Thr Glu Glu Thr Asn Asp Ala Glu Pro Cys Cys Ile
660 665 670

Cys Gln Glu Glu Tyr Lys Asp Gly Glu Asp Leu Gly Lys Leu Asp Cys
675 680 685

Gly His Asp Phe His Ala Asp Cys Val Lys Gln Trp Leu Met Gln Lys
690 695 700

Asn Leu Cys Pro Ile Cys Lys Thr Thr Gly Leu Asn Thr Ser Gly Lys
705 710 715 720

Gln

<210> 244
<211> 2097
<212> DNA
<213> Lycopersicon esculentum

<400> 244
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gaaaacaacg aaaacagaag agaaaaagat ataaatggtg cttcgtgtaa gacatggatg 180
aatatcctgt taaaagagct gggaatgggc ttgtcgccgc cagaagaggt ttaagggaca 240
ctgctgaaaa caagataaa aatgttcagt attgttctag acttggatgt agtggccggg 300
tcaattatac taagagtacc agagttggag gcatggagaa accgagacca ctaaggccta 360
ctttcggttc atcaaacgga aaggaagtag ttgggagttc atctgtgaca tcctctggaa 420
tgactactgc aagaaggta ggcaaggaat ctcaacagaa gtactcttct aacattgaag 480
ataagcgatc agataccagt tccttacgta aagagtcaca agtttttaaaa cagatgcagt 540
catcaacgga gcgtcaattc caatttgatt cagcaaagag agatactgga tccagcaaag 600
ttgtatttac agaagttggt tgctctagtg gaacatcgaa cagtagacct cgaaaaatat 660
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cgtctaaatc cattagtgtc gggacaagga gcagtagtag tggagaggga tacaggttga 780
gaaatctgaa gtgcaattcc acacctgatg tcctcccata tagttcttca tcatcagaat 840
caagtattag tcgaaggga acagtaaaaa ggagaaatac tgaaggtgaa agcagttcat 900
catctaaagg gaaaaaatg agtggtgcat cgccaaatga agggcgtgca gttcgtcctg 960
ctactggaat ctccatctct gattcaagga gtagtagaag ctcgatttc agtgacggta 1020
atcgtgctgt atcagttcgg accgcaggt caatgaatgt gagtactagg ttaaggggtc 1080
ctgttcagga ttcatgcat actaagtctt ctggcttaag ccaaaattta cctgagcatg 1140

PF59082PF60142_PCT_SEQ_LIST.txt

```

gaactccaaa tctagatatg cctagttcat ccagtcaact tttcatggat tcttcatcaa 1200
gtgattatag cacatatagt ttacctgcaa atgattatga tgatgacgac gaagatgaag 1260
atgaagatga tgatttacct ggtgtagtac cattcacttc agcagaaatc tgcattaacg 1320
gtatgaaccg tgaagcattg cagagatata acatggatgg agtcgctcag gtattgctgg 1380
cacttgagag aatcgaacaa gatgaagagt tatcttatga gcgactactg gcgttggagt 1440
ccaatttggt cctcagtggc cttactttt atgaccagca tagagacatg agactagata 1500
ttgatgacat gtcctatgag gaattattag cacttgagga gaggattggc tctgttagta 1560
ccgctctgcc cgaggaagaa ctattaaagt gcctcaggag aaacatttat cagggtatgg 1620
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gtcaggagga gtacgtgatc ggagatgaaa tagggaacct gggttgtgaa cacgggtatc 1740
atatggagtg cataaagcag tggtttaagc tcaagaactg gtgccctatc tgtaaggctg 1800
cagtagaatc atcgaaaccg acatcttagt tgcaaaatgg ttagatacct taaaccccag 1860
atgtgggaaa gctgttaaac agtttccctg tgtacaaatt catctggggg tggtttttgt 1920
ggattcctgc aattcatatt tactgttctc ttttccctct attctcttga actttttttt 1980
gtctcttttc ttttgcttaa ttgctctctt gccatatgaa ccaataaacc caggccttct 2040
tctggctttg tggtggtgaa tgttttcata ttcatttctt tcaaaaaaaaa aaaaaaa 2097

```

```

<210> 245
<211> 551
<212> PRT
<213> Lycopersicon esculentum
<400> 245

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

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PF59082PF60142_PCT_SEQ_LIST.txt

Lys Glu Ser Gln Val Leu Lys Gln Met Gln Ser Ser Thr Glu Arg Gln
115 120 125

Phe Gln Phe Asp Ser Ala Lys Arg Asp Thr Gly Ser Ser Lys Val Val
130 135 140

Phe Thr Glu Val Gly Cys Ser Ser Gly Thr Ser Asn Ser Arg Pro Arg
145 150 155 160

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

Asn Ser Ser Ile Ser Ser Ser Ser Lys Ser Ile Ser Ala Gly Thr Arg
180 185 190

Ser Ser Ser Ser Gly Glu Gly Tyr Arg Leu Arg Asn Leu Lys Cys Asn
195 200 205

Ser Thr Pro Asp Val Leu Pro Tyr Ser Ser Ser Ser Glu Ser Ser
210 215 220

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

Ser Ser Ser Ser Lys Gly Lys Lys Met Ser Gly Ala Ser Pro Asn Glu
245 250 255

Gly Arg Ala Val Arg Pro Ala Thr Gly Ile Ser Ile Ser Asp Ser Arg
260 265 270

Ser Ser Arg Ser Ser Asp Phe Ser Asp Gly Asn Arg Ala Val Ser Val
275 280 285

Arg Thr Arg Arg Ser Met Asn Val Ser Thr Arg Leu Arg Gly Pro Val
290 295 300

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

Glu His Gly Thr Pro Asn Leu Asp Met Pro Ser Ser Ser Ser Gln Leu
325 330 335

Phe Met Asp Ser Ser Ser Ser Asp Tyr Ser Thr Tyr Ser Leu Pro Ala
340 345 350

Asn Asp Tyr Asp Asp Asp Asp Glu Asp Glu Asp Glu Asp Asp Asp Leu
355 360 365

Pro Gly Val Val Pro Phe Thr Ser Ala Glu Ile Cys Ile Asn Gly Met
370 375 380

Asn Arg Glu Ala Leu Gln Arg Tyr Asn Met Asp Gly Val Ala Gln Val

385 390 395 400

Leu Leu Ala Leu Glu Arg Ile Glu Gln Asp Glu Glu Leu Ser Tyr Glu
405 410 415

Arg Leu Leu Ala Leu Glu Ser Asn Leu Phe Leu Ser Gly Leu Asn Phe
420 425 430

Tyr Asp Gln His Arg Asp Met Arg Leu Asp Ile Asp Asp Met Ser Tyr
435 440 445

Glu Glu Leu Leu Ala Leu Glu Glu Arg Ile Gly Ser Val Ser Thr Ala
450 455 460

Leu Pro Glu Glu Glu Leu Leu Lys Cys Leu Arg Arg Asn Ile Tyr Gln
465 470 475 480

Gly Met Ala Ser Glu Thr Glu Thr Leu Glu Ala Asp Glu Asp Gly Asp
485 490 495

Asp Ile Lys Cys Ser Ile Cys Gln Glu Glu Tyr Val Ile Gly Asp Glu
500 505 510

Ile Gly Asn Leu Gly Cys Glu His Gly Tyr His Met Glu Cys Ile Lys
515 520 525

Gln Trp Phe Lys Leu Lys Asn Trp Cys Pro Ile Cys Lys Ala Ala Val
530 535 540

Glu Ser Ser Lys Pro Thr Ser
545 550

<210> 246
<211> 2043
<212> DNA
<213> Glycine max

<400> 246
atgattaact gtcgtgatat ttttttctt ttcaatccac acccaccgta taacacaaac 60
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ccttgatgata tgaactcatc ctatgacaat tctattatta atcatgaatg gcaaaatttg 180
agtggatgga gcttagggga gccaagttcc agtaatacac caaatgagat caacaataat 240
gagcaaaaaa gagaacttgg atggatcatc accattactg ctggtgcatt ggctggtcca 300
agcctagaag aaaggcgcct tgaaccaacc aatgctcttt cactagacaa tgtcaataca 360
ggcctatct acatctgtag cccaattct catttgatgt ccagaatct caacttaaat 420
gcaggtttag cggacagtgg cagtgatgat agtcaacatc tggagctccc taacttaaac 480
aagtctagtg ggtcagcaa cgagtgtata ccacctaag ttggatctgg ttcttttctg 540
cttccttctg gaaataatgc cttcctggtg gaagatactg atggtaggcc tagttgttct 600

PF59082PF60142_PCT_SEQ_LIST.txt

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gcaagacttg gcctgggtat cggggatgaa gcatctgaaa atgtttctga ttcaaaaact 840
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atgtccagaa atatgttaga acatccagtc tttcaacctg caactgattt aagaaattta 1260
gttcaaaatc caacagttag agcttcaagt tcaagtagtg taaatttaag tattccagga 1320
aatgttgctt catcacggac tggatcaaat ccagctacca atccctcatc tgccccaact 1380
tgggtttctc ctccaatcc tccacagcat ccacggaggt tatctgaata tgtccgtcgg 1440
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cgctctgggtt tttctacatc tgaaccaagg gcgttatcat ctgggagtggt ggcaaaccgg 1560
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cgacttgatg ttgataacat gtcttatgag gagttgttgg ctctggaaga gcgcattgga 1800
aatgtgagta ctggattgag tgaggaaacc ctatcgaaac tcttgaaaca gagaaagcac 1860
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ggtgatggga atgatattgg aacgcttgat tgtggccatg atttccatag cagctgtatc 1980
aaacagtggc taatgcaaaa gaatctgtgt cccatttgta agacaacggg cttggcaaca 2040
tga 2043

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<210> 247
 <211> 680
 <212> PRT
 <213> Glycine max

<400> 247

Met Ile Asn Cys Arg Asp Ile Ile Phe Leu Phe Asn Pro His Pro Pro
 1 5 10 15

Tyr Asn Thr Asn Lys Arg Glu Lys Glu Val Ser His Ser His Glu Asn
 20 25 30

Gln Ile Pro Asp Tyr Ile Leu Ser Pro Cys Asp Met Asn Ser Ser Tyr
 35 40 45

PF59082PF60142_PCT_SEQ_LIST.txt

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

PF59082PF60142_PCT_SEQ_LIST.txt

Ser Pro Ser Ser Gln Val Ser Gln Arg Leu His Ser Val Asn Asn Ser
325 330 335

Leu Asn Ser Arg Ser Ala Pro Pro Ile Asp Asn Val Val Pro Gln Ser
340 345 350

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

Phe Arg Trp Ser Gly Gly Ser Ser Ser Arg Asn Ile His Ser Ser Asn
370 375 380

Ser Ile Ile Ser Pro Ala Arg Asp Gln Glu Asp Ala Ser Ser Arg Arg
385 390 395 400

Met Ser Arg Asn Met Leu Glu His Pro Val Phe Gln Pro Ala Thr Asp
405 410 415

Leu Arg Asn Leu Val Gln Asn Pro Thr Val Arg Ala Ser Ser Ser Ser
420 425 430

Ser Val Asn Leu Ser Ile Pro Gly Asn Val Ala Ser Ser Arg Thr Gly
435 440 445

Ser Asn Pro Ala Thr Asn Pro Ser Ser Ala Pro Thr Trp Val Ser Pro
450 455 460

Pro Asn Pro Pro Gln His Pro Arg Arg Leu Ser Glu Tyr Val Arg Arg
465 470 475 480

Ser Leu Phe Ser Pro Ser Ser Asp Ala Ile Gly Ser Pro Ser Asn Asn
485 490 495

Tyr Ser Ser Leu Arg Ser Gly Phe Ser Thr Ser Glu Pro Arg Ala Leu
500 505 510

Ser Ser Gly Ser Gly Ala Asn Pro Arg Ser Ser Ser Trp Leu Glu Arg
515 520 525

Gln Gly Gly Ser Glu Phe Gly Ile Pro Tyr Ser Leu Arg Thr Leu Ala
530 535 540

Val Ala Ser Glu Gly Ser Ser Arg Leu Val Ser Glu Asp Val Val Ile
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Leu Glu His Gln Ser Phe Leu Ser Gly Ile Ala Asp Val His Asp Arg
565 570 575

His Gly Asp Met Arg Leu Asp Val Asp Asn Met Ser Tyr Glu Glu Leu
580 585 590

Leu Ala Leu Glu Glu Arg Ile Gly Asn Val Ser Thr Gly Leu Ser Glu

595

600

605

Glu Thr Leu Ser Lys Leu Leu Lys Gln Arg Lys His Ser Val Glu Lys
 610 615 620

Gly Ser Glu Thr Asp Ala Glu Pro Cys Cys Val Cys Gln Glu Asp Tyr
 625 630 635 640

Gly Asp Gly Asn Asp Ile Gly Thr Leu Asp Cys Gly His Asp Phe His
 645 650 655

Ser Ser Cys Ile Lys Gln Trp Leu Met Gln Lys Asn Leu Cys Pro Ile
 660 665 670

Cys Lys Thr Thr Gly Leu Ala Thr
 675 680

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 <211> 2073
 <212> DNA
 <213> Glycine max

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PF59082PF60142_PCT_SEQ_LIST.txt

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<210> 249
 <211> 690
 <212> PRT
 <213> Glycine max

<400> 249

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Cys Trp Asn Asn Val Asn Pro Ala Glu Asn Gln Ile Pro Asp Tyr Ile
 35 40 45

Leu Ser Pro Cys Asp Met Asn Ser Ser Tyr Glu Asn Ser Ile Ile Asn
 50 55 60

His Glu Trp Gln Asn Leu Ser Gly Trp Ser Leu Gly Glu Pro Ser Ser
 65 70 75 80

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

Gly Trp Ser Ser Thr Ile Thr Ala Gly Ala Leu Ala Gly Pro Ser Leu
 100 105 110

Glu Glu Arg Arg Leu Glu Pro Thr Asn Ala Leu Ser Leu Asp Asn Val
 115 120 125

PF59082PF60142_PCT_SEQ_LIST.txt

Asn Thr Gly Pro Ile Tyr Ile Cys Ser Pro Asn Ser His Leu Met Ser
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 Gln Asn Leu Asn Leu Asn Ala Gly Leu Ala Asp Ser Gly Ser Asp Asp
 145 150 155 160
 Ser Gln His Leu Glu Leu Pro Asn Leu Asn Lys Ser Ser Gly Ser Ala
 165 170 175
 Asn Glu Cys Ile Pro Pro Asn Val Gly Ser Gly Ser Phe Leu Leu Pro
 180 185 190
 Ser Gly Asn Asn Ala Phe Leu Val Glu Asp Thr Asp Gly Arg Pro Ser
 195 200 205
 Cys Ser Leu Asp Thr Arg Arg Val Ser Cys Lys Arg Lys Ala Val Glu
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 Gly Asn Asn Gly Gln Ser Ser Asp Ala Gly Ser Ser Ser Tyr Ser Gln
 225 230 235 240
 His Thr Asp Gly Ser Ala Trp His Thr Ile Pro Thr Gln Asp Asn Ala
 245 250 255
 Gly Ser Ser Ser Arg Arg Ser Ile Pro Ser Glu Glu Val Asn Ala Arg
 260 265 270
 Leu Gly Leu Gly Ile Gly Asp Glu Ala Ser Glu Asn Val Ser Asp Ser
 275 280 285
 Asn Thr Ala Gly Cys Ser Glu Ser Phe His Arg Asn Phe Arg Leu Arg
 290 295 300
 Leu Asn Pro Ser Asn Pro Ala Asn Ser Val Pro Pro Thr Ala Phe Ser
 305 310 315 320
 Thr Gly Ser Met Ile Arg His Ser Gly Val Ser Pro Ser Ser Gln Val
 325 330 335
 Ser Gln Arg Leu His Ser Val Asp Asn Ser Met Asn Ser Arg Ser Ala
 340 345 350
 Pro Pro Ile Asp Asn Val Val Pro Gln Ser Gln Pro His Val Ile His
 355 360 365
 Val Pro Ala Leu Pro Arg Asn Arg Gln Ser Phe Arg Trp Ser Gly Gly
 370 375 380
 Ser Ser Ser Arg Asn Ile His Ser Ser Asn Ser Ile Ile Cys Pro Ala
 385 390 395 400

PF59082PF60142_PCT_SEQ_LIST.txt

Arg Asp Gln Glu Asp Ala Ser Ser Arg Arg Met Ser Arg Asn Met Leu
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Glu His Pro Val Phe Gln Pro Ala Thr Asp Leu Ser Asn Leu Val Gln
420 425 430

Asn Pro Thr Val Arg Ala Ser Ser Ser Ser Ser Val Asn Leu Ser Ile
435 440 445

Pro Gly Asn Val Ala Ser Ser Gln Thr Gly Ser Asn Pro Ala Thr Asn
450 455 460

Pro Ser Ser Ala Pro Thr Trp Val Ser Pro Pro Asn Pro Pro Gln His
465 470 475 480

Pro Gln Arg Leu Ser Glu Tyr Val Arg Arg Ser Leu Phe Ser Pro Ser
485 490 495

Ser Asp Ala Thr Gly Ser Pro Ser Asn Asn Phe Ser Ser Leu Arg Ser
500 505 510

Gly Phe Ser Thr Ser Glu Pro Arg Ala Leu Ser Ser Gly Ser Gly Ala
515 520 525

Asn Pro Arg Ser Ser Ser Trp Leu Glu Arg Gln Gly Gly Ser Glu Phe
530 535 540

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

Ser Arg Leu Val Ser Glu Asp Val Val Ile Leu Glu His Gln Ser Phe
565 570 575

Leu Ser Arg Ile Ala Asp Val His Asp Arg His Arg Asp Met Arg Leu
580 585 590

Asp Val Asp Asn Met Ser Tyr Glu Glu Leu Leu Ala Leu Glu Glu Arg
595 600 605

Ile Gly Asn Val Ser Thr Gly Leu Ser Glu Glu Thr Leu Ser Lys Leu
610 615 620

Leu Lys Gln Arg Lys His Ser Val Glu Lys Gly Ser Glu Thr Asp Ala
625 630 635 640

Glu Pro Cys Cys Val Cys Gln Glu Asp Tyr Gly Asp Gly Asn Asp Ile
645 650 655

Gly Thr Leu Asp Cys Gly His Asp Phe His Ser Ser Cys Ile Lys Gln
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Trp Leu Met His Lys Asn Leu Cys Pro Ile Cys Lys Thr Thr Gly Leu

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PF59082PF60142_PCT_SEQ_LIST.txt
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<211> 1592
<212> DNA
<213> Zinnia elegans

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<210> 251

<211> 463
 <212> PRT
 <213> *Zinnia elegans*

<400> 251

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Pro Phe Gly Pro Ser Ser Asp Pro Phe Glu Leu Glu Ala Arg Gln Val
35     40     45

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

Gly Val Gly Ser Ser Thr Met Phe Gln Gly Ser Glu Gly Gly Pro Pro
65     70     75     80

Ala Asp Pro Thr Ile Pro Arg Leu Gly Leu Ser Ile Gly Glu His Pro
85     90     95

Val Val Glu Asn Thr Arg Arg Asn Val Gly Leu Arg Ile Asn Ser Ala
100    105    110

Arg Gln Gln Val Asp Ala Leu Pro Ala Asn Asn Ala Asn Arg Glu Ser
115    120    125

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

His Gln Gly Gln Pro Val Leu Arg Val Pro Ala Leu Arg Arg Asn Phe
145    150    155    160

Gln Ser Thr Ser Arg Trp Arg Ala Ser Arg Ser Ala Asn Val Ala Met
165    170    175

Ser Gly Ala Arg Asn Glu Val Asp Ser Ile Ser Asp His Pro Leu Phe
180    185    190

Thr Pro Pro Ser Asn Ala Thr Thr Pro Ser Gln Thr Glu Leu Asn Trp
195    200    205

Ser Ser Asn Ser Gly Gly Asn Gly Pro Ser Ser Gly Ser Ser Thr Ser
210    215    220

His His Ser Arg Arg Leu Ser Ala Phe Leu Arg Arg Ser Leu Leu Pro
225    230    235    240

Val Ala Asp Pro Glu Asp Gly Val Gly Gln Asn Gly Asn Ile Phe Pro
245    250    255

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PF59082PF60142_PCT_SEQ_LIST.txt

Arg Val Pro Pro Ala Leu Ser Gly Ser Ser Ser Ser Ser Gln Asp Val
260 265 270

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

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

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

Ile Arg Gln Ile Arg Asn Val Leu Asp Leu Met Arg Arg Gly Glu Pro
325 330 335

Leu Arg Phe Glu Asp Leu Met Ile Leu Asp Gln Ser Val Phe Tyr Gly
340 345 350

Val Ala Asp Ile His Asp Arg His Arg Asp Met Arg Leu Asp Ile Asp
355 360 365

Asn Met Ser Tyr Glu Glu Leu Leu Ala Leu Glu Glu Arg Ile Gly Asn
370 375 380

Val Asn Thr Gly Leu Thr Glu Glu Thr Ile Leu Lys His Ile Arg Gln
385 390 395 400

Lys Gln Tyr Val Val Gly Asn Gly Ser Ala Arg Cys Arg Pro Cys Cys
405 410 415

Ile Cys Gln Glu Glu Tyr Lys Asp Gly Asp Asp Leu Gly Thr Leu Asp
420 425 430

Cys Thr His Asp Phe His Tyr Gly Cys Ile Lys Gln Trp Leu Gln Gln
435 440 445

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

<210> 252
<211> 2103
<212> DNA
<213> Lotus japonicus

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PF59082PF60142_PCT_SEQ_LIST.txt

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 <211> 549
 <212> PRT
 <213> Lotus japonicus

<400> 253

PF59082PF60142_PCT_SEQ_LIST.txt

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Leu Gly Arg Thr Ser Thr Ala Glu Asn Gly Ser Tyr Phe Tyr Pro Val
35 40 45

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

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

Pro Pro His Gln Ser Asp Thr Ser Gly Ala Ser Asn Asp His Phe Ile
85 90 95

His Ser Ser Ser Ala Gly Ala Phe Phe Ala Val Ser Asn Asn Cys Val
100 105 110

Pro Gln Pro Pro Ala Ala Asn Tyr Asp Arg Pro Pro Phe Gln Val Asp
115 120 125

Gly Gly Phe Ile Asp Leu Thr Met Gly Ser Gly Arg Gly Pro His Lys
130 135 140

Arg Lys Ser Pro Gly Ile Pro Ser Val Tyr Glu Arg Gly Gly Ser Ser
145 150 155 160

Arg Tyr Phe Asn Ala Gly Ser Ser Thr Asp Val Pro Ile Ser Ser Glu
165 170 175

Ser Arg Pro Glu Lys Pro Asn Ile Asp Ser Gln Tyr Met Pro Trp Asp
180 185 190

His Val Pro Met Thr Ser Thr Val Arg Gly Ala Gly His Ser Ile Lys
195 200 205

Gly Glu Ser Ser Leu Arg Asn Val Arg Ser Arg Ser Ala Leu Asp Leu
210 215 220

Glu Ser Asn Leu Ser Arg Thr His Leu Pro Ser Asn His Ser His Asn
225 230 235 240

Ser Tyr Ser Thr Ile Pro Pro Val Asp His Ser Ser Met Met Asp Leu
245 250 255

Ser Gly Gln Ile Ser Thr Ser Leu Thr Gly Asp Trp Ser Gln Met Asn
260 265 270

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

Gly Leu Glu Ser Ser His Phe Leu Ala Gly Ser Gly Ala Thr Ala Ser
 290 295 300

Asn Ala Ser Val Asp Val Gly Ser Phe His His Glu Phe Gly Thr Ser
 305 310 315 320

Arg Asn Pro Thr Gly Pro Gln Ser Phe His Asn Leu Thr Gln Thr Ala
 325 330 335

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

Ala Ser Ser Ser Thr His Leu Gly His Val Thr Pro Leu Asp Asp Gly
 355 360 365

Leu Pro Met Val Ala Glu Ser Tyr Ser Ser Arg His Gln Arg Pro Leu
 370 375 380

Ser Ser Ile Gly Trp Arg Asn Ser Asp Arg Asn Gly Arg Ala Arg Ile
 385 390 395 400

Ser Ser Glu Arg Tyr Arg Ser Leu Ala Asn Glu Ala Gly Leu His Gly
 405 410 415

Arg Ile Ser Pro Glu Val Phe Met Ile Val Asp Arg Ala Ser Met Tyr
 420 425 430

Gly Ser Arg Asn Met Leu Asp Gln His Arg Asp Met Arg Met Asp Ile
 435 440 445

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

His Val Asn Thr Gly Leu Ser Glu Asp Ser Phe Ser Gln Cys Met Thr
 465 470 475 480

Glu Thr Ile Tyr Cys Ser Ser Glu Gln Gly Gln Asp Glu Gly Ser Cys
 485 490 495

Val Ile Cys Leu Glu Glu Tyr Lys Asn Met Asp Asp Val Gly Thr Leu
 500 505 510

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

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 <211> 1494
 <212> DNA
 <213> Arabidopsis thaliana

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 <212> PRT
 <213> Arabidopsis thaliana

<400> 255

Met Asp Arg Trp Ser Ser Lys Arg Ala Met Glu Ala Arg Pro Asp Ser
 1 5 10 15

PF59082PF60142_PCT_SEQ_LIST.txt

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

PF59082PF60142_PCT_SEQ_LIST.txt

Asp Gly Leu Ser Ser Val Thr Ala Ala Glu Met Ser Gln Thr Glu Thr
290 295 300

Ser Asn Asn Leu Asn Ser Pro Val Ser Leu Glu Leu Phe Ser Gly Phe
305 310 315 320

Pro Glu Phe Gly Leu Ser Gly Ser Leu Leu Ser His Asp Ser Phe Arg
325 330 335

Ser Tyr Asn Leu Asp Gly Ile Ser Glu Ile Leu Pro Glu Leu Asp Arg
340 345 350

Ile Glu Gln Asp Ile Glu Leu Asn Tyr Glu Asp Leu Leu Ile Met Glu
355 360 365

Thr Gly Leu Leu Leu Gly Gly Leu Ser Phe His Asp Gln His Arg Asp
370 375 380

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

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

Ser Lys Cys Leu Lys Thr Ser Ile Tyr Gln Met Lys Pro Leu Ser Tyr
420 425 430

Gly Ser Ile Thr Lys Ser Pro Ser Asp Asn Lys Glu Asp Ala Lys Cys
435 440 445

Ser Ile Cys Gln Glu Glu Tyr Thr Ile Gly Asp Glu Val Gly Arg Leu
450 455 460

His Cys Glu His Thr Tyr His Val Lys Cys Val Gln Glu Trp Leu Arg
465 470 475 480

Ile Lys Ser Trp Cys Pro Ile Cys Lys Ala Thr Ala Glu Thr Ser Ser
485 490 495

Lys

<210> 256
<211> 1485
<212> PRT
<213> Arabidopsis thaliana

<400> 256

Ala Thr Gly Gly Gly Ala Cys Ala Ala Ala Gly Ala Ala Ala Thr Ala
1 5 10 15

Gly Gly Ala Ala Thr Gly Thr Thr Gly Ala Thr Thr Thr Ala Gly Ala
Seite 251

20

25

30

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 35 40 45

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Cys Ala Ala Gly Cys Ala Gly Thr Cys Ala Cys Gly Gly Thr Gly Thr
 305 310 315 320
 Ala Gly Thr Thr Gly Gly Thr Gly Thr Ala Ala Gly Thr Cys Cys Thr
 325 330 335
 Gly Ala Thr Cys Ala Thr Gly Ala Ala Thr Ala Cys Gly Ala Ala Ala
 340 345 350
 Gly Ala Ala Ala Thr Gly Cys Thr Cys Ala Thr Thr Thr Thr Ala Thr
 355 360 365
 Gly Gly Ala Thr Cys Ala Cys Ala Cys Ala Ala Gly Ala Gly Gly Gly
 370 375 380
 Ala Cys Ala Thr Ala Cys Ala Ala Gly Cys Gly Ala Ala Ala Gly Ala
 385 390 395 400
 Ala Cys Gly Cys Thr Gly Ala Ala Gly Gly Ala Ala Thr Ala Cys Cys
 405 410 415
 Cys Gly Gly Ala Cys Ala Ala Cys Cys Thr Cys Ala Ala Thr Ala Thr
 420 425 430
 Thr Thr Ala Ala Gly Thr Ala Cys Cys Thr Thr Ala Gly Cys Ala Gly
 435 440 445
 Cys Thr Cys Cys Ala Thr Thr Thr Ala Ala Cys Ala Cys Ala Cys Cys
 450 455 460
 Gly Gly Ala Gly Ala Cys Ala Ala Thr Ala Gly Cys Cys Cys Cys Thr
 465 470 475 480
 Thr Thr Thr Gly Gly Ala Gly Gly Cys Gly Cys Thr Ala Gly Gly Ala
 485 490 495
 Ala Cys Ala Gly Ala Cys Cys Ala Gly Gly Ala Gly Cys Thr Gly Thr
 500 505 510
 Thr Ala Cys Ala Gly Thr Gly Ala Ala Cys Ala Cys Thr Gly Thr Thr
 515 520 525
 Cys Thr Thr Cys Cys Thr Thr Cys Thr Cys Ala Thr Gly Cys Thr Cys
 530 535 540
 Cys Ala Ala Ala Cys Ala Ala Cys Thr Thr Cys Ala Thr Thr Cys Ala
 545 550 555 560
 Ala Gly Gly Ala Ala Ala Cys Thr Ala Thr Gly Cys Ala Gly Gly Thr
 565 570 575

PF59082PF60142_PCT_SEQ_LIST.txt

Cys Ala Thr Cys 580 Ala Thr Cys Cys Thr 585 Thr Thr Thr Cys Cys 590 Ala Cys
 Cys Thr Cys 595 Cys Thr Gly Gly Cys 600 Thr Cys Ala Ala Thr 605 Gly Thr Gly
 Gly Thr 610 Ala Thr Gly Ala Thr 615 Cys Ala Ala Cys Ala Cys Cys Ala Cys
 Gly 625 Gly Cys Ala Gly Ala 630 Thr Cys Thr Gly Ala 635 Thr Gly Gly Cys Thr 640
 Cys Ala Cys Cys Thr 645 Thr Cys Gly Thr Thr 650 Cys Thr Gly Gly Cys 655 Cys
 Cys Ala Cys Ala 660 Cys Cys Thr Thr Ala 665 Cys Ala Thr Gly Cys 670 Ala Cys
 Gly Gly Thr 675 Ala Gly Thr Ala Ala 680 Cys Ala Thr Thr Thr 685 Thr Cys Gly
 Cys Thr 690 Gly Gly Thr Thr Cys 695 Cys Ala Thr Ala Gly 700 Ala Gly Thr Cys
 Thr 705 Ala Gly Thr Ala Gly 710 Cys Ala Gly Ala Ala 715 Ala Cys Cys Cys Thr 720
 Ala Cys Ala Thr Cys 725 Ala Thr Thr Thr Ala 730 Thr Gly Thr Ala Thr 735 Cys
 Cys Thr Thr Cys 740 Thr Cys Ala Gly Thr 745 Thr Ala Ala Ala Cys 750 Cys Cys
 Gly Ala Gly 755 Gly Gly Ala Cys Cys 760 Ala Cys Thr Ala Thr 765 Thr Ala Thr
 Ala Gly 770 Thr Cys Ala Thr Cys 775 Ala Thr Cys Ala Cys 780 Cys Ala Cys Cys
 Cys 785 Gly Gly Cys Ala Cys 790 Cys Thr Cys Cys Thr 795 Cys Cys Thr Gly Thr 800
 Ala Cys Ala Ala Gly 805 Gly Cys Ala Thr Gly 810 Ala Gly Ala Gly 815 Cys
 Cys Ala Gly Ala 820 Ala Thr Gly Cys Cys 825 Ala Cys Ala Thr Thr 830 Ala Thr
 Ala Thr Cys 835 Cys Cys Cys Ala Cys 840 Ala Cys Ala Gly Cys 845 Thr Thr Cys

Thr Thr Cys Thr Gly Cys Thr Thr Cys Ala Thr Ala Cys Ala Gly Ala
 850 855 860
 Gly Thr Thr Cys Cys Thr Cys Cys Ala Gly Gly Gly Ala Gly Thr Thr
 865 870 875 880
 Thr Thr Ala Cys Thr Cys Cys Thr Cys Ala Gly Ala Ala Cys Ala Cys
 885 890 895
 Ala Ala Thr Gly Ala Ala Thr Ala Gly Thr Gly Gly Thr Cys Cys Cys
 900 905 910
 Thr Thr Gly Gly Gly Gly Thr Cys Ala Gly Ala Gly Ala Thr Gly Gly
 915 920 925
 Gly Cys Thr Cys Gly Ala Gly Thr Cys Ala Cys Ala Thr Gly Gly Gly
 930 935 940
 Thr Cys Cys Gly Gly Thr Thr Cys Ala Ala Cys Cys Ala Ala Cys Cys
 945 950 955 960
 Gly Gly Gly Thr Thr Thr Cys Gly Gly Ala Thr Ala Thr Ala Cys Cys
 965 970 975
 Ala Gly Cys Ala Thr Cys Ala Thr Cys Ala Gly Cys Gly Ala Gly Ala
 980 985 990
 Thr Gly Ala Thr Thr Cys Thr Gly Thr Ala Cys Cys Thr Gly Thr Ala
 995 1000 1005
 Gly Cys Ala Ala Cys Thr Cys Thr Thr Ala Gly Ala Cys Ala Ala
 1010 1015 1020
 Cys Ala Cys Cys Gly Thr Gly Gly Ala Gly Gly Ala Gly Thr Thr
 1025 1030 1035
 Cys Cys Thr Cys Gly Gly Cys Thr Thr Ala Gly Ala Gly Thr Gly
 1040 1045 1050
 Ala Thr Gly Cys Cys Thr Gly Ala Thr Gly Ala Thr Gly Ala Ala
 1055 1060 1065
 Gly Thr Thr Gly Cys Gly Cys Thr Thr Thr Thr Gly Gly Ala Gly
 1070 1075 1080
 Thr Thr Thr Gly Gly Ala Gly Ala Cys Thr Thr Cys Cys Thr Thr
 1085 1090 1095
 Gly Gly Thr Gly Gly Thr Thr Cys Thr Gly Gly Ala Ala Ala Thr
 1100 1105 1110
 Ala Ala Thr Cys Ala Cys Ala Thr Thr Gly Ala Thr Cys Ala Thr
 1115 1120 1125

1115														
Cys	Ala	Thr	Cys	Gly	Ala	Gly	Ala	Thr	Ala	Thr	Gly	Cys	Gly	Ala
	1130					1135					1140			
Thr	Thr	Gly	Gly	Ala	Cys	Ala	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Ala
	1145					1150					1155			
Ala	Thr	Gly	Thr	Cys	Thr	Thr	Ala	Cys	Gly	Ala	Gly	Gly	Ala	Gly
	1160					1165					1170			
Cys	Thr	Thr	Cys	Thr	Thr	Gly	Cys	Thr	Thr	Thr	Gly	Ala	Gly	Thr
	1175					1180					1185			
Gly	Ala	Gly	Cys	Gly	Ala	Ala	Thr	Thr	Gly	Gly	Ala	Ala	Cys	Ala
	1190					1195					1200			
Gly	Thr	Ala	Ala	Ala	Cys	Ala	Cys	Thr	Gly	Gly	Gly	Thr	Thr	Gly
	1205					1210					1215			
Cys	Cys	Gly	Gly	Ala	Gly	Gly	Ala	Ala	Gly	Ala	Thr	Gly	Thr	Thr
	1220					1225					1230			
Ala	Ala	Gly	Ala	Ala	Thr	Cys	Ala	Thr	Thr	Thr	Gly	Ala	Ala	Ala
	1235					1240					1245			
Ala	Cys	Ala	Ala	Gly	Ala	Ala	Cys	Ala	Thr	Gly	Thr	Thr	Cys	Thr
	1250					1255					1260			
Gly	Gly	Ala	Ala	Thr	Cys	Ala	Ala	Cys	Thr	Thr	Thr	Gly	Ala	Ala
	1265					1270					1275			
Ala	Ala	Ala	Gly	Ala	Gly	Thr	Cys	Gly	Thr	Cys	Gly	Thr	Cys	Cys
	1280					1285					1290			
Cys	Cys	Ala	Cys	Gly	Ala	Ala	Cys	Thr	Ala	Ala	Ala	Gly	Ala	Thr
	1295					1300					1305			
Thr	Thr	Ala	Gly	Ala	Ala	Ala	Cys	Cys	Gly	Ala	Ala	Cys	Cys	Gly
	1310					1315					1320			
Thr	Gly	Cys	Ala	Cys	Thr	Ala	Thr	Ala	Thr	Gly	Thr	Cys	Ala	Gly
	1325					1330					1335			
Gly	Ala	Ala	Ala	Gly	Cys	Thr	Thr	Cys	Ala	Ala	Gly	Ala	Ala	Cys
	1340					1345					1350			
Gly	Ala	Ala	Gly	Ala	Ala	Ala	Ala	Gly	Ala	Thr	Thr	Gly	Cys	Gly
	1355					1360					1365			
Ala	Cys	Thr	Thr	Thr	Gly	Gly	Ala	Thr	Thr	Gly	Cys	Gly	Gly	Gly
	1370					1375					1380			

PF59082PF60142_PCT_SEQ_LIST.txt

Cys Ala Cys Gly Ala Gly Thr Ala Thr Cys Ala Thr Gly Cys Ala
1385 1390 1395

Gly Ala Gly Thr Gly Cys Thr Thr Gly Gly Ala Gly Ala Ala Ala
1400 1405 1410

Thr Gly Gly Cys Thr Gly Ala Thr Thr Gly Thr Gly Ala Ala Gly
1415 1420 1425

Ala Ala Cys Gly Thr Thr Thr Gly Cys Cys Cys Ala Ala Thr Cys
1430 1435 1440

Thr Gly Thr Ala Ala Ala Thr Cys Ala Gly Ala Gly Gly Cys Ala
1445 1450 1455

Cys Thr Gly Gly Thr Cys Ala Thr Gly Gly Ala Gly Ala Ala Gly
1460 1465 1470

Ala Gly Ala Ala Ala Gly Gly Thr Ala Thr Ala Gly
1475 1480 1485

<210> 257
<211> 494
<212> PRT
<213> Arabidopsis thaliana
<400> 257

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1 5 10 15

Ser Gln Ala Ser Leu Gln Ala Glu Pro Cys Ile Leu Leu Gly Ser Phe
20 25 30

Pro Gln Gln Pro Asp Asn Asn Asn Met Pro Ala Met Val Ala His Val
35 40 45

Pro Asn Leu Glu Pro His Ser Leu Gln Asp Pro Thr Tyr Asp Asn Ser
50 55 60

Ala Met Phe Tyr Gly Leu Pro Gln Tyr His His His Pro His Gln Arg
65 70 75 80

Val Pro Thr Asn Phe Tyr Val Pro Tyr Val Ala Phe Gln Ala Pro Pro
85 90 95

Gly Gln Leu Pro Ser Ser Ser Ser His Gly Val Val Gly Val Ser Pro
100 105 110

Asp His Glu Tyr Glu Arg Asn Ala His Phe Met Asp His Thr Arg Gly
115 120 125

PF59082PF60142_PCT_SEQ_LIST.txt

Thr Tyr Lys Arg Lys Asn Ala Glu Gly Ile Pro Gly Gln Pro Gln Tyr
130 135 140

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

Phe Gly Gly Ala Arg Asn Arg Pro Gly Ala Val Thr Val Asn Thr Val
165 170 175

Leu Pro Ser His Ala Pro Asn Asn Phe Ile Gln Gly Asn Tyr Ala Gly
180 185 190

His His Pro Phe Pro Pro Pro Gly Ser Met Trp Tyr Asp Gln His His
195 200 205

Gly Arg Ser Asp Gly Ser Pro Ser Phe Trp Pro Thr Pro Tyr Met His
210 215 220

Gly Ser Asn Ile Phe Ala Gly Ser Ile Glu Ser Ser Ser Arg Asn Pro
225 230 235 240

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

Ser His His His His Pro Ala Pro Pro Val Gln Gly Met Arg Gly
260 265 270

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

Val Pro Pro Gly Ser Phe Thr Pro Gln Asn Thr Met Asn Ser Gly Pro
290 295 300

Leu Gly Ser Glu Met Gly Ser Ser His Met Gly Pro Val Gln Pro Thr
305 310 315 320

Gly Phe Arg Ile Tyr Gln His His Gln Arg Asp Asp Ser Val Pro Val
325 330 335

Ala Thr Leu Arg Gln His Arg Gly Gly Val Pro Arg Leu Arg Val Met
340 345 350

Pro Asp Asp Glu Val Ala Leu Leu Glu Phe Gly Asp Phe Leu Gly Gly
355 360 365

Ser Gly Asn Asn His Ile Asp His His Arg Asp Met Arg Leu Asp Ile
370 375 380

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

Thr Val Asn Thr Gly Leu Pro Glu Glu Asp Val Lys Asn His Leu Lys

405

410

415

Thr Arg Thr Cys Ser Gly Ile Asn Phe Glu Lys Glu Ser Ser Ser Pro
 420 425 430

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

Phe Lys Asn Glu Glu Lys Ile Ala Thr Leu Asp Cys Gly His Glu Tyr
 450 455 460

His Ala Glu Cys Leu Glu Lys Trp Leu Ile Val Lys Asn Val Cys Pro
 465 470 475 480

Ile Cys Lys Ser Glu Ala Leu Val Met Glu Lys Arg Lys Val
 485 490

<210> 258
 <211> 1641
 <212> DNA
 <213> Arabidopsis thaliana

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 aacagatcac atgtttatcc agcagaaaac atgttgaatg aaggaatgcc agtgtcttct 180
 cattggaact cttctccagg accaaatgct tatactgact caggatcatag tgtggagaga 240
 ccacactaca atccgggggt ttcggggccg tcccatgata cttccgtgaa ttcaacagtt 300
 ccaactttct ctgctccaca tgagaattat gtgacatttg catcttcttc aagctacaac 360
 agccagacat ggtcaaatgc tagttatgtt gatcatcaat ctatggaaag tgtgagagga 420
 gcacaaaaga gaaaacgacc atgtccttct tccatctatg aaatgggtag ttcaagccaa 480
 tatcacggtg acagaactcc tgcagacact catttccctc cggaattgca cttgggaaaa 540
 tcaataacgc atgatcatga ccctcattac atgccatggc ttatgaaccc aacttacaga 600
 agtaataatc tctcgatcag gggagagagc tcttcaagga atgtccggag tcgtcctaca 660
 cttgattcag agaccagctt aggtagaaat aatttgccaa gaagcttgag ctttgattct 720
 cattctacac accaccacag tgttgatcat tatggctcag gtcaatttcc tggtcagaca 780
 tctcacggaa ataaagactg gaactgtgct agattgtccc cagttcttag agatataaat 840
 ggcttttagtc cagagacaaa taatttcctt cctgcaagaa gtgttggtcaa cagcttatct 900
 gttaataactt ccggctatca tcaccatgag cttaccggaa acagaaaacc tacagtttcc 960
 cacgggggtc ctggaacttc aacactatct acaagcagca gccgcttctc tcataggtca 1020
 acatccacct atagatcttc ttcacacggt tcgcatcggt gacatgtagc atcttcttct 1080
 ggagacaggt ctcatgtgtt cactgagact tatccgtcta ggcatttaag gccaccacca 1140
 cacatttcat ggcgtagcgg tgatcgcca gggagacgca gaagttccta tgagaggttt 1200

PF59082PF60142_PCT_SEQ_LIST.txt

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 gaagatcgcc aaccacaata ctacggatcc agaaacatgc ttgatcacca cagagacatg 1320
 aggcttgaca tcgataacat gagctatgag gaactccttg atcttgagga aaggattggg 1380
 agtgtcaaca ctgggtctatc cgacagcgca atctccagtt gcttgtttagc aacaatgtat 1440
 tatccatcat atcaaacaga ggagcaaaga aaatgtgcaa tctgcctgga ggagtacaag 1500
 gaaaaagaag agttagggga agttaagggg tgtgggtcatg actaccatgg gaggtgcatc 1560
 aagaaatggg tgtctatgaa gaactcttgc cctatttgca aatcccctgc tttacctgat 1620
 gcttctaaga actcatcata a 1641

<210> 259
 <211> 546
 <212> PRT
 <213> Arabidopsis thaliana
 <400> 259

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

180

185

190

Trp Leu Met Asn Pro Thr Tyr Arg Ser Asn Asn Leu Ser Ile Arg Gly
 195 200 205
 Glu Ser Ser Ser Arg Asn Val Arg Ser Arg Pro Thr Leu Asp Ser Glu
 210 215 220
 Thr Ser Leu Gly Arg Asn Asn Leu Pro Arg Ser Leu Ser Leu Asp Ser
 225 230 235 240
 His Ser Thr His His His Ser Val Asp His Tyr Gly Ser Gly Gln Phe
 245 250 255
 Pro Gly Gln Thr Ser His Gly Asn Lys Asp Trp Asn Cys Ala Arg Leu
 260 265 270
 Ser Pro Val Leu Arg Asp Ile Asn Gly Phe Ser Pro Glu Thr Asn Asn
 275 280 285
 Phe Leu Pro Ala Arg Ser Val Val Asn Ser Leu Ser Val Asn Thr Ser
 290 295 300
 Gly Tyr His His His Glu Leu Thr Gly Asn Arg Asn Pro Thr Val Ser
 305 310 315 320
 His Gly Val Pro Gly Thr Ser Thr Leu Ser Thr Ser Ser Ser Arg Phe
 325 330 335
 Ser His Arg Ser Thr Ser Thr Tyr Arg Ser Ser Ser His Gly Ser Arg
 340 345 350
 Ser Gly His Val Ala Ser Ser Ser Gly Asp Arg Ser His Leu Val Thr
 355 360 365
 Glu Thr Tyr Pro Ser Arg His Leu Arg Pro Pro Pro His Ile Ser Trp
 370 375 380
 Arg Ser Gly Asp Arg Pro Gly Arg Arg Arg Ser Ser Tyr Glu Arg Phe
 385 390 395 400
 Gln Pro Pro Phe Asp Glu Val Ala Leu His Glu Arg Phe Ser Ser Glu
 405 410 415
 Glu Phe Met Val Glu Asp Arg Gln Pro Gln Tyr Tyr Gly Ser Arg Asn
 420 425 430
 Met Leu Asp His His Arg Asp Met Arg Leu Asp Ile Asp Asn Met Ser
 435 440 445
 Tyr Glu Glu Leu Leu Asp Leu Gly Glu Arg Ile Gly Ser Val Asn Thr
 450 455 460

PF59082PF60142_PCT_SEQ_LIST.txt

Gly Leu Ser Asp Ser Ala Ile Ser Ser Cys Leu Leu Ala Thr Met Tyr
465 470 475 480

Tyr Pro Ser Tyr Gln Thr Glu Glu Gln Arg Lys Cys Ala Ile Cys Leu
485 490 495

Glu Glu Tyr Lys Glu Lys Glu Glu Leu Gly Glu Val Lys Gly Cys Gly
500 505 510

His Asp Tyr His Gly Arg Cys Ile Lys Lys Trp Leu Ser Met Lys Asn
515 520 525

Ser Cys Pro Ile Cys Lys Ser Pro Ala Leu Pro Asp Ala Ser Lys Asn
530 535 540

Ser Ser
545

<210> 260
<211> 1563
<212> DNA
<213> Arabidopsis thaliana

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agaattgggtt gcagttccag ggtagtttcc actaagggag atttgattga tcataaagca      180
aaagctactg tgtcttcggt tcgatctcct ttgagtggaa aggaaaccgt tggtagttca      240
tctcgaagta tgagtggatt tgggtgtaca aaaaaggctt ccaaggttat tggtaggaga      300
caactctctt ctcttttggg catggattct tcagagagca gcagtgttaa tgaagactca      360
cccacaagtg agcgttccct tcctcgtgga aagacaaaag aaagcactat tagtgttcat      420
tctgaaagta gtgtctctgg agaagttgtg acagaggcag gaagctcgag tagaggaact      480
ggtagaagca ttcacagag acctgatttg gtctcccgag atgctcgtgt gagtaatagt      540
gagcaaaatg caagagctag tgtgaacaag aatggattaa gagacttgag gaacaaatct      600
ggttctgatg ttcttccatc taattcaact ccgacaagaa aaagtaacat ctttagaaag      660
aaaacctctg atggtgagag cagctcttcg agtagaggga ataagacgga aggatcagtg      720
gttgggggaa agaataattag ttcccctcag gggaatggca tcaccatgtc tgaacctagg      780
aggaacagaa acttaccaag tgtaggggac aacagtgttg tttcaagtag tactaggaga      840
tcaactgggtt attatggtag aacaggacgt gctggagcgg ttgcaacact acaagcacct      900
cggcctccaa caagagctga tctcaatcct tctagatcgg cagaagcttc gcgtagtcct      960
ttaaatagtt acagtaggcc aatcagtagt aatggcaggt tacgtagcct gatgatgcct     1020
ggtagcccct cagaagccgg ctttctcgc tctttgatga accgtgatac tttcagacgg     1080
tataacatga atggagttgc agaggtattg ttggccctgg aaaggattga gcaagacgaa     1140
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PF59082PF60142_PCT_SEQ_LIST.txt

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 agcttccacg atcagcatag agatatgagg cttagacattg acaacatgtc gtatgaggaa 1260
 ctgttagcat tagaggagaa aatgggtaca gtgagcactg ctctaagcga agaagcgctt 1320
 ctgaaaagcc tcaagtcaag tatttaccgt ccaaacgatg aatccgacga catttgacctg 1380
 aacaaagatg atgatgtcaa gtgcagcatt tgccaggaag agtatgttga tggagatgaa 1440
 gtagggactt tgccttgcca acataaatac cacgtgagct gcgcgcaaca atggctacgg 1500
 atgaagaatt ggtgtcctat atgtaaaacc tctgcagaat ctcagccaca tccattttca 1560
 tga 1563

<210> 261
 <211> 520
 <212> PRT
 <213> Arabidopsis thaliana
 <400> 261

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

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

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

Ser Ser Phe Arg Ser Pro Leu Ser Gly Lys Glu Thr Val Gly Ser Ser
 65 70 75 80

Ser Arg Ser Met Ser Gly Phe Gly Gly Thr Lys Lys Ala Ser Lys Val
 85 90 95

Ile Gly Arg Arg Gln Leu Ser Ser Leu Leu Asp Met Asp Ser Ser Glu
 100 105 110

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

Arg Gly Lys Thr Lys Glu Ser Thr Ile Ser Val His Ser Glu Ser Ser
 130 135 140

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

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

Val Ser Asn Ser Glu Gln Asn Ala Arg Ala Ser Val Asn Lys Asn Gly
180 185 190

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

Ser Thr Pro Thr Arg Lys Ser Asn Ile Phe Arg Lys Lys Thr Ser Asp
210 215 220

Gly Glu Ser Ser Ser Ser Arg Gly Asn Lys Thr Glu Gly Ser Val
225 230 235 240

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

Ser Glu Pro Arg Arg Asn Arg Asn Leu Pro Ser Val Arg Asp Asn Ser
260 265 270

Val Val Ser Ser Ser Thr Arg Arg Ser Thr Gly Tyr Tyr Gly Arg Thr
275 280 285

Gly Arg Ala Gly Ala Val Ala Thr Leu Gln Ala Pro Arg Pro Pro Thr
290 295 300

Arg Ala Asp Leu Asn Pro Ser Arg Ser Ala Glu Ala Ser Arg Ser Pro
305 310 315 320

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

Leu Met Met Pro Gly Ser Pro Ser Glu Ala Gly Leu Ser Arg Ser Leu
340 345 350

Met Asn Arg Asp Thr Phe Arg Arg Tyr Asn Met Asn Gly Val Ala Glu
355 360 365

Val Leu Leu Ala Leu Glu Arg Ile Glu Gln Asp Glu Glu Leu Thr Tyr
370 375 380

Glu Gln Leu Ala Val Leu Glu Thr Asn Leu Phe Leu Asn Gly Met Ser
385 390 395 400

Ser Phe His Asp Gln His Arg Asp Met Arg Leu Asp Ile Asp Asn Met
405 410 415

Ser Tyr Glu Glu Leu Leu Ala Leu Glu Glu Lys Met Gly Thr Val Ser
420 425 430

Thr Ala Leu Ser Glu Glu Ala Leu Leu Lys Ser Leu Lys Ser Ser Ile
435 440 445

Tyr Arg Pro Asn Asp Glu Ser Asp Asp Ile Cys Leu Asn Lys Asp Asp

450

Asp Val Lys Cys Ser Ile Cys Gln Glu Glu Tyr Val Asp Gly Asp Glu
465 470 475 480

Val Gly Thr Leu Pro Cys Gln His Lys Tyr His Val Ser Cys Ala Gln
485 490 495

Gln Trp Leu Arg Met Lys Asn Trp Cys Pro Ile Cys Lys Thr Ser Ala
500 505 510

Glu Ser Gln Pro His Pro Phe Ser
515 520

<210> 262
<211> 2076
<212> DNA
<213> Arabidopsis thaliana

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PF59082PF60142_PCT_SEQ_LIST.txt

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caggaggaat acaccgaagg agaagacatg gggacactag aatgtgggca tgaattccat	1980
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<210> 263
 <211> 691
 <212> PRT
 <213> Arabidopsis thaliana

<400> 263

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

Asn Ile His Ser Leu Gly Asp Asn Asp Leu Gln Asp Tyr Met Ile Ala
 35 40 45

Asn Ser Glu Ser Asn Thr Ser Leu Ala Asn Ser Val Tyr His Glu Gln
 50 55 60

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

Lys Asp Glu Ala Ser Ser His Asn Glu Gln Arg Met Glu Thr Arg Cys
 85 90 95

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

Gln Pro Ser Gly Thr Asn Gln Pro Val Gln Asn Val Asn Leu Asn Ala
 115 120 125

Glu Tyr Ile Glu Ile His Glu Asp Ile Asn Pro Tyr Arg Gly Arg Ser
 130 135 140

PF59082PF60142_PCT_SEQ_LIST.txt

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145 150 155 160

Arg Ser Phe Glu Glu Asn Gly Val Gly Thr Gly Ser Ser Val Glu Gly
165 170 175

Arg Arg Ala Ser Cys Lys Arg Lys Ala Leu Glu Gly Ser Ile Ser Gln
180 185 190

Ser Ser Ser Gly Gly Tyr His Asp Phe Gln Arg Gly Glu Ser Ser Ser
195 200 205

Trp Thr Pro Gly Ser Thr Val Phe Arg Pro Gly Asn Gly Leu Asn Ile
210 215 220

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

Pro Asn Phe Pro Val Ser Ala Pro Asn Phe Pro Val Ser Ala Ile Ala
245 250 255

Glu Ser Ser Ser Arg Asn Ile Cys Val Arg Ser Asn Pro Ser Asp His
260 265 270

Gln Glu Thr Val Asn Pro Ser Thr Phe Ala Ala Gly Thr Val Val Arg
275 280 285

Arg Pro Val Pro Pro Ser Gln Leu Asn Leu Ser Arg His Leu Pro Ala
290 295 300

Asp Gln His Ser Leu Asp Leu Arg Pro Gly Gln Ser Phe Val Val Ser
305 310 315 320

Arg Asn Pro Asn Ser Thr Pro Val Ser Ile Pro Pro Gly Ser Arg Thr
325 330 335

Met Leu Pro Pro Phe Arg Trp Thr Gly Ser Ser Leu Val Gly Gly Thr
340 345 350

Ser Asn Ser Thr Ala Pro Val Glu Arg Asn Leu His Leu Asp Glu Thr
355 360 365

Arg Ser Arg Ser Ile Pro Gly Asn Thr Leu Glu Ile Pro Met Phe Ala
370 375 380

Ala Pro Glu Val Gly Asn Phe Ala Arg Ser Gln Ser Ser Arg Asn Val
385 390 395 400

Thr Asn Gly Asn Leu Asn Ser Ala Ser Ser Val Ser Arg Thr Gly Ser
405 410 415

Thr Thr Ser Val Pro Pro Pro Pro Pro Ser Ser Asn Leu Ala Trp
420 425 430

Thr Ser Tyr Gln Asn Ser Pro His Tyr Gln Arg Arg Arg Thr Glu Arg
435 440 445

Ser Glu Leu Ala Arg Arg Ser Leu Leu Ser Ser Leu Ala Ala Asp Ala
450 455 460

Thr Asn Gln Arg Ser Gly Asp His Pro Thr Leu Arg Ser Leu Ala Pro
465 470 475 480

Pro Ala Ser Ser Asp Gly Leu Val Leu Gln Pro Gly Gly Asp Asn Ser
485 490 495

Gln Met His Asn Arg Ala Tyr Ser Arg Ala Gly Pro Leu Phe Asp Arg
500 505 510

Gln Gly Asp Ser Val Val Gly Ile Pro His Pro Leu Arg Ala Leu Ala
515 520 525

Ala Ala Ser Arg Gly Arg Ser Arg Leu Met Val Ser Gln Met Gln Asn
530 535 540

Val Leu Asp Val Met Arg Arg Asp Ala Asn Asn Asn Leu Arg Leu
545 550 555 560

Glu Asp Val Met Leu Leu Asn His Ser Val Leu Phe Asp Gly Ala Thr
565 570 575

Gly His Asp Arg Tyr Arg Asp Met Arg Leu Asp Val Asp Asn Met Ser
580 585 590

Tyr Glu Glu Leu Leu Ala Leu Glu Glu Arg Ile Gly Asp Val Cys Thr
595 600 605

Gly Val Asn Glu Glu Thr Ile Ser Asn Arg Leu Lys Gln Arg Lys Tyr
610 615 620

Lys Ser Asn Thr Lys Ser Pro Gln Asp Ala Glu Pro Cys Cys Val Cys
625 630 635 640

Gln Glu Glu Tyr Thr Glu Gly Glu Asp Met Gly Thr Leu Glu Cys Gly
645 650 655

His Glu Phe His Ser Gln Cys Ile Lys Glu Trp Leu Lys Gln Lys Asn
660 665 670

Leu Cys Pro Ile Cys Lys Thr Thr Gly Leu Asn Thr Ala Lys Lys Arg
675 680 685

Arg Ile Ala

690

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 <211> 2001
 <212> DNA
 <213> *Arabidopsis thaliana*

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tttcacactg cctgcgtcaa gcaatggctg atgctcaaga atctctgccc aatttgtaag 1980
actgtggctt tatcgacata a 2001

<210> 265
<211> 666
<212> PRT
<213> Arabidopsis thaliana
<400> 265

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

Ser Gly Arg Pro Thr Tyr Ala Ser Ser Ser Ser His Val Val Gln Asn
50 55 60

His Asn Trp Trp Ser Phe Gly Glu Ser Ser Ser Arg Leu Gly Pro Ser
65 70 75 80

Asp His Leu Asn Ser Asn Gly Ser Lys Thr Asp Arg Gln Leu Leu Ser
85 90 95

Asp Gly Tyr Gly Phe Glu Glu Gly Gln Ser Gly Met Leu Leu Pro Gly
100 105 110

Glu Ser Phe Leu Arg Gly Ser Ser Ser Ser His Met Leu Ser His Val
115 120 125

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

Val Val Ile Arg His Asn Asn Cys Glu Thr Ser Leu Gly Ser Ser Ser
145 150 155 160

Gln Thr Ala Glu Glu Arg Ser Ser Gly Pro Gly Ser Ser Leu Gly Gly
165 170 175

Leu Gly Ser Ser Cys Lys Arg Lys Ala Leu Glu Gly Ala Pro Ser His
180 185 190

Ser Phe Pro Gly Glu Ser His Gly Cys Phe Phe Gln Thr Glu Asn Gly
195 200 205

Ala Trp Asn Glu Gly Leu Ala Gln Tyr Asp Ala Ser Ser Ser Leu Ser
Seite 270

210

Leu Ser Met Pro Ser Gln Asn Ser Pro Asn Val Asn Asn Gln Ser Gly
225 230 235 240

Leu Pro Glu Pro Arg Phe Gly Leu Gly Gly Gly Arg Ala Val Thr Ala
245 250 255

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

Arg Arg Leu Asn Pro Gly Gln Pro Pro Glu Ser Val Ala Phe Ser Phe
275 280 285

Thr Gln Ser Gly Ser Ser Val Arg Gln Gln Gln Gln Leu Pro Ala Thr
290 295 300

Ser Pro Phe Val Asp Pro Leu Asp Ala Arg Ala Ile Pro Val Thr Gly
305 310 315 320

Ser Ser Ser Ser Gly Asp Gly Gln Pro Ser Met Ile His Leu Pro Ala
325 330 335

Leu Thr Arg Asn Ile His Gln Phe Ala Trp Ser Ala Ser Ser Ser Ser
340 345 350

Arg Ala Asn Ser Met Pro Glu Glu Gly Leu Ser Pro Trp Asp Ala Pro
355 360 365

Arg Ile Asn Ser Glu Gln Pro Val Phe Thr Thr Pro Ala Asn Glu Thr
370 375 380

Arg Asn Pro Val Gln Asp Gln Phe Cys Trp Ser Phe Thr Arg Gly Asn
385 390 395 400

Pro Ser Thr Ser Gly Asp Ser Pro Phe Val Pro Arg Ala Gly Ser Ser
405 410 415

Ser Gly Ile His Gly Leu Gln Pro Asn Pro Thr Trp Val Thr Pro His
420 425 430

Asn Gln Ser Arg Ile Ser Glu Val Ala Pro Trp Ser Leu Phe Pro Ser
435 440 445

Ile Glu Ser Glu Ser Ala Thr His Gly Ala Ser Leu Pro Leu Leu Pro
450 455 460

Thr Gly Pro Ser Val Ser Ser Asn Glu Ala Ala Ala Pro Ser Gly Ser
465 470 475 480

Ser Ser Arg Ser His Arg Ser Arg Gln Arg Arg Ser Gly Leu Leu Leu
485 490 495

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Glu Arg Gln Asn Asp His Leu His Leu Arg His Leu Gly Arg Ser Leu
500 505 510

Ala Ala Asp Asn Asp Gly Arg Asn Arg Leu Ile Ser Glu Ile Arg Gln
515 520 525

Val Leu Ser Ala Met Arg Arg Gly Glu Asn Leu Arg Phe Glu Asp Tyr
530 535 540

Met Val Phe Asp Pro Leu Ile Tyr Gln Gly Met Ala Glu Met His Asp
545 550 555 560

Arg His Arg Asp Met Arg Leu Asp Val Asp Asn Met Ser Tyr Glu Glu
565 570 575

Leu Leu Ala Leu Gly Glu Arg Ile Gly Asp Val Ser Thr Gly Leu Ser
580 585 590

Glu Glu Val Ile Leu Lys Val Met Lys Gln His Lys His Thr Ser Ser
595 600 605

Ala Ala Gly Ser His Gln Asp Met Glu Pro Cys Cys Val Cys Gln Glu
610 615 620

Glu Tyr Ala Glu Gly Asp Asp Leu Gly Thr Leu Gly Cys Gly His Glu
625 630 635 640

Phe His Thr Ala Cys Val Lys Gln Trp Leu Met Leu Lys Asn Leu Cys
645 650 655

Pro Ile Cys Lys Thr Val Ala Leu Ser Thr
660 665

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<211> 1938
<212> DNA
<213> Arabidopsis thaliana

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tctcagaacc caaatgctcc tgctactcat atgccccctg tttcaagaaa tacatttcaa    960
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gaagaagaag aaataggaag gctggaatgt ggacacgact ttcatagtca atgcatcaaa   1860
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 <211> 645
 <212> PRT
 <213> Arabidopsis thaliana

<400> 267

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 20 25 30

Arg Trp Glu Asn Leu His Asn Tyr Gly Asp Asn Asp Leu Gln Asp Tyr
 35 40 45

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Met Ser Ser Ala Ala Asp Thr Asn Pro Thr Phe Ala Asn Ser Val Tyr
50 55 60

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

Ser Gly Thr Lys Asn Glu Gly Ala Ser Leu Thr Glu Gln Trp Lys Gly
85 90 95

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

Leu Phe Val Gln Pro Ser Asn Gly Ser Arg Val Val Arg Asp Val Asn
115 120 125

Leu Asn Ala Glu Tyr Asn Glu His Leu Glu Asp Met Asn Pro Val Thr
130 135 140

Val His Pro Gly His Phe Glu Val Asn Gly Leu Arg Ser Glu Phe Leu
145 150 155 160

Leu Asp Asn Ser Val Arg Ala Gly Ser Ser Val Asp Gly Arg Arg Ala
165 170 175

Ser Cys Lys Arg Lys Ala Leu Asp Ala Ser Gly Gly Gln Ser Ser Ser
180 185 190

Thr Gly Gly Phe Arg Glu Phe Gln Arg Gly Val Ser Ser Ser Trp Ile
195 200 205

Ser Gly Pro Thr Tyr Tyr Ser Pro Ala Met Thr Ala Asn Asp Leu Asn
210 215 220

Ile Ser Leu Asp His Gly Arg Arg Gly Leu Val Ser Ser Ala Val Pro
225 230 235 240

Asn Leu Ser Pro Pro Thr Ile Thr Glu Ser Ser Ser Arg Asn Tyr Pro
245 250 255

Val Trp Val Asn Pro Thr Tyr Gln Gln Glu Thr Val Ser Asn Phe Ala
260 265 270

Pro Ser Leu Asn Ser Pro Gly Leu Ile Pro Ala Asp His Gln Gln Ile
275 280 285

Ser Met Arg Tyr Gly His Ala Leu Gly Asn Phe Ala Ser Gln Asn Pro
290 295 300

Asn Ala Pro Ala Thr His Met Pro Pro Val Ser Arg Asn Thr Phe Gln
305 310 315 320

Trp Asn Thr Ser Pro Val Ala Ala Val Ile Ser Ser Ser Ser Ala Thr

325

330

335

Pro Val Asp Arg Asn Val Ile His Arg Asn Ala Thr Arg Gln Arg Ser
 340 345 350

Asn Thr Leu Glu Ile Pro Leu Phe Val Pro Ala Pro Glu Leu Arg Asn
 355 360 365

Val Ala His Gly His Ile Ser Arg Asn Ala Ser Gly Ala Arg His Val
 370 375 380

Ala Ser Ser Ser Ser Arg Thr Ser Val Gln Pro Ser Pro Ser Ser Pro
 385 390 395 400

Ala Leu Thr Pro Tyr Gln Asn Asn Ser Leu His Asn Gln Arg Arg Leu
 405 410 415

Ser Glu Asn Phe Arg Arg Ser Leu Leu Ser Ser Leu Val Thr Gln Gln
 420 425 430

Arg Ala Ala Arg Ser Leu Ala His Pro Ala Ser Pro Asn Glu His Val
 435 440 445

Leu Gln Ser Gly Gly Asp Asn Thr Ser Gln Val His Asn Arg Ala Ser
 450 455 460

Ser Arg Ala Gly Pro Arg Gln Gly Gln Asp Ala Thr Gly Ile Ser His
 465 470 475 480

Ser Leu Arg Gly Leu Ala Ser Thr Ser Arg Gly Arg Thr Arg Met Gly
 485 490 495

Ala Ser Glu Ile Arg Asn Ile Leu Glu His Met Arg Arg Ala Gly Asn
 500 505 510

Leu Arg Leu Glu Asp Val Met Leu Leu Asn Gln Ser Ile Met Leu Gly
 515 520 525

Ala Ala Asp Ile His Asp Arg Tyr Arg Asp Met Arg Leu Asp Val Asp
 530 535 540

Asn Met Thr Tyr Glu Glu Leu Leu Ser Leu Glu Glu Arg Ile Gly Asp
 545 550 555 560

Val Cys Thr Gly Leu Asn Glu Glu Thr Ile Ser Asn Arg Leu Lys Gln
 565 570 575

Gln Lys Tyr Lys Ser Ser Thr Arg Ser Ser Gln Glu Val Glu Pro Cys
 580 585 590

Cys Val Cys Gln Glu Glu Tyr Lys Glu Glu Glu Glu Ile Gly Arg Leu
 595 600 605

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Glu Cys Gly His Asp Phe His Ser Gln Cys Ile Lys Glu Trp Leu Lys
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Asn Lys Pro Gln Arg
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<211> 2115
<212> DNA
<213> Arabidopsis thaliana

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cctaaccgca ttgttcagac tgaaaatagt gcttcgcatg caagtctttc tcaatatggt 720
gcttcaagta gcttaagttt ggctacacct tcacaaagtt ctccaaatgt tactaatcat 780
tttggccgga cagaacaaat gtttgatctt ggtgggtggaa gagcagttgc agccagtgtc 840
tttcattcta caagaaacac tgacacctta tctagagctg gcagacgatt aaatcccagg 900
cagcctcaag agtctgtagc attcagcgtc tcacatggtg ggacttctgt acgtcccact 960
ggttctttgc aacagaactt accattaaac tctccttttg tagatcctcc agatgtgaga 1020
tcatcatcaa ttactagtgg ctcaaacact ggtgagaatc agacaaatat agtcacctc 1080
ccagctttga ccaggaatat acaccaatat gcttgggatg cttctttcag ttctagagcc 1140
agtaatcctt cgggtatttg gatgcctgca gagcgattag gaccacagtg ggaaacaccg 1200
agaagcaacc aagagcagcc cttgtttgca cctgcaactg acatgagaca gccggtgcat 1260
gatctttgga atttcgcacg tggaagccct ggttcatctg tagattctct ctttgttcct 1320
cgagcagggc cgagttcagc tattcatatc ccacagccta atcccacatg gattcctcct 1380
cagaatgccc caccacataa tccatcgaga acatcagaac tttctccttg gtctttatct 1440
cctagtattg aatctccatc tgctagtcat ggtggccctc ttccattatt acccgagggc 1500

PF59082PF60142_PCT_SEQ_LIST.txt

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tcacggcata gaagatcagg tttgttattg gagagacaaa atgaacttct ccacttgcgt 1620
cacataggga ggagcttagc tgctgacggt aatggaagga atcaaatcat ttctgagata 1680
cgtcagggtg tgcatgccat gagaagagga gaaaatctac gggttgagga ttacatggtg 1740
ttcgatccac ttatctacca gggtatgact gacatgcatg ataggcatcg ggaaatgcgg 1800
cttgatgtgg acaacatgtc gtatgaggag ctattggcac ttggggaacg cataggtgat 1860
gtgagcactg gcctaagtga agaggtcatt ttgaaagcaa tgaacaaca caaacatata 1920
tcttcgtctc cttcttctgt tgagttgcat cagaacatag agccatgctg catttgcag 1980
gaagagtatg tagaagggtg taatctagga accttgaaat gtggacatga attccacaag 2040
gactgtatca agcaatgggt catgatcaag aatctctgcc ccatttgtaa gaccgaagca 2100
ttaaagacgc cgtag 2115

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<210> 269
<211> 704
<212> PRT
<213> Arabidopsis thaliana
<400> 269

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Met Asn Pro Met Gln Gly Pro Arg Ser Ile Gly Gly Ser Ser Thr Glu
1      5      10

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```

Val Asn Gln Val Asp Gly Glu Ser Ile Tyr Cys Thr Glu Thr Ser Leu
20      25      30

```

```

Asn Thr Met Leu Asn Pro Ala Asp Thr Gly Phe Pro Asn Asn Ser Thr
35      40      45

```

```

Pro Ser Gly Arg Pro Thr Tyr Ala Ser Ser Ser Ser His Ala Ala Gln
50      55      60

```

```

Asp His Thr Trp Trp Arg Phe Gly Glu Ser Ser Ser Ile Pro Gly Pro
65      70      75      80

```

```

Ser Asp Gln Val Asn Ser Ile Gly Ile Lys Thr Ser His Gln Leu Pro
85      90      95

```

```

Gln Asp Gly Thr His His Phe Val Gly Tyr Gly Ser Glu Gly Arg Gln
100      105      110

```

```

Thr Gly Leu Asn Gly Met Met Val Asp Gly Gly Val His Ala Gly Ser
115      120      125

```

```

His Ile Arg Asn Val Pro Ser Phe Leu Arg Gly Ser Ser Ser Asn Pro
130      135      140

```

```

Met Pro Gln His Val Asp Met Ser Met Asp Met Asp Ser Asp Asn Cys
145      150      155      160

```

PF59082PF60142_PCT_SEQ_LIST.txt

Asn Ala Gln Thr Ser₁₆₅ Gly Val Val Ile Arg₁₇₀ His Asn Ser Tyr Gly₁₇₅ Ser
 Ser Leu Gly Ser₁₈₀ Ser Val Gln Ala Ala₁₈₅ Gly Glu Ser Ser Ser₁₉₀ Gly Pro
 Ala Ser Pro₁₉₅ Phe Gly Gly Trp Gly₂₀₀ Ser Ser Cys Lys Arg₂₀₅ Lys Ala Leu
 Glu Gly₂₁₀ Ser Pro Ser His Tyr₂₁₅ Phe Ser Gly Glu Thr₂₂₀ Pro Asn Arg Ile
 Val₂₂₅ Gln Thr Glu Asn Ser₂₃₀ Ala Ser His Ala Ser₂₃₅ Leu Ser Gln Tyr Gly₂₄₀
 Ala Ser Ser Ser₂₄₅ Leu Ser Leu Ala Thr Pro₂₅₀ Ser Gln Ser Ser Pro₂₅₅ Asn
 Val Thr Asn His₂₆₀ Phe Gly Arg Thr Glu₂₆₅ Gln Met Phe Gly Ser₂₇₀ Gly Gly
 Gly Arg Ala₂₇₅ Val Ala Ala Ser Ala₂₈₀ Phe His Ser Thr Arg₂₈₅ Asn Thr Asp
 Thr Leu₂₉₀ Ser Arg Ala Gly Arg₂₉₅ Arg Leu Asn Pro Arg₃₀₀ Gln Pro Gln Glu
 Ser₃₀₅ Val Ala Phe Ser Val₃₁₀ Ser His Gly Gly Thr₃₁₅ Ser Val Arg Pro Thr₃₂₀
 Gly Ser Leu Gln Gln₃₂₅ Asn Leu Pro Leu Asn₃₃₀ Ser Pro Phe Val Asp₃₃₅ Pro
 Pro Asp Val Arg₃₄₀ Ser Ser Ser Ile Thr₃₄₅ Ser Gly Ser Asn Thr₃₅₀ Gly Glu
 Asn Gln Thr₃₅₅ Asn Ile Val His Leu₃₆₀ Pro Ala Leu Thr Arg₃₆₅ Asn Ile His
 Gln Tyr₃₇₀ Ala Trp Asp Ala Ser₃₇₅ Phe Ser Ser Arg Ala₃₈₀ Ser Asn Pro Ser
 Gly Ile Gly Met Pro Ala₃₉₀ Glu Arg Leu Gly Pro₃₉₅ Gln Trp Glu Thr Pro₄₀₀
 Arg Ser Asn Gln Glu₄₀₅ Gln Pro Leu Phe Ala₄₁₀ Pro Ala Thr Asp Met₄₁₅ Arg
 Gln Pro Val His₄₂₀ Asp Leu Trp Asn Phe₄₂₅ Ala Arg Gly Ser Pro₄₃₀ Gly Ser

PF59082PF60142_PCT_SEQ_LIST.txt

Ser Val Asp Ser Leu Phe Val Pro Arg Ala Gly Pro Ser Ser Ala Ile
435 440 445

His Thr Pro Gln Pro Asn Pro Thr Trp Ile Pro Pro Gln Asn Ala Pro
450 455 460

Pro His Asn Pro Ser Arg Thr Ser Glu Leu Ser Pro Trp Ser Leu Phe
465 470 475 480

Pro Ser Ile Glu Ser Pro Ser Ala Ser His Gly Gly Pro Leu Pro Leu
485 490 495

Leu Pro Ala Gly Pro Ser Val Ser Ser Asn Glu Val Thr Met Pro Ser
500 505 510

Ser Ser Asn Ser Arg Ser His Arg Ser Arg His Arg Arg Ser Gly Leu
515 520 525

Leu Leu Glu Arg Gln Asn Glu Leu Leu His Leu Arg His Ile Gly Arg
530 535 540

Ser Leu Ala Ala Asp Gly Asn Gly Arg Asn Gln Ile Ile Ser Glu Ile
545 550 555 560

Arg Gln Val Leu His Ala Met Arg Arg Gly Glu Asn Leu Arg Val Glu
565 570 575

Asp Tyr Met Val Phe Asp Pro Leu Ile Tyr Gln Gly Met Thr Asp Met
580 585 590

His Asp Arg His Arg Glu Met Arg Leu Asp Val Asp Asn Met Ser Tyr
595 600 605

Glu Glu Leu Leu Ala Leu Gly Glu Arg Ile Gly Asp Val Ser Thr Gly
610 615 620

Leu Ser Glu Glu Val Ile Leu Lys Ala Met Lys Gln His Lys His Thr
625 630 635 640

Ser Ser Ser Pro Ser Ser Val Glu Leu His Gln Asn Ile Glu Pro Cys
645 650 655

Cys Ile Cys Gln Glu Glu Tyr Val Glu Gly Asp Asn Leu Gly Thr Leu
660 665 670

Lys Cys Gly His Glu Phe His Lys Asp Cys Ile Lys Gln Trp Val Met
675 680 685

Ile Lys Asn Leu Cys Pro Ile Cys Lys Thr Glu Ala Leu Lys Thr Pro
690 695 700

PF59082PF60142_PCT_SEQ_LIST.txt

<210> 270
<211> 1107
<212> DNA
<213> Arabidopsis thaliana

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<400> 270
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cgatcatctcc acgccgccga cgatgatccg ccgctaagcc acgtcgttct tccgatttca      120
caacctaatc gcttctgtaa ctccgcaatg tcttccttct tccccctccc gacttcctcc      180
tccaacgaaa gcacgaggaa gaaaccgtac caaacgtcgt cgtttcgagg gatggggtgc      240
tatgccgcag cagcagcagc agtcaagag gtttctgttc cctccgtcat tcgctactcc      300
gcggatttgg atgccagaat tagaaaagat aagaagaaga agaagcataa gcataagaaa      360
aagaaaaaga agaataaagg aagctacgaa gatgggttcga ttaggatttt aagcgaagaa      420
gctagagacg ttattgatgt ttggtgcaga cctggattag gcttctccac ggatgctgta      480
attggtcgat cggttgatcc tcctcgggga aggaatatcc cgtcgtctcg tcgcaaaatt      540
gatgtggata acaacaatta taatcacaca ctgggttctt ctgttcttcc cattcggttt      600
ctcaatcaag aaactcattc tcatgatatc ttcaactctg attctacttt tgtgacatca      660
tcacgcgctg aaccaacgat gttgtcaagt agatgtcgtg gccatcttcc acgctcttac      720
cctgatgatc ttaccgagat gaggatgctc cagaatgggt ttgtaatggg aagaataaca      780
gattcccgtg ataactacca cgaattgagg ctcatgttg atagcatgtc atacgagcaa      840
cttcttgagc ttggtgatag aattggttat gtgaatactg gactaaaaga aagcgagata      900
catcgttgtc ttgggaaaat caaacatcc gtatcacata ctcttggtga tagaaaatgt      960
agcatctgtc aggatgagta tgagagagag gatgagggtg gggaattgaa ctgtggacac     1020
agctttcatg tccattgcgt gaaacaatgg ctttcgagga agaatgcttg tccggtctgt     1080
aagaaggcag catatggcaa gccttaa                                     1107

```

<210> 271
<211> 368
<212> PRT
<213> Arabidopsis thaliana

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<400> 271
Met Ser Ser Thr Thr Ile Gly Glu His Ile Arg Leu Arg Arg Ala Arg
1           5           10           15

Asn Gln Thr Ile Arg His Leu His Ala Ala Asp Asp Asp Pro Pro Leu
          20           25           30

Ser His Val Val Leu Pro Ile Ser Gln Pro Asn Arg Phe Cys Asn Ser
          35           40           45

Ala Met Ser Ser Phe Phe Pro Leu Pro Thr Ser Ser Ser Asn Glu Ser
          50           55           60

Thr Arg Lys Lys Pro Tyr Gln Thr Ser Ser Phe Arg Gly Met Gly Cys

```

65 70 75 80
 Tyr Ala Ala Ala Ala Ala Ala Ala Gln Glu Val Ser Val Pro Ser Val
 85 90 95
 Ile Arg Tyr Ser Ala Asp Leu Asp Ala Arg Ile Arg Lys Asp Lys Lys
 100 105 110
 Lys Lys Lys His Lys His Lys Lys Lys Lys Lys Asn Lys Gly Ser
 115 120 125
 Tyr Glu Asp Gly Ser Ile Arg Ile Leu Ser Glu Glu Ala Arg Asp Val
 130 135 140
 Ile Asp Val Trp Cys Arg Pro Gly Leu Gly Phe Ser Thr Asp Ala Val
 145 150 155 160
 Ile Gly Arg Ser Val Asp Pro Pro Arg Gly Arg Asn Ile Pro Ser Ser
 165 170 175
 Arg Arg Lys Ile Asp Val Asp Asn Asn Asn Tyr Asn His Thr Leu Gly
 180 185 190
 Ser Ser Val Leu Pro Ile Arg Phe Leu Asn Gln Glu Thr His Ser His
 195 200 205
 Asp Ile Phe Asn Ser Asp Ser Thr Phe Val Thr Ser Ser Arg Ala Glu
 210 215 220
 Pro Thr Met Leu Ser Ser Arg Cys Arg Gly His Leu Pro Arg Ser Tyr
 225 230 235 240
 Pro Asp Asp Leu Thr Glu Met Arg Met Leu Gln Asn Gly Phe Val Met
 245 250 255
 Gly Arg Ile Thr Asp Ser Arg Asp Asn Tyr His Glu Leu Arg Leu Asp
 260 265 270
 Val Asp Ser Met Ser Tyr Glu Gln Leu Leu Glu Leu Gly Asp Arg Ile
 275 280 285
 Gly Tyr Val Asn Thr Gly Leu Lys Glu Ser Glu Ile His Arg Cys Leu
 290 295 300
 Gly Lys Ile Lys Pro Ser Val Ser His Thr Leu Val Asp Arg Lys Cys
 305 310 315 320
 Ser Ile Cys Gln Asp Glu Tyr Glu Arg Glu Asp Glu Val Gly Glu Leu
 325 330 335
 Asn Cys Gly His Ser Phe His Val His Cys Val Lys Gln Trp Leu Ser
 340 345 350

PF59082PF60142_PCT_SEQ_LIST.txt

Arg Lys Asn Ala Cys Pro Val Cys Lys Lys Ala Ala Tyr Gly Lys Pro
355 360 365

<210> 272
<211> 1578
<212> DNA
<213> Arabidopsis thaliana

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<400> 272
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ggtcttacct tgcgtgagaa tatgaacaag acagatggta agaatgttcc tttctgcagc    120
cgagttgggt gtactgcaaa ggtaacttct accaagagat ctcggattgg ctctacggat    180
aacaatacaa aagttgggtc gcctccggtt ccatctacct taaatagaaa ggaaattggt    240
gggagctcat ctcgtactcc tgggtgattt ggatacttga gaaagccagc caaagttact    300
gcaagaagac agccgtcatc tagtttagac actgaatctt cggaaacgag ttgtattcat    360
gatgatccag ctgcaacaga gcccacactt ccacgccaaa agactaaaag agtcacaatc    420
aatgttcatc ctcaaagcgc tgtctctaga gaagttgtaa taacaaaggc aggaagctca    480
agtagaggaa ccagcagaat tagtcatcca aagtctgaat tgggtacctg cgatgctctg    540
acgggtcctt ctgtttctac atcttctggt aacagtgagc aactgttaag aggcgggttg    600
agtaggcata gattgaggaa cttgagctgc aattctgtgt ctgatgttct tccaactaac    660
tcaaactcag caacaaaaat cagtgtgact aaaaagaaaa acgctgatgg agagagcagc    720
ttatctagca aaggtagtaa gactagtgtg ttggttccaa aggtaaggaa tcaaatttct    780
tctcatggca atggcgtcac agtttctgat aacagaagaa atcgagtagt accaagtatt    840
agggacagca gtactgttgt ttcaaattgg ttaggagagag ctgggtattt tggtagatca    900
gagcgacttg gagctactgc atcctctgct acttctcgac aaatgcctca tcctacaaca    960
ccaaccgatc ccaatccttc tctttcgttt tgtccatcaa atatatacag tagtactgga   1020
cgcgtaacata gcaatatgcc tggtagcccc acggaagctg acccttcaag ctctttggtg   1080
aaccgggatg gtttgagtca ctacaacatg aatggaattg cagaggtatt gttggccctg   1140
gaaaggattg aacatgatga agagcttaca tatgagcaac tggcttctat agagaccaat   1200
ctatttctcaa gtggtatggt cagattctat gatcagcata gagatatgag gcttgacatc   1260
gataacatgt catatgagga gttactagct ttgggggata aaatgggtac agtgagcaca   1320
gctctaagcg aagaagcact ctcaagaagc ctttaagcaa gcatttatca ggagacagat   1380
gaaaccgggt ccatctctct gtataaggat gatgatatca agtgcagtat ttgccaggaa   1440
gagtatgttg atggagatga attagggact attccatgtc aacatatgta ccatgtgagc   1500
tgtgtacaac aatggctgcg gatgaagaat tggtgcccaa tctgcaaaac ctctgcggaa   1560
gaagagaagt cgatttag                                     1578
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<210> 273
<211> 525

<212> PRT

<213> Arabidopsis thaliana

<400> 273

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

Arg Lys Ala Ser Gly Leu Thr Leu Arg Glu Asn Met Asn Lys Thr Asp
 20 25 30

Gly Lys Asn Val Pro Phe Cys Ser Arg Val Gly Cys Thr Ala Lys Val
 35 40 45

Thr Ser Thr Lys Arg Ser Arg Ile Gly Ser Thr Asp Asn Asn Thr Lys
 50 55 60

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

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

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

Ser Ser Glu Thr Ser Cys Ile His Asp Asp Pro Ala Ala Thr Glu Pro
 115 120 125

Thr Leu Pro Arg Gln Lys Thr Lys Arg Val Thr Ile Asn Val His Pro
 130 135 140

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

Ser Arg Gly Thr Ser Arg Ile Ser His Pro Lys Ser Glu Leu Gly Thr
 165 170 175

Arg Asp Ala Leu Thr Gly Pro Ser Val Ser Thr Ser Ser Gly Asn Ser
 180 185 190

Glu His Thr Val Arg Gly Gly Leu Ser Arg His Arg Leu Arg Asn Leu
 195 200 205

Ser Cys Asn Ser Val Ser Asp Val Leu Pro Thr Asn Ser Asn Ser Ala
 210 215 220

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

Leu Ser Ser Lys Gly Ser Lys Thr Ser Val Leu Val Pro Lys Val Arg
 245 250 255

Asn Gln Ile Ser Ser His Gly Asn Gly Val Thr Val Ser Asp Asn Arg
 260 265 270
 Arg Asn Arg Val Val Pro Ser Ile Arg Asp Ser Ser Thr Val Val Ser
 275 280 285
 Asn Gly Cys Arg Arg Ala Gly Tyr Phe Gly Arg Ser Glu Arg Leu Gly
 290 295 300
 Ala Thr Ala Ser Ser Ala Thr Ser Arg Gln Met Pro His Pro Thr Thr
 305 310 315 320
 Pro Thr Asp Pro Asn Pro Ser Leu Ser Phe Cys Pro Ser Asn Ile Tyr
 325 330 335
 Ser Ser Thr Gly Arg Val His Ser Asn Met Pro Gly Ser Pro Thr Glu
 340 345 350
 Ala Asp Pro Ser Ser Ser Leu Val Asn Arg Asp Gly Leu Ser His Tyr
 355 360 365
 Asn Met Asn Gly Ile Ala Glu Val Leu Leu Ala Leu Glu Arg Ile Glu
 370 375 380
 His Asp Glu Glu Leu Thr Tyr Glu Gln Leu Ala Ser Ile Glu Thr Asn
 385 390 395 400
 Leu Phe Ser Ser Gly Met Phe Arg Phe Tyr Asp Gln His Arg Asp Met
 405 410 415
 Arg Leu Asp Ile Asp Asn Met Ser Tyr Glu Glu Leu Leu Ala Leu Gly
 420 425 430
 Asp Lys Met Gly Thr Val Ser Thr Ala Leu Ser Glu Glu Ala Leu Ser
 435 440 445
 Arg Ser Leu Lys Gln Ser Ile Tyr Gln Glu Thr Asp Glu Thr Gly Ser
 450 455 460
 Ile Ser Leu Tyr Lys Asp Asp Asp Ile Lys Cys Ser Ile Cys Gln Glu
 465 470 475 480
 Glu Tyr Val Asp Gly Asp Glu Leu Gly Thr Ile Pro Cys Gln His Met
 485 490 495
 Tyr His Val Ser Cys Val Gln Gln Trp Leu Arg Met Lys Asn Trp Cys
 500 505 510
 Pro Ile Cys Lys Thr Ser Ala Glu Glu Glu Lys Ser Ile
 515 520 525

<210> 274

<211> 1461

<212> DNA

<213> *Arabidopsis thaliana*

<400> 274

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atgcgacaaa gaaatatgat gactggttca gacatggagc agaattctca aagctttggt      60
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actgttcctc atttagaagc tcattctctg caagaacctt atgataacaa ctcaatgttc      180
tacgggcctc cacagtacca tcatcaacat gcttcaaadc ttggttctgg catgtcaacc      240
gcaccaaatt tctatgtccc ttatgtgaat tatgaagctc caccgagttt tctgtttgtct      300
catggaagta atgatgcagt tgttgagatt acttccactg aacatgagag aaatgcccat      360
tttatggatc acggattcaa aagaaagagt tctgaagtaa tacctggaaa ttctcagtat      420
ccagttgctc cttgttcttt ccctcaattg aatacatcgg agacagcacc tttttcattc      480
ccacattttg gtacttatcc acaaccacta gatcagagaa gtgtgaggaa cagagcagga      540
gcagctacaa tggatccact tctctctcat ggtcataaca acttcagtca aggaaactat      600
gcagctcatc cttttccacc tcttggtctc atctgggatg accaactctg taatggcaac      660
agatctgatg gatcatcttc gctttggtct caagcacctg cgttacctta tatgcatggt      720
aacattgcta ctggatctat agaatctggt aatgtttgct tccaagata ccatgaaaca      780
tctagtagca gaaacccac gccatctgta taccaaagga accactatat tagccatcac      840
cccgtacctc ctctcccat cgtataccct cacatgcctt cagcctcata cgctgagact      900
ttgcatcctg cttcatacag tcatatggga caggttcaat caaccggatt caggataaac      960
caatatcccg gagaagattt tgtacctgca gcaattctaa gacaccgtga attgcctcac     1020
tttagagcaa tgcccgcgaa tgaaaatgca ttttggaag taggagactt ctacaatgct     1080
gttaattatg tcgatcatca tcaagacatg cgcttagaca tagaagatat gtcatatgag     1140
gagcttcttg ctttgagcga ccagattgga actgtgaaga caggcttgct atcagaagat     1200
gttaaagaac ttctgaaaag aagaacctg accagaatta acctggaaga aggtccatct     1260
actgatctag agactgattc ttgcacgata tgccaggaaa actacaagaa cgaagataag     1320
atcgcaacgc tggattgcat gcacaaatac catgcagaat gcttgaagaa gtggttggtt     1380
atcaagaacg tttgccaat ctgtaaatca gaggcattgg tcatagagaa gaagaagaag     1440
ctaagggttaa gtagtagatg a                                     1461

```

<210> 275

<211> 486

<212> PRT

<213> *Arabidopsis thaliana*

<400> 275

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Met Arg Gln Arg Asn Met Met Thr Gly Ser Asp Met Glu Gln Asn Ser
1           5           10           15

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

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PF59082PF60142_PCT_SEQ_LIST.txt

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

PF59082PF60142_PCT_SEQ_LIST.txt

Ser Tyr Ser His Met Gly Gln Val Gln Ser Thr Gly Phe Arg Ile Asn
305 310 315 320

Gln Tyr Pro Gly Glu Asp Phe Val Pro Ala Ala Ile Leu Arg His Arg
325 330 335

Glu Leu Pro His Phe Arg Ala Met Pro Ala Asn Glu Asn Ala Phe Trp
340 345 350

Glu Val Gly Asp Phe Tyr Asn Ala Val Asn Tyr Val Asp His His Gln
355 360 365

Asp Met Arg Leu Asp Ile Glu Asp Met Ser Tyr Glu Glu Leu Leu Ala
370 375 380

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

Val Lys Glu Leu Leu Lys Arg Arg Thr Ser Thr Arg Ile Asn Leu Glu
405 410 415

Glu Gly Pro Ser Thr Asp Leu Glu Thr Asp Ser Cys Thr Ile Cys Gln
420 425 430

Glu Asn Tyr Lys Asn Glu Asp Lys Ile Ala Thr Leu Asp Cys Met His
435 440 445

Lys Tyr His Ala Glu Cys Leu Lys Lys Trp Leu Val Ile Lys Asn Val
450 455 460

Cys Pro Ile Cys Lys Ser Glu Ala Leu Val Ile Glu Lys Lys Lys Lys
465 470 475 480

Leu Arg Leu Ser Ser Arg
485

<210> 276
<211> 1104
<212> DNA
<213> Arabidopsis thaliana

<400> 276	
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ctccaacgac ctaggaatca tcgaaatctc ccacccatth ccaccgccga cgaacctcta	120
atcccaaac ctagccgcgt ctctaaatcc gccatgtctt ccttcttctt cttgccagaa	180
actactaaga agaaacccaa cggaacggcg tcgtttcgtg gtctaggctg cacaacctcc	240
gcatctcagc aagtttcagt cccggcagtg attcgctcct ccgcggattg ggatgctagt	300
aatttcaaaa ttaagaagac gaagaagaag aacaagaaca agggtagtag tagctacaat	360
ggtggttcga ttaagatctt gagcgaagct agtactagta gtagcgtcgc ttgcgcagcg	420

PF59082PF60142_PCT_SEQ_LIST.txt

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attcctgatg tttggtgtgg tcctggagtt gggttttcaa cggatgctgt cgtcggagggc 480
tccattgaca cagttgtttc agatcctccg agaaggaata ttccggtgag acgcaaaatc 540
gatggagata aaaccaatag taacagtaat aatcatagag agggttcttc ttctcttctt 600
cctagacgat ctctcaatca agagtctaat ccttattttg attctgattc gagttttttg 660
acatcgcggg ctgagcagac tgatagatat catcgtcatc taagactgcc ttaccctgat 720
ggactcgctg agatgatgat gatgcagaat ggttttgtga tgggaggagt attaagctca 780
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gagcttggtg aaagaattgg gcatgtgaac actggactta ctgaaaaaca gatcaaaagt 900
tgtcttcgga aagtcaaacc atgccggcaa gatacaacag ttgctgatag aaagtgcac 960
atctgtcaag acgagtatga ggcgaaggac gaggtagggg aattacgatg tgggcacagg 1020
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acgatggcgt acaataagtc ttag 1104

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<210> 277
<211> 367
<212> PRT
<213> Arabidopsis thaliana
<400> 277

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

Gln His Met Arg Leu Gln Arg Pro Arg Asn His Arg Asn Leu Pro Pro
      20     25     30

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

Lys Ser Ala Met Ser Ser Phe Phe Leu Leu Pro Glu Thr Thr Lys Lys
      50     55     60

Lys Pro Asn Gly Thr Ala Ser Phe Arg Gly Leu Gly Cys Thr Thr Ser
65      70     75     80

Ala Ser Gln Gln Val Ser Val Pro Ala Val Ile Arg Ser Ser Ala Asp
      85     90     95

Trp Asp Ala Ser Asn Phe Lys Ile Lys Lys Thr Lys Lys Lys Asn Lys
      100    105    110

Asn Lys Gly Ser Ser Ser Tyr Asn Gly Gly Ser Ile Lys Ile Leu Ser
      115    120    125

Glu Ala Ser Thr Ser Ser Ser Val Ala Cys Ala Ala Ile Pro Asp Val
      130    135    140

Trp Cys Gly Pro Gly Val Gly Phe Ser Thr Asp Ala Val Val Gly Gly

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145 150 155 160

Ser Ile Asp Thr Val Val Ser Asp Pro Pro Arg Arg Asn Ile Pro Val
165 170 175

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

Arg Glu Gly Ser Ser Ser Leu Leu Pro Arg Arg Ser Leu Asn Gln Glu
195 200 205

Ser Asn Pro Tyr Phe Asp Ser Asp Ser Ser Phe Leu Thr Ser Arg Ala
210 215 220

Glu Gln Thr Asp Arg Tyr His Arg His Leu Arg Leu Pro Tyr Pro Asp
225 230 235 240

Gly Leu Ala Glu Met Met Met Met Gln Asn Gly Phe Val Met Gly Gly
245 250 255

Val Leu Ser Ser Phe Asp Gln Phe Arg Asp Met Arg Leu Asn Val Asp
260 265 270

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

Val Asn Thr Gly Leu Thr Glu Lys Gln Ile Lys Ser Cys Leu Arg Lys
290 295 300

Val Lys Pro Cys Arg Gln Asp Thr Thr Val Ala Asp Arg Lys Cys Ile
305 310 315 320

Ile Cys Gln Asp Glu Tyr Glu Ala Lys Asp Glu Val Gly Glu Leu Arg
325 330 335

Cys Gly His Arg Phe His Ile Asp Cys Val Asn Gln Trp Leu Val Arg
340 345 350

Lys Asn Ser Cys Pro Val Cys Lys Thr Met Ala Tyr Asn Lys Ser
355 360 365

<210> 278

<211> 1742

<212> DNA

<213> Populus trichocarpa

<400> 278

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agagatcaaa aagctcagtt ttgcaaccga attggatgca gtggcagact gaactctagt 180

aaagggtact aaataagttc agaaaaagcc aaatcttcaa ggccaaggcc attaatttca 240

PF59082PF60142_PCT_SEQ_LIST.txt

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gaatccttag	aaactgggag	tggtcaggat	gaagttacac	caccttctgg	aaggattaag	420
ttagaccttc	gccctgaaac	cgatggagct	gcttctagt	atattacctc	aatggaagct	480
ggaagctccg	gtatatcaaa	aagtacaaga	tctcattgga	attttcatca	gaaatcagga	540
ttggtaaacc	ccgagactgt	agtgggggtca	cctgtttctt	tggcatccaa	aagcaccatt	600
cagggaaactc	gactgaatgc	cagcagggtt	ggtcacagaa	atcttagatg	caatacagta	660
tctgattctt	cctcttcagg	ttcttcatca	tcagatttaa	atctaagtag	acggaaagac	720
acattcaaca	agagaatttg	tgatggagaa	agtagttcct	ttgccagggg	gaaaaggatg	780
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cgacctggca	gtagcaatgg	gagtttacgg	ggtattaggg	catccagtcc	agaagttagc	1140
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atgagactgg	atatcgacaa	tatgtcatat	gaggaactat	tagctcttga	agagagaatg	1380
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gagcatggat	atcacatgtc	ctgcatacat	caatggctaa	gtctgaaaaa	ttggtgccct	1620
atttgcaagg	catcagtggc	tccgtcgcca	ccatcctcgt	aaacaattaa	taaactggat	1680
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tt						1742

<210> 279
 <211> 543
 <212> PRT
 <213> Populus trichocarpa

<400> 279

Met Asp Asp Tyr Ser Gly Lys Arg Ala Gly Asp Arg Phe Ile Val Ser
 1 5 10 15

Arg Lys Gly Ser Pro His Val Leu Arg Asp Thr Ala Asn Asn Arg Asp
 20 25 30

Gln Lys Ala Gln Phe Cys Asn Arg Ile Gly Cys Ser Gly Arg Leu Asn
 Seite 290

35

40

45

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

PF59082PF60142_PCT_SEQ_LIST.txt

Gln Pro Asp Met Ser₃₂₅ Leu Asp Leu Asn Ala₃₃₀ Pro Ser Ser Ser His₃₃₅ His

Phe Ser Val Glu₃₄₀ Ala Ser Leu Gly Arg₃₄₅ Pro Ser Ser Tyr Ser₃₅₀ Arg Pro

Gly Ser Ser₃₅₅ Asn Gly Ser Leu Arg₃₆₀ Gly Ile Arg Pro Ser₃₆₅ Ser Pro Glu

Val Ser₃₇₀ Asn Ala Gln Ser Leu₃₇₅ Met Asn Arg Glu Ser₃₈₀ Phe Gln Arg Tyr

Asn Met Val Gly Ile Ala₃₉₀ Glu Val Leu Leu Ala₃₉₅ Leu Gln Arg Ile Glu₄₀₀

Gln Asp Glu Glu₄₀₅ Leu Thr Tyr Glu Gln₄₁₀ Leu Val Leu Glu Thr₄₁₅ Ser

Leu Val Leu Asn₄₂₀ Gly Leu Asn Phe His₄₂₅ Asp Gln His Arg Asp₄₃₀ Met Arg

Leu Asp Ile₄₃₅ Asp Asn Met Ser Tyr₄₄₀ Glu Glu Leu Leu Ala₄₄₅ Leu Glu Glu

Arg Met Gly Thr Val Ser₄₅₅ Thr Ala Leu Thr Glu Glu₄₆₀ Ala Leu Ser Glu

Cys₄₆₅ Leu Lys Thr Ser Ile₄₇₀ Tyr His Ser Thr Pro₄₇₅ Met Glu Asp Ala Thr₄₈₀

Ala Asn Leu Glu Gly₄₈₅ Asp Lys Asp Asp Ile₄₉₀ Lys Cys Ser Ile Cys₄₉₅ Gln

Glu Glu Tyr Val₅₀₀ Val Gly Asp Glu Val₅₀₅ Gly Arg Leu Gln Cys₅₁₀ Glu His

Gly Tyr His₅₁₅ Met Ser Cys Ile His₅₂₀ Gln Trp Leu Ser Leu₅₂₅ Lys Asn Trp

Cys Pro₅₃₀ Ile Cys Lys Ala Ser₅₃₅ Val Ala Pro Ser Pro₅₄₀ Pro Ser Ser

<210> 280

<211> 476

<212> DNA

<213> Populus trichocarpa

<400> 280

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gaggagtgc tggctttgga agagcgcatt ggaaatgtca gtactggatt gagcgaagaa 180

PF59082PF60142_PCT_SEQ_LIST.txt

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gctgaaccat gctgcatttg ccaggaggaa tacaatgatg gagaagatct tggaacactg 300
gactgcggac atgatttcca cgcgggggtgt gttaagcagt ggctgatgca caagaattgg 360
tgcccatct gcaaaacaac aggacttgct acatgagaaa gggtaaagat gttcaggcca 420
ttacacacgg ttggtacacg gttgtacgag gaaaacgtga gaggcgtggc cctaga 476

<210> 281
<211> 121
<212> PRT
<213> Populus trichocarpa

<400> 281

Met Ile Leu Asp Gln Ser Val Leu Phe Gly Ala Ala Asp Met Tyr Asp
1 5 10 15

Arg His Arg Asp Met Arg Leu Asp Val Asp Asn Met Ser Tyr Glu Glu
20 25 30

Leu Leu Ala Leu Glu Glu Arg Ile Gly Asn Val Ser Thr Gly Leu Ser
35 40 45

Glu Glu Thr Ile Val Asn Asn Leu Lys Gln Gln Lys Tyr Ser Val Ala
50 55 60

Val Gly Ala Lys Val Glu Ala Glu Pro Cys Cys Ile Cys Gln Glu Glu
65 70 75 80

Tyr Asn Asp Gly Glu Asp Leu Gly Thr Leu Asp Cys Gly His Asp Phe
85 90 95

His Ala Gly Cys Val Lys Gln Trp Leu Met His Lys Asn Trp Cys Pro
100 105 110

Ile Cys Lys Thr Thr Gly Leu Ala Thr
115 120

<210> 282
<211> 2210
<212> DNA
<213> Populus trichocarpa

<400> 282

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aatgatgatg ggataaaaaat ggaagaatgg ttgtctactt cagtcaatgc ttatcctgca 240
gttgggtcaaa gatcagagga aaggctatctt gaaacaacta atatcctttt cccaggcaga 300
gtcagtacgg ggattagtgg caatcaggtt agaagtggac ctttattctt gcagggtccc 360

PF59082PF60142_PCT_SEQ_LIST.txt

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ggaagttctg	gttatatagt	agaggagaca	aatggtggtt	caggatcttc	tattgggggtt	600
tggggcttat	cctgcaagag	aaaggccctt	gaaggtacta	ctggacagtc	ttttcctggt	660
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cgttggtcct	tgagcattc	tcgcagacct	gtctcagtta	gtgactatct	ggagtcaaga	1020
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catttctccc	ctttgtcttc	tggtccttcc	tctgcacagg	acacacagat	ttcttctgga	1560
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ccttgctgta	tctgtcagga	ggaatatgtg	gatggggatg	atatgggaat	aatcgactgt	2040
gggcatgact	ttcataccaa	ctgcatcaaa	cagtggctaa	tgagaaaaa	tctatgtcca	2100
atttgaaga	tgacggccct	gctcacttga	gaggaagat	aatgccagtt	cctggaaatt	2160
ttattttctt	aaaaacaaat	caacatccaa	atactgggtg	gatgatatcc		2210

<210> 283
 <211> 708
 <212> PRT
 <213> Populus trichocarpa
 <400> 283

PF59082PF60142_PCT_SEQ_LIST.txt

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

Ala Leu Thr His Asp Val Gln Ser Phe Ser Gly Trp Asn Ser Gly Glu
35 40 45

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

Lys Met Glu Glu Trp Leu Ser Thr Ser Val Asn Ala Tyr Pro Ala Val
65 70 75 80

Gly Gln Arg Ser Glu Glu Arg Leu Phe Glu Thr Thr Asn Ile Leu Phe
85 90 95

Pro Gly Arg Val Ser Thr Gly Ile Ser Gly Asn Gln Val Arg Ser Gly
100 105 110

Pro Leu Phe Leu Gln Gly Ser Ser Ser Asn His Ile Ala Pro Asn Val
115 120 125

Cys Pro Asn Ser Gly His Ile Gly Asp Thr Thr Ile Gly Arg Pro Ile
130 135 140

Thr Gly Ala Val Leu Gly Leu Asn Gln Leu Asn Pro Gly Gly Gly Leu
145 150 155 160

Glu Ile Glu Arg Ala Ser Ser Ser Gly Val Ser Ser Ser Asp Val Gly
165 170 175

Thr Ser Ser Gly Ser Ser Gly Tyr Ile Val Glu Glu Thr Asn Gly Gly
180 185 190

Ser Gly Ser Ser Ile Gly Val Trp Gly Leu Ser Cys Lys Arg Lys Ala
195 200 205

Leu Glu Gly Thr Thr Gly Gln Ser Phe Pro Gly Gly Ser Ser Ser Cys
210 215 220

Phe Pro Gln Ala Glu Ser Ser Ala Trp His Asn Gly Pro Asn Asn His
225 230 235 240

Ser Val Ser Ser Ser Leu Ser Leu Ser Thr Pro Ser Pro Asn Thr Pro
245 250 255

Ser Val Ala Pro Pro Glu Gln Leu Asn Pro Arg Phe Gly Tyr Gly Met
260 265 270

PF59082PF60142_PCT_SEQ_LIST.txt

Arg Gly Ala Pro Pro Asp Ala Phe Pro Ser Ser Asn Val Ser Gly Asn
275 280 285

Ala Asp Ser Leu Arg Asn Phe Gly Arg Arg Ile Ser Pro Gly His Gln
290 295 300

Gln Glu Ser Val Thr Phe Asn Leu Ser Thr Thr Gly Gly Ser Arg Arg
305 310 315 320

Trp Ser Leu Gln His Ser Arg Arg Pro Val Ser Val Ser Asp Tyr Leu
325 330 335

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

Leu His Ala Ile Asn Pro Ser Ser Leu Ser Ser Ser Leu Pro Cys Trp
355 360 365

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

Pro Gly Glu Leu Gly Ala Ala Ser Arg Glu Glu Ala Asn Leu Arg Ser
385 390 395 400

Phe Gln Thr Asn Asn Ala Asp His Pro Met Phe Ala Pro Ala Thr Glu
405 410 415

Met Arg Arg Met Gly Gln Asp Pro Thr Arg Trp Gly Leu Ala Thr Gly
420 425 430

Asn Met Ser Ala Ser Gly Ser Val Ser Ser Thr Arg Ile Gly Ser Ser
435 440 445

Thr Arg Met Gly Pro Ser Ser Ser Val His Pro Phe Pro Thr Pro Gly
450 455 460

Trp Ile His His Asn Pro Thr Thr His Asn Gln Gln Arg Ile Ser Glu
465 470 475 480

Phe Ser Thr Trp Ser Leu Phe Pro Pro Met Ala Ser Glu Ser Gly Gly
485 490 495

His Ser Cys His Phe Ser Pro Leu Ser Ser Gly Pro Ser Ser Ala Gln
500 505 510

Asp Thr Gln Ile Ser Ser Gly Ser Ser Ser Gln Gly His Asn Pro Pro
515 520 525

Pro Phe Pro Arg Ser Ala Phe Leu Thr Glu Glu Gln Ser Asp Asp Val
530 535 540

Leu Gly Met Pro Arg Ser Leu Arg Ala Leu Ala Ala Asp Ile Glu Gly

545 550 555 560

Arg His Arg Leu Ile Ser Glu Ile Arg Gln Val Leu Asn Ala Met Arg
565 570 575

Arg Gly Glu Asn Leu Arg Val Glu Asp Tyr Met Leu Phe Asp Pro Met
580 585 590

Ile Tyr His Gly Met Ala Glu Met His Asp Arg His Arg Asp Met Arg
595 600 605

Leu Asp Val Asp Asn Met Ser Tyr Glu Glu Leu Leu Ala Leu Glu Glu
610 615 620

Arg Ile Gly Asp Val Ser Thr Gly Leu Ser Glu Glu Thr Ile Leu Lys
625 630 635 640

Leu Leu Lys Gln Glu Lys His Val Pro Ile Ser Thr Glu Ser Pro Ala
645 650 655

Asp Leu Glu Pro Cys Cys Ile Cys Gln Glu Glu Tyr Val Asp Gly Asp
660 665 670

Asp Met Gly Ile Ile Asp Cys Gly His Asp Phe His Thr Asn Cys Ile
675 680 685

Lys Gln Trp Leu Met Gln Lys Asn Leu Cys Pro Ile Cys Lys Met Thr
690 695 700

Ala Leu Leu Thr
705

<210> 284
<211> 1247
<212> DNA
<213> Populus trichocarpa

<400> 284
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acagatccaa acccacatat ctctaggacc tccaaatcca atacaataat ctctccctc 180
ttccactctc acttcactgc aacccacact gaccaaacia agaagaaagg tgcaaccttt 240
agaggcctag gatgcactgc tggagcagca cagcaggtgt cggtgccggc ggtgataagg 300
tcatcggtg gctgggaagg gaaaagggc aagaagaaaa agggatcatca gaaaagaaag 360
aaagaaagct tgaaactttc cagtgacaac aacaacaata gtaataatag caatggtgat 420
ggtgatctta gtggagatgg taatcttggg aattgcatgg ttatgcaaga tgtttggtgt 480
ggacctggaa ttgggttttc aggtgctgat gctgttggtg ggtcagttga ctgtgtgtgc 540
gttagaagga acgcgtcatc cggaagaggg aagattgatg aaggagagaa atttaatcaa 600

PF59082PF60142_PCT_SEQ_LIST.txt

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agggaaagag agaggggggag agagagagag cgtccttggt tatctaggcg ggctgcagtg      660
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atagaagttt ttggaactcg gtattatcgc catatccgac atccttcccc agatggactt      780
gctaggatga tgatgctcca gaatagtttt atcatgggag gaagattgga tcgatttagc      840
aactggagac ttgatattga tcacatgaca tatgagcaac tgctcgattt aggtgataga      900
attggttatg tgaatactgg attgaaagaa gatgagatca gcagctgtgt caagaaaatt      960
aatccctcaa tcatcgaaga actgccatca catttacaca tgacattgga aaagaagtgc     1020
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ggttttcaca tacaatgtat aaagaaatgg cttgcacaga aaaatacatg cccgggtctgt     1140
aaaactgaac cgggtggctcg agcctaatat cttcaaactg ctgctattta cctgttggtg     1200
tgtatagatt tcatttccta tacgtattca agcatccatt ctttagc                       1247

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<210> 285
<211> 708
<212> PRT
<213> Populus trichocarpa
<400> 285

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Met Ser Gln Gln Thr Pro Phe Ser Asn Met Leu Asn Pro Val Asp Ser
1          5          10          15

Arg Leu Ser Asn Asn Ala Val Ser Ser Gly Asn Ala Ser Cys Ser Asn
          20          25          30

Ala Leu Thr His Asp Val Gln Ser Phe Ser Gly Trp Asn Ser Gly Glu
          35          40          45

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

Lys Met Glu Glu Trp Leu Ser Thr Ser Val Asn Ala Tyr Pro Ala Val
65          70          75          80

Gly Gln Arg Ser Glu Glu Arg Leu Phe Glu Thr Thr Asn Ile Leu Phe
          85          90          95

Pro Gly Arg Val Ser Thr Gly Ile Ser Gly Asn Gln Val Arg Ser Gly
          100          105          110

Pro Leu Phe Leu Gln Gly Ser Ser Ser Asn His Ile Ala Pro Asn Val
          115          120          125

Cys Pro Asn Ser Gly His Ile Gly Asp Thr Thr Ile Gly Arg Pro Ile
          130          135          140

Thr Gly Ala Val Leu Gly Leu Asn Gln Leu Asn Pro Gly Gly Gly Leu
145          150          155          160

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PF59082PF60142_PCT_SEQ_LIST.txt

Glu Ile Glu Arg Ala Ser Ser Ser Gly Val Ser Ser Ser Asp Val Gly
165 170 175

Thr Ser Ser Gly Ser Ser Gly Tyr Ile Val Glu Glu Thr Asn Gly Gly
180 185 190

Ser Gly Ser Ser Ile Gly Val Trp Gly Leu Ser Cys Lys Arg Lys Ala
195 200 205

Leu Glu Gly Thr Thr Gly Gln Ser Phe Pro Gly Gly Ser Ser Ser Cys
210 215 220

Phe Pro Gln Ala Glu Ser Ser Ala Trp His Asn Gly Pro Asn Asn His
225 230 235 240

Ser Val Ser Ser Ser Leu Ser Leu Ser Thr Pro Ser Pro Asn Thr Pro
245 250 255

Ser Val Ala Pro Pro Glu Gln Leu Asn Pro Arg Phe Gly Tyr Gly Met
260 265 270

Arg Gly Ala Pro Pro Asp Ala Phe Pro Ser Ser Asn Val Ser Gly Asn
275 280 285

Ala Asp Ser Leu Arg Asn Phe Gly Arg Arg Ile Ser Pro Gly His Gln
290 295 300

Gln Glu Ser Val Thr Phe Asn Leu Ser Thr Thr Gly Gly Ser Arg Arg
305 310 315 320

Trp Ser Leu Gln His Ser Arg Arg Pro Val Ser Val Ser Asp Tyr Leu
325 330 335

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

Leu His Ala Ile Asn Pro Ser Ser Leu Ser Ser Ser Leu Pro Cys Trp
355 360 365

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

Pro Gly Glu Leu Gly Ala Ala Ser Arg Glu Glu Ala Asn Leu Arg Ser
385 390 395 400

Phe Gln Thr Asn Asn Ala Asp His Pro Met Phe Ala Pro Ala Thr Glu
405 410 415

Met Arg Arg Met Gly Gln Asp Pro Thr Arg Trp Gly Leu Ala Thr Gly
420 425 430

Asn Met Ser Ala Ser Gly Ser Val Ser Ser Thr Arg Ile Gly Ser Ser
 435 440 445

Thr Arg Met Gly Pro Ser Ser Val His Pro Phe Pro Thr Pro Gly
 450 455 460

Trp Ile His His Asn Pro Thr Thr His Asn Gln Gln Arg Ile Ser Glu
 465 470 475 480

Phe Ser Thr Trp Ser Leu Phe Pro Pro Met Ala Ser Glu Ser Gly Gly
 485 490 495

His Ser Cys His Phe Ser Pro Leu Ser Ser Gly Pro Ser Ser Ala Gln
 500 505 510

Asp Thr Gln Ile Ser Ser Gly Ser Ser Ser Gln Gly His Asn Pro Pro
 515 520 525

Pro Phe Pro Arg Ser Ala Phe Leu Thr Glu Glu Gln Ser Asp Asp Val
 530 535 540

Leu Gly Met Pro Arg Ser Leu Arg Ala Leu Ala Ala Asp Ile Glu Gly
 545 550 555 560

Arg His Arg Leu Ile Ser Glu Ile Arg Gln Val Leu Asn Ala Met Arg
 565 570 575

Arg Gly Glu Asn Leu Arg Val Glu Asp Tyr Met Leu Phe Asp Pro Met
 580 585 590

Ile Tyr His Gly Met Ala Glu Met His Asp Arg His Arg Asp Met Arg
 595 600 605

Leu Asp Val Asp Asn Met Ser Tyr Glu Glu Leu Leu Ala Leu Glu Glu
 610 615 620

Arg Ile Gly Asp Val Ser Thr Gly Leu Ser Glu Glu Thr Ile Leu Lys
 625 630 635 640

Leu Leu Lys Gln Glu Lys His Val Pro Ile Ser Thr Glu Ser Pro Ala
 645 650 655

Asp Leu Glu Pro Cys Cys Ile Cys Gln Glu Glu Tyr Val Asp Gly Asp
 660 665 670

Asp Met Gly Ile Ile Asp Cys Gly His Asp Phe His Thr Asn Cys Ile
 675 680 685

Lys Gln Trp Leu Met Gln Lys Asn Leu Cys Pro Ile Cys Lys Met Thr
 690 695 700

Ala Leu Leu Thr

705

<210> 286
 <211> 2297
 <212> DNA
 <213> Populus trichocarpa

<400> 286
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 caaacttctt ttggtaacat gctaaatcca gtagatagca gattgtcaaa taatgctgta 180
 tcttctggcg atgtatcatg ttcaaagtct atgactcatg atattcagaa cttcagtggc 240
 tggaattcag gtgaatctag ctcaagttta agtttgcaaa atcagctgaa tgatgatgag 300
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 ggggatgata tgggaataat cgattgtgga catgactttc atgccaactg catcaaacag 2160
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<210> 287
 <211> 728
 <212> PRT
 <213> Populus trichocarpa

<400> 287

Met His Arg Gln Arg Gly Ala Phe His Thr Phe Ser Glu Thr Ile Asp
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Ile Asp Gln Gly Ser Val Ser Asp Asn Ile Gly Thr Ser Gln Gln Thr
 20 25 30

Ser Phe Gly Asn Met Leu Asn Pro Val Asp Ser Arg Leu Ser Asn Asn
 35 40 45

Ala Val Ser Ser Gly Asp Val Ser Cys Ser Asn Ala Met Thr His Asp
 50 55 60

Ile Gln Asn Phe Ser Gly Trp Asn Ser Gly Glu Ser Ser Ser Ser Leu
 65 70 75 80

Ser Leu Gln Asn Gln Leu Asn Asp Asp Glu Ile Lys Thr Glu Glu Arg
 85 90 95

Trp Ser Ser Ser Val Asn Ala Tyr Pro Ala Val Gly Gln Arg Ser Asp
 100 105 110

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

Met Gly Ile Ser Gly Asn Gln Val Arg Ser Gly Pro Leu Phe Leu Gln
 130 135 140

Gly Ser Ser Ser Asn His Ile Pro Pro Asn Glu Ser Pro Asn Ala Gly
 145 150 155 160

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

PF59082PF60142_PCT_SEQ_LIST.txt

Gly Leu Asn Arg Leu Asn Pro Gly Gly Leu Glu Ile Glu Leu Ala Ser
180 185 190

Ser Ser Gly Val Ser Ser Asp Asp Val Gly Thr Ser Ser Gly Ser Ser
195 200 205

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

Gly Trp Gly Leu Ser Cys Lys Arg Lys Ala Leu Glu Gly Thr Ser Gly
225 230 235 240

Gln Ser Phe Pro Gly Ala Ser Ser Ser Cys Phe Pro Gln Ala Glu Asn
245 250 255

Ser Ala Trp His Asn Gly Pro Asn Asn His Ser Val Ser Ser Ser Leu
260 265 270

Ser Leu Ser Thr Pro Thr Trp Asn Ala Pro Ser Val Thr Pro Pro Glu
275 280 285

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

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

Phe Asp Arg Arg Thr Ser Pro Gly Leu Gln Gln Glu Ser Ala Ala Phe
325 330 335

Asn Val Ser Thr Thr Gly Gly Ser Arg Arg Trp Ser Leu Gln His Pro
340 345 350

Pro Arg Pro Val Ser Val Ser Asp Tyr Leu Glu Ser Arg Ser Pro Glu
355 360 365

Pro Ala Asn Ser Asn Ala Thr Gln Gly Gln Leu His Ala Ile Asn Pro
370 375 380

Ser Ala Leu Ser Arg Ser Met Leu Arg Trp Asn Asp Phe Ser Ser Ser
385 390 395 400

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

Ala Leu Arg Glu Glu Thr Asn Ser Arg Arg Phe Gln Arg Asn Asn Ala
420 425 430

Glu His Pro Met Phe Ala Pro Ala Thr Glu Met Arg Ser Met Ile Gln
435 440 445

Asp Pro Thr Cys Trp Gly Leu Ala Thr Gly Asn Met Ser Thr Ser Gly
 450 455 460
 Ser Val Ser Ser Thr Arg Ile Gly Pro Ser Ser Ser Val Arg Pro Phe
 465 470 475 480
 Pro Thr Pro Arg Trp Ile His Arg Asn Pro Thr Thr His Asn Gln Gln
 485 490 495
 Arg Phe Ser Glu Phe Ser Thr Trp Ser Leu Phe Pro Pro Met Asp Ser
 500 505 510
 Glu Pro Gly Gly His Ser Gly His Phe Ser Pro Leu Ser Ser Gly Pro
 515 520 525
 Ser Ser Ser Ala Gln Asp Thr Val Ile Ser Ser Gly Ser Asn Ser Gln
 530 535 540
 Gly His Asn Pro Pro Phe Pro Arg Ser Ala Leu Leu Met Glu Glu Gln
 545 550 555 560
 Ser Asp Asp Ile Leu Gly Met Pro Arg Ser Leu Arg Val Leu Ala Ala
 565 570 575
 Asp Ile Glu Gly Arg His Arg Leu Ile Ser Glu Ile Arg Gln Val Leu
 580 585 590
 Asn Ala Met Arg Arg Gly Glu Asn Leu Arg Val Glu Asp Tyr Met Leu
 595 600 605
 Phe Asp Pro Leu Ile Tyr His Gly Met Ala Glu Met His Asp Gln His
 610 615 620
 Arg Asp Met Arg Leu Asp Val Asp Asn Met Ser Tyr Glu Glu Leu Leu
 625 630 635 640
 Ala Leu Glu Glu Arg Ile Gly Asp Val Ser Thr Gly Leu Ser Gly Glu
 645 650 655
 Thr Ile Leu Lys Leu Met Lys Lys Gln Lys His Val Pro Val Ser Thr
 660 665 670
 Glu Ser Pro Ala Asp Leu Glu Pro Cys Cys Ile Cys Gln Glu Glu Tyr
 675 680 685
 Val Asp Gly Asp Asp Met Gly Ile Ile Asp Cys Gly His Asp Phe His
 690 695 700
 Ala Asn Cys Ile Lys Gln Trp Leu Met Gln Lys Asn Leu Cys Pro Ile
 705 710 715 720
 Cys Lys Met Thr Ala Leu Ile Thr

<210> 288
 <211> 1280
 <212> DNA
 <213> Populus trichocarpa

<400> 288
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 caaccatttt caactgaaac agatccaaac ccacatgctt ccaagtcata caaatccaac 180
 acaattatct cctccctctt ccactctcac ttctctacaa cccacactga ccaatccaag 240
 aagaaaggtg ccacctttag aggcctagga tgcactgctg gagcagctca gcaagtatcg 300
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<210> 289
 <211> 389
 <212> PRT
 <213> Populus trichocarpa

<400> 289
 Met Pro Val Phe Ala Glu Ser Ser Ser Ser Thr Pro Ala Ala Ile Ala
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 Asp Gln Ile Lys Leu Arg Lys Pro Arg Ser Gln Gln Glu Leu Gln Pro
 20 25 30

PF59082PF60142_PCT_SEQ_LIST.txt

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

Ser Asn Thr Ile Ile Ser Ser Leu Phe His Ser His Phe Ser Thr Thr
50 55 60

Pro Pro Asp Gln Ser Lys Lys Lys Gly Ala Thr Phe Arg Gly Leu Gly
65 70 75 80

Cys Thr Ala Gly Ala Ala Gln Gln Val Ser Val Pro Ala Val Ile Arg
85 90 95

Ser Ser Ala Asp Trp Glu Gly Lys Lys Val Lys Lys Lys Lys Gly His
100 105 110

Pro Lys Arg Lys Lys Glu Ser Leu Lys Leu Cys Ser Asp Asn Asn Asn
115 120 125

Thr Ser Asn Ser Asn Gly Asp Val Asn Gly Asp Gly Asn Phe Ala Asn
130 135 140

Cys Met Val Met Gln Asp Val Trp Cys Gly Pro Gly Met Gly Leu Ser
145 150 155 160

Gly Ala Asp Ala Val Val Gly Ser Val Asp Cys Val Val Ala Arg Arg
165 170 175

Asn Val Ser Ile Gly Arg Gly Lys Ile Asp Gly Gly Glu Lys Ile Asn
180 185 190

Gln Arg Glu Arg Glu Arg Glu Arg Glu Arg Glu Arg Asp Arg Glu Arg
195 200 205

Glu Arg Glu Arg Pro Cys Ile Val Arg Arg Ala Ala Val Asn Pro Glu
210 215 220

Thr Leu Ser Phe Leu Asp Thr Asp Pro Ala Phe Ile Thr Ser Arg Pro
225 230 235 240

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

Ser Pro Asp Gly Leu Ala Glu Ile Met Met Leu Gln Asn Ser Phe Ile
260 265 270

Met Gly Gly Arg Met Asp Arg Phe Ser Asn Trp Arg Leu Asp Ile Asp
275 280 285

His Met Thr Tyr Glu Gln Leu Leu Asp Leu Gly Asp Arg Ile Gly Tyr
290 295 300

Val Asn Thr Gly Leu Lys Glu Asp Glu Ile Ser Arg Cys Val Lys Lys

305 310 315 320

Ile Asn Pro Ser Phe Ile Lys Glu Leu Ser Ser His Leu Pro Met Val
325 330 335

Leu Glu Lys Lys Cys Ser Ile Cys Gln Asp Asp Tyr Glu Glu Asp Gly
340 345 350

Glu Val Gly Lys Leu Asp Cys Gly His Gly Phe His Ile Gln Cys Ile
355 360 365

Lys Gln Trp Leu Gly Gln Lys Asn Thr Cys Pro Val Cys Lys Thr Glu
370 375 380

Pro Val Gly Arg Gly
385

<210> 290
<211> 1748
<212> DNA
<213> Populus trichocarpa

<400> 290
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<210> 291
 <211> 545
 <212> PRT
 <213> Populus trichocarpa

<400> 291

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 20 25 30

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

Asn Pro Pro Ser Ile Asp Gly Pro Ser Cys Ala Ser Arg Arg Asn Leu
 50 55 60

Glu Asn Arg Ala Leu Glu His Ser Ser Thr Tyr Phe Arg Ser Glu Gly
 65 70 75 80

Pro Gln Val His Ala Pro Leu Ser Ala Pro Arg His Asp Val Phe Pro
 85 90 95

His Cys Pro Ala Gly Gly Ser Phe Tyr Pro Pro Pro Glu Leu Glu Ala
 100 105 110

Thr His Val His Ser Asn His His Asn Arg His Gly Ile His Glu Gly
 115 120 125

Glu Gly Gly Leu Leu Asp His Thr Met Ser Ala Gly Arg Gly Pro Phe
 130 135 140

Lys Arg Lys Ser Pro Gly Val Pro Thr Ser Trp Glu Arg Gly Gly Thr
 145 150 155 160

Ser Ser Met Tyr Ser Ala Gly Ser Ser Ser Asn Ser Phe Glu Leu His
 Seite 308

165

170

175

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

Gly Leu Pro Pro Tyr Met Gly Ser Ser Leu Ser Ile Gly Gly Glu Asp
 195 200 205

Pro Pro Arg Asn Val Arg Ser Arg Ser Arg Leu Asp Leu Glu Pro Asn
 210 215 220

Pro Arg Arg Thr His Ser Ser Ser Tyr Thr Ser His Pro Phe Ser Ser
 225 230 235 240

Thr Ser His Leu Arg Asn His Pro Gly Pro Val Asp Val Ala Asn Leu
 245 250 255

Asn Ala Asp Arg Thr Ala Tyr Glu Gln Asn Gln Ile Gly Val Pro Pro
 260 265 270

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

Glu Met Asn Gln His Tyr Ala Gly Gly Asn Pro Thr Asp Ile Arg Arg
 290 295 300

Tyr Asn His Asp Ser Ile Leu Ser Arg Asn Pro Ile Ala Pro Pro Arg
 305 310 315 320

His Leu His Gly Phe His Ala Gln Ala Ser Arg Glu Gly Gln Asn Ser
 325 330 335

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

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

Ser Glu Thr His Ser Ser Arg Tyr Ser Arg Pro Leu Leu Ser Gly Gly
 370 375 380

Trp His Ser Asn His Arg Glu Gly Arg Ser Arg Ile Ser Ile Glu Arg
 385 390 395 400

Phe Gln Ser Leu Ser Asn Val Val Asp Val Arg Asp Arg Met Gly Ser
 405 410 415

Glu Ala Leu Met Met Leu Asp His Ser Tyr Leu Tyr Gly Ser Arg Asn
 420 425 430

Phe Leu Asp Gln Tyr Arg Asp Met Arg Leu Asp Val Asp Ser Met Ser
 435 440 445

PF59082PF60142_PCT_SEQ_LIST.txt

Tyr Glu Glu Leu Leu Ala Leu Gly Glu Arg Ile Gly Ile Val Asn Thr
450 455 460

Gly Leu Pro Glu Asp Val Phe Ser Lys Cys Leu Val Glu Thr Arg Cys
465 470 475 480

His Ser Ser Asp Lys Ala Gln Glu Glu Thr Ser Cys Ala Ile Cys Leu
485 490 495

Glu Glu Tyr Lys Ser Met Asp Lys Val Gly Met Ile Arg Asn Cys Gly
500 505 510

His Val Tyr His Val Asp Cys Ile Lys Lys Trp Leu Ser Met Lys Asn
515 520 525

Met Cys Pro Ile Cys Lys Ala Pro Ala Val Ala Asp Gly Ser Asn Lys
530 535 540

Glu
545

<210> 292
<211> 1766
<212> DNA
<213> Populus trichocarpa

<400> 292
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atccttttag ggggtgtgac aaacttccga ccatctgata ttccaacat ggtagcagct 180
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tggtactcaga ccactgctat tccttacatg catgggaaca atctcaatgg aggtcctata 900
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PF59082PF60142_PCT_SEQ_LIST.txt

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gatattggac ttaggcatct aggatcagtt caaccaactg gccttagaat gtacaggtct 1200
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cgcttgaaga atgtctgccc catctgcaaa tcagaagcct taaacacgga aagaatggat 1680
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gtgacagttt ctttctcata atttgt 1766

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<210> 293
<211> 551
<212> PRT
<213> Populus trichocarpa

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<400> 293

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Met Gly Gln Arg Asn Met Leu Cys Thr Asn Gln Met Ile Asp Leu Glu
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Met Asp Gln Gln Ser Gln Gly Tyr Leu His Pro Glu Pro Cys Ile Leu
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```

Leu Gly Gly Val Thr Asn Phe Arg Pro Ser Asp Ile Pro Thr Met Val
          35          40          45

```

```

Ala Ala Ser Gly Asn Thr Asn Asn Arg Asp Ala His Leu Val Asp His
          50          55          60

```

```

Tyr Asp Gly Ala Met Phe Tyr Gly Met Pro Gln Tyr His Gly Leu His
65          70          75          80

```

```

Pro His Arg Gln Tyr His Gly Pro Asn Leu Asp Leu Ser Val Ala Thr
          85          90          95

```

```

Ala Pro Asn Phe Tyr Val Pro Tyr Met Thr Pro Ser Ser Gly Ile Pro
          100         105         110

```

```

Ile Ser His Gly Pro Cys Asp Gln Leu Ser Ser Ser Asn Asn Tyr Gly
          115         120         125

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Val Ile Glu Val Ser Ala Asp Glu Tyr Gly Thr Asn Ser His Phe Met
          130         135         140

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PF59082PF60142_PCT_SEQ_LIST.txt

Asp Asn Ala Arg Gly Ser Phe Lys Arg Lys Asn Ala Glu Gly Asn Pro
 145 150 155 160
 Gly Asn Phe Gln Tyr Leu Asn Ala Ser Ala Ser Ser Ser Ser Ser Val
 165 170 175
 Ala Pro Leu Asn Thr Arg His Ser Glu Gly Gly Ala Leu Met Asp Ala
 180 185 190
 Thr Ser Phe Thr Pro Pro His Tyr Arg Gly Ser Ser Ala Ser Ser Ile
 195 200 205
 Arg Asp Val Gly Ser Gln Ser Ser Val Arg Asn Arg Leu Gly Ala Ala
 210 215 220
 Gly Leu Asp Pro Ala Leu Ala His Asn Leu Asn His Phe Ile Gln Gly
 225 230 235 240
 Asn Tyr Leu Gly Gln Pro Tyr Gln Pro Ser Gly Ser Leu Trp Leu Asp
 245 250 255
 Gln His Leu Ser Asn Ser Gly Thr Asp Ala Gly Thr Ser Gly Trp Thr
 260 265 270
 Gln Thr Thr Ala Ile Pro Tyr Met His Gly Asn Asn Leu Asn Gly Gly
 275 280 285
 Pro Ile Glu Ile Gly Asn Met Gly Leu Gln Arg Tyr His Glu Pro Ala
 290 295 300
 Ser Asn Arg Ser Asn Ala Ser Phe Ser Arg Pro Ser Ala Val Asn Leu
 305 310 315 320
 Gln His His Asn Phe His His Met Ser Pro Pro Ile Gln Gly Met Arg
 325 330 335
 Gly His Asn Ile Asn Ile Leu Pro Gln Ala Pro Ala Ala Ser Phe Arg
 340 345 350
 Val Pro Thr Ala Asn Ala Ser Gln Ile Thr Met Asn Pro Ser Gln Asp
 355 360 365
 Gly Leu Asp Ile Gly Leu Arg His Leu Gly Ser Val Gln Pro Thr Gly
 370 375 380
 Leu Arg Met Tyr Arg Ser His Arg Glu Gly Val Val Pro Glu Thr Thr
 385 390 395 400
 Leu Arg His Arg Asn Leu Pro Gln Leu Arg Val Leu Pro Thr Asp Gly
 405 410 415

PF59082PF60142_PCT_SEQ_LIST.txt

Val Ala Ile Leu Gly Phe Pro Asp Tyr Tyr Glu Val Glu Asn His Val
420 425 430

Asp His His Arg Asp Met Arg Leu Asp Ile Glu Asp Met Ser Tyr Glu
435 440 445

Glu Leu Leu Ala Leu Gly Glu Arg Ile Gly Asn Val Asn Thr Gly Leu
450 455 460

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

Ser Pro Ser Ile Asn Leu Glu Glu Ala Ala Cys Met Asp Gln Glu Ala
485 490 495

Asp Ser Cys Ile Ile Cys Gln Asp Asp Tyr Lys Ser Lys Glu Lys Ile
500 505 510

Ala Ala Leu Asp Cys Gly His Glu Tyr His Ala Val Cys Leu Lys Lys
515 520 525

Trp Leu Arg Leu Lys Asn Val Cys Pro Ile Cys Lys Ser Glu Ala Leu
530 535 540

Asn Thr Glu Arg Met Asp Val
545 550

<210> 294
<211> 1763
<212> DNA
<213> Populus trichocarpa

<400> 294
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cagatgattg atttagaaat ggatcaacaa agccagggat atctacatcc tgagtcctgc 120
attcttctag ggggtgtgac aaacttccga ccacctgata ttcctaccat gttaacagct 180
tcagggaaca ctatcaatcg tgacgccccat ctagctgatac gttatgatgg tgctatgttt 240
tatgggatgc cccaatacca tgggtgttcac cctcatcctc agtatcacag cccaaatcct 300
gatttaagtg tggctactgc acccaacttc tatgttcctt acatgactcc atcttctggt 360
attcctatca gtcatgcatc ttgtgatcaa ttatcttcac ccaacaatta tggagtgatt 420
ggagtttctg ctgatgagta tggaacaaac agtcacttca tggataatgc tagaagttca 480
tacaagagaa agaatgctga aggaaatcca gggaatttcc actatctgaa tgcctcagca 540
agctctagtt cctcagttcc cccaatgaat acaaggcatc ccgagggggg tgctctgatg 600
gatgctacat cattcaccct gccacattac aggggggacta gtgcttcatac aatcaggggaa 660
gtaggatctc aaagaagtgt gaggaataga ttaggttctg tggggctcga tcctgccttg 720
acacacaacc cgaaccattt tattcaagga aactatttgg gccaaccta tcagccaggt 780

PF59082PF60142_PCT_SEQ_LIST.txt

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ggctctctct ggttagaaca acacttaagc aacgggttcta ctgatgcagg cgcttcagta      840
tggactcaga cccctactat tccttacatg cacgggaaca atgtcaatgg agttcctata      900
gaaactggga gcatgggtcc acagcgggtat catgagccag ctagcaacag aagtaatgcc      960
agtttctcgc acccttctcc agtaaaccct cagcaccata attttcatca cctgtctcca     1020
ccaattcaag gaattagagg tcacaatatt aatattcttc ctcaagcacc agcagcttca     1080
ttcagagttc ctacagccaa tgcctcacia agcactatga atctatctca agatgggttta     1140
gatattggac ttaggaatcc gggatctgtt caaccaaccg gccttcgaat gtaccggcct     1200
cgccatgagg gagttgcacc tgagaccaca ctaagacatc gcaacctccc tcgcttaaga     1260
gtgttgccaa cagatgcaac aatactaggg ttccctgact attatgaagt agagaattat     1320
gctgaccacc acagagatat gcgcttgat atagaggaca tgtcttatga ggagcttctt     1380
gcacttgggg agcgtattgg taatgtaaat actggcttat cagatgcaac tatcagaagt     1440
caattaaaaa caagaactta tttatcatct cttattcaa tcaatttgga agtatcttgt     1500
atggatcaag aagctgattc ttgcattatt tgccaggatg attataagag taaggagaaa     1560
attgcatctc ttgattgtgg acacgagtat catgcagatt gcttgaagaa gtggctacgc     1620
ttgaagaatg tctgccccat ctgcaaact gaagccttaa ccatggaagg aaaggatgtt     1680
taagggtggtg atcctgcttg tataaaataa aaggaaaaat aaagcggagg aaaggggtga     1740
cagctttata ggcgagcatt caa                                             1763

```

<210> 295
 <211> 550
 <212> PRT
 <213> Populus trichocarpa

<400> 295

Met Gly Gln Arg Asn Met Leu Cys Thr Asn Gln Met Ile Asp Leu Glu
 1 5 10 15

Met Asp Gln Gln Ser Gln Gly Tyr Leu His Pro Glu Ser Cys Ile Leu
 20 25 30

Leu Gly Gly Val Thr Asn Phe Arg Pro Pro Asp Ile Pro Thr Met Leu
 35 40 45

Thr Ala Ser Gly Asn Thr Ile Asn Arg Asp Ala His Leu Ala Asp Arg
 50 55 60

Tyr Asp Gly Ala Met Phe Tyr Gly Met Pro Gln Tyr His Gly Val His
 65 70 75 80

Pro His Pro Gln Tyr His Ser Pro Asn Leu Asp Leu Ser Val Ala Thr
 85 90 95

Ala Pro Asn Phe Tyr Val Pro Tyr Met Thr Pro Ser Ser Gly Ile Pro
 100 105 110

PF59082PF60142_PCT_SEQ_LIST.txt

Ile Ser His Ala Ser Cys Asp Gln Leu Ser Ser Ser Asn Asn Tyr Gly
115 120 125

Val Ile Gly Val Ser Ala Asp Glu Tyr Gly Thr Asn Ser His Phe Met
130 135 140

Asp Asn Ala Arg Ser Ser Tyr Lys Arg Lys Asn Ala Glu Gly Asn Pro
145 150 155 160

Gly Asn Phe His Tyr Leu Asn Ala Ser Ala Ser Ser Ser Ser Ser Val
165 170 175

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

Thr Ser Phe Thr Leu Pro His Tyr Arg Gly Thr Ser Ala Ser Ser Ile
195 200 205

Arg Glu Val Gly Ser Gln Arg Ser Val Arg Asn Arg Leu Gly Ser Val
210 215 220

Gly Leu Asp Pro Ala Leu Thr His Asn Pro Asn His Phe Ile Gln Gly
225 230 235 240

Asn Tyr Leu Gly Gln Pro Tyr Gln Pro Gly Gly Ser Leu Trp Leu Glu
245 250 255

Gln His Leu Ser Asn Gly Ser Thr Asp Ala Gly Ala Ser Val Trp Thr
260 265 270

Gln Thr Pro Thr Ile Pro Tyr Met His Gly Asn Asn Val Asn Gly Val
275 280 285

Pro Ile Glu Thr Gly Ser Met Gly Pro Gln Arg Tyr His Glu Pro Ala
290 295 300

Ser Asn Arg Ser Asn Ala Ser Phe Ser His Pro Ser Pro Val Asn Pro
305 310 315 320

Gln His His Asn Phe His His Leu Ser Pro Pro Ile Gln Gly Ile Arg
325 330 335

Gly His Asn Ile Asn Ile Leu Pro Gln Ala Pro Ala Ala Ser Phe Arg
340 345 350

Val Pro Thr Ala Asn Ala Ser Gln Ser Thr Met Asn Leu Ser Gln Asp
355 360 365

Gly Leu Asp Ile Gly Leu Arg Asn Pro Gly Ser Val Gln Pro Thr Gly
370 375 380

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Arg Met Tyr Arg Pro Arg His Glu Gly Val Ala Pro Glu Thr Thr
385 390 395 400

Leu Arg His Arg Asn Leu Pro Arg Leu Arg Val Leu Pro Thr Asp Ala
405 410 415

Thr Ile Leu Gly Phe Pro Asp Tyr Tyr Glu Val Glu Asn Tyr Ala Asp
420 425 430

His His Arg Asp Met Arg Leu Asp Ile Glu Asp Met Ser Tyr Glu Glu
435 440 445

Leu Leu Ala Leu Gly Glu Arg Ile Gly Asn Val Asn Thr Gly Leu Ser
450 455 460

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

Pro Tyr Ser Ile Asn Leu Glu Val Ser Cys Met Asp Gln Glu Ala Asp
485 490 495

Ser Cys Ile Ile Cys Gln Asp Asp Tyr Lys Ser Lys Glu Lys Ile Ala
500 505 510

Ser Leu Asp Cys Gly His Glu Tyr His Ala Asp Cys Leu Lys Lys Trp
515 520 525

Leu Arg Leu Lys Asn Val Cys Pro Ile Cys Lys Ser Glu Ala Leu Thr
530 535 540

Met Glu Gly Lys Asp Val
545 550

<210> 296
<211> 743
<212> DNA
<213> Populus trichocarpa

<400> 296
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gaggatgaag agagaaaaca ggcacgcagt agggctctgtt ataccaact cgaacagggtt 120
cattcagatt ttgcaatagc aatggttttg caggaacaag aaagggcttt cacaatcctc 180
acaagcatcg aaagcgatag taacgaggaa gaaagtgatg aagcttcaag ttctgaaagc 240
ggtgctgatg acaatgacta tgagttcttt cagagccatg aattcgaatc tgaaatggaa 300
tttctgcagg aaggagagga tagtaacagc gatgaagata tggaagagga tgaggttgac 360
ccagacgagc tatcttacga agacttgatt gcgctgggag agtttgtagg gcaagagaag 420
aggggactgt caagaaatga aatctctacg tgcttgcgct catgtaagta cgagtccttta 480
gcaagcaaaa ctgggactga tcggtgtgtg atttgtcaaa tggaatatga agaagatgaa 540
tcattggtag ctctttcttg tgatcatcct tatcatcctg aatgcatagc caactggctt 600

PF59082PF60142_PCT_SEQ_LIST.txt

caaatcaata agatttgccc catttgtagc accgaagtat catcgcccta taagagtgtt 660
tagttattat ccatttgata tgcgttgtaa aattcccaag attcaagatt aatttgattg 720
taacatttgc gttcatgtac tcg 743

<210> 297
<211> 210
<212> PRT
<213> Populus trichocarpa

<400> 297

Met Asp Asn Asp Gly Arg Lys Glu Pro Val Glu Asp Glu Glu Arg Lys
1 5 10 15

Gln Ala Ser Ser Arg Val Cys Tyr Thr Gln Leu Glu Gln Val His Ser
20 25 30

Asp Phe Ala Ile Ala Met Val Leu Gln Glu Gln Glu Arg Ala Phe Thr
35 40 45

Ile Leu Thr Ser Ile Glu Ser Asp Ser Asn Glu Glu Glu Ser Asp Glu
50 55 60

Ala Ser Ser Ser Glu Ser Gly Ala Asp Asp Asn Asp Tyr Glu Phe Phe
65 70 75 80

Gln Ser His Glu Phe Glu Ser Glu Met Glu Phe Leu Gln Glu Gly Glu
85 90 95

Asp Ser Asn Ser Asp Glu Asp Met Glu Glu Asp Glu Val Asp Pro Asp
100 105 110

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

Glu Lys Arg Gly Leu Ser Arg Asn Glu Ile Ser Thr Cys Leu Arg Pro
130 135 140

Cys Lys Tyr Glu Ser Leu Ala Ser Lys Thr Gly Thr Asp Arg Cys Val
145 150 155 160

Ile Cys Gln Met Glu Tyr Glu Glu Asp Glu Ser Leu Val Ala Leu Ser
165 170 175

Cys Asp His Pro Tyr His Pro Glu Cys Ile Ala Asn Trp Leu Gln Ile
180 185 190

Asn Lys Ile Cys Pro Ile Cys Thr Thr Glu Val Ser Ser Pro Tyr Lys
195 200 205

Ser Val
210

<210> 298
 <211> 1805
 <212> DNA
 <213> *Medicago truncatula*

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<400> 298
atggatgaat attctagtaa gagagccaat gatgggggtga tagttcctag aaaggggatg      60
agcaccatgt ttaaagatac tgccactacc cgagatcgaa atggtcaagt atgtagccgc      120
cttggttgca gcagcaaagt caactcttct aaaggtgctc aaattggttc ttctgaaaag      180
ggtaaattctt tgaggccttc atttcggttc tcatcaaattg gcaaggaaac aattggtagc      240
tcctctagaa cgttctccgg gagtagtagc ccaggaaaac cccatagaaa gcctcagaaa      300
aagttatcat ctcatagata gacagattca tctgaaacta atagtgtaca agatgaacca      360
gaagtttcaa agctcacacc tccacaaaaa aaccagaggg gtcttcaagc cgaaggggaa      420
aacacagatt ctagtaatgg ggtgctgatg gaagtaggaa gttctagttt agcctctaata      480
acaagatcta ggaggaattt tcatccaaaa cctggattac gtagtcaaga aattcaaagc      540
accggtccag ggacacgtgc tgggtaccagt aggtatgggt taaggaacct caaatgcaac      600
tccatttctg atgtcatgcc cgtcggttgt acaccatctg attcaaccct aaacaaaaag      660
aaggatgcga taaaaaagag aaattgtgaa ggagaaagta gttctacagc tagaggcaaa      720
aaaattaacg ggccgttaat tgatggacgg aattctgtat ccagaaatgg cctatctatc      780
tctgattcaa gaatatctag aaatgccct catagggaca gggcagacag caacatagcg      840
tctggtagaa cacgaagatc aattggcggg catggtaggg gaagggtttc tggccaagga      900
aatgctaata ctgtggcccc taatcagtcc cttatcatgg taccttcctt ttcttattct      960
ggaaatctta attctcctgg tgtacaacat cataattctc tggagactcc ttcaagtcca     1020
agttcttaca gtggagcagg tactagtagt gaggaactgt acggtgttat gccaacgtct     1080
cctacagaat acgggctcac ccattctcta ataaatcggg atagctttcg acgacgctac     1140
aacatggatg gtattgcaga ggtactgttg gcacttgaga ggattgaaca agatgtcgag     1200
ctaacacacg agcaaattca cttgttgagg tccaacttgt tccttactgg actaaacttc     1260
tttgatcagc atagagatat gcgactggac atcgataata tgtcatatga ggaattactg     1320
gctctggaag aaaggatggg tactgtgagc accgctgtaa cagaggaaga tctatcagaa     1380
tgcctaaaga gaagtttcta tcaatcctca ccctcagaca atgcaaccaa gtgttgcaat     1440
gagaataagg atgatatcaa atgctgcata tgccaggagg agtatgtgga ggaagatgaa     1500
gtgggggagtc tactatgcga gcacaaatat catgttgttt gcatacagca gtggctacga     1560
ctaaagaact ggtgtcctat ttgcaaagca tcagtgcacac cgtcaagttc gccgtcgtcc     1620
cactagttaa gttttaggcc agacaatgga tattgatttc tttctacccc tctttctggt     1680
cattttaatt ttcacttttg taaaaatac agtttctctt cacctcttct tattagtctt     1740
ttgtacataa ccaatatctt cataccaatt attatcaaat aatacaagcc actggcttga     1800
tagat

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1805

<210> 299
 <211> 541
 <212> PRT
 <213> Medicago truncatula

<400> 299

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Met Asp Glu Tyr Ser Ser Lys Arg Ala Asn Asp Gly Val Ile Val Pro
1      5      10      15

Arg Lys Gly Met Ser Thr Met Phe Lys Asp Thr Ala Thr Thr Arg Asp
      20      25      30

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

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

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

Ser Ser Arg Thr Phe Ser Gly Ser Ser Ser Pro Gly Lys Pro His Arg
      85      90      95

Lys Pro Gln Lys Lys Leu Ser Ser Gln Ile Glu Thr Asp Ser Ser Glu
      100      105      110

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

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

Ser Asn Gly Val Leu Met Glu Val Gly Ser Ser Ser Leu Ala Ser Asn
      145      150      155      160

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

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

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

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

Lys Lys Arg Asn Cys Glu Gly Glu Ser Ser Ser Thr Ala Arg Gly Lys
      225      230      235      240

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PF59082PF60142_PCT_SEQ_LIST.txt

Lys Ile Asn Gly Pro Leu Ile Asp Gly Arg Asn Ser Val Ser Arg Asn
 245 250 255
 Gly Leu Ser Ile Ser Asp Ser Arg Ile Ser Arg Asn Ala Pro His Arg
 260 265 270
 Asp Arg Ala Asp Ser Asn Ile Ala Ser Gly Arg Thr Arg Arg Ser Ile
 275 280 285
 Gly Gly His Gly Arg Gly Arg Val Ser Gly Gln Gly Asn Ala Asn Pro
 290 295 300
 Val Ala Pro Asn Gln Ser Leu Ile Met Val Pro Ser Phe Ser Tyr Ser
 305 310 315 320
 Gly Asn Leu Asn Ser Pro Gly Val Gln His His Asn Ser Leu Glu Thr
 325 330 335
 Pro Ser Ser Pro Ser Ser Tyr Ser Gly Ala Gly Thr Ser Ser Glu Glu
 340 345 350
 Leu Tyr Gly Val Met Pro Thr Ser Pro Thr Glu Tyr Gly Leu Thr His
 355 360 365
 Ser Leu Ile Asn Arg Asp Ser Phe Arg Arg Arg Tyr Asn Met Asp Gly
 370 375 380
 Ile Ala Glu Val Leu Leu Ala Leu Glu Arg Ile Glu Gln Asp Val Glu
 385 390 395 400
 Leu Thr His Glu Gln Ile His Leu Leu Glu Ser Asn Leu Phe Leu Thr
 405 410 415
 Gly Leu Asn Phe Phe Asp Gln His Arg Asp Met Arg Leu Asp Ile Asp
 420 425 430
 Asn Met Ser Tyr Glu Glu Leu Leu Ala Leu Glu Glu Arg Met Gly Thr
 435 440 445
 Val Ser Thr Ala Val Thr Glu Glu Asp Leu Ser Glu Cys Leu Lys Arg
 450 455 460
 Ser Phe Tyr Gln Ser Ser Pro Ser Asp Asn Ala Thr Lys Cys Cys Asn
 465 470 475 480
 Glu Asn Lys Asp Asp Ile Lys Cys Cys Ile Cys Gln Glu Glu Tyr Val
 485 490 495
 Glu Glu Asp Glu Val Gly Ser Leu Leu Cys Glu His Lys Tyr His Val
 500 505 510
 Val Cys Ile Gln Gln Trp Leu Arg Leu Lys Asn Trp Cys Pro Ile Cys
 Seite 320

515

520

525

Lys Ala Ser Val Thr Pro Ser Ser Ser Pro Ser Ser His
 530 535 540

<210> 300
 <211> 2330
 <212> DNA
 <213> *Medicago truncatula*

<400> 300
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 gcgcaaaatg cagtagattt ccggctgtca gattataggg ggtcttcttg tgagactgca 120
 tgtttacgtg gtactggtcc taatgtgagc tttaatggct ggaataccgg tgaacccagt 180
 tctggactga atctgggtcaa ccaagtcaac gatgatggtc taaaatctga acaaagggtt 240
 tcttcgtcat gcagtgtctat tgctgaggat ggtctaagac ccgaggaaag gcaattactt 300
 gggaaccaat ccagaattca tccttccttt ttgcaagggt ccagctccaa tcatacagcc 360
 caaggtatta attttgggtat ggagcacatt gctaactcat ctgatcgcg gaaaggtaaa 420
 gaaactggta gcggtgttaa taacaacgat ctttttggtat tagatagaga gaagacatca 480
 attggcagtt cttcattcaa ccaaacaggt gcttcacag caagctcttg gtacatggca 540
 tggggagata gtggcagttc aagttcttct ttagctaatt ggggtccttc ctgcaaaaga 600
 aaggcccttg aagatagttc tatgcaactg tgtactggag gaagctcgag ttcccttgta 660
 caatctgaaa atggttactg gcttactgat tctgttgatc ttaatgttcc tggaagctta 720
 ggtgatttgt cacctttaga ggatttccgt gttactagcc ctccatttca gcagaataca 780
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 aatgtggaaa ggcctctacg aaactttgat aggagaatga cccatctaca tcatccggaa 900
 tctgtacctc tcaatttaac atcaacaggg agtgctagac atcataatta tccttctccg 960
 catcaaatac ccggctctct ctcatttaac gaatccttgg atttaagggt agcagctgga 1020
 gtaacagctg ctaattctgc tgtgccgcaa aaccagtcac catccctgca catgcatcct 1080
 tttccgtgga atagagctgc taatcctaga gtggccagat cttcaagttc ttatagctca 1140
 ggagaaagag cagtacgtga tgattttaat ttaagaatct tccaagaga tagtaccgag 1200
 catcccatga acatgcctgc atcttcagga catgaacctg caggttggta ttcattctct 1260
 agtaatttga acaatgctgg aggcatacct cctccatcct ggattggatc tacttcaaac 1320
 gtccactcgt tacctaattc tagctggaca ttttaaccatg aagtcccaac agaaaatcta 1380
 cagagagttt cagagttcag tccttggtcc ctttttcctt caatcagctc agcatctggt 1440
 actcataatg gtcattcctc ctctacttcc ggccctcctt ctttttctca gggttctagt 1500
 agtaatcaac cacatccaag accatcattt atgacggaaa gaaggggttg tgatgttctc 1560
 tctgctcctc attcattgcg aacattacc tttgacaatg aggggagacg ccggctcata 1620
 tctgagattc gccaagtcct gctagcaatg cggaggggtg agaacttacg agctgaggat 1680

PF59082PF60142_PCT_SEQ_LIST.txt

tatatgctct ttgacccttt cctatatcat ggcattggctg aaatgcacga cagacacaga	1740
gaaatgcgcc ttgacgttga taatatgtct tatgaggaat tgttggcatt ggaggagcgt	1800
ataggagacg taagcactgg actgagtga gatataatta ataagttgat gaaacagcga	1860
ttttacatgt ctctcatgac agagtcttct tctgatctcg aaccttgctg tatctgtcag	1920
gaggaatatg ttgatggaca aaatctcggg ttgctagatt gtggggcacga gttccacagt	1980
aactgcatca cacagtggct aatgcagaag aatctgtgcc caatttgcaa aacaacggcc	2040
ttggcctcgt gacgaggaga atctctccct cttcacatat catttccatt tatcagtttt	2100
tatcttttgt tggttctatc tattactttg ttttattcaa tgaacttcct ctcatcttag	2160
attgggaacg aaaacacaca taaaaaata gacataaaga aatattggtg gttaagctct	2220
atagtagaat tacatttata ctgtgataat ggacaattac atgtccttta tgatatctaa	2280
aagcacttga attatattat tgattttcat tataagttta agactgttga	2330

<210> 301
 <211> 683
 <212> PRT
 <213> Medicago truncatula

<400> 301

Met Met Gln Gly Pro Ser Ser Asn Gly Thr Asp Met Asn His Gln Ser	
1 5 10 15	

Ser Leu Asn His Ala Gln Asn Ala Val Asp Phe Arg Leu Ser Asp Tyr	
20 25 30	

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

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

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

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

Arg Gln Leu Leu Gly Asn Gln Ser Arg Ile His Pro Ser Phe Leu Gln	
100 105 110	

Gly Ser Ser Ser Asn His Thr Ala Gln Gly Ile Asn Phe Gly Met Glu	
115 120 125	

His Ile Ala Asn Ser Ser Asp Arg Gly Lys Gly Lys Glu Thr Gly Ser	
130 135 140	

Gly Val Asn Asn Asn Asp Pro Phe Gly Leu Asp Arg Glu Lys Thr Ser	
145 150 155 160	

PF59082PF60142_PCT_SEQ_LIST.txt

Ile Gly Ser Ser Ser Phe Asn Gln Thr Gly Ala Ser Ser Ala Ser Ser
165 170 175

Gly Tyr Met Ala Trp Gly Asp Ser Gly Ser Ser Ser Ser Ser Leu Ala
180 185 190

Asn Trp Gly Pro Ser Cys Lys Arg Lys Ala Leu Glu Asp Ser Ser Met
195 200 205

Gln Leu Cys Thr Gly Gly Ser Ser Ser Ser Leu Val Gln Ser Glu Asn
210 215 220

Gly Tyr Trp Leu Thr Asp Ser Val Asp Leu Asn Val Pro Gly Ser Leu
225 230 235 240

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

Gln Gln Asn Thr Arg Asn Glu Val Arg Gln Glu Ala Ser Asn Ala Phe
260 265 270

Pro Ser Met Val Ser Ile Ala Glu Asn Val Glu Arg Pro Leu Arg Asn
275 280 285

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

Asn Leu Thr Ser Thr Gly Ser Ala Arg His His Asn Tyr Pro Ser Pro
305 310 315 320

His Gln Ile Pro Gly Ser Leu Ser Phe Asn Glu Ser Leu Asp Leu Arg
325 330 335

Leu Ala Ala Gly Val Thr Ala Ala Asn Ser Ala Val Pro Gln Asn Gln
340 345 350

Ser Pro Ser Leu His Met His Pro Phe Pro Trp Asn Arg Ala Ala Asn
355 360 365

Pro Arg Val Ala Arg Ser Ser Ser Ser Tyr Ser Ser Gly Glu Arg Ala
370 375 380

Val Arg Asp Asp Phe Asn Leu Arg Ile Phe Pro Arg Asp Ser Thr Glu
385 390 395 400

His Pro Met Asn Met Pro Ala Ser Ser Gly His Glu Pro Ala Gly Trp
405 410 415

Tyr Ser Ser Ser Ser Asn Leu Asn Asn Ala Gly Gly Ile Pro Pro Pro
420 425 430

PF59082PF60142_PCT_SEQ_LIST.txt

Ser Trp Ile Gly Ser Thr Ser Asn Val His Ser Leu Pro Asn Pro Ser
435 440 445

Trp Thr Phe Asn His Glu Val Pro Thr Glu Asn Leu Gln Arg Val Ser
450 455 460

Glu Phe Ser Pro Trp Ser Leu Phe Pro Ser Ile Ser Ser Ala Ser Gly
465 470 475 480

Thr His Asn Gly His Ser Ser Ser Thr Ser Gly Pro Pro Ser Phe Ser
485 490 495

Gln Gly Ser Ser Ser Asn Gln Pro His Pro Arg Pro Ser Phe Met Thr
500 505 510

Glu Arg Arg Gly Gly Asp Val Leu Ser Ala Pro His Ser Leu Arg Thr
515 520 525

Leu Pro Phe Asp Asn Glu Gly Arg Arg Arg Leu Ile Ser Glu Ile Arg
530 535 540

Gln Val Leu Leu Ala Met Arg Arg Gly Glu Asn Leu Arg Ala Glu Asp
545 550 555 560

Tyr Met Leu Phe Asp Pro Phe Leu Tyr His Gly Met Ala Glu Met His
565 570 575

Asp Arg His Arg Glu Met Arg Leu Asp Val Asp Asn Met Ser Tyr Glu
580 585 590

Glu Leu Leu Ala Leu Glu Glu Arg Ile Gly Asp Val Ser Thr Gly Leu
595 600 605

Ser Glu Asp Ile Ile Asn Lys Leu Met Lys Gln Arg Phe Tyr Met Ser
610 615 620

Leu Met Thr Glu Ser Ser Ser Asp Leu Glu Pro Cys Cys Ile Cys Gln
625 630 635 640

Glu Glu Tyr Val Asp Gly Gln Asn Leu Gly Leu Leu Asp Cys Gly His
645 650 655

Glu Phe His Ser Asn Cys Ile Thr Gln Trp Leu Met Gln Lys Asn Leu
660 665 670

Cys Pro Ile Cys Lys Thr Thr Ala Leu Ala Ser
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<210> 302
<211> 1894
<212> DNA
<213> Medicago truncatula

PF59082PF60142_PCT_SEQ_LIST.txt

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<400> 302
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aattatgaca gacaagcatt tcatgttgat agtgggtttta ttgatcttac aatggggagt 420
ggacgagcgc atcacaagag gaagagccct ggaattcctt cagtctatga gagaggcagt 480
tcaagtgggt atttcaatgc tgggacttca agtgatcttc cgatacctcc agaatcatgg 540
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ggtttgcttc tatttttaat aacaaaagaa acta 1894

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<210> 303
<211> 556
<212> PRT

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<213> Medicago truncatula

<400> 303

Met Gly His Arg His Leu Phe Asn Ala Ser Pro Met Phe Glu Gly Glu
1 5 10 15Ala Asp Pro Asn Trp Asn Asn Met Leu Thr Asp Gln His His Val Asn
20 25 30His Gly Gly Thr Ser Ser Ser Glu Asn Gly Ser Phe Ile Tyr Pro Val
35 40 45Glu Asn Met Ser Ile Asp Asn Ile Tyr Phe Pro Ser His Trp Asn Ala
50 55 60Asn Thr Arg Ser Asn Gly Tyr Ala Ser Ser Gly Pro Asn Ile Glu Val
65 70 75 80Pro Pro Pro His Gln Leu Asp Thr Ser Gly Thr Ser Thr Asn Asp His
85 90 95Phe Met His Ser Ser Ser Ala Gly Pro Phe Phe Ala Val Ser Glu Asn
100 105 110Phe Val His Gln Pro Ser Ser Ser Asn Tyr Asp Arg Gln Ala Phe His
115 120 125Val Asp Ser Gly Phe Ile Asp Leu Thr Met Gly Ser Gly Arg Ala His
130 135 140His Lys Arg Lys Ser Pro Gly Ile Pro Ser Val Tyr Glu Arg Gly Ser
145 150 155 160Ser Ser Gly Tyr Phe Asn Ala Gly Thr Ser Ser Asp Leu Pro Ile Pro
165 170 175Pro Glu Ser Trp Pro Glu Lys Pro Asn Met Asp Pro Gln Tyr Met Pro
180 185 190Trp Asp His Ala Ala Met Ala Pro Thr Phe Arg Gly Ala Gly Leu Ser
195 200 205Met Lys Gly Glu Ser Ser Val Arg Asn Val Arg Ser Arg Ser Ser Leu
210 215 220Asp Leu Glu Ser Asn Leu Cys Arg Thr His Leu Ser Ser Ser His Ser
225 230 235 240His Asn Ser Tyr Pro Thr Val Pro Pro Val Ser His Ser Ser Leu Ala
245 250 255Asp Leu Ser Gln Val Ser Thr Ser Leu Thr Arg Asp Trp Ser Gln Met
Seite 326

260

265

270

Asn Val Thr Pro Ala Asn Gly Arg Val Leu Leu Pro Asp Ala Ser Thr
 275 280 285
 Phe Gly Leu Glu Thr Ser His Phe Pro Val Gly Asn Ala Ala Ala Ala
 290 300
 Ala Ala Ala Ser Asn Ala Thr Val Asp Val Gly Ser Phe His His Asp
 305 310 315 320
 Phe Gly Thr Ser Arg Asn Pro Thr Thr Ala Gln Ser Phe Gln Asn Leu
 325 330 335
 Thr Gln Thr Ala Arg Gly Thr Arg Ser Asn Tyr Ser Gln Arg Ser Thr
 340 345 350
 Pro Ala Tyr Arg Ala Ser Ser Ser Leu Arg Leu Gly Gln Ala Thr Pro
 355 360 365
 Ser Asp Asn Gly Leu Pro Met Val Ala Glu Gly Tyr Pro Ser Arg His
 370 375 380
 Pro Arg Pro Leu Asn Thr Val Gly Trp Arg Asn Ser Asp Arg Asn Gly
 385 390 395 400
 Arg Ser Arg Ile Ser Ser Glu Arg Tyr Arg Ser Leu Ala Asp Gln Ala
 405 410 415
 Ala Leu His Ala Arg Leu Ser Ser Ser Glu Val Pro Gly Phe Met Ile
 420 425 430
 Val Glu Arg Ala Ser Leu Tyr Gly Ser Arg Asn Val Leu Asp Gln His
 435 440 445
 Arg Glu Met Arg Met Asp Ile Asp Asn Met Ser Tyr Glu Glu Leu Leu
 450 455 460
 Ala Leu Gly Glu Arg Ile Gly Gln Val Asn Thr Gly Leu Ser Glu Asp
 465 470 475 480
 Val Leu Ser Lys Cys Val Thr Glu Thr Ile Tyr Cys Ser Ser Asp Gln
 485 490 495
 Cys Gln Asp Glu Gly Ser Cys Val Ile Cys Leu Glu Glu Tyr Lys Asn
 500 505 510
 Met Asp Asp Val Gly Thr Leu Lys Thr Cys Gly His Asp Tyr His Val
 515 520 525
 Ser Cys Ile Lys Lys Trp Leu Ser Met Lys Lys Leu Cys Pro Ile Cys
 530 535 540

PF59082PF60142_PCT_SEQ_LIST.txt

Lys Ser Ser Ala Leu Pro Glu Asp Lys Lys Asp Lys
545 550 555

<210> 304
<211> 2433
<212> DNA
<213> *Medicago truncatula*

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gccgaaaatc ggatacccgga gtttatgctt tccccaagtg agatgaaccc gcctcacggg      180
aattctctaa accatgaatg gcagaacttg agcggatgga gcttaggaga accaagttcc      240
agtaatacac agaacgaagt taacaacaat gagctgaaaa gggagttagg gttatcacct      300
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agtgcatttt cattggataa cgtcaataca ggtcctatgt atatgtgcag cccaatttct      420
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agctatcatg tggaagttga acatcccaac atgcacaaat ccagtgggtc tctaaatgag      540
catattccac ctccgattac ttctggttct tttttgcttc cttctggttg aagtaacagc      600
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gaatcaagaa atctgccatc tgggaccaac cctggatcat ctccatggat ggagaggtca     1620
gctgatagtg aatttggaat tccctattcc ttacgatcgt tggctgctgc tgggtgaagga     1680
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PF59082PF60142_PCT_SEQ_LIST.txt

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<210> 305
 <211> 708
 <212> PRT
 <213> Medicago truncatula

<400> 305

Met Gln Gly Gln Arg Gly Thr Ile Gly Ser Ser Ser Glu Thr Phe Glu
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Phe Asp Cys Gly Ser Thr Ser Ser Thr Ala Ala Val Asp Gln His Ile
20 25 30

Phe Trp Asn Asn Met His Thr Pro Ala Glu Asn Arg Ile Pro Glu Phe
35 40 45

Met Leu Ser Pro Ser Glu Met Asn Pro Pro His Gly Asn Ser Leu Asn
50 55 60

His Glu Trp Gln Asn Leu Ser Gly Trp Ser Leu Gly Glu Pro Ser Ser
65 70 75 80

Ser Asn Thr Gln Asn Glu Val Asn Asn Asn Glu Leu Lys Arg Glu Leu
85 90 95

Gly Leu Ser Pro Pro Ile Asn Gly Gly Ala Ile Ala Gly Pro Arg Leu
100 105 110

Glu Glu Arg His Phe Glu Pro Thr Ser Ala Phe Ser Leu Asp Asn Val
115 120 125

Asn Thr Gly Pro Met Tyr Met Cys Ser Pro Asn Ser His Leu Val Pro
130 135 140

PF59082PF60142_PCT_SEQ_LIST.txt

Gln Asn Leu Asn Leu Asn Ala Ser Leu Thr Asp Asn Gly Ile Asp Asn
145 150 155 160

Ser Tyr His Val Glu Val Glu His Pro Asn Met His Lys Ser Ser Gly
165 170 175

Pro Leu Asn Glu His Ile Pro Pro Pro Ile Thr Ser Gly Ser Phe Leu
180 185 190

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

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

Ala Val Glu Gly Asn Gly Gly Gln Ser Ser Asp Gly Gly Ser Ser Ser
225 230 235 240

Tyr Ser Gln His Thr Val Gly Ser Ala Trp Asn Thr Leu Pro Thr Gln
245 250 255

Asp Tyr Ala Gly Ser Asn Phe Asn Gln Ser Ala Pro Ala Glu Gln Val
260 265 270

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

Pro Gly Ser Thr Val Ala Gly Ser Ser Glu Ser Phe His Arg Asn Phe
290 295 300

Arg Leu Arg Ile Asn Pro Ser Ser Gln Gln Ile Ser Leu Pro Pro Ala
305 310 315 320

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

Ala Pro Met Leu Gln Arg Tyr His Pro Ile Asn Asn Pro Leu Asp Leu
340 345 350

Arg Ser Val Gln Pro Val Asn Val Met His Pro Gln Ser Glu Pro Leu
355 360 365

Leu Val His Val Pro Ala Leu Pro Arg Ser Ala Gln Ser Ile Arg Trp
370 375 380

Ser Gly Gly Ser Ser Ser Thr Asn Asn His Ser Ser Asn Ser Val Leu
385 390 395 400

Gly Leu Asp Arg Asp Thr Gln Pro His Glu Glu Ala Gly Ser Arg Ala
405 410 415

Met Ala Arg Asn Ile Leu Asp His Pro Val Phe Val Pro Ala Asn Val

420

425

430

Arg Asn Ala Ala Arg Asn Pro Ala Arg Ser Ser Ser Ser Ala Asn Leu
 435 440 445

Ser Ile Pro Gly Asn Val Ala Ser Ser Ser Arg Thr Ala Pro Asn Pro
 450 455 460

Pro Ala Leu Asn Pro Ser Ser Val Ser Ala Trp Val Ser Arg Pro Asn
 465 470 475 480

Pro Gln Gln Tyr Pro Arg Arg Leu Ser Glu Tyr Val Arg Arg Ser Leu
 485 490 495

Phe Ser Pro Gly Ser Glu Gly Gly Ser Ser Ser Asn Asn Tyr Pro Ser
 500 505 510

Leu Arg Gly Pro Ser Thr Ser Ser Glu Ser Arg Asn Leu Pro Ser Gly
 515 520 525

Thr Asn Pro Gly Ser Ser Pro Trp Met Glu Arg Ser Ala Asp Ser Glu
 530 535 540

Phe Gly Ile Pro Tyr Ser Leu Arg Ser Leu Ala Ala Ala Gly Glu Gly
 545 550 555 560

Ser Ser Arg Leu Val Ser Glu Leu Arg Asn Val Leu Gly Ile Met Arg
 565 570 575

Arg Gly Gly Asn Leu Arg Phe Glu Asp Val Met Ile Leu Asp His Ser
 580 585 590

Met Phe Ala Gly Ile Ala Asp Met His Asp Arg His Arg Asp Met Arg
 595 600 605

Leu Asp Val Asp Asn Met Ser Tyr Glu Glu Leu Leu Ala Leu Glu Glu
 610 615 620

Arg Ile Gly Asn Val Ser Thr Gly Leu Asn Glu Glu Thr Ile Met Lys
 625 630 635 640

His Leu Lys Gln Lys Lys Tyr Ser Val Asp Gly Leu Gly Ser Gln Ser
 645 650 655

Glu Thr Glu Pro Cys Cys Val Cys Gln Glu Glu Phe Lys Asn Glu Asp
 660 665 670

Asp Ile Gly Ser Leu Asp Cys Gly His Asp Tyr His Ile Asp Cys Ile
 675 680 685

Lys Gln Trp Leu Thr His Lys Asn Ile Cys Pro Ile Cys Lys Thr Thr
 690 695 700

Gly Leu Ala Thr
705

<210> 306
<211> 52
<212> PRT
<213> Artificial sequence

<220>
<223> RING domain

<400> 306

Cys Glu Arg Lys Cys Ser Ile Cys Gln Glu Glu Tyr Ser Asp Gly Glu
1 5 10 15

Glu Val Gly Lys Met Val Cys Lys His Tyr Tyr His Phe Ser Cys Ile
20 25 30

Lys Asn Trp Leu Arg Gln Lys Asn Trp Cys Pro Ile Cys Lys Ser Val
35 40 45

Ala Leu Asn Thr
50

<210> 307
<211> 52
<212> PRT
<213> Artificial sequence

<220>
<223> RING domain

<400> 307

Asp Asp Ile Lys Cys Ser Ile Cys Gln Glu Glu Tyr Ile Glu Gly Glu
1 5 10 15

Glu Val Gly Arg Leu Gly Cys Glu His Gln Tyr His Val Cys Cys Ile
20 25 30

His Gln Trp Leu Arg Gln Lys Asn Trp Cys Pro Ile Cys Lys Ala Ser
35 40 45

Ala Glu Pro Ser
50

<210> 308
<211> 51
<212> PRT
<213> Artificial sequence

<220>
<223> RING domain

<400> 308

Val Glu Pro Cys Cys Ile Cys Gln Glu Glu Tyr Ala Glu Gly Glu Asp
Seite 332

1 5 10 15
 Met Gly Arg Leu Asp Cys Gly His Asp Phe His Thr Ala Cys Ile Lys
 20 25 30
 Gln Trp Leu Val Ile Lys Asn Leu Cys Pro Ile Cys Lys Lys Thr Gly
 35 40 45
 Leu Gly Thr
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<210> 309
 <211> 50
 <212> PRT
 <213> Artificial sequence

<220>
 <223> RING domain

<400> 309

Asp Asp Gly Lys Cys Ala Ile Cys Leu Glu Glu Tyr Lys Asp Asn Ser
 1 5 10 15

Leu Leu Gly Ile Leu Lys Cys Asn His Asp Phe His Thr Asp Cys Val
 20 25 30

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

Ala Ala
 50

<210> 310
 <211> 52
 <212> PRT
 <213> Artificial sequence

<220>
 <223> RING domain

<400> 310

Val Glu Arg Asn Cys Ser Ile Cys Gln Glu Glu Phe Glu Ala Asn Glu
 1 5 10 15

Glu Thr Gly Arg Leu Ile Cys Gly His Ser Tyr His Val Gln Cys Ile
 20 25 30

Lys Gln Trp Leu Ser Arg Lys Asn Thr Cys Pro Val Cys Lys Thr Val
 35 40 45

Val Ser Lys Thr
 50

<210> 311
 <211> 52

<212> PRT
 <213> Artificial sequence
 <220>
 <223> RING domain
 <400> 311
 Asp Asn Glu Arg Cys Val Ile Cys Leu Glu Glu Tyr Lys His Glu Asp
 1 5 10 15
 Thr Leu Gly Arg Leu Lys Cys Gly His Gly Phe His Cys Asn Cys Ile
 20 25 30
 Lys Lys Trp Leu Gln Val Lys Asn Thr Cys Pro Val Cys Lys Ala Ala
 35 40 45
 Ala Ala Asp Glu
 50

<210> 312
 <211> 52
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> RING domain
 <400> 312
 Glu Lys Asp Ala Cys Ile Ile Cys Gln Glu Glu Tyr Glu Ala Lys Glu
 1 5 10 15
 Leu Val Gly Thr Leu Gly Cys Gly His Lys Tyr His Ala Met Cys Ile
 20 25 30
 Lys Gly Trp Leu Met Val Lys Asn Leu Cys Pro Ile Cys Lys Thr Thr
 35 40 45
 Ala Leu Pro Ala
 50

<210> 313
 <211> 51
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> RING domain
 <400> 313
 Met Glu Gln Cys Val Ile Cys Arg Val Glu Phe Glu Glu Gly Glu Ser
 1 5 10 15
 Leu Val Ala Leu Pro Cys Lys His Ser Tyr His Ser Glu Cys Ile Asn
 20 25 30
 Gln Trp Leu Gln Leu Asn Lys Val Cys Pro Met Cys Ser Ala Glu Val
 Seite 334

35

40

45

Pro Thr Ser
50

<210> 314
<211> 52
<212> PRT
<213> Artificial sequence

<220>
<223> RING domain

<400> 314

Met Glu Arg Lys Cys Ser Ile Cys Gln Glu Glu Phe Glu Thr Asn Glu
1 5 10 15

Glu Met Gly Arg Leu Asp Cys Gly His Ser Tyr His Val Tyr Cys Ile
20 25 30

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

Val Ser Lys Asn
50

<210> 315
<211> 52
<212> PRT
<213> Artificial sequence

<220>
<223> RING domain

<400> 315

Asp Pro Glu Pro Cys Cys Ile Cys Gln Glu Glu Tyr Ala Asp Gly Asp
1 5 10 15

Asp Leu Gly Arg Leu Asp Cys Gly His Asp Phe His Ala Gly Cys Ile
20 25 30

Lys Gln Trp Leu Val Val Lys Asn Val Cys Pro Ile Cys Lys Ser Thr
35 40 45

Ala Leu Lys Lys
50

<210> 316
<211> 52
<212> PRT
<213> Artificial sequence

<220>
<223> RING domain

<400> 316

Asp Asp Ile Lys Cys Ser Ile Cys Gln Glu Glu Phe Val Lys Gly Glu
1 5 10 15

Glu Val Gly Arg Leu Arg Cys Glu His Gln Tyr His Val Cys Cys Ile
20 25 30

Arg Gln Trp Leu Leu Gln Lys Asn Trp Cys Pro Val Cys Lys Ala Pro
35 40 45

Ala Leu Pro Ser
50

<210> 317
<211> 52
<212> PRT
<213> Artificial sequence

<220>
<223> RING domain

<400> 317

Glu Phe Glu Pro Cys Cys Ile Cys Gln Glu Asp Tyr Val Glu Gly Asp
1 5 10 15

Asp Leu Gly Thr Leu His Cys Gly His Asp Phe His Ala Ser Cys Ile
20 25 30

Ser Gln Trp Leu Val Val Lys Asn Leu Cys Pro Ile Cys Lys Ser Thr
35 40 45

Ala Leu Lys Thr
50

<210> 318
<211> 52
<212> PRT
<213> Artificial sequence

<220>
<223> RING domain

<400> 318

Cys Asp Arg Lys Cys Ser Ile Cys Gln Glu Glu Tyr Ser Gly Gly Glu
1 5 10 15

Glu Val Gly Asn Met Ala Cys Lys His Tyr Tyr His Ile Thr Cys Ile
20 25 30

Gln His Trp Leu Arg Gln Lys Asn Trp Cys Pro Ile Cys Lys Ser Val
35 40 45

Ala Ala Lys Thr
50

<210> 319

<211> 52
 <212> PRT
 <213> Artificial sequence

<220>
 <223> RING domain

<400> 319

Leu Glu Arg Gln Cys Thr Ile Cys Gln Glu Glu Tyr Glu Ala Glu Asp
 1 5 10 15

Glu Met Gly Lys Leu Asp Cys Gly His Phe Tyr His Ile Arg Cys Ile
 20 25 30

Lys Gln Trp Leu Ser Gln Lys Asn Ser Cys Pro Val Cys Lys Ser Ala
 35 40 45

Ala Met Ser Asn
 50

<210> 320
 <211> 52
 <212> PRT
 <213> Artificial sequence

<220>
 <223> RING domain

<400> 320

Asp Ala Glu Pro Cys Cys Ile Cys Gln Glu Glu Tyr Lys Asp Gly Glu
 1 5 10 15

Asp Leu Gly Lys Leu Asp Cys Gly His Asp Phe His Ala Asp Cys Val
 20 25 30

Lys Gln Trp Leu Met Gln Lys Asn Leu Cys Pro Ile Cys Lys Thr Thr
 35 40 45

Gly Leu Asn Thr
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<210> 321
 <211> 52
 <212> PRT
 <213> Artificial sequence

<220>
 <223> RING domain

<400> 321

Asp Asp Ile Lys Cys Ser Ile Cys Gln Glu Glu Tyr Val Ile Gly Asp
 1 5 10 15

Glu Ile Gly Asn Leu Gly Cys Glu His Gly Tyr His Met Glu Cys Ile
 20 25 30

Lys Gln Trp Phe Lys Leu Lys Asn Trp Cys Pro Ile Cys Lys Ala Ala
35 40 45

Val Glu Ser Ser
50

<210> 322
<211> 52
<212> PRT
<213> Artificial sequence

<220>
<223> RING domain

<400> 322

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

Asp Ile Gly Thr Leu Asp Cys Gly His Asp Phe His Ser Ser Cys Ile
20 25 30

Lys Gln Trp Leu Met Gln Lys Asn Leu Cys Pro Ile Cys Lys Thr Thr
35 40 45

Gly Leu Ala Thr
50

<210> 323
<211> 52
<212> PRT
<213> Artificial sequence

<220>
<223> RING domain

<400> 323

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

Asp Ile Gly Thr Leu Asp Cys Gly His Asp Phe His Ser Ser Cys Ile
20 25 30

Lys Gln Trp Leu Met His Lys Asn Leu Cys Pro Ile Cys Lys Thr Thr
35 40 45

Gly Leu Ala Thr
50

<210> 324
<211> 52
<212> PRT
<213> Artificial sequence

<220>
<223> RING domain

<400> 324

PF59082PF60142_PCT_SEQ_LIST.txt

Arg Cys Arg Pro Cys Cys Ile Cys Gln Glu Glu Tyr Lys Asp Gly Asp
1 5 10 15

Asp Leu Gly Thr Leu Asp Cys Thr His Asp Phe His Tyr Gly Cys Ile
20 25 30

Lys Gln Trp Leu Gln Gln Lys Asn Leu Cys Pro Thr Cys Lys Ser Thr
35 40 45

Gly Phe Ala Ser
50

<210> 325
<211> 52
<212> PRT
<213> Artificial sequence

<220>
<223> RING domain

<400> 325

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

Val Gly Thr Leu Lys Thr Cys Gly His Asp Tyr His Val Asn Cys Ile
20 25 30

Lys Lys Trp Leu Ser Met Lys Lys Leu Cys Pro Ile Cys Lys Ala Ser
35 40 45

Val Met Pro Glu
50

<210> 326
<211> 52
<212> PRT
<213> Artificial sequence

<220>
<223> RING domain

<400> 326

Glu Asp Ala Lys Cys Ser Ile Cys Gln Glu Glu Tyr Thr Ile Gly Asp
1 5 10 15

Glu Val Gly Arg Leu His Cys Glu His Thr Tyr His Val Lys Cys Val
20 25 30

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

Ala Glu Thr Ser
50

<210> 327
<211> 52
<212> PRT
<213> Artificial sequence

<220>
<223> RING domain

<400> 327

Glu Thr Glu Pro Cys Thr Ile Cys Gln Glu Ser Phe Lys Asn Glu Glu
1 5 10 15

Lys Ile Ala Thr Leu Asp Cys Gly His Glu Tyr His Ala Glu Cys Leu
20 25 30

Glu Lys Trp Leu Ile Val Lys Asn Val Cys Pro Ile Cys Lys Ser Glu
35 40 45

Ala Leu Val Met
50

<210> 328
<211> 52
<212> PRT
<213> Artificial sequence

<220>
<223> RING domain

<400> 328

Gln Arg Lys Cys Ala Ile Cys Leu Glu Glu Tyr Lys Glu Lys Glu Glu
1 5 10 15

Leu Gly Glu Val Lys Gly Cys Gly His Asp Tyr His Gly Arg Cys Ile
20 25 30

Lys Lys Trp Leu Ser Met Lys Asn Ser Cys Pro Ile Cys Lys Ser Pro
35 40 45

Ala Leu Pro Asp
50

<210> 329
<211> 52
<212> PRT
<213> Artificial sequence

<220>
<223> RING domain

<400> 329

Asp Asp Val Lys Cys Ser Ile Cys Gln Glu Glu Tyr Val Asp Gly Asp
1 5 10 15

Glu Val Gly Thr Leu Pro Cys Gln His Lys Tyr His Val Ser Cys Ala
20 25 30

Gln Gln Trp Leu Arg Met Lys Asn Trp Cys Pro Ile Cys Lys Thr Ser
35 40 45

Ala Glu Ser Gln
50

<210> 330
<211> 52
<212> PRT
<213> Artificial sequence

<220>
<223> RING domain

<400> 330

Asp Ala Glu Pro Cys Cys Val Cys Gln Glu Glu Tyr Thr Glu Gly Glu
1 5 10 15

Asp Met Gly Thr Leu Glu Cys Gly His Glu Phe His Ser Gln Cys Ile
20 25 30

Lys Glu Trp Leu Lys Gln Lys Asn Leu Cys Pro Ile Cys Lys Thr Thr
35 40 45

Gly Leu Asn Thr
50

<210> 331
<211> 52
<212> PRT
<213> Artificial sequence

<220>
<223> RING domain

<400> 331

Asp Met Glu Pro Cys Cys Val Cys Gln Glu Glu Tyr Ala Glu Gly Asp
1 5 10 15

Asp Leu Gly Thr Leu Gly Cys Gly His Glu Phe His Thr Ala Cys Val
20 25 30

Lys Gln Trp Leu Met Leu Lys Asn Leu Cys Pro Ile Cys Lys Thr Val
35 40 45

Ala Leu Ser Thr
50

<210> 332
<211> 52
<212> PRT
<213> Artificial sequence

<220>
<223> RING domain

<400> 332

Glu Val Glu Pro Cys Cys Val Cys Gln Glu Glu Tyr Lys Glu Glu Glu
 1 5 10 15

Glu Ile Gly Arg Leu Glu Cys Gly His Asp Phe His Ser Gln Cys Ile
 20 25 30

Lys Glu Trp Leu Lys Gln Lys Asn Leu Cys Pro Ile Cys Lys Thr Thr
 35 40 45

Gly Leu Asn Thr
 50

<210> 333

<211> 52

<212> PRT

<213> Artificial sequence

<220>

<223> RING domain

<400> 333

Asn Ile Glu Pro Cys Cys Ile Cys Gln Glu Glu Tyr Val Glu Gly Asp
 1 5 10 15

Asn Leu Gly Thr Leu Lys Cys Gly His Glu Phe His Lys Asp Cys Ile
 20 25 30

Lys Gln Trp Val Met Ile Lys Asn Leu Cys Pro Ile Cys Lys Thr Glu
 35 40 45

Ala Leu Lys Thr
 50

<210> 334

<211> 52

<212> PRT

<213> Artificial sequence

<220>

<223> RING domain

<400> 334

Val Asp Arg Lys Cys Ser Ile Cys Gln Asp Glu Tyr Glu Arg Glu Asp
 1 5 10 15

Glu Val Gly Glu Leu Asn Cys Gly His Ser Phe His Val His Cys Val
 20 25 30

Lys Gln Trp Leu Ser Arg Lys Asn Ala Cys Pro Val Cys Lys Lys Ala
 35 40 45

Ala Tyr Gly Lys
 50

<210> 335
 <211> 52
 <212> PRT
 <213> Artificial sequence

<220>
 <223> RING domain

<400> 335

Asp Asp Ile Lys Cys Ser Ile Cys Gln Glu Glu Tyr Val Asp Gly Asp
 1 5 10 15

Glu Leu Gly Thr Ile Pro Cys Gln His Met Tyr His Val Ser Cys Val
 20 25 30

Gln Gln Trp Leu Arg Met Lys Asn Trp Cys Pro Ile Cys Lys Thr Ser
 35 40 45

Ala Glu Glu Glu
 50

<210> 336
 <211> 52
 <212> PRT
 <213> Artificial sequence

<220>
 <223> RING domain

<400> 336

Glu Thr Asp Ser Cys Thr Ile Cys Gln Glu Asn Tyr Lys Asn Glu Asp
 1 5 10 15

Lys Ile Ala Thr Leu Asp Cys Met His Lys Tyr His Ala Glu Cys Leu
 20 25 30

Lys Lys Trp Leu Val Ile Lys Asn Val Cys Pro Ile Cys Lys Ser Glu
 35 40 45

Ala Leu Val Ile
 50

<210> 337
 <211> 52
 <212> PRT
 <213> Artificial sequence

<220>
 <223> RING domain

<400> 337

Ala Asp Arg Lys Cys Ile Ile Cys Gln Asp Glu Tyr Glu Ala Lys Asp
 1 5 10 15

Glu Val Gly Glu Leu Arg Cys Gly His Arg Phe His Ile Asp Cys Val
 20 25 30

Asn Gln Trp Leu Val Arg Lys Asn Ser Cys Pro Val Cys Lys Thr Met
 35 40 45

Ala Tyr Asn Lys
 50

<210> 338
 <211> 52
 <212> PRT
 <213> Artificial sequence

<220>
 <223> RING domain

<400> 338

Asp Asp Ile Lys Cys Ser Ile Cys Gln Glu Glu Tyr Val Val Gly Asp
 1 5 10 15

Glu Val Gly Arg Leu Gln Cys Glu His Gly Tyr His Met Ser Cys Ile
 20 25 30

His Gln Trp Leu Ser Leu Lys Asn Trp Cys Pro Ile Cys Lys Ala Ser
 35 40 45

Val Ala Pro Ser
 50

<210> 339
 <211> 52
 <212> PRT
 <213> Artificial sequence

<220>
 <223> RING domain

<400> 339

Glu Ala Glu Pro Cys Cys Ile Cys Gln Glu Glu Tyr Asn Asp Gly Glu
 1 5 10 15

Asp Leu Gly Thr Leu Asp Cys Gly His Asp Phe His Ala Gly Cys Val
 20 25 30

Lys Gln Trp Leu Met His Lys Asn Trp Cys Pro Ile Cys Lys Thr Thr
 35 40 45

Gly Leu Ala Thr
 50

<210> 340
 <211> 52
 <212> PRT
 <213> Artificial sequence

<220>
 <223> RING domain

<400> 340

Asp Leu Glu Pro Cys Cys Ile Cys Gln Glu Glu Tyr Val Asp Gly Asp
1 5 10 15

Asp Met Gly Ile Ile Asp Cys Gly His Asp Phe His Thr Asn Cys Ile
20 25 30

Lys Gln Trp Leu Met Gln Lys Asn Leu Cys Pro Ile Cys Lys Met Thr
35 40 45

Ala Leu Leu Thr
50

<210> 341

<211> 52

<212> PRT

<213> Artificial sequence

<220>

<223> RING domain

<400> 341

Asp Leu Glu Pro Cys Cys Ile Cys Gln Glu Glu Tyr Val Asp Gly Asp
1 5 10 15

Asp Met Gly Ile Ile Asp Cys Gly His Asp Phe His Thr Asn Cys Ile
20 25 30

Lys Gln Trp Leu Met Gln Lys Asn Leu Cys Pro Ile Cys Lys Met Thr
35 40 45

Ala Leu Leu Thr
50

<210> 342

<211> 52

<212> PRT

<213> Artificial sequence

<220>

<223> RING domain

<400> 342

Asp Leu Glu Pro Cys Cys Ile Cys Gln Glu Glu Tyr Val Asp Gly Asp
1 5 10 15

Asp Met Gly Ile Ile Asp Cys Gly His Asp Phe His Ala Asn Cys Ile
20 25 30

Lys Gln Trp Leu Met Gln Lys Asn Leu Cys Pro Ile Cys Lys Met Thr
35 40 45

Ala Leu Ile Thr
50

<210> 343
 <211> 52
 <212> PRT
 <213> Artificial sequence

<220>
 <223> RING domain

<400> 343

Leu Glu Lys Lys Cys Ser Ile Cys Gln Asp Asp Tyr Glu Glu Asp Gly
 1 5 10 15

Glu Val Gly Lys Leu Asp Cys Gly His Gly Phe His Ile Gln Cys Ile
 20 25 30

Lys Gln Trp Leu Gly Gln Lys Asn Thr Cys Pro Val Cys Lys Thr Glu
 35 40 45

Pro Val Gly Arg
 50

<210> 344
 <211> 52
 <212> PRT
 <213> Artificial sequence

<220>
 <223> RING domain

<400> 344

Glu Thr Ser Cys Ala Ile Cys Leu Glu Glu Tyr Lys Ser Met Asp Lys
 1 5 10 15

Val Gly Met Ile Arg Asn Cys Gly His Val Tyr His Val Asp Cys Ile
 20 25 30

Lys Lys Trp Leu Ser Met Lys Asn Met Cys Pro Ile Cys Lys Ala Pro
 35 40 45

Ala Val Ala Asp
 50

<210> 345
 <211> 52
 <212> PRT
 <213> Artificial sequence

<220>
 <223> RING domain

<400> 345

Glu Ala Asp Ser Cys Ile Ile Cys Gln Asp Asp Tyr Lys Ser Lys Glu
 1 5 10 15

Lys Ile Ala Ala Leu Asp Cys Gly His Glu Tyr His Ala Val Cys Leu
 Seite 346

20

25

30

Lys Lys Trp Leu Arg Leu Lys Asn Val Cys Pro Ile Cys Lys Ser Glu
 35 40 45

Ala Leu Asn Thr
 50

<210> 346
 <211> 52
 <212> PRT
 <213> Artificial sequence

<220>
 <223> RING domain

<400> 346

Glu Ala Asp Ser Cys Ile Ile Cys Gln Asp Asp Tyr Lys Ser Lys Glu
 1 5 10 15

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

Lys Lys Trp Leu Arg Leu Lys Asn Val Cys Pro Ile Cys Lys Ser Glu
 35 40 45

Ala Leu Thr Met
 50

<210> 347
 <211> 50
 <212> PRT
 <213> Artificial sequence

<220>
 <223> RING domain

<400> 347

Asp Arg Cys Val Ile Cys Gln Met Glu Tyr Glu Glu Asp Glu Ser Leu
 1 5 10 15

Val Ala Leu Ser Cys Asp His Pro Tyr His Pro Glu Cys Ile Ala Asn
 20 25 30

Trp Leu Gln Ile Asn Lys Ile Cys Pro Ile Cys Thr Thr Glu Val Ser
 35 40 45

Ser Pro
 50

<210> 348
 <211> 52
 <212> PRT
 <213> Artificial sequence

<220>

<223> RING domain

<400> 348

Asp Asp Ile Lys Cys Cys Ile Cys Gln Glu Glu Tyr Val Glu Glu Asp
1 5 10 15

Glu Val Gly Ser Leu Leu Cys Glu His Lys Tyr His Val Val Cys Ile
20 25 30

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

Val Thr Pro Ser
50

<210> 349

<211> 52

<212> PRT

<213> Artificial sequence

<220>

<223> RING domain

<400> 349

Asp Leu Glu Pro Cys Cys Ile Cys Gln Glu Glu Tyr Val Asp Gly Gln
1 5 10 15

Asn Leu Gly Leu Leu Asp Cys Gly His Glu Phe His Ser Asn Cys Ile
20 25 30

Thr Gln Trp Leu Met Gln Lys Asn Leu Cys Pro Ile Cys Lys Thr Thr
35 40 45

Ala Leu Ala Ser
50

<210> 350

<211> 52

<212> PRT

<213> Artificial sequence

<220>

<223> RING domain

<400> 350

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

Val Gly Thr Leu Lys Thr Cys Gly His Asp Tyr His Val Ser Cys Ile
20 25 30

Lys Lys Trp Leu Ser Met Lys Lys Leu Cys Pro Ile Cys Lys Ser Ser
35 40 45

Ala Leu Pro Glu

50

<210> 351
 <211> 52
 <212> PRT
 <213> Artificial sequence

<220>
 <223> RING domain

<400> 351

Glu Thr Glu Pro Cys Cys Val Cys Gln Glu Glu Phe Lys Asn Glu Asp
 1 5 10 15

Asp Ile Gly Ser Leu Asp Cys Gly His Asp Tyr His Ile Asp Cys Ile
 20 25 30

Lys Gln Trp Leu Thr His Lys Asn Ile Cys Pro Ile Cys Lys Thr Thr
 35 40 45

Gly Leu Ala Thr
 50

<210> 352
 <211> 44
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DAR1 domain

<400> 352

Phe Asn Asp Arg Tyr Arg Gly Met Arg Met Asp Ile Asp Gly Met Ser
 1 5 10 15

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

Gly Leu Ser Glu Asp Ala Leu Ser Lys Cys Leu Asp
 35 40

<210> 353
 <211> 44
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DAR1 domain

<400> 353

Phe Asn Asp Arg Tyr Arg Gly Met Arg Met Asp Ile Asp Gly Met Ser
 1 5 10 15

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

Gly Leu Ser Glu Asp Ala Leu Ser Lys Cys Leu Asp
 35 40

<210> 354
 <211> 44
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DAR1 domain

<400> 354

Ser His Asp Gln His Ser Asp Met Arg Met Asp Ile Asp Asn Met Ser
 1 5 10 15

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

Ala Leu Ser Glu Glu Gln Phe Val Lys Cys Leu Arg
 35 40

<210> 355
 <211> 44
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DAR1 domain

<400> 355

Leu Ile Asp Arg His Arg Asp Met Arg Leu Asp Val Asp Asn Met Ser
 1 5 10 15

Tyr Glu Glu Leu Leu Ala Leu Gly Glu Arg Ile Gly Tyr Val Asn Thr
 20 25 30

Gly Leu Ser Glu Asp Lys Ile Arg Thr Gly Leu Lys
 35 40

<210> 356
 <211> 44
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DAR1 domain

<400> 356

Ala Gln Asp Pro His Arg Ala Met Arg Leu Asp Ile Asp Asn Met Ser
 1 5 10 15

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

Gly Leu Val Asp Glu Lys Ile Ser Gly Cys Val Arg
 35 40

<210> 357
 <211> 44
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DAR1 domain

<400> 357

Met His Asp Gln His Gln Asp Trp Arg Leu Asp Val Asp Asn Met Thr
 1 5 10 15

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

Gly Leu His Asp Asp Glu Ile Ala Arg Ser Leu Arg
 35 40

<210> 358
 <211> 44
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DAR1 domain

<400> 358

Ala Phe Asp Pro His Trp Asp Met Arg Leu Asp Ile Asp Asp Met Ser
 1 5 10 15

Tyr Glu Glu Leu Leu Ala Leu Glu Glu Arg Ile Gly His Val Asn Thr
 20 25 30

Gly Leu Ala Asp Glu Lys Ile Ser Gly Cys Val Met
 35 40

<210> 359
 <211> 44
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DAR1 domain

<400> 359

Val Ile Asp Glu His Arg Asp Met Arg Leu Asp Val Asp Ser Met Thr
 1 5 10 15

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

Gly Phe Thr Glu Ser Tyr Ile Glu Glu Asn Leu Lys
 35 40

<210> 360
 <211> 44

<212> PRT
 <213> Artificial sequence
 <220>
 <223> DAR1 domain
 <400> 360
 Asp Asp Pro Gln Asp Ala Trp Glu Asp Val Asp Pro Asp Glu Tyr Ser
 1 5 10 15
 Tyr Glu Glu Leu Val Ala Leu Gly Glu Val Val Gly Thr Glu Ser Arg
 20 25 30
 Gly Leu Ser Ala Asp Thr Leu Ala Ser Leu Pro Ser
 35 40
 <210> 361
 <211> 44
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> DAR1 domain
 <400> 361
 Met Tyr Asp Arg Tyr Gln Asp Trp Arg Leu Asp Val Asp Asn Met Thr
 1 5 10 15
 Tyr Glu Glu Leu Leu Glu Leu Gly Asp Lys Ile Gly Tyr Val Asn Thr
 20 25 30
 Gly Leu Arg Asp Asp Glu Ile Thr Arg Asn Leu Arg
 35 40
 <210> 362
 <211> 44
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> DAR1 domain
 <400> 362
 Ile His Asp Arg His Arg Asp Met Arg Leu Asp Ile Asp Asn Met Ser
 1 5 10 15
 Tyr Glu Glu Leu Leu Ala Leu Glu Glu Arg Ile Gly Asn Val Gly Thr
 20 25 30
 Gly Leu Ser Glu Glu Ala Val Ile Arg Leu Leu Lys
 35 40
 <210> 363
 <211> 44
 <212> PRT
 <213> Artificial sequence

<220>

<223> DAR1 domain

<400> 363

Ser His Asp His His Ser Asp Met Arg Met Asp Ile Asp Asn Met Ser
 1 5 10 15

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

Ala Leu Ser Glu Glu Gln Phe Ala Lys Cys Ile Arg
 35 40

<210> 364

<211> 44

<212> PRT

<213> Artificial sequence

<220>

<223> DAR1 domain

<400> 364

Ile His Asp Arg His Arg Asp Met Arg Leu Asp Ile Asp Asn Met Ser
 1 5 10 15

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

Gly Leu Thr Glu Asn Asp Val Met Lys Leu Leu Lys
 35 40

<210> 365

<211> 44

<212> PRT

<213> Artificial sequence

<220>

<223> DAR1 domain

<400> 365

Leu Ser Asp Arg His Arg Ala Met Arg Met Asp Ile Asp Gly Met Ser
 1 5 10 15

Tyr Glu Glu Leu Leu Ala Leu Gly Asp Arg Ile Gly Thr Val Asn Thr
 20 25 30

Gly Leu Ser Glu Asp Ala Leu Tyr Lys Cys Leu Lys
 35 40

<210> 366

<211> 44

<212> PRT

<213> Artificial sequence

<220>

<223> DAR1 domain

<400> 366

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

Tyr Glu Glu Leu Leu Glu Leu Gly Asp Arg Ile Gly Tyr Val Asn Thr
 20 25 30

Gly Leu Arg Glu Asp Glu Ile Ala Arg Cys Val Arg
 35 40

<210> 367

<211> 44

<212> PRT

<213> Artificial sequence

<220>

<223> DAR1 domain

<400> 367

Ile Gln Asp Arg His Arg Asp Met Arg Leu Asp Val Asp Asn Met Ser
 1 5 10 15

Tyr Glu Glu Leu Leu Ala Leu Glu Glu Arg Ile Gly Asn Val Cys Thr
 20 25 30

Gly Leu Thr Glu Glu Thr Ile Leu Asn Arg Leu Lys
 35 40

<210> 368

<211> 44

<212> PRT

<213> Artificial sequence

<220>

<223> DAR1 domain

<400> 368

Phe Tyr Asp Gln His Arg Asp Met Arg Leu Asp Ile Asp Asp Met Ser
 1 5 10 15

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

Ala Leu Pro Glu Glu Glu Leu Leu Lys Cys Leu Arg
 35 40

<210> 369

<211> 44

<212> PRT

<213> Artificial sequence

<220>

<223> DAR1 domain

<400> 369

Val His Asp Arg His Gly Asp Met Arg Leu Asp Val Asp Asn Met Ser
 Seite 354

1 5 10 15
 Tyr Glu Glu Leu Leu Ala Leu Glu Glu Arg Ile Gly Asn Val Ser Thr
 20 25 30
 Gly Leu Ser Glu Glu Thr Leu Ser Lys Leu Leu Lys
 35 40
 <210> 370
 <211> 44
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> DAR1 domain
 <400> 370
 Val His Asp Arg His Arg Asp Met Arg Leu Asp Val Asp Asn Met Ser
 1 5 10 15
 Tyr Glu Glu Leu Leu Ala Leu Glu Glu Arg Ile Gly Asn Val Ser Thr
 20 25 30
 Gly Leu Ser Glu Glu Thr Leu Ser Lys Leu Leu Lys
 35 40
 <210> 371
 <211> 44
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> DAR1 domain
 <400> 371
 Ile His Asp Arg His Arg Asp Met Arg Leu Asp Ile Asp Asn Met Ser
 1 5 10 15
 Tyr Glu Glu Leu Leu Ala Leu Glu Glu Arg Ile Gly Asn Val Asn Thr
 20 25 30
 Gly Leu Thr Glu Glu Thr Ile Leu Lys His Ile Arg
 35 40
 <210> 372
 <211> 44
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> DAR1 domain
 <400> 372
 Met Leu Asp Gln His Arg Asp Met Arg Met Asp Ile Asp Asn Met Ser
 1 5 10 15

Tyr Glu Glu Leu Leu Ala Leu Gly Glu Arg Ile Gly His Val Asn Thr
20 25 30

Gly Leu Ser Glu Asp Ser Phe Ser Gln Cys Met Thr
35 40

<210> 373
<211> 44
<212> PRT
<213> Artificial sequence

<220>
<223> DAR1 domain

<400> 373

Phe His Asp Gln His Arg Asp Met Arg Leu Asp Ile Asp Asn Met Ser
1 5 10 15

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

Ala Leu Thr Glu Glu Ala Ile Ser Lys Cys Leu Lys
35 40

<210> 374
<211> 44
<212> PRT
<213> Artificial sequence

<220>
<223> DAR1 domain

<400> 374

His Ile Asp His His Arg Asp Met Arg Leu Asp Ile Glu Glu Met Ser
1 5 10 15

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

Gly Leu Pro Glu Glu Asp Val Lys Asn His Leu Lys
35 40

<210> 375
<211> 44
<212> PRT
<213> Artificial sequence

<220>
<223> DAR1 domain

<400> 375

Met Leu Asp His His Arg Asp Met Arg Leu Asp Ile Asp Asn Met Ser
1 5 10 15

Tyr Glu Glu Leu Leu Asp Leu Gly Glu Arg Ile Gly Ser Val Asn Thr
20 25 30

Gly Leu Ser Asp Ser Ala Ile Ser Ser Cys Leu Leu
35 40

<210> 376
<211> 44
<212> PRT
<213> Artificial sequence

<220>
<223> DAR1 domain

<400> 376

Phe His Asp Gln His Arg Asp Met Arg Leu Asp Ile Asp Asn Met Ser
1 5 10 15

Tyr Glu Glu Leu Leu Ala Leu Glu Glu Lys Met Gly Thr Val Ser Thr
20 25 30

Ala Leu Ser Glu Glu Ala Leu Leu Lys Ser Leu Lys
35 40

<210> 377
<211> 44
<212> PRT
<213> Artificial sequence

<220>
<223> DAR1 domain

<400> 377

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

Tyr Glu Glu Leu Leu Ala Leu Glu Glu Arg Ile Gly Asp Val Cys Thr
20 25 30

Gly Val Asn Glu Glu Thr Ile Ser Asn Arg Leu Lys
35 40

<210> 378
<211> 44
<212> PRT
<213> Artificial sequence

<220>
<223> DAR1 domain

<400> 378

Met His Asp Arg His Arg Asp Met Arg Leu Asp Val Asp Asn Met Ser
1 5 10 15

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

Gly Leu Ser Glu Glu Val Ile Leu Lys Val Met Lys
35 40

<210> 379
 <211> 44
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DAR1 domain

<400> 379

Ile His Asp Arg Tyr Arg Asp Met Arg Leu Asp Val Asp Asn Met Thr
 1 5 10 15

Tyr Glu Glu Leu Leu Ser Leu Glu Glu Arg Ile Gly Asp Val Cys Thr
 20 25 30

Gly Leu Asn Glu Glu Thr Ile Ser Asn Arg Leu Lys
 35 40

<210> 380
 <211> 44
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DAR1 domain

<400> 380

Met His Asp Arg His Arg Glu Met Arg Leu Asp Val Asp Asn Met Ser
 1 5 10 15

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

Gly Leu Ser Glu Glu Val Ile Leu Lys Ala Met Lys
 35 40

<210> 381
 <211> 44
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DAR1 domain

<400> 381

Ser Arg Asp Asn Tyr His Glu Leu Arg Leu Asp Val Asp Ser Met Ser
 1 5 10 15

Tyr Glu Gln Leu Leu Glu Leu Gly Asp Arg Ile Gly Tyr Val Asn Thr
 20 25 30

Gly Leu Lys Glu Ser Glu Ile His Arg Cys Leu Gly
 35 40

<210> 382

<211> 44
<212> PRT
<213> Artificial sequence

<220>
<223> DAR1 domain

<400> 382

Phe Tyr Asp Gln His Arg Asp Met Arg Leu Asp Ile Asp Asn Met Ser
1 5 10 15

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

Ala Leu Ser Glu Glu Ala Leu Ser Arg Ser Leu Lys
35 40

<210> 383
<211> 44
<212> PRT
<213> Artificial sequence

<220>
<223> DAR1 domain

<400> 383

Tyr Val Asp His His Gln Asp Met Arg Leu Asp Ile Glu Asp Met Ser
1 5 10 15

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

Gly Leu Ser Ser Glu Asp Val Lys Glu Leu Leu Lys
35 40

<210> 384
<211> 44
<212> PRT
<213> Artificial sequence

<220>
<223> DAR1 domain

<400> 384

Ser Phe Asp Gln Phe Arg Asp Met Arg Leu Asn Val Asp Asn Met Thr
1 5 10 15

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

Gly Leu Thr Glu Lys Gln Ile Lys Ser Cys Leu Arg
35 40

<210> 385
<211> 44
<212> PRT
<213> Artificial sequence

<220>

<223> DAR1 domain

<400> 385

Phe His Asp Gln His Arg Asp Met Arg Leu Asp Ile Asp Asn Met Ser
1 5 10 15

Tyr Glu Glu Leu Leu Ala Leu Glu Glu Arg Met Gly Thr Val Ser Thr
20 25 30

Ala Leu Thr Glu Glu Ala Leu Ser Glu Cys Leu Lys
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Gly Leu Ser Glu Glu Thr Ile Val Asn Asn Leu Lys
35 40

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Met His Asp Arg His Arg Asp Met Arg Leu Asp Val Asp Asn Met Ser
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Arg Met Asp Arg Phe Ser Asn Trp Arg Leu Asp Ile Asp His Met Thr
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<400> 391

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<220>
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His Val Asp His His Arg Asp Met Arg Leu Asp Ile Glu Asp Met Ser
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Gly Leu Ser Glu Gly Thr Ile Arg Ser Gln Leu Lys
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Ala Val Thr Glu Glu Asp Leu Ser Glu Cys Leu Lys
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<400> 398

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20      25      30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa His
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Xaa Xaa Xaa His Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50      55      60

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<213> Oryza sativa

<400> 409

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35 40 45

Trp Glu Gly Arg Gly Arg Gly Thr Arg Ser Pro Val Gly Trp Leu Arg
50 55 60

Gln Ala Ile Ser Ala Ser Glu Gly Asp Val Val Ala Val Gly Gly Val
65 70 75 80

Asp Ala Ala Val Tyr Leu Val Phe Leu Ser Ser Val Leu Ser Ile Leu
85 90 95

Val Phe Ser Gly Ile Val Leu Leu Pro Val Leu Leu Pro Val Ala Ala
100 105 110

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

Lys Thr Pro Gln Asn Phe Thr Glu Leu Glu Lys Leu Ala Leu Gly Asn
130 135 140

Val Gln Glu His Ser Arg Arg Leu Trp Ala Phe Leu Leu Ser Val Tyr
145 150 155 160

Trp Val Ser Phe Val Thr Tyr Phe Val Leu Trp Lys Ser Tyr Lys His
165 170 175

Val Ser Asn Met Arg Ala Ala Ala Arg Ser Thr Pro Asp Val Lys Pro
180 185 190

Glu Glu Phe Ala Val Leu Val Arg Asp Val Pro Lys Pro Pro Pro Asp
195 200 205

PF59082PF60142_PCT_SEQ_LIST.txt

Gln Thr Ile Lys Asp Ser Val Asp Ser Tyr Phe Arg Ala Leu His Pro
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Asp Thr Phe Tyr Arg Ser Met Val Val Thr Asp His Thr Lys Ala Asp
225 230 235 240

Lys Ile Tyr Gln Glu Ile Glu Gly His Lys Gln Lys Ile Ala Arg Ala
245 250 255

Glu Val Val Tyr Ala Glu Ser Lys Thr Thr Gly Lys Pro Glu Gly Thr
260 265 270

Lys Pro Thr His Arg Ile Gly Phe Leu Gly Leu Ile Gly Lys Lys Val
275 280 285

Asp Thr Ile Glu Tyr Cys Asn Asp Gln Ile Lys Glu Leu Leu Pro Lys
290 295 300

Leu Glu Ala Glu Gln Lys Thr Thr Leu Arg Glu Lys Gln Gln Gln Ala
305 310 315 320

Ala Ile Val Phe Phe Asn Arg Arg Ser Ala Ala Ala Ser Ala Ser Gln
325 330 335

Thr Leu His Ala Gln Met Phe Asp Lys Trp Thr Val Glu Gln Ala Pro
340 345 350

Glu Pro Arg Gln Ile Ile Trp Ser Asn Pro Ser Lys Lys Ile Tyr Glu
355 360 365

Arg Gln Ile Arg Gln Val Val Val Tyr Thr Ile Val Phe Leu Thr Val
370 375 380

Val Phe Tyr Met Ile Pro Ile Thr Ala Ile Ser Ala Leu Thr Thr Leu
385 390 395 400

Glu Lys Leu Arg Glu Lys Leu Pro Phe Leu Lys Val Val Val Asp Gln
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Pro Lys Ile Lys Thr Val Leu Gln Ala Tyr Leu Pro
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<212> DNA
<213> Oryza sativa

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 <212> PRT
 <213> Oryza sativa

<400> 411

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Ile Asn Asp Arg Val Tyr Phe Pro Lys Trp Tyr Leu Lys Gly Ala Arg
 35 40 45

Glu Ser Pro Ser His Gly Gly Ala Phe Val Arg Lys Phe Val Asn Leu
 50 55 60

Asp Met Arg Ser Tyr Leu Lys Val Leu Ser Trp Met Pro Ala Ala Leu
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Lys Met Pro Glu Asp Glu Leu Ile Ser His Ala Gly Leu Asp Ser Ala
 85 90 95

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

Thr Leu Gln Ser Ser Lys Val Gln His Ser Asp Ile Asp Lys Leu Ser
 130 135 140

Ile Ser Asn Ile Pro Val Gly Ser Lys Arg Phe Ala Ala His Leu Thr
 145 150 155 160

Met Ala Tyr Val Phe Thr Phe Trp Thr Cys Tyr Val Leu Leu Arg Glu
 165 170 175

Tyr Glu Ile Val Ala Thr Met Arg Leu Arg Phe Leu Ala Ser Glu Lys
 180 185 190

Arg Arg Pro Asp Gln Phe Thr Val Leu Val Arg Asn Ile Pro Pro Asp
 195 200 205

Pro Asp Glu Ser Ile Gly Glu Leu Val Glu His Phe Phe Leu Val Asn
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His Pro Asp His Tyr Leu Thr His Gln Val Val Tyr Asn Ala Asn Lys
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 Lys Thr Gly₂₇₅ Phe Leu Gly Cys Phe₂₈₀ Gly Ser Lys Val₂₈₅ Asp Ala Ile Glu
 Tyr Tyr Thr Ser Glu Ile Glu₂₉₅ Arg Ile Glu Lys Glu₃₀₀ Glu Thr Asp Glu
 Arg Gly Lys Ile Met Lys₃₁₀ Asp Pro Lys Ser Val₃₁₅ Val Pro Ala Ala Phe₃₂₀
 Val Ser Phe Arg Ser₃₂₅ Arg Trp Gly Ala₃₃₀ Val Cys Ala Gln Thr₃₃₅ Gln
 Gln Thr Ser Asn₃₄₀ Pro Thr Val Trp Leu₃₄₅ Thr Glu Trp Ala Pro₃₅₀ Glu Pro
 Arg Asp Val₃₅₅ Tyr Trp Asp Asn Leu₃₆₀ Ser Ile Pro Phe Val₃₆₅ Tyr Leu Thr
 Ile Arg Arg Leu Ile Ile Ala₃₇₅ Val Ala Phe Phe Phe₃₈₀ Leu Asn Phe Phe
 Tyr Val Leu Pro Ile Ala₃₉₀ Phe Val Gln Ser Leu₃₉₅ Ala Asn Ile Glu Gly₄₀₀
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 Phe Leu Ile₄₃₅ Leu Leu Pro Ser Ile₄₄₀ Leu Met Phe Met Ser₄₄₅ Lys Val Glu
 Gly Leu₄₅₀ Thr Ser Val Ser Ser₄₅₅ Leu Glu Arg Arg Ser₄₆₀ Ala Phe Lys Tyr
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 Ser Ala Leu Glu Gln₄₈₅ Leu Lys Thr Phe Leu₄₉₀ His Gln Ser Ala Asn₄₉₅ Glu
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PF59082PF60142_PCT_SEQ_LIST.txt

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Leu Val Tyr Ala Val Val Thr Pro Phe Leu Leu Pro Phe Ile Leu Ile
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Phe Phe Gly Leu Ala Tyr Val Val Tyr Arg His Gln Ile Ile Asn Val
595 600 605

Tyr Asn Gln Glu Tyr Glu Ser Ala Ala Ala Phe Trp Pro Ser Val His
610 615 620

Gly Arg Ile Ile Val Ala Leu Ile Val Ser Gln Leu Leu Leu Leu Gly
625 630 635 640

Leu Leu Ser Thr Lys Gly Ala Gly Gln Ser Thr Pro Val Leu Leu Val
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Leu Pro Val Val Thr Phe Tyr Phe Tyr Lys Tyr Cys Lys Asn Arg Tyr
660 665 670

Glu Pro Ala Phe Val Glu Tyr Pro Leu Gln Asp Ala Met Arg Lys Asp
675 680 685

Thr Leu Glu Arg Ala Arg Glu Pro Gly Phe Asp Leu Lys Gly Tyr Leu
690 695 700

Met Asn Ala Tyr Ile His Pro Val Phe Lys Gly Asp Glu Asp Asp Glu
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Lys Phe Ser Ile Ser Asp Glu Pro Glu Ala Glu Gln Val Leu Val Ala
725 730 735

Thr Lys Arg Gln Ser Arg Arg Asn Thr Pro Val Pro Ser Lys Tyr Asn
740 745 750

Gly Ser Glu Ser Pro Ser Leu Ala Glu Ile Val Asn Asp Gln Arg Leu
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<212> DNA
<213> Oryza sativa

PF59082PF60142_PCT_SEQ_LIST.txt

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<213> Oryza sativa

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Asn Ala Pro Val Tyr Leu Ala Arg Arg Met Ala Ala Gly Gly Gly Gly
35 40 45

Gly Gly Leu Pro Leu Gly His Gly Arg Leu Thr Pro Ser Phe Arg Trp
50 55 60

Ile Arg Ala Ala Leu Arg Leu Ser Glu Asp Asp Val Leu Arg Arg His
65 70 75 80

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

Cys Phe Ala Val Cys Ser Ile Val Gly Leu Phe Ile Leu Ala Pro Thr
100 105 110

Asn Tyr Ser Cys Glu Gly Leu Gln Asp Thr Lys Arg Ser Asn Ser Met
115 120 125

Glu Leu Phe Thr Val Ser Asn Val Ala Arg Gly Ser Asn Arg Leu Trp
130 135 140

Val His Phe Ala Cys Leu Cys Phe Ile Ser Phe Tyr Val Val Tyr Leu
145 150 155 160

Leu His Lys Glu His Lys Glu Met Ser Ser Arg Arg Ile Ala His Leu
165 170 175

Lys Tyr His Arg Lys Arg Pro Asp Gln Tyr Thr Ile Leu Val Arg Gly
180 185 190

Ile Pro Leu Cys Pro Asp His Gly Thr Tyr Gly Cys Tyr Ala Asp His
195 200 205

Phe Phe Ser Lys His Tyr Arg Thr Tyr Gln Ser Tyr His Ile Val His
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 260 265 270
 Glu Glu Lys Leu Lys Asn Val His His Ser Ile Arg Leu Leu Gln Cys
 275 280 285
 Glu Asn Met Leu Lys Arg Lys Glu Leu Pro Val Ala Phe Val Ser Phe
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 Lys Ser Gln Leu Asp Ala Ala Gln Ala Ala Glu Met Gln Gln His Val
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 Asn Pro Leu Ser Leu Val Thr Thr Tyr Ala Pro Glu Pro Pro Asp Ala
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 Pro Val Thr Ala Val Gln Gly Ile Val Gln Phe Glu Lys Ile Lys Ile
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 Trp Phe Pro Pro Ala Arg Ala Val Glu Leu Ile Pro Gly Leu Asn Ser
 385 390 395 400
 Val Val Thr Gly Tyr Leu Pro Ser Met Ile Leu Asn Gly Phe Ile Tyr
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 465 470 475 480
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 Leu Thr Asp Gly Met Ser Gly Phe Ser Leu Glu Val Leu Gln Phe Gly
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500

505

510

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Gln Pro Tyr Leu Tyr Gly Phe Pro Tyr Tyr Arg Val Val Pro Ile Val
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Ser Leu Ala Val Leu Ile Gly Leu Val Tyr Ala Val Val Ala Pro Leu
 545 550 555 560

Leu Leu Pro Ile Leu Val Ile Tyr Phe Leu Leu Gly Tyr Ala Val Tyr
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Ile Asn Gln Met Glu Asp Val Tyr Glu Ile Thr Tyr Asp Thr Cys Gly
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Gln Tyr Trp Pro Asn Ile His Arg Tyr Ile Phe Leu Ser Val Thr Leu
 595 600 605

Met Gln Ile Thr Met Leu Lys Ser Lys Pro Gly Ala Ser Phe Ala Thr
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Val Pro Leu Leu Val Ser Thr Ile Leu Phe Asn Glu Tyr Cys Lys Val
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Arg Phe Leu Pro Thr Phe Leu His Arg Pro Val Gln Val Ala Lys Glu
 645 650 655

Asn Asp Asp Leu Asn Glu Ala Glu Gly Met Arg Gly Asp Leu Asp His
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Ala Ile Ser Ala Tyr Lys Pro Pro Trp Met Arg Pro Thr Asn Phe Ser
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 <213> Oryza sativa

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agtttgtag tcttttataa	attgctgccc tctagaagtg	atcgcttcca gccatccttg	2280
ttggaaggga tgcagacagt	taatagcttt gtagatggtc	caacagatta tgaagttttt	2340
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<210> 415
 <211> 792
 <212> PRT
 <213> Oryza sativa

<400> 415

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 20 25 30

Ala Ala Ser Cys Val Leu Leu Phe Leu Leu Val Lys Leu Arg Phe Asp
 35 40 45

His Arg Arg Ile Pro Gly Pro Ser Ala Leu Ala Ala Lys Leu Leu Ala
 50 55 60

Val Tyr His Ala Thr Ala Pro Gln Ile Ala Leu His Cys Gly Ala Asp
 65 70 75 80

Ala Ala Gln Phe Leu Leu Phe Glu Arg Ala Ser Phe Leu Val Leu Ala
 85 90 95

Ala Val Ala Ala Ala Ala Val Ala Ala Ala Leu Pro Leu Asn Leu Leu
 100 105 110

Ala Gly Asp Ala Ala Ile Ala Asp Gln Phe Ala Ala Thr Thr Ile Ser
 115 120 125

His Ile Pro Lys Ser Ser Pro Leu Leu Trp Leu His Leu Leu Leu Thr
 130 135 140

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

Ala Leu Arg Ile Thr Arg Phe Arg Asp Gly Asn Gly Asn Pro Ser Asp
 165 170 175

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

Pro Lys Thr Leu Ala Ala Asp Lys Thr Pro Leu Lys Asp Tyr Phe Glu
 195 200 205

His Lys Tyr Pro Gly Lys Val Tyr Arg Val Ile Val Pro Phe Asp Leu
 210 215 220

Cys Thr Leu Glu Tyr Leu Ala Glu Glu Trp Gly Lys Val Arg Asn Arg
 225 230 235 240

Ile Ser Trp Leu Glu Ala Arg Met Asp Ala Arg Asn Leu Phe Asp Glu
 245 250 255

PF59082PF60142_PCT_SEQ_LIST.txt

Phe Ala Gln Gly Gly Arg His Ser Glu Glu His Trp Ile Val Arg Arg
 260 265 270
 Cys Lys Glu Leu Trp Val Met Thr Ala Glu Arg Phe Gly Phe Thr Asp
 275 280 285
 Glu Glu Met Leu Arg Arg Leu Gln Thr Lys Lys Leu Val Leu Gly Ser
 290 295 300
 Arg Leu Ser Asp Tyr Lys Asp Gly Arg Ala Pro Gly Ala Gly Ile Ala
 305 310 315 320
 Phe Val Val Phe Lys Asp Val Tyr Thr Ala Asn Lys Ala Val Arg Asp
 325 330 335
 Phe Arg Met Glu Arg Lys Lys Thr Pro Ile Gly Arg Phe Phe Pro Val
 340 345 350
 Met Glu Leu Gln Leu Glu Arg Ser Arg Trp Thr Val Glu Arg Ala Pro
 355 360 365
 Pro Ala Ser Asp Ile Tyr Trp Asn His Leu Gly Leu Ser Lys Thr Ser
 370 375 380
 Leu Gly Leu Arg Arg Ile Ala Val Asn Thr Cys Leu Ile Leu Met Leu
 385 390 395 400
 Leu Phe Phe Ser Ser Pro Leu Ala Ile Ile Ser Gly Met Gln Ser Ala
 405 410 415
 Ala Arg Ile Ile Asn Val Glu Ala Met Asp Asn Ala Lys Ser Trp Leu
 420 425 430
 Val Trp Leu Gln Ser Ser Ser Trp Phe Trp Thr Ile Ile Phe Gln Phe
 435 440 445
 Leu Pro Asn Val Leu Ile Phe Val Ser Met Tyr Ile Ile Ile Pro Ser
 450 455 460
 Val Leu Ser Tyr Phe Ser Lys Phe Glu Cys His Leu Thr Val Ser Gly
 465 470 475 480
 Glu Gln Arg Ala Ala Leu Leu Lys Met Val Cys Phe Phe Leu Val Asn
 485 490 495
 Leu Ile Leu Leu Arg Ala Leu Val Glu Ser Ser Leu Glu Ser Trp Ile
 500 505 510
 Leu Ser Met Gly Arg Cys Tyr Leu Asp Ser Val Asp Cys Lys Gln Ile
 515 520 525

PF59082PF60142_PCT_SEQ_LIST.txt

Glu Gln Tyr Leu Ser Pro Ser Phe Leu Ser Arg Ser Ser Leu Ser Ser
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 Leu Ala Phe Leu Ile Thr Cys Thr Phe Leu Gly Ile Ser Phe Asp Leu
 545 550 555 560
 Leu Ala Pro Ile Pro Trp Ile Lys His Val Met Lys Lys Phe Arg Lys
 565 570 575
 Asn Asp Met Val Gln Leu Val Pro Glu Glu Asn Glu Asp Tyr Gln Leu
 580 585 590
 Met His Asp Gly Glu Glu Thr Asn Asn Leu Arg Ala Pro Leu Met Ser
 595 600 605
 Glu Arg Glu Asp Ser Gly Ile Leu Asn Gly Ile Glu Glu His Asp Leu
 610 615 620
 Ser Leu Tyr Pro Ile Asn Arg Ser Phe His Met Pro Lys Gln Thr Phe
 625 630 635 640
 Asp Phe Ala Gln Tyr Tyr Ala Phe Asp Ile Thr Ile Phe Ala Leu Thr
 645 650 655
 Met Ile Tyr Ser Leu Phe Ala Pro Leu Thr Val Pro Val Gly Ala Val
 660 665 670
 Tyr Phe Gly Tyr Arg Tyr Leu Val Asp Lys Tyr Asn Phe Leu Phe Ile
 675 680 685
 Tyr Arg Val Arg Gly Phe Pro Ala Gly Asn Asp Gly Lys Leu Met Asp
 690 695 700
 Met Val Ile Cys Ile Met Gln Phe Cys Val Ile Phe Phe Leu Val Ala
 705 710 715 720
 Met Leu Leu Phe Phe Ala Val Gln Gly Asp Pro Met Lys Leu Gln Ala
 725 730 735
 Ile Cys Thr Leu Ser Leu Leu Val Phe Tyr Lys Leu Leu Pro Ser Arg
 740 745 750
 Ser Asp Arg Phe Gln Pro Ser Leu Leu Glu Gly Met Gln Thr Val Asn
 755 760 765
 Ser Phe Val Asp Gly Pro Thr Asp Tyr Glu Val Phe Ser Gln Pro Asp
 770 775 780
 Leu Asp Trp Ser Leu Tyr Gln Ser
 785 790

PF59082PF60142_PCT_SEQ_LIST.txt

<210> 416
 <211> 2334
 <212> DNA
 <213> Oryza sativa

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<400> 416
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aggattgctg aggagaatag taggctcagg gaggctttta ttttgagagag atttgttcca 180
tccgctagct ggattttgag aagtcttcga tgcacggagg atgaactctt agctactgct 240
gggttggtatg cagttgtctt caataggatt cttgtattta gcatacgcac attctcctta 300
gccgctttcc tttgtgtact tggagttctt ccactgaatt attttggaaca agatatgctc 360
catgtacgga ttccttcagc atcattggag acatttaca ttggaaatat gcaagagaga 420
tcaagatggc tctgggtcca ttgtgttgca ctgtacatca tatctggtgt ggcttgcctt 480
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catcagatta ttataaaagt cgggaaactt cagaagattg tgactggtgc aaagaaggct 720
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PF59082PF60142_PCT_SEQ_LIST.txt

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gttcacgttg acagagatgc agatgcaagc ggaagtccg gtgaatctag ctgcaaagaa 2160
gacaccaacc aaccacaac cagtacatt tctcacccta cactggaagg actccctgta 2220
aaccggctac ggcatgcagt gaggtcgtc agttccatca tcaggttaca gaagagaggc 2280
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<210> 417
<211> 777
<212> PRT
<213> Oryza sativa

<400> 417

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

Leu Arg Glu Ala Phe Ile Leu Glu Arg Phe Val Pro Ser Ala Ser Trp
50 55 60

Ile Leu Arg Ser Leu Arg Cys Thr Glu Asp Glu Leu Leu Ala Thr Ala
65 70 75 80

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

Ile Phe Ser Leu Ala Ala Phe Leu Cys Val Leu Gly Val Leu Pro Leu
100 105 110

Asn Tyr Phe Gly Gln Asp Met Leu His Val Arg Ile Pro Ser Ala Ser
115 120 125

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

Trp Val His Cys Val Ala Leu Tyr Ile Ile Ser Gly Val Ala Cys Leu
145 150 155 160

Leu Leu Tyr Leu Glu Tyr Lys His Ile Ala Arg Leu Arg Leu Leu His
165 170 175

Val Ser Arg Ala Ser Thr Asn Pro Ser His Phe Thr Val Leu Val Arg
180 185 190

PF59082PF60142_PCT_SEQ_LIST.txt

Gly Val Pro Lys Ser Thr Lys Glu Ser Ile Ser Cys Thr Val Glu Ser
195 200 205

Phe Phe Thr Lys Tyr His Val Ser Ser Tyr Leu Ser His Gln Ile Ile
210 215 220

Tyr Lys Val Gly Lys Leu Gln Lys Ile Val Thr Gly Ala Lys Lys Ala
225 230 235 240

Tyr Lys Lys Phe Lys His Phe Lys Gly Thr Thr Val Asp Gln Arg Cys
245 250 255

Gly Pro Ile Thr Tyr Arg Cys Gly Leu Cys Gly Ala Ser Ser Lys Ser
260 265 270

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

Val Lys Asp Ser Glu Leu Ser Leu Pro Asp Lys Asp Cys Gly Ala Ala
290 295 300

Phe Val Phe Phe Lys Thr Arg Tyr Ala Ala Leu Val Val Ser Glu Ile
305 310 315 320

Val Gln Thr Ser Asn Pro Met Glu Trp Val Thr Ser Leu Ala Pro Asp
325 330 335

Arg Asp Asp Val Tyr Trp Ser Asn Leu Trp Leu Pro Tyr Lys Gln Leu
340 345 350

Trp Ile Arg Arg Ile Val Thr Leu Ser Gly Ser Ile Val Phe Met Phe
355 360 365

Leu Phe Leu Ile Pro Val Thr Phe Ile Gln Gly Leu Thr Gln Leu Glu
370 375 380

Gln Leu Gln Gln Arg Leu Pro Phe Leu Asn Gly Ile Leu Lys Lys Lys
385 390 395 400

Tyr Ile Thr Gln Leu Val Thr Gly Tyr Leu Pro Ser Val Ile Leu Gln
405 410 415

Ile Phe Leu Tyr Thr Val Pro Pro Thr Met Met Phe Phe Ser Thr Leu
420 425 430

Glu Gly Pro Val Ser His Ser Glu Arg Lys Arg Ser Ala Cys Cys Lys
435 440 445

Val Leu Tyr Phe Thr Ile Trp Asn Val Phe Phe Val Asn Val Leu Ser
450 455 460

PF59082PF60142_PCT_SEQ_LIST.txt

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

Pro Met Val Leu Ala Arg Ala Val Pro Val Gln Ala Thr Phe Phe Thr
485 490 495

Thr Tyr Val Leu Thr Ser Gly Trp Ala Ser Leu Ser Ser Glu Leu Met
500 505 510

Gln Leu Phe Gly Leu Thr Trp Asn Phe Ile Met Lys Tyr Val Leu Arg
515 520 525

Met Lys Glu Asp Ser Tyr Phe Val Pro Ser Phe Pro Tyr His Thr Glu
530 535 540

Val Pro Lys Val Leu Leu Phe Gly Leu Leu Gly Phe Thr Cys Ser Val
545 550 555 560

Leu Ala Pro Leu Ile Leu Pro Phe Leu Leu Val Tyr Phe Phe Leu Gly
565 570 575

Tyr Val Val Tyr Arg Asn Gln Phe Leu Asn Val Tyr Cys Thr Lys Tyr
580 585 590

Asp Thr Gly Gly Leu Tyr Trp Pro Ile Ala His Tyr Thr Thr Ile Phe
595 600 605

Ser Ile Val Leu Thr Gln Ile Ile Cys Leu Gly Val Phe Gly Leu Lys
610 615 620

Glu Ser Pro Val Ala Ala Gly Phe Thr Val Pro Leu Ile Ile Leu Thr
625 630 635 640

Leu Leu Phe Asn Gln Tyr Cys Ser Asn Arg Leu Arg Pro Leu Phe Lys
645 650 655

Thr Leu Pro Ala Gln Asp Leu Ile Asp Met Asp Arg Glu Asp Glu Gln
660 665 670

Ser Gly Arg Met Asp Asp Ile His His Arg Leu His Ser Ala Tyr Cys
675 680 685

Gln Phe Ala Asp Thr Asp Asp Ile Pro Leu Lys Gly Val His Val Asp
690 695 700

Arg Asp Ala Asp Ala Ser Gly Ser Ser Gly Glu Ser Ser Cys Lys Glu
705 710 715 720

Asp Thr Asn Gln Pro Thr Thr Ser Asp Ile Ser His Pro Thr Leu Glu
725 730 735

PF59082PF60142_PCT_SEQ_LIST.txt

Gly Leu Pro Val Asn Arg Leu Arg His Ala Val Arg Ser Leu Ser Ser
740 745 750

Ile Ile Arg Leu Gln Lys Arg Gly Leu Ser Pro Gln Pro Ala Gly Pro
755 760 765

Ser Ala Asp Val Asn Pro Gln Thr Ala
770 775

<210> 418
<211> 2232
<212> DNA
<213> Oryza sativa

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cggctcgccg aggagaagtt ccggcagcag gtcgactact tctcgcttga gaggctcttg 180
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ataacttctc ttgtttgcat atttggagtg cttcctgtta attaccatgg gaaagaaacg 360
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tcacatcaga tgatctaccg gaaaggaagt atgcagaaat ttgtggataa tgcagagagg 720
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tgtccagggt ctatagtatt cttcaagact cgctatgcgg caattgttgc ttcacgaatt 960
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gcagctagtg ttgccttcat gtttgttttt attgtccccg ttgcattcgt ccaaagcatg 1140
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PF59082PF60142_PCT_SEQ_LIST.txt

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atggcacctc tcatactgcc cttcttgcta gtctactttt gcctcggcta cctagtgtat 1740
cgcaatcaga tcctaaatgt ctactacca aagtacgaaa tgggagggaa actgtggcca 1800
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gacgagatgt ga 2232

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<210> 419
 <211> 743
 <212> PRT
 <213> Oryza sativa

<400> 419

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

Gln Gln Val Asp Tyr Phe Ser Leu Glu Arg Leu Leu Pro Thr Ala Gly
 50 55 60

Trp Ile Val Lys Ala Tyr Trp Cys Thr Glu Glu Glu Ile Arg Arg Val
 65 70 75 80

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

Arg Ile Phe Ser Ile Thr Ser Leu Val Cys Ile Phe Gly Val Leu Pro
 100 105 110

Val Asn Tyr His Gly Lys Glu Thr Asn His Gly Arg Ile Pro Ala Glu
 115 120 125

Ser Leu Asn Val Phe Thr Ile Ala Asn Leu Lys Glu Gly Ser Arg Met
 130 135 140

Leu Trp Val His Cys Val Ala Leu Tyr Val Ile Thr Ile Ser Ala Cys
 145 150 155 160
 Ile Leu Leu Tyr Tyr Glu Tyr Lys Tyr Ile Ser Arg Lys Arg Leu Ala
 165 170 175
 His Ile Thr Gly Ser Pro Pro Gly Pro Gly His Phe Ser Val Ile Val
 180 185 190
 Arg Ser Ile Pro Lys Ser Asp Asn Glu Leu Leu Asp Asp Thr Ile Arg
 195 200 205
 Asn Phe Phe Val Asn Tyr His Gly Ser Ser Tyr Leu Ser His Gln Met
 210 215 220
 Ile Tyr Arg Lys Gly Ser Met Gln Lys Phe Val Asp Asn Ala Glu Arg
 225 230 235 240
 Val Tyr Arg Lys Phe Val Arg Val Lys Met Ser Ser Phe Gly Gln Ser
 245 250 255
 Arg Arg Ser Asp Leu Ser Arg Cys Gly Leu Cys Gly Val Arg Ala Ser
 260 265 270
 Ser Phe Gln Gln Tyr Arg Asn Lys Phe Ile Asn Ser Lys Lys Pro Asp
 275 280 285
 Leu Ser Asp Pro Glu Val Ile Glu Ala Gln Lys Asp Cys Pro Gly Ala
 290 295 300
 Ile Val Phe Phe Lys Thr Arg Tyr Ala Ala Ile Val Ala Ser Arg Ile
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 Pro Arg Asp Val Tyr Trp Ser Asn Leu Trp Ile Pro Tyr Arg Gln Ile
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 Trp Leu Arg Lys Ile Ala Thr Leu Ala Ala Ser Val Ala Phe Met Phe
 355 360 365
 Val Phe Ile Val Pro Val Ala Phe Val Gln Ser Met Met Gln Leu Asp
 370 375 380
 Gln Ile Glu Gln Leu Phe Pro Ser Leu Lys Asn Met Leu Lys Lys Pro
 385 390 395 400
 Phe Phe Val Lys Leu Val Thr Gly Tyr Leu Pro Ser Val Val Leu Leu
 405 410 415
 Leu Ser Leu Tyr Thr Val Pro Pro Leu Met Met Phe Phe Ser Ser Ile
 Seite 392

420

425

430

Glu Gly Ser Ile Ser Arg Ser Gly Arg Lys Lys Ser Ala Cys Cys Lys
 435 440 445

Ile Leu Phe Phe Thr Ile Trp Asn Val Phe Phe Val Asn Val Leu Ser
 450 455 460

Gly Ser Val Leu Asn Gln Leu Asn Val Phe Thr Arg Pro Arg Asp Met
 465 470 475 480

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

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

Gln Val Tyr Asn Leu Val Tyr Asn Phe Phe Arg Lys Cys Ile Phe Cys
 515 520 525

Tyr Arg Asp Asp Pro Glu Tyr Gly Tyr Ser Phe Pro Tyr His Thr Glu
 530 535 540

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

Met Ala Pro Leu Ile Leu Pro Phe Leu Leu Val Tyr Phe Cys Leu Gly
 565 570 575

Tyr Leu Val Tyr Arg Asn Gln Ile Leu Asn Val Tyr Tyr Pro Lys Tyr
 580 585 590

Glu Met Gly Gly Lys Leu Trp Pro Ile Met His Ser Thr Leu Val Phe
 595 600 605

Ala Leu Val Leu Thr Gln Thr Ile Ala Leu Gly Val Phe Thr Ile Lys
 610 615 620

His Ala Thr Ile Ser Ser Gly Phe Thr Val Leu Leu Ile Ile Gly Thr
 625 630 635 640

Val Leu Phe His Gln Tyr Cys Arg His Arg Phe Ser Ser Ile Phe Asn
 645 650 655

Ser Phe Ser Ala Gln Asp Leu Ile Glu Met Asp Arg Asp Asp Glu Gln
 660 665 670

Ser Gly Arg Met Glu Glu Ile His Lys His Leu Leu Asp Ala Tyr Ser
 675 680 685

Gln Gly Thr Thr Asn Met Asp Asn Ser Ser Ser Ser Arg Asn Gly Gly
 690 695 700

PF59082PF60142_PCT_SEQ_LIST.txt

Ala Pro Ile Glu Met Ile Met Glu Asp Pro Ala Gln Asp Ala Gln Asp
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Ser Asn Gln Glu Leu Cys Asp Ala Val Lys Glu Val Thr Gly Ser Ile
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Gln Glu His Ala Asp Glu Met
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<210> 420
<211> 2304
<212> DNA
<213> Oryza sativa

<400> 420
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gtgatggcct atgtatttac gttttggacg tttttcgtgt tgtatcgtga atacaaggtt 540
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caggaagatg aggagagaca caaggtgatc actgatccta atgctattat gccagctgca 960
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PF59082PF60142_PCT_SEQ_LIST.txt

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<210> 421
 <211> 767
 <212> PRT
 <213> Oryza sativa

<400> 421

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Ser Ala Leu Gly Phe Leu Leu Ala Phe Ala Val Leu Arg Ile Gln Pro
 20 25 30

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

Ser Ser Pro Arg Ser Met Gly Thr Val Phe Ser Lys Phe Val Asn Ala
 50 55 60

Asp Leu Ser Thr Tyr Ile Arg Phe Leu Asn Trp Met Pro Ala Ala Leu
 65 70 75 80

Gln Met Pro Glu Pro Glu Leu Ile Glu His Ala Gly Leu Asp Ser Ala
 85 90 95

Val Tyr Val Arg Ile Tyr Leu Leu Gly Leu Lys Ile Phe Val Pro Ile
 100 105 110

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

PF59082PF60142_PCT_SEQ_LIST.txt

Thr Leu Glu Lys Glu Lys Ser Leu Ser Tyr Asp Gln Ile Asp Lys Leu
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145 150 155 160

Val Met Ala Tyr Val Phe Thr Phe Trp Thr Phe Phe Val Leu Tyr Arg
165 170 175

Glu Tyr Lys Val Val Thr Thr Met Arg Leu Arg Phe Leu Ala Ile Gln
180 185 190

Asn Arg Arg Ala Asp Gln Phe Thr Val Leu Val Arg Asn Val Pro Pro
195 200 205

Asp Pro Asp Glu Thr Val Ser Glu His Val Glu His Phe Phe Ala Val
210 215 220

Asn His Arg Asp His Tyr Leu Ser His Gln Thr Val Tyr Asn Ala Asn
225 230 235 240

Thr Leu Ala Gly Leu Val Glu Gln Lys Lys Gly Leu Gln Asn Trp Leu
245 250 255

Val Tyr Tyr Glu Asn Gln His Ala Lys Asn Pro Ala Lys Lys Pro Thr
260 265 270

Met Lys Thr Gly Leu Trp Gly Leu Trp Gly Lys Arg Val Asp Ala Ile
275 280 285

Glu His Tyr Thr Thr Ala Ile Glu Glu Leu Cys Lys Gln Glu Asp Glu
290 295 300

Glu Arg His Lys Val Ile Thr Asp Pro Asn Ala Ile Met Pro Ala Ala
305 310 315 320

Phe Val Ser Phe Lys Ser Arg Trp Gly Ala Ala Val Cys Ala Gln Thr
325 330 335

Gln Gln Thr Ser Asn Pro Thr Leu Trp Leu Thr Glu Trp Ala Pro Glu
340 345 350

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

Ser Val Arg Arg Leu Ile Met Ala Val Ala Leu Phe Phe Leu Thr Phe
370 375 380

Phe Phe Met Ile Pro Ile Ala Ile Val Gln Ser Met Ala Asn Leu Asp
385 390 395 400

Asp Ile Glu Arg Met Leu Pro Phe Leu Lys Pro Ile Ile Glu Arg Asn
Seite 396

405

410

415

Ser Leu Lys Ser Ile Val Gln Gly Phe Leu Pro Gly Ile Ala Leu Lys
 420 425 430

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

Glu Gly His Thr Ser Leu Ser Gly Leu Asp Arg Arg Thr Ala Ser Lys
 450 455 460

Tyr Tyr Leu Phe Leu Phe Val Asn Val Phe Leu Gly Ser Val Ile Thr
 465 470 475 480

Gly Thr Ala Phe Gln Gln Leu Asn Asn Phe Ile His Gln Ser Ala Asn
 485 490 495

Lys Ile Pro Glu Ile Val Gly Glu Ser Ile Pro Met Lys Ala Thr Phe
 500 505 510

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

Val Leu Arg Leu Lys Pro Leu Val Met Phe His Ile Lys Asn Thr Phe
 530 535 540

Leu Val Arg Thr Glu Arg Asp Arg Glu Gln Ala Met Asp Pro Gly Ser
 545 550 555 560

Leu Asp Phe Gly Thr Thr Glu Pro Arg Ile Gln Leu Tyr Phe Leu Leu
 565 570 575

Gly Leu Val Tyr Ala Val Val Thr Pro Ile Leu Leu Pro Phe Ile Ile
 580 585 590

Val Phe Phe Ser Leu Ala Tyr Leu Val Phe Arg His Gln Ile Ile Asn
 595 600 605

Val Tyr Asn Gln Gln Tyr Glu Ser Gly Ala Gln Phe Trp Pro Asp Val
 610 615 620

Gln Arg Arg Leu Val Ile Ala Leu Ile Val Ser Gln Ile Leu Leu Leu
 625 630 635 640

Gly Leu Leu Ser Thr Gln Glu Ala Glu Lys Ser Thr Val Ala Leu Leu
 645 650 655

Pro Leu Pro Val Leu Ser Ile Trp Phe His Tyr Val Cys Lys Gly Arg
 660 665 670

Phe Glu Pro Ala Phe Ile Lys Phe Pro Leu Gln Asp Ala Met Val Lys
 675 680 685

PF59082PF60142_PCT_SEQ_LIST.txt

Asp Thr Leu Glu Arg Ala Asn Asp Pro Thr Leu Asn Leu Arg Glu Tyr
690 695 700

Leu Lys Asp Ala Tyr Val His Pro Val Phe Gln Lys Asn Asp Ile Tyr
705 710 715 720

Glu Phe Ala Gly Ile Asp Glu Glu Glu Lys Asn Pro Met Val Ala Thr
725 730 735

Lys Arg Gln Ser Arg Met Asn Thr Pro Val Asp Ser Lys Phe Asn Ser
740 745 750

Ser Ser Gly Thr Asn Glu Gly Glu Phe Ser Arg Met Ala Pro Thr
755 760 765

<210> 422
<211> 2301
<212> DNA
<213> Oryza sativa

<400> 422
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gttgtcaatt taaacatgag atcatacttg aaatttttta gttggatgcc ggctgctctc 240
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cttgtgcgga atatacctcc agatcctgat gaatcaatta gtgagctcgt ggagcatttc 660
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gaagctgatg agcgtcaaaa gatcatgaag gatccccagt cagctgttcc agcagccttt 960
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tccattccat ttgtgtccct cacagttagg aggctgatag ttgctgtggc attcttcttc 1140
ctcaactttt tttatgtcat tccaatagca ttcgtgcaat ctcttgcaag ctttgaagga 1200
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PF59082PF60142_PCT_SEQ_LIST.txt

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gcatctaaat attatatctt cttgttcttc aatgtatttt tgggaagcat cgttacagga 1440
tctgctttag atcagcttaa ggcatacatt catcagtcgg caaatgaaat accgagaacc 1500
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aatatgtcaa tatccgagga tgtcgggatg gaggaggtga tcgtgccgac caagcgtcaa 2220
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gaaactgtac acgaacgata g 2301

<210> 423
<211> 766
<212> PRT
<213> Oryza sativa

<400> 423

Met Ala Thr Val Ser Asp Ile Gly Leu Ser Ala Ala Ile Asn Val Ser
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Met Ala Val Ala Phe Leu Leu Val Phe Ala Phe Leu Arg Leu Gln Pro
20 25 30

Ile Asn Asp Arg Val Tyr Phe Pro Lys Trp Tyr Leu Arg Gly Met Arg
35 40 45

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

Asn Met Arg Ser Tyr Leu Lys Phe Leu Ser Trp Met Pro Ala Ala Leu
65 70 75 80

Lys Met Pro Glu Asp Glu Leu Ile Asn His Ala Gly Leu Asp Ser Ala
85 90 95

PF59082PF60142_PCT_SEQ_LIST.txt

Val Tyr Leu Arg Ile Tyr Leu Thr Gly Ile Lys Ile Phe Val Pro Ile
100 105 110

Ser Ile Leu Ala Ser Leu Val Leu Phe Pro Val Asn Trp Thr Asn Asp
115 120 125

Thr Leu Asp Ser Met Lys Val Val His Ser Lys Ile Asp Lys Leu Ser
130 135 140

Ile Ser Asn Ile Pro Tyr Gly Ser Asn Arg Phe Val Thr His Leu Val
145 150 155 160

Met Ala Tyr Ala Val Thr Phe Trp Thr Cys Tyr Val Leu Phe Arg Glu
165 170 175

Tyr Glu Ile Ile Thr Thr Met Arg Leu Arg Phe Leu Ala Ser Glu Lys
180 185 190

Arg Arg Pro Asp Gln Phe Thr Val Leu Val Arg Asn Ile Pro Pro Asp
195 200 205

Pro Asp Glu Ser Ile Ser Glu Leu Val Glu His Phe Phe Leu Val Asn
210 215 220

His Pro Asp His Tyr Leu Arg His Gln Val Val Tyr Asn Ala Asn Lys
225 230 235 240

Leu Ala Asp Leu Val Glu Lys Lys Lys Lys Leu Gln Asn Trp Leu Asp
245 250 255

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

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

Tyr Tyr Lys Ala Glu Ile Glu Lys Ile Gly Lys Glu Glu Ala Asp Glu
290 295 300

Arg Gln Lys Ile Met Lys Asp Pro Gln Ser Ala Val Pro Ala Ala Phe
305 310 315 320

Val Ser Phe Arg Ser Arg Trp Gly Ala Ala Val Cys Ala Gln Thr Gln
325 330 335

Gln Thr Ser Asn Pro Thr Val Trp Ile Thr Glu Trp Ala Pro Glu Pro
340 345 350

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

Val Arg Arg Leu Ile Val Ala Val Ala Phe Phe Phe Leu Asn Phe Phe

370

Tyr Val Ile Pro Ile Ala Phe Val Gln Ser Leu Ala Ser Leu Glu Gly
385 390 395 400

Ile Glu Lys Ala Leu Pro Phe Leu Lys Pro Leu Ile Lys Ile Asp Val
405 410 415

Ile Lys Ser Phe Ile Gln Gly Phe Leu Pro Gly Ile Ala Leu Lys Val
420 425 430

Phe Leu Ile Leu Leu Pro Thr Ile Leu Met Phe Met Ser Lys Phe Glu
435 440 445

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

Tyr Ile Phe Leu Phe Phe Asn Val Phe Leu Gly Ser Ile Val Thr Gly
465 470 475 480

Ser Ala Leu Asp Gln Leu Lys Ala Tyr Ile His Gln Ser Ala Asn Glu
485 490 495

Ile Pro Arg Thr Ile Gly Val Ala Ile Pro Met Arg Ala Thr Phe Phe
500 505 510

Ile Thr Tyr Val Met Val Asp Gly Trp Thr Gly Val Ala Gly Glu Ile
515 520 525

Leu Arg Leu Arg Ala Leu Ile Ile Phe His Leu Lys Asn Phe Phe Leu
530 535 540

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

Cys Phe Asp Trp Cys Glu Pro Arg Ile Gln Leu Tyr Phe Leu Leu Gly
565 570 575

Leu Val Tyr Ala Val Val Thr Pro Leu Leu Leu Pro Phe Ile Leu Val
580 585 590

Phe Phe Gly Leu Ala Tyr Val Val Tyr Arg His Gln Ile Ile Asn Val
595 600 605

Tyr Asn Gln Gln Tyr Glu Ser Gly Ala Gln Phe Trp Pro Ser Val His
610 615 620

Gly Arg Ile Ile Ile Ala Leu Ile Val Ser Gln Leu Leu Leu Ile Gly
625 630 635 640

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

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Pro Val Leu Thr Phe Trp Phe Tyr Lys Tyr Cys Lys Asn Arg Phe
660 665 670

Glu Pro Ala Phe Val Arg Asn Pro Leu Gln Glu Ala Met Arg Lys Asp
675 680 685

Thr Leu Glu Arg Ala Arg Glu Pro Thr Phe Asp Leu Lys Ala Tyr Leu
690 695 700

Ala Asn Ala Tyr Leu His Pro Val Phe Lys Gly Arg Glu Glu Glu Asp
705 710 715 720

Asn Met Ser Ile Ser Glu Asp Val Gly Met Glu Glu Val Ile Val Pro
725 730 735

Thr Lys Arg Gln Ser Arg Arg Asn Thr Pro Ala Gln Ser Lys Tyr Glu
740 745 750

Gly Ser Asp Thr Leu Ser Leu Pro Glu Thr Val His Glu Arg
755 760 765

<210> 424
<211> 2196
<212> DNA
<213> Oryza sativa

<400> 424
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gcaattgtgt ttttcaacag aagatctgct gcagcttctg catctcagac tctccatgct 1020

PF59082PF60142_PCT_SEQ_LIST.txt

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tacatcccgg cttgcctgaa gcctgagaag ctagaggatg tggatatctt cgaagacgcc 2160
cagttgcaca ccacctccag agcccatcc atctaa 2196

<210> 425
<211> 731
<212> PRT
<213> Oryza sativa
<400> 425

Met Asp Thr Ala Ser Phe Val Thr Ser Leu Leu Thr Ser Phe Val Ile
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Phe Val Val Leu Val Leu Val Phe Thr Trp Leu Ser Ser Arg Pro Gly
20 25 30

Asn Ala Pro Val Tyr Tyr Pro Ser Val Leu Leu Arg Gly Leu Asp Pro
35 40 45

Trp Glu Gly Arg Gly Arg Gly Thr Arg Ser Pro Val Gly Trp Leu Arg
50 55 60

Gln Ala Ile Ser Ala Ser Glu Gly Asp Val Val Ala Ala Gly Gly Val
65 70 75 80

PF59082PF60142_PCT_SEQ_LIST.txt

Asp Ala Ala Val Tyr 85 Leu Val Phe Leu 90 Ser Ser Val Leu Ser Ile 95 Leu

Val Phe Ser Gly 100 Ile Val Leu Leu 105 Pro Val Leu Leu Pro Val 110 Ala Ala

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

Lys Thr 130 Pro Gln Asn Phe Thr 135 Glu Leu Glu Lys Leu 140 Ala Leu Gly Asn

Val 145 Gln Glu His Ser Arg 150 Arg Leu Trp Ala Phe 155 Leu Leu Ser Val Tyr 160

Trp Val Ser Phe Val 165 Thr Tyr Phe Val Leu 170 Trp Lys Ser Tyr Lys 175 His

Val Ser Asn Met 180 Arg Ala Ala Ala Arg 185 Ser Thr Pro Asp Val 190 Lys Pro

Glu Glu Phe 195 Ala Val Leu Val Arg 200 Asp Val Pro Lys Pro 205 Pro Pro Asp

Gln Thr 210 Ile Lys Asp Ser Val 215 Asp Ser Tyr Phe Arg 220 Ala Leu His Pro

Asp Thr 225 Phe Tyr Arg Ser 230 Met Val Val Thr Asp 235 His Thr Lys Ala Asp 240

Lys Ile Tyr Gln Glu 245 Ile Glu Gly His Lys 250 Gln Lys Ile Ala Arg 255 Ala

Glu Val Val Tyr 260 Ala Glu Ser Lys Thr 265 Thr Gly Lys Pro Glu 270 Gly Thr

Lys Pro Thr 275 His Arg Ile Gly Phe 280 Leu Gly Leu Ile Gly 285 Lys Lys Val

Asp Thr 290 Ile Glu Tyr Cys Asn 295 Asp Gln Ile Lys Glu 300 Leu Leu Pro Lys

Leu 305 Glu Ala Glu Gln Lys 310 Thr Thr Leu Arg Glu 315 Lys Gln Gln Gln Ala 320

Ala Ile Val Phe Phe 325 Asn Arg Arg Ser Ala 330 Ala Ala Ser Ala 335 Ser Gln

Thr Leu His Ala 340 Gln Met Phe Asp Lys 345 Trp Thr Val Glu Gln 350 Ala Pro

Glu Pro Arg Gln Ile Ile Trp Ser Asn Leu Ser Lys Lys Ile Tyr Glu

355

360

365

Arg Gln Ile Arg Gln Val Val Val Tyr Thr Ile Val Phe Leu Thr Val
 370 375 380

Val Phe Tyr Met Ile Pro Ile Thr Ala Ile Ser Ala Leu Thr Thr Leu
 385 390 395 400

Glu Lys Leu Arg Glu Lys Leu Pro Phe Leu Lys Val Val Val Asp Gln
 405 410 415

Pro Lys Ile Lys Thr Val Leu Gln Ala Tyr Leu Pro Gln Leu Ala Leu
 420 425 430

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

Leu Glu Gly Ile Pro Ser Gln Gly His Thr Val Arg Ala Ala Ala Gly
 450 455 460

Lys Tyr Phe Tyr Phe Ile Val Phe Asn Val Phe Leu Gly Val Thr Ile
 465 470 475 480

Ser Ser Thr Leu Phe Ser Ala Leu Thr Thr Ile Ile Asn Asn Pro Pro
 485 490 495

Gly Ile Val Asn Met Leu Ala Ser Ser Leu Pro Gly Ser Ala Thr Phe
 500 505 510

Phe Leu Thr Phe Val Ala Leu Lys Phe Phe Val Gly Tyr Gly Leu Glu
 515 520 525

Leu Ser Arg Leu Val Pro Leu Ile Ile Phe His Leu Lys Arg Lys Tyr
 530 535 540

Leu Cys Lys Thr Glu Asp Glu Val Arg Ala Ala Trp Ala Pro Gly Asp
 545 550 555 560

Leu Gly Tyr Asn Thr Arg Val Pro Asn Asp Met Leu Ile Val Thr Ile
 565 570 575

Val Leu Cys Tyr Ser Val Ile Ala Pro Leu Ile Ile Pro Phe Gly Val
 580 585 590

Ala Tyr Phe Ala Leu Gly Trp Ile Ile Val Lys Asn Gln Val Leu Arg
 595 600 605

Val Tyr Val Pro Ser Tyr Glu Ser Asn Gly Arg Met Trp Pro His Met
 610 615 620

His Thr Arg Ile Ile Ala Ala Leu Leu Ile Tyr Gln Ile Thr Met Val
 625 630 635 640

PF59082PF60142_PCT_SEQ_LIST.txt

Gly Val Ile Leu Leu Lys Lys Phe Leu Tyr Ser Pro Val Leu Val Pro
645 650 655

Leu Ile Pro Ile Ser Phe Ile Phe Ala Tyr Ile Cys His Met Arg Phe
660 665 670

Tyr Pro Ala Phe Ala Lys Thr Pro Leu Glu Val Val Gln His Asn Val
675 680 685

Lys Asp Thr Pro Asn Met Asp Ala Val Tyr Thr Ser Tyr Ile Pro Ala
690 695 700

Cys Leu Lys Pro Glu Lys Leu Glu Asp Val Asp Ile Phe Glu Asp Ala
705 710 715 720

Gln Leu His Thr Thr Ser Arg Ala Pro Ser Ile
725 730

<210> 426
<211> 2433
<212> DNA
<213> Oryza sativa

<400> 426
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aagctctacc tcaactggcca gcgacgccac caccctcacc ctcatggctt cgtcaacctc 180
gacctctgct cctacctccg cttcctcgcc tgggtccccg gcgccctccg catgtcccag 240
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PF59082PF60142_PCT_SEQ_LIST.txt

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<210> 427
 <211> 810
 <212> PRT
 <213> Oryza sativa

<400> 427

Met Ala Thr Leu Pro Asp Leu Gly Val Ser Ala Phe Ile Asn Ile Leu
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Gly Ala Phe Val Phe Leu Leu Ile Phe Ala Ala Leu Arg Leu Gln Pro
 20 25 30

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

Arg His His Pro His Pro His Gly Phe Val Asn Leu Asp Leu Cys Ser
 50 55 60

PF59082PF60142_PCT_SEQ_LIST.txt

Tyr Leu Arg Phe Leu Ala Trp Val Pro Gly Ala Leu Arg Met Ser Gln
65 70 75 80

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

Ile Tyr Thr Leu Gly Leu Lys Ile Phe Leu Pro Ile Met Thr Val Ala
100 105 110

Leu Leu Val Leu Ile Pro Val Asn Val Ser Gly Gly Thr Leu Leu Asn
115 120 125

Leu Arg Lys Glu Ile Val Phe Ser Asp Ile Asp Lys Leu Ser Ile Ser
130 135 140

Asn Val Asn Pro Gly Ser Asn Arg Phe Phe Ile His Leu Leu Met Ala
145 150 155 160

Tyr Val Phe Thr Phe Trp Thr Cys Phe Met Leu Tyr Lys Glu Tyr Ser
165 170 175

Asn Val Ala Phe Met Arg Leu His Phe Leu Ala Ser Gln Lys Arg Cys
180 185 190

Ala Asp Gln Phe Thr Val Ile Val Arg Asn Ile Pro His Val Ser Ser
195 200 205

His Ser Thr Ser Glu Thr Val Asp Glu Phe Phe Arg Arg Asn His Pro
210 215 220

Asp His Tyr Leu Gly Gln Gln Ala Val Tyr Asn Ala Asn Arg Tyr Ala
225 230 235 240

Lys Leu Val Lys Lys Lys Glu Arg Leu Gln Asn Trp Leu Asp Tyr Tyr
245 250 255

Gln Leu Lys Phe Glu Arg His Pro Gly Lys Arg Pro Ile Gly Arg Thr
260 265 270

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

Arg Ala Arg Ile Ser Glu Leu Asp Lys Lys Leu Ala Ser Glu Arg Gln
290 295 300

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

Phe Asp Ser Arg Trp Gly Ala Ala Val Cys Ala Gln Thr Gln Gln Ser
325 330 335

Lys Asn Pro Thr Gln Trp Leu Thr Asp Trp Ala Pro Glu Pro Arg Asp
Seite 408

340

345

350

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

Lys Phe Leu Ile Ser Ile Ala Val Phe Ala Leu Val Phe Phe Tyr Met
 370 375 380

Ile Pro Ile Ala Phe Val Gln Ser Leu Ala Asn Leu Glu Gly Ile Glu
 385 390 395 400

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

Ser Phe Leu Gln Gly Phe Leu Pro Gly Leu Ala Leu Lys Ile Phe Leu
 420 425 430

Tyr Ile Leu Pro Thr Val Leu Met Ile Met Ser Lys Val Glu Gly Tyr
 435 440 445

Val Ser Leu Ser Ser Leu Glu Arg Arg Ala Ala Ser Lys Tyr Tyr Tyr
 450 455 460

Phe Met Leu Val Asn Val Phe Leu Gly Ser Ile Ile Ala Gly Thr Ala
 465 470 475 480

Phe Glu Gln Leu Asn Ala Phe Phe His Gln Pro Pro Ser Gln Ile Pro
 485 490 495

Arg Thr Ile Gly Val Ala Ile Pro Met Lys Ala Thr Phe Phe Met Thr
 500 505 510

Tyr Ile Met Val Asp Gly Trp Ala Gly Ile Ala Asn Glu Ile Leu Arg
 515 520 525

Val Lys Pro Leu Val Ile Tyr His Leu Lys Asn Met Phe Ile Val Lys
 530 535 540

Thr Glu Arg Asp Arg Glu Arg Ala Met Asp Pro Gly Ser Ile Gly Leu
 545 550 555 560

Ala Glu Asn Leu Pro Ser Leu Gln Leu Tyr Phe Leu Leu Gly Leu Val
 565 570 575

Tyr Ala Val Val Thr Pro Ile Leu Leu Pro Phe Ile Ile Ile Phe Phe
 580 585 590

Ala Phe Ala Phe Leu Val Tyr Arg His Gln Ile Ile Asn Val Tyr Asn
 595 600 605

Gln Glu Tyr Glu Ser Ala Ala Ala Phe Trp Pro Gln Val His Ser Arg
 610 615 620

PF59082PF60142_PCT_SEQ_LIST.txt

Ile Ile Ala Ser Leu Leu Ile Ser His Val Thr Leu Phe Gly Leu Met
625 630 635 640

Ser Thr Met Lys Ala Ala Tyr Ser Thr Pro Leu Leu Ile Phe Leu Pro
645 650 655

Leu Leu Thr Ile Trp Phe His Lys Tyr Cys Lys Ser Arg Phe Glu Pro
660 665 670

Ala Phe Arg Lys Tyr Pro Leu Glu Glu Ala Met Glu Lys Asp Asn Leu
675 680 685

Glu Arg Thr Ser Glu Pro Asn Leu Asn Leu Lys Ser Tyr Leu Gln Asn
690 695 700

Ala Tyr Leu His Pro Ile Phe His Met Phe Glu Gln Gln Gln Gln Gln
705 710 715 720

Glu Gln Glu Gln Gln Arg Glu Glu Lys Val Glu Val Arg Ile Asp Lys
725 730 735

Ala Gln Gln His His His Arg Gln Val Glu Glu Glu Glu Glu Glu ser
740 745 750

Lys Ser Ser Gln Ala Thr Thr His Tyr Tyr His His His His Glu Gln
755 760 765

Thr Thr Thr Thr Thr His His His Tyr His Gln His Glu His Met Ser
770 775 780

His Tyr His Met Gly Pro Ser Asp Thr Ala Asp Ser Pro Ser Pro Pro
785 790 795 800

His Phe Val Tyr His Tyr Gly Val Asp Pro
805 810

<210> 428
<211> 2088
<212> DNA
<213> Oryza sativa

<400> 428
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gcggcggcgt acacgctgct ccggcggcgc ccgccgtacg tcgccgtgta ctgccgcggg 120
cggccgtacg cgccgccgga gccgtggctg cccgcggcgt ggcgccgcac cgaggccgac 180
gtccacgccg ccgccgggct cgacggcgct gtcttcctcc gcatcttcgt cttcagcatt 240
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PF59082PF60142_PCT_SEQ_LIST.txt

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taccattcat ctacctactt gtcacacact gttgttcatc aaactggcaa actccgccgc 660
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<210> 429
 <211> 695
 <212> PRT
 <213> Oryza sativa
 <400> 429

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Thr Val Leu Leu Ala Ala Ala Tyr Thr Leu Leu Arg Arg Arg Pro Pro
20 25 30

Tyr Val Ala Val Tyr Ser Pro Arg Arg Pro Tyr Ala Pro Pro Glu Pro
35 40 45

Trp Leu Pro Ala Ala Trp Arg Arg Thr Glu Ala Asp Val His Ala Ala
50 55 60

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

Arg Val Phe Ala Ala Ala Ala Val Val Gly Val Gly Val Leu Met Pro
85 90 95

Val Asn Phe Met Gly Asp Gln Leu Arg Gln Ile Asp Phe Ser Asp Leu
100 105 110

Pro Asn Lys Ser Val Asp Leu Phe Ser Val Ser Asn Val Gln Asp Gly
115 120 125

Ser Asn Lys Leu Trp Leu His Phe Ser Ala Val Tyr Ile Ile Thr Gly
130 135 140

Ile Thr Cys Tyr Leu Leu Tyr Tyr Glu Tyr Lys Tyr Ile Ser Gly Lys
145 150 155 160

Arg Leu Glu Tyr Phe Met Thr Ser Lys Pro Leu Pro Gln His Phe Thr
165 170 175

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

Ala Val Asp Lys Phe Phe Lys Glu Tyr His Ser Ser Thr Tyr Leu Ser
195 200 205

His Thr Val Val His Gln Thr Gly Lys Leu Arg Arg Leu Leu Asn Asp
210 215 220

Ala Glu Asn Ile Cys Thr Lys Leu Ala Asn Leu Lys Ser Val Arg Arg
225 230 235 240

Thr Ser Gly Asp Pro Pro Gly Lys Phe Leu Gly Ile Phe Gly Arg Asn
245 250 255

Asp Leu Val Gly Lys Tyr Gln Lys Arg Leu Glu Asp Leu Glu Glu Asn
260 265 270

Val Arg Met Glu Gln Ser Asp Thr Thr Arg Ser Arg Gln Glu Val Pro
275 280 285

Ala Ala Phe Val Ser Phe Arg Ser Arg Tyr Gly Ala Ala Asn Ala Ile

290

Tyr Ile Arg Gln Ser Asp Lys Pro Thr Glu Trp Gln Thr Glu His Ala
305 310 315 320

Pro Asp Pro His Asp Val Tyr Trp Pro Phe Phe Ser Thr Ser Phe Met
325 330 335

Asp Arg Trp Ile Ser Lys Phe Val Val Ser Val Ala Ser Ile Leu Leu
340 345 350

Ile Leu Val Phe Leu Leu Val Ser Ala Phe Val Gln Gly Leu Thr Tyr
355 360 365

Met Glu Gln Leu Glu Thr Trp Leu Pro Phe Leu Arg Asn Ile Leu Glu
370 375 380

Ile Ala Val Val Ser Gln Leu Val Thr Gly Tyr Leu Pro Ser Val Ile
385 390 395 400

Leu His Phe Leu Ser Ser Tyr Val Pro Ser Ile Met Lys Leu Phe Ser
405 410 415

Thr Met Gln Gly Phe Ile Ser Val Ser Gly Ile Glu Arg Ser Ala Cys
420 425 430

Asn Lys Met Leu Arg Phe Thr Ile Trp Ser Val Phe Phe Ala Asn Val
435 440 445

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

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

Phe Ile Thr Tyr Val Val Thr Ser Trp Thr Ser Ile Ala Ser Glu Leu
485 490 495

Thr Gln Thr Ala Ala Leu Leu Phe His Leu Trp Gly Ser Cys Ala Lys
500 505 510

Cys Cys Lys Arg Asp Glu Ser Lys Pro Pro Ser Met His Tyr His Ser
515 520 525

Glu Ile Pro Arg Val Leu Leu Phe Gly Leu Leu Gly Leu Thr Tyr Phe
530 535 540

Ile Val Ser Pro Leu Ile Leu Pro Phe Val Leu Val Tyr Phe Cys Leu
545 550 555 560

Gly Tyr Phe Ile Tyr Arg Asn Gln Leu Phe Asn Val Tyr Ser Pro Lys
565 570 575

PF59082PF60142_PCT_SEQ_LIST.txt

Tyr Asp Thr Gly Gly Arg Phe Trp Pro Ile Val His Gly Gly Thr Ile
580 585 590

Phe Ser Leu Val Leu Met His Val Ile Ala Ile Gly Val Phe Gly Leu
595 600 605

Lys Lys Leu Pro Leu Ala Ser Ser Leu Leu Val Pro Leu Pro Val Leu
610 615 620

Thr Leu Leu Phe Asn Glu Tyr Cys Arg Asn Arg Phe Leu Pro Ile Phe
625 630 635 640

Glu Ala Tyr Ser Thr Glu Ser Leu Ile Lys Lys Asp Arg Glu Glu Glu
645 650 655

Ser Lys Pro Glu Met Ala Glu Phe Phe Ser Asn Leu Val Asn Ala Tyr
660 665 670

Cys Asp Pro Ala Met Lys Pro Ile Gln His Ser Ser Asn Ser Asp Glu
675 680 685

Arg Thr Thr Pro Leu Leu Ser
690 695

<210> 430
<211> 2292
<212> DNA
<213> Oryza sativa

<400> 430
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aggattgccg aggagcataa tcggctccga gaagctttta tcttggagag atttgtacca 180
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tacaggaaat tcaaacattt tacagacagc actattgatc agaggtgtcg agcaatttca 780
taccggtgct gtctgtgcgg agcctcatct aattctttcc agctgttggc aactgggctt 840
gagcagaatc aggggaaatc tgaccttcaa gattccagct tgaaactaga tgatcaggaa 900

PF59082PF60142_PCT_SEQ_LIST.txt

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tattggtcaa atctttggct accttataag cagctttgga ttcgccgaat agctacgctc 1080
cttggttcaa ttgtttttat gttattcttt ctgataccag tgacatttat acaaggacta 1140
tctcagctag agcagttgca gcagaggctt cttttcctga aggggatact ggagaagaaa 1200
tacatgagcc agcttgtaac tgggtacctt cccagtgtca tactgcaaata atttttatat 1260
gccgttgcac cgataatgat attatcttct acattagagg ggcctatatc tcacagtgaa 1320
aggaagagga gtgcttgctg taaagtgtg tacttctactg tttggaacat attctttgga 1380
aatgtactat ctggtactgt cataagccaa ttgaatgtgt tatcaagccc aaaggacatc 1440
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acatcaggat gggccagttt atcatctgaa cttatgcaat tatttggttt aatatggaac 1560
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caggatttaa ttgacatgga cagggaagac gaacggctag gaagaatgga tgaaattcac 2040
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gaaagcttcg aggaaccag agcggagttg tctcaccaa cactgaatgg actcccagtt 2220
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ttgtcagaat ag 2292

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<210> 431
 <211> 763
 <212> PRT
 <213> Oryza sativa

<400> 431

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

Asn Val Arg Val Tyr Phe Gly Arg Arg Ile Ala Glu Glu His Asn Arg
 35 40 45

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Arg Glu Ala Phe Ile Leu Glu Arg Phe Val Pro Ser Thr Gly Trp
50 55 60

Ile Val Lys Ala Leu Gln Cys Thr Glu Glu Glu Ile Leu Ala Ala Ala
65 70 75 80

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

Ile Phe Ser Leu Ala Ala Ile Leu Cys Val Phe Gly Ile Leu Pro Leu
100 105 110

Asn Tyr Phe Gly Gln Asp Ile His His Val Arg Ile Pro Ser Glu Ser
115 120 125

Leu Asp Ile Phe Thr Ile Gly Asn Val Lys Val Arg Ser Arg Trp Leu
130 135 140

Trp Val His Cys Val Ala Leu Tyr Ile Ile Ser Gly Val Ala Cys Ile
145 150 155 160

Leu Leu Tyr Leu Glu Tyr Lys His Ile Ala Arg Leu Arg Leu Arg His
165 170 175

Leu Thr Cys Ala Met Pro Asn Pro Ser His Phe Thr Val Leu Val Arg
180 185 190

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

Phe Phe Thr Lys Tyr His Gly Ser Ser Tyr Leu Phe His Gln Val Val
210 215 220

Tyr Lys Val Gly Lys Val Gln Lys Ile Met Thr Gly Ala Lys Lys Ala
225 230 235 240

Tyr Arg Lys Phe Lys His Phe Thr Asp Ser Thr Ile Asp Gln Arg Cys
245 250 255

Arg Ala Ile Ser Tyr Arg Cys Cys Leu Cys Gly Ala Ser Ser Asn Ser
260 265 270

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

Leu Gln Asp Ser Ser Leu Lys Leu Asp Asp Gln Glu Cys Ala Ala Ala
290 295 300

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

Leu Gln Thr Ser Asn Pro Met Lys Trp Val Thr Asp Leu Ala Pro Glu

325

330

335

Pro Asp Asp Val Tyr Trp Ser Asn Leu Trp Leu Pro Tyr Lys Gln Leu
 340 345 350

Trp Ile Arg Arg Ile Ala Thr Leu Leu Gly Ser Ile Val Phe Met Leu
 355 360 365

Phe Phe Leu Ile Pro Val Thr Phe Ile Gln Gly Leu Ser Gln Leu Glu
 370 375 380

Gln Leu Gln Gln Arg Leu Pro Phe Leu Lys Gly Ile Leu Glu Lys Lys
 385 390 395 400

Tyr Met Ser Gln Leu Val Thr Gly Tyr Leu Pro Ser Val Ile Leu Gln
 405 410 415

Ile Phe Leu Tyr Ala Val Ala Pro Ile Met Ile Leu Phe Ser Thr Leu
 420 425 430

Glu Gly Pro Ile Ser His Ser Glu Arg Lys Arg Ser Ala Cys Cys Lys
 435 440 445

Val Leu Tyr Phe Thr Val Trp Asn Ile Phe Phe Gly Asn Val Leu Ser
 450 455 460

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

Pro Val Gln Leu Ala Arg Ala Ile Pro Val Gln Ala Thr Phe Phe Ile
 485 490 495

Thr Tyr Val Leu Thr Ser Gly Trp Ala Ser Leu Ser Ser Glu Leu Met
 500 505 510

Gln Leu Phe Gly Leu Ile Trp Asn Phe Val Arg Lys Tyr Ile Leu Arg
 515 520 525

Met Pro Glu Asp Thr Glu Phe Val Pro Ser Phe Pro Tyr His Thr Glu
 530 535 540

Val Pro Lys Val Leu Leu Phe Gly Leu Leu Gly Phe Thr Cys Ser Val
 545 550 555 560

Leu Ala Pro Leu Ile Leu Pro Phe Leu Leu Val Tyr Phe Phe Leu Gly
 565 570 575

Tyr Ile Val Tyr Arg Asn Gln Leu Leu Asn Val Tyr Arg Thr Arg Tyr
 580 585 590

Asp Thr Gly Gly Leu Tyr Trp Pro Ile Ala His Asn Ala Val Ile Phe
 595 600 605

PF59082PF60142_PCT_SEQ_LIST.txt

Ser Leu Val Leu Thr Gln Ile Ile Cys Leu Gly Val Phe Gly Leu Lys
610 615 620

Glu Ser Pro Val Ala Ala Gly Phe Thr Ile Pro Leu Ile Ile Leu Thr
625 630 635 640

Leu Leu Phe Asn Gln Tyr Cys Arg Asn Arg Leu Leu Pro Leu Phe Arg
645 650 655

Thr Thr Pro Ala Gln Asp Leu Ile Asp Met Asp Arg Glu Asp Glu Arg
660 665 670

Ser Gly Arg Met Asp Glu Ile His His Arg Leu His Ser Ala Tyr Cys
675 680 685

Gln Phe His Asp Thr Glu Asp Ile Pro Leu Glu Lys Ile Gln Thr Val
690 695 700

Gly Ser Asp Glu Glu Gln Gly Cys Ser Ser Asp Lys Ser Asn Gly Lys
705 710 715 720

Glu Ser Phe Glu Glu Pro Arg Ala Glu Leu Ser His Pro Thr Leu Asn
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Leu Val Lys Ala Trp Glu Thr Thr Glu Glu Glu Met Leu Ala Ala Ala
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Gly Leu Asp Ala Val Val Phe Ile Arg Met Val Ile Cys Ser Ile Arg
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Ile Phe Ser Ile Val Ala Val Val Cys Leu Ala Phe Val Leu Pro Val
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Asn Tyr Tyr Gly Gln Lys Met Glu His Lys Glu Val His Leu Glu Ser
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Trp Val His Cys Leu Ser Leu Tyr Ile Ile Ser Ser Ala Ala Cys Ala
145 150 155 160

Leu Leu Tyr Phe Glu Tyr Lys Asn Ile Ala Lys Lys Arg Leu Ala His
165 170 175

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

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Tyr Phe Thr Asn Tyr Tyr Ala Pro Ser Tyr Val Ser His Leu Met Val
210 215 220

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

Glu Ser Tyr Glu Thr Leu Arg Phe Pro Tyr His Thr Glu Ile Pro Arg
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Leu Leu Leu Phe Gly Leu Leu Gly Phe Thr Asn Ser Val Ile Ala Pro
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Leu Ser Gln Val Ile Ala Leu Gly Phe Phe Gly Leu Lys Leu Ser Thr
610 615 620

Val Ala Ser Gly Phe Thr Ile Pro Leu Ile Leu Leu Thr Leu Leu Phe
625 630 635 640

Ser Glu Tyr Cys Arg Gln Arg Phe Ala Pro Ile Phe Gln Lys Tyr Pro
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Ala Glu Ile Leu Ile Ala Met Asp Arg Ala Asp Glu Met Thr Gly Lys
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690 695 700

Asp Gln Glu Leu Pro Asp Ser Glu Glu Leu Lys Pro Glu Lys Glu Asn
705 710 715 720

Leu Lys Ala Asp Tyr Ile Trp Glu Phe Gln Arg Ser Lys Ser Gly Leu
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Ser Ser Pro Leu His Ser Gly Ala Leu Val Ser Lys Phe Val Asn Val
 50 55 60

Asn Leu Gly Ser Tyr Leu Arg Phe Leu Asn Trp Met Pro Ala Ala Leu
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Val Tyr Leu Arg Ile Tyr Leu Ile Gly Leu Lys Ile Phe Val Pro Ile
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Ala Leu Leu Ala Trp Ser Ile Leu Val Pro Val Asn Trp Thr Ser His
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180 185 190

Asn Glu Gln Arg Arg Pro Asp Gln Phe Thr Val Leu Val Arg Asn Val
195 200 205

Pro Ala Asp Pro Asp Glu Ser Ile Ser Asp Ser Val Glu His Phe Phe
210 215 220

Leu Val Asn His Pro Asp His Tyr Leu Thr His Gln Val Val Tyr Asn
225 230 235 240

Ala Asn Asp Leu Ala Ala Leu Val Glu Gln Lys Lys Ser Thr Gln Asn
245 250 255

Trp Leu Asp Tyr Tyr Gln Leu Lys Tyr Thr Arg Asn Gln Glu His Lys
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Pro Arg Ile Lys Thr Gly Phe Leu Gly Leu Trp Gly Lys Lys Val Asp
275 280 285

Ala Ile Asp His Tyr Ile Ala Glu Ile Glu Lys Leu Asn Glu Gln Ile
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Met Glu Glu Arg Lys Lys Val Lys Lys Asp Asp Thr Ser Val Met Pro
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Cys Ser Ser Leu Leu Leu Leu Pro Thr Leu Leu Pro Leu Ala Ala Thr
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Asp Asn Asn Ile Lys Asn Thr Lys Asn Ala Thr Asp Thr Thr Ser Lys
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Lys Glu Phe Ile Asp Ser Tyr Phe Arg Glu Ile Tyr Pro Glu Thr Phe
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Tyr Arg Ser Leu Val Ala Thr Glu Asn Ser Lys Val Asn Lys Ile Trp
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 275 280 285
 Asn Glu Ser Val Ala Lys Leu Glu Thr Glu Gln Lys Ala Val Leu Ala
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 Glu Lys Gln Gln Thr Ala Ala Val Val Phe Phe Thr Thr Arg Val Ala
 305 310 315 320
 Ala Ala Ser Ala Ala Gln Ser Leu His Cys Gln Met Val Asp Lys Trp
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 Thr Val Thr Glu Ala Pro Glu Pro Arg Gln Leu Leu Trp Gln Asn Leu
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 Asn Ile Lys Leu Phe Ser Arg Ile Ile Arg Gln Tyr Phe Ile Tyr Phe
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 Ser Ala Ile Thr Thr Leu Lys Asn Leu Gln Arg Ile Ile Pro Phe Ile
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Gly Asp Met Leu Ile Leu Thr Ile Thr Phe Cys Tyr Ser Val Ile Ala
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Pro Leu Ile Leu Ile Phe Gly Ile Thr Tyr Phe Gly Leu Gly Trp Leu
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Val Leu Arg Asn Gln Ala Leu Lys Val Tyr Val Pro Ser Tyr Glu Ser
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Ile Phe Arg Ala Tyr Ile Pro His Ser Leu Ser Ser His Lys Pro Glu
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<210> 439
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 <212> PRT
 <213> Arabidopsis thaliana

<400> 439

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PF59082PF60142_PCT_SEQ_LIST.txt

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Lys Glu Ile₃₅ His Leu Glu Ser₄₀ Ser Glu Val Phe Thr Ile₄₅ Glu Asn Leu
Lys Glu₅₀ Gly Ser Lys Trp₅₅ Trp Val His Cys₆₀ Leu Ala Leu Tyr Ile
Ile Thr Ser Ala Ala Cys₇₀ Leu Leu Leu Tyr Phe₇₅ Glu Tyr Ser Thr Ile₈₀
Ala Lys Met Arg₈₅ Leu Gly His Ile Thr Gly₉₀ Cys Ala Ser Lys₉₅ Pro Ser
Gln Phe Thr Val₁₀₀ Leu Ile Arg Ala Ile₁₀₅ Pro Trp Ser Pro Glu₁₁₀ Gln Ser
Tyr Ser Asp₁₁₅ Thr Leu Ser Lys Phe₁₂₀ Phe Thr Asn Tyr Tyr₁₂₅ Ser Ser Ser
Tyr Val₁₃₀ Ser His Gln Met Val₁₃₅ Tyr His Asn Gly Ile₁₄₀ Ile Gln Arg Leu
Leu Arg Asp Ala Glu Arg₁₅₀ Met Cys Gln Thr Leu₁₅₅ Lys His Val Ser Pro₁₆₀
Glu Ile Asn Cys Lys₁₆₅ Pro Ser Leu Arg Pro₁₇₀ Cys Thr Phe Cys Gly₁₇₅ Gly
Pro Thr Ala Thr₁₈₀ Ser Ser Phe His Ile₁₈₅ Leu Ser Asn Glu Ala₁₉₀ Asp Ser
Val Lys Gly₁₉₅ Met Glu Leu Gly Glu₂₀₀ Leu Thr Met Thr Thr₂₀₅ Thr Thr Thr
Glu Gln Glu Arg Ser Ala Ala₂₁₅ Phe Val Phe Phe Lys₂₂₀ Thr Arg Tyr Asp
Ala Leu Val Val Ser Glu Val Leu Gln Ser Ser₂₃₅ Asn Pro Met Leu Trp₂₄₀
Val Thr Asp Leu Ala₂₄₅ Pro Glu Pro His Asp₂₅₀ Val Tyr Trp Lys Asn₂₅₅ Leu
Asn Ile Pro Tyr₂₆₀ Arg Gln Leu Trp Ile₂₆₅ Arg Lys Ile Ala Thr₂₇₀ Leu Val
Gly Ala Val₂₇₅ Ala Phe Met Phe Val₂₈₀ Phe Leu Ile Pro Val₂₈₅ Thr Phe Ile

PF59082PF60142_PCT_SEQ_LIST.txt

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

Leu Pro Ser Val Ile Leu Ile Leu Phe Phe Tyr Ala Val Pro Pro Leu
325 330 335

Met Met Tyr Phe Ser Ala Leu Glu Gly Cys Ile Ser Arg Ser Ile Arg
340 345 350

Lys Lys Ser Ala Cys Ile Lys Val Leu Tyr Phe Thr Ile Trp Asn Val
355 360 365

Phe Phe Val Asn Ile Leu Ser Gly Ser Val Ile Arg Gln Leu Asn Val
370 375 380

Phe Ser Ser Val Arg Asp Ile Pro Ala Gln Leu Ala Arg Ala Val Pro
385 390 395 400

Thr Gln Ala Gly Phe Phe Met Thr Tyr Cys Phe Thr Ser Gly Trp Ala
405 410 415

Ser Leu Ala Cys Glu Ile Met Gln Pro Met Ala Leu Ile Trp Asn Leu
420 425 430

Val Ala Lys Val Val Thr Lys Asn Glu Asp Glu Ser Tyr Glu Thr Leu
435 440 445

Arg Phe Pro Tyr His Thr Glu Ile Pro Arg Leu Leu Leu Phe Gly Leu
450 455 460

Leu Gly Phe Thr Asn Ser Val Ile Ala Pro Leu Ile Leu Pro Phe Leu
465 470 475 480

Leu Ile Tyr Phe Phe Leu Ala Tyr Leu Ile Tyr Lys Asn Gln Ile Leu
485 490 495

Asn Val Tyr Ile Thr Lys Tyr Glu Ser Gly Gly Gln Tyr Trp Pro Ile
500 505 510

Phe His Asn Thr Thr Ile Phe Ser Leu Ile Leu Thr Gln Ile Ile Ala
515 520 525

Leu Gly Phe Phe Gly Leu Lys Leu Ser Thr Val Ala Ser Gly Phe Thr
530 535 540

Ile Pro Leu Ile Leu Leu Thr Leu Leu Phe Ser Glu Tyr Cys Arg Gln
545 550 555 560

PF59082PF60142_PCT_SEQ_LIST.txt

Arg Phe Ala Pro Ile Phe Asn Lys Asn Pro Ala Gln Val Leu Ile Asp
565 570 575

Met Asp Arg Ala Asp Glu Ile Ser Gly Lys Met Glu Glu Leu His Lys
580 585 590

Lys Leu His Asn Val Tyr Ser Gln Ile Pro Leu His Ser Gln Lys Ser
595 600 605

Ser Ser Lys Ala Glu Cys Ser Asn Pro Phe Lys Lys Gln Glu Leu Pro
610 615 620

Asp Pro Glu Lys Leu Lys Pro Glu Glu Gly Asp Ala Ile Ala Lys Glu
625 630 635 640

Leu Trp Gly Phe Gln Gly Asn Glu Ser Gly Gln Glu His Asp Thr Lys
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Ser

<210> 440
<211> 2310
<212> DNA
<213> Arabidopsis thaliana

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attatgaatt tggactttcg atcatacgtt cggtttttaa actggatgcc tgatgctctt 240
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gagaaaattg ctgcaatgcg gttatctttt ctccaatcag agaagcgacg tgctgatcaa 600
ttcactgttc tggttaggaa cgtaccaccg gactcagacg agtcgattag cgaaaacgtg 660
cagcatttct ttcttgtaa ccaccagac cattatctta cacatcaggt ggtgtacaat 720
gcaaatgaat tggctaaatt ggtagaagac aagaagaaaa tgcagaattg gttagattac 780
taccagttga agtatacaag aaacaaggaa caacggccac ggatgggatt tctcgggcta 840
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PF59082PF60142_PCT_SEQ_LIST.txt

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 <211> 769
 <212> PRT
 <213> Arabidopsis thaliana

<400> 441

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Phe Asn Asp Arg Val Tyr Phe Pro Lys Trp Tyr Leu Lys Gly Val Arg
 35 40 45

Ser Ser Pro Val Asn Ser Gly Ala Phe Val Ser Lys Ile Met Asn Leu
 50 55 60

Asp Phe Arg Ser Tyr Val Arg Phe Leu Asn Trp Met Pro Asp Ala Leu
 65 70 75 80

PF59082PF60142_PCT_SEQ_LIST.txt

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

PF59082PF60142_PCT_SEQ_LIST.txt

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

Phe Phe Ile Ile Pro Ile Ala Phe Val Gln Ser Leu Ala Ser Ile Glu
385 390 395 400

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

Leu Met Lys Ser Leu Ile Gln Gly Phe Leu Pro Gly Ile Val Leu Lys
420 425 430

Leu Phe Leu Ile Phe Leu Pro Thr Ile Leu Met Ile Met Ser Lys Phe
435 440 445

Glu Gly Phe Ile Ser Ile Ser Ser Leu Glu Arg Arg Ala Ala Phe Arg
450 455 460

Tyr Tyr Ile Phe Asn Leu Val Asn Val Phe Leu Gly Ser Val Ile Thr
465 470 475 480

Gly Ser Ala Phe Glu Gln Leu Asp Ser Phe Leu Lys Gln Ser Ala Asn
485 490 495

Asp Ile Pro Arg Thr Val Gly Val Ala Ile Pro Ile Lys Ala Thr Phe
500 505 510

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

Ile Phe Arg Leu Lys Pro Leu Val Ile Phe His Leu Lys Asn Phe Phe
530 535 540

Phe Val Lys Thr Glu Lys Asp Arg Glu Glu Ala Met Asp Pro Gly Gln
545 550 555 560

Ile Asp Phe Tyr Ala Thr Glu Pro Arg Ile Gln Leu Tyr Phe Leu Leu
565 570 575

Gly Leu Val Tyr Ala Pro Val Thr Pro Val Leu Leu Pro Phe Ile Ile
580 585 590

Phe Phe Phe Gly Phe Ala Tyr Leu Val Phe Arg His Gln Lys Tyr Glu
595 600 605

Ser Ala Gly Ala Phe Trp Pro Asp Val His Gly Arg Ile Ile Ser Ala
610 615 620

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Ile Ile Ser Gln Ile Leu Leu Leu Gly Leu Met Ser Thr Lys Gly
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Lys Val Gln Ser Thr Pro Phe Leu Leu Val Leu Ala Ile Leu Thr Phe
645 650 655

Gly Phe His Arg Phe Cys Lys Gly Arg Tyr Glu Ser Ala Phe Val Ile
660 665 670

Asn Pro Leu Gln Glu Ala Met Ile Lys Asp Thr Leu Glu Arg Ala Arg
675 680 685

Glu Pro Asn Leu Asn Leu Lys Gly Phe Leu Gln Asn Ala Tyr Val His
690 695 700

Pro Val Phe Lys Asp Glu Glu Asp Ser Asp Glu Glu Gly Leu Ile Glu
705 710 715 720

Asp Ser Asp Asp Glu Asp Cys Val Val Val Gln Thr Lys Arg Gln Arg
725 730 735

Ser Arg Arg Thr Thr Val Ala Ser Ser Asn Ala Ser Arg Gly Ser Ser
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755 760 765

Thr

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<211> 2136
<212> DNA
<213> Arabidopsis thaliana

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PF59082PF60142_PCT_SEQ_LIST.txt

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 <212> PRT
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<400> 443

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

Arg Arg Arg Asn Lys Val Ala Arg Tyr Ile Pro Ser Leu Lys Trp Ile
50 55 60

Trp Lys Ser Trp Arg Pro Thr Glu Lys Glu Leu Met Glu Ser Ser Gly
65 70 75 80

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

Phe Leu Phe Ala Gly Ile Ile Gly Val Phe Val Leu Leu Pro Val Asn
100 105 110

Cys Phe Gly Asp Gln Leu Thr Val Ile Asp Tyr Ala Asp Trp Ser Ala
115 120 125

Asn Ser Leu Asp Leu Phe Ser Val Ala Asn Leu Lys Val Arg Ser Gln
130 135 140

Trp Leu Trp Val His Phe Gly Ala Ile Tyr Leu Val Thr Val Phe Val
145 150 155 160

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

Glu His Phe Tyr Ser Ser Lys Pro Lys Pro Glu Gln Phe Thr Ile Leu
180 185 190

Val Arg Asn Ile Pro Ser Ser Asp Gly Ser Ser Val Ser Asp Thr Val
195 200 205

Asp Arg Phe Phe Gly Glu Asn His Ser Ser Thr Tyr Phe Ser His Val
210 215 220

Val Ile His Arg Thr Ser Lys Leu Arg Ser Val Val Asp Lys Ala Lys
225 230 235 240

Lys Leu Tyr Lys Glu Val Lys His Lys Lys Pro Val Lys Lys Thr Pro
245 250 255

Met Arg Phe Phe Ser Arg Lys Asp Asn Thr Glu Gly His Tyr Glu Ser
260 265 270

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

Ser Ala Pro Gly Lys Glu Val Arg Ala Ala Phe Val Ser Phe Lys Ser
290 295 300

Arg Tyr Gly Ala Ala Thr Ala Leu His Met Pro Gln Ser Ile Asn Pro
305 310 315 320

Thr Tyr Trp Leu Thr Glu Pro Ala Pro Glu Pro His Asp Val His Trp
Seite 438

325

330

335

Pro Phe Phe Ser Ala Ser Phe Met Gln Lys Trp Leu Ala Lys Ile Leu
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 355 360 365

Val Leu Val Gln Gly Leu Thr Asn Leu Pro Ala Leu Glu Phe Met Phe
 370 375 380

Pro Phe Leu Ser Leu Ile Leu Ser Met Lys Val Val Ser Gln Ile Ile
 385 390 395 400

Thr Gly Tyr Leu Pro Ser Leu Ile Leu Gln Thr Ser Leu Lys Val Val
 405 410 415

Pro Pro Thr Met Glu Phe Leu Ser Ser Ile Gln Gly His Ile Cys His
 420 425 430

Ser Asp Ile Gln Lys Ser Ala Cys Asn Lys Val Ile Trp Phe Thr Ile
 435 440 445

Trp Asn Val Phe Phe Ala Thr Val Phe Ser Gly Ser Ala Phe Tyr Lys
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Leu Ser Val Ile Leu Asp Pro Lys Gln Ile Pro Leu Lys Leu Ala Val
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Val Ser Tyr Ile Lys Arg Ser Phe Glu Pro Ser Asp Glu Asn Glu Phe
 515 520 525

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 530 535 540

Phe Gly Leu Leu Gly Ile Thr Tyr Phe Phe Leu Ala Pro Leu Ile Leu
 545 550 555 560

Pro Phe Ile Leu Leu Tyr Phe Ile Leu Ala Tyr Ile Ile Tyr Arg Asn
 565 570 575

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Trp Pro Met Ile His Tyr Thr Met Ile Phe Ser Leu Val Leu Met Gln
 595 600 605

PF59082PF60142_PCT_SEQ_LIST.txt

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625 630 635 640

Cys Arg Lys Arg Phe Met Pro Ile Phe Thr Asp Tyr Pro Ala Glu Val
645 650 655

Leu Thr Lys Arg Asp Lys Glu Asp Arg Asn Asp Pro Thr Met Pro Glu
660 665 670

Phe Tyr Asn Asn Leu Val Ser Ala Tyr Lys Asp Pro Ala Leu Leu Pro
675 680 685

Leu Arg Phe Ser Gly Ser Gly Ser Arg Asn Asp Ser Leu Thr Ser Pro
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<213> Arabidopsis thaliana

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PF59082PF60142_PCT_SEQ_LIST.txt

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<210> 445
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Asn Val Thr Val Tyr Gly Pro Arg Leu Val Lys Lys Asp Gly Lys Ser
35 40 45

Gln Gln Ser Asn Glu Phe Asn Leu Glu Arg Leu Leu Pro Thr Ala Gly
50 55 60

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

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

PF59082PF60142_PCT_SEQ_LIST.txt

Arg Val Phe Ser₁₀₀ Phe Ala Ser Val Val₁₀₅ Gly Ile Phe Ile Leu₁₁₀ Leu Pro
 Val Asn Tyr₁₁₅ Met Gly Thr Glu Phe₁₂₀ Glu Glu Phe Phe Asp₁₂₅ Leu Pro Lys
 Lys Ser₁₃₀ Met Asp Asn Phe Ser₁₃₅ Ile Ser Asn Val Asn₁₄₀ Asp Gly Ser Asn
 Lys₁₄₅ Leu Trp Ile His Phe₁₅₀ Cys Ala Ile Tyr Ile₁₅₅ Phe Thr Ala Val Val₁₆₀
 Cys Ser Leu Leu Tyr₁₆₅ Tyr Glu His Lys Tyr₁₇₀ Ile Leu Thr Lys Arg₁₇₅ Ile
 Ala His Leu Tyr₁₈₀ Ser Ser Lys Pro Gln₁₈₅ Pro Gln Glu Phe Thr₁₉₀ Val Leu
 Val Ser Gly₁₉₅ Val Pro Leu Val Ser₂₀₀ Gly Asn Ser Ile Ser₂₀₅ Glu Thr Val
 Glu Asn₂₁₀ Phe Phe Arg Glu Tyr₂₁₅ His Ser Ser Ser Tyr₂₂₀ Leu Ser His Ile
 Val₂₂₅ Val His Arg Thr Asp₂₃₀ Lys Leu Lys Val Leu₂₃₅ Met Asn Asp Ala Glu₂₄₀
 Lys Leu Tyr Lys Lys₂₄₅ Leu Thr Arg Val Lys₂₅₀ Ser Gly Ser Ile Ser₂₅₅ Arg
 Gln Lys Ser Arg₂₆₀ Trp Gly Gly Phe Leu₂₆₅ Gly Met Phe Gly Asn₂₇₀ Asn Val
 Asp Val Val₂₇₅ Asp His Tyr Gln Lys₂₈₀ Lys Leu Asp Lys Leu₂₈₅ Glu Asp Asp
 Met Arg₂₉₀ Leu Lys Gln Ser Leu₂₉₅ Leu Ala Gly Glu Glu₃₀₀ Val Pro Ala Ala
 Phe Val Ser Phe Arg Thr₃₁₀ Arg His Gly Ala Ala₃₁₅ Ile Ala Thr Asn Ile₃₂₀
 Gln Gln Gly Ile Asp₃₂₅ Pro Thr Gln Trp Leu₃₃₀ Thr Glu Ala Ala Pro Glu₃₃₅
 Pro Glu Asp Val₃₄₀ His Trp Pro Phe Phe₃₄₅ Thr Ala Ser Phe Val₃₅₀ Arg Arg
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PF59082PF60142_PCT_SEQ_LIST.txt

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 Leu Phe Leu Leu Ile Val Pro Pro Ile Met Leu Leu Leu Ser Ser Met
 420 425 430
 Gln Gly Phe Ile Ser His Ser Gln Ile Glu Lys Ser Ala Cys Ile Lys
 435 440 445
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 465 470 475 480
 Pro Arg Val Leu Ala Ala Ala Val Pro Ala Gln Ala Ser Phe Phe Val
 485 490 495
 Ser Tyr Val Val Thr Ser Gly Trp Thr Gly Leu Ser Ser Glu Ile Leu
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 Arg Leu Val Pro Leu Leu Trp Ser Phe Ile Thr Lys Leu Phe Gly Lys
 515 520 525
 Glu Asp Asp Lys Glu Phe Glu Val Pro Ser Thr Pro Phe Cys Gln Glu
 530 535 540
 Ile Pro Arg Ile Leu Phe Phe Gly Leu Leu Gly Ile Thr Tyr Phe Phe
 545 550 555 560
 Leu Ser Pro Leu Ile Leu Pro Phe Leu Leu Val Tyr Tyr Cys Leu Gly
 565 570 575
 Tyr Ile Ile Tyr Arg Asn Gln Leu Leu Asn Val Tyr Ala Ala Lys Tyr
 580 585 590
 Glu Thr Gly Gly Lys Phe Trp Pro Ile Val His Ser Tyr Thr Ile Phe
 595 600 605
 Ser Leu Val Leu Met His Ile Ile Ala Val Gly Leu Phe Gly Leu Lys
 610 615 620
 Glu Leu Pro Val Ala Ser Ser Leu Thr Ile Pro Leu Pro Val Leu Thr
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PF59082PF60142_PCT_SEQ_LIST.txt

Val Leu Phe Ser Ile Tyr Cys Gln Arg Arg Phe Leu Pro Asn Phe Lys
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Ser Tyr Pro Thr Gln Cys Leu Val Asn Lys Asp Lys Ala Asp Glu Arg
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675 680 685

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690 695 700

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<211> 2271
<212> DNA
<213> Arabidopsis thaliana

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PF59082PF60142_PCT_SEQ_LIST.txt

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<212> PRT
<213> Arabidopsis thaliana
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Val Asn Asp Arg Val Tyr Phe Pro Lys Trp Tyr Leu Lys Gly Leu Arg
      35      40      45
Ser Ser Pro Ile Lys Thr Gly Gly Phe Ala Ser Lys Phe Val Asn Leu
50      55      60
Asp Phe Arg Ser Tyr Ile Arg Phe Leu Asn Trp Met Pro Gln Ala Leu
65      70      75      80
Arg Met Pro Glu Pro Glu Leu Ile Asp His Ala Gly Leu Asp Ser Val
      85      90      95
Val Tyr Leu Arg Ile Tyr Leu Leu Gly Leu Lys Ile Phe Phe Pro Ile
100      105      110
Ala Cys Ile Ala Phe Thr Val Met Val Pro Val Asn Trp Thr Asn Ser
115      120      125

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Cys Met Ala Tyr Val Ile Thr Phe Trp Thr Cys Phe Val Leu Gln Arg
165 170 175

Glu Tyr Lys His Ile Ala Ser Met Arg Leu Gln Phe Leu Ala Ser Glu
180 185 190

His Arg Arg Pro Asp Gln Phe Thr Val Leu Val Arg Asn Ile Pro Pro
195 200 205

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

Asn His Pro Asp Tyr Tyr Leu Thr Tyr Gln Ala Val Tyr Asn Ala Asn
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Lys Leu Ser Glu Leu Val Gln Lys Arg Met Lys Leu Gln Asn Trp Leu
245 250 255

Asp Tyr Tyr Gln Asn Lys His Ser Arg Asn Pro Ser Lys Arg Pro Leu
260 265 270

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

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

Phe Val Ser Phe Lys Lys Arg Trp Gly Ala Val Val Cys Ser Gln Thr
325 330 335

Gln Gln Ser Arg Asn Pro Thr Glu Trp Leu Thr Glu Trp Ala Pro Glu
340 345 350

Pro Arg Asp Ile Tyr Trp Asp Asn Leu Ala Leu Pro Tyr Val Gln Leu
355 360 365

Thr Ile Arg Arg Leu Val Ile Ala Val Ala Phe Phe Phe Leu Thr Phe
370 375 380

Phe Phe Met Ile Pro Ile Ala Phe Val Gln Thr Leu Ala Asn Ile Glu
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Gly Ile Glu Lys Ala Val Pro Phe Leu Lys Pro Leu Ile Glu Val Lys

405

410

415

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

Glu Gly Phe Ile Ser Lys Ser Ser Leu Glu Arg Arg Cys Ala Ser Arg
 450 455 460

Tyr Tyr Met Phe Gln Phe Ile Asn Val Phe Leu Cys Ser Ile Ile Ala
 465 470 475 480

Gly Thr Ala Leu Gln Gln Leu Asp Ser Phe Leu Asn Gln Ser Ala Thr
 485 490 495

Glu Ile Pro Lys Thr Ile Gly Val Ser Ile Pro Met Lys Ala Thr Phe
 500 505 510

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

Ile Leu Arg Leu Lys Pro Leu Ile Ile Tyr His Leu Lys Asn Phe Phe
 530 535 540

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

Gly Leu Val Tyr Ala Ala Val Ser Pro Ile Leu Leu Pro Phe Ile Leu
 580 585 590

Val Phe Phe Ala Leu Ala Tyr Val Val Tyr Arg His Gln Ile Ile Asn
 595 600 605

Val Tyr Asn Gln Glu Tyr Glu Ser Ala Ala Ala Phe Trp Pro Asp Val
 610 615 620

His Arg Arg Val Val Ile Ala Leu Ile Val Ser Gln Leu Leu Leu Met
 625 630 635 640

Gly Leu Leu Ser Thr Lys Lys Ala Ala Arg Ser Thr Pro Leu Leu Phe
 645 650 655

Ile Leu Pro Val Leu Thr Ile Gly Phe His Lys Phe Cys Gln Gly Arg
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Tyr Gln Pro Ile Phe Val Thr Tyr Pro Leu Gln Asp Ala Met Val Lys
 675 680 685

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725 730 735

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Glu Thr Phe Thr
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Tyr Ala Leu Phe Leu Leu His Lys Glu Tyr Lys Glu Ile Leu Val Ile
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Arg Leu Gln Gln Met Lys Glu Leu Arg His Arg Ala Asp Gln Phe Thr
85 90 95
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Cys Ala Val Asp His Phe Phe Ser Lys His His Arg Phe Ser Tyr His
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Ser His Gln Met Leu Tyr Asp Gly Arg Asp Leu Glu Tyr Leu Leu Gly
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Lys Gln Lys Lys Leu Lys Lys Glu Leu Glu Asp Lys Arg His Thr Glu
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Ile Leu Ser Asn Gly Ser Gln Glu His Lys Gln Ile Ser Thr Ser Glu
 165 170 175

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

Ser Arg Arg Asn Ala Ala Leu Ala Ala Gln Thr Gln Gln His Ser Asn
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Pro Leu Glu Leu Ile Thr Glu Met Ala Pro Glu Pro Arg Asp Val Ser
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Trp Arg Asn Leu Ala Ile Pro Gln Lys Ile Leu Pro Leu Asn Lys Ile
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Val Thr Ala Val Gln Gly Ile Ala Lys Tyr Glu Lys Leu Lys Lys Trp
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Glu Ile Gly Glu Tyr Leu Thr His Pro Arg Asp Ile Pro Ser His Leu
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Arg Thr Pro Tyr Leu Phe Ser Phe Pro Tyr Phe Arg Val Ile Pro Thr
 Seite 450

435

440

445

Val Ser Leu Ser Ile Met Ile Gly Met Ile Tyr Ala Val Val Ala Pro
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Leu Met Leu Pro Phe Leu Val Gly Tyr Phe Cys Leu Gly Tyr Ile Val
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Tyr Phe Asn Gln Met Glu Asp Val Tyr Glu Thr Thr Tyr Asp Thr Cys
485 490 495

Gly Arg Phe Trp Pro Phe Ile His His Tyr Ile Phe Val Ser Ile Ile
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Leu Met Gln Ile Thr Met Val Gly Leu Phe Gly Leu Lys Ser Lys Pro
515 520 525

Ser Ala Ala Ile Ala Thr Val Pro Leu Ile Leu Ile Thr Ile Ala Tyr
530 535 540

Asn Glu Tyr Cys Lys Ile Arg Phe Leu Pro Ser Phe Lys His Phe Pro
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Ile Gln Thr Ala Val Glu Ile Asp Glu Glu Asp Glu Lys Asn Gly Glu
565 570 575

Met Glu Thr His Tyr Val Asp Ala Ala Thr Ala Tyr Asn Arg His Gln
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 <211> 785
 <212> PRT
 <213> Arabidopsis thaliana

<400> 451

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 35      40      45

Gly Ser Pro Thr Arg Ser Arg Gly Ile Met Thr Arg Phe Val Asn Leu
 50      55      60

Asp Trp Thr Thr Tyr Val Lys Phe Leu Asn Trp Met Pro Ala Ala Leu
 65      70      75      80

Gln Met Pro Glu Pro Glu Leu Ile Glu His Ala Gly Leu Asp Ser Ala
 85      90      95

Val Tyr Ile Arg Ile Tyr Leu Leu Gly Leu Lys Met Phe Val Pro Ile
100      105      110

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

Thr Leu Glu Asn Ile Asp Asp Leu Thr Phe Ser Asn Val Asp Lys Leu
130      135      140

Ser Ile Ser Asn Val Pro Pro Gly Ser Pro Arg Phe Trp Ala His Ile
145      150      155      160

Thr Met Thr Tyr Val Ile Thr Phe Trp Thr Cys Tyr Ile Leu Tyr Met
165      170      175

Glu Tyr Lys Ala Val Ala Asn Met Arg Leu Arg His Leu Ala Ala Glu
180      185      190

Ser Arg Arg Pro Asp Gln Leu Thr Val Leu Val Arg Asn Val Pro Pro
195      200      205

Asp Pro Asp Glu Ser Val Asn Glu His Val Glu His Phe Phe Cys Val
210      215      220

Asn His Pro Asp His Tyr Leu Cys His Gln Val Val Tyr Asn Ala Asn
225      230      235      240

Asp Leu Ala Lys Leu Val Ala Gln Arg Lys Ala Met Gln Asn Trp Leu
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PF59082PF60142_PCT_SEQ_LIST.txt

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Glu Arg Glu Lys Ile Met Asn Asp Pro Lys Ala Ile Met Pro Ala Ala
305 310 315 320

Phe Val Ser Phe Arg Ser Arg Trp Gly Thr Ala Val Cys Ala Gln Thr
325 330 335

Gln Gln Cys His Asn Pro Thr Ile Trp Leu Thr Glu Trp Ala Pro Glu
340 345 350

Pro Arg Asp Val Phe Trp Asp Asn Leu Ala Ile Pro Tyr Val Glu Leu
355 360 365

Ser Ile Arg Arg Leu Leu Thr Thr Val Ala Leu Phe Phe Leu Ile Phe
370 375 380

Cys Phe Met Ile Pro Ile Ala Phe Val Gln Ser Leu Ala Asn Leu Glu
385 390 395 400

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

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

Ile Phe Leu Ile Ile Leu Pro Thr Ile Leu Met Thr Met Ser Gln Ile
435 440 445

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

Gly Thr Ala Phe Gln Gln Leu Lys Ser Phe Leu Glu Gln Pro Pro Thr
485 490 495

Glu Ile Pro Lys Thr Val Gly Val Ser Ile Pro Met Lys Ala Thr Phe
500 505 510

Phe Ile Thr Tyr Ile Met Val Asp Gly Trp Ala Gly Ile Ala Ala Glu
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Ile Leu Arg Val Val Pro Leu Val Ile Phe His Leu Lys Asn Thr Phe
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PF59082PF60142_PCT_SEQ_LIST.txt

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Gly Leu Val Tyr Ala Ala Val Ala Pro Ile Leu Leu Pro Phe Ile Ile
580 585 590

Val Phe Phe Ala Phe Ala Tyr Val Val Phe Arg His Gln Val Ile Asn
595 600 605

Val Tyr Asp Gln Lys Tyr Glu Ser Gly Ala Arg Tyr Trp Pro Asp Val
610 615 620

His Arg Arg Leu Ile Ile Cys Leu Ile Ile Ser Gln Leu Leu Met Met
625 630 635 640

Gly Leu Leu Ser Thr Lys Lys Phe Ala Lys Val Thr Ala Leu Leu Leu
645 650 655

Pro Gln Pro Ile Leu Thr Phe Trp Phe Tyr Arg Tyr Cys Ala Gly Arg
660 665 670

Phe Glu Ser Ala Phe Ser Lys Phe Pro Leu Gln Glu Ala Met Val Lys
675 680 685

Asp Thr Leu Glu Lys Ala Thr Glu Pro Asn Leu Asn Leu Lys Glu Tyr
690 695 700

Leu Lys Asp Ala Tyr Val His Pro Val Phe Lys Gly Asn Asp Phe Asp
705 710 715 720

Arg Pro Arg Val Val Asp Glu Glu Glu Ser Asn Pro Leu Val Arg Thr
725 730 735

Lys Arg Thr Ser Gln Gly Thr Thr Arg Tyr Asn Ser Glu Ala Ser Ser
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<211> 2319
<212> DNA
<213> Arabidopsis thaliana

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aagatgcctg agcgtgagct gattgatcat gctggtttag actctgttgt ctatctccgg    300
atttactggc tcgggcttaa gatttttgct ccaatagcaa tgcttgcttg ggcagttctt    360
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PF59082PF60142_PCT_SEQ_LIST.txt

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 <213> Arabidopsis thaliana

<400> 453

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

Val Tyr Leu Arg Ile Tyr Trp Leu Gly Leu Lys Ile Phe Ala Pro Ile
 100 105 110

Ala Met Leu Ala Trp Ala Val Leu Val Pro Val Asn Trp Thr Asn Asn
 115 120 125

Glu Leu Glu Leu Ala Lys His Phe Lys Asn Val Thr Ser Ser Asp Ile
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 145 150 155 160

Ala His Ile Ile Met Ala Tyr Ala Phe Thr Ile Trp Thr Cys Tyr Met
 165 170 175

Leu Met Lys Glu Tyr Glu Thr Val Ala Asn Met Arg Leu Gln Phe Leu
 180 185 190

Ala Ser Glu Gly Arg Arg Pro Asp Gln Phe Thr Val Leu Val Arg Asn
 195 200 205

PF59082PF60142_PCT_SEQ_LIST.txt

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 245 250 255
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 Ile Arg Pro Ile Thr Lys Leu Gly Cys Leu Gly Leu Cys Gly Gln Lys
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 Glu Ile Ala Glu Glu Arg Glu Asn Val Val Asn Asp Gln Lys Ser Val
 305 310 315 320
 Met Pro Ala Ser Phe Val Ser Phe Lys Thr Arg Trp Ala Ala Ala Val
 325 330 335
 Cys Ala Gln Thr Thr Gln Thr Arg Asn Pro Thr Glu Trp Leu Thr Glu
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 Tyr Val Ser Leu Thr Val Arg Arg Leu Val Met Asn Val Ala Phe Phe
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 385 390 395 400
 Ala Thr Ile Glu Gly Ile Glu Lys Val Ala Pro Phe Leu Lys Val Ile
 405 410 415
 Ile Glu Lys Asp Phe Ile Lys Ser Leu Ile Gln Gly Leu Leu Ala Gly
 420 425 430
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PF59082PF60142_PCT_SEQ_LIST.txt

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Gln Ser Pro Asn Gln Ile Pro Lys Thr Ile Gly Met Ala Ile Pro Met
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Val Ala Gly Glu Ile Leu Met Leu Lys Pro Leu Ile Ile Tyr His Leu
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Lys Asn Ala Phe Leu Val Lys Thr Glu Lys Asp Arg Glu Glu Ala Met
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Asn Pro Gly Ser Ile Gly Phe Asn Thr Gly Glu Pro Gln Ile Gln Leu
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Tyr Phe Leu Leu Gly Leu Val Tyr Ala Pro Val Thr Pro Met Leu Leu
580 585 590

Pro Phe Ile Leu Val Phe Phe Ala Leu Ala Tyr Val Val Tyr Arg His
595 600 605

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610 615 620

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Cys Lys Gly Arg Phe Glu Pro Ala Phe Val Arg Tyr Pro Leu Gln Glu
675 680 685

Ala Met Met Lys Asp Thr Leu Glu Arg Ala Arg Glu Pro Asn Leu Asn
690 695 700

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Gly Asp Asn Asp Asp Gly Asp Met Ile Gly Lys Leu Glu Asn Glu
725 730 735

Val Ile Ile Val Pro Thr Lys Arg Gln Ser Arg Arg Asn Thr Pro Ala
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<210> 455
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50          55          60

Asp Phe Arg Ser Tyr Ile Arg Phe Leu Asn Trp Met Pro Glu Ala Leu
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Lys Met Pro Glu Pro Glu Leu Val Asp His Ala Gly Leu Asp Ser Val
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Val Tyr Leu Arg Ile Tyr Leu Leu Gly Leu Lys Ile Phe Phe Pro Ile
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Ala Cys Val Ala Phe Thr Thr Met Val Pro Val Asn Trp Thr Asn Lys
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PF59082PF60142_PCT_SEQ_LIST.txt

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Pro	Ala 210	Asp	Pro	His	Glu	Ser 215	Ile	Cys	Glu	Leu	Val 220	Glu	His	Phe	Phe
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Gly	Ile 290	Lys	Tyr	Tyr	Thr	Ser 295	Val	Val	Glu	Gly	Leu 300	Thr	Arg	Glu	Ile
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Asp	Leu 370	Lys	Ile	Arg	Arg	Leu 375	Ile	Val	Gly	Val	Ala 380	Tyr	Phe	Phe	Leu
Thr 385	Phe	Phe	Phe	Met	Ile 390	Pro	Ile	Ala	Phe	Val 395	Gln	Ser	Leu	Ala	Asn 400
Ile	Glu	Gly	Ile	Glu 405	Lys	Ala	Phe	Pro	Phe 410	Leu	Lys	Pro	Leu	Ile 415	Glu
Val	Lys	Leu	Leu 420	Lys	Ser	Ile	Ile	Gln 425	Gly	Phe	Leu	Pro	Gly 430	Ile	Ala

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Lys Ile Phe Leu Leu Phe Leu Pro Arg Ile Leu Met Gln Met Ser
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 Lys Phe Glu Gly Phe Val Ser Thr Ser Ser Leu Glu Arg Arg Ala Ala
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 Thr Arg Phe Tyr Met Phe Gln Phe Ile Asn Val Phe Leu Gly Ser Ile
 465 470 475 480
 Val Thr Gly Thr Ala Phe Gln Gln Leu Asn Ser Phe Leu Asn Gln Ser
 485 490 495
 Ala Asn Asp Ile Pro Lys Thr Ile Gly Val Ser Ile Pro Met Lys Ala
 500 505 510
 Thr Phe Phe Ile Thr Tyr Ile Met Val Asp Gly Trp Ala Gly Val Ala
 515 520 525
 Gly Glu Ile Leu Arg Leu Lys Pro Leu Ile Ile Tyr His Leu Lys Asn
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 Ser Phe Leu Val Arg Thr Glu Lys Asp Arg Glu Glu Ala Thr Asp Pro
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 Gly Thr Ile Gly Phe Asn Thr Gly Glu Pro Gln Ile Gln Leu Tyr Phe
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 Leu Leu Gly Leu Val Tyr Ala Ala Val Ser Pro Ile Leu Leu Pro Phe
 580 585 590
 Ile Leu Val Phe Phe Gly Leu Ala Phe Val Val Tyr Arg His Gln Val
 595 600 605
 Ile Asn Val Tyr Asn Gln Lys Tyr Glu Ser Ala Gly Lys Phe Trp Pro
 610 615 620
 Asp Val His Arg Arg Val Val Thr Ala Leu Val Val Ser Gln Leu Leu
 625 630 635 640
 Leu Met Gly Leu Leu Ser Thr Lys His Ala Ser Lys Ser Thr Pro Leu
 645 650 655
 Leu Leu Val Leu Pro Leu Leu Thr Ile Gly Phe His Lys His Cys Lys
 660 665 670
 Asn Arg Tyr Gln Pro Ala Phe Val Thr Tyr Pro Leu Gln Gln Glu Ala
 675 680 685
 Met Ile Lys Asp Thr Leu Asp Arg Ile Arg Glu Pro Asn Leu Asn Leu
 690 695 700

PF59082PF60142_PCT_SEQ_LIST.txt

Lys Ala Phe Leu Arg Asp Ala Tyr Ala His Pro Glu Phe Arg Val Gly
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Glu Asp Pro Glu Pro Glu Glu Lys Leu Glu Ser Asp Met Ser Pro Pro
725 730 735

Asp Leu Val Ala Thr Lys Arg Trp Ser Trp Arg Asn Thr Pro Leu Pro
740 745 750

Ser Lys Asp Ser Cys Arg Glu Ile Pro
755 760

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PF59082PF60142_PCT_SEQ_LIST.txt

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<213> Arabidopsis thaliana

<400> 457

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Phe Asn Asp Arg Val Tyr Phe Ser Lys Trp Tyr Leu Lys Gly Leu Arg
35 40 45

Ser Ser Pro Ala Arg Gly Gly Ala Phe Ala Gln Arg Phe Val Asn Leu
50 55 60

Asp Phe Arg Ser Tyr Met Lys Phe Leu Asn Trp Met Pro Glu Ala Leu
65 70 75 80

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

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

PF59082PF60142_PCT_SEQ_LIST.txt

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 145 150 155 160
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 165 170 175
 Leu Met Lys Glu Tyr Glu Thr Ile Ala Asn Met Arg Leu Gln Phe Val
 180 185 190
 Ala Ser Glu Ala Arg Arg Pro Asp Gln Phe Thr Val Leu Val Arg Asn
 195 200 205
 Val Pro Pro Asp Ala Asp Glu Ser Val Ser Glu Leu Val Glu His Phe
 210 215 220
 Phe Leu Val Asn His Pro Asp His Tyr Leu Thr His Gln Val Val Cys
 225 230 235 240
 Asn Ala Asn Lys Leu Ala Asp Leu Val Lys Lys Lys Lys Lys Leu Gln
 245 250 255
 Asn Trp Leu Asp Tyr Tyr Gln Leu Lys Tyr Ala Arg Asn Asn Ser Gln
 260 265 270
 Arg Ile Met Val Lys Leu Gly Phe Leu Gly Leu Trp Gly Gln Lys Val
 275 280 285
 Asp Ala Ile Glu His Tyr Ile Ala Glu Ile Asp Lys Ile Ser Lys Glu
 290 295 300
 Ile Ser Lys Glu Arg Glu Glu Val Val Asn Asp Pro Lys Ala Ile Met
 305 310 315 320
 Pro Ala Ala Phe Val Ser Phe Lys Thr Arg Trp Ala Ala Ala Val Cys
 325 330 335
 Ala Gln Thr Gln Gln Thr Arg Asn Pro Thr Gln Trp Leu Thr Glu Trp
 340 345 350
 Ala Pro Glu Pro Arg Asp Val Phe Trp Ser Asn Leu Ala Ile Pro Tyr
 355 360 365
 Val Ser Leu Thr Val Arg Arg Leu Ile Met His Val Ala Phe Phe Phe
 370 375 380
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Asp Asp Lys Phe Met Lys Ser Val Ile Gln Gly Phe Leu Pro Gly Ile
420 425 430

Ala Leu Lys Leu Phe Leu Ala Phe Leu Pro Ser Ile Leu Met Ile Met
435 440 445

Ser Lys Phe Glu Gly Phe Thr Ser Ile Ser Ser Leu Glu Arg Arg Ala
450 455 460

Ala Phe Arg Tyr Tyr Ile Phe Asn Leu Val Asn Val Phe Leu Ala Ser
465 470 475 480

Val Ile Ala Gly Ala Ala Phe Glu Gln Leu Asn Ser Phe Leu Asn Gln
485 490 495

Ser Ala Asn Gln Ile Pro Lys Thr Ile Gly Val Ala Ile Pro Met Lys
500 505 510

Ala Thr Phe Phe Ile Thr Tyr Ile Met Val Asp Gly Trp Ala Gly Val
515 520 525

Ala Gly Glu Ile Leu Met Leu Lys Pro Leu Ile Met Phe His Leu Lys
530 535 540

Asn Ala Phe Leu Val Lys Thr Asp Lys Asp Arg Glu Glu Ala Met Asp
545 550 555 560

Pro Gly Ser Ile Gly Phe Asn Thr Gly Glu Pro Arg Ile Gln Leu Tyr
565 570 575

Phe Leu Leu Gly Leu Val Tyr Ala Pro Val Thr Pro Met Leu Leu Pro
580 585 590

Phe Ile Leu Val Phe Phe Ala Leu Ala Tyr Ile Val Tyr Arg His Gln
595 600 605

Ile Ile Asn Val Tyr Asn Gln Glu Tyr Glu Ser Ala Ala Ala Phe Trp
610 615 620

Pro Asp Val His Gly Arg Val Ile Ala Ala Leu Val Ile Ser Gln Leu
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Leu Leu Met Gly Leu Leu Gly Thr Lys His Ala Ala Leu Ala Ala Pro
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Phe Leu Ile Ala Leu Pro Val Leu Thr Ile Gly Phe His His Phe Cys
660 665 670

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Met Met Lys Asp Thr Leu Glu Thr Ala Arg Glu Pro Asn Leu Asn Leu
690 695 700

Lys Gly Tyr Leu Gln Asn Ala Tyr Val His Pro Val Phe Lys Gly Asp
705 710 715 720

Glu Asp Asp Tyr Asp Ile Asp Asp Lys Leu Gly Lys Phe Glu Asp Glu
725 730 735

Ala Ile Ile Val Pro Thr Lys Arg Gln Ser Arg Arg Asn Thr Pro Ala
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Pro Ser Ile Ile Ser Gly Asp Asp Ser Pro Ser Leu Pro Phe Ser Gly
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Lys Leu Val
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PF59082PF60142_PCT_SEQ_LIST.txt

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 <212> PRT
 <213> Arabidopsis thaliana

<400> 459

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Ser Val Ile Gly Leu Leu Cys Cys Val Ser Ile Phe Leu Phe Val Lys
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PF59082PF60142_PCT_SEQ_LIST.txt

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 Cys Gly Ala Asp Ala Ala Gln Phe Leu Leu Ile Glu Gly Gly Ser Phe
 100 105 110
 Val Leu Leu Phe Ser Ile Ala Val Leu Ala Val Ser Val Met Leu Pro
 115 120 125
 Leu Asn Leu Tyr Ala Gly Thr Ala Leu Leu Ser Asp Glu Leu Ser Lys
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 Thr Met Ile Thr His Ile Gln Lys Gly Ser Ala Leu Leu Trp Leu His
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 Phe Val Phe Val Val Ile Val Val Val Ile Ser His Phe Gly Ile Ala
 165 170 175
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 180 185 190
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 195 200 205
 Val Gln Gly Leu Pro Lys Asn Leu Gly Ser Asp Arg Val Glu Phe Glu
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 225 230 235 240
 Pro Met Asp Leu Cys Ala Leu Asp Asp Leu Ala Thr Glu Leu Val Arg
 245 250 255
 Val Arg Asp Glu Ile Thr Trp Leu Val Ala Lys Met Asp Ser Arg Leu
 260 265 270
 Leu Pro Asp Glu Tyr Glu Asn Val Gly Asp Asn Gly Leu Val Phe Cys
 275 280 285
 Val Cys Ser Leu Trp Val Arg Val Lys Val Leu Trp Ser Gln Ile Thr
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PF59082PF60142_PCT_SEQ_LIST.txt

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Ala Asn Lys Ala Val Gln Asp Phe Arg Asn Glu Arg Ser Arg Arg Thr
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370 375 380

Lys Val Asp Arg Ala Pro Leu Ala Thr Asp Ile Tyr Trp Asn His Leu
385 390 395 400

Gly Leu Thr Lys Val Ala Leu Ile Val Arg Arg Val Ile Val Asn Thr
405 410 415

Ile Leu Leu Leu Ile Leu Val Phe Phe Ser Ser Pro Leu Ala Leu Ile
420 425 430

Ser Ala Leu Val Ser Ala Gly Arg Ile Phe Asn Ala Glu Ala Leu Asp
435 440 445

Ser Ala Gln Tyr Trp Leu Thr Trp Val Gln Thr Ser Gly Trp Ile Gly
450 455 460

Ser Leu Ile Phe Gln Phe Leu Pro Asn Val Phe Ile Phe Val Ser Met
465 470 475 480

Tyr Ile Val Ile Pro Ser Ala Leu Ser Tyr Leu Ser Lys Phe Glu Arg
485 490 495

His Leu Thr Val Ser Gly Glu Gln Arg Ala Ala Leu Leu Lys Met Val
500 505 510

Cys Phe Phe Leu Val Asn Leu Ile Ile Leu Lys Ala Leu Val Glu Ser
515 520 525

Ser Leu Glu Ser Ala Leu Leu Lys Met Ser Arg Cys Tyr Leu Asp Gly
530 535 540

Glu Asp Cys Lys Arg Ile Glu Glu Tyr Met Ser Pro Ser Phe Leu Ser
545 550 555 560

Arg Ser Cys Val Ser Ala Leu Ala Phe Leu Ile Thr Ser Thr Phe Leu
565 570 575

Gly Ile Ser Phe Asp Leu Leu Ala Pro Ile Pro Trp Ile Lys Lys Lys
580 585 590

Ile Gln Lys Phe Arg Lys Asn Asp Met Leu Gln Leu Val Pro Glu Gln
595 600 605

Asn Glu Glu Tyr Ala Leu Glu Asn Gln Glu Pro Ser Ser Asn Leu Glu
610 615 620

Thr Pro Leu Leu Pro Glu Asn Met Phe Glu Ser Pro Arg Phe Gly Asp
625 630 635 640

Ile Glu Pro Met Ser Gln Asp Leu Ser Glu Tyr Pro Ile Ser Arg Thr
645 650 655

Ser Pro Ile Pro Lys Gln Lys Phe Asp Phe Ala Gln Tyr Tyr Ala Phe
660 665 670

Asn Leu Thr Ile Phe Ala Leu Thr Met Ile Tyr Ser Ser Phe Ala Pro
675 680 685

Leu Val Val Pro Val Gly Ala Val Tyr Phe Gly Tyr Arg Tyr Ile Val
690 695 700

Asp Lys Tyr Asn Phe Leu Tyr Val Tyr Arg Val Arg Gly Phe Pro Ala
705 710 715 720

Gly Asn Glu Gly Lys Leu Met Asp Thr Val Leu Cys Ile Met Arg Phe
725 730 735

Cys Val Asp Leu Tyr Leu Val Ser Met Leu Leu Phe Phe Ser Val Lys
740 745 750

Gly Asp Ser Thr Lys Leu Gln Ala Ile Phe Thr Leu Gly Val Leu Val
755 760 765

Met Tyr Lys Leu Leu Pro Ser Asp Thr Asp Arg Tyr His Pro Ala Leu
770 775 780

Leu Arg Ser Ile Gln Thr Val Asp Ser Ile Ile Asp Gly Pro Val Asp
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Arg

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<211> 2363
<212> DNA
<213> Aquilegia spp.

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Seite 472

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ctattttataa	ctcctacatt	ccaccttgct	tgagttcata	taagtttgat	gaaactcaag	2160
agtttgggtca	tgctttatct	gcatttcgag	aaacgggatc	attggtttga	ttgcaagtac	2220
actgaatttc	agcattctat	gttaagaagt	gtggtgtggt	taaattttta	gtcgtgtggt	2280

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 gttgtgactt tctgggtcac tcg 2363

<210> 461
 <211> 707
 <212> PRT
 <213> Aquilegia spp.

<400> 461

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Asn Ser Val Ile Tyr Tyr Pro Asn Arg Ile Val Lys Gly Leu Lys Pro
 35 40 45

Tyr Glu Gly Val Arg Thr Arg Ser Pro Phe Ala Trp Ile Lys Glu Ser
 50 55 60

Ile Thr Ser Thr Glu Asp Asp Ile Ile Ser Ile Ser Gly Val Asp Thr
 65 70 75 80

Ala Val Tyr Phe Val Phe Leu Ser Thr Val Leu Gly Ile Leu Val Ser
 85 90 95

Ser Gly Thr Leu Leu Leu Pro Ser Leu Leu Pro Ile Ala Gly Thr Ala
 100 105 110

Lys Gly Asp Ala Lys Asn Asn Ser Asn Phe Thr Ser Leu Glu Arg Ile
 115 120 125

Ser Met Ala Asn Val Glu Glu Lys Ser Pro Arg Leu Trp Ala Phe Leu
 130 135 140

Leu Ala Thr Tyr Val Val Ser Phe Ser Thr Leu Tyr Met Leu Trp Lys
 145 150 155 160

Ala Tyr Ile His Val Ser Glu Leu Arg Ser Thr Ala Leu Ser Ala Pro
 165 170 175

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

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

Leu Leu His Gly Asp Thr Phe Tyr Arg Ser Met Val Val Thr Asp Asn
 210 215 220

Ile Glu Val Asn Lys Ile Trp Glu Asp Leu Glu Asn Tyr Arg Lys Lys
 Seite 474

225 230 235 240
 Arg Ala Arg Ala Glu Ala Ile Leu Glu Ala Ser Lys Thr Arg Pro Met
 245 250 255
 Asn Lys Thr Gly Phe Leu Ser Gly Asp Lys Val Asn Thr Ile Lys His
 260 265 270
 Cys Thr Glu Met Ile His Glu Leu Val Pro Lys Leu Lys Ile Glu Gln
 275 280 285
 Glu Asn Thr Ile Arg Glu Lys Gln Gln Ser Ser Ala Leu Ile Phe Phe
 290 295 300
 Thr Asn Arg Ile Ala Ala Thr Ser Ala Ala Gln Thr Ile His Ala Lys
 305 310 315 320
 Lys Val Asp Thr Trp Thr Val Val Glu Ala Pro Glu Pro Arg Gln Ile
 325 330 335
 Ile Trp Arg Asn Leu Lys Met Lys Phe Tyr Gln Arg Lys Leu Lys Lys
 340 345 350
 Asp Ile Val Phe Val Ile Val Ala Leu Thr Ile Phe Phe Tyr Met Ile
 355 360 365
 Pro Ile Ala Phe Ile Ser Ala Phe Thr Thr Met Lys Asn Leu Lys Lys
 370 375 380
 Leu Leu Pro Phe Met Lys Pro Ile Val Asp Gln Pro Gln Val Lys Thr
 385 390 395 400
 Val Leu Glu Ala Tyr Leu Pro Gln Ile Ala Leu Ile Val Phe Leu Ala
 405 410 415
 Leu Ile Pro Lys Ile Leu Met Phe Leu Ser Lys Thr Glu Gly Pro Ser
 420 425 430
 Ile Ser Tyr Val Val Arg Ala Ser Ser Gly Lys Tyr Phe Tyr Phe Ile
 435 440 445
 Ile Leu Asn Val Phe Ile Gly Val Thr Ile Ser Gly Thr Leu Phe Lys
 450 455 460
 Thr Ile Lys Glu Val Lys Pro Asn Gln Ile Trp Gly Leu Leu Gly Lys
 465 470 475 480
 Ser Leu Pro Gln Asn Ala Thr Phe Phe Leu Thr Leu Val Ala Leu Lys
 485 490 495
 Phe Phe Ile Gly Tyr Gly Leu Glu Leu Ser Arg Leu Val Pro Leu Ile
 500 505 510

PF59082PF60142_PCT_SEQ_LIST.txt

Ile Phe His Leu Lys Arg Lys Tyr Phe Cys Lys Thr Asp Asp Glu Val
515 520 525

Arg Glu Ala Trp Ala Pro Gly Asp Ile Asn Tyr Ala Thr Arg Val Pro
530 535 540

Asn Asp Leu Leu Ile Val Thr Ile Val Leu Cys Tyr Ser Val Ile Ala
545 550 555 560

Pro Ile Ile Ile Pro Phe Gly Val Ala Tyr Phe Gly Val Gly Trp Leu
565 570 575

Val Leu Arg Asn Gln Ala Leu Lys Val Tyr Val Pro Ser Tyr Glu Ser
580 585 590

Tyr Gly Arg Met Trp Pro His Met His Ala Arg Ile Leu Ala Ala Leu
595 600 605

Ile Ile Tyr Gln Val Thr Met Ile Gly Tyr Phe Ser Ile Lys Lys Phe
610 615 620

Leu Tyr Ser Pro Phe Ala Ile Pro Leu Pro Ile Phe Ser Ile Val Phe
625 630 635 640

Ala Leu Met Cys Arg Arg Lys Phe Tyr Asn Ser Phe Leu Tyr Thr Pro
645 650 655

Leu Glu Val Val Cys Ala Lys Thr Lys Glu Thr Pro Asn Leu Glu Thr
660 665 670

Ile Tyr Asn Ser Tyr Ile Pro Pro Cys Leu Ser Ser Tyr Lys Phe Asp
675 680 685

Glu Thr Gln Glu Phe Gly His Ala Leu Ser Ala Phe Arg Glu Thr Gly
690 695 700

Ser Leu Val
705

<210> 462
<211> 2295
<212> DNA
<213> Medicago truncatula

<400> 462
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ttcgttgctg aaggaaaggt taaagaaggt ggtcaattta acttggaacg cctgtttacct 180
actgctgggt ggggtgagaaa ggcatgggag ccaacagaag acgaattttt atcgacttca 240
ggcttagatg cctttgtttt catgcgcatg tttgtcttta gcttgaaagt atttactttt 300
Seite 476

PF59082PF60142_PCT_SEQ_LIST.txt

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tcaaacaggt	tatggatcca	tttttctgct	gcatatgttt	tcactggagt	tgtttgctat	480
cttctttatt	atgagtatcg	atacatttcg	tccaaacgaa	tagcttgctt	ttattcttct	540
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ggttgttgtg	gactctttgg	gcctaaagtt	gatactgtag	atcactatga	aaggagactt	840
gggaatatag	aagataatgt	gagaatggaa	cagtcctcat	tggcatcaaa	ggaagttcct	900
gctgcattcg	tttcatttaa	aactcgattt	ggtgctgcaa	tagctttaca	cattcaagaa	960
ggtgtcaatc	caacagaatg	gattaccgag	gaagctcccg	aacctcatga	tgtttattgg	1020
cctttcttta	ccgtttcatt	ccttaaaaga	tggatcagca	agctggtagt	ttatgttgca	1080
tatactactc	tcacagttct	gtttttaatc	ccggttgcaa	tagtacaagg	tcttactcat	1140
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agccaagtta	taacaggata	ccttccaagt	ttgattcttc	agttgtttct	atcatatggt	1260
ccacctacta	tgattatgct	ttcatctttg	caaggataca	tttcatggag	tcagatacaa	1320
aaaagtgcac	gcactaaagt	gttactgttt	accatatgga	acattttctt	tgcaaagtga	1380
ctatcagggt	ctgctcttta	tcgagtgaac	atctttcttg	agccgaaaaa	catccaaga	1440
gtattagccg	aagctgtacc	ctcacaggca	tcgttcttca	ttgcatatgt	tgtgacatct	1500
ggatggacca	caatagcatc	agagctcttt	cgattatcta	cacttatttc	caatttttta	1560
agtagaactt	tttgtaaaaa	cggcgatgat	gattttgagc	ccccgtcaat	tccttaccac	1620
agcgaaattc	ccaggattcg	tctcttcggt	cttcttggtg	tgacatactt	ctttcttgct	1680
ccactcatac	ttccatttct	cttgatttac	ttttgtttgg	gatacatcat	tttccgcaac	1740
cagtttttga	aagtttatgt	gccaaagttt	gagactggag	gagagttttg	gcctacagtg	1800
cataactcca	cgatattttc	attgatacta	atgcatgtaa	tagccattgg	gatttttggt	1860
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ttcaacgagt	attgccagaa	acggttccga	cctatattca	agaattttcc	agctgagtg	1980
ttgattaaga	aggacagagc	agacgaaatc	gagcataata	tgtctgaatt	ttatgataaa	2040
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agtcaaagat	caccacttct	tcatagttct	caattttaat	tcatattatg	aggctggttg	2160
ctactatgaa	aatcagcata	ccctcagttt	gatttcccga	tttctgttaa	aattttattg	2220
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gaatggaagc	ttagc					2295

PF59082PF60142_PCT_SEQ_LIST.txt

<210> 463
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 <212> PRT
 <213> Medicago truncatula

<400> 463

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 20 25 30

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

Glu Gly Gly Gln Phe Asn Leu Glu Arg Leu Leu Pro Thr Ala Gly Trp
 50 55 60

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

Gly Leu Asp Ala Phe Val Phe Met Arg Met Phe Val Phe Ser Leu Lys
 85 90 95

Val Phe Thr Phe Gly Ala Ile Ile Gly Ile Val Leu Ile Pro Ile Asn
 100 105 110

Tyr Met Gly Ser Gln Leu Thr Asp Asp Ser Asp Phe Gln His Lys Ser
 115 120 125

Leu Asp Ser Phe Ser Ile Ser Asn Val Asn Asn Gly Ser Asn Arg Leu
 130 135 140

Trp Ile His Phe Ser Ala Ala Tyr Val Phe Thr Gly Val Val Cys Tyr
 145 150 155 160

Leu Leu Tyr Tyr Glu Tyr Arg Tyr Ile Ser Ser Lys Arg Ile Ala Cys
 165 170 175

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

Gly Ile Pro Ile Pro Pro Gly Ser Thr Cys Thr Asp Ala Val Gln Arg
 195 200 205

Phe Phe Ser Glu Tyr His Pro Ser Thr Tyr Leu Ser His Ser Val Val
 210 215 220

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

Tyr Lys Lys Leu Thr Asn Leu Lys Gln Lys Asn Asp Ala Pro Lys Arg

245

250

255

Gln Thr Arg Glu Gly Cys Cys Gly Leu Phe Gly Pro Lys Val Asp Thr
 260 265 270
 Val Asp His Tyr Glu Arg Arg Leu Gly Asn Ile Glu Asp Asn Val Arg
 275 280 285
 Met Glu Gln Ser Ser Leu Ala Ser Lys Glu Val Pro Ala Ala Phe Val
 290 295 300
 Ser Phe Lys Thr Arg Phe Gly Ala Ala Ile Ala Leu His Ile Gln Glu
 305 310 315 320
 Gly Val Asn Pro Thr Glu Trp Ile Thr Glu Glu Ala Pro Glu Pro His
 325 330 335
 Asp Val Tyr Trp Pro Phe Phe Thr Val Ser Phe Leu Lys Arg Trp Ile
 340 345 350
 Ser Lys Leu Val Val Tyr Val Ala Tyr Thr Thr Leu Thr Val Leu Phe
 355 360 365
 Leu Ile Pro Val Ala Ile Val Gln Gly Leu Thr His Leu Glu Gln Leu
 370 375 380
 Glu Thr Phe Phe Pro Phe Leu Lys Gly Val Leu Arg Leu Ser Val Val
 385 390 395 400
 Ser Gln Val Ile Thr Gly Tyr Leu Pro Ser Leu Ile Leu Gln Leu Phe
 405 410 415
 Leu Ser Tyr Val Pro Pro Thr Met Ile Met Leu Ser Ser Leu Gln Gly
 420 425 430
 Tyr Ile Ser Trp Ser Gln Ile Gln Lys Ser Ala Cys Thr Lys Val Leu
 435 440 445
 Leu Phe Thr Ile Trp Asn Ile Phe Phe Ala Asn Val Leu Ser Gly Ser
 450 455 460
 Ala Leu Tyr Arg Val Asn Ile Phe Leu Glu Pro Lys Asn Ile Pro Arg
 465 470 475 480
 Val Leu Ala Glu Ala Val Pro Ser Gln Ala Ser Phe Phe Ile Ala Tyr
 485 490 495
 Val Val Thr Ser Gly Trp Thr Thr Ile Ala Ser Glu Leu Phe Arg Leu
 500 505 510
 Ser Thr Leu Ile Ser Asn Phe Leu Ser Arg Thr Phe Cys Lys Asn Gly
 515 520 525

PF59082PF60142_PCT_SEQ_LIST.txt

Asp Asp Asp Phe Glu Pro Pro Ser Ile Pro Tyr His Ser Glu Ile Pro
530 535 540

Arg Ile Arg Leu Phe Gly Leu Leu Gly Val Thr Tyr Phe Phe Leu Ala
545 550 555 560

Pro Leu Ile Leu Pro Phe Leu Leu Ile Tyr Phe Cys Leu Gly Tyr Ile
565 570 575

Ile Phe Arg Asn Gln Phe Leu Lys Val Tyr Val Pro Lys Phe Glu Thr
580 585 590

Gly Gly Glu Phe Trp Pro Thr Val His Asn Ser Thr Ile Phe Ser Leu
595 600 605

Ile Leu Met His Val Ile Ala Ile Gly Ile Phe Gly Leu Lys Lys Leu
610 615 620

Pro Leu Ala Ser Ala Leu Thr Leu Pro Leu Pro Ile Leu Thr Leu Leu
625 630 635 640

Phe Asn Glu Tyr Cys Gln Lys Arg Phe Arg Pro Ile Phe Lys Asn Phe
645 650 655

Pro Ala Glu Cys Leu Ile Lys Lys Asp Arg Ala Asp Glu Ile Glu His
660 665 670

Asn Met Ser Glu Phe Tyr Asp Lys Met Glu Asn Ala Tyr Asn Asp Pro
675 680 685

Ala Leu Met Pro Val Gln Tyr Ser Glu Arg Phe Asp Ser Gln Arg Ser
690 695 700

Pro Leu Leu His Ser Ser Gln Phe
705 710

<210> 464
<211> 2460
<212> DNA
<213> Medicago truncatula

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ttagtttccg aaggaaaact ccaagagggc aatcaagata acttggaaca tttgttacct 180
acttctggtt gggtgagaag agcatgggag ctttctgatg atgaatttat atcaactgca 240
ggcttagatg ctttcgtctt catccgtata ttgtcttta gtttaaaagt atttgccttt 300
gctggaattg ttgggacaat ctttcttctt ccagttaatt acatggggac tcagatttgt 360
gatgattccg agtctcagaa aacgtcattg gattccttta gtatttcaaa cgttaacaat 420
Seite 480

PF59082PF60142_PCT_SEQ_LIST.txt

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tcgaagccgg	agcctcgtca	gtttagtata	ttagtacgag	gtattccggt	tcctcctgga	600
tgtacatgta	gtgaagctgt	cgaacaattc	tttatggagt	atcacccttc	tgcttatcat	660
tcacattcag	ttgttcgtcg	aagcagcaaa	cttcaaattc	tagttactga	tacagataga	720
ctgtacaaaa	ggcttaccca	attgaaagat	aaagaaaact	ctcctcaaag	gcataggcgt	780
gatggatttt	taggactttt	tgggcaaaaa	gttgatctgt	tagatcatta	cgaaaagaaa	840
ttgggagaca	ttgcagataa	tgtgagaata	gaacagtctg	cattggcagg	aaaggaagtt	900
ccagcagcat	ttgtctcatt	taagtcacga	ttcggtgctg	caatagcttt	gaactcgcaa	960
ccaggtgtca	atccccacaca	ctggatcacc	gaaccagcgc	cagagcctca	tgatgtttat	1020
tggcctttct	tttctgtcac	attcattcga	agatggatca	gcaggctggc	agtttttggt	1080
gcttgcatg	ctcttacaat	tctattttta	atcccagttg	cagtagttca	aggccttacc	1140
catctcgatc	aattagaaac	catgttccca	cctctgagaa	gcatactgag	actgacactt	1200
gtgagtcaag	ttataacagg	ataccttccc	attcagattc	tacagttggt	tctgtctttt	1260
gtgccagcta	ttatgatttt	tctttcatcc	ttgcaaggat	atatttcatg	gagtcagata	1320
caaaaaagtg	catgcactaa	agtattatgg	tttaccatct	ggaacatttt	ctttgcaaac	1380
gtattatcag	ggtcggctct	ctaccgattg	aactactttc	ttgagcccaa	agagtttcct	1440
agagtactag	ctgaagctgt	accagctcag	gcatcattct	tcatggcgta	tattgtggca	1500
ttcggatgga	ctaataatagc	atcagaactt	tttcaattga	ttccactttc	ttacaattat	1560
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gctcctctca	tactgccatt	tatcttggtc	tacttttggt	tgggatacat	catttaccgc	1740
aaccagctat	tatatgttta	tgtgcaaaaa	ttcgagactg	gaggagaatt	ttggcctata	1800
gtacacaact	gcacaatttt	ttcaatggtg	ctaatagcaca	tcatagtaat	tgggatattt	1860
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cttttcaatg	aatactgcc	gaagcggttc	attcctatat	tcaacgctta	tcctgccgaa	1980
tgtttgatca	agaaagatag	agcagatcaa	aatgatccga	acatgtccga	gttttatgat	2040
aagttaacca	atgcatacaa	tgatccagct	ctaatagc	tcaagtatcc	cggacggttt	2100
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cttccccgtt	cccataccca	actctcatgt	acttacctgt	tattctaccc	atattcagcg	2280
gggataagaa	atcgattctc	atccccatct	ccgacgggtt	tgggtatccc	cgccctcatcc	2340
ccatccccga	atcggataac	ttttcttaaa	taaaaataga	agcatttgct	agccccgagc	2400
gtaatgttgt	aatacattat	ccagcaaaga	gatgatggtg	atcaattgat	atggtgatgg	2460

PF59082PF60142_PCT_SEQ_LIST.txt

<210> 465
 <211> 790
 <212> PRT
 <213> Medicago truncatula

<400> 465

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

Glu Gly Asn Gln Asp Asn Leu Glu His Leu Leu Pro Thr Ser Gly Trp
 50 55 60

Val Arg Arg Ala Trp Glu Pro Ser Asp Asp Glu Phe Ile Ser Thr Ala
 65 70 75 80

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

Val Phe Ala Phe Ala Gly Ile Val Gly Thr Ile Phe Leu Leu Pro Val
 100 105 110

Asn Tyr Met Gly Thr Gln Ile Cys Asp Asp Ser Glu Ser Gln Lys Thr
 115 120 125

Ser Leu Asp Ser Phe Ser Ile Ser Asn Val Asn Asn Gly Ser His Arg
 130 135 140

Leu Trp Ile His Phe Ser Ala Val Tyr Ile Phe Thr Gly Val Val Cys
 145 150 155 160

Ile Leu Leu Tyr Tyr Glu Tyr Glu Tyr Ile Ala Ser Lys Arg Ile Ala
 165 170 175

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

Arg Gly Ile Pro Val Pro Pro Gly Cys Thr Cys Ser Glu Ala Val Glu
 195 200 205

Gln Phe Phe Met Glu Tyr His Pro Ser Ala Tyr His Ser His Ser Val
 210 215 220

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

Leu Tyr Lys Arg Leu Thr Gln Leu Lys Asp Lys Glu Asn Ser Pro Gln
 Seite 482

245

250

255

Arg His Arg Arg Asp Gly Phe Leu Gly Leu Phe Gly Gln Lys Val Asp
 260 265 270
 Leu Leu Asp His Tyr Glu Lys Lys Leu Gly Asp Ile Ala Asp Asn Val
 275 280 285
 Arg Ile Glu Gln Ser Ala Leu Ala Gly Lys Glu Val Pro Ala Ala Phe
 290 295 300
 Val Ser Phe Lys Ser Arg Phe Gly Ala Ala Ile Ala Leu Asn Ser Gln
 305 310 315 320
 Pro Gly Val Asn Pro Thr His Trp Ile Thr Glu Pro Ala Pro Glu Pro
 325 330 335
 His Asp Val Tyr Trp Pro Phe Phe Ser Val Thr Phe Ile Arg Arg Trp
 340 345 350
 Ile Ser Arg Leu Ala Val Phe Val Ala Cys Ile Ala Leu Thr Ile Leu
 355 360 365
 Phe Leu Ile Pro Val Ala Val Val Gln Gly Leu Thr His Leu Asp Gln
 370 375 380
 Leu Glu Thr Met Phe Pro Pro Leu Arg Ser Ile Leu Arg Leu Thr Leu
 385 390 395 400
 Val Ser Gln Val Ile Thr Gly Tyr Leu Pro Ile Gln Ile Leu Gln Leu
 405 410 415
 Phe Leu Ser Phe Val Pro Ala Ile Met Ile Phe Leu Ser Ser Leu Gln
 420 425 430
 Gly Tyr Ile Ser Trp Ser Gln Ile Gln Lys Ser Ala Cys Thr Lys Val
 435 440 445
 Leu Trp Phe Thr Ile Trp Asn Ile Phe Phe Ala Asn Val Leu Ser Gly
 450 455 460
 Ser Ala Leu Tyr Arg Leu Asn Tyr Phe Leu Glu Pro Lys Glu Phe Pro
 465 470 475 480
 Arg Val Leu Ala Glu Ala Val Pro Ala Gln Ala Ser Phe Phe Met Ala
 485 490 495
 Tyr Ile Val Ala Phe Gly Trp Thr Asn Ile Ala Ser Glu Leu Phe Gln
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 Leu Ile Pro Leu Ser Tyr Asn Tyr Val Asn Arg Tyr Phe Gly Gly Asn
 515 520 525

PF59082PF60142_PCT_SEQ_LIST.txt

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 545 550 555 560
 Ala Pro Leu Ile Leu Pro Phe Ile Leu Val Tyr Phe Cys Leu Gly Tyr
 565 570 575
 Ile Ile Tyr Arg Asn Gln Leu Leu Tyr Val Tyr Val Gln Lys Phe Glu
 580 585 590
 Thr Gly Gly Glu Phe Trp Pro Ile Val His Asn Cys Thr Ile Phe Ser
 595 600 605
 Met Val Leu Met His Ile Ile Val Ile Gly Ile Phe Gly Leu Lys Glu
 610 615 620
 Leu Pro Ile Ala Ser Gly Phe Thr Leu Pro Leu Pro Ile Val Thr Leu
 625 630 635 640
 Leu Phe Asn Glu Tyr Cys Gln Lys Arg Phe Ile Pro Ile Phe Asn Ala
 645 650 655
 Tyr Pro Ala Glu Cys Leu Ile Lys Lys Asp Arg Ala Asp Gln Asn Asp
 660 665 670
 Pro Asn Met Ser Glu Phe Tyr Asp Lys Leu Thr Asn Ala Tyr Asn Asp
 675 680 685
 Pro Ala Leu Met Pro Ile Lys Tyr Pro Gly Arg Phe Ser Ser His Arg
 690 695 700
 Ser Pro Leu Leu Gly Ser Ser Glu Ser Asn Thr Asn Val Leu Val Ala
 705 710 715 720
 Thr Glu Gly Leu Phe Val Leu Asp Arg Asp Gly Asn Gly Ala Gly Trp
 725 730 735
 Asp Gly Phe Tyr Leu Pro Arg Ser His Thr Gln Leu Ser Cys Thr Tyr
 740 745 750
 Leu Leu Phe Tyr Pro Tyr Ser Ala Gly Ile Arg Asn Arg Phe Ser Ser
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 Pro Ser Pro Thr Gly Leu Gly Ile Pro Ala Ser Ser Pro Ser Pro Asn
 770 775 780
 Arg Ile Thr Phe Leu Lys
 785 790

PF59082PF60142_PCT_SEQ_LIST.txt

<210> 466
 <211> 2613
 <212> DNA
 <213> *Medicago truncatula*

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aaatggtata tgaaggggtt aagggtccagt ccattgcaag gaggggcatt tgtgagcaaa      180
tttgtcaata tagacttcag gtcatacata aggttcttga actggatgcc tgctgcattg      240
caaatgccgg aaccggaact aattgaacat gcaggccttg attctgctgt atacttgagg      300
atctacttac tcgggctgaa aatatttgtc ccaatttcac tcctagcatt ttctgttatg      360
gtccctgtca attggaccaa tgacaccttg aaacgttcaa atgtgggttta taccagcatc      420
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ccaacaatat ggttgactga atgggctcca gagccccgtg acatatactg ggataacatg     1080
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<210> 467
 <211> 766
 <212> PRT
 <213> *Medicago truncatula*

<400> 467

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

Ser Ser Pro Leu Gln Gly Gly Ala Phe Val Ser Lys Phe Val Asn Ile
 50 55 60

Asp Phe Arg Ser Tyr Ile Arg Phe Leu Asn Trp Met Pro Ala Ala Leu
 65 70 75 80

Gln Met Pro Glu Pro Glu Leu Ile Glu His Ala Gly Leu Asp Ser Ala
 85 90 95

Val Tyr Leu Arg Ile Tyr Leu Leu Gly Leu Lys Ile Phe Val Pro Ile
 100 105 110

Ser Leu Leu Ala Phe Ser Val Met Val Pro Val Asn Trp Thr Asn Asp
 115 120 125

Thr Leu Lys Arg Ser Asn Val Val Tyr Thr Ser Ile Asp Lys Leu Ser
 130 135 140

PF59082PF60142_PCT_SEQ_LIST.txt

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165 170 175

Tyr Gln Ile Val Ala Ala Met Arg Leu Ser Phe Leu Ala Ser Glu Arg
180 185 190

Arg Arg Pro Asp Gln Phe Thr Val Leu Val Arg Asn Val Pro Pro Asp
195 200 205

Ala Asp Glu Ser Val Ser Glu Leu Val Glu His Phe Phe Leu Val Asn
210 215 220

His Pro Asp Gln Tyr Leu Thr His Gln Val Val Tyr Asp Ala Lys Lys
225 230 235 240

Leu Ser Ser Leu Val Ala Lys Lys Lys Lys Gln Gln Asn Trp Leu Asp
245 250 255

Tyr Tyr Glu Leu Lys Tyr Ser Arg Asn Glu Ser Val Arg Pro Thr Lys
260 265 270

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

Phe Tyr Thr Ala Ala Ile Glu Arg Leu Ser Arg Asp Ile Glu Leu Glu
290 295 300

Lys Asp Lys Val Thr Lys Asn Pro Lys Ser Ile Met Pro Ala Ala Phe
305 310 315 320

Val Ser Phe Lys Thr Arg Trp Gly Ala Ala Val Cys Ala Gln Thr Gln
325 330 335

Gln Thr Arg Asn Pro Thr Ile Trp Leu Thr Glu Trp Ala Pro Glu Pro
340 345 350

Arg Asp Ile Tyr Trp Asp Asn Met Ala Ile Pro Tyr Val Ser Leu Ser
355 360 365

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

Phe Met Ile Pro Ile Ala Phe Val Gln Ser Leu Ala Asn Ile Glu Gly
385 390 395 400

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

PF59082PF60142_PCT_SEQ_LIST.txt

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Phe Leu Ile Phe Leu Pro Thr Ile Leu Met Ile Met Ser Lys Phe Glu
435 440 445

Gly Phe Ile Ser Gln Ser Ser Leu Glu Arg Arg Cys Ala Ser Arg Tyr
450 455 460

Tyr Ile Phe Gln Phe Ile Asn Val Phe Leu Gly Ser Ile Ile Thr Gly
465 470 475 480

Thr Ala Phe Gln Gln Leu Asp Lys Phe Ile His Gln Ser Ala Asn Glu
485 490 495

Ile Pro Lys Thr Ile Gly Val Ser Ile Pro Met Lys Ala Thr Phe Phe
500 505 510

Ile Thr Tyr Ile Met Val Asp Gly Trp Ala Gly Cys Ala Gly Glu Ile
515 520 525

Leu Arg Leu Lys Pro Leu Ile Phe Tyr His Leu Lys Asn Phe Leu Leu
530 535 540

Val Lys Thr Glu Lys Asp Arg Glu Glu Ala Met Asp Pro Gly Thr Ile
545 550 555 560

Gly Phe Asn Thr Gly Glu Pro Gln Ile Gln Leu Tyr Phe Leu Leu Gly
565 570 575

Leu Val Tyr Ser Val Val Thr Pro Phe Leu Leu Pro Tyr Ile Ile Val
580 585 590

Phe Phe Gly Leu Ala Tyr Leu Val Tyr Arg His Gln Ile Ile Asn Val
595 600 605

Tyr Asn Gln Glu Tyr Glu Ser Ala Gly Ala Phe Trp Pro Asp Val His
610 615 620

Gly Arg Ile Val Phe Ala Leu Val Val Ser Gln Leu Leu Leu Met Gly
625 630 635 640

Leu Leu Ser Thr Lys Glu Ala Ala Asn Ser Thr Pro Leu Leu Ile Ala
645 650 655

Leu Pro Val Leu Thr Ile Trp Phe His Arg Phe Cys Lys Gly Ser Tyr
660 665 670

Glu Pro Ala Phe Thr Thr His Pro Leu Gln Glu Ala Met Val Lys Asp
675 680 685

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

690

His Asp Ala Tyr Ile His Pro Val Phe Asn Asp Asp Gly Asp Thr Asp
705 710 715 720

Ser Asp Val Met Ser Gln Glu Trp Lys Glu Glu Pro Val Ile Val Gln
725 730 735

Thr Lys Arg Gln Ser Arg Lys Asn Thr Pro Ala Pro Ser Lys His Ser
740 745 750

Gly Gly Ser Leu Gln Thr Ser Met His Gly Thr Thr Asp Val
755 760 765

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<211> 1386
<212> DNA
<213> Medicago truncatula

<400> 468
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tgcaaagaca tgctcaagga aaaggagtta cctgtcgctt ttgttacatt caagtcgcgt 180
tctgctgctg tagtagcagc tcagttgcag cagcattcac atccacttct ttgggtcact 240
gaacttgctc cagaaccaag ggatgtttcc tggaggaatt tgagattatc ctacagagtc 300
cttccgcttt gtagactagg cgttgctcatt gcggcatcat tgcttacaat tttctttgcc 360
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ccagctatgg ctgtgcagtt gataccagga ttaagctcta ttgtgacagg atatcttcca 480
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caagcagatt tctttgtgac atacatcttg acagatggac tatctgggtt tcttttgaa 780
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atcattctca tgcagattac catgatcggc ctatttggaac tcaagttaaa gccagctgct 1140
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cgttttctcc cttcctttca ccatcagtct ctcaaggatg cggctgaaaa tgatgaactt 1260
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tcatga 1386

<210> 469
<211> 461
<212> PRT
<213> Medicago truncatula
<400> 469

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Cys His Lys Ile His Gln Leu Gln Cys Lys Asp Met Leu Lys Glu Lys
35 40 45

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

Val Ala Ala Gln Leu Gln Gln His Ser His Pro Leu Leu Trp Val Thr
65 70 75 80

Glu Leu Ala Pro Glu Pro Arg Asp Val Ser Trp Arg Asn Leu Arg Leu
85 90 95

Ser Tyr Arg Val Leu Pro Leu Cys Arg Leu Gly Val Val Ile Ala Ala
100 105 110

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

Ile Ala Lys Tyr Glu Lys Leu Lys Lys Trp Phe Pro Pro Ala Met Ala
130 135 140

Val Gln Leu Ile Pro Gly Leu Ser Ser Ile Val Thr Gly Tyr Leu Pro
145 150 155 160

Ser Val Val Leu Lys Gly Phe Ile Tyr Val Val Pro Phe Ala Met Phe
165 170 175

Ala Met Ala Lys Val Ala Gly Cys Val Ala Arg Ser Lys Glu Glu Ile
180 185 190

Lys Ala Cys Asn Met Val Phe Tyr Phe Leu Val Gly Asn Val Phe Phe
195 200 205

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

Ser Arg Pro Lys Ser Ile Pro Asn Glu Leu Ala Thr Ala Val Ser Ala
Seite 490

225 230 235 240
 Gln Ala Asp Phe Phe Val Thr Tyr Ile Leu Thr Asp Gly Leu Ser Gly
 245 250 255
 Phe Ser Leu Glu Ile Leu Gln Pro Gly Leu Leu Ile Trp Asn Ile Leu
 260 265 270
 Thr Ser Cys Thr Pro Gly Arg Gln Arg Glu Arg Asn Pro Tyr Leu Tyr
 275 280 285
 Ser Leu Pro Tyr Phe Arg Ile Ile Pro Phe Val Ser Leu Ser Ile Leu
 290 295 300
 Ile Gly Leu Val Tyr Ala Val Val Ala Pro Leu Leu Leu Pro Phe Leu
 305 310 315 320
 Ile Val Tyr Phe Cys Leu Gly Tyr Val Val Tyr Ile Asn Gln Ile Glu
 325 330 335
 Asp Met Tyr Glu Thr Thr Tyr Glu Thr Cys Gly Gln Tyr Trp Pro Tyr
 340 345 350
 Ile His His Tyr Ile Leu Leu Ala Ile Ile Leu Met Gln Ile Thr Met
 355 360 365
 Ile Gly Leu Phe Gly Leu Lys Leu Lys Pro Ala Ala Ser Ile Ser Thr
 370 375 380
 Ile Pro Leu Leu Leu Phe Thr Leu Met Phe Asn Glu Tyr Cys Lys Leu
 385 390 395 400
 Arg Phe Leu Pro Ser Phe His His Gln Ser Leu Lys Asp Ala Ala Glu
 405 410 415
 Asn Asp Glu Leu Asp Glu Lys Cys Gly Gln Leu Glu Phe His Tyr Lys
 420 425 430
 Asn Ala Gly Asn Ala Tyr Tyr Pro Ser Gly Leu Gln Pro Val Ser Phe
 435 440 445
 Ala Val Ser Glu Ser Ser Ser Thr Pro Leu Val Ser Ser
 450 455 460

<210> 470
 <211> 1016
 <212> DNA
 <213> Populus trichocarpa

<400> 470
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PF59082PF60142_PCT_SEQ_LIST.txt

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atgaagactg gtttccttgg gcatttttggg ggaaaagtgg atgcaatcga tcatcacata	300
tcagagattg aggaactgtc aaaagaaata gaagaagaga ggacaagggg tttaaaggat	360
ccaaagtcta tcatgccagc agcattttgtt tcattcaaga ctcgatgggg tgcagctgtg	420
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cagtctgcta acgagtatgt tactctcaca aattgattaa atattcatgt cttcattatt	960
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<210> 471
 <211> 301
 <212> PRT
 <213> Populus trichocarpa
 <400> 471

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Glu	His	Phe	Phe	Leu	Val	Asn	His	Pro	Asp	His	Tyr	Leu	Thr	His	Gln
			20					25					30		
Val	Val	Cys	Asn	Ala	Asn	Lys	Leu	Ala	Ser	Leu	Val	Lys	Lys	Lys	Lys
		35					40					45			
Lys	Lys	Gln	Asn	Trp	Leu	Asp	Tyr	Tyr	Gln	Leu	Lys	Tyr	Ser	Arg	Asn
	50					55					60				
Gln	Ser	Gln	Arg	Pro	Gln	Met	Lys	Thr	Gly	Phe	Leu	Gly	His	Phe	Gly
65					70					75					80
Gly	Lys	Val	Asp	Ala	Ile	Asp	His	His	Ile	Ser	Glu	Ile	Glu	Glu	Leu
				85					90					95	
Ser	Lys	Glu	Ile	Glu	Glu	Glu	Arg	Thr	Arg	Val	Leu	Lys	Asp	Pro	Lys
			100					105					110		
Ser	Ile	Met	Pro	Ala	Ala	Phe	Val	Ser	Phe	Lys	Thr	Arg	Trp	Gly	Ala
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PF59082PF60142_PCT_SEQ_LIST.txt

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

Thr Glu Trp Ala Pro Glu Pro Arg Asp Val Tyr Trp Gln Asn Leu Ala
145 150 155 160

Ile Pro Tyr Met Ser Leu Lys Val Arg Arg Leu Ile Ile Gly Val Ala
165 170 175

Phe Leu Leu Leu Thr Phe Phe Phe Ile Ile Pro Ile Ala Ser Val Gln
180 185 190

Ala Leu Ala Ser Ile Glu Gly Ile Glu Lys Arg Ala Pro Phe Leu Lys
195 200 205

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

Pro Gly Ile Val Leu Lys Leu Phe Leu Ile Phe Leu Pro Thr Ile Leu
225 230 235 240

Met Ile Met Ser Lys Phe Glu Gly Phe Ile Ser Leu Ser Ser Leu Glu
245 250 255

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

Leu Gly Ser Ile Leu Thr Gly Ala Ala Phe Glu Gln Leu Asn Ser Phe
275 280 285

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

<210> 472
<211> 941
<212> DNA
<213> Populus trichocarpa

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gctgggattg ctggggaagt tttaatgttg aaaccactga tattctacca cttgaaaaat 180
ttccttttgg tgaagactga aaaagacagg gaagaggcaa tggatcctgg aagtcttggt 240
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gtgacaccag ttctccttcc attcatagtt attttcttcg ccttcgccta tttagtgttc 360
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PF59082PF60142_PCT_SEQ_LIST.txt

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<210> 473
<211> 276
<212> PRT
<213> Populus trichocarpa
<400> 473

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

PF59082PF60142_PCT_SEQ_LIST.txt

Ala Met Met Lys Asp Thr Leu Glu Arg Ala Arg Asp Pro Asn Phe Asn
195 200 205

Leu Lys Ala Cys Leu His Ser Ala Tyr Val His Pro Ile Phe Lys Gly
210 215 220

Asp Asp Asp Asp Glu Asp Asp Leu Ser Val Glu Met Glu Thr Glu Ser
225 230 235 240

Val Leu Val Pro Thr Lys Arg Gln Ser Gln Arg Asn Thr Pro Val Pro
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Ser Lys Ile Ser Gly Gly Tyr Ser Pro Ser Leu Pro Glu Ala Val Lys
260 265 270

Asn Gly Glu Leu
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<210> 474
<211> 2438
<212> DNA
<213> Populus trichocarpa

<400> 474
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caacctttca atgatagggg ttactttccg aaatgggtatc tcaagggctt aagaaacagt 180
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tgggggtgcag cagtttgtgc acaaactcaa caatcaagaa atccaacttt gtggttaaca 1080
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PF59082PF60142_PCT_SEQ_LIST.txt

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 <211> 775
 <212> PRT
 <213> Populus trichocarpa

<400> 475

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Phe Asn Asp Arg Val Tyr Phe Pro Lys Trp Tyr Leu Lys Gly Leu Arg
 35 40 45

Asn Ser Pro Ser Arg Ser Arg Ala Leu Val Ser Arg Phe Val Asn Leu
 50 55 60

Asp Cys Arg Ser Tyr Ile Gln Phe Leu Asn Trp Met Pro Gln Ala Leu

				70				75				80			
Lys	Met	Pro	Glu	Pro ₈₅	Glu	Leu	Ile	Asp	His ₉₀	Ala	Gly	Leu	Asp	Ser ₉₅	Ala
Val	Tyr	Leu	Arg ₁₀₀	Ile	Tyr	Leu	Met	Gly ₁₀₅	Leu	Lys	Ile	Phe	Val ₁₁₀	Pro	Ile
Thr	Ile	Leu ₁₁₅	Ala	Trp	Val	Val	Leu ₁₂₀	Val	Pro	Val	Asn	Tyr ₁₂₅	Thr	Asn	Asn
Ala	Leu ₁₃₀	Glu	Ala	Glu	Lys	Met ₁₃₅	Ala	Ala	Asn	Val	Thr ₁₄₀	Ala	Ser	Asp	Ile
Asp ₁₄₅	Lys	Leu	Ser	Ile	Ser ₁₅₀	Asn	Val	Pro	Leu	Lys ₁₅₅	Ser	Gln	Arg	Phe	Trp ₁₆₀
Ala	His	Ile	Val	Met ₁₆₅	Ala	Tyr	Ala	Phe	Thr ₁₇₀	Phe	Trp	Thr	Cys	Tyr ₁₇₅	Val
Leu	Leu	Lys	Glu ₁₈₀	Tyr	Glu	Lys	Val	Ala ₁₈₅	Ser	Met	Arg	Leu	Gln ₁₉₀	Phe	Leu
Ser	Ser	Glu ₁₉₅	Arg	Arg	Arg	Pro	Asp ₂₀₀	Gln	Phe	Thr	Val	Leu ₂₀₅	Val	Arg	Asn
Val	Pro ₂₁₀	Pro	Asp	Pro	Asp	Glu ₂₁₅	Ser	Val	Ser	Glu	Leu ₂₂₀	Val	Glu	His	Phe
Phe ₂₂₅	Leu	Val	Asn	His	Pro ₂₃₀	Asp	His	Tyr	Leu	Thr ₂₃₅	Gln	Gln	Val	Val	Cys ₂₄₀
Asn	Ala	Asn	Asn	Leu ₂₄₅	Ala	Ser	Leu	Val	Lys ₂₅₀	Lys	Asn	Glu	Gly	Met ₂₅₅	Gln
Asn	Trp	Leu	Asp ₂₆₀	Tyr	Tyr	Arg	Phe	Lys ₂₆₅	Tyr	Ser	Arg	Asn	Arg ₂₇₀	Ser	Gln
Arg	Pro	Gln ₂₇₅	Thr	Lys	Thr	Gly	Phe ₂₈₀	Leu	Gly	Leu	Trp	Gly ₂₈₅	Ala	Lys	Val
Asp	Ala ₂₉₀	Ile	Asp	Tyr	Tyr	Ile ₂₉₅	Ser	Glu	Ile	Glu	Lys ₃₀₀	Leu	Ser	Lys	Glu
Ile ₃₀₅	Thr	Glu	Glu	Arg	Glu ₃₁₀	Lys	Val	Leu	Asn	Asp ₃₁₅	Pro	Asn	Cys	Ile	Met ₃₂₀
Pro	Ala	Ala	Phe	Val ₃₂₅	Ser	Phe	Lys	Thr	Arg ₃₃₀	Trp	Gly	Ala	Ala	Val ₃₃₅	Cys
Ala	Gln	Thr	Gln ₃₄₀	Gln	Ser	Arg	Asn	Pro ₃₄₅	Thr	Leu	Trp	Leu	Thr ₃₅₀	Glu	Trp

PF59082PF60142_PCT_SEQ_LIST.txt

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Val Ser Leu Ser Val Arg Arg Leu Ile Ile Gly Val Ser Phe Phe Phe
370 375 380

Leu Ala Phe Phe Phe Met Ile Pro Ile Ala Phe Val Gln Ser Leu Ala
385 390 395 400

Ser Ile Glu Gly Ile Glu Lys Ser Leu Pro Phe Leu Lys Pro Val Ile
405 410 415

Glu Val Glu Phe Ile Lys Ser Val Val Gln Gly Phe Leu Pro Gly Ile
420 425 430

Ala Leu Lys Leu Phe Leu Ile Leu Leu Pro Thr Leu Leu Met Met Met
435 440 445

Ser Lys Phe Glu Gly Leu Thr Ser Leu Ser Ser Leu Glu Arg Arg Ser
450 455 460

Ala Met Arg Tyr Tyr Ile Phe Ile Ile Ile Asn Val Phe Leu Gly Ser
465 470 475 480

Ile Leu Thr Gly Ala Ala Phe Glu Gln Leu Asp Ser Phe Ile Lys Gln
485 490 495

Ser Ala Ser Glu Ile Pro Lys Thr Ile Gly Val Ala Ile Pro Met Lys
500 505 510

Ala Thr Phe Phe Ile Thr Tyr Ile Met Val Asp Gly Trp Ala Gly Ile
515 520 525

Ala Gly Glu Val Leu Met Leu Lys Pro Leu Ile Ile Tyr His Leu Lys
530 535 540

Asn Phe Phe Leu Val Lys Thr Glu Lys Asp Arg Lys Glu Ala Met Asp
545 550 555 560

Ala Gly Ser Leu Gly Phe Asn Thr Gly Glu Pro Arg Ile Gln Leu Tyr
565 570 575

Phe Leu Leu Gly Leu Val Tyr Ala Pro Val Thr Pro Ile Leu Leu Pro
580 585 590

Phe Ile Val Met Phe Phe Gly Phe Ala Tyr Val Val Tyr Arg His Gln
595 600 605

Ile Ile Asn Val Tyr Asn Gln Glu Tyr Glu Ser Gly Ala Ala Phe Trp
610 615 620

PF59082PF60142_PCT_SEQ_LIST.txt

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Leu Met Met Gly Leu Leu Ser Thr Lys Gln Ala Ser Ser Thr Thr Pro
645 650 655

Phe Leu Ile Ala Leu Pro Val Leu Thr Ile Trp Phe His Val Phe Cys
660 665 670

Asn Gly Arg Tyr Lys Ser Ala Phe Val Lys Tyr Pro Leu Gln Glu Ala
675 680 685

Met Met Lys Asp Ser Leu Glu Arg Ala Ser Ser Pro Asn Phe Asn Phe
690 695 700

Arg Ser Tyr Leu Glu Lys Ala Tyr Val His Pro Val Phe Lys Gly Asp
705 710 715 720

Gly Asn Asp Asp Asp Tyr Glu Gln Tyr Leu Ser Glu Asn Gln Glu Ala
725 730 735

Asp Ala Glu Asn Val Leu Val Pro Thr Arg Arg His Ser Arg Arg Asn
740 745 750

Ser Pro Ala Val Ser Arg Ala Ala Ser Pro Ala Leu Ser Glu Glu Val
755 760 765

Gln Ser Val Glu His Arg Val
770 775

<210> 476
<211> 2435
<212> DNA
<213> Populus trichocarpa

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caacccttca atgatagagt ttactttcca aaatggatc tgaagggtt aagaagcagc 180
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PF59082PF60142_PCT_SEQ_LIST.txt

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<210> 477

<211> 774

<212> PRT

<213> Populus trichocarpa

<400> 477

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Ser Ser Pro Ser Arg Ser Gly Ala Phe Val Arg Arg Val Val Asn Leu
50          55          60
Asp Phe Arg Ser Tyr Ile Arg Phe Leu Asn Trp Met Pro Glu Ala Leu
65          70          75          80
Lys Met Pro Glu Pro Glu Leu Ile Asp His Ala Gly Leu Asp Tyr Ala
85          90          95
Val Tyr Leu Arg Ile Tyr Leu Met Gly Leu Lys Ile Phe Val Pro Ile
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Thr Phe Leu Ala Trp Ala Ile Leu Val Pro Val Asn Tyr Thr Asn Asp
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Thr His Ile Val Met Ala Tyr Ala Phe Thr Phe Trp Thr Cys Tyr Val
165         170         175
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180         185         190
Ser Ser Glu Arg Arg Arg Pro Asp Gln Phe Thr Val Leu Val Arg Asn
195         200         205
Val Pro Pro Asp Pro Asp Glu Thr Val Ser Glu Leu Val Glu His Phe
210         215         220
Phe Leu Val Asn His Pro Asp His Tyr Leu Thr His Arg Val Val Cys
225         230         235         240
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245         250         255
Asn Trp Leu Asp Tyr Tyr Gln Leu Lys Tyr Ser Arg Asn Gln Ser Gln
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Arg Pro Gln Met Lys Thr Gly Phe Leu Gly His Phe Gly Gly Lys Val
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PF59082PF60142_PCT_SEQ_LIST.txt

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 Ala Pro Glu Pro Arg Asp Val Tyr Trp Gln Asn Leu Ala Ile Pro Tyr
 355 360 365
 Met Ser Leu Lys Val Lys Arg Leu Ile Ile Gly Val Ala Phe Phe Phe
 370 375 380
 Leu Thr Phe Phe Phe Met Ile Pro Ile Ala Ser Val Gln Ala Leu Ala
 385 390 395 400
 Ser Ile Glu Gly Ile Glu Lys Arg Ala Pro Phe Leu Lys Ser Val Ile
 405 410 415
 Glu Ile Lys Phe Ile Lys Ser Val Ile Gln Gly Phe Leu Pro Gly Ile
 420 425 430
 Ala Leu Lys Leu Phe Leu Ile Phe Leu Pro Thr Ile Leu Met Ile Met
 435 440 445
 Ser Lys Phe Glu Gly Phe Val Ser Leu Ser Ser Leu Glu Arg Arg Ser
 450 455 460
 Ala Thr Arg Tyr Tyr Ile Phe Leu Ile Ile Asn Val Phe Leu Gly Ser
 465 470 475 480
 Ile Leu Thr Gly Ala Ala Phe Asp Gln Leu Asn Ala Phe Ile Asn Gln
 485 490 495
 Ser Ala Asn Glu Ile Pro Lys Thr Ile Gly Val Ala Val Pro Met Lys
 500 505 510
 Ala Thr Phe Phe Ile Thr Tyr Ile Met Val Asp Gly Trp Ala Gly Ile
 515 520 525
 Ala Gly Glu Val Leu Met Leu Lys Pro Leu Ile Phe Tyr His Leu Lys
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 545 550 555 560

PF59082PF60142_PCT_SEQ_LIST.txt

Pro Gly Ser Leu Gly Phe His Thr Gly Glu Pro Arg Ile Gln Leu Tyr
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580 585 590

Phe Ile Val Ile Phe Phe Ala Phe Ala Tyr Leu Val Phe Arg His Gln
595 600 605

Ile Ile Asn Val Tyr Asn His Glu Tyr Glu Ser Gly Ala Ala Phe Trp
610 615 620

Pro Asp Val His Gly Arg Val Ile Thr Ala Leu Val Ile Ser Gln Leu
625 630 635 640

Ala Leu Met Gly Leu Met Ser Thr Lys Glu Ala Ala Gln Ser Thr Pro
645 650 655

Phe Leu Ile Ala Leu Pro Val Leu Thr Ile Trp Phe His Arg Phe Cys
660 665 670

Asn Gly Arg His Lys Ser Ala Phe Val Lys Tyr Pro Leu Gln Glu Ala
675 680 685

Met Met Lys Asp Thr Leu Glu Arg Ala Arg Asp Pro Asn Phe Asn Leu
690 695 700

Lys Ala Tyr Leu Gln Ser Ala Tyr Val His Pro Val Phe Lys Gly Gly
705 710 715 720

Asp Asp Asp Ile Asp Glu Asp Asp Leu Leu Ser Gly Lys Met Glu Thr
725 730 735

Glu Ser Val Leu Val Pro Thr Lys Arg Gln Ser Arg Arg Asn Thr Pro
740 745 750

Ala Pro Ser Lys Ile Ser Gly Gly Ser Ser Pro Ser Leu Pro Glu Thr
755 760 765

Val Lys Asn Gly Glu Pro
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<210> 478
<211> 2606
<212> DNA
<213> Populus trichocarpa

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caacccatca atgacagagt ttactttccg aagtgggtaca ttagtggagg aaggagcaac 180

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<211> 831
<212> PRT
<213> Populus trichocarpa
<400> 479

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Ser Asn Pro Arg Arg Ala Gly Asn Phe Val Gly Lys Phe Val Asn Leu
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Asn Val Lys Thr Tyr Phe Thr Phe Leu Asn Trp Met Pro Gln Ala Leu
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Lys Met Thr Glu Ala Glu Ile Ile Asn His Ala Gly Leu Asp Ser Ala
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Val Phe Leu Arg Ile Tyr Thr Leu Gly Leu Lys Ile Phe Val Pro Ile
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Thr Ile Leu Ala Leu Leu Ile Leu Ile Pro Val Asn Val Ser Ser Gly
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Thr Leu Phe Phe Leu Arg Lys Glu Leu Val Met Ser Asp Ile Asp Lys
130 135 140

Leu Ser Ile Ser Asn Val Arg Pro Gln Ser Ile Arg Gln Val Phe Ala
145 150 155 160

Phe Ala Tyr Glu Glu Lys Gly Lys Ser Met Ile Met Phe Phe Ile His
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Ile Ala Leu Glu Tyr Ala Phe Thr Ile Trp Ile Cys Phe Met Leu Tyr
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PF59082PF60142_PCT_SEQ_LIST.txt

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 260 265 270
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 275 280 285
 Thr Arg Lys Asn Gly Phe Leu Gly Leu Trp Gly Glu Arg Val Asp Ser
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 Ile Glu His Tyr Lys Gln Gln Met Lys His Leu Glu Lys Asn Met Ala
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 Ser Phe Val Ser Phe Asn Ser Arg Trp Gly Ala Ala Val Cys Ala Gln
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 Thr Gln Gln Ser Lys Asn Pro Thr Leu Trp Leu Thr Asn Trp Ala Pro
 355 360 365
 Glu Pro Arg Asp Ile Tyr Trp Arg Asn Leu Ala Ile Pro Phe Met Ser
 370 375 380
 Leu Thr Val Arg Lys Leu Ile Ile Ser Val Thr Val Phe Ala Leu Val
 385 390 395 400
 Phe Phe Tyr Met Ile Pro Ile Ala Phe Val Gln Ser Leu Ala Asn Leu
 405 410 415
 Glu Gly Leu Glu Lys Val Ala Pro Phe Leu Arg Pro Val Ile Glu Leu
 420 425 430
 Lys Phe Ile Lys Ser Phe Leu Gln Gly Phe Leu Pro Gly Leu Ala Leu
 435 440 445
 Lys Ile Phe Leu Tyr Ile Leu Pro Thr Val Leu Met Ile Met Ser Lys
 450 455 460
 Ile Glu Gly Tyr Ile Ala His Ser Thr Leu Glu Arg Arg Ala Ala Ala
 Seite 506

465 470 475 480
 Lys Tyr Tyr Tyr Phe Met Leu Val Asn Val Phe Leu Gly Ser Ile Ile
 485 490 495
 Ala Gly Thr Ala Phe Glu Gln Leu Asp Ala Phe Leu His Gln Ser Pro
 500 505 510
 Thr Gln Ile Pro Arg Thr Ile Gly Val Ser Ile Pro Met Lys Ala Thr
 515 520 525
 Phe Phe Ile Thr Tyr Ile Met Val Asp Gly Trp Ala Gly Ile Ala Gly
 530 535 540
 Glu Ile Leu Arg Leu Lys Pro Leu Ile Ile Phe His Leu Lys Asn Met
 545 550 555 560
 Phe Leu Val Lys Thr Glu Arg Asp Ile Glu Arg Ala Met Asp Pro Gly
 565 570 575
 Ser Val Asp Phe Pro Glu Thr Leu Pro Ser Leu Gln Leu Tyr Phe Leu
 580 585 590
 Leu Gly Ile Val Tyr Ala Val Val Thr Pro Ile Leu Leu Pro Phe Val
 595 600 605
 Leu Val Phe Phe Ala Phe Ala Tyr Leu Val Tyr Arg His Gln Ile Val
 610 615 620
 Asn Val Tyr Asn Gln Gln Tyr Glu Ser Ala Ala Ala Phe Trp Pro His
 625 630 635 640
 Val His Ser Arg Ile Ile Ala Ser Leu Leu Ile Ser Gln Leu Leu Leu
 645 650 655
 Leu Gly Leu Leu Ser Thr Lys Lys Ala Ala Asn Ser Thr Pro Leu Leu
 660 665 670
 Val Ile Leu Pro Val Leu Thr Leu Ser Phe His Lys Tyr Cys Lys Ile
 675 680 685
 Arg Phe Glu Pro Ala Phe Arg Lys Tyr Pro Leu Glu Glu Ala Met Ala
 690 695 700
 Lys Asp Ile Thr Asp Arg Thr Ala Glu Ser Asp Met Asn Leu Lys Ala
 705 710 715 720
 Tyr Leu Ala Asp Ala Tyr Leu His Pro Ile Phe Arg Ser Phe Glu Glu
 725 730 735
 Pro Leu Val Glu Val Lys Val Glu Lys Asn Lys Pro Gln Thr Ala Ser
 740 745 750

PF59082PF60142_PCT_SEQ_LIST.txt

Asp Arg Ile Ser Glu Leu Ser Ser Pro Ser Pro Pro His Gln Val Asn
755 760 765

His Pro Ser Ser Pro Pro His Gln Val Asn His Pro Ser Ser Pro Pro
770 775 780

His Tyr Val Tyr His Pro Ser Ser Pro Pro Gln His Val Tyr Asp Pro
785 790 795 800

Ser Ser Pro Ser His Tyr Ala Tyr His Tyr Glu Asn Asp Ile Phe His
805 810 815

Ala Pro Thr Pro Pro His Tyr Ala Tyr His Tyr Glu Asn Glu Pro
820 825 830

<210> 480
<211> 2285
<212> DNA
<213> Populus trichocarpa

<400> 480
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cctggaaact cttcgtgta ttacccaac cggatcttga aaggctctgga accctgggat 180
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gacaagttat taatgggaaa tgttaagggg gggagtccaa ggctgtgggc attcttgatt 480
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PF59082PF60142_PCT_SEQ_LIST.txt

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<210> 481
<211> 724
<212> PRT
<213> Populus trichocarpa
<400> 481

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20 25 30

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

Trp Asp Gly Ala Ser Arg Ser Arg Asn Pro Phe Ala Trp Ile Arg Glu
50 55 60

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

Thr Ala Val Tyr Phe Val Phe Leu Ser Thr Ala Leu Ala Ile Leu Val
85 90 95

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Ser Gly Leu Val Leu Leu Pro Val Leu Leu Pro Val Ala Ala Thr
100 105 110

Asp Asp Asn Val Lys Thr Gln Lys Asp Lys Gly Asn Gln Ser Phe Ser
115 120 125

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

Leu Trp Ala Phe Leu Ile Ala Thr Tyr Trp Val Ser Leu Val Thr Tyr
145 150 155 160

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

Ala Leu Met Ser Pro Glu Leu Thr Pro Glu Gln Phe Ala Val Leu Val
180 185 190

Arg Asp Ile Pro Pro Val Pro Glu Gly Arg Thr Arg Lys Glu Gln Val
195 200 205

Asp Ser Tyr Phe Lys Ser Ile Tyr Pro Glu Thr Phe Tyr Arg Ser Met
210 215 220

Val Val Thr Asn Asn Lys Glu Val Asn Lys Ile Tyr Ile Glu Leu Glu
225 230 235 240

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

Lys Lys Thr Gly Lys Pro Glu Gly Leu Arg Pro Thr Ile Arg Thr Gly
260 265 270

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

Glu Lys Ile Lys Glu Leu Ile Pro Lys Leu Glu Ala Glu Gln Lys Val
290 295 300

Thr Leu Arg Glu Asn Gln Gln Ala Cys Ala Phe Ala Phe Phe Thr Asn
305 310 315 320

Arg Val Thr Ala Ala Ser Ala Ala Gln Ser Leu His Ala Gln Met Val
325 330 335

Asp Thr Trp Thr Val Met Glu Ala Pro Glu Pro Arg Gln Ile Ile Trp
340 345 350

Ser Asn Leu Lys Ile Lys Tyr Phe Gln Arg Ile Ile Arg Gln Tyr Val
355 360 365

Val Cys Phe Ile Val Ala Leu Thr Ile Leu Phe Tyr Met Ile Pro Ile

370

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

Pro Phe Leu Lys Pro Ile Val Asn Ile Val Ala Val Lys Thr Val Leu
405 410 415

Glu Ala Tyr Leu Pro Gln Ile Ala Leu Ile Val Phe Leu Ala Leu Leu
420 425 430

Pro Lys Leu Leu Leu Ala Leu Ser Lys Ala Glu Gly Ile Pro Ser Val
435 440 445

Gly His Ala Val Arg Ala Thr Ser Gly Lys Tyr Phe Tyr Phe Thr Ile
450 455 460

Leu Asn Val Phe Ile Gly Val Thr Leu Gly Gly Thr Leu Phe Thr Thr
465 470 475 480

Phe Lys Ser Ile Glu Glu Lys Pro Asn Ser Ile Val Ser Leu Leu Ala
485 490 495

Ser Ser Leu Pro Gly Asn Ala Thr Phe Phe Leu Thr Phe Val Ala Leu
500 505 510

Lys Phe Phe Val Gly Tyr Gly Leu Glu Leu Ser Arg Ile Val Pro Leu
515 520 525

Ile Ile Phe His Leu Lys Lys Lys Tyr Leu Cys Lys Thr Glu Ala Glu
530 535 540

Leu Lys Glu Ala Trp Phe Pro Gly Asp Leu Gly Tyr Ala Thr Arg Ile
545 550 555 560

Pro Gly Asp Met Leu Val Leu Thr Ile Val Leu Cys Tyr Ser Val Ile
565 570 575

Ala Pro Leu Ile Ile Pro Phe Gly Val Val Tyr Phe Gly Leu Gly Trp
580 585 590

Leu Val Leu Arg Asn Gln Ala Leu Lys Val Tyr Ala Pro Ser Phe Glu
595 600 605

Thr Tyr Gly Arg Met Trp Pro His Ile His Thr Arg Val Ile Ala Ala
610 615 620

Leu Ile Leu Phe Gln Val Thr Met Phe Gly Tyr Phe Val Val Lys Lys
625 630 635 640

Phe Ser Phe Ser Thr Phe Leu Leu Ile Pro Leu Pro Ile Leu Ser Leu
645 650 655

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Phe Ala Tyr Val Cys His Lys Lys Phe Tyr Arg Ser Phe Ser Asp
660 665 670

Thr Ala Leu Glu Val Ala Cys Arg Glu Leu Lys Glu Ile Pro Asn Met
675 680 685

Glu Arg Ile Tyr Arg Ser Phe Ile Pro Pro Ser Leu Ser Ser Glu Lys
690 695 700

Ala Asp Asp Asp His Phe Glu Asp Ala Leu Ser Gln Val Ser Arg Val
705 710 715 720

Gly Ser Phe Ala

<210> 482
<211> 2231
<212> DNA
<213> Populus trichocarpa

<400> 482
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ccaagcaaca cgatttgtta tttcggggcgg aggcttgctt ctttaaacia cagaaatagc 180
agaaatcatt tctccttcga aaggttttgtg ccctctccca gttggatcgt caaggcatgg 240
gaaacaacag aaaatgaaat cttggccatt ggtggccttg atgctgtggt tttccagagg 300
atacttgttt tcagttgtat acagtatcag agtcttttct attgcagctg ttacgtgtct 360
gttcctggtg cttccagtga attattatgg gcaggagatg aaacacaagc atatccatgc 420
cgagtccctc aatgtattta caattgcaaa tgtgaaagaa ggctccagat ggctttgggc 480
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tgtaccaatg tgtaagatt attaacaaca ccccttctc tccaggaata caaaagcatc 600
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gtacaaggct tgactcaact agagaagctg tcacaaacat ttccttttct gagagggttt 1260

PF59082PF60142_PCT_SEQ_LIST.txt

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 tgaagagaag t 2231

<210> 483
 <211> 706
 <212> PRT
 <213> Populus trichocarpa
 <400> 483

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

Asn Thr Ile Val Tyr Phe Gly Arg Arg Leu Ala Ser Leu Asn Asn Arg
 35 40 45

Asn Ser Arg Asn His Phe Ser Phe Glu Arg Phe Val Pro Ser Pro Ser
 50 55 60

Trp Ile Val Lys Ala Trp Glu Thr Thr Glu Asn Glu Ile Leu Ala Ile
 65 70 75 80

Gly Gly Leu Asp Ala Val Val Phe Gln Arg Ile Leu Val Phe Ser Cys
 85 90 95

Ile Gln Tyr Gln Ser Leu Phe Tyr Cys Ser Cys Tyr Val Ser Val Pro
 100 105 110

PF59082PF60142_PCT_SEQ_LIST.txt

Gly Ala Ser Ser Glu Leu Leu Trp Ala Gly Asp Glu Thr Gln Ala Tyr
115 120 125

Pro Cys Arg Val Pro Gln Cys Ile Tyr Asn Cys Lys Cys Glu Arg Arg
130 135 140

Leu Gln Met Ala Leu Gly Thr Leu Ser Arg Ile Ile Tyr His Ile Leu
145 150 155 160

Leu Ser Leu Cys Ser Ser Leu Leu Phe Val Cys Thr Asn Val Leu Arg
165 170 175

Leu Leu Thr Thr Pro Pro Ser Leu Gln Glu Tyr Lys Ser Ile Thr Lys
180 185 190

Met Arg Leu Ala His Ile Thr Thr Ser Pro Pro Asn Pro Ser His Phe
195 200 205

Thr Ile Leu Val Arg Ser Ile Pro Tyr Ser Val Gly Glu Ser Tyr Ser
210 215 220

Asn Ser Val Lys Lys Phe Phe Thr Asn Tyr Tyr Ala Ser Ser Tyr Leu
225 230 235 240

Ser His Gln Ile Val Tyr Arg Cys Gly Leu Val Gln Lys Leu Met Val
245 250 255

Asp Ala Glu Lys Ile Cys Met Arg Ile Lys Ala Ala Pro Lys Gly Gln
260 265 270

Ser Ser Leu Lys Pro Cys Cys Leu Cys Gly Gly Ser Thr Ser Phe Lys
275 280 285

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

Asn Leu Asn Leu Ala Thr Arg Asp Asn Glu Arg Ser Ala Ala Phe Val
305 310 315 320

Ile Phe Lys Thr Arg Tyr Ala Ala Val Val Ala Thr Gln Met Leu Gln
325 330 335

Ser Pro Asn Pro Met Ser Trp Val Thr Glu Leu Ala Pro Glu Pro His
340 345 350

Asp Val Leu Trp Ser Asn Leu Cys Ile Pro Phe Arg Gln Leu Trp Leu
355 360 365

Arg Lys Ile Ala Thr Leu Leu Ala Ser Ile Val Phe Met Val Leu Phe
370 375 380

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Ala Pro Val Thr Phe Val Gln Gly Leu Thr Gln Leu Glu Lys Leu
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 405 410 415
 Ile Pro Val Glu Leu Ala Lys Ala Ile Pro Asn Gln Ala Ser Phe Phe
 420 425 430
 Val Thr Tyr Val Leu Thr Ser Gly Trp Ala Ser Leu Ser Cys Glu Val
 435 440 445
 Met Gln Pro Phe Ser Leu Leu Cys Asn Phe Leu Lys Lys His Leu Leu
 450 455 460
 Arg Asn His Glu Asp Ser Ser Asp Gly Leu Val Ser Phe Pro Tyr His
 465 470 475 480
 Thr Glu Val Pro Arg Val Leu Leu Phe Gly Leu Ile Gly Phe Thr Tyr
 485 490 495
 Ser Val Met Ala Pro Leu Ile Leu Pro Phe Leu Leu Ile Tyr Phe Leu
 500 505 510
 Leu Ala Tyr Leu Val Tyr Arg Asn Gln Ile Val Asn Val Tyr Ile Thr
 515 520 525
 Lys Tyr Glu Gly Gly Gly Gln Leu Trp Pro Ile Val His Asn Thr Thr
 530 535 540
 Ile Phe Ser Leu Val Leu Thr Gln Met Ile Ser Leu Gly Val Phe Gly
 545 550 555 560
 Ile Lys Lys Ser Pro Val Ala Ser Gly Phe Thr Ile Pro Leu Ile Ile
 565 570 575
 Cys Thr Leu Leu Phe Asn Glu Tyr Cys Arg Gln Arg Phe Phe Pro Ile
 580 585 590
 Phe Lys Lys Asn Val Ala Gln Val Ile Met Arg Asn Trp Phe Ala Phe
 595 600 605
 Glu Ser Leu Ser Ser Cys Leu Ser Lys Val Asn Lys Leu Phe Cys Pro
 610 615 620
 Val Gln Val Leu Leu Glu Met Asp Arg Arg Asp Glu Gln Ser Gly Arg
 625 630 635 640
 Met Glu Glu Ile His Gln Gln Leu His Ser Ala Tyr Cys Gln Leu Pro
 645 650 655

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Thr Ser His Glu Phe Cys Glu Ser Val His Lys Leu Cys Gln Asp
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Asn Ile Arg Gly Arg Glu Gly Thr Lys Ser Gly Lys Glu Pro Ser Glu
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Val Ser Glu Pro Cys Ala Val Cys Asn Phe Gly Lys Glu Gly Ser Ile
690 695 700

Gly Glu
705

<210> 484
<211> 2414
<212> DNA
<213> Populus trichocarpa

<400> 484
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PF59082PF60142_PCT_SEQ_LIST.txt

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<210> 485
<211> 767
<212> PRT
<213> Populus trichocarpa
<400> 485

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Thr Ala Phe Ala Phe Phe Phe Ala Phe Ala Ile Leu Arg Ile Gln Pro
          20          25          30

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Val Asn Asp Arg Val Tyr Phe Pro Lys Trp Tyr Ile Lys Gly Leu Arg
          35          40          45

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

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Asp Phe Arg Ser Tyr Val Arg Phe Leu Asn Trp Met Pro Ala Ala Leu
65          70          75          80

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His Met Pro Glu Pro Glu Leu Ile Asp His Ala Gly Leu Asp Ser Ala
          85          90          95

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Val Tyr Leu Arg Ile Tyr Leu Ile Gly Leu Lys Ile Phe Val Pro Ile
          100          105          110

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PF59082PF60142_PCT_SEQ_LIST.txt

Ala Phe Leu Ala Phe Thr Ile Leu Val Pro Val Asn Trp Thr Asn Ser
115 120 125

Thr Leu Glu Arg Ser Asn Leu Thr Tyr Ser Asp Leu Asp Lys Leu Ser
130 135 140

Ile Ser Asn Ile Pro Thr Gly Ser Asn Arg Phe Trp Thr His Leu Val
145 150 155 160

Met Ala Tyr Ala Ser Thr Phe Trp Thr Cys Tyr Val Leu Lys Lys Glu
165 170 175

Tyr Glu Ile Val Ala Lys Met Arg Leu His Phe Leu Ala Ser Glu Lys
180 185 190

Arg Arg Pro Asp Gln Phe Thr Val Leu Val Arg Asn Val Pro Pro Asp
195 200 205

Ala Asp Glu Ser Val Ser Glu Leu Val Glu His Phe Phe Leu Val Asn
210 215 220

His Pro Asn Asp Tyr Leu Thr Tyr Gln Val Val Tyr Asn Ala Asn Gln
225 230 235 240

Leu Ser His Leu Val Asn Glu Lys Lys Lys Met Lys Asn Trp Leu Asp
245 250 255

Tyr Tyr Gln Ile Lys Tyr Ser Arg Asn Lys Ser Arg Met Pro Ser Leu
260 265 270

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

His Tyr Thr Ser Glu Ile Glu Arg Leu Ser Arg Lys Ile Ser Leu Glu
290 295 300

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

Val Ser Phe Lys Thr Arg Trp Gly Ala Ala Val Cys Ala Gln Thr Gln
325 330 335

Gln Ser Arg Asn Pro Ala Met Trp Leu Thr Glu Trp Ala Pro Glu Pro
340 345 350

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

Leu Arg Arg Leu Val Ile Ala Val Thr Phe Phe Phe Leu Thr Phe Phe
370 375 380

PF59082PF60142_PCT_SEQ_LIST.txt

Phe Met Val Pro Ile Ala Phe Val Gln Ser Leu Ala Asn Ile Glu Gly
 385 390 395 400
 Ile Glu Lys Ala Leu Pro Phe Leu Lys Pro Ile Ile Glu Met Lys Val
 405 410 415
 Ile Lys Ser Phe Ile Gln Gly Phe Leu Pro Gly Ile Ala Leu Lys Ile
 420 425 430
 Phe Leu Ile Phe Leu Pro Ser Ile Leu Met Leu Met Ser Lys Phe Glu
 435 440 445
 Gly Phe Ile Ser Ile Ser Gly Leu Glu Arg Arg Ser Ala Ala Arg Tyr
 450 455 460
 Tyr Ile Phe Gln Phe Ile Asn Val Phe Leu Gly Ser Ile Ile Thr Gly
 465 470 475 480
 Thr Ala Phe Gln Gln Leu Asp Asn Phe Ile His Gln Ser Ala Thr Glu
 485 490 495
 Ile Pro Lys Thr Ile Gly Val Ser Ile Pro Met Lys Ala Thr Phe Phe
 500 505 510
 Ile Thr Tyr Ile Met Val Asp Gly Trp Ala Gly Val Ala Gly Glu Ile
 515 520 525
 Leu Arg Leu Lys Pro Leu Ile Ile Tyr His Leu Lys Met Phe Phe Met
 530 535 540
 Val Lys Thr Glu Lys Asp Met Glu Glu Ala Met Asp Pro Gly Thr Leu
 545 550 555 560
 Gly Phe Asn Thr Gly Glu Pro Gln Ile Gln Leu Tyr Phe Leu Leu Gly
 565 570 575
 Leu Val Tyr Ala Val Val Ser Pro Ile Leu Leu Pro Phe Ile Ile Val
 580 585 590
 Phe Phe Ala Leu Ala Phe Val Val Tyr Arg His Gln Ile Ile Asn Val
 595 600 605
 Tyr Asn Gln Glu Tyr Glu Ser Ala Ala Ala Phe Trp Pro Asp Val His
 610 615 620
 Gly Arg Ile Ile Val Ala Val Ile Val Ser Gln Leu Leu Leu Met Gly
 625 630 635 640
 Leu Leu Ser Thr Lys Glu Ala Ala Gln Ser Thr Pro Leu Leu Ile Thr
 645 650 655

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Pro Val Leu Thr Ile Trp Phe His Leu Phe Cys Lys Gly Arg Tyr
660 665 670

Glu Pro Ala Phe Val Arg Tyr Pro Leu Gln Glu Ala Met Met Lys Asp
675 680 685

Thr Leu Glu Arg Ala Lys Glu Pro Asn Leu Asn Leu Lys Ser Phe Leu
690 695 700

Gln Asn Ala Tyr Ile His Pro Val Phe Lys Gly Glu Asp Asp Ser Asp
705 710 715 720

Ser Asp Glu Ala Pro Glu Glu Phe Glu Lys Glu Pro Asp Leu Val Pro
725 730 735

Thr Lys Arg Gln Ser Arg Arg Asn Thr Pro Leu Pro Ser Lys His Gly
740 745 750

Ser Ala Ala Ser Ser Gln Pro Glu Ala Gln Asp Tyr Pro Leu Leu
755 760 765

<210> 486
<211> 2291
<212> DNA
<213> Populus trichocarpa

<400> 486
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ccttctaattg cctccattta ctacgctcgt cgcctctcca aacgacacca tgatcacttt 180
gagcagtctt tcaactcttc ccgctttctt ccttcagttg cttggattcc tcgtgctttt 240
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ctcttcaaatt ttgggatata tttctttgga atttgttctc ttattggatt agtggtactt 360
ctgccaatca atttcggtga ccaagatgaa caatctagca tctaccattc catggatcct 420
ttcacaatat caaatattag tgcagggttcg aacagggttg gtttcccatc ttgcttatgg 480
ttgttcaggc tttgggtgca ttttacgtgc ttgtggttga tatcatttta tggattatat 540
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aggcatcaac ctgatcgggtt taatgttctt gttcggcaag ttcccttctg caatgaacac 660
aacgcttatg ggtgctctgt tgatcacttc ttctctaaac atcatcctaa cagttactgt 720
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cagcaagaaa atgttcgtaa gattcgtcaa ttacagaacg aaagtatgct gaaaggaaaag 960
gagttgcctg ttgcctttgt tacattcaag tcccgacgtg gtgcagcatt agtttcccaa 1020
actcaacagc actcacatcc actcatatgg atcacggaaa tggctccaga accaagggat 1080

PF59082PF60142_PCT_SEQ_LIST.txt

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atagctaaac ttgagaaact taagaaatgg ttccccccag ccatggctat ggagctaata 1260
ccaggattaa gtcaccattat tacagggtat cttccaagtg ccattctcaa aggctttata 1320
tatgttggtc cctttgcaat gcttggcatg gctaaattag gcggttcgat ttcaaagagc 1380
aaggaggaga ttaaagcttg caatatggtt ttctactttc tcgtgggaaa tgtattcttt 1440
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ttattgctta ctataatgtt caatgagtac tgcaagatac gttttctacc tacttttcgc 2040
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ttcatggcat caaagtctac ttcctcgag ccattgggtt cttcattgtg atatcttaac 2220
attgtaattc attttcttcc tttctcttgt actttcgagt acattcacct gagttttccg 2280
aaaaattatt a 2291

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<210> 487
 <211> 726
 <212> PRT
 <213> Populus trichocarpa

<400> 487

Met Asn Pro Glu Ser Leu Thr Ala Ser Ala Ala Ile Asn Phe Gly Leu
 1 5 10 15

Ala Phe Ile Val Leu Ser Leu Phe Ser Ile Phe Lys Lys Gln Pro Ser
 20 25 30

Asn Ala Ser Ile Tyr Tyr Ala Arg Arg Leu Ser Lys Arg His His Asp
 35 40 45

His Phe Glu Gln Ser Phe Thr Leu Ser Arg Phe Leu Pro Ser Val Ala
 50 55 60

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

PF59082PF60142_PCT_SEQ_LIST.txt

Gly Gly Leu Asp Ala₈₅ Leu Ile Ile Ile Arg₉₀ Leu Phe Lys Phe Gly₉₅ Ile
 Tyr Phe Phe Gly₁₀₀ Ile Cys Ser Leu Ile₁₀₅ Gly Leu Val Val Leu₁₁₀ Leu Pro
 Ile Asn Phe₁₁₅ Gly Asp Gln Asp Glu₁₂₀ Gln Ser Ser Ile Tyr₁₂₅ His Ser Met
 Asp Pro₁₃₀ Phe Thr Ile Ser Asn₁₃₅ Ile Ser Ala Gly Ser₁₄₀ Asn Arg Leu Gly
 Phe₁₄₅ Pro Ser Cys Leu Trp₁₅₀ Leu Phe Arg Leu Trp₁₅₅ Val His Phe Thr Cys₁₆₀
 Leu Trp Leu Ile Ser₁₆₅ Phe Tyr Gly Leu Tyr₁₇₀ Leu Leu Tyr Lys Glu₁₇₅ Tyr
 Asp Gly Ile Ser₁₈₀ Val Lys Arg Ile Gln₁₈₅ Leu Leu Arg Asn Leu₁₉₀ Arg His
 Gln Pro Asp₁₉₅ Arg Phe Asn Val Leu₂₀₀ Val Arg Gln Val Pro₂₀₅ Phe Cys Asn
 Glu His₂₁₀ Asn Ala Tyr Gly Cys₂₁₅ Ser Val Asp His Phe₂₂₀ Phe Ser Lys His
 His₂₂₅ Pro Asn Ser Tyr Cys₂₃₀ Ser Tyr Gln Met Ile₂₃₅ Tyr Asp Gly Lys Asp₂₄₀
 Ile Glu Asp Leu₂₄₅ Leu His Gln Ala Lys Tyr₂₅₀ Val Ala Arg Lys Ile Glu₂₅₅
 Asp Met Arg Gly₂₆₀ Lys Leu Thr Val Lys₂₆₅ Lys Arg Asp Lys Glu₂₇₀ Ser Leu
 Leu Leu Asp₂₇₅ Val Ser Gln Glu Asp₂₈₀ Asp Val Lys Ile Ala₂₈₅ Leu Phe Glu
 Glu Lys₂₉₀ Gln Gln Glu Asn Val₂₉₅ Arg Lys Ile Arg Gln₃₀₀ Leu Gln Asn Glu
 Ser Met Leu Lys Gly Lys₃₁₀ Glu Leu Pro Val Ala₃₁₅ Phe Val Thr Phe Lys₃₂₀
 Ser Arg Arg Gly Ala₃₂₅ Ala Leu Val Ser Gln₃₃₀ Thr Gln Gln His Ser His₃₃₅
 Pro Leu Ile Trp₃₄₀ Ile Thr Glu Met Ala₃₄₅ Pro Glu Pro Arg Asp₃₅₀ Val Ser

PF59082PF60142_PCT_SEQ_LIST.txt

Trp Arg Ser₃₅₅ Leu Glu Ile Pro Phe₃₆₀ Lys Ile Leu Pro Leu₃₆₅ Cys Lys Ile

Gly Val₃₇₀ Val Val Ala Ala Ser₃₇₅ Leu Leu Thr Ile Phe₃₈₀ Phe Ala Val Pro

Val₃₈₅ Thr Ala Val Gln Gly₃₉₀ Ile Ala Lys Leu Glu₃₉₅ Lys Leu Lys Lys Trp₄₀₀

Phe Pro Pro Ala Met₄₀₅ Ala Met Glu Leu Ile₄₁₀ Pro Gly Leu Ser Ser₄₁₅ Ile

Ile Thr Gly Tyr₄₂₀ Leu Pro Ser Ala Ile₄₂₅ Leu Lys Gly Phe Ile₄₃₀ Tyr Val

Val Pro Phe₄₃₅ Ala Met Leu Gly Met₄₄₀ Ala Lys Leu Gly Gly₄₄₅ Ser Ile Ser

Lys Ser₄₅₀ Lys Glu Glu Ile Lys₄₅₅ Ala Cys Asn Met Val₄₆₀ Phe Tyr Phe Leu

Val₄₆₅ Gly Asn Val Phe Phe₄₇₀ Leu Ser Leu Ile Ser₄₇₅ Gly Ser Leu Leu Asp₄₈₀

Glu Leu Gly Glu Tyr₄₈₅ Phe Thr His Pro Arg₄₉₀ Ser Ile Pro Ser His₄₉₅ Leu

Ala Ser Ala Val₅₀₀ Ser Ser Gln Ala Asp₅₀₅ Phe Phe Val Thr Tyr₅₁₀ Ile Leu

Thr Asp Gly₅₁₅ Leu Ser Gly Phe Ser₅₂₀ Leu Glu Ile Leu Gln₅₂₅ Pro Gly Leu

Leu Val₅₃₀ Trp Asp Ala Val Lys₅₃₅ Ser His Thr Val Gly₅₄₀ Gly Ser Gly Asp

Glu₅₄₅ Glu Asn Pro Tyr Leu₅₅₀ Tyr Ser Leu Pro Tyr₅₅₅ Phe Arg Ile Ile Pro₅₆₀

ser Val Ser Leu Ser₅₆₅ Ile Leu Ile Gly Met₅₇₀ Val Tyr Ala Val Val₅₇₅ Ala

Pro Leu Leu Leu₅₈₀ Pro Phe Leu Val Gly₅₈₅ Tyr Phe Tyr Leu Gly₅₉₀ Tyr Val

Val Tyr Val₅₉₅ Asn Gln Ile Glu Asp₆₀₀ Val Tyr Glu Thr Ala₆₀₅ Tyr Asp Thr

Cys Gly₆₁₀ Gln Tyr Trp Pro Tyr₆₁₅ Val His His Tyr Ile₆₂₀ Phe Val Gly Ile

PF59082PF60142_PCT_SEQ_LIST.txt

Ile Leu Met Gln Ile Thr Met Ile Gly Leu Phe Gly Leu Lys Ser Lys
625 630 635 640

Pro Ser Ala Ser Ile Ala Thr Ile Pro Leu Leu Leu Leu Thr Ile Met
645 650 655

Phe Asn Glu Tyr Cys Lys Ile Arg Phe Leu Pro Thr Phe Arg His Tyr
660 665 670

Ser Val Lys Asp Ala Asp Glu His Asp Glu Leu Asp Arg Lys Phe Gly
675 680 685

Lys Met Glu Ile Asn Cys Glu Asn Ala Arg Ser Ala Tyr Cys Gln Pro
690 695 700

Thr Leu Gln Pro Ala Asn Phe Met Ala Ser Lys Ser Thr Ser Ser Gln
705 710 715 720

Pro Leu Val Ser Ser Leu
725

<210> 488
<211> 1661
<212> DNA
<213> Populus trichocarpa

<400> 488
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atggcatcgg agcgccaaaa aattcttgaa gactcaaaat ctatcttgcc agtttctttt 120
gtttctttta attcacgctg gggggcagct gtttgtgcac aaacacaaca aagcaagaac 180
ccaacattat ggctgacaaa ttgggctcca gaacctcgcg atatctattg gcgtaatttg 240
gctataccat tcgtgtcact gactgttcga aagcttataa tatctttgtc agtgtttgct 300
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gcagcaaagt attattactt tatgttagtg aatgtattct tggggagcat aatagctgga 600
acggcattcg agcagctgga tgctttcctt caccaatcac caaccagat tcctagaact 660
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taccgtcatc agataatcaa tgtctacaat caacaatacg agagtgtctg tgcattttgg 1020
ccacatgttc acagccgtat aattgcaagt ttattgatat ctcaactttt acttttgggc 1080

PF59082PF60142_PCT_SEQ_LIST.txt

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cttgaggaag ccatggagaa agacatatta gatcgaacta cagaatctga tataaacttg 1260
aaagcatact tggctgatgc atatttgcac ccaattttcc actcatttga ggaagaagag 1320
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accgaaatca accccccctc tccaccacat caagtcaacc atcctttttc cccaccgcat 1440
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cattatgaaa acgagccttg atattatgga ggtactaatc tacaagttca actgctaacc 1620
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<210> 489
 <211> 516
 <212> PRT
 <213> Populus trichocarpa
 <400> 489

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

Phe Asn Ser Arg Trp Gly Ala Ala Val Cys Ala Gln Thr Gln Gln Ser
 35 40 45

Lys Asn Pro Thr Leu Trp Leu Thr Asn Trp Ala Pro Glu Pro Arg Asp
 50 55 60

Ile Tyr Trp Arg Asn Leu Ala Ile Pro Phe Val Ser Leu Thr Val Arg
 65 70 75 80

Lys Leu Ile Ile Ser Leu Ser Val Phe Ala Leu Val Phe Phe Tyr Met
 85 90 95

Ile Pro Ile Ala Phe Val Gln Ser Leu Ala Asn Leu Glu Gly Leu Glu
 100 105 110

Lys Val Ala Pro Phe Leu Arg Pro Val Ile Glu Leu Lys Phe Ile Lys
 115 120 125

Ser Phe Leu Gln Gly Phe Leu Pro Gly Leu Ala Leu Lys Ile Phe Leu
 130 135 140

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

PF59082PF60142_PCT_SEQ_LIST.txt

Ile Ala His Ser Thr₁₆₅ Leu Glu Arg Arg Ala₁₇₀ Ala Ala Lys Tyr Tyr₁₇₅ Tyr

Phe Met Leu Val₁₈₀ Asn Val Phe Leu Gly₁₈₅ Ser Ile Ile Ala Gly₁₉₀ Thr Ala

Phe Glu Gln₁₉₅ Leu Asp Ala Phe Leu₂₀₀ His Gln Ser Pro Thr₂₀₅ Gln Ile Pro

Arg Thr₂₁₀ Ile Gly Val Ser Ile₂₁₅ Pro Met Lys Ala Thr₂₂₀ Phe Phe Ile Thr

Tyr₂₂₅ Ile Met Val Asp Gly₂₃₀ Trp Ala Gly Ile Ala₂₃₅ Gly Glu Ile Leu Arg₂₄₀

Leu Lys Pro Leu Ile₂₄₅ Ile Phe His Leu Lys₂₅₀ Asn Met Phe Leu Val₂₅₅ Lys

Thr Glu Arg Asp₂₆₀ Arg Glu Lys Ala Met₂₆₅ Asn Pro Gly Ser Val₂₇₀ Asp Phe

Pro Glu Thr₂₇₅ Leu Pro Ser Leu Gln₂₈₀ Leu Tyr Phe Leu Leu₂₈₅ Gly Ile Val

Tyr Ala Val Val Thr Pro Ile₂₉₅ Leu Leu Pro Phe Ile₃₀₀ Leu Val Phe Phe

Ala Phe Ala Tyr Leu Val₃₁₀ Tyr Arg His Gln Ile₃₁₅ Ile Asn Val Tyr Asn₃₂₀

Gln Gln Tyr Glu Ser₃₂₅ Ala Ala Ala Phe Trp₃₃₀ Pro His Val His Ser₃₃₅ Arg

Ile Ile Ala Ser₃₄₀ Leu Leu Ile Ser Gln₃₄₅ Leu Leu Leu Leu Gly₃₅₀ Leu Leu

Ser Thr Lys₃₅₅ Lys Ala Ala Asn Ser₃₆₀ Thr Pro Leu Leu Val₃₆₅ Ile Leu Pro

Ile Leu Thr Leu Ser Phe His₃₇₅ Lys Phe Cys Lys Ser₃₈₀ Arg Phe Glu Pro

Ala Phe Arg Arg Tyr Pro₃₉₀ Leu Glu Glu Ala Met₃₉₅ Glu Lys Asp Ile Leu₄₀₀

Asp Arg Thr Thr Glu₄₀₅ Ser Asp Ile Asn Leu₄₁₀ Lys Ala Tyr Leu Ala₄₁₅ Asp

Ala Tyr Leu His₄₂₀ Pro Ile Phe His Ser₄₂₅ Phe Glu Glu Glu Glu₄₃₀ Leu Val

Glu Val Glu Val Lys Val Glu Arg Asn Lys Ser His Thr Ala Ser Asp

435

440

445

Pro Thr Thr Glu Ile Asn Pro Pro Ser Pro Pro His Gln Val Asn His
450 455 460

Pro Phe Ser Pro Pro His Tyr Met Tyr His Pro Ser Ser Pro Pro Gln
465 470 475 480

His Val Tyr Glu Pro Ser Ser Pro Ser His Tyr Ala Tyr His Tyr Glu
485 490 495

Asn Asp Ile Tyr His Pro Pro Ser Pro Pro His Tyr Ala Tyr His Tyr
500 505 510

Glu Asn Glu Pro
515

<210> 490
<211> 1421
<212> DNA
<213> Populus trichocarpa

<400> 490
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cctggtaatt ttacgtgta tgcaccccggt ttggctgata aagagaaatc tcagccacag 180
gagagtgatg atttttactt ggaaagggtta ttgccttctg ctggttgggt tagaaatgct 240
tggcagcttt ctgaagatga aatcttgtca atttcgggtt tagatgggtct cgtgttaact 300
cggatcttca cttcagctt gaaagtgttc accgttgctg gggttattgg aatctccatc 360
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cacttttctg ctgcatatat ttttactgga gttgtctgct atcttctgta ttacgagcat 540
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gagagttttt tcacagagta tcatccttct acttatcttt cacattcaat ggttcatcga 720
acaagcaaaa ttcaagatct cattaatgat gcggacaaat tgtatagaaa gcttgactgc 780
atgaaatcaa acaaccattc tcagcaaaac ttcagacgtg atggcttttt aggactcact 840
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ttcattaaaa gatggatctt caaactggtg aactgttgct agtcaagtaa ttacaggata 1140
tcttccaagt ctattctgc agttatttct ttcttttggt ccaccaatta tgtaaacatt 1200

PF59082PF60142_PCT_SEQ_LIST.txt

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tctagtcaat gtcttccttg agcccaaaaa tattcccagg gtgctagctg aagctgtccc 1380
aggtcaggtg ggaatgcac tctgttctgt atattctttt a 1421

<210> 491
<211> 436
<212> PRT
<213> Populus trichocarpa

<400> 491
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Cys Leu Leu Phe Phe Thr Leu Tyr Ser Ile Leu Arg Lys Gln Pro Gly
20 25 30

Asn Phe Tyr Val Tyr Ala Pro Arg Leu Val Asp Lys Glu Lys Ser Gln
35 40 45

Pro Gln Glu Ser Asp Asp Phe Tyr Leu Glu Arg Leu Leu Pro Ser Ala
50 55 60

Gly Trp Val Arg Asn Ala Trp Gln Leu Ser Glu Asp Glu Ile Leu Ser
65 70 75 80

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

Leu Lys Val Phe Thr Val Ala Gly Val Ile Gly Ile Ser Ile Leu Leu
100 105 110

Pro Ile Asn Tyr Phe Gly Asn Gln Leu Ser Asp Asp Phe Gly His Leu
115 120 125

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

Ser Asn Arg Leu Trp Val His Phe Ser Ala Ala Tyr Ile Phe Thr Gly
145 150 155 160

Val Val Cys Tyr Leu Leu Tyr Tyr Glu His Asn Tyr Met Ser Ala Lys
165 170 175

Arg Ile Ala Tyr Phe Tyr Ser Ser Lys Pro Gln Pro His Gln Phe Thr
180 185 190

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

Thr Val Glu Ser Phe Phe Thr Glu Tyr His Pro Ser Thr Tyr Leu Ser
210 215 220

PF59082PF60142_PCT_SEQ_LIST.txt

His Ser Met Val His Arg Thr Ser Lys Ile Gln Asp Leu Ile Asn Asp
 225 230 235 240

Ala Asp Lys Leu Tyr Arg Lys Leu Asp Cys Met Lys Ser Asn Asn His
 245 250 255

Ser Gln Gln Asn Phe Arg Arg Asp Gly Phe Leu Gly Leu Thr Gly Arg
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Lys Val Asn Leu Leu Asp Leu Tyr Glu Lys Lys Leu Glu Asp Leu Glu
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Asp Asn Leu Arg Lys Glu Gln Asn Leu Leu Ala Gly Glu Glu Val Pro
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Ala Ala Phe Val Ser Phe Lys Ser Arg Phe Gly Ala Ala Val Ala Leu
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His Ile Gln Gln Gly Val Asn Pro Thr Glu Trp Val Thr Glu Arg Ala
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Pro Glu Pro Gln Asp Val His Trp Ala Phe Phe Ser Ala Ser Phe Ile
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Arg Ile Ser Ser Lys Ser His Ser Ala Val Ile Ser Phe Phe Cys Ser
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Thr Asn Tyr Val Asn Ile Phe Arg His Ser Arg Ile His Phe Ser Gln
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Ser Asn Arg Lys Lys Phe Leu Phe Gln Asp Ala Met Val Tyr His Met
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 <213> Populus trichocarpa

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 Val Phe Ser Phe Ala Gly Ile Ile Gly Ile Phe Ile Leu Leu Pro Val
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 180 185 190
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 Val Glu Ser Phe Phe Thr Glu Tyr Tyr Pro Thr Thr Tyr Leu Ser His
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 Glu Gln Ser Glu Val Ser Leu Ala Lys Asp Thr His Ala Ala Phe Val
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 Ser Phe Lys Thr Arg Tyr Gly Ala Ser Thr Val Phe His Leu Gln Gln
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 Ser Thr Asn Pro Thr His Trp Leu Thr Glu Glu Ala Pro Gln Pro Asn
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 Asp Val Phe Trp Pro Phe Phe Ser Ser Ser Phe Met Gly Arg Trp Ile
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 Glu Val Trp Phe Pro Phe Leu Lys Ser Ile Leu Thr Leu Ala Phe Val
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 Ser Gln Ile Val Thr Gly Tyr Leu Pro Ser Leu Ile Leu Met Leu Phe
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 Leu Lys Ile Val Pro Pro Ile Met Glu Phe Leu Ser Ser Ile Gln Gly
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 Tyr Ile Ser His Ser Glu Ile Glu Arg Ser Ala Cys Asn Lys Val Leu
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 Trp Phe Thr Val Trp Asn Ile Phe Phe Ala Thr Val Phe Ser Gly Ser
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 Val Leu Asn Gln Ile Ser Ile Ala Leu Asp Pro Lys Asn Ile Pro Thr
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 Lys Leu Ala Val Val Val Pro Ala Gln Ala Ser Phe Phe Ile Ala Tyr
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Ala Gly Lys Phe Trp Pro Ile Val His Asn Leu Val Ile Phe Ser Leu
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<212> DNA

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

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Tyr His Leu Lys Asn Ile Phe Leu Val Lys Thr Glu Lys Asp Arg Gln
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Glu Ala Met Asp Ala Gly Ser Leu Gly Phe Asn Thr Ser Glu Thr Arg
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Met Gln Leu Tyr Phe Leu Leu Gly Leu Val Asn Ala Ala Val Thr Pro
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Ile Leu Leu Pro Phe Ile Val Ile Phe Phe Ser Phe Ser Tyr Val Val
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Phe Arg His Gln Ile Ile Asn Val Tyr Asn Gln Glu Tyr Glu Ser Gly
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Ala Val Phe Trp Pro Ser Val His Gly Arg Ile Ile Thr Ala Leu Val
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<400> 497

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Ser Ser Ala Ser His Ser Gly Ala Phe Ala Arg Arg Ile Val Asn Leu
 50 55 60

Asp Phe Arg Ser Tyr Thr Arg Phe Leu Asn Trp Met Pro Glu Ala Leu
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Lys Met Pro Glu Pro Glu Leu Ile Asp His Ala Gly Leu Asp Ser Ala
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Val Tyr Leu Arg Ile Tyr Leu Met Gly Leu Lys Ile Phe Val Pro Ile
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Ala Phe Leu Ala Trp Ala Ile Leu Val Pro Val Asn Tyr Thr Asn Asp
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Thr Leu Glu Lys Ala Gln Leu Val Ser Asn Val Thr Ala Ser Asp Ile
 130 135 140

Asp Lys Leu Ser Ile Ser Asn Val Pro Leu Lys Ser Gln Arg Phe Trp
 145 150 155 160

Ala His Ile Val Met Ala Tyr Ala Phe Thr Phe Trp Thr Cys Tyr Val
 165 170 175

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 180 185 190

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

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 Arg Pro Leu₂₇₅ Lys Lys Thr Gly Phe₂₈₀ Leu Gly Leu Trp Gly₂₈₅ Glu Lys Val
 Asp Ala₂₉₀ Ile Asp His His Ile₂₉₅ Ser Glu Ile Lys Lys₃₀₀ Leu Ser Glu Glu
 Ile₃₀₅ Glu Glu Glu Arg Glu₃₁₀ Lys Val Leu Lys Asp₃₁₅ Pro Lys Ser Ile Met₃₂₀
 Pro Ala Ala Phe Val₃₂₅ Ser Phe Lys Thr Arg₃₃₀ Trp Gly Ala Ala Val₃₃₅ Cys
 Ala Gln Thr Gln₃₄₀ Gln Ser Arg Asn Pro₃₄₅ Thr Leu Trp Leu Thr₃₅₀ Glu Trp
 Ala Pro Glu₃₅₅ Pro Arg Asp Val Tyr₃₆₀ Trp Glu Asn Leu Ala₃₆₅ Ile Pro Tyr
 Met Ser₃₇₀ Leu Ser Val Arg Arg₃₇₅ Leu Ile Ile Gly Val₃₈₀ Ala Phe Phe Phe
 Leu₃₈₅ Thr Phe Phe Phe Met₃₉₀ Ile Pro Ile Ala Ser₃₉₅ Val Gln Ala Leu Ala₄₀₀
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Pro Gly Ser Leu Gly Phe Asn Thr Gly Glu Pro Arg Ile Gln Leu Tyr
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Ala Leu Leu Gly Leu Met Ser Thr Lys Glu Ala Ala Gln Ser Ala Pro
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Asn Gly Arg His Lys Ser Ala Phe Val Lys Tyr Pro Leu Gln Leu Asp
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675 680 685

Gln Glu Tyr Glu Ser Ala Ala Ala Phe Trp Pro Asp Val His Gly Arg
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785 790 795 800

Glu Ala Pro Glu Glu Phe Glu Lys Glu Pro Asp Leu Val Pro Thr Lys
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Tyr Cys Asn Glu Lys Ile Lys Glu Leu Leu Pro Lys Leu Glu Asp Glu
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Ala Lys Thr Pro Leu Glu Val Ala Ser Gln Gln Leu Lys Glu Thr Pro
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Ile Thr Gly Leu Trp Ile Ser Gly Val Val Gly Thr Ala Val Ile Ile
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Leu Ile Ser Phe Ile Asp Trp Ala Ile Lys Ser Ile Ser Val Ser Asp
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Val Asp Phe Ile Leu Ser Ala Gly Leu Asp Ala Leu Ile Met Val Lys
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Thr Ala Val Leu Ile Pro Leu His Trp Thr Gly Gly Ala Ser Lys Gln
145 150 155 160

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

Pro His Gly Ser Lys Val Phe Trp Val His Leu Gly Phe Val Tyr Ile
180 185 190

Tyr Leu Gly Trp Ala Met Val Leu Leu His Trp His Tyr His Gln Tyr
195 200 205

Leu Thr Ile Arg Gln His Tyr Leu Arg Lys Gly Asp Asp Val Asn Leu
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PF59082PF60142_PCT_SEQ_LIST.txt

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 Lys Glu Pro Arg Gly Ser Glu Phe Ile Asn Gly Leu Leu Arg Ser Val
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 Gln Leu Ile Lys Ala Leu Met Pro Ser Gly Val Pro Val Ser Gly Pro
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 Thr Ser Leu Pro Ala Asp Gly Arg Asp Glu Glu Asp Glu Asp Glu Glu
 275 280 285
 Glu Asp Glu Gly Phe Ala Met Gly Gly Met Pro Leu Pro Leu Glu Leu
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 Arg Arg Thr Thr Leu Gly Gly Leu Asp Pro Val Gly Ala Arg Ser Pro
 305 310 315 320
 Arg Gly Ser Val Asp Gly Cys Gly Arg Val Val His Val Arg Gly His
 325 330 335
 Gly Asp Leu Trp Ala Gly Glu Trp Ser Gln Ser Arg Val Leu Gln Leu
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 Ser Gly Ala His Asp Ala Pro Thr Ala Gly Ser Gly Thr Ser Ser Arg
 355 360 365
 Leu Ser Arg Arg Thr Leu Ala Gln Ala Ile Arg Asn Arg Val Thr Gly
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 Ser Gly Ser Thr Val Leu Arg Ala Ser Gly Ala Gln Asp His Gly Ser
 385 390 395 400
 Arg Leu Ile His Arg Ala Ala Tyr Ser Ile Gly Pro Arg Ala Val Ala
 405 410 415
 Ala Pro Ser Asp Gln Ala Leu Gln His Met Arg Pro Gln Leu Ser Leu
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 Asp Arg Gly Gly Arg Arg Gly Met Ser Pro Ala Arg Gly Gln Ser Tyr
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 Leu Lys Ser Ser Glu Pro Val Ser Leu Gln Leu Lys Glu Ser Ser Asp
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Ala His Leu Leu Glu Trp Trp Leu Glu Arg Pro Glu Ala Thr Val Gln
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Ser Arg Ser Arg Ala Leu Arg Ala Gln Leu Glu Lys Ala Leu Asn Gly
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Arg Asp Met Asp Leu Lys Arg Pro Ser Val Gly His Arg Lys Thr Val
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Asn Ala Glu Phe Ser Asp Gly Thr Arg Val Ala Val Leu Ala Gln His
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Tyr Ala Val Leu Val Thr Asp Val Thr Ser Arg Arg Pro Arg Leu Ser
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Arg Arg Asn Ser Arg Gly Pro Ala Gln Pro Thr Leu Val Thr Leu Pro
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Arg Pro Ala Gly Cys Cys Leu Pro Pro Trp Leu Trp Ser Trp Cys Asp
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Ala Thr Leu Ser Glu Glu Leu Leu Ala Pro Val Pro Ser Gly Ala Asn
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Arg Thr Ile Ala Ser Met Thr Ala Leu Ala Arg Gly Ser Thr Pro Tyr
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His Cys Ser Pro Arg Gly Ser Gly Asp Gly Arg Val Val Pro Ala Leu
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Leu Ser Gly Asn Arg Thr Cys Ser Val Asn Thr Pro Ser His Ala Gln
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Pro Leu Ser Ala Leu Gln Thr Thr Ser Thr Ala Gly Arg Ile Asp Leu
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Asn Pro Asp Ser Ser Pro Lys Met Ala Gly Arg Trp His Gln Ala Val
740 745 750

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Gly Ser Gly Ser Gly Ser Gly Ser Glu Arg Leu Ile Arg Leu Leu Glu

770

775

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Met Met Ala Arg Glu Ala Gln Gly Lys Leu Ala Ala Met Ser Thr Gly
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His Thr Gly Thr Gly Ser Gly Thr Gly Thr Ser His Pro Val Pro Thr
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Ser Ser Val Arg Ala Val Ala Leu Pro Arg Ser Phe Gly Thr Gly Pro
 835 840 845

Ser Ser Ser His Gln Gln Leu Gln His Gln Gly Val Pro His Arg Phe
 850 855 860

Thr Glu Pro Gly Pro Ala Ala Ala Ala Ala Ser Gly Gly Gln Ala Ala
 865 870 875 880

Ala Arg Arg Gly Gln Ala Ala Ser Pro Arg Ala Gly Ser Gly Pro Ile
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Ile Ile Ser Pro Arg Val Pro Val Gly Ala Ser Leu Arg Gly Val Ala
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Ala Leu Gly Gln Arg Glu Gly Pro Ser Thr Ser Gly Thr Gly Ala Gly
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Pro Val Ala Glu Ala Ser Leu Glu Ile Arg Glu Glu Gly Gln Ala Gly
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Asp Ala Ala Gly Ser Glu Gly Val Ile Gln Glu Gly Asn His Val Ala
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Gly Ser Ala Gly Ala Ser Ala Ala Ala Gly Val Gly Ala Gly Ala Gly
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Gln Asp Gly Gly Arg Thr Val Val Asp Ala Ala Thr Ser Gln Arg Gln
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Glu Gly Ser Pro Pro Gly Asp Glu Val Glu Ala Asn Pro Val Ser Gln
 995 1000 1005

Gln Pro Thr Glu Arg Glu Arg Leu Arg Ala Ala Ala Leu Ala Gly
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Trp Glu Val Val Arg Gln Ala Val Trp Asp Gly Arg Val Ala Glu
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Leu Pro Trp Arg Tyr Arg Tyr Ser Val Val Ser Ala Thr Phe Leu
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PF59082PF60142_PCT_SEQ_LIST.txt

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Ala	Gln 1085	Tyr	Glu	Tyr	Ala	Ile 1090	Lys	Tyr	Glu	Glu	Lys 1095	Thr	Gly	Lys
Pro	Leu 1100	Tyr	Gly	Cys	Leu	Gly 1105	Phe	Cys	Gly	Leu	Val 1110	Gly	Glu	Arg
Cys	Arg 1115	Val	Arg	Asp	His	His 1120	Arg	Asp	Lys	Ile	Asn 1125	Asp	Leu	Leu
Val	Gln 1130	Val	Arg	Lys	Ala	Arg 1135	Val	Ala	Ala	Ala	Asn 1140	Lys	Ala	His
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Leu	Trp 1190	Ser	Asn	Phe	Arg	Asp 1195	Arg	Asp	Leu	Arg	Arg 1200	Asn	Leu	Met
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Ala	Pro 1280	Ser	Gln	Gln	Leu	Ser 1285	Trp	Glu	Trp	Tyr	Cys 1290	Gly	Gln	Lys
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PF59082PF60142_PCT_SEQ_LIST.txt

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Val	Phe	Asn	Val	Phe	Leu	Gly	Gly	Val	Ala	Gly	Ser	Thr	Ile	Ile
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Gln	Gly	Ile	Asn	Ser	Ala	Ile	Glu	Lys	Gly	Pro	Ser	Glu	Ile	Phe
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Leu Arg Phe Gly Val Tyr Leu Phe Phe Pro Leu Thr Ile Phe Cys Ile
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Ile Val Val Leu Pro Pro Asn Met Lys Ser Asn Gly Ile Glu Ala Ile
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Lys Gly Asp Leu Glu Phe Ser Asp Phe Asp His Tyr Ser Leu Ser Asn
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Val Glu Ala Ala Ser Pro Lys Met Trp Ala His Leu Phe Ala Val Tyr
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Cys Val Val Leu Tyr Thr Leu Trp Leu Leu Trp Arg Phe Asn Arg Glu
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PF59082PF60142_PCT_SEQ_LIST.txt

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Leu Pro Gly Ser Ser Thr Lys Pro Glu Val Val Glu Leu Lys Ser Ala
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Ala Gly Gly Ala Ser Phe Val Val Lys Ala Gly Gly Asn Ser Arg Phe
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Leu Glu Leu Ala Arg Val Gly Lys Thr Asn Glu Glu Ile Leu Lys Glu
385 390 395 400

Leu Gln Val Met Glu Lys Asp Asp Leu Val Lys Gly Leu Pro Glu Lys
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Leu Gly Val Asp Thr Arg Pro Leu Pro Pro Thr Arg Arg Asn Thr Lys
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Arg Tyr Glu Tyr Asp Leu Lys Thr Thr Val Leu Asp Pro Val His Glu
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Ala Leu Glu Thr Leu Arg Lys Gly Val Thr Pro Gln Gln Leu Val Ala
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Arg Glu Phe Ala Leu Val Tyr Gly Thr Ser Asn Val Ala Ala Val Asn
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Met Ile Gln Asp Thr Ser Ala Leu Glu Pro Leu Ala Glu Glu Tyr Asn
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Gln Ala Arg Val Cys Gln Asp Leu Asp Asp Tyr Leu Glu Met Ala Lys
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Lys Tyr Leu Arg Glu Arg Ile Lys Ile Glu Gln Ala Lys Cys Val Arg
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Lys Met Ala Pro Ser Ala Phe Val Thr Phe Asn Thr Arg Met Ala Gln
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Ala Val Ser Ala Asn Ser Leu His Ser His Asp Glu Asn Ala Trp Arg
595 600 605

Val Gln Asn Ala Pro Ala Pro Phe Glu Val Val Trp Lys Asn Leu Ser
610 615 620

Leu Thr Met Pro Ile Lys Asn Gly Arg Leu Tyr Leu Leu Trp Ala Ala
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Phe Trp Gly Met Thr Ile Phe Phe Met Val Pro Val Ser Phe Ile Gln
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Gly Met Ile Glu Val Pro Lys Leu Ala Ser Ile Pro Val Leu Gly Asp
660 665 670

Ile Val Thr Thr Pro Pro Ile Lys Gln Leu Leu Gln Ala Val Ile Pro
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Gly Leu Val Leu Lys Ile Phe Leu Ala Leu Val Pro Thr Ile Leu Arg
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Ile Met Ala Gln Leu Ser Gly Ala Thr Ser Val Ser Glu Ile Asp Phe
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Gly Val Val Lys Arg Phe Phe Leu Phe Gln Thr Val Val Val Phe Phe
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Gly Ser Ile Ile Leu Gly Ser Phe Phe Asn Gln Leu Lys Gln Trp Val
740 745 750

Lys Glu Pro Ser Ser Val Ile Ala Thr Leu Gly Lys Ser Ile Pro Met
755 760 765

Thr Ser Thr Phe Phe Ile Thr Tyr Leu Leu Val Asn Gly Leu Gly Val
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Lys Ser Phe Ala Phe Ile Arg Leu Pro Asn Phe Val Ile Tyr Trp Ile

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Asp Ser Asp Asp Glu Glu Asp Ala Gly Gly Ala Ala Gly Gly Asn
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Pro Asn Ser Thr Thr Asn Asn Asn Lys Asn Asp Thr Ala Ala Ala
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Ser Tyr Pro Ile Ser Ala Gly Ser Ser Thr Leu Glu Thr His Ser Tyr
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Thr Asn Ala Arg Ile Thr Phe Asn Gly Thr Ser Thr Asp Leu Leu Leu
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Thr Gly Thr Asn Val Asp Thr Gly Val Val Thr Tyr Met Phe Leu Arg
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Asn Val Ser Pro Gly Asp Glu Val Met Trp Cys His Met Val Ala Val
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Thr Asp Val Pro Tyr Val Asn Glu Ala Pro Ser Met Lys Gln Ala Ala
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Gly Gly Lys Ala Pro Gly Pro Gly Pro Glu Gly Ala Gly Leu Ala Phe
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Val Asp Thr Arg Val Leu Lys Pro Asp Arg Arg Ala Leu Lys Arg Phe
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Arg Tyr Asp Val Lys Thr Met Lys Ala Arg Asn Glu Ile Thr Glu Thr
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 Gly Trp Thr Ser Ser Ala Arg Thr Val Asp Ala Val Thr Tyr Trp Leu
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 Tyr Ser Arg Pro Trp Ser Val Thr Ala Leu His Asp Ala Ala Glu Met
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Val Val Gln Leu Leu Leu Pro Pro Leu Asn Gln Phe Val Ser Glu
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Tyr Lys Leu Tyr Arg Arg Gly Val Lys Ala Ser Lys Leu Lys Gly
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<210> 509
 <211> 1429
 <212> PRT
 <213> Chlamydomonas reinhardtii

<400> 509

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 20 25 30

Lys Pro Lys Arg Met Ser Ser Phe Tyr Leu Gly Trp Val Lys Pro Ile
 35 40 45

Met Leu Tyr Lys Glu Glu Asp Ile Ile Asp Glu Val Gly Leu Asp Ala
 50 55 60

PF59082PF60142_PCT_SEQ_LIST.txt

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

Leu Thr Leu Ile Cys Ile Pro Leu Val Leu Pro Thr Asn Met Thr Ser
85 90 95

Gly Glu Ile Glu Arg Leu Leu Ala Gln Ala Glu Glu Ala Gln Ser Leu
100 105 110

Val Leu Asn Asn Ser Val Val Val Gln Pro Arg Asn Thr Ser Leu Leu
115 120 125

Gly Asp Asp Asn His Asn Asp Val Arg Phe Met Tyr Met Ser Gln Gly
130 135 140

Thr Val Val Ala Asn Asn Met Ala Pro Trp Asn Thr Ser Ile Thr Phe
145 150 155 160

Asn Ala Thr Met Val Glu Asn Asn Val Thr Phe Val Gln Asp Phe Phe
165 170 175

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

Ala Tyr Asn Met Thr Tyr Val Arg Ile Ser Gly Thr Lys Arg Tyr Asn
195 200 205

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

Trp Gln Asn Met Ser Val Ile Pro Ala Ser Leu Gln Ala Val Asn Asn
225 230 235 240

Ser Gly Phe Asp Tyr Ile Ile Val Trp Ser Leu Glu Gly Glu Thr Glu
245 250 255

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

Asp Lys Tyr Ser Leu Ser Asn Ile Pro Ala Gly Ser Ala Lys Met Trp
275 280 285

Ala His Val Val Ala Leu Trp Leu Val Thr Leu Phe Thr Met Trp Arg
290 295 300

Leu Arg Glu Tyr Asn Leu Gln Ser Val Tyr Leu Arg Leu Leu Phe Leu
305 310 315 320

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

Val Pro Phe Val Ser Asp Ala Val Ala Cys Gly Leu Arg Ala Glu Glu
340 345 350

Tyr Arg Glu Lys His Gly Leu Pro Ala Ser Val Thr Ser Leu Lys Lys
355 360 365

Ser Met Ser Ile Lys Asn Pro Met Tyr Glu Gly Tyr Glu Ser Leu Glu
370 375 380

Gly Gly Pro Asp Gly Arg Thr Ala Val Gly Val Pro Val Ser Thr Ser
385 390 395 400

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

Pro Gly Gly Lys Asn Gly Ala Gly Gly Ala Ala Gln Gln Pro Ala Ser
420 425 430

Ser Leu Arg Ser Ser Gln Ala Ala Ser Leu Lys Gln Ser Gln Ala Gly
435 440 445

Ala Leu Lys Val His Thr Thr Asn Gly Gly Gly Ala Tyr Ala Ala Glu
450 455 460

Thr Pro Arg Ala Asn Gly Gly Gly Ser Thr Ala Gln Ser Gly Asp Met
465 470 475 480

Arg Val Ser Glu Phe Ala Ser Ala Thr Tyr Glu Ala Glu Ser Ala Ala
485 490 495

Gly Gly Asp Lys Arg Ser Ala Ala Gly Asp Ser Gly Val Gly Gly Lys
500 505 510

Glu Gly Gly Ala Val Val Gln Ala Val Gly Val Pro Ile Glu Glu Cys
515 520 525

Leu Lys Tyr Arg Leu His Asp Pro Glu Val Glu Pro Arg His Ala Ala
530 535 540

Thr Gly Gly Arg Leu Leu Met Ala Arg Val Gly Arg Thr Thr Glu Glu
545 550 555 560

Leu Arg Arg Asp Val Leu Arg Glu Asp Pro Glu Pro Thr Trp Leu Pro
565 570 575

Pro Gly Tyr Gly Val Asp Thr Arg Val Leu Lys Pro Asp Arg Arg Ser
580 585 590

Leu Lys Arg Phe Arg Tyr Asp Val Lys Thr Leu Gly Lys Lys Pro Gly
595 600 605

Asp Met Val Leu Trp Met Arg Asp Lys Ala Ala Gln Leu Leu Gly Gly
Seite 573

610

615

620

Lys Ser His Glu Asp Lys Glu Lys Glu Lys Ala Glu Leu Asp Ala Ala
625 630 635 640

Arg Met Lys Arg Glu Ala Glu Asp Lys Asp His Ile Gly Pro Arg Phe
645 650 655

Arg Pro Pro Val Asn Ala Thr Ala Met Asp Pro Lys Glu Gln Ala Lys
660 665 670

Ala Lys Leu Arg Ser Gly Leu Thr Pro Gln Gln Met Val Ala Gln Glu
675 680 685

Phe Ala Leu Val Tyr Gln Pro Tyr Asn Ile Ala Ala Val Asn Met Ile
690 695 700

Gln Asp Thr Thr Gly Leu Glu Pro Leu Val Ala Glu Tyr Leu Lys Ile
705 710 715 720

Glu Gln Ser Leu Glu Asp Tyr Leu Asp Met Ala Lys Leu Arg Leu Lys
725 730 735

Leu Arg Lys Ala Leu Pro Met Lys Ile Val Arg Ile Ser Pro Lys Leu
740 745 750

Gln Gly Asp Ala Trp Pro Ala Val Gln Ser Glu Met Ile Arg Ile Val
755 760 765

Lys Ser Gln Tyr Glu Tyr Met Arg Glu Gln Ala His Ala Arg Ser Lys
770 775 780

Gln Ala Leu Glu Leu His Asp Arg Glu Ile Asn Pro Lys Ala Ser Arg
785 790 795 800

Ser Ser Arg Arg Ala Glu Lys Asp Val Leu Gln Lys Arg Ala Val Ala
805 810 815

Leu Gly Ala Glu Glu Ala Asn Leu Pro Arg Gln Glu Ala Glu Ala Leu
820 825 830

Ala Ala Ile Gln Lys Ile Met Pro Lys Arg Trp Ser Ala Lys Val Asp
835 840 845

Ala Val Thr Tyr Trp Leu Ala Arg Leu Lys Tyr Leu Arg Glu Cys Ile
850 855 860

Lys Ile Gln Gln Ala Val Ala Ser Arg Lys Ile Ala Pro Ser Ala Phe
865 870 875 880

Val Thr Phe Asn Thr Arg Met Ala Gln Gly Val Ala Ser Asn Ser Leu
885 890 895

PF59082PF60142_PCT_SEQ_LIST.txt

His Ala His Asp Glu Thr Ser Trp Arg Ile Met Pro Ala Pro Ala Pro
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 Ile Glu Val Val Trp Gly Asn Leu Met Met Thr His Pro Val Arg Thr
 915 920 925

 Gly Arg Leu Trp Leu Ile Trp Val Ala Phe Trp Ala Met Thr Leu Phe
 930 935 940

 Phe Met Ile Pro Val Thr Leu Ile Gln Ala Leu Ile Glu Val Pro Lys
 945 950 955 960

 Leu Ala Ser Ile Pro Val Leu Gly Asp Ile Val Thr Ala Pro Val Val
 965 970 975

 Lys Gln Leu Leu Glu Ala Ile Ile Pro Gly Thr Cys Arg Val Val Val
 980 985 990

 Val Phe Phe Gly Ser Ile Ile Ala Gly Ser Phe Phe Asn Gln Ile Thr
 995 1000 1005

 Gln Trp Val Lys Asp Pro Ala Ser Val Ile Ser Val Leu Gly Lys
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 Ser Ile Pro Met Thr Ala Thr Phe Phe Ile Thr Tyr Leu Phe Val
 1025 1030 1035

 Asn Gly Leu Ala Val Arg Ser Ile Gln Phe Val Arg Leu Ser Asp
 1040 1045 1050

 Phe Val Val Phe Trp Ile Leu Ser Lys Phe Ala Gly Ser Pro Arg
 1055 1060 1065

 Ala Arg Glu Arg Met Trp Met Asn Gln Val Gln Phe Tyr Gly Lys
 1070 1075 1080

 Thr Val Pro Asp His Thr Ile Ala Met Leu Leu Gly Leu Val Phe
 1085 1090 1095

 Cys Cys Met Asn Pro Ile Val Cys Pro Ala Ala Leu Ala Tyr Phe
 1100 1105 1110

 Leu Val Ala Cys Val Gly Glu Arg Tyr Asn Val Ile Tyr Val Tyr
 1115 1120 1125

 Arg Pro Gln Tyr Glu Ser Ala Gly Arg Leu Trp Lys Thr Val Tyr
 1130 1135 1140

 Asn Gln Ile Met Val Ala Ile Tyr Ile Met Leu Leu Ala Met Phe
 1145 1150 1155

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	1190					1195					1200			
Glu	Met	Asp	Met	Leu	Glu	Ala	Asp	Gln	Arg	Arg	Glu	His	Leu	Leu
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Ala	Met	Ala	Arg	Asp	Glu	Arg	Lys	Lys	Ala	Lys	Leu	Glu	Gln	Lys
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Gln	Arg	Tyr	Glu	Thr	Ala	Cys	Ile	Ala	Ala	Glu	Lys	Glu	Asp	Lys
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Pro	Ala	Pro	Pro	Ala	Ser	Asp	Phe	Phe	Thr	Glu	Ile	Lys	Pro	Gly
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Lys	Ala	Glu	Arg	Leu	Leu	Tyr	Glu	Thr	Leu	Glu	Gly	Glu	Gly	Phe
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Ser	Leu	Asn	Ser	Ala	Glu	Lys	Lys	Glu	Ile	Ala	Asp	Met	Ala	Val
	1280					1285					1290			
Pro	Pro	Thr	Cys	Leu	Glu	Gly	Gly	Val	Arg	Met	His	Leu	Glu	His
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Leu	Glu	Glu	Val	Glu	Lys	Leu	Ala	Arg	Val	Val	Gln	Ser	Leu	Leu
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Pro	Ser	Leu	Asn	Gln	Phe	Val	Ser	Glu	Tyr	Lys	Asn	Tyr	Arg	Arg
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Thr	Val	Lys	Ala	His	Lys	Ile	Lys	Gly	Asp	Thr	Ala	Thr	Gly	Ala
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Glu	Val	Pro	His	Met	Pro	Glu	Asp	Leu	Thr	Ile	Phe	Asp	Asn	Asp
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Pro	Arg	Leu	Val	Ser	Leu	Asp	Gln	Glu	Met	Ala	Asp	Arg	Pro	Asp
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Asp	Ala	Ala	Ser	Leu	Ser	Ala	Ala	Glu	Ala	Ser	Asp	Asp	Asp	Glu
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Val

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 <211> 2976
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 <213> *Saccharomyces cerevisiae*

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PF59082PF60142_PCT_SEQ_LIST.txt

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 <211> 991
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 511

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Pro Lys Asn Arg Arg Val Tyr Glu Pro Arg Ser Leu Lys Asp Ile Gln
 35 40 45

Thr Ile Pro Glu Glu Glu Arg Thr Glu Pro Val Pro Glu Gly Tyr Phe
 50 55 60

PF59082PF60142_PCT_SEQ_LIST.txt

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 His Thr Ser Val Asp Gly Tyr Phe Leu Leu Arg Tyr Ile Gly Ile Val
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 Gly Ser Leu Ser Phe Val Gly Cys Leu Leu Leu Leu Pro Ile Leu Leu
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 Pro Val Asn Ala Thr Asn Gly Asn Asn Leu Gln Gly Phe Glu Leu Leu
 115 120 125
 Ser Phe Ser Asn Val Thr Asn Lys Asn Arg Phe Tyr Ala His Val Phe
 130 135 140
 Leu Ser Trp Ile Phe Phe Gly Leu Phe Thr Tyr Val Ile Tyr Lys Glu
 145 150 155 160
 Leu Tyr Tyr Tyr Val Val Phe Arg His Ala Met Gln Thr Thr Pro Leu
 165 170 175
 Tyr Asp Gly Leu Leu Ser Ser Arg Thr Val Ile Val Thr Glu Leu His
 180 185 190
 Lys Ser Ile Ala Gln Glu Gly Glu Met Gln Met Arg Phe Pro Lys Ala
 195 200 205
 Ser Asn Val Ala Phe Ala Tyr Asp Leu Ser Asp Leu Gln Glu Leu Cys
 210 215 220
 Lys Glu Arg Ala Lys Asn Ala Ala Lys Tyr Glu Ala Ala Leu Asn Lys
 225 230 235 240
 Val Leu Asn Lys Cys Val Lys Met Thr Arg Asn Lys Thr Gln Lys Gln
 245 250 255
 Leu Asp Lys Leu Tyr Asn Asn Gly Thr Lys Pro Lys Asp Asp Leu Glu
 260 265 270
 Thr Tyr Val Pro His Lys Lys Arg Pro Lys His Arg Leu Gly Lys Leu
 275 280 285
 Pro Leu Cys Leu Gly Gly Lys Lys Val Asn Thr Leu Ser Tyr Ser Ser
 290 295 300
 Lys Arg Ile Gly Glu Leu Asn Glu Glu Ile His Glu Lys Gln Ala Asp
 305 310 315 320
 Trp Ala Ser Asn Asp Arg Gln Pro Ala Cys Phe Ile Gln Phe Glu Thr
 325 330 335
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 Seite 579

340

345

350

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

Asn Trp Gly Ser Met Arg Leu Ser Ser Lys Glu Arg His Ser Arg Arg
 370 375 380

Ala Val Ala Asn Thr Ile Met Val Leu Leu Ile Ile Phe Trp Ala Phe
 385 390 395 400

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

Lys Val Pro Phe Leu Arg Phe Ile Asn Asn Met Pro Thr Phe Leu Met
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Gly Val Ile Thr Gly Leu Leu Pro Thr Ile Ala Leu Val Val Leu Met
 435 440 445

Ser Leu Val Pro Pro Phe Ile Val Met Leu Gly Lys Leu Ser Gly Cys
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Val Thr Arg Gln Glu Thr Asp Leu Tyr Ser Gln Ala Trp Tyr Tyr Ala
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Phe Ala Val Ile Gln Ile Phe Leu Val Val Thr Ala Thr Ser Ser Ala
 485 490 495

Ser Ser Thr Val Asp Ser Ile Ile Asp Arg Pro Arg Ser Ala Met Thr
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Leu Leu Ala Asn Asn Leu Pro Lys Ala Ser Asn Phe Tyr Ile Met Tyr
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Phe Ile Leu Lys Gly Leu Thr Gly Pro Thr Trp Thr Ile Leu Gln Ala
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Val Asn Leu Leu Leu Ser Lys Val Leu Gly Arg Val Leu Asp Ser Thr
 545 550 555 560

Pro Arg Gln Lys Trp Asn Arg Tyr Asn Thr Leu Ala Thr Pro Arg Met
 565 570 575

Gly Ile Val Tyr Pro Gly Ile Glu Ile Leu Val Cys Ile Tyr Ile Cys
 580 585 590

Tyr Ser Ile Ile Ala Pro Ile Leu Leu Phe Phe Ser Thr Val Met Leu
 595 600 605

Thr Leu Leu Tyr Val Ala Tyr Leu Tyr Asn Leu Asn Tyr Val Phe Gly
 610 615 620

PF59082PF60142_PCT_SEQ_LIST.txt

Phe Ser Phe Asp Leu Lys Gly Arg Asn Tyr Pro Arg Ala Leu Phe Gln
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 645 650 655
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 660 665 670
 Val Val Thr Ala Leu Ala His Ile Tyr Met Lys Arg Lys Phe Ile Pro
 675 680 685
 Leu Phe Asp Ala Val Pro Leu Ser Ala Ile Arg His Ala Arg Gly Glu
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 Gly Ile Leu Thr Pro Val Thr Lys Asp Asp Leu Lys Lys Ala Asn Leu
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 Thr Leu Ser Ser Ser Thr Lys Asp Asn Asn Glu Ser Thr Phe Val Pro
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 Glu Gly Ala Val Pro Val Asn Ala Asp Ala Gly Val Ile Tyr Ser Asp
 850 855 860
 Pro Ala Ala Val Met Lys Glu Pro Gln Ala Phe Pro Pro Asp Val Leu
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 Glu Thr Asn Thr Trp Thr Arg Arg Ile Leu Gln Phe Phe Asn Pro Arg
 885 890 895

PF59082PF60142_PCT_SEQ_LIST.txt

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915 920 925

Asp Pro Cys Val Arg Glu Lys Asp Pro Ile Val Trp Cys Cys Lys Asp
930 935 940

Pro Leu Gly Val Ser Lys Gln Gln Ile Gln Glu Ala Arg Ser Asn Gly
945 950 955 960

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Ile Phe Thr Tyr Asn Pro Pro Asp Tyr Glu Pro Glu Ala Lys Lys
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<211> 2616
<212> DNA
<213> Schizosaccharomyces pombe

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PF59082PF60142_PCT_SEQ_LIST.txt

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<210> 513
 <211> 871
 <212> PRT
 <213> Schizosaccharomyces pombe

<400> 513

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Val Phe Asn Phe Ala Ile Phe Cys Ala Phe Ile Gly Leu Phe Leu Cys
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Leu Arg Pro Arg Glu Lys His Val Tyr Gln Pro Arg Cys Ile Ile Asp
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PF59082PF60142_PCT_SEQ_LIST.txt

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 Gly Leu Phe Ala Tyr Val Val Lys Arg Ser Glu Thr Tyr Leu Ile Gln
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 Gly Ala Leu Cys Ile Leu Gly Cys Leu Val Leu Phe Pro Ile Leu Leu
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 Pro Val Asn Ala Thr Asn Gly Val Gly Glu Lys Gly Phe Asp Ile Leu
 115 120 125
 Ser Phe Ser Asn Val Lys Asn His Asn Arg Phe Tyr Ala His Val Phe
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 Leu Ser Trp Leu Phe Phe Gly Phe Thr Ile Phe Ile Ile Tyr Arg Glu
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 Leu Arg Tyr Tyr Val Ile Phe Arg His Ala Met Gln Ser Ser Gly Leu
 165 170 175
 Tyr Asn Asn Leu Pro Ser Ser Ser Thr Met Leu Leu Thr Glu Leu Pro
 180 185 190
 Asn Ser Val Leu Asn Asp Glu Glu Thr Leu His Glu Leu Phe Pro Asn
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 Ala Ser Glu Phe Thr Cys Val Arg Asp Leu Lys Lys Leu Glu Lys Lys
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 Val Lys Lys Arg Ser Asp Leu Gly Asn Lys Tyr Glu Ser Thr Leu Asn
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 Ser Leu Ile Asn Lys Ser Val Lys Lys His Asn Lys Leu Val Lys Lys
 245 250 255
 His Lys Pro Leu Pro Ser Thr Leu Asp Tyr Thr Ala Tyr Val Lys Lys
 260 265 270
 Arg Pro Thr His Arg Leu Lys Phe Leu Ile Gly Lys Lys Val Asp Thr
 275 280 285
 Ile Asp Tyr Cys Arg Asp Thr Ile Ala Glu Leu Asp Glu Val Val Asp
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 Lys Leu Gln Thr Ser Leu Glu Glu Arg Lys Lys Val Gly Ser Val Phe
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Ile Arg Phe Arg Ser₃₂₅ Gln Thr Asp Leu Gln₃₃₀ Thr Ala Tyr Gln₃₃₅ Ala Phe

Leu Tyr Ser Lys₃₄₀ Lys Phe Arg Lys Tyr₃₄₅ Arg Phe Gly Arg Ala₃₅₀ Leu Val

Gly Ile Ala₃₅₅ Pro Glu Asp Ile Val₃₆₀ Trp Ser Asn Leu Asp₃₆₅ Leu Ser Met

Tyr Thr₃₇₀ Arg Arg Gly Lys Lys₃₇₅ Thr Ile Ser Asn Thr₃₈₀ Ile Leu Thr Leu

Met₃₈₅ Ile Ile Phe Trp Ala₃₉₀ Phe Pro Val Ala₃₉₅ Val Val Gly Cys Ile Ser₄₀₀

Asn Val Asn Tyr Leu₄₀₅ Ile Glu Lys Val His₄₁₀ Phe Leu Lys Phe Ile₄₁₅ Asp

His Met Pro Pro₄₂₀ Lys Leu Leu Gly Ile₄₂₅ Ile Thr Gly Ile₄₃₀ Leu Pro Ser

Val Ala Leu₄₃₅ Ser Ile Leu Met Ser₄₄₀ Leu Val Pro Pro₄₄₅ Phe Ile Lys Phe

Leu Gly₄₅₀ Lys Phe Gly Gly Ala₄₅₅ Leu Thr Val Gln Glu₄₆₀ Ile Glu Asn Tyr

Cys Gln Asn Trp Tyr Tyr₄₇₀ Ala Phe Gln Val Val₄₇₅ Gln Val Phe Leu Val₄₈₀

Thr Thr Met Thr Ser₄₈₅ Ala Ala Thr Ser Ala₄₉₀ Val Val Gln Val Ile₄₉₅ Lys

Glu Pro Ala Ser₅₀₀ Ser Met Thr Leu Leu₅₀₅ Ala Ser Asn Leu Pro₅₁₀ Lys Ala

Ser Asn Phe₅₁₅ Tyr Ile Ser Tyr Phe₅₂₀ Leu Leu Gln Gly Leu₅₂₅ Ser Ile Pro

Gly Gly₅₃₀ Ala Leu Leu Gln Ile₅₃₅ Val Thr Leu Leu Leu₅₄₀ Ser Lys Val Leu

Gly₅₄₅ Arg Ile Phe Asp Asn₅₅₀ Thr Pro Arg Lys Lys₅₅₅ Trp Asn Arg Trp Asn₅₆₀

Gln Leu Ser Ala Pro₅₆₅ Ser Trp Gly Thr Val₅₇₀ Tyr Pro Val Tyr Ser₅₇₅ Leu

Leu Val Thr Ile₅₈₀ Met Ile Cys Tyr Ser₅₈₅ Ile Ile Ala Pro Ile₅₉₀ Ile Ile

Gly Phe Ala Ala Val Ala Phe Val Leu Ile Tyr Phe Ala Tyr Ser Tyr

595

600

605

Asn Leu Ile Tyr Val Leu Gly His Asn Ala Asp Ala Lys Gly Arg Asn
 610 615 620

Tyr Pro Arg Ala Leu Phe Gln Val Phe Val Gly Leu Tyr Leu Ala Glu
 625 630 635 640

Val Cys Leu Ile Gly Leu Phe Val Leu Ala Lys Asn Trp Gly Ala Thr
 645 650 655

Val Leu Glu Ala Val Phe Leu Gly Phe Thr Val Ala Cys His Leu Tyr
 660 665 670

Phe Lys Tyr Lys Phe Leu Pro Leu Met Asp Ala Val Pro Ile Ser Ala
 675 680 685

Ile Glu Ser Val Ser Glu Arg Pro Glu Ile Lys Tyr Pro Met Asp Leu
 690 695 700

Gly Thr Ser Glu Met Lys Asn Val Gly Arg Ala Tyr Pro Glu Ile Leu
 705 710 715 720

Glu Lys Leu Ser Ser Ser Gly Ser Asp Glu Phe Leu Glu Thr Ser
 725 730 735

Ser Arg Thr Ser Glu Asn Thr Lys Glu Lys Ile Asp Lys Asp Asp Glu
 740 745 750

Gly Phe Ala Ile Thr Asn Ile Ser Ser Val His Lys Met Pro Ser Phe
 755 760 765

Val Leu Ser Tyr Phe Ser Asp Leu Ala Ala Ser Asn Arg Ile Leu Thr
 770 775 780

Gly Phe Asp Arg Val Leu Gln Leu Leu Pro Ser Phe Tyr Asp Ile Pro
 785 790 795 800

Val Arg Val Arg Asn Val Gln Tyr Val Ser Pro Ala Leu Lys Ala Thr
 805 810 815

Pro Pro Ser Val Trp Ile Pro Lys Asp Pro Leu Gly Leu Ser Thr Tyr
 820 825 830

Ala Ile Glu Asp Ala Arg Gly Lys Val Asp Ile Phe Asp Asp Asn Thr
 835 840 845

Thr Phe Asn Glu Lys Gly Asn Leu Gln Tyr Thr Gly Pro Pro Pro Asp
 850 855 860

Tyr Asp Glu Ala Ile Arg Ser
 865 870

PF59082PF60142_PCT_SEQ_LIST.txt

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 <211> 2628
 <212> DNA
 <213> Ashbya gossypii

<400> 514
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PF59082PF60142_PCT_SEQ_LIST.txt

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<210> 515
<211> 875
<212> PRT
<213> Ashbya gossypii

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<400> 515

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Met Ala Asp Ala Asn Asp Ser Ser Asp Ser Asn Ser Thr Ser Ser Phe
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Val Ser Ala Leu Ile Leu Tyr Gly Ile Ile Gly Leu Val Tyr Thr Leu
          20          25          30

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Ile Phe Leu Ala Leu Arg Lys Arg Tyr Arg Arg Val Tyr Glu Pro Arg
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```

```

Thr Leu Asp Asp Val Arg Thr Leu Gln Pro Ser Glu Arg Val Glu Ser
          50          55          60

```

```

Ala Pro Ala Gly Tyr Val Trp Trp Leu Pro His Leu Leu Tyr Lys Pro
65          70          75          80

```

```

His Lys Ser Leu Leu Gln His Met Gly Val Asp Ala Tyr Phe Phe Ala
          85          90          95

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Arg Tyr Leu Ala Val Phe Gly Thr Leu Ala Leu Ile Gly Cys Phe Ile
          100          105          110

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Leu Leu Pro Ile Leu Leu Pro Val Asn Ala Ala Gly Gly Arg His Leu
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Arg Gly Phe Glu Arg Ile Ser Phe Ser Asn Val Ala Met Ser Arg Arg
          130          135          140

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PF59082PF60142_PCT_SEQ_LIST.txt

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

PF59082PF60142_PCT_SEQ_LIST.txt

Thr Glu Lys Val His Phe Leu Arg Phe Ile Asn Asn Leu Pro Asp Val
420 425 430

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

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

Gly Ser Ile Ser Arg Gln Glu Thr Gln Leu Tyr Cys Gln Arg Trp Phe
465 470 475 480

Tyr Ala Phe Gln Val Val His Val Val Leu Val Val Met Leu Ala Ser
485 490 495

Ser Ala Ala Ser Thr Val Thr Ala Ile Ile Asp Asp Pro Asn Asn Ala
500 505 510

Phe Glu Gln Leu Ala Gln Asn Met Pro Leu Ser Ala Asn Phe Tyr Leu
515 520 525

Ser Tyr Val Met Leu Phe Ala Phe Ile Phe Ala Ser Gly Val Leu Leu
530 535 540

Gln Leu Thr Gly Phe Val Leu Ser Phe Ile Leu Gly Arg Ile Leu Asp
545 550 555 560

Ser Thr Pro Arg Gln Lys Trp Thr Arg Tyr Asn Thr Leu Asn Leu Pro
565 570 575

Thr Trp Gly Val Met Tyr Pro Leu Met Glu Leu Gln Val Cys Ile Met
580 585 590

Leu Ala Tyr Ala Ile Val Thr Pro Val Leu Leu Ile Ile Ser Thr Leu
595 600 605

Ala Leu Leu Phe Ala Tyr Val Ala Tyr Met Tyr Val Phe Asn Tyr Val
610 615 620

Tyr Gly Leu Lys His Asp Tyr Lys Gly Arg Asn Tyr Val Asn Ala Leu
625 630 635 640

Phe Gln Val Phe Val Gly Leu Tyr Leu Ala Glu Val Phe Leu Phe Ala
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Leu Phe Ile Met Gly Arg Ala Trp Gly Pro Leu Val Leu Asn Val Ile
660 665 670

Met Leu Ala Phe Thr Val Leu Val His Leu Tyr Leu Gln Arg Arg Phe
675 680 685

Leu Pro Leu Val Asp Ala Val Pro Leu Ser Leu Leu Asp Gly Ala Ala
690 695 700

Gly Ser Val Gly Lys Asp Gln Gly Trp Ala Glu Val Val Arg Ala Gly
705 710 715 720

Arg Ala Arg Pro Leu Asp Gly Leu Val Ala Leu Thr Asn Arg Leu Thr
725 730 735

Gly Ala Ala Thr Pro Ala His Pro Ala Pro Val Asn Pro Asp Ala Glu
740 745 750

Lys Ala Ala Leu Ser Arg Ser Ala Pro Ala Ala Ala Ser Ser Ala Leu
755 760 765

Ala Arg Val Lys Asn Phe Phe His Pro Ser Ala Ala Tyr Asn Tyr Asp
770 775 780

Leu Ala Lys Ser Arg Leu Pro Asp Thr Tyr Asp Lys Pro Leu Glu Tyr
785 790 795 800

Ala Glu Gly Tyr Thr Arg Ser Ala Tyr Thr Asp Pro Cys Ile Arg Asp
805 810 815

Lys Glu Pro Val Leu Trp Val Pro Glu Asp Pro Met Gly Val Ala Ala
820 825 830

Arg Gln Ala Ala Ile Ala Glu Gln His Gly Val Lys Val Ser Thr Ser
835 840 845

His Thr Gly Phe Asp Glu Lys Gly Ala Ala Ile Tyr Thr Asp Asn Pro
850 855 860

Pro Asp Tyr Thr Pro Tyr Asp Tyr Val Asn His
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<211> 2904
<212> DNA
<213> Kluyveromyces lactis

<400> 516
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PF59082PF60142_PCT_SEQ_LIST.txt

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

PF59082PF60142_PCT_SEQ_LIST.txt

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

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

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

Thr Leu Asn Gly Val Ile Thr Lys Ser Val Lys Lys Lys Leu Lys Ala
245 250 255

Asp Lys Lys Gly Glu Lys Val Ala Glu Gly Thr Thr Asn Leu Asp Gln
260 265 270

Pro Gln Asn Asp Leu Glu Thr Tyr Ile Pro Leu Lys Lys Arg Pro Lys
275 280 285

His Arg Leu Ser Lys Ile Pro Ile Leu Asn Ile Cys Leu Ser Glu Lys
290 295 300

Val Asp Thr Leu Asp Tyr Ser Val Lys His Ile Ser Glu Leu Asn Glu
305 310 315 320

Lys Ile Gly Thr Glu Gln Glu Ser Trp Glu Asp Asn Asn Thr Val Gly
325 330 335

Ser Ala Phe Ile Glu Phe Lys Thr Gln Tyr Asp Ala Gln Arg Ala Tyr
340 345 350

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

Ile Gly Tyr Gly Pro Asp Asp Val Ile Trp Glu Ser Thr Ser Met Asn
370 375 380

Arg Lys Thr Arg Lys Val Lys Arg Leu Gly Gly Asn Thr Ile Leu Thr
385 390 395 400

Leu Met Ile Ile Phe Trp Ala Ile Pro Val Ala Val Val Gly Cys Ile
405 410 415

Ser Asn Ile Asn Phe Leu Thr Asp Lys Val Pro Phe Leu Arg Phe Ile
420 425 430

Asp Asn Met Pro Asp Val Leu Met Gly Val Ile Thr Gly Leu Leu Pro
435 440 445

Thr Ile Leu Leu Ala Leu Leu Met Ser Leu Val Pro Val Phe Ile Lys
450 455 460

PF59082PF60142_PCT_SEQ_LIST.txt

Lys Val Ala Met Met Thr Gly Ala Leu Thr Arg Gln Glu Ile Glu Leu
 465 470 475 480
 Tyr Cys His Ala Trp Tyr Tyr Ala Phe Gln Val Val Gln Val Phe Ile
 485 490 495
 Val Val Thr Leu Ala Ser Ser Ala Ser Ser Thr Val Thr Asp Ile Ile
 500 505 510
 Asp Glu Pro Asp Ser Ala Met Thr Leu Leu Ala Gln Asn Leu Pro Lys
 515 520 525
 Ala Ser Asn Phe Tyr Ile Ala Tyr Phe Leu Leu Gln Gly Leu Thr Val
 530 535 540
 Pro Ser Gly Ala Leu Leu Gln Val Val Ala Leu Ile Leu Ser Lys Val
 545 550 555 560
 Leu Gly Arg Val Leu Asp Lys Thr Pro Arg Gln Lys Trp Ala Arg Tyr
 565 570 575
 Asn Thr Leu Ser Gln Pro Ser Trp Gly Val Val Tyr Pro Val Leu Glu
 580 585 590
 Leu Leu Val Cys Ile Phe Ile Thr Tyr Ser Ile Ile Ala Pro Ile Ile
 595 600 605
 Leu Val Phe Ser Thr Val Ala Leu Gly Phe Phe Phe Leu Ala Tyr Leu
 610 615 620
 Tyr Asn Leu Thr Tyr Val Met Ser Phe Ser Tyr Asp Leu Arg Gly Arg
 625 630 635 640
 Asn Tyr Pro Arg Ala Leu Phe Gln Val Phe Val Gly Leu Tyr Leu Ala
 645 650 655
 Glu Ile Cys Leu Ile Gly Leu Phe Ile Met Ala Lys Thr Trp Gly Pro
 660 665 670
 Leu Val Leu Glu Ala Val Phe Leu Ala Ala Thr Ala Leu Ala His Ile
 675 680 685
 Tyr Phe Lys Arg Arg Phe Ile Pro Leu Phe Asp Ala Val Pro Leu Ser
 690 695 700
 Ala Ile Arg Tyr Ala Arg Gly Glu Glu Gly Ser Tyr Tyr Pro Ala Lys
 705 710 715 720
 Asp Gln Gly Leu Asn Glu Ile Gln Val Glu Gly Lys Lys Leu Ala Glu
 725 730 735
 Asn Ile Leu Ser Glu Asp Arg Asn Gly Val Phe Gln Glu Thr Thr Lys
 Seite 595

740

745

750

Gln Asp Leu Gln Arg Val Asn Met Leu Pro Asp Glu Tyr Glu Asp Ser
755 760 765

Leu Glu Asn Asp Ser Lys Ser Asn Asn Gly Asn Gly Thr Ile Ser Gly
770 775 780

Ser Ser Lys Gln Asn Pro Ser Thr Phe Val Asn Asp Ser Glu Gln Phe
785 790 795 800

His Lys Thr Lys Val Pro Pro Gln Ile Pro Pro Pro Glu Val His Gln
805 810 815

Glu Glu Arg Asp Pro Asn Ile Ile Val Asn Arg Ala Asp Ala Gly Gln
820 825 830

Val Ile Ser Asp Val Lys Gly Tyr Pro Ile Asn Ala Pro Glu Glu Gln
835 840 845

Leu Gly Leu Pro Ser Asp Leu Ile Arg Pro Lys Ser Ile Val Ala Arg
850 855 860

Cys Lys Leu Phe Phe Gln Pro Gln Lys Tyr Tyr Asp Phe Ala Ile Val
865 870 875 880

Arg Gln Thr Leu Pro Tyr Val Phe Asn Asp Val Ile Arg Tyr Asp Leu
885 890 895

Glu Tyr Leu Glu Thr Ala Phe Thr Glu Pro Cys Val Arg Glu Lys Glu
900 905 910

Pro Ile Ile Trp Cys Ala Arg Asp Pro Met Gly Leu Ser His Gln Gln
915 920 925

Ile Ser Ile Ala Ser Ala Ser Gly Val Asp Val Arg Asp Asp Phe Ala
930 935 940

Gly Tyr Asp Glu Thr Gly Lys Thr Thr Tyr Ser Asn Ser Pro Pro Asp
945 950 955 960

Tyr Glu Met Ile Ala Lys Lys
965

<210> 518
<211> 124
<212> PRT
<213> Artificial sequence

<220>
<223> DUF221 domain

<400> 518

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Glu Ala Glu Gln Lys Thr Thr Leu Arg Glu Lys Gln Gln Gln Ala
1 5 10 15

Ala Ile Val Phe Phe Asn Arg Arg Ser Ala Ala Ala Ser Ala Ser Gln
20 25 30

Thr Leu His Ala Gln Met Phe Asp Lys Trp Thr Val Glu Gln Ala Pro
35 40 45

Glu Pro Arg Gln Ile Ile Trp Ser Asn Pro Ser Lys Lys Ile Tyr Glu
50 55 60

Arg Gln Ile Arg Gln Val Val Val Tyr Thr Ile Val Phe Leu Thr Val
65 70 75 80

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

Glu Lys Leu Arg Glu Lys Leu Pro Phe Leu Lys Val Val Val Asp Gln
100 105 110

Pro Lys Ile Lys Thr Val Leu Gln Ala Tyr Leu Pro
115 120

<210> 519
<211> 414
<212> PRT
<213> Artificial sequence

<220>
<223> DUF221 domain

<400> 519

Glu Thr Asp Glu Arg Gly Lys Ile Met Lys Asp Pro Lys Ser Val Val
1 5 10 15

Pro Ala Ala Phe Val Ser Phe Arg Ser Arg Trp Gly Ala Ala Val Cys
20 25 30

Ala Gln Thr Gln Gln Thr Ser Asn Pro Thr Val Trp Leu Thr Glu Trp
35 40 45

Ala Pro Glu Pro Arg Asp Val Tyr Trp Asp Asn Leu Ser Ile Pro Phe
50 55 60

Val Tyr Leu Thr Ile Arg Arg Leu Ile Ile Ala Val Ala Phe Phe Phe
65 70 75 80

Leu Asn Phe Phe Tyr Val Leu Pro Ile Ala Phe Val Gln Ser Leu Ala
85 90 95

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

PF59082PF60142_PCT_SEQ_LIST.txt

Glu Met Arg Thr Ile Lys Ser Phe Ile Gln Gly Phe Leu Pro Gly Ile
115 120 125

Ala Leu Lys Ile Phe Leu Ile Leu Leu Pro Ser Ile Leu Met Phe Met
130 135 140

Ser Lys Val Glu Gly Leu Thr Ser Val Ser Ser Leu Glu Arg Arg Ser
145 150 155 160

Ala Phe Lys Tyr Tyr Ile Phe Leu Phe Phe Asn Val Phe Leu Gly Ser
165 170 175

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

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

Ala Thr Phe Phe Ile Thr Tyr Val Met Val Asp Gly Trp Ala Gly Val
210 215 220

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

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

Pro Gly Ser Ile Gly Phe Asp Ser Asn Glu Pro Gln Ile Gln Leu Tyr
260 265 270

Phe Leu Leu Gly Leu Val Tyr Ala Val Val Thr Pro Phe Leu Leu Pro
275 280 285

Phe Ile Leu Ile Phe Phe Gly Leu Ala Tyr Val Val Tyr Arg His Gln
290 295 300

Ile Ile Asn Val Tyr Asn Gln Glu Tyr Glu Ser Ala Ala Ala Phe Trp
305 310 315 320

Pro Ser Val His Gly Arg Ile Ile Val Ala Leu Ile Val Ser Gln Leu
325 330 335

Leu Leu Leu Gly Leu Leu Ser Thr Lys Gly Ala Gly Gln Ser Thr Pro
340 345 350

Val Leu Leu Val Leu Pro Val Val Thr Phe Tyr Phe Tyr Lys Tyr Cys
355 360 365

Lys Asn Arg Tyr Glu Pro Ala Phe Val Glu Tyr Pro Leu Gln Asp Ala
370 375 380

Met Arg Lys Asp Thr Leu Glu Arg Ala Arg Glu Pro Gly Phe Asp Leu
385 390 395 400

Lys Gly Tyr Leu Met Asn Ala Tyr Ile His Pro Val Phe Lys
405 410

<210> 520
<211> 399
<212> PRT
<213> Artificial sequence

<220>
<223> DUF221 domain

<400> 520

Ser Ile Arg Leu Leu Gln Cys Glu Asn Met Leu Lys Arg Lys Glu Leu
1 5 10 15

Pro Val Ala Phe Val Ser Phe Lys Ser Gln Leu Asp Ala Ala Gln Ala
20 25 30

Ala Glu Met Gln Gln His Val Asn Pro Leu Ser Leu Val Thr Thr Tyr
35 40 45

Ala Pro Glu Pro Pro Asp Ala Leu Trp Thr Asn Leu Ala Ile Pro Phe
50 55 60

Cys Arg Ile Ala Ile Tyr Lys Leu Gly Val Phe Ile Ala Ala Phe Leu
65 70 75 80

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

Gln Phe Glu Lys Ile Lys Ile Trp Phe Pro Pro Ala Arg Ala Val Glu
100 105 110

Leu Ile Pro Gly Leu Asn Ser Val Val Thr Gly Tyr Leu Pro Ser Met
115 120 125

Ile Leu Asn Gly Phe Ile Tyr Leu Ile Pro Phe Ala Met Leu Gly Met
130 135 140

Ala Ser Phe Glu Gly Cys Ile Ala Lys Ser Gln Lys Glu Ile Lys Ala
145 150 155 160

Cys Asn Met Val Phe Tyr Phe Leu Leu Gly Asn Val Phe Phe Leu Ser
165 170 175

Ile Leu Ser Gly Ser Leu Leu His Gln Ile Gly Glu Ser Phe Thr His
180 185 190

Pro Lys Asp Ile Pro Ser Arg Leu Ala Arg Ala Val Ser Ala Gln Ser
195 200 205

PF59082PF60142_PCT_SEQ_LIST.txt

Asp Phe Phe Ile Thr Tyr Ile Leu Thr Asp Gly Met Ser Gly Phe Ser
210 215 220

Leu Glu Val Leu Gln Phe Gly Leu Leu Thr Trp His Phe Phe Lys Ala
225 230 235 240

His Ser Ile Gly His Ser Glu Gln Pro Tyr Leu Tyr Gly Phe Pro Tyr
245 250 255

Tyr Arg Val Val Pro Ile Val Ser Leu Ala Val Leu Ile Gly Leu Val
260 265 270

Tyr Ala Val Val Ala Pro Leu Leu Leu Pro Ile Leu Val Ile Tyr Phe
275 280 285

Leu Leu Gly Tyr Ala Val Tyr Ile Asn Gln Met Glu Asp Val Tyr Glu
290 295 300

Ile Thr Tyr Asp Thr Cys Gly Gln Tyr Trp Pro Asn Ile His Arg Tyr
305 310 315 320

Ile Phe Leu Ser Val Thr Leu Met Gln Ile Thr Met Leu Lys Ser Lys
325 330 335

Pro Gly Ala Ser Phe Ala Thr Val Pro Leu Leu Val Ser Thr Ile Leu
340 345 350

Phe Asn Glu Tyr Cys Lys Val Arg Phe Leu Pro Thr Phe Leu His Arg
355 360 365

Pro Val Gln Val Ala Lys Glu Asn Asp Asp Leu Asn Glu Ala Glu Gly
370 375 380

Met Arg Gly Asp Leu Asp His Ala Ile Ser Ala Tyr Lys Pro Pro
385 390 395

<210> 521
<211> 451
<212> PRT
<213> Artificial sequence

<220>
<223> DUF221 domain

<400> 521

Lys Lys Leu Val Leu Gly Ser Arg Leu Ser Asp Tyr Lys Asp Gly Arg
1 5 10 15

Ala Pro Gly Ala Gly Ile Ala Phe Val Val Phe Lys Asp Val Tyr Thr
20 25 30

Ala Asn Lys Ala Val Arg Asp Phe Arg Met Glu Arg Lys Lys Thr Pro
35 40 45

PF59082PF60142_PCT_SEQ_LIST.txt

Ile Gly Arg Phe Phe Pro Val Met Glu Leu Gln Leu Glu Arg Ser Arg
50 55 60

Trp Thr Val Glu Arg Ala Pro Pro Ala Ser Asp Ile Tyr Trp Asn His
65 70 75 80

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

Thr Cys Leu Ile Leu Met Leu Leu Phe Phe Ser Ser Pro Leu Ala Ile
100 105 110

Ile Ser Gly Met Gln Ser Ala Ala Arg Ile Ile Asn Val Glu Ala Met
115 120 125

Asp Asn Ala Lys Ser Trp Leu Val Trp Leu Gln Ser Ser Ser Trp Phe
130 135 140

Trp Thr Ile Ile Phe Gln Phe Leu Pro Asn Val Leu Ile Phe Val Ser
145 150 155 160

Met Tyr Ile Ile Ile Pro Ser Val Leu Ser Tyr Phe Ser Lys Phe Glu
165 170 175

Cys His Leu Thr Val Ser Gly Glu Gln Arg Ala Ala Leu Leu Lys Met
180 185 190

Val Cys Phe Phe Leu Val Asn Leu Ile Leu Leu Arg Ala Leu Val Glu
195 200 205

Ser Ser Leu Glu Ser Trp Ile Leu Ser Met Gly Arg Cys Tyr Leu Asp
210 215 220

Ser Val Asp Cys Lys Gln Ile Glu Gln Tyr Leu Ser Pro Ser Phe Leu
225 230 235 240

Ser Arg Ser Ser Leu Ser Ser Leu Ala Phe Leu Ile Thr Cys Thr Phe
245 250 255

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

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

Glu Asn Glu Asp Tyr Gln Leu Met His Asp Gly Glu Glu Thr Asn Asn
290 295 300

Leu Arg Ala Pro Leu Met Ser Glu Arg Glu Asp Ser Gly Ile Leu Asn
305 310 315 320

PF59082PF60142_PCT_SEQ_LIST.txt

Gly Ile Glu Glu His Asp Leu Ser Leu Tyr Pro Ile Asn Arg Ser Phe
325 330 335

His Met Pro Lys Gln Thr Phe Asp Phe Ala Gln Tyr Tyr Ala Phe Asp
340 345 350

Ile Thr Ile Phe Ala Leu Thr Met Ile Tyr Ser Leu Phe Ala Pro Leu
355 360 365

Thr Val Pro Val Gly Ala Val Tyr Phe Gly Tyr Arg Tyr Leu Val Asp
370 375 380

Lys Tyr Asn Phe Leu Phe Ile Tyr Arg Val Arg Gly Phe Pro Ala Gly
385 390 395 400

Asn Asp Gly Lys Leu Met Asp Met Val Ile Cys Ile Met Gln Phe Cys
405 410 415

Val Ile Phe Phe Leu Val Ala Met Leu Leu Phe Phe Ala Val Gln Gly
420 425 430

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

Tyr Lys Leu
450

<210> 522
<211> 408
<212> PRT
<213> Artificial sequence

<220>
<223> DUF221 domain

<400> 522

Lys His Asp Val Lys Asp Ser Glu Leu Ser Leu Pro Asp Lys Asp Cys
1 5 10 15

Gly Ala Ala Phe Val Phe Phe Lys Thr Arg Tyr Ala Ala Leu Val Val
20 25 30

Ser Glu Ile Val Gln Thr Ser Asn Pro Met Glu Trp Val Thr Ser Leu
35 40 45

Ala Pro Asp Arg Asp Asp Val Tyr Trp Ser Asn Leu Trp Leu Pro Tyr
50 55 60

Lys Gln Leu Trp Ile Arg Arg Ile Val Thr Leu Ser Gly Ser Ile Val
65 70 75 80

Phe Met Phe Leu Phe Leu Ile Pro Val Thr Phe Ile Gln Gly Leu Thr
85 90 95

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

PF59082PF60142_PCT_SEQ_LIST.txt

Leu Phe Lys Thr Leu Pro Ala Gln Asp Leu Ile Asp Met Asp Arg Glu
370 375 380

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

Ala Tyr Cys Gln Phe Ala Asp Thr
405

<210> 523
<211> 408
<212> PRT
<213> Artificial sequence

<220>
<223> DUF221 domain

<400> 523

Lys Pro Asp Leu Ser Asp Pro Glu Val Ile Glu Ala Gln Lys Asp Cys
1 5 10 15

Pro Gly Ala Ile Val Phe Phe Lys Thr Arg Tyr Ala Ala Ile Val Ala
20 25 30

Ser Arg Ile Leu Gln Ser Ser Asn Pro Met Leu Trp Val Thr Asp Phe
35 40 45

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

Arg Gln Ile Trp Leu Arg Lys Ile Ala Thr Leu Ala Ala Ser Val Ala
65 70 75 80

Phe Met Phe Val Phe Ile Val Pro Val Ala Phe Val Gln Ser Met Met
85 90 95

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

Lys Lys Pro Phe Phe Val Lys Leu Val Thr Gly Tyr Leu Pro Ser Val
115 120 125

Val Leu Leu Leu Ser Leu Tyr Thr Val Pro Pro Leu Met Met Phe Phe
130 135 140

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

Cys Cys Lys Ile Leu Phe Phe Thr Ile Trp Asn Val Phe Phe Val Asn
165 170 175

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

PF59082PF60142_PCT_SEQ_LIST.txt

Arg Asp Met Pro Ser Met Leu Ala Glu Leu Val Pro Lys Gln Ala Thr
195 200 205

Phe Phe Ile Thr Tyr Val Leu Thr Ser Gly Trp Ala Ser Leu Cys Ser
210 215 220

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

Ile Phe Cys Tyr Arg Asp Asp Pro Glu Tyr Gly Tyr Ser Phe Pro Tyr
245 250 255

His Thr Glu Val Pro Lys Val Leu Leu Phe Asn Leu Leu Gly Phe Thr
260 265 270

Phe Ser Ile Met Ala Pro Leu Ile Leu Pro Phe Leu Leu Val Tyr Phe
275 280 285

Cys Leu Gly Tyr Leu Val Tyr Arg Asn Gln Ile Leu Asn Val Tyr Tyr
290 295 300

Pro Lys Tyr Glu Met Gly Gly Lys Leu Trp Pro Ile Met His Ser Thr
305 310 315 320

Leu Val Phe Ala Leu Val Leu Thr Gln Thr Ile Ala Leu Gly Val Phe
325 330 335

Thr Ile Lys His Ala Thr Ile Ser Ser Gly Phe Thr Val Leu Leu Ile
340 345 350

Ile Gly Thr Val Leu Phe His Gln Tyr Cys Arg His Arg Phe Ser Ser
355 360 365

Ile Phe Asn Ser Phe Ser Ala Gln Asp Leu Ile Glu Met Asp Arg Asp
370 375 380

Asp Glu Gln Ser Gly Arg Met Glu Glu Ile His Lys His Leu Leu Asp
385 390 395 400

Ala Tyr Ser Gln Gly Thr Thr Asn
405

<210> 524
<211> 414
<212> PRT
<213> Artificial sequence

<220>
<223> DUF221 domain

<400> 524

Glu Asp Glu Glu Arg His Lys Val Ile Thr Asp Pro Asn Ala Ile Met
Seite 605

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

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PF59082PF60142_PCT_SEQ_LIST.txt

Phe Ile Ile Val Phe Phe Ser Leu Ala Tyr Leu Val Phe Arg His Gln
290 295 300

Ile Ile Asn Val Tyr Asn Gln Gln Tyr Glu Ser Gly Ala Gln Phe Trp
305 310 315 320

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

Leu Leu Leu Gly Leu Leu Ser Thr Gln Glu Ala Glu Lys Ser Thr Val
340 345 350

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

Lys Gly Arg Phe Glu Pro Ala Phe Ile Lys Phe Pro Leu Gln Asp Ala
370 375 380

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

Arg Glu Tyr Leu Lys Asp Ala Tyr Val His Pro Val Phe Gln
405 410

<210> 525
<211> 414
<212> PRT
<213> Artificial sequence

<220>
<223> DUF221 domain

<400> 525

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

Pro Ala Ala Phe Val Ser Phe Arg Ser Arg Trp Gly Ala Ala Val Cys
20 25 30

Ala Gln Thr Gln Gln Thr Ser Asn Pro Thr Val Trp Ile Thr Glu Trp
35 40 45

Ala Pro Glu Pro Arg Asp Val Tyr Trp Asn Asn Leu Ser Ile Pro Phe
50 55 60

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

Leu Asn Phe Phe Tyr Val Ile Pro Ile Ala Phe Val Gln Ser Leu Ala
85 90 95

Ser Leu Glu Gly Ile Glu Lys Ala Leu Pro Phe Leu Lys Pro Leu Ile
Seite 607

100

105

110

Lys Ile Asp Val Ile Lys Ser Phe Ile Gln Gly Phe Leu Pro Gly Ile
 115 120 125

Ala Leu Lys Val Phe Leu Ile Leu Leu Pro Thr Ile Leu Met Phe Met
 130 135 140

Ser Lys Phe Glu Gly Leu Ile Ser Gln Ser Ser Leu Glu Arg Arg Ser
 145 150 155 160

Ala Ser Lys Tyr Tyr Ile Phe Leu Phe Phe Asn Val Phe Leu Gly Ser
 165 170 175

Ile Val Thr Gly Ser Ala Leu Asp Gln Leu Lys Ala Tyr Ile His Gln
 180 185 190

Ser Ala Asn Glu Ile Pro Arg Thr Ile Gly Val Ala Ile Pro Met Arg
 195 200 205

Ala Thr Phe Phe Ile Thr Tyr Val Met Val Asp Gly Trp Thr Gly Val
 210 215 220

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

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

Pro Gly Ser Ile Cys Phe Asp Trp Cys Glu Pro Arg Ile Gln Leu Tyr
 260 265 270

Phe Leu Leu Gly Leu Val Tyr Ala Val Val Thr Pro Leu Leu Leu Pro
 275 280 285

Phe Ile Leu Val Phe Phe Gly Leu Ala Tyr Val Val Tyr Arg His Gln
 290 295 300

Ile Ile Asn Val Tyr Asn Gln Gln Tyr Glu Ser Gly Ala Gln Phe Trp
 305 310 315 320

Pro Ser Val His Gly Arg Ile Ile Ile Ala Leu Ile Val Ser Gln Leu
 325 330 335

Leu Leu Ile Gly Leu Leu Ser Thr Lys Gly Phe Glu Glu Thr Thr Pro
 340 345 350

Val Leu Val Val Leu Pro Val Leu Thr Phe Trp Phe Tyr Lys Tyr Cys
 355 360 365

Lys Asn Arg Phe Glu Pro Ala Phe Val Arg Asn Pro Leu Gln Glu Ala
 370 375 380

PF59082PF60142_PCT_SEQ_LIST.txt

Met Arg Lys Asp Thr Leu Glu Arg Ala Arg Glu Pro Thr Phe Asp Leu
385 390 395 400

Lys Ala Tyr Leu Ala Asn Ala Tyr Leu His Pro Val Phe Lys
405 410

<210> 526
<211> 411
<212> PRT
<213> Artificial sequence

<220>
<223> DUF221 domain

<400> 526

Leu Glu Ala Glu Gln Lys Thr Thr Leu Arg Glu Lys Gln Gln Gln Ala
1 5 10 15

Ala Ile Val Phe Phe Asn Arg Arg Ser Ala Ala Ala Ser Ala Ser Gln
20 25 30

Thr Leu His Ala Gln Met Phe Asp Lys Trp Thr Val Glu Gln Ala Pro
35 40 45

Glu Pro Arg Gln Ile Ile Trp Ser Asn Leu Ser Lys Lys Ile Tyr Glu
50 55 60

Arg Gln Ile Arg Gln Val Val Val Tyr Thr Ile Val Phe Leu Thr Val
65 70 75 80

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

Glu Lys Leu Arg Glu Lys Leu Pro Phe Leu Lys Val Val Val Asp Gln
100 105 110

Pro Lys Ile Lys Thr Val Leu Gln Ala Tyr Leu Pro Gln Leu Ala Leu
115 120 125

Ile Val Phe Leu Ala Leu Leu Pro Ser Leu Leu Met Phe Leu Ser Lys
130 135 140

Leu Glu Gly Ile Pro Ser Gln Gly His Thr Val Arg Ala Ala Ala Gly
145 150 155 160

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

Ser Ser Thr Leu Phe Ser Ala Leu Thr Thr Ile Ile Asn Asn Pro Pro
180 185 190

Gly Ile Val Asn Met Leu Ala Ser Ser Leu Pro Gly Ser Ala Thr Phe
Seite 609

195

200

205

Phe Leu Thr Phe Val Ala Leu Lys Phe Phe Val Gly Tyr Gly Leu Glu
 210 215 220

Leu Ser Arg Leu Val Pro Leu Ile Ile Phe His Leu Lys Arg Lys Tyr
 225 230 235 240

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

Leu Gly Tyr Asn Thr Arg Val Pro Asn Asp Met Leu Ile Val Thr Ile
 260 265 270

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

Ala Tyr Phe Ala Leu Gly Trp Ile Ile Val Lys Asn Gln Val Leu Arg
 290 295 300

Val Tyr Val Pro Ser Tyr Glu Ser Asn Gly Arg Met Trp Pro His Met
 305 310 315 320

His Thr Arg Ile Ile Ala Ala Leu Leu Ile Tyr Gln Ile Thr Met Val
 325 330 335

Gly Val Ile Leu Leu Lys Lys Phe Leu Tyr Ser Pro Val Leu Val Pro
 340 345 350

Leu Ile Pro Ile Ser Phe Ile Phe Ala Tyr Ile Cys His Met Arg Phe
 355 360 365

Tyr Pro Ala Phe Ala Lys Thr Pro Leu Glu Val Val Gln His Asn Val
 370 375 380

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

Cys Leu Lys Pro Glu Lys Leu Glu Asp Val Asp
 405 410

<210> 527
 <211> 414
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DUF221 domain

<400> 527

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

PF59082PF60142_PCT_SEQ_LIST.txt

Pro Val Ala Phe Val Thr Phe Asp Ser Arg Trp Gly Ala Ala Val Cys
20 25 30

Ala Gln Thr Gln Gln Ser Lys Asn Pro Thr Gln Trp Leu Thr Asp Trp
35 40 45

Ala Pro Glu Pro Arg Asp Val Tyr Trp Gln Asn Leu Ala Ile Pro Phe
50 55 60

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

Leu Val Phe Phe Tyr Met Ile Pro Ile Ala Phe Val Gln Ser Leu Ala
85 90 95

Asn Leu Glu Gly Ile Glu Lys Val Ala Pro Phe Leu Arg Pro Val Ile
100 105 110

Asp Thr Pro Val Val Lys Ser Phe Leu Gln Gly Phe Leu Pro Gly Leu
115 120 125

Ala Leu Lys Ile Phe Leu Tyr Ile Leu Pro Thr Val Leu Met Ile Met
130 135 140

Ser Lys Val Glu Gly Tyr Val Ser Leu Ser Ser Leu Glu Arg Arg Ala
145 150 155 160

Ala Ser Lys Tyr Tyr Tyr Phe Met Leu Val Asn Val Phe Leu Gly Ser
165 170 175

Ile Ile Ala Gly Thr Ala Phe Glu Gln Leu Asn Ala Phe Phe His Gln
180 185 190

Pro Pro Ser Gln Ile Pro Arg Thr Ile Gly Val Ala Ile Pro Met Lys
195 200 205

Ala Thr Phe Phe Met Thr Tyr Ile Met Val Asp Gly Trp Ala Gly Ile
210 215 220

Ala Asn Glu Ile Leu Arg Val Lys Pro Leu Val Ile Tyr His Leu Lys
225 230 235 240

Asn Met Phe Ile Val Lys Thr Glu Arg Asp Arg Glu Arg Ala Met Asp
245 250 255

Pro Gly Ser Ile Gly Leu Ala Glu Asn Leu Pro Ser Leu Gln Leu Tyr
260 265 270

Phe Leu Leu Gly Leu Val Tyr Ala Val Val Thr Pro Ile Leu Leu Pro
275 280 285

Phe Ile Ile Ile Phe Phe Ala Phe Ala Phe Leu Val Tyr Arg His Gln
Seite 611

290

Ile Ile Asn Val Tyr Asn Gln Glu Tyr Glu Ser Ala Ala Ala Phe Trp
305 310 315 320

Pro Gln Val His Ser Arg Ile Ile Ala Ser Leu Leu Ile Ser His Val
325 330 335

Thr Leu Phe Gly Leu Met Ser Thr Met Lys Ala Ala Tyr Ser Thr Pro
340 345 350

Leu Leu Ile Phe Leu Pro Leu Leu Thr Ile Trp Phe His Lys Tyr Cys
355 360 365

Lys Ser Arg Phe Glu Pro Ala Phe Arg Lys Tyr Pro Leu Glu Glu Ala
370 375 380

Met Glu Lys Asp Asn Leu Glu Arg Thr Ser Glu Pro Asn Leu Asn Leu
385 390 395 400

Lys Ser Tyr Leu Gln Asn Ala Tyr Leu His Pro Ile Phe His
405 410

<210> 528
<211> 407
<212> PRT
<213> Artificial sequence

<220>
<223> DUF221 domain

<400> 528

Asn Val Arg Met Glu Gln Ser Asp Thr Thr Arg Ser Arg Gln Glu Val
1 5 10 15

Pro Ala Ala Phe Val Ser Phe Arg Ser Arg Tyr Gly Ala Ala Asn Ala
20 25 30

Ile Tyr Ile Arg Gln Ser Asp Lys Pro Thr Glu Trp Gln Thr Glu His
35 40 45

Ala Pro Asp Pro His Asp Val Tyr Trp Pro Phe Phe Ser Thr Ser Phe
50 55 60

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

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

Tyr Met Glu Gln Leu Glu Thr Trp Leu Pro Phe Leu Arg Asn Ile Leu
100 105 110

Glu Ile Ala Val Val Ser Gln Leu Val Thr Gly Tyr Leu Pro Ser Val
 115 120 125
 Ile Leu His Phe Leu Ser Ser Tyr Val Pro Ser Ile Met Lys Leu Phe
 130 135 140
 Ser Thr Met Gln Gly Phe Ile Ser Val Ser Gly Ile Glu Arg Ser Ala
 145 150 155 160
 Cys Asn Lys Met Leu Arg Phe Thr Ile Trp Ser Val Phe Phe Ala Asn
 165 170 175
 Val Leu Thr Gly Ser Val Leu Gly Gln Leu Glu Ile Phe Leu Asp Pro
 180 185 190
 Lys Glu Ile Pro Lys Arg Leu Ala Val Val Val Pro Ala Gln Ala Ser
 195 200 205
 Phe Phe Ile Thr Tyr Val Val Thr Ser Trp Thr Ser Ile Ala Ser Glu
 210 215 220
 Leu Thr Gln Thr Ala Ala Leu Leu Phe His Leu Trp Gly Ser Cys Ala
 225 230 235 240
 Lys Cys Cys Lys Arg Asp Glu Ser Lys Pro Pro Ser Met His Tyr His
 245 250 255
 Ser Glu Ile Pro Arg Val Leu Leu Phe Gly Leu Leu Gly Leu Thr Tyr
 260 265 270
 Phe Ile Val Ser Pro Leu Ile Leu Pro Phe Val Leu Val Tyr Phe Cys
 275 280 285
 Leu Gly Tyr Phe Ile Tyr Arg Asn Gln Leu Phe Asn Val Tyr Ser Pro
 290 295 300
 Lys Tyr Asp Thr Gly Gly Arg Phe Trp Pro Ile Val His Gly Gly Thr
 305 310 315 320
 Ile Phe Ser Leu Val Leu Met His Val Ile Ala Ile Gly Val Phe Gly
 325 330 335
 Leu Lys Lys Leu Pro Leu Ala Ser Ser Leu Leu Val Pro Leu Pro Val
 340 345 350
 Leu Thr Leu Leu Phe Asn Glu Tyr Cys Arg Asn Arg Phe Leu Pro Ile
 355 360 365
 Phe Glu Ala Tyr Ser Thr Glu Ser Leu Ile Lys Lys Asp Arg Glu Glu
 370 375 380
 Glu Ser Lys Pro Glu Met Ala Glu Phe Phe Ser Asn Leu Val Asn Ala
 Seite 613

385 390 395 400

Tyr Cys Asp Pro Ala Met Lys
405

<210> 529
<211> 408
<212> PRT
<213> Artificial sequence

<220>
<223> DUF221 domain
<400> 529

Lys Ser Asp Leu Gln Asp Ser Ser Leu Lys Leu Asp Asp Gln Glu Cys
1 5 10 15

Ala Ala Ala Phe Val Tyr Phe Arg Thr Arg Tyr Ala Ala Leu Val Ala
20 25 30

Ser Glu Ile Leu Gln Thr Ser Asn Pro Met Lys Trp Val Thr Asp Leu
35 40 45

Ala Pro Glu Pro Asp Asp Val Tyr Trp Ser Asn Leu Trp Leu Pro Tyr
50 55 60

Lys Gln Leu Trp Ile Arg Arg Ile Ala Thr Leu Leu Gly Ser Ile Val
65 70 75 80

Phe Met Leu Phe Phe Leu Ile Pro Val Thr Phe Ile Gln Gly Leu Ser
85 90 95

Gln Leu Glu Gln Leu Gln Gln Arg Leu Pro Phe Leu Lys Gly Ile Leu
100 105 110

Glu Lys Lys Tyr Met Ser Gln Leu Val Thr Gly Tyr Leu Pro Ser Val
115 120 125

Ile Leu Gln Ile Phe Leu Tyr Ala Val Ala Pro Ile Met Ile Leu Phe
130 135 140

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

Cys Cys Lys Val Leu Tyr Phe Thr Val Trp Asn Ile Phe Phe Gly Asn
165 170 175

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

Lys Asp Ile Pro Val Gln Leu Ala Arg Ala Ile Pro Val Gln Ala Thr
195 200 205

Phe Phe Ile Thr Tyr Val Leu Thr Ser Gly Trp Ala Ser Leu Ser Ser
210 215 220

Glu Leu Met Gln Leu Phe Gly Leu Ile Trp Asn Phe Val Arg Lys Tyr
225 230 235 240

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

His Thr Glu Val Pro Lys Val Leu Leu Phe Gly Leu Leu Gly Phe Thr
260 265 270

Cys Ser Val Leu Ala Pro Leu Ile Leu Pro Phe Leu Leu Val Tyr Phe
275 280 285

Phe Leu Gly Tyr Ile Val Tyr Arg Asn Gln Leu Leu Asn Val Tyr Arg
290 295 300

Thr Arg Tyr Asp Thr Gly Gly Leu Tyr Trp Pro Ile Ala His Asn Ala
305 310 315 320

Val Ile Phe Ser Leu Val Leu Thr Gln Ile Ile Cys Leu Gly Val Phe
325 330 335

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

Ile Leu Thr Leu Leu Phe Asn Gln Tyr Cys Arg Asn Arg Leu Leu Pro
355 360 365

Leu Phe Arg Thr Thr Pro Ala Gln Asp Leu Ile Asp Met Asp Arg Glu
370 375 380

Asp Glu Arg Ser Gly Arg Met Asp Glu Ile His His Arg Leu His Ser
385 390 395 400

Ala Tyr Cys Gln Phe His Asp Thr
405

<210> 530
<211> 406
<212> PRT
<213> Artificial sequence

<220>
<223> DUF221 domain

<400> 530

Glu Leu Gly Glu Leu Thr Leu Thr Thr Thr Glu Glu Glu Arg Pro Val
1 5 10 15

Ala Phe Val Phe Phe Lys Ser Arg Tyr Asp Ala Leu Val Val Ser Glu
20 25 30

PF59082PF60142_PCT_SEQ_LIST.txt

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

PF59082PF60142_PCT_SEQ_LIST.txt

Tyr Glu Ser Gly Gly Gln Tyr Trp Pro Val Phe His Asn Thr Thr Ile
305 310 315 320

Phe Ser Leu Ile Leu Ser Gln Val Ile Ala Leu Gly Phe Phe Gly Leu
325 330 335

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

Thr Leu Leu Phe Ser Glu Tyr Cys Arg Gln Arg Phe Ala Pro Ile Phe
355 360 365

Gln Lys Tyr Pro Ala Glu Ile Leu Ile Ala Met Asp Arg Ala Asp Glu
370 375 380

Met Thr Gly Lys Met Glu Glu Ile His Asn Asn Leu Lys Val Ala Tyr
385 390 395 400

Ser Gln Ile Pro Thr Cys
405

<210> 531
<211> 72
<212> PRT
<213> Artificial sequence

<220>
<223> DUF221 domain

<400> 531

Ile Met Glu Glu Arg Lys Lys Val Lys Lys Asp Asp Thr Ser Val Met
1 5 10 15

Pro Ala Ala Phe Val Ser Phe Lys Thr Arg Trp Gly Ala Ala Val Ser
20 25 30

Ala Gln Thr Gln Gln Ser Ser Asp Pro Thr Glu Trp Leu Thr Glu Trp
35 40 45

Ala Pro Glu Ala Arg Glu Val Phe Trp Ser Asn Leu Ala Ile Pro Tyr
50 55 60

Val Ser Leu Thr His Arg Arg His
65 70

<210> 532
<211> 413
<212> PRT
<213> Artificial sequence

<220>
<223> DUF221 domain

<400> 532

Leu Glu Thr Glu Gln Lys Ala Val Leu Ala Glu Lys Gln Gln Thr Ala
Seite 617

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

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PF59082PF60142_PCT_SEQ_LIST.txt

Gly Ile Thr Tyr Phe Gly Leu Gly Trp Leu Val Leu Arg Asn Gln Ala
290 295 300

Leu Lys Val Tyr Val Pro Ser Tyr Glu Ser Tyr Gly Arg Met Trp Pro
305 310 315 320

His Ile His Gln Arg Ile Leu Ala Ala Leu Phe Leu Phe Gln Val Val
325 330 335

Met Phe Gly Tyr Leu Gly Ala Lys Thr Phe Phe Tyr Thr Ala Leu Val
340 345 350

Ile Pro Leu Ile Ile Thr Ser Leu Ile Phe Gly Tyr Val Cys Arg Gln
355 360 365

Lys Phe Tyr Gly Gly Phe Glu His Thr Ala Leu Glu Val Ala Cys Arg
370 375 380

Glu Leu Lys Gln Ser Pro Asp Leu Glu Glu Ile Phe Arg Ala Tyr Ile
385 390 395 400

Pro His Ser Leu Ser Ser His Lys Pro Glu Glu His Glu
405 410

<210> 533
<211> 408
<212> PRT
<213> Artificial sequence

<220>
<223> DUF221 domain

<400> 533

Glu Leu Gly Glu Leu Thr Met Thr Thr Thr Thr Glu Gln Glu Arg
1 5 10 15

Ser Ala Ala Phe Val Phe Phe Lys Thr Arg Tyr Asp Ala Leu Val Val
20 25 30

Ser Glu Val Leu Gln Ser Ser Asn Pro Met Leu Trp Val Thr Asp Leu
35 40 45

Ala Pro Glu Pro His Asp Val Tyr Trp Lys Asn Leu Asn Ile Pro Tyr
50 55 60

Arg Gln Leu Trp Ile Arg Lys Ile Ala Thr Leu Val Gly Ala Val Ala
65 70 75 80

Phe Met Phe Val Phe Leu Ile Pro Val Thr Phe Ile Gln Gly Leu Thr
85 90 95

Gln Leu Val Gln Leu Ser His Ala Phe Pro Phe Leu Arg Gly Ile Leu
Seite 619

100

105

110

Ser Lys Asn Phe Ile Asn Gln Val Ile Thr Gly Tyr Leu Pro Ser Val
 115 120 125

Ile Leu Ile Leu Phe Phe Tyr Ala Val Pro Pro Leu Met Met Tyr Phe
 130 135 140

Ser Ala Leu Glu Gly Cys Ile Ser Arg Ser Ile Arg Lys Lys Ser Ala
 145 150 155 160

Cys Ile Lys Val Leu Tyr Phe Thr Ile Trp Asn Val Phe Phe Val Asn
 165 170 175

Ile Leu Ser Gly Ser Val Ile Arg Gln Leu Asn Val Phe Ser Ser Val
 180 185 190

Arg Asp Ile Pro Ala Gln Leu Ala Arg Ala Val Pro Thr Gln Ala Gly
 195 200 205

Phe Phe Met Thr Tyr Cys Phe Thr Ser Gly Trp Ala Ser Leu Ala Cys
 210 215 220

Glu Ile Met Gln Pro Met Ala Leu Ile Trp Asn Leu Val Ala Lys Val
 225 230 235 240

Val Thr Lys Asn Glu Asp Glu Ser Tyr Glu Thr Leu Arg Phe Pro Tyr
 245 250 255

His Thr Glu Ile Pro Arg Leu Leu Leu Phe Gly Leu Leu Gly Phe Thr
 260 265 270

Asn Ser Val Ile Ala Pro Leu Ile Leu Pro Phe Leu Leu Ile Tyr Phe
 275 280 285

Phe Leu Ala Tyr Leu Ile Tyr Lys Asn Gln Ile Leu Asn Val Tyr Ile
 290 295 300

Thr Lys Tyr Glu Ser Gly Gly Gln Tyr Trp Pro Ile Phe His Asn Thr
 305 310 315 320

Thr Ile Phe Ser Leu Ile Leu Thr Gln Ile Ile Ala Leu Gly Phe Phe
 325 330 335

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

Leu Leu Thr Leu Leu Phe Ser Glu Tyr Cys Arg Gln Arg Phe Ala Pro
 355 360 365

Ile Phe Asn Lys Asn Pro Ala Gln Val Leu Ile Asp Met Asp Arg Ala
 370 375 380

PF59082PF60142_PCT_SEQ_LIST.txt

Asp Glu Ile Ser Gly Lys Met Glu Glu Leu His Lys Lys Leu His Asn
385 390 395 400

Val Tyr Ser Gln Ile Pro Leu His
405

<210> 534
<211> 407
<212> PRT
<213> Artificial sequence

<220>
<223> DUF221 domain

<400> 534

Ile Met Glu Glu Arg Lys Arg Ile Lys Lys Asp Asp Lys Ser Val Met
1 5 10 15

Gln Ala Ala Phe Val Ser Phe Lys Thr Arg Trp Gly Ala Ala Val Cys
20 25 30

Ala Gln Thr Gln Gln Thr Lys Asn Pro Thr Glu Trp Leu Thr Glu Trp
35 40 45

Ala Pro Glu Ala Arg Glu Met Tyr Trp Pro Asn Leu Ala Met Pro Tyr
50 55 60

Val Ser Leu Thr Val Arg Arg Phe Val Met His Ile Ala Phe Phe Phe
65 70 75 80

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

Ser Ile Glu Gly Ile Glu Lys Ser Ala Pro Phe Leu Ser Pro Ile Val
100 105 110

Lys Asn Lys Leu Met Lys Ser Leu Ile Gln Gly Phe Leu Pro Gly Ile
115 120 125

Val Leu Lys Leu Phe Leu Ile Phe Leu Pro Thr Ile Leu Met Ile Met
130 135 140

Ser Lys Phe Glu Gly Phe Ile Ser Ile Ser Ser Leu Glu Arg Arg Ala
145 150 155 160

Ala Phe Arg Tyr Tyr Ile Phe Asn Leu Val Asn Val Phe Leu Gly Ser
165 170 175

Val Ile Thr Gly Ser Ala Phe Glu Gln Leu Asp Ser Phe Leu Lys Gln
180 185 190

Ser Ala Asn Asp Ile Pro Arg Thr Val Gly Val Ala Ile Pro Ile Lys
Seite 621

195

200

205

Ala Thr Phe Phe Ile Thr Tyr Ile Met Val Asp Gly Trp Ala Gly Val
 210 215 220

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

Asn Phe Phe Phe Val Lys Thr Glu Lys Asp Arg Glu Glu Ala Met Asp
 245 250 255

Pro Gly Gln Ile Asp Phe Tyr Ala Thr Glu Pro Arg Ile Gln Leu Tyr
 260 265 270

Phe Leu Leu Gly Leu Val Tyr Ala Pro Val Thr Pro Val Leu Leu Pro
 275 280 285

Phe Ile Ile Phe Phe Phe Gly Phe Ala Tyr Leu Val Phe Arg His Gln
 290 295 300

Lys Tyr Glu Ser Ala Gly Ala Phe Trp Pro Asp Val His Gly Arg Ile
 305 310 315 320

Ile Ser Ala Leu Ile Ile Ser Gln Ile Leu Leu Leu Gly Leu Met Ser
 325 330 335

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

Leu Thr Phe Gly Phe His Arg Phe Cys Lys Gly Arg Tyr Glu Ser Ala
 355 360 365

Phe Val Ile Asn Pro Leu Gln Glu Ala Met Ile Lys Asp Thr Leu Glu
 370 375 380

Arg Ala Arg Glu Pro Asn Leu Asn Leu Lys Gly Phe Leu Gln Asn Ala
 385 390 395 400

Tyr Val His Pro Val Phe Lys
 405

<210> 535
 <211> 408
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DUF221 domain

<400> 535

Asn Ile Arg Leu Gly Gln Ala Glu Val Ser Ala Pro Gly Lys Glu Val
 1 5 10 15

Arg Ala Ala Phe Val Ser Phe Lys Ser Arg Tyr Gly Ala Ala Thr Ala
20 25 30

Leu His Met Pro Gln Ser Ile Asn Pro Thr Tyr Trp Leu Thr Glu Pro
35 40 45

Ala Pro Glu Pro His Asp Val His Trp Pro Phe Phe Ser Ala Ser Phe
50 55 60

Met Gln Lys Trp Leu Ala Lys Ile Leu Val Val Phe Ala Cys Leu Leu
65 70 75 80

Leu Thr Ile Leu Phe Leu Val Pro Val Val Leu Val Gln Gly Leu Thr
85 90 95

Asn Leu Pro Ala Leu Glu Phe Met Phe Pro Phe Leu Ser Leu Ile Leu
100 105 110

Ser Met Lys Val Val Ser Gln Ile Ile Thr Gly Tyr Leu Pro Ser Leu
115 120 125

Ile Leu Gln Thr Ser Leu Lys Val Val Pro Pro Thr Met Glu Phe Leu
130 135 140

Ser Ser Ile Gln Gly His Ile Cys His Ser Asp Ile Gln Lys Ser Ala
145 150 155 160

Cys Asn Lys Val Ile Trp Phe Thr Ile Trp Asn Val Phe Phe Ala Thr
165 170 175

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

Lys Gln Ile Pro Leu Lys Leu Ala Val Ala Val Pro Ala Gln Ala Ser
195 200 205

Phe Phe Ile Ala Tyr Val Val Thr Thr Gly Trp Thr Asp Thr Leu Thr
210 215 220

Glu Leu Phe Arg Val Val Pro Phe Met Val Ser Tyr Ile Lys Arg Ser
225 230 235 240

Phe Glu Pro Ser Asp Glu Asn Glu Phe Val Val Pro Pro Met Arg Tyr
245 250 255

His Arg Asp Thr Pro Arg Val Leu Phe Phe Gly Leu Leu Gly Ile Thr
260 265 270

Tyr Phe Phe Leu Ala Pro Leu Ile Leu Pro Phe Ile Leu Leu Tyr Phe
275 280 285

Ile Leu Ala Tyr Ile Ile Tyr Arg Asn Gln Phe Met Asn Val Tyr Ala

290

Pro Lys Phe Asp Thr Gly Gly Met Phe Trp Pro Met Ile His Tyr Thr
305 310 315 320

Met Ile Phe Ser Leu Val Leu Met Gln Ala Ile Ala Ile Gly Leu Phe
325 330 335

Ala Leu Lys Lys Met Glu Leu Ala Thr Tyr Leu Leu Val Pro Leu Pro
340 345 350

Val Phe Thr Leu Leu Phe Asn Glu Phe Cys Arg Lys Arg Phe Met Pro
355 360 365

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

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

Ala Tyr Lys Asp Pro Ala Leu Leu
405

<210> 536
<211> 309
<212> PRT
<213> Artificial sequence

<220>
<223> DUF221 domain

<400> 536

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

Ala Phe Val Ser Phe Arg Thr Arg His Gly Ala Ala Ile Ala Thr Asn
20 25 30

Ile Gln Gln Gly Ile Asp Pro Thr Gln Trp Leu Thr Glu Ala Ala Pro
35 40 45

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

Arg Trp Ile Ser Asn Val Val Val Leu Val Ala Phe Val Ala Leu Leu
65 70 75 80

Ile Leu Tyr Ile Val Pro Val Val Leu Val Gln Gly Leu Ala Asn Leu
85 90 95

His Gln Leu Glu Thr Trp Phe Pro Phe Leu Lys Gly Ile Leu Asn Met
100 105 110

PF59082PF60142_PCT_SEQ_LIST.txt

Lys Ile Val Ser Gln Val Ile Thr Gly Tyr Leu Pro Ser Leu Ile Phe
115 120 125

Gln Leu Phe Leu Leu Ile Val Pro Pro Ile Met Leu Leu Leu Ser Ser
130 135 140

Met Gln Gly Phe Ile Ser His Ser Gln Ile Glu Lys Ser Ala Cys Ile
145 150 155 160

Lys Leu Leu Ile Phe Thr Val Trp Asn Ser Phe Phe Ala Asn Val Leu
165 170 175

Ser Gly Ser Ala Leu Tyr Arg Val Asn Val Phe Leu Glu Pro Lys Thr
180 185 190

Ile Pro Arg Val Leu Ala Ala Ala Val Pro Ala Gln Ala Ser Phe Phe
195 200 205

Val Ser Tyr Val Val Thr Ser Gly Trp Thr Gly Leu Ser Ser Glu Ile
210 215 220

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

Lys Glu Asp Asp Lys Glu Phe Glu Val Pro Ser Thr Pro Phe Cys Gln
245 250 255

Glu Ile Pro Arg Ile Leu Phe Phe Gly Leu Leu Gly Ile Thr Tyr Phe
260 265 270

Phe Leu Ser Pro Leu Ile Leu Pro Phe Leu Leu Val Tyr Tyr Cys Leu
275 280 285

Gly Tyr Ile Ile Tyr Arg Asn Gln Val Thr Glu Pro Ile Ser Leu Leu
290 295 300

Ser Ile Ile Leu Cys
305

<210> 537
<211> 414
<212> PRT
<213> Artificial sequence

<220>
<223> DUF221 domain

<400> 537

Ile Ser Glu Glu Lys Glu Thr Val Met Ser Ser Thr Lys Ser Leu Val
1 5 10 15

Pro Ala Ala Phe Val Ser Phe Lys Lys Arg Trp Gly Ala Val Val Cys
20 25 30

PF59082PF60142_PCT_SEQ_LIST.txt

Ser Gln Thr Gln Gln Ser Arg Asn Pro Thr Glu Trp Leu Thr Glu Trp
35 40 45

Ala Pro Glu Pro Arg Asp Ile Tyr Trp Asp Asn Leu Ala Leu Pro Tyr
50 55 60

Val Gln Leu Thr Ile Arg Arg Leu Val Ile Ala Val Ala Phe Phe Phe
65 70 75 80

Leu Thr Phe Phe Phe Met Ile Pro Ile Ala Phe Val Gln Thr Leu Ala
85 90 95

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

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

Ala Leu Lys Ile Phe Leu Ile Val Leu Pro Ser Ile Leu Met Leu Met
130 135 140

Ser Lys Phe Glu Gly Phe Ile Ser Lys Ser Ser Leu Glu Arg Arg Cys
145 150 155 160

Ala Ser Arg Tyr Tyr Met Phe Gln Phe Ile Asn Val Phe Leu Cys Ser
165 170 175

Ile Ile Ala Gly Thr Ala Leu Gln Gln Leu Asp Ser Phe Leu Asn Gln
180 185 190

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

Ala Thr Phe Phe Ile Thr Tyr Ile Met Val Asp Gly Trp Ala Gly Val
210 215 220

Ala Gly Glu Ile Leu Arg Leu Lys Pro Leu Ile Ile Tyr His Leu Lys
225 230 235 240

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

Pro Gly Thr Ile Gly Phe Asn Thr Gly Glu Pro Gln Ile Gln Leu Tyr
260 265 270

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

Phe Ile Leu Val Phe Phe Ala Leu Ala Tyr Val Val Tyr Arg His Gln
290 295 300

PF59082PF60142_PCT_SEQ_LIST.txt

Ile Ile Asn Val Tyr Asn Gln Glu Tyr Glu Ser Ala Ala Ala Phe Trp
305 310 315 320

Pro Asp Val His Arg Arg Val Val Ile Ala Leu Ile Val Ser Gln Leu
325 330 335

Leu Leu Met Gly Leu Leu Ser Thr Lys Lys Ala Ala Arg Ser Thr Pro
340 345 350

Leu Leu Phe Ile Leu Pro Val Leu Thr Ile Gly Phe His Lys Phe Cys
355 360 365

Gln Gly Arg Tyr Gln Pro Ile Phe Val Thr Tyr Pro Leu Gln Asp Ala
370 375 380

Met Val Lys Asp Thr Leu Glu Arg Met Arg Glu Pro Asn Leu Asn Leu
385 390 395 400

Lys Thr Phe Leu Gln Asn Ala Tyr Ala His Pro Val Phe Lys
405 410

<210> 538
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<213> Artificial sequence

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<223> DUF221 domain

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

Ala Gln Thr Gln Gln His Ser Asn Pro Leu Glu Leu Ile Thr Glu Met
35 40 45

Ala Pro Glu Pro Arg Asp Val Ser Trp Arg Asn Leu Ala Ile Pro Gln
50 55 60

Lys Ile Leu Pro Leu Asn Lys Ile Gly Val Ile Leu Ala Ala Ala Leu
65 70 75 80

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

Lys Tyr Glu Lys Leu Lys Lys Trp Phe Pro Pro Ala Met Ala Ile Glu
100 105 110

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

PF59082PF60142_PCT_SEQ_LIST.txt

Ile Leu Lys Gly Phe Met Tyr Ile Ile Pro Phe Ala Met Leu Gly Leu
130 135 140

Ala Tyr Leu Gly Gly Ser Ile Ser Asn Ser Lys Glu Glu Ile Lys Ala
145 150 155 160

Cys Asn Met Val Phe Tyr Phe Leu Met Gly Asn Val Phe Phe Leu Ser
165 170 175

Leu Ile Ser Gly Ser Leu Leu Asp Glu Ile Gly Glu Tyr Leu Thr His
180 185 190

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

Glu Phe Phe Met Thr Tyr Ile Leu Thr Asp Gly Leu Ser Gly Phe Ser
210 215 220

Leu Glu Ile Leu Gln Leu Gly Leu Ile Leu Phe Asp Ile Ile Arg Ser
225 230 235 240

Tyr Thr Tyr Gly Arg Gly Lys Glu Arg Thr Pro Tyr Leu Phe Ser Phe
245 250 255

Pro Tyr Phe Arg Val Ile Pro Thr Val Ser Leu Ser Ile Met Ile Gly
260 265 270

Met Ile Tyr Ala Val Val Ala Pro Leu Met Leu Pro Phe Leu Val Gly
275 280 285

Tyr Phe Cys Leu Gly Tyr Ile Val Tyr Phe Asn Gln Met Glu Asp Val
290 295 300

Tyr Glu Thr Thr Tyr Asp Thr Cys Gly Arg Phe Trp Pro Phe Ile His
305 310 315 320

His Tyr Ile Phe Val Ser Ile Ile Leu Met Gln Ile Thr Met Val Gly
325 330 335

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

Leu Ile Leu Ile Thr Ile Ala Tyr Asn Glu Tyr Cys Lys Ile Arg Phe
355 360 365

Leu Pro Ser Phe Lys His Phe Pro Ile Gln Thr Ala Val Glu Ile Asp
370 375 380

Glu Glu Asp Glu Lys Asn Gly Glu Met Glu Thr His Tyr Val Asp Ala
385 390 395 400

Ala Thr Ala Tyr Asn Arg His Gln Pro Cys
405 410

<210> 539
<211> 414
<212> PRT
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<400> 539

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

Ala Gln Thr Gln Gln Ser Lys Asn Pro Thr Leu Trp Leu Thr Ser Ser
35 40 45

Ala Pro Glu Pro Arg Asp Ile Tyr Trp Gln Asn Leu Ala Ile Pro Phe
50 55 60

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

Leu Val Phe Phe Tyr Met Ile Pro Ile Ala Phe Val Gln Ser Leu Ala
85 90 95

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

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

Ala Leu Lys Ile Phe Leu Trp Ile Leu Pro Thr Val Leu Leu Ile Met
130 135 140

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

Ala Ala Lys Tyr Tyr Tyr Phe Met Leu Val Asn Val Phe Leu Gly Ser
165 170 175

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

Ser Pro Ser Gln Ile Pro Arg Thr Ile Gly Val Ser Ile Pro Met Lys
195 200 205

Ala Thr Phe Phe Ile Thr Tyr Ile Met Val Asp Gly Trp Ala Gly Ile
210 215 220

PF59082PF60142_PCT_SEQ_LIST.txt

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

Asn Met Phe Ile Val Lys Thr Glu Glu Asp Arg Val Arg Ala Met Asp
245 250 255

Pro Gly Phe Val Asp Phe Lys Glu Thr Ile Pro Ser Leu Gln Leu Tyr
260 265 270

Phe Leu Leu Gly Ile Val Tyr Thr Ala Val Thr Pro Ile Leu Leu Pro
275 280 285

Phe Ile Leu Ile Phe Phe Ala Phe Ala Tyr Leu Val Tyr Arg His Gln
290 295 300

Ile Ile Asn Val Tyr Asn Gln Gln Tyr Glu Ser Cys Gly Ala Phe Trp
305 310 315 320

Pro His Val His Gly Arg Ile Ile Ala Ser Leu Leu Ile Ser Gln Leu
325 330 335

Leu Leu Met Gly Leu Leu Ala Ser Lys Lys Ala Ala Asp Ser Thr Pro
340 345 350

Leu Leu Ile Ile Leu Pro Ile Leu Thr Leu Ser Phe His Lys Tyr Cys
355 360 365

Lys His Arg Phe Glu Pro Ala Phe Arg Gln Tyr Pro Leu Glu Glu Ala
370 375 380

Met Ala Lys Asp Lys Leu Glu Lys Glu Thr Glu Pro Glu Leu Asn Met
385 390 395 400

Lys Ala Asp Leu Ala Asp Ala Tyr Leu His Pro Ile Phe His
405 410

<210> 540
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<212> PRT
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<223> DUF221 domain
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Ile Ala Glu Glu Arg Glu Asn Val Val Asn Asp Gln Lys Ser Val Met
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Pro Ala Ser Phe Val Ser Phe Lys Thr Arg Trp Ala Ala Ala Val Cys
20 25 30

Ala Gln Thr Thr Gln Thr Arg Asn Pro Thr Glu Trp Leu Thr Glu Trp
35 40 45

PF59082PF60142_PCT_SEQ_LIST.txt

Ala Ala Glu Pro Arg Asp Ile Tyr Trp Pro Asn Leu Ala Ile Pro Tyr
50 55 60

Val Ser Leu Thr Val Arg Arg Leu Val Met Asn Val Ala Phe Phe Phe
65 70 75 80

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

Thr Ile Glu Gly Ile Glu Lys Val Ala Pro Phe Leu Lys Val Ile Ile
100 105 110

Glu Lys Asp Phe Ile Lys Ser Leu Ile Gln Gly Leu Leu Ala Gly Ile
115 120 125

Ala Leu Lys Leu Phe Leu Ile Phe Leu Pro Ala Ile Leu Met Thr Met
130 135 140

Ser Lys Phe Glu Gly Phe Thr Ser Val Ser Phe Leu Glu Arg Arg Ser
145 150 155 160

Ala Ser Arg Tyr Tyr Ile Phe Asn Leu Val Asn Val Phe Leu Gly Ser
165 170 175

Val Ile Ala Gly Ala Ala Phe Glu Gln Leu Asn Ser Phe Leu Asn Gln
180 185 190

Ser Pro Asn Gln Ile Pro Lys Thr Ile Gly Met Ala Ile Pro Met Lys
195 200 205

Ala Thr Phe Phe Ile Thr Tyr Ile Met Val Asp Gly Trp Ala Gly Val
210 215 220

Ala Gly Glu Ile Leu Met Leu Lys Pro Leu Ile Ile Tyr His Leu Lys
225 230 235 240

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

Pro Gly Ser Ile Gly Phe Asn Thr Gly Glu Pro Gln Ile Gln Leu Tyr
260 265 270

Phe Leu Leu Gly Leu Val Tyr Ala Pro Val Thr Pro Met Leu Leu Pro
275 280 285

Phe Ile Leu Val Phe Phe Ala Leu Ala Tyr Val Val Tyr Arg His Gln
290 295 300

Ile Ile Asn Val Tyr Asn Gln Glu Tyr Glu Ser Ala Ala Ala Phe Trp
305 310 315 320

PF59082PF60142_PCT_SEQ_LIST.txt

Pro Asp Val His Gly Arg Val Ile Thr Ala Leu Ile Ile Ser Gln Leu
325 330 335

Leu Leu Met Gly Leu Leu Gly Thr Lys His Ala Ala Ser Ala Ala Pro
340 345 350

Phe Leu Ile Ala Leu Pro Val Ile Thr Ile Gly Phe His Arg Phe Cys
355 360 365

Lys Gly Arg Phe Glu Pro Ala Phe Val Arg Tyr Pro Leu Gln Glu Ala
370 375 380

Met Met Lys Asp Thr Leu Glu Arg Ala Arg Glu Pro Asn Leu Asn Leu
385 390 395 400

Lys Gly Tyr Leu Gln Asp Ala Tyr Ile His Pro Val Phe Lys
405 410

<210> 541

<211> 415

<212> PRT

<213> Artificial sequence

<220>

<223> DUF221 domain

<400> 541

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

Ala Gln Thr Gln Gln Thr Arg Asn Pro Thr Glu Trp Leu Thr Glu Trp
35 40 45

Ala Ala Glu Pro Arg Asp Ile Tyr Tyr Asp Asn Leu Ala Leu Pro Tyr
50 55 60

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

Leu Thr Phe Phe Phe Met Ile Pro Ile Ala Phe Val Gln Ser Leu Ala
85 90 95

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

Glu Val Lys Leu Leu Lys Ser Ile Ile Gln Gly Phe Leu Pro Gly Ile
115 120 125

Ala Leu Lys Ile Phe Leu Leu Phe Leu Pro Arg Ile Leu Met Gln Met
130 135 140

PF59082PF60142_PCT_SEQ_LIST.txt

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

Ala Thr Arg Phe Tyr Met Phe Gln Phe Ile Asn Val Phe Leu Gly Ser
165 170 175

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

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

Ala Thr Phe Phe Ile Thr Tyr Ile Met Val Asp Gly Trp Ala Gly Val
210 215 220

Ala Gly Glu Ile Leu Arg Leu Lys Pro Leu Ile Ile Tyr His Leu Lys
225 230 235 240

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

Pro Gly Thr Ile Gly Phe Asn Thr Gly Glu Pro Gln Ile Gln Leu Tyr
260 265 270

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

Phe Ile Leu Val Phe Phe Gly Leu Ala Phe Val Val Tyr Arg His Gln
290 295 300

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

Pro Asp Val His Arg Arg Val Val Thr Ala Leu Val Val Ser Gln Leu
325 330 335

Leu Leu Met Gly Leu Leu Ser Thr Lys His Ala Ser Lys Ser Thr Pro
340 345 350

Leu Leu Leu Val Leu Pro Leu Leu Thr Ile Gly Phe His Lys His Cys
355 360 365

Lys Asn Arg Tyr Gln Pro Ala Phe Val Thr Tyr Pro Leu Gln Gln Glu
370 375 380

Ala Met Ile Lys Asp Thr Leu Asp Arg Ile Arg Glu Pro Asn Leu Asn
385 390 395 400

Leu Lys Ala Phe Leu Arg Asp Ala Tyr Ala His Pro Glu Phe Arg
405 410 415

PF59082PF60142_PCT_SEQ_LIST.txt

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Ile Ser Lys Glu Arg Glu Glu Val Val Asn Asp Pro Lys Ala Ile Met
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Pro Ala Ala Phe Val Ser Phe Lys Thr Arg Trp Ala Ala Ala Val Cys
 20 25 30

Ala Gln Thr Gln Gln Thr Arg Asn Pro Thr Gln Trp Leu Thr Glu Trp
 35 40 45

Ala Pro Glu Pro Arg Asp Val Phe Trp Ser Asn Leu Ala Ile Pro Tyr
 50 55 60

Val Ser Leu Thr Val Arg Arg Leu Ile Met His Val Ala Phe Phe Phe
 65 70 75 80

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

Thr Ile Glu Gly Ile Val Lys Ala Ala Pro Phe Leu Lys Phe Ile Val
 100 105 110

Asp Asp Lys Phe Met Lys Ser Val Ile Gln Gly Phe Leu Pro Gly Ile
 115 120 125

Ala Leu Lys Leu Phe Leu Ala Phe Leu Pro Ser Ile Leu Met Ile Met
 130 135 140

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

Ala Phe Arg Tyr Tyr Ile Phe Asn Leu Val Asn Val Phe Leu Ala Ser
 165 170 175

Val Ile Ala Gly Ala Ala Phe Glu Gln Leu Asn Ser Phe Leu Asn Gln
 180 185 190

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

Ala Thr Phe Phe Ile Thr Tyr Ile Met Val Asp Gly Trp Ala Gly Val
 210 215 220

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

PF59082PF60142_PCT_SEQ_LIST.txt

Asn Ala Phe Leu Val₂₄₅ Lys Thr Asp Lys Asp₂₅₀ Arg Glu Glu Ala Met₂₅₅ Asp
 Pro Gly Ser Ile₂₆₀ Gly Phe Asn Thr Gly₂₆₅ Glu Pro Arg Ile Gln₂₇₀ Leu Tyr
 Phe Leu Leu₂₇₅ Gly Leu Val Tyr Ala₂₈₀ Pro Val Thr Pro Met₂₈₅ Leu Leu Pro
 Phe Ile₂₉₀ Leu Val Phe Phe Ala₂₉₅ Leu Ala Tyr Ile Val₃₀₀ Tyr Arg His Gln
 Ile₃₀₅ Ile Asn Val Tyr Asn₃₁₀ Gln Glu Tyr Glu Ser₃₁₅ Ala Ala Ala Phe Trp₃₂₀
 Pro Asp Val His Gly₃₂₅ Arg Val Ile Ala₃₃₀ Leu Val Ile Ser Gln₃₃₅ Leu
 Leu Leu Met Gly₃₄₀ Leu Leu Gly Thr Lys₃₄₅ His Ala Ala Leu Ala₃₅₀ Ala Pro
 Phe Leu Ile₃₅₅ Ala Leu Pro Val Leu₃₆₀ Thr Ile Gly Phe His₃₆₅ His Phe Cys
 Lys Gly₃₇₀ Arg Tyr Glu Pro Ala₃₇₅ Phe Ile Arg Tyr Pro₃₈₀ Leu Gln Glu Ala
 Met₃₈₅ Met Lys Asp Thr Leu₃₉₀ Glu Thr Ala Arg Glu₃₉₅ Pro Asn Leu Asn₄₀₀ Leu
 Lys Gly Tyr Leu Gln₄₀₅ Asn Ala Tyr Val His₄₁₀ Pro Val Phe Lys

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Leu Arg Ala Asp Leu₅ Glu Ser Gln Leu Ala₁₀ Ala Tyr Lys Glu Gly₁₅ Arg
 Ala Gln Gly Ala₂₀ Gly Val Ala Phe Val₂₅ Met Phe Lys Asp Val₃₀ Tyr Thr
 Ala Asn Lys₃₅ Ala Val Gln Asp Phe₄₀ Arg Asn Glu Arg Ser₄₅ Arg Arg Thr
 Gly Lys Phe Phe Ser Val Thr Glu Leu Arg Leu Gln Arg Asn Gln Trp
 Seite 635

50

Lys Val Asp Arg Ala Pro Leu Ala Thr Asp Ile Tyr Trp Asn His Leu
65 70 75 80

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

Ile Leu Leu Leu Ile Leu Val Phe Phe Ser Ser Pro Leu Ala Leu Ile
100 105 110

Ser Ala Leu Val Ser Ala Gly Arg Ile Phe Asn Ala Glu Ala Leu Asp
115 120 125

Ser Ala Gln Tyr Trp Leu Thr Trp Val Gln Thr Ser Gly Trp Ile Gly
130 135 140

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

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

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

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

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

Glu Asp Cys Lys Arg Ile Glu Glu Tyr Met Ser Pro Ser Phe Leu Ser
225 230 235 240

Arg Ser Cys Val Ser Ala Leu Ala Phe Leu Ile Thr Ser Thr Phe Leu
245 250 255

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

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

Asn Glu Glu Tyr Ala Leu Glu Asn Gln Glu Pro Ser Ser Asn Leu Glu
290 295 300

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

Ile Glu Pro Met Ser Gln Asp Leu Ser Glu Tyr Pro Ile Ser Arg Thr
325 330 335

PF59082PF60142_PCT_SEQ_LIST.txt

Ser Pro Ile Pro Lys Gln Lys Phe Asp Phe Ala Gln Tyr Tyr Ala Phe
340 345 350

Asn Leu Thr Ile Phe Ala Leu Thr Met Ile Tyr Ser Ser Phe Ala Pro
355 360 365

Leu Val Val Pro Val Gly Ala Val Tyr Phe Gly Tyr Arg Tyr Ile Val
370 375 380

Asp Lys Tyr Asn Phe Leu Tyr Val Tyr Arg Val Arg Gly Phe Pro Ala
385 390 395 400

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

Cys Val Asp Leu Tyr Leu Val Ser Met Leu Leu Phe Phe Ser Val Lys
420 425 430

Gly Asp Ser Thr Lys Leu Gln Ala Ile Phe Thr Leu Gly Val Leu Val
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Met Tyr Lys Leu
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