

2577-166.ST25
SEQUENCE LISTING

<110> Unknown, Draft

<120> Novel Plant Homeodomain Protein-encoding Genes and Their Uses

<130> 2577-166

<160> 68

<170> PatentIn version 3.3

<210> 1

<211> 1010

<212> DNA

<213> Gossypium hirsutum

<400> 1

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tcaaaatcca aatcaaacc tcattttctt tatctgcaaa tggaaggtgg cggcggcggc      180
ggtggtggag ggaattcacg gtggaacccg acgaaggagc aaataagcat gcttgaaagc      240
ttgtacaagc aagggataag aaccccaagt gctgatcaga tacagcaa at aaccagtagg      300
ctcaaagctt atggcaccat tgaaggcaaa aacgtgttct attggttcca aaatcataaa      360
gctcgtcaaa ggcagaaaca aaagcaagag aatttggctt atatcaaccg ttacattcac      420
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ggtccatatt ttgtaccaca agctgatcat caccatcatc taggctttta cctcagtg      540
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ggaaagtctc tatttttaca cggaatgct tatgatcata ccatggttcc atcacctgat      660
actgaaaact tataactgg agcattcaac aatggcggcg gcgccactaa tcatcacgag      720
acattgccat tgtttccatt gcaccogact ggtgtttccg aagagacgtt aatggcttca      780
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ttgggggggtg ggggaggaaa tggaaataaa aatcaagggt tttgattcaa agaacattga      960
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<212> PRT

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<213> Gossypium hirsutum

<400> 2

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Pro Thr Lys Glu Gln Ile Ser Met Leu Glu Ser Leu Tyr Lys Gln Gly
 20 25 30

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

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

Asn His Lys Ala Arg Gln Arg Gln Lys Gln Lys Gln Glu Asn Leu Ala
 65 70 75 80

Tyr Ile Asn Arg Tyr Ile His His His His Arg Ala Gln Pro Val Phe
 85 90 95

His Pro Pro Pro Cys Thr Asn Val Val Cys Ala Gly Pro Tyr Phe Val
 100 105 110

Pro Gln Ala Asp His His His His Leu Gly Phe Tyr Pro Gln Cys Pro
 115 120 125

Lys Val Leu Leu Pro Ser Arg Ser Ile Lys Arg Arg Gly Arg Pro Ile
 130 135 140

Gly Lys Thr Gly Lys Ser Leu Phe Tyr Asn Gly Asn Ala Tyr Asp His
 145 150 155 160

Thr Met Val Pro Ser Pro Asp Thr Glu Asn Leu Tyr Thr Gly Ala Phe
 165 170 175

Asn Asn Gly Gly Gly Ala Thr Asn His His Glu Thr Leu Pro Leu Phe
 180 185 190

Pro Leu His Pro Thr Gly Val Ser Glu Glu Thr Leu Met Ala Ser Ser
 195 200 205

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Ser Pro Thr Gly Ser Thr Ser Cys Glu Thr Thr Ile Ser Ala Gly Gly
 210 215 220

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

Ile Asp Phe Phe

<210> 3
 <211> 1236
 <212> DNA
 <213> Arabidopsis thaliana

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 ccgatcagat tcagcagatc accggtaggc ttcggtcgta cggccatata gaaggtaaaa 180
 acgtctttta ctggttccag aaccataagg ctaggcaacg caaaagcag aaacaggagc 240
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 gctcaaacgg cactagttc ttatcctttt ctcttactta tccgtatcta atcttcgacg 360
 ttctatttta taatcttaaa aaaattgtag tccatacgtt ataggttctt tttgttgacg 420
 acgttttctt tccgtattaa agaaatgaaa ataaagcgta tgaattacat ctggactatg 480
 aaagaactta caaaaacatg tcattaaata catatataaa tatataatcc agttttggcc 540
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 tgcgaaagga ttatatcata tgggactatt ttgagatggt tatcagcaaa ttatgtactc 660
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 <211> 260
 <212> PRT
 <213> Arabidopsis thaliana

<400> 4

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Pro Thr Lys Asp Gln Ile Thr Leu Leu Glu Asn Leu Tyr Lys Glu Gly
 20 25 30

Ile Arg Thr Pro Ser Ala Asp Gln Ile Gln Gln Ile Thr Gly Arg Leu
 35 40 45

Arg Ala Tyr Gly His Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe Gln
 50 55 60

Asn His Lys Ala Arg Gln Arg Gln Lys Gln Lys Gln Glu Arg Met Ala
 65 70 75 80

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

Pro Cys Ser Asn Val Gly Cys Val Ser Pro Tyr Tyr Leu Gln Gln Ala
 100 105 110

Ser Asp His His Met Asn Gln His Gly Ser Val Tyr Thr Asn Asp Leu
 115 120 125

Leu His Arg Asn Asn Val Met Ile Pro Ser Gly Gly Tyr Glu Lys Arg
 130 135 140

Thr Val Thr Gln His Gln Lys Gln Leu Ser Asp Ile Arg Thr Thr Ala
 145 150 155 160

Ala Thr Arg Met Pro Ile Ser Pro Ser Ser Leu Arg Phe Asp Arg Phe
 165 170 175

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

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

Ser Asn Ala Asp Gly Met Gly Ser Ser Ser Phe Ala Leu Gly Ser Asp
 210 215 220

Ser Pro Val Asp Cys Ser Ser Asp Gly Ala Gly Arg Glu Gln Pro Phe
 225 230 235 240

Ile Asp Phe Phe Ser Gly Gly Ser Thr Ser Thr Arg Phe Asp Ser Asn
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Gly Asn Gly Leu
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<210> 5
 <211> 708
 <212> DNA
 <213> Arabidopsis thaliana

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 gcagttgaag atattgactg atctgtttcg agccggtctt agaactccaa caactgatca 180
 gattcagaag atctctacgg agctcagttt ctacggcaag atagagagca agaatgtttt 240
 ctattggttt cagaatcata aggctagggg gaggcagaaa cgtcgtaaaa totccattga 300
 ttttgatcat catcatcatc aaccatcaac tagagatgtt tttgaaataa gcgaagaaga 360
 ttgtcaagag gaagagaagg tgatagagac attacaactc tttccggtga attcatttga 420
 agactccaac tccaaggtgg acaaaatgag agctagaggc aataaccagt accgtgaata 480
 tattcgagag accaccacga cgtcgttttc tccatactca tcatgtggag ctgaaatgga 540
 acatccaccg ccattagatc ttcgattaag ctttctttta gtcattgacc acaataacaa 600
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<210> 6

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<211> 182

<212> PRT

<213> Arabidopsis thaliana

<400> 6

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 20 25 30

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

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

Glu Ser Lys Asn Val Phe Tyr Trp Phe Gln Asn His Lys Ala Arg Glu
 65 70 75 80

Arg Gln Lys Arg Arg Lys Ile Ser Ile Asp Phe Asp His His His His
 85 90 95

Gln Pro Ser Thr Arg Asp Val Phe Glu Ile Ser Glu Glu Asp Cys Gln
 100 105 110

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

Phe Glu Asp Ser Asn Ser Lys Val Asp Lys Met Arg Ala Arg Gly Asn
 130 135 140

Asn Gln Tyr Arg Glu Tyr Ile Arg Glu Thr Thr Thr Thr Ser Phe Ser
 145 150 155 160

Pro Tyr Ser Ser Cys Gly Ala Glu Met Glu His Pro Pro Pro Leu Asp
 165 170 175

Leu Arg Leu Ser Phe Leu
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<210> 7

<211> 775

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<212> DNA

<213> *Arabidopsis thaliana*

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tctccggcag cctccctcc cctccttctt ctctctccgg cgtoacttca gccacttttg      180
accttaaaaa cttcattaga cccgatcaaa ccggtccgac aaaatttgaa cacaaacgag      240
accctctca tcaattggag acgcacccgg gagggacaag gtggaacccg actcaagaac      300
agatagggat acttgagatg ttgtacaaag gtggaatgcg tactcctaata gctcaacaga      360
ttgagcatat cacattgcaa ctcggttaagt acgggaaaat cgaagggaaa aatgtgttct      420
attggttcca gaaccacaaa gcccgcgaga gacagaagca gaagaggaac aacctcatca      480
gcctaagttg ccaaagcagc ttcaagacca ctggtgtctt taatccgagt gtaactatga      540
agacaagaac atcatcgtca ctagacatta tgagagaacc aatggtggag aaggaggagt      600
tagtgggaaga gaatgagtac aagaggacat gtaggagctg gggatttgag aacttgagaga      660
tagagaacag gagaacaaaa aatagtagta ctatggcaac tacttttaata aaaatcattg      720
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<210> 8

<211> 251

<212> PRT

<213> *Arabidopsis thaliana*

<400> 8

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His Asp Ser Thr Ser Ser Leu Ser Leu Ser Cys Lys Arg Leu Arg Pro
          20           25           30

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

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

Gln Ile Gly Ile Leu Glu Met Leu Tyr Lys Gly Gly Met Arg Thr Pro
 100 105 110

Asn Ala Gln Gln Ile Glu His Ile Thr Leu Gln Leu Gly Lys Tyr Gly
 115 120 125

Lys Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe Gln Asn His Lys Ala
 130 135 140

Arg Glu Arg Gln Lys Gln Lys Arg Asn Asn Leu Ile Ser Leu Ser Cys
 145 150 155 160

Gln Ser Ser Phe Thr Thr Thr Gly Val Phe Asn Pro Ser Val Thr Met
 165 170 175

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

Glu Lys Glu Glu Leu Val Glu Glu Asn Glu Tyr Lys Arg Thr Cys Arg
 195 200 205

Ser Trp Gly Phe Glu Asn Leu Glu Ile Glu Asn Arg Arg Asn Lys Asn
 210 215 220

Ser Ser Thr Met Ala Thr Thr Phe Asn Lys Ile Ile Asp Asn Val Thr
 225 230 235 240

Leu Glu Leu Phe Pro Leu His Pro Glu Gly Arg
 245 250

<210> 9

<211> 689

<212> DNA

<213> Artificial

<220>

<223> Synthetic Construct, Chimera of GhCIR1 HD domain and VP16 activation domain

<400> 9

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tcaaaatcca aatcaaacc ctcattttctt tatctgcaaa tggaaggtgg cggcggcggc    180
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ttgtacaagc aagggataag aaccccaagt gctgatcaga tacagcaaat aaccagtagg    300
ctcaaagctt atggcaccat tgaaggcaaa aacgtgttct attggttcca aaatcataaa    360
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catcatcatc gagctcaatt aattaacgcc ccccgaccg atgtcagcct gggggacgag    480
ctccacttag acggcgagga cgtggcgatg gcgcatgccg acgcgctaga cgatttcgat    540
ctggacatgt tgggggacgg ggattccccg ggtccgggat ttacccccca cgactccgcc    600
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<210> 10
 <211> 176
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct, Chimera of GhCIR1 HD domain and VP16
 activation domain

<400> 10

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Pro Thr Lys Glu Gln Ile Ser Met Leu Glu Ser Leu Tyr Lys Gln Gly
 20 25 30

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

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

Asn His Lys Ala Arg Gln Arg Gln Lys Gln Lys Gln Glu Asn Leu Ala
 65 70 75 80

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Tyr Ile Asn Arg Tyr Ile His His His His Arg Ala Gln Leu Ile Asn
 85 90 95

Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp Gly
 100 105 110

Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp Leu
 115 120 125

Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro His
 130 135 140

Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe Glu
 145 150 155 160

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

<210> 11
 <211> 1652
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic Construct, Chimera of GhCIR1 HD domain, VP16 activation domain, estrogen regulatory domain and putative nuclear localization signal

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 atcatcatcg agctcaatta attaacgccc ccccgaccga tgtcagcctg ggggacgagc 480
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 tggacatgtt gggggacggg gattccccgg gtccgggatt tccccccac gactccgccc 600
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<210> 12
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 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct, Chimera of GhCIR1 HD domain, VP16 activation domain, estrogen regulatory domain and putative nuclear localization signal

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Pro Thr Lys Glu Gln Ile Ser Met Leu Glu Ser Leu Tyr Lys Gln Gly
 20 25 30

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

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

Asn His Lys Ala Arg Gln Arg Gln Lys Gln Lys Gln Glu Asn Leu Ala
 65 70 75 80

Tyr Ile Asn Arg Tyr Ile His His His His Arg Ala Gln Leu Ile Asn
 85 90 95

Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp Gly
 100 105 110

Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp Leu
 115 120 125

Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro His
 130 135 140

Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe Glu
 145 150 155 160

Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Asp Pro
 165 170 175

Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 180 185 190

Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
 195 200 205

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
 210 215 220

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

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
 245 250 255

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

Leu Leu Glu Cys Ala Trp Leu Glu Ile Leu Met Ile Gly Leu Val Trp
 275 280 285

Arg Ser Met Glu His Pro Val Lys Leu Leu Phe Ala Pro Asn Leu Leu
 290 295 300

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Met Val Glu Ile Phe
 305 310 315 320

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

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
 340 345 350

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
 355 360 365

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
 370 375 380

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

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
 405 410 415

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
 420 425 430

Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
 435 440 445

Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
 450 455 460

Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
 465 470 475 480

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Pro Thr Lys Glu Gln Ile Ser Met Leu Glu Ser Leu Tyr Lys Gln Gly
 20 25 30

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

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

Asn His Lys Ala Arg Gln Arg Gln Lys Gln Lys Gln Glu Asn Leu Ala
 65 70 75 80

Tyr Ile Asn Arg Tyr Ile His His His His Arg Ala Gln Leu Ile Asn
 85 90 95

Pro Ser Thr Arg Asp Val Phe Glu Ile Ser Glu Glu Asp Cys Gln Glu
 100 105 110

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

Glu Asp Ser Asn Ser Lys Val Asp Lys Met Arg Ala Arg Gly Asn Asn
 130 135 140

Gln Tyr Arg Glu Tyr Ile Arg Glu Thr Thr Thr Thr Ser Phe Ser Pro
 145 150 155 160

Tyr Ser Ser Cys Gly Ala Glu Met Glu His Pro Pro Pro Leu Asp Leu
 165 170 175

Arg Leu Ser Phe Leu
 180

<210> 15

<211> 1001

<212> DNA

<213> Artificial

<220>

<223> Synthetic Construct, Chimera of HD-domain of GhCIR1 and the
 C-terminal domain of AtCIR2

<400> 15

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aactttaatt aatccatcaa ctagagatgt ttttgaaata agcgaagaag attgtcaaga      660
ggaagagaag gtgatagaga cattacaact ctttccggtg aattcatttg aagactccaa      720
ctccaagggtg gacaaaatga gagctagagg caataaccag taccgtgaat atattcgaga      780
gaccaccacg acgtcgtttt ctccatactc atcatgtgga gctgaaatgg aacatccacc      840
gccattagat cttcgattaa gctttcttta agtcattgac cacaataaca aaagaaaaaa      900
aacagatgct ttagccttta aaatgttggt gtattttgaa ttatgacata ttatccgatg      960
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<210> 16
 <211> 235
 <212> PRT
 <213> Artificial

<220>
 <223> Chimera of HD-domain of GhCIR1 and the C-terminal domain of AtCIR2

<400> 16

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Met Glu Gly Gly Gly Gly Gly Gly Gly Gly Gly Asn Ser Arg Trp Asn
1           5           10           15

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Pro Thr Lys Glu Gln Ile Ser Met Leu Glu Ser Leu Tyr Lys Gln Gly
20           25           30

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

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2577-166.ST25

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

Asn His Lys Ala Arg Gln Arg Gln Lys Gln Lys Gln Glu Asn Leu Ala
 65 70 75 80

Tyr Ile Asn Arg Tyr Ile His His His His Arg Ala Gln Pro Val Phe
 85 90 95

His Pro Pro Pro Cys Thr Asn Val Val Cys Ala Gly Pro Tyr Phe Val
 100 105 110

Pro Gln Ala Asp His His His His Leu Gly Phe Tyr Pro Gln Cys Pro
 115 120 125

Lys Val Leu Leu Pro Ser Arg Ser Ile Lys Arg Arg Gly Arg Pro Ile
 130 135 140

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

Glu Glu Asp Cys Gln Glu Glu Glu Lys Val Ile Glu Thr Leu Gln Leu
 165 170 175

Phe Pro Val Asn Ser Phe Glu Asp Ser Asn Ser Lys Val Asp Lys Met
 180 185 190

Arg Ala Arg Gly Asn Asn Gln Tyr Arg Glu Tyr Ile Arg Glu Thr Thr
 195 200 205

Thr Thr Ser Phe Ser Pro Tyr Ser Ser Cys Gly Ala Glu Met Glu His
 210 215 220

Pro Pro Pro Leu Asp Leu Arg Leu Ser Phe Leu
 225 230 235

<210> 17
 <211> 260
 <212> PRT
 <213> Arabidopsis thaliana
 <400> 17

2577-166.ST25

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

2577-166.ST25

Ser Pro Val Asp Cys Ser Ser Asp Gly Ala Gly Arg Glu Gln Pro Phe
 225 230 235 240

Ile Asp Phe Phe Ser Gly Gly Ser Thr Ser Thr Arg Phe Asp Ser Asn
 245 250 255

Gly Asn Gly Leu
 260

<210> 18
 <211> 244
 <212> PRT
 <213> Arabidopsis thaliana

<400> 18

Met Ser Pro Val Ala Ser Thr Arg Trp Cys Pro Thr Pro Glu Gln Leu
 1 5 10 15

Met Ile Leu Glu Glu Met Tyr Arg Ser Gly Ile Arg Thr Pro Asn Ala
 20 25 30

Val Gln Ile Gln Gln Ile Thr Ala His Leu Ala Phe Tyr Gly Arg Ile
 35 40 45

Glu Gly Lys Asn Val Phe Tyr Trp Phe Gln Asn His Lys Ala Arg Asp
 50 55 60

Arg Gln Lys Leu Arg Lys Lys Leu Ala Lys Gln Leu His Gln Gln Gln
 65 70 75 80

His Gln Leu Gln Leu Gln Leu Gln Gln Ile Lys Pro Lys Pro Ile Ser
 85 90 95

Ser Met Ile Ser Gln Pro Val Asn Lys Asn Ile Ile Asp His His Asn
 100 105 110

Pro Tyr His His His His His Asn His His His Asn His His Arg Pro
 115 120 125

Tyr Asp His Met Ser Phe Asp Cys Cys Ser His Pro Ser Pro Met Cys
 130 135 140

2577-166.ST25

Leu Pro His Gln Gly Thr Gly Val Gly Glu Ala Pro Ser Lys Val Met
 145 150 155 160

Asn Glu Tyr Tyr Cys Thr Lys Ser Gly Ala Glu Glu Ile Leu Met Gln
 165 170 175

Lys Ser Ile Thr Gly Pro Asn Ser Ser Tyr Gly Arg Asp Trp Met Met
 180 185 190

Met Met Asp Met Gly Pro Arg Pro Ser Tyr Pro Ser Ser Ser Ser Ser
 195 200 205

Pro Ile Ser Cys Cys Asn Met Met Met Ser Ser Pro Lys Ile Pro Leu
 210 215 220

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

Ser Thr Lys Leu

<210> 19
 <211> 292
 <212> PRT
 <213> Arabidopsis thaliana

<400> 19

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

Ser Gly Asn Asn Asn Asn Asn Lys Ser Gly Ser Gly Gly Tyr Thr Cys
 20 25 30

Arg Gln Thr Ser Thr Arg Trp Thr Pro Thr Thr Glu Gln Ile Lys Ile
 35 40 45

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

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

Gly Lys Asn Val Phe Tyr Trp Phe Gln Asn His Lys Ala Arg Glu Arg

2577-166.ST25

85

90

95

Gln Lys Lys Arg Phe Asn Gly Thr Asn Met Thr Thr Pro Ser Ser Ser
 100 105 110

Pro Asn Ser Val Met Met Ala Ala Asn Asp His Tyr His Pro Leu Leu
 115 120 125

His His His His Gly Val Pro Met Gln Arg Pro Ala Asn Ser Val Asn
 130 135 140

Val Lys Leu Asn Gln Asp His His Leu Tyr His His Asn Lys Pro Tyr
 145 150 155 160

Pro Ser Phe Asn Asn Gly Asn Leu Asn His Ala Ser Ser Gly Thr Glu
 165 170 175

Cys Gly Val Val Asn Ala Ser Asn Gly Tyr Met Ser Ser His Val Tyr
 180 185 190

Gly Ser Met Glu Gln Asp Cys Ser Met Asn Tyr Asn Asn Val Gly Gly
 195 200 205

Gly Trp Ala Asn Met Asp His His Tyr Ser Ser Ala Pro Tyr Asn Phe
 210 215 220

Phe Asp Arg Ala Lys Pro Leu Phe Gly Leu Glu Gly His Gln Glu Glu
 225 230 235 240

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

Leu Phe Pro Met His Gly Glu Asp His Ile Asn Gly Gly Ser Gly Ala
 260 265 270

Ile Trp Lys Tyr Gly Gln Ser Glu Val Arg Pro Cys Ala Ser Leu Glu
 275 280 285

Leu Arg Leu Asn
 290

<210> 20

2577-166.ST25

<211> 307

<212> PRT

<213> Petunia

<400> 20

Met Glu Thr Ala Gln His Gln Gln Asn Asn Gln Gln His Tyr Leu His
1 5 10 15

Gln His Leu Ser Ile Gly Gln Gly Thr Asn Ile Glu Asp Gly Ser Asn
20 25 30

Lys Asn Asn Ser Ser Asn Phe Met Cys Arg Gln Asn Ser Thr Arg Trp
35 40 45

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

Asn Gly Val Arg Ser Pro Thr Ala Glu Gln Ile Gln Arg Ile Ser Ala
65 70 75 80

Lys Leu Arg Gln Tyr Gly Lys Ile Glu Gly Lys Asn Val Phe Tyr Trp
85 90 95

Phe Gln Asn His Lys Ala Arg Glu Arg Gln Lys Lys Arg Leu Ile Ala
100 105 110

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

Arg Gly Val Trp Arg Ser Ser Ala Asp Asp Pro Ile His His Lys Tyr
130 135 140

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

Ala Val Gly Gln Asn Gly Asn His Gly Tyr Gly Ala Leu Ala Met Glu
165 170 175

Lys Ser Phe Arg Asp Cys Ser Ile Ser Pro Gly Ser Ser Met Ser His
180 185 190

His His His Gln Asn Phe Ala Trp Ala Gly Val Asp Pro Tyr Ser Ser
195 200 205

2577-166.ST25

Thr Thr Thr Tyr Pro Phe Leu Glu Lys Thr Lys His Phe Glu Asn Glu
 210 215 220

Thr Leu Glu Ala Asp Glu Glu Gln Gln Glu Glu Asp Gln Glu Asn Tyr
 225 230 235 240

Tyr Tyr Gln Arg Thr Thr Ser Ala Ile Glu Thr Leu Pro Leu Phe Pro
 245 250 255

Met His Glu Glu Asn Ile Ser Ser Phe Cys Asn Leu Lys His Gln Glu
 260 265 270

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

Ala Ala Ala Arg Ala Ser Leu Glu Leu Ser Leu Asn Ser Phe Ile Gly
 290 295 300

Asn Ser Ser
 305

<210> 21
 <211> 272
 <212> PRT
 <213> Tomato

<400> 21

Met Glu His Gln His Asn Ile Glu Asp Gly Gly Lys Asn Ser Asn Asn
 1 5 10 15

Ser Phe Leu Cys Arg Gln Ser Ser Ser Arg Trp Thr Pro Thr Ser Asp
 20 25 30

Gln Ile Arg Ile Leu Lys Asp Leu Tyr Tyr Asn Asn Gly Val Arg Ser
 35 40 45

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

Gly Lys Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe Gln Asn His Lys
 65 70 75 80

2577-166.ST25

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

Asp Asn Asn Asn Ile Ser Ser Met Gln Met Ile Pro His Leu Trp Arg
 100 105 110

Ser Pro Asp Asp His His Lys Tyr Asn Thr Ala Thr Thr Asn Pro Gly
 115 120 125

Val Gln Cys Pro Ser Pro Ser Ser His Gly Val Leu Pro Val Val Gln
 130 135 140

Thr Gly Asn Tyr Gly Tyr Gly Thr Leu Ala Met Glu Lys Ser Phe Arg
 145 150 155 160

Glu Cys Ser Ile Ser Pro Pro Gly Gly Ser Tyr His Gln Asn Leu Thr
 165 170 175

Trp Val Gly Val Asp Pro Tyr Asn Asn Met Ser Thr Thr Ser Pro Ala
 180 185 190

Thr Tyr Pro Phe Leu Glu Lys Ser Asn Asn Lys His Tyr Glu Glu Thr
 195 200 205

Leu Asp Glu Glu Gln Glu Glu Glu Asn Tyr Gln Arg Gly Asn Ser Ala
 210 215 220

Leu Glu Thr Leu Ser Leu Phe Pro Met His Glu Glu Asn Ile Ile Ser
 225 230 235 240

Asn Phe Cys Ile Lys His His Glu Ser Ser Gly Gly Trp Tyr His Ser
 245 250 255

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

<210> 22
 <211> 200
 <212> PRT
 <213> rice

<400> 22

2577-166.ST25

Met Glu Ala Leu Ser Gly Arg Val Gly Val Lys Cys Gly Arg Trp Asn
 1 5 10 15

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

Leu Arg Thr Pro Ser Thr Glu Gln Ile Gln Arg Ile Ser Thr His Leu
 35 40 45

Ser Ala Phe Gly Lys Val Glu Ser Lys Asn Val Phe Tyr Trp Phe Gln
 50 55 60

Asn His Lys Ala Arg Glu Arg His His His Lys Lys Arg Arg Arg Gly
 65 70 75 80

Ala Ser Ser Pro Asp Ser Gly Ser Asn Asp Asp Asp Gly Arg Ala Ala
 85 90 95

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

Arg Glu Ala Arg Ser Tyr Gly His His His Arg Leu Met Thr Cys Tyr
 115 120 125

Val Arg Asp Val Val Glu Thr Glu Ala Met Trp Glu Arg Pro Thr Arg
 130 135 140

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

Val Asp Lys Val Arg Tyr Val Arg Gly Gly Gly Gly Glu Gln Cys Arg
 165 170 175

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

Leu Arg Leu Cys Ser Phe Gly Leu
 195 200

<210> 23
 <211> 220
 <212> PRT
 <213> Zea May

2577-166.ST25

<400> 23

Met Glu Ala Leu Ser Gly Arg Val Gly Val Lys Cys Gly Arg Trp Asn
 1 5 10 15

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

Leu Arg Thr Pro Ser Thr Glu Gln Ile Gln Arg Ile Ser Thr His Leu
 35 40 45

Ser Ala Phe Gly Lys Val Glu Ser Lys Asn Val Phe Tyr Trp Phe Gln
 50 55 60

Asn His Lys Ala Arg Glu Arg His His His Lys Lys Arg Arg Arg Gly
 65 70 75 80

Ala Ser Ser Ser Ser Pro Asp Ser Gly Ser Gly Arg Gly Ser Asn Asn
 85 90 95

Glu Glu Asp Gly Arg Gly Ala Ala Ser Gln Ser His Asp Ala Asp Ala
 100 105 110

Asp Ala Asp Leu Val Leu Gln Pro Pro Glu Ser Lys Arg Glu Ala Arg
 115 120 125

Ser Tyr Gly His His His Arg Leu Val Thr Cys Tyr Val Arg Asp Val
 130 135 140

Val Glu Gln Gln Glu Ala Ser Pro Ser Trp Glu Arg Pro Thr Arg Glu
 145 150 155 160

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

Ala Ala Glu Lys Val Arg Ser Tyr Val Arg Gly Ile Ala Ala Thr Ser
 180 185 190

Glu Gln Cys Arg Glu Leu Ser Phe Phe Asp Val Ser Ala Gly Arg Asp
 195 200 205

Pro Pro Leu Glu Leu Arg Leu Cys Ser Phe Gly Pro

2577-166.ST25

210

215

220

<210> 24
 <211> 240
 <212> PRT
 <213> Zea May

<400> 24

Met Ala Ala Asn Ala Gly Gly Gly Gly Ala Gly Gly Gly Ser Gly Ser
 1 5 10 15

Gly Ser Val Ala Ala Pro Ala Val Cys Arg Pro Ser Gly Ser Arg Trp
 20 25 30

Thr Pro Thr Pro Glu Gln Ile Arg Met Leu Lys Glu Leu Tyr Tyr Gly
 35 40 45

Cys Gly Ile Arg Ser Pro Ser Ser Glu Gln Ile Gln Arg Ile Thr Ala
 50 55 60

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

Phe Gln Asn His Lys Ala Arg Glu Arg Gln Lys Arg Arg Leu Thr Ser
 85 90 95

Leu Asp Val Asn Val Pro Ala Ala Gly Ala Ala Asp Ala Thr Thr Ser
 100 105 110

Gln Leu Gly Val Leu Ser Leu Ser Ser Pro Pro Pro Ser Gly Ala Ala
 115 120 125

Pro Pro Ser Pro Thr Leu Gly Leu Tyr Ala Ala Gly Asn Gly Gly Gly
 130 135 140

Ser Ala Val Leu Leu Asp Thr Ser Ser Asp Trp Gly Ser Ser Gly Ala
 145 150 155 160

Ala Met Ala Thr Glu Thr Cys Phe Leu Gln Val Gly Ala Val Val Arg
 165 170 175

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

2577-166.ST25

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

Gly Ala Arg Pro Gln Asp Tyr Met Gly Val Thr Asp Thr Gly Ser Ser
 210 215 220

Ser Gln Trp Pro Arg Phe Ser Ser Ser Asp Thr Ile Met Ala Ala Ala
 225 230 235 240

<210> 25
 <211> 237
 <212> PRT
 <213> Zea May

<400> 25

Met Ala Ala Asn Ala Gly Gly Gly Gly Ala Gly Gly Gly Ser Gly Ser
 1 5 10 15

Gly Ser Val Ala Ala Pro Ala Val Cys Arg Pro Ser Gly Ser Arg Trp
 20 25 30

Thr Pro Thr Pro Glu Gln Ile Arg Met Leu Lys Glu Leu Tyr Tyr Gly
 35 40 45

Cys Gly Ile Arg Ser Pro Ser Ser Glu Gln Ile Gln Arg Ile Thr Ala
 50 55 60

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

Phe Gln Asn His Lys Ala Arg Glu Arg Gln Lys Arg Arg Leu Thr Ser
 85 90 95

Leu Asp Val Asn Val Pro Ala Ala Gly Ala Ala Asp Ala Thr Thr Ser
 100 105 110

Gln Leu Gly Val Leu Ser Leu Ser Ser Pro Pro Pro Ser Gly Ala Ala
 115 120 125

Pro Pro Ser Pro Thr Leu Gly Phe Tyr Ala Ala Gly Asn Gly Gly Gly
 130 135 140

29/52

2577-166.ST25

Ser Ala Val Leu Leu Asp Thr Ser Ser Asp Trp Gly Ser Ser Gly Ala
 145 150 155 160

Ala Met Ala Thr Glu Thr Cys Phe Leu Gln Val Gly Ala Val Val Arg
 165 170 175

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

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

Gly Ala Arg Pro Gln Asp Tyr Met Gly Val Thr Asp Thr Gly Ser Ser
 210 215 220

Ser Gln Trp Pro Arg Phe Ala Ser Ser Asp Thr Ile Met
 225 230 235

<210> 26
 <211> 253
 <212> PRT
 <213> Zea May

<400> 26

Met Glu Gly Gly Leu Ser Pro Glu Arg His Ala Ala Ala Glu Pro Val
 1 5 10 15

Arg Ser Arg Trp Thr Pro Lys Pro Glu Gln Ile Leu Ile Leu Glu Ser
 20 25 30

Ile Phe Asn Ser Gly Met Val Asn Pro Pro Lys Asp Glu Thr Val Arg
 35 40 45

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

Phe Tyr Trp Phe Gln Asn Arg Arg Ser Arg Ser Arg Arg Arg Gln Arg
 65 70 75 80

Gln Leu Gln Ala Gln Ala Ala Ala Ser Ser Ser Ser Ser Gly Ser Pro
 85 90 95

2577-166.ST25

Pro Thr Ser Gly Leu Ala Pro Gly His Ala Thr Ala Ser Ser Thr Ala
 100 105 110

Gly Met Phe Ala His Gly Ala Thr Tyr Gly Ser Ser Ala Ser Ala Ser
 115 120 125

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

Gly Gly Gly Asp Asp Leu Phe Ala Ile Ser Arg Gln Met Gly Tyr Ala
 145 150 155 160

Ser Gly Gly Gly Ser Gly Ser Ala Ser Ser Ala Ala Val Ala His His
 165 170 175

Glu Gln Gln Gln Gln Leu Tyr Tyr Ser Pro Cys Gln Pro Ala Ser Met
 180 185 190

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

Asp Leu Arg Ser Met Phe Gly Gln Asp Val Met Leu Val His Ser Thr
 210 215 220

Ala Gly Leu Leu Pro Val Asn Glu Tyr Gly Val Leu Thr Gln Ser Leu
 225 230 235 240

Gln Met Gly Glu Ser Tyr Phe Leu Val Thr Arg Gly Tyr
 245 250

<210> 27
 <211> 227
 <212> PRT
 <213> Zea May

<400> 27

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

Glu Gly Leu Tyr Glu His Gly Leu Arg Thr Pro Ser Ala Glu Gln Ile
 20 25 30

Gln Gln Ile Thr Gly Arg Leu Arg Glu His Gly Ala Ile Glu Gly Lys

2577-166.ST25

35

40

45

Asn Val Phe Tyr Trp Phe Gln Asn His Lys Ala Arg Gln Arg Gln Arg
 50 55 60

Gln Lys Gln Asp Ser Phe Ala Tyr Phe Ser Arg Leu Leu Arg Arg Pro
 65 70 75 80

Pro Pro Leu Pro Val Leu Ser Met Pro Pro Ala Pro Pro Tyr His His
 85 90 95

Ala Arg Val Pro Ala Pro Pro Ala Ile Pro Met Pro Met Ala Pro Pro
 100 105 110

Pro Pro Ala Ala Cys Asn Asp Asn Gly Gly Ala Arg Val Ile Tyr Arg
 115 120 125

Asn Pro Phe Tyr Val Ala Ala Pro Gln Ala Pro Pro Ala Asn Ala Ala
 130 135 140

Tyr Tyr Tyr Pro Gln Pro Gln Gln Gln Gln Gln Gln Val Thr Val
 145 150 155 160

Met Tyr Gln Tyr Pro Arg Met Glu Val Ala Gly Gln Asp Lys Met Met
 165 170 175

Thr Arg Ala Ala Ala His Gln Gln Gln Gln His Asn Gly Ala Gly Gln
 180 185 190

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

Pro Pro Pro Ala His Leu Arg Ala Ala Ala Arg Gln Gly Ala Arg Arg
 210 215 220

Gln Arg Gln
 225

<210> 28
 <211> 134
 <212> PRT
 <213> Zea May

2577-166.ST25

<400> 28

Met Glu Ser Ser His Ser Thr Ala Glu Asp Glu Ser Gly Trp Lys Gly
 1 5 10 15

Ser Ser Gly Ala His Ser Ser Val Ser Arg Trp Ser Pro Thr Lys Glu
 20 25 30

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

Ser Thr Glu Gln Ile Gln Gln Ile Thr Ser Arg Leu Arg Ala Tyr Gly
 50 55 60

Tyr Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe Gln Asn His Lys Ala
 65 70 75 80

Arg Gln Arg Gln Lys Leu Lys Gln Lys Gln Gln Ser Ile Ala Tyr Cys
 85 90 95

Asn Cys Phe Leu His Ala Ser His Pro Ile Cys Gln Asn Val Val Cys
 100 105 110

Val His Ile Val Cys Lys Arg Val Asp Ser Ala Phe Ile Leu Thr Asn
 115 120 125

Gln Arg Cys Leu Gln Val
 130

<210> 29

<211> 225

<212> PRT

<213> Zea May

<400> 29

Met Glu Ser His Ser Thr Ala Glu Asp Glu Ser Gly Trp Lys Gly Ser
 1 5 10 15

Ser Gly Ala His Ser Ser Val Ser Arg Trp Ser Pro Thr Lys Glu Gln
 20 25 30

Ile Asp Met Glu Thr Leu Glu Asn Phe Tyr Lys Gln Gly Ile Arg Thr
 35 40 45

2577-166.ST25

Pro Ser Thr Glu Gln Ile Gln Gln Ile Thr Ser Arg Leu Arg Ala Tyr
 50 55 60

Gly Tyr Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe Gln Asn His Lys
 65 70 75 80

Ala Arg Gln Arg Gln Lys Leu Lys Gln Lys Gln Gln Ser Ile Ala Tyr
 85 90 95

Cys Asn Cys Phe Leu His Ala Ser His Pro Ile Cys Gln Asn Val Val
 100 105 110

Cys Ala Pro Tyr Cys Leu Gln Lys Ser Gly Phe Ser Phe Tyr Pro His
 115 120 125

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

Gly Ser Phe Gly Met Glu Thr Leu Arg Ile Cys Asp Gly Met Glu Thr
 145 150 155 160

Gln Ser Glu His Pro Asp Tyr Asn Tyr Ser Thr Ser Asn Arg Glu Ala
 165 170 175

Leu Thr Leu Phe Pro Leu His Pro Thr Gly Ile Leu Glu Glu Lys Thr
 180 185 190

Thr His His Ser Val Asp Val Thr Asp Lys Ser Phe Val Ser Ile Ala
 195 200 205

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

Tyr
 225

<210> 30
 <211> 212
 <212> PRT
 <213> Glycin Max

<400> 30

2577-166.ST25

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

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

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

Gln Gln Ile Thr Ser Arg Leu Arg Ala Tyr Gly His Ile Glu Gly Lys
 50 55 60

Asn Val Phe Tyr Trp Phe Gln Asn His Lys Ala Arg Gln Arg Gln Lys
 65 70 75 80

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

Ser His Pro Ile Cys Gln Asn Val Ala Cys Ala Pro Tyr Cys Leu Gln
 100 105 110

Arg Ser Gly Phe Ser Phe Tyr Pro Gln Gln Ser Lys Val Leu Ala Ser
 115 120 125

Gly Gly Ile Ser Ser Thr Gly Pro Leu Gly Met Gln Arg Met Phe Asp
 130 135 140

Gly Met Gln Ser Ser Glu His Pro Asp Cys Asn Arg Glu Val Leu Thr
 145 150 155 160

Leu Phe Pro Leu His Pro Thr Gly Ile Leu Lys Glu Lys Thr Thr His
 165 170 175

Gln Val Pro Ser Leu Ala Ser Thr Ser Val Val Ala Val Asp Glu Asp
 180 185 190

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

Arg Ser Arg Glu
 210

2577-166.ST25

<210> 31
<211> 236
<212> PRT
<213> Glycine Max

<220>
<221> misc_feature
<222> (162)..(162)
<223> Xaa can be any naturally occurring amino acid

<400> 31

Met Leu Lys Leu Ser Met Lys Val His Gln Phe Ala Arg Gly Phe Trp
1 5 10 15

Glu His Glu Pro Ser Leu Thr Leu Gly Cys Lys Arg Leu Arg Pro Leu
20 25 30

Ala Pro Lys Leu Ser Asn Thr Asp Thr Ile Ser Pro Pro His His Pro
35 40 45

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

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

Pro Ser Ser Pro Gln Gly Gln Ala Glu Thr His Ile Pro Gly Gly Thr
85 90 95

Arg Trp Asn Pro Thr Gln Glu Gln Ile Gly Ile Leu Glu Met Leu Tyr
100 105 110

Arg Gly Gly Met Arg Thr Pro Asn Ala Gln Gln Ile Glu Gln Ile Thr
115 120 125

Ala Gln Leu Ser Lys Tyr Gly Lys Ile Glu Gly Lys Asn Val Phe Tyr
130 135 140

Trp Phe Gln Asn His Lys Ala Arg Glu Arg Gln Lys Gln Lys Arg Asn
145 150 155 160

Asn Xaa Gly Leu Ala His Ser Pro Arg Thr Thr Leu Thr Thr Ser Pro
165 170 175

2577-166.ST25

Pro Phe Ser Cys Cys Val Ile Thr Thr Met Asp Thr Thr Lys Arg Gly
 180 185 190

Glu Val Val Glu Arg Glu Glu Glu Asp Ser Pro Leu Lys Lys Cys Arg
 195 200 205

Ser Trp Ala Phe Glu Tyr Leu Glu Asp Gln Arg Glu Glu Glu His Arg
 210 215 220

Thr Leu Glu Leu Phe Pro Leu His Pro Glu Gly Arg
 225 230 235

<210> 32
 <211> 222
 <212> PRT
 <213> Glycine Max

<400> 32

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

Pro Phe Leu Thr Leu Gly Cys Lys Arg Leu Arg Pro Leu Ala Pro Lys
 20 25 30

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

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

Lys Lys Asp Pro Pro Ser Pro Gln Gly Gln Ile Glu Thr His Pro Gly
 65 70 75 80

Gly Thr Arg Trp Asn Pro Thr Gln Glu Gln Ile Gly Ile Leu Glu Met
 85 90 95

Leu Tyr Lys Gly Gly Met Arg Thr Pro Asn Ala Gln Gln Ile Glu Gln
 100 105 110

Ile Thr Val Gln Leu Gly Lys Tyr Gly Lys Ile Glu Gly Lys Asn Val
 115 120 125

2577-166.ST25

Phe Tyr Trp Phe Gln Asn His Lys Ala Arg Glu Arg Gln Lys Gln Lys
 130 135 140

Arg Ser Ser Leu Ala Ser Ser His Ser Pro Arg Thr Pro Thr Ile His
 145 150 155 160

Ser Val Val Thr Leu Glu Thr Thr Arg Gly Glu Val Val Glu Arg Asp
 165 170 175

His Glu Glu Asp Ser Pro Tyr Lys Lys Lys Cys Arg Arg Trp Val Phe
 180 185 190

Asp Cys Leu Glu Glu Gln Asn Met Ser Ser Pro Cys Glu Gln Glu Glu
 195 200 205

His Arg Thr Leu Glu Leu Phe Pro Leu His Pro Glu Gly Arg
 210 215 220

<210> 33

<211> 44

<212> DNA

<213> Artificial

<220>

<223> Synthetic Construct, GeneRacer RNA oligo

<220>

<221> misc_feature

<222> (5)..(5)

<223> n = u

<220>

<221> misc_feature

<222> (21)..(21)

<223> n = u

<220>

<221> misc_feature

<222> (26)..(26)

<223> n = u

<220>

<221> misc_feature

<222> (31)..(31)

<223> n = u

<220>

<221> misc_feature

<222> (39)..(39)

2577-166.ST25

<223> n = u

<400> 33

cgacnnggagc acgaggacac ngacangggac ngaaggagna gaaa

44

<210> 34

<211> 54

<212> DNA

<213> Artificial

<220>

<223> Synthetic Construct, GeneRacer oligo dT primer

<400> 34

gctgtcaacg atacgctacg taacggcatg acagtgtttt tttttttttt tttt

54

<210> 35

<211> 40

<212> DNA

<213> Artificial

<220>

<223> PCR primer GR5-2

<400> 35

ttttggcgcg cgggacactg acttggactg aaggagtaga

40

<210> 36

<211> 38

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38

<210> 37

<211> 33

<212> DNA

<213> Artificial

<220>

<223> PCR primer GR3-2P

<400> 37

tttttaatta agctacgtaa cggcatgaca gtg

33

<210> 38

<211> 32

2577-166.ST25

<212> DNA

<213> Artificial

<220>

<223> PCR primer 59340U

<400> 38

aaggcgcgcc atggaaaacg aagtaaacgc ag

32

<210> 39

<211> 34

<212> DNA

<213> Artificial

<220>

<223> PCR primer 59340L

<400> 39

cgttaattaa ttacaacca ttaccattac tatc

34

<210> 40

<211> 34

<212> DNA

<213> Artificial

<220>

<223> PCR primer 11260U

<400> 40

aaggcgcgcc agttgaggac ttacatctg aaca

34

<210> 41

<211> 30

<212> DNA

<213> Artificial

<220>

<223> PCR primer 11260L

<400> 41

aattaattaa ccatgcattg gaaaatatct

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<210> 42

<211> 37

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<220>

<223> PCR primer 46480U

<400> 42

aggcgcgcc aaatgaaggt tcatgagttt tcgaatg

37

2577-166.ST25

<210> 43
<211> 34
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<400> 43
agttaattaa tcatctccct tcaggatgga gagg

34

<210> 44
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<210> 45
<211> 36
<212> DNA
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36

<210> 46
<211> 34
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34

<210> 47
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2577-166.ST25

<223> PCR primer VP16U

<400> 47

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34

<210> 48

<211> 33

<212> DNA

<213> Artificial

<220>

<223> PCR primer VP16L

<400> 48

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33

<210> 49

<211> 30

<212> DNA

<213> Artificial

<220>

<223> PCR primer GhCIR1N2L

<400> 49

gattaattaa agttttacca ataggcctgc

30

<210> 50

<211> 33

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<223> PCR primer At3g11260U2

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33

<210> 51

<211> 26

<212> DNA

<213> Artificial

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<223> PCR primer GhCIR1T188AU

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26

<210> 52

<211> 26

2577-166.ST25

<212> DNA

<213> Artificial

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<223> PCR primer GhCIR1T188AL

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gaaacaatgg caaggcctcg tgatga

26

<210> 53

<211> 27

<212> DNA

<213> Artificial

<220>

<223> PCR primer GhCIR1T188DU

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tcatcacgag gatttgccat tgtttcc

27

<210> 54

<211> 27

<212> DNA

<213> Artificial

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<223> PCR primer GhCIR1T188DL

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ggaaacaatg gcaaatactc gtgatga

27

<210> 55

<211> 28

<212> DNA

<213> Artificial

<220>

<223> PCR primer GhCIR1deltaC45

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ttaattaaaa caccagtcgg gtgcaatg

28

<210> 56

<211> 41

<212> DNA

<213> Artificial

<220>

<223> PCR primer GhCIR1E236A

<400> 56

ttttaattaa gaagaaatca atgaaacgat gtgccccaga a

41

2577-166.ST25

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<211> 735
<212> DNA
<213> *Gossypium hirsutum*

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caaataagca tgcttgaaag cttgtacaag caagggataa gaacccaag tgctgatcag 120
atacagcaaa taaccagtag gctcaaagct tatggcacca ttgaaggcaa aaacgtgttc 180
tattggttcc aaaatcataa agctcgtcaa aggcagaaac aaaagcaaga gaatttggct 240
tatatcaacc gttacattca ccatcatcat cgagctcaac ctgtttttca tctcctcct 300
tgcaccaatg ttgtttgtgc tgggccatat ttgtaccac aagctgatca tcaccatcat 360
ctaggctttt accctcagtg tccaagggtt cttctcccta gtagatcaat taaaagaaga 420
ggcaggccta ttggtaaaac tggaaagtct ctattttaca acggaaatgc ttatgatcat 480
accatgggtc catcacctga tactgaaaac ttatacactg gagcattcaa caatggcggc 540
ggcgccacta atcatcacga gacattgcca ttgtttccat tgcacccgac tgggtgttcc 600
gaagagacgt taatgggttc atcatcacca actggttcaa cttcatgtga gacgacgata 660
tctgctggtg gtgttgataa ccatgaaagt aataatgaag gttctgggga acatcgtttc 720
attgatttct tctga 735

<210> 58
<211> 708
<212> DNA
<213> *Gossypium hirsutum*

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caaataagca tgcttgaaag cttgtacaag caagggataa gaacccaag tgctgatcag 120
atacagcaaa taaccagtag gctcaaagct tatggcacca ttgaaggcaa aaacgtgttc 180
tattggttcc aaaatcataa agctcgtcaa aggcagaaac aaaagcaaga gaatttggct 240
tatatcaacc gttacattca ccatcatcat cgagctcaac ctgtttttca tctcctcct 300
tgcaccaatg ttgtttgtgc tgggccatat ttgtaccac aagctgatca tcaccatcat 360
ctaggctttt accctcagtg tccaagggtt cttctcccta gtagatcaat taaaagaaga 420
ggcaggccta ttggtaaaac tttaattaat ccatcaacta gagatgtttt tgaaataagc 480

2577-166.ST25

gaagaagatt gtcaagagga agagaaggtg atagagacat tacaactcct tccggtgaat 540
tcatttgaag actccaactc caaggtggac aaaatgagag ctagaggcaa taaccagtac 600
cgtgaatata ttcgagagac caccacgacg tcgttttctc catactcatc atgtggagct 660
gaaatggaac atccaccgcc attagatcct cgattaagct ttctttaa 708

<210> 59
<211> 6
<212> PRT
<213> Gossypium hirsutum

<400> 59

Lys Arg Arg Gly Arg Pro
1 5

<210> 60
<211> 73
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct, signature sequence

<220>
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<222> (1)..(1)
<223> X = a polypeptide chain of any number of amino acid residues
between 13 and 23 residues

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> X = K or V

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> X = D or E

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> X = I or L

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> X = S, T or K

2577-166.ST25

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> X = M, I or L

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> X = E or T

<220>
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<222> (15)..(15)
<223> X = S, N or D

<220>
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<222> (17)..(17)
<223> X = F or Y

<220>
<221> MISC_FEATURE
<222> (18)..(18)
<223> X = K or R

<220>
<221> MISC_FEATURE
<222> (19)..(19)
<223> X = Q, E or A

<220>
<221> misc_feature
<222> (21)..(21)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (25)..(25)
<223> X = S or T

<220>
<221> MISC_FEATURE
<222> (26)..(26)
<223> X = A or T

<220>
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<222> (31)..(31)
<223> X = Q or K

<220>
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<220>

2577-166.ST25

<221> MISC_FEATURE
<222> (34)..(34)
<223> X = G, S or T

<220>
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<222> (35)..(35)
<223> X = R or E

<220>
<221> MISC_FEATURE
<222> (37)..(37)
<223> X = K, R or S

<220>
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<222> (38)..(38)
<223> X = A or F

<220>
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<222> (41)..(41)
<223> X = K, H or T

<220>
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<222> (44)..(44)
<223> X = G or S

<220>
<221> MISC_FEATURE
<222> (58)..(58)
<223> X = Q or E

<220>
<221> MISC_FEATURE
<222> (62)..(62)
<223> X = Q or R

<220>
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<222> (63)..(63)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (64)..(64)
<223> X = a polypeptide chain of any number of amino acid residues
between 29 and 101 residues

<220>
<221> MISC_FEATURE
<222> (65)..(65)
<223> X = E or K

<220>

2577-166.ST25

<221> MISC_FEATURE
<222> (66)..(66)
<223> X = S, T, A, C, I, G, V, L, M, N, Q or P

<220>
<221> MISC_FEATURE
<222> (68)..(68)
<223> X = P or Q

<220>
<221> misc_feature
<222> (72)..(72)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (73)..(73)
<223> X = a polypeptide chain of any number of amino acid residues between 13 and 57 residues

<400> 60

Xaa Arg Trp Asn Pro Thr Xaa Xaa Gln Xaa Xaa Xaa Leu Xaa Xaa Leu
1 5 10 15

Xaa Xaa Xaa Gly Xaa Arg Thr Pro Xaa Xaa Asp Gln Ile Gln Xaa Ile
20 25 30

Xaa Xaa Xaa Leu Xaa Xaa Tyr Gly Xaa Ile Glu Xaa Lys Asn Val Phe
35 40 45

Tyr Trp Phe Gln Asn His Lys Ala Arg Xaa Arg Gln Lys Xaa Xaa Xaa
50 55 60

Xaa Xaa Leu Xaa Leu Phe Pro Xaa Xaa
65 70

<210> 61
<211> 73
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct, expanded signature sequence

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<223> X = a polypeptide chain of any number of amino acid residues between 13 and 23 residues

2577-166.ST25

<220>
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<222> (7)..(7)
<223> X = K, E, Q, R, I, M, L or V

<220>
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<222> (8)..(8)
<223> X = E, D, N, K or Q

<220>
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<222> (10)..(10)
<223> X = I, L, M or V

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<222> (11)..(11)
<223> X = E, K, N, S, T, Q or R

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<222> (12)..(12)
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<223> X = D, E, K, Q, S or T

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<223> X = A, D, E, H, N, S or T

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<223> X = A, D, E, K, R, Q or S

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2577-166.ST25

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<222> (25)..(26)

<223> X = A, S or T

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<221> MISC_FEATURE

<222> (31)..(31)

<223> X = E, K, Q or R

<220>

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<222> (33)..(33)

<223> X = A, S or T

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<223> X = A, G, S or T

<220>

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<222> (35)..(35)

<223> X = D, E, K, Q or R

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> X = A, E, Q, K, R, S or T

<220>

<221> MISC_FEATURE

<222> (38)..(38)

<223> X = A, S, F, W or Y

<220>

<221> MISC_FEATURE

<222> (41)..(41)

<223> X = E, Q, H, K, T or Y

<220>

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<222> (44)..(44)

<223> X = A, G, S or T

<220>

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<223> X = D, E, Q, K or R

<220>

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<222> (62)..(63)

<223> X = E, K, Q or R

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2577-166.ST25

<221> MISC_FEATURE
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<223> X = a polypeptide chain of any number of amino acid residues
between 29 and 101 residues

<220>
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<223> X = D, E, K, Q or R

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<223> X = S, T, A, C, I, G, V, L, M, N, Q or P

<220>
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<222> (68)..(68)
<223> X = E, P, Q, K or R

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<222> (72)..(72)
<223> X = M, I, L or V

<220>
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<223> X = a polypeptide chain of any number of amino acid residues
between 13 and 57 residues

<400> 61

Xaa Arg Trp Asn Pro Thr Xaa Xaa Gln Xaa Xaa Xaa Leu Xaa Xaa Leu
1 5 10 15

Xaa Xaa Xaa Gly Xaa Arg Thr Pro Xaa Xaa Asp Gln Ile Gln Xaa Ile
20 25 30

Xaa Xaa Xaa Leu Xaa Xaa Tyr Gly Xaa Ile Glu Xaa Lys Asn Val Phe
35 40 45

Tyr Trp Phe Gln Asn His Lys Ala Arg Xaa Arg Gln Lys Xaa Xaa Xaa
50 55 60

Xaa Xaa Leu Xaa Leu Phe Pro Xaa Xaa
65 70

<210> 62
<211> 99
<212> DNA

2577-166.ST25

<213> Artificial

<220>

<223> Synthetic Construct

<400> 62

ctgtacaagt taattaacta cccctatgat gtacctgact atgcataccc ttatgatgta 60

ccagactatg ctcacatca ccacatcac tgactagtc 99

<210> 63

<211> 30

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 63

Leu Tyr Lys Leu Ile Asn Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Tyr
1 5 10 15Pro Tyr Asp Val Pro Asp Tyr Ala His His His His His His
20 25 30

<210> 64

<211> 4

<212> PRT

<213> Agrobacterium tumefaciens

<400> 64

Arg Lys Gly Lys

1

<210> 65

<211> 6

<212> PRT

<213> Gossypium hirsutum

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> X = any amino acids

<400> 65

Thr Leu Xaa Leu Phe Pro

1

5

2577-166.ST25

<210> 66
<211> 6
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<213> Artificial

<220>
<223> Synthetic Construct, signature sequence

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<400> 66

Arg Trp Asn Pro Thr Xaa
1 5

<210> 67
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<223> Synthetic Construct, signature sequence

<400> 67

Arg Trp Asn Pro Thr Lys
1 5

<210> 68
<211> 6
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<220>
<223> Synthetic Construct, signature sequence

<400> 68

Arg Trp Asn Pro Thr Val
1 5