

LISTADO DE SECUENCIAS

<110> Monsanto Technology LLC
 <120> PROTEÍNAS INHIBIDORAS DE INSECTOS NOVEDOSAS
 <130> MONS:530WO
 <150> US 63/219.604
 <151> 2021-07-08
 <150> US 63/348.278
 <151> 2022-06-02
 <160> 18
 <170> PatentIn versión 3.5
 <210> 1
 <211> 2160
 <212> ADN
 <213> Bacillus thuringiensis
 <220>
 <221> característica_misc
 <222> (1)..(2160)
 <223> Secuencia de ácido nucleico que codifica una proteína plaguicida TIC2199 obtenida de la especie EG8639 Bacillus thuringiensis
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 atgaaaccaa agaatcaaaa tatgtatcaa agcttgtcta gcaatgtgac agttgataaa 60
 atctctacaa atccactaaa aatgaaaca gatatagaat tacaaaatat taatcatgaa 120
 gcttgtttaa aatgtctaa gtataaaaat gtagcgccat ttgttagcgc atcaacaatt 180
 caaacgggga ttggaattgc tggttaagatt cttggtactc taggtgttcc ttttgctgga 240
 caaatagcta gcctctatag ttttatctta ggcgagcttt ggcttaaagg gaaaagtcaa 300
 tgggaaatct ttatggaaca tgtagaagag attattaatc aaaaaatatc aacttatgca 360
 agaaataaag ctctttcaga cttgagagga ttaggggatg ctttagccgt ctacatgaa 420
 tcgcttgaaa gttgggttga aaatcgtaat aacactcgag cgaggagtgt agtcaagaac 480
 caatatatcg cattagaact gatgtttgtt caaaaactac cttcttttgc agtatctggt 540
 gaggaagtac cattattacc gatatacgcc caagctgcca atttacattt gttgttatta 600
 agagatgtat ctatTTTTGG aaaagaatgg ggattatcag cttcagaaat ttcaacattt 660
 tataaccgtc aagtcgaacg aacaagagat tattccgacc attgtgtaaa atggtataat 720

acaggcctaa ataacttgag ggggtacaaat gccaaaagtt gggtttcgtta taatcaat	780
cgtaaagata tgacattaat ggtattagat ttagttgcgc tattcccaag ctatgataca	840
cttgatatatc ctattaaaac cacttcacaa cttacaagag aagtatatac agacgcaatt	900
gggaccgtgc atccgaatca agcttttgca agtacgactt ggtataataa taatgcacct	960
tcgttctctg ccatagaggc tgctgttatc cgaagtccac acctacttga ttttctagaa	1020
aaagttacaa tatacagctt attaagtcgg tggagtaata ctacgtatat gaatatgtgg	1080
ggaggacata gacttgaatc ccgcccata ggaggggcat taaatacctc aacacaagga	1140
tctaccaata cttcgattaa tccagtaaca ttacagttca cgtctcgaga cgtttatagg	1200
actgaatcat gggcagggct gaatttattt ttaactcaac ctgttaatgg agtacctaga	1260
gttgatttcc attggaaatt cgtcacacat ccgatcgcat ctgataattt ctattatcca	1320
gggtatgctg gaattgggac acaattacaa gattcagaaa atgaattacc acctgaaaca	1380
acaggacagc caaattatga atcatatagt catagattat ctcatatagg actcatttca	1440
gcatcacatg tgaaagcatt ggtatattct tggacgcac gtagtgcaga tcgtacaaat	1500
acaattgagc caaatagcat tacacaaata ccattagtaa aagcgttcaa tctttcttca	1560
ggtgccgctg ttgtgagagg accaggattt acaggtgggg atatccttcg aagaacgaat	1620
actggtacat ttggggatat acgagtaaatt attaatccac ctttgcaca aaggtatcgc	1680
gtaaggattc gctatgcttc tactacagat ttacaattcc atacgtcaat taacggtaaa	1740
gctattaatc aaggtaattt ttcagcaact atgaatagag gagaggactt agactataaa	1800
acctttagaa ctgtaggctt taccactcca tttagctttt cagatgtaca aagtacattc	1860
acaatagggtg cttggaactt ctcttcaggt aacgaagttt atatagatag aattgaattt	1920
gttccggtag aagttacata tggggcagaa tatgattttg aaaaagcgca agagaagggt	1980
actgcactgt ttacatctac gaatccaaga gaattaaaaa tagatgtaac ggattatcat	2040
attgaccagg tatcaaattt agtagagtct ctattagacg aattctatct tgatgaaaag	2100
agagaattat tcgagatagt taaatacgcg aagcaactct atattgagcg taacatgtag	2160

<210> 2

<211> 719

<212> PRT

<213> Bacillus thuringiensis

<220>

<221> característica_misc

<222> (1)..(719)

<223> Secuencia de aminoácidos de la proteína plaguicida TIC2199.

<400> 2

Met Lys Pro Lys Asn Gln Asn Met Tyr Gln Ser Leu Ser Ser Asn Val
1 5 10 15

Thr Val Asp Lys Ile Ser Thr Asn Pro Leu Lys Asn Glu Thr Asp Ile
20 25 30

Glu Leu Gln Asn Ile Asn His Glu Ala Cys Leu Lys Met Ser Lys Tyr
35 40 45

Lys Asn Val Ala Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
50 55 60

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

Gln Ile Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
85 90 95

Gly Lys Ser Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
100 105 110

Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Ser Asp Leu
115 120 125

Arg Gly Leu Gly Asp Ala Leu Ala Val Tyr His Glu Ser Leu Glu Ser
130 135 140

Trp Val Glu Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Asn
145 150 155 160

Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
165 170 175

Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala

180

185

190

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

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

Val Glu Arg Thr Arg Asp Tyr Ser Asp His Cys Val Lys Trp Tyr Asn
 225 230 235 240

Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Lys Ser Trp Val Arg
 245 250 255

Tyr Asn Gln Phe Arg Lys Asp Met Thr Leu Met Val Leu Asp Leu Val
 260 265 270

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

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

Pro Asn Gln Ala Phe Ala Ser Thr Thr Trp Tyr Asn Asn Asn Ala Pro
 305 310 315 320

Ser Phe Ser Ala Ile Glu Ala Ala Val Ile Arg Ser Pro His Leu Leu
 325 330 335

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

Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Arg Leu Glu Ser Arg
 355 360 365

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

Ser Ile Asn Pro Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg
 385 390 395 400

Thr Glu Ser Trp Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn
405 410 415

Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile
420 425 430

Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile Gly Thr Gln
435 440 445

Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Thr Thr Gly Gln Pro
450 455 460

Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser
465 470 475 480

Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala
485 490 495

Asp Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu
500 505 510

Val Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro
515 520 525

Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe
530 535 540

Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg
545 550 555 560

Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser
565 570 575

Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn
580 585 590

Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr Val Gly Phe Thr
595 600 605

Thr Pro Phe Ser Phe Ser Asp Val Gln Ser Thr Phe Thr Ile Gly Ala

610

615

620

Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe
 625 630 635 640

Val Pro Val Glu Val Thr Tyr Gly Ala Glu Tyr Asp Phe Glu Lys Ala
 645 650 655

Gln Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro Arg Glu Leu
 660 665 670

Lys Ile Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val
 675 680 685

Glu Ser Leu Leu Asp Glu Phe Tyr Leu Asp Glu Lys Arg Glu Leu Phe
 690 695 700

Glu Ile Val Lys Tyr Ala Lys Gln Leu Tyr Ile Glu Arg Asn Met
 705 710 715

<210> 3

<211> 2160

<212> ADN

<213> Artificial

<220>

<223> Secuencia codificadora sintética usada para la expresión en una célula
 vegetal
 que codifica TIC2199

<400> 3

atgaagccca agaatcagaa catgtaccag tccctcagct cgaacgtcac cgtcgataag 60

attagcacca acccgctcaa gaatgagacc gacatcgaat tacagaacat taaccacgag 120

gcgtgcctca agatgtctaa gtacaagaac gtcgcaccct tcgtctcggc ttctacgatac 180

cagacgggca ttggcatcgc cgggaagata ctcggcacac tcggcgtccc gttcgtggt 240

caaatcgcct cgctctactc cttcatactc ggtgaactgt ggccgaaggg caagtcgcag 300

tgggaaatct tcatggagca cgtggaggag atcatcaacc agaagataag cacctacgcc 360

cgtaacaagg cgctgagcga cctccgtggg ctgggcgatg cgctggcggg gtaccacgag 420

tcgctggagt cgtgggtgga gaaccgcaac aacaccgcg cccggtccgt ggtcaagaac 480

cagtacattg ccctggagct gatgttcgtg cagaagctcc cgtccttcgc ggtgtccggc	540
gaggaagtgc cactgttgcc catctacgcc caagcagcca acctgcacct ctttctcctc	600
cgggacgtca gcatcttcgg gaaggagtgg ggcctttcag cgtcagagat ttcaaccttc	660
tacaacaggc aagttgagcg cacgcgcgac tactcggacc actgcgtcaa gtggtacaac	720
accggcctca acaacctgcg tggaacgaac gccaagagct ggggccgcta caaccagttt	780
cgaaggaca tgacctcat ggtgctggac cttgtggcct tgttcccgtc ctacgacacc	840
ctcgtttatc cgattaagac tacatctcaa cttacccgcg aggtttacac agacgccata	900
gggaccgtgc atcctaacca ggcgttcgca tcgacaactt ggtacaacaa caacgcgccc	960
tcgttctcag ccatcgaggc cgccgtgatc cgttcaccgc acctcctgga cttcctggag	1020
aaggttacca tctactccct cttgtctcgc tggagtaata ctcagtacat gaacatgtgg	1080
ggaggacatc gcctcgaatc tcgaccgatt ggcggcgcgc ttaacacatc cacacagggc	1140
tccacgaaca ccagcatcaa cccggtgacg ttgcaattca cttcacgcga tgtctatcgg	1200
accgagagct gggctggcct gaacctgttc ctaactcagc ccgtgaacgg tgtgcccaga	1260
gtcgatttcc actggaaatt cgtcactcat cccatcgcca gcgacaactt ctactacca	1320
ggctacgccg gtatcggcac acagcttcaa gactccgaga acgaactgcc tcccagagact	1380
actggccagc cgaactacga gagttactcc cataggcttt cgcacatcgg cctaattctca	1440
gcttcgcatg ttaaagcact cgtgtactca tggacacaca gaagcgccga cagaacgaac	1500
accattgagc caaactctat cacgcagatc ccgctggtta aggcgttcaa cttgtcgagc	1560
ggcgctgcgg tcgtgcgcgg acctggattc accggtggcg acattctgcg ccgcaccaac	1620
acaggaacct tcggcgacat ccgggtgaac atcaaccgcg cgtttgcaca acgctatcgc	1680
gtcaggatac ggtacgcatc cacgacggac ctccagttcc acaccagcat caacgggaag	1740
gctatcaacc agggaaactt tagcgccacg atgaaccgtg gtgaggactt ggactacaag	1800
acattccgga cggtcggctt cacgacgcc tttagcttta gcgacgtcca gtccaccttc	1860
accatcggag catggaactt cagtagcggc aacgaggtgt acatcgaccg aatcgagttc	1920
gtcccggttg aggtgacctc cggagccgaa tacgacttcg agaaggcaca ggagaagggtg	1980
actgctctgt ttacaagcac aaatcctcgg gaactaaaga tcgacgtcac agactaccac	2040
atcgaccaag ttagcaacct cgtcgagagc ctcttgacg agttctatctt ggacgagaag	2100

cgggagctgt tcgagatcgt gaaatacgcc aagcagttgt acatcgagcg taacatgtga 2160

<210> 4
<211> 611
<212> PRT
<213> Bacillus thuringiensis

<220>
<221> característica_misc
<222> (1)..(611)
<223> Una secuencia de aminoácidos de un fragmento de TIC2199 donde el péptido de secreción del extremo N y el dominio protoxina han sido eliminados.

<400> 4

Met Ser Lys Tyr Lys Asn Val Ala Pro Phe Val Ser Ala Ser Thr Ile
1 5 10 15

Gln Thr Gly Ile Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val
20 25 30

Pro Phe Ala Gly Gln Ile Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu
35 40 45

Leu Trp Pro Lys Gly Lys Ser Gln Trp Glu Ile Phe Met Glu His Val
50 55 60

Glu Glu Ile Ile Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala
65 70 75 80

Leu Ser Asp Leu Arg Gly Leu Gly Asp Ala Leu Ala Val Tyr His Glu
85 90 95

Ser Leu Glu Ser Trp Val Glu Asn Arg Asn Asn Thr Arg Ala Arg Ser
100 105 110

Val Val Lys Asn Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys
115 120 125

Leu Pro Ser Phe Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile
130 135 140

Tyr Ala Gln Ala Ala Asn Leu His Leu Leu Leu Leu Arg Asp Val Ser
145 150 155 160

Ile Phe Gly Lys Glu Trp Gly Leu Ser Ala Ser Glu Ile Ser Thr Phe
165 170 175

Tyr Asn Arg Gln Val Glu Arg Thr Arg Asp Tyr Ser Asp His Cys Val
180 185 190

Lys Trp Tyr Asn Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Lys
195 200 205

Ser Trp Val Arg Tyr Asn Gln Phe Arg Lys Asp Met Thr Leu Met Val
210 215 220

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

Ile Lys Thr Thr Ser Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile
245 250 255

Gly Thr Val His Pro Asn Gln Ala Phe Ala Ser Thr Thr Trp Tyr Asn
260 265 270

Asn Asn Ala Pro Ser Phe Ser Ala Ile Glu Ala Ala Val Ile Arg Ser
275 280 285

Pro His Leu Leu Asp Phe Leu Glu Lys Val Thr Ile Tyr Ser Leu Leu
290 295 300

Ser Arg Trp Ser Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Arg
305 310 315 320

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

Ser Thr Asn Thr Ser Ile Asn Pro Val Thr Leu Gln Phe Thr Ser Arg
340 345 350

Asp Val Tyr Arg Thr Glu Ser Trp Ala Gly Leu Asn Leu Phe Leu Thr
355 360 365

Gln Pro Val Asn Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val
370 375 380

Thr His Pro Ile Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly
385 390 395 400

Ile Gly Thr Gln Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Thr
405 410 415

Thr Gly Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile
420 425 430

Gly Leu Ile Ser Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr
435 440 445

His Arg Ser Ala Asp Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr
450 455 460

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

Val Arg Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn
485 490 495

Thr Gly Thr Phe Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala
500 505 510

Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln
515 520 525

Phe His Thr Ser Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser
530 535 540

Ala Thr Met Asn Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr
545 550 555 560

Val Gly Phe Thr Thr Pro Phe Ser Phe Ser Asp Val Gln Ser Thr Phe
565 570 575

Thr Ile Gly Ala Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp
580 585 590

Arg Ile Glu Phe Val Pro Val Glu Val Thr Tyr Gly Ala Glu Tyr Asp
595 600 605

Phe Glu Lys
610

<210> 5
<211> 1836
<212> ADN
<213> Artificial

<220>
<223> Una secuencia de ADN que codifica la proteína truncada TIC2199 de SEQ ID NO:4 para la expresión en bacterias.

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ggaattgctg gtaagattct tgggtactcta ggtgttcctt ttgctggaca aatagctagc 120
ctctatagtt ttatcttagg cgagctttgg cctaaaggga aaagtcaatg ggaaatcttt 180
atggaacatg tagaagagat tattaatcaa aaaatatcaa cttatgcaag aaataaagct 240
ctttcagact tgagaggatt aggggatgct ttagccgtct accatgaatc gcttgaaagt 300
tgggttgaaa atcgtaataa cactcgagcg aggagtgtag tcaagaacca atatatcgca 360
ttagaactga tgtttggtca aaaactacct tcttttgcag tatctggtga ggaagtacca 420
ttattaccga tatacgcca agctgccaat ttacatttgt tgttattaag agatgtatct 480
atttttggaa aagaatgggg attatcagct tcagaaattt caacatttta taaccgtcaa 540
gtcgaacgaa caagagatta ttccgaccat tgtgtaaaat ggtataatac aggcctaaat 600
aacttgaggg gtacaaatgc caaaagttgg gttcgttata atcaatttcg taaagatatg 660
acattaatgg tattagattt agttgcgcta ttcccaagct atgatacact tgtatatcct 720
attaaaacca cttcacaact tacaagagaa gtatatacag acgcaattgg gaccgtgcat 780
ccgaatcaag cttttgcaag tacgacttgg tataataata atgcaccttc gttctctgcc 840
atagaggctg ctgttatccg aagtccacac ctacttgatt ttctagaaaa agttacaata 900
tacagcttat taagtcggtg gagtaatact cagtatatga atatgtgggg aggacataga 960

cttgaatccc gcccaatagg aggggcatta aatacctcaa cacaaggatc taccaatact	1020
tcgattaatc cagtaacatt acagttcacg tctcgagacg tttataggac tgaatcatgg	1080
gcagggctga atttattttt aactcaacct gttaatggag tacctagagt tgatttccat	1140
tggaaattcg tcacacatcc gatcgcacgt gataatttct attatccagg gtatgctgga	1200
attgggacac aattacaaga ttcagaaaat gaattaccac ctgaaacaac aggacagcca	1260
aattatgaat catatagtca tagattatct catataggac tcatttcagc atcacatgtg	1320
aaagcattgg tatattcttg gacgcatcgt agtgcagatc gtacaaatac aattgagcca	1380
aatagcatta cacaataacc attagtaaaa gcgttcaatc tttcttcagg tgccgctgtt	1440
gtgagaggac caggatttac aggtggggat atccttcgaa gaacgaatac tggtacattt	1500
ggggatatac gagtaaatat taatccacca tttgcacaaa ggtatcgcgt aaggattcgc	1560
tatgcttcta ctacagattt acaattccat acgtcaatta acggtaaagc tattaatcaa	1620
ggtaattttt cagcaactat gaatagagga gaggacttag actataaaac ctttagaact	1680
gtaggcttta ccactccatt tagcttttca gatgtacaaa gtacattcac aataggtgct	1740
tggaacttct cttcaggtaa cgaagtttat atagatagaa ttgaatttgt tccggtagaa	1800
gttacatatg gggcagaata tgattttgaa aaatag	1836

<210> 6
 <211> 1836
 <212> ADN
 <213> Artificial

<220>

<223> Una secuencia codificadora sintética que codifica la TIC2199 truncada de SEQ ID NO:4 y es capaz de ser usada en una célula vegetal.

<400> 6

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ggcatcgccg ggaagatact cggcacactc ggcgtcccgt tcgctggtca aatcgccctcg	120
ctctactcct tcatactcgg tgaactgtgg ccgaagggca agtcgcagtg ggaaatcttc	180
atggagcacg tggaggagat catcaaccag aagataagca cctacgcccg taacaaggcg	240
ctgagcgacc tccgtgggct gggcgatgcg ctggcgggtgt accacgagtc gctggagtcg	300
tgggtggaga accgcaacaa caccgcgcc cggtccgtgg tcaagaacca gtacattgcc	360
ctggagctga tgttcgtgca gaagctcccg tccttcgcgg tgtccggcga ggaagtgcc	420

ctgttgccca tctacgcca agcagccaac ctgcacctcc ttctcctccg ggacgtcagc	480
atcttcggga aggagtgggg cctttcagcg tcagagattt caaccttcta caacaggcaa	540
gttgagcgca cgcgcgacta ctcggaccac tgcgtcaagt ggtacaacac cggcctcaac	600
aacctgcgtg gaacgaacgc caagagctgg gtccgctaca accagtttcg aaaggacatg	660
accctcatgg tgctggacct tgtggccttg ttcccgtcct acgacaccct cgtttatccg	720
attaagacta catctcaact taccgcgag gtttacacag acgcatagg gaccgtgcat	780
cctaaccagg cgttcgcac gacaacttgg tacaacaaca acgcgccctc gttctcagcc	840
atcgaggccg ccgtgatccg ttcaccgcac ctcttgact tcctggagaa ggttaccatc	900
tactccctct tgtctcgctg gagtaatact cagtacatga acatgtgggg aggacatcgc	960
ctcgaatctc gaccgattgg cggcgcgctt aacacatcca cacagggtc cacgaacacc	1020
agcatcaacc cggtgacgtt gcaattcact tcacgcgatg tctatcggac cgagagctgg	1080
gctggcctga acctgttcct aactcagccc gtgaacggtg tgcccagagt cgatttccac	1140
tggaatttcg tcatcatcc catcgccagc gacaacttct actaccagg ctacgccggt	1200
atcggcacac agcttcaaga ctccgagaac gaactgcctc ccgagactac tggccagccg	1260
aactacgaga gttactccca taggccttcg cacatcggcc taatctcagc ttcgcatgtt	1320
aaagcactcg tgtactcatg gacacacaga agcgccgaca gaacgaacac cattgagcca	1380
aactctatca cgcagatccc gctgggtaag gcgttcaact tgtcgagcgg cgctgcggtc	1440
gtgcgcggac ctggattcac cgggtggcgac attctgcgcc gcaccaacac aggaaccttc	1500
ggcgacatcc ggggtgaacat caaccgccg tttgcacaac gctatcgcgt caggatacgg	1560
tacgcatcca cgacggacct ccagttccac accagcatca acgggaaggc tatcaaccag	1620
ggaaacttta gcgccacgat gaaccgtggt gaggacttgg actacaagac attccggacg	1680
gtcggcttca cgacgccctt cagctttagc gacgtccagt ccaccttcac catcggagca	1740
tggaacttca gtagcggcaa cgaggtgtac atcgaccgaa tcgagttcgt cccggttgag	1800
gtgacctacg gagccgaata cgacttcgag aagtga	1836

<210> 7
 <211> 675
 <212> PRT
 <213> Artificial

<220>

<223> Una secuencia de aminoácidos de una variante de TIC2199, TIC2199_1, en la cual los 44 aminoácidos del extremo N que comprenden un péptido de secreción han sido eliminados.

<400> 7

Met Ser Lys Tyr Lys Asn Val Ala Pro Phe Val Ser Ala Ser Thr Ile
1 5 10 15

Gln Thr Gly Ile Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val
20 25 30

Pro Phe Ala Gly Gln Ile Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu
35 40 45

Leu Trp Pro Lys Gly Lys Ser Gln Trp Glu Ile Phe Met Glu His Val
50 55 60

Glu Glu Ile Ile Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala
65 70 75 80

Leu Ser Asp Leu Arg Gly Leu Gly Asp Ala Leu Ala Val Tyr His Glu
85 90 95

Ser Leu Glu Ser Trp Val Glu Asn Arg Asn Asn Thr Arg Ala Arg Ser
100 105 110

Val Val Lys Asn Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys
115 120 125

Leu Pro Ser Phe Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile
130 135 140

Tyr Ala Gln Ala Ala Asn Leu His Leu Leu Leu Leu Arg Asp Val Ser
145 150 155 160

Ile Phe Gly Lys Glu Trp Gly Leu Ser Ala Ser Glu Ile Ser Thr Phe
165 170 175

Tyr Asn Arg Gln Val Glu Arg Thr Arg Asp Tyr Ser Asp His Cys Val
180 185 190

Lys Trp Tyr Asn Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Lys
195 200 205

Ser Trp Val Arg Tyr Asn Gln Phe Arg Lys Asp Met Thr Leu Met Val
210 215 220

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

Ile Lys Thr Thr Ser Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile
245 250 255

Gly Thr Val His Pro Asn Gln Ala Phe Ala Ser Thr Thr Trp Tyr Asn
260 265 270

Asn Asn Ala Pro Ser Phe Ser Ala Ile Glu Ala Ala Val Ile Arg Ser
275 280 285

Pro His Leu Leu Asp Phe Leu Glu Lys Val Thr Ile Tyr Ser Leu Leu
290 295 300

Ser Arg Trp Ser Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Arg
305 310 315 320

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

Ser Thr Asn Thr Ser Ile Asn Pro Val Thr Leu Gln Phe Thr Ser Arg
340 345 350

Asp Val Tyr Arg Thr Glu Ser Trp Ala Gly Leu Asn Leu Phe Leu Thr
355 360 365

Gln Pro Val Asn Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val
370 375 380

Thr His Pro Ile Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly
385 390 395 400

Ile Gly Thr Gln Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Thr
405 410 415

Thr Gly Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile
420 425 430

Gly Leu Ile Ser Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr
435 440 445

His Arg Ser Ala Asp Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr
450 455 460

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

Val Arg Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn
485 490 495

Thr Gly Thr Phe Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala
500 505 510

Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln
515 520 525

Phe His Thr Ser Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser
530 535 540

Ala Thr Met Asn Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr
545 550 555 560

Val Gly Phe Thr Thr Pro Phe Ser Phe Ser Asp Val Gln Ser Thr Phe
565 570 575

Thr Ile Gly Ala Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp
580 585 590

Arg Ile Glu Phe Val Pro Val Glu Val Thr Tyr Gly Ala Glu Tyr Asp
595 600 605

Phe Glu Lys Ala Gln Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn
610 615 620

Pro Arg Glu Leu Lys Ile Asp Val Thr Asp Tyr His Ile Asp Gln Val
625 630 635 640

Ser Asn Leu Val Glu Ser Leu Leu Asp Glu Phe Tyr Leu Asp Glu Lys
645 650 655

Arg Glu Leu Phe Glu Ile Val Lys Tyr Ala Lys Gln Leu Tyr Ile Glu
660 665 670

Arg Asn Met
675

<210> 8
<211> 2028
<212> ADN
<213> Artificial

<220>
<223> Una secuencia de ADN que codifica la variante TIC2199_1
de SEQ ID NO:7.

<400> 8
atgtctaagt ataaaaatgt agcgccattt gttagcgcac caacaattca aacgggggatt 60
ggaattgctg gtaagattct tgggtactcta ggtgttcctt ttgctggaca aatagctagc 120
ctctatagtt ttatcttagg cgagcttttg cctaaaggga aaagtcaatg ggaaatcttt 180
atggaacatg tagaagagat tattaatcaa aaaatatcaa cttatgcaag aaataaagct 240
ctttcagact tgagaggatt aggggatgct ttagccgtct accatgaatc gcttgaaagt 300
tgggttgaaa atcgtaataa cactcgagcg aggagtgtag tcaagaacca atatatcgca 360
ttagaactga tgtttgttca aaaactacct tcttttgcag tatctggtga ggaagtacca 420
ttattaccga tatacgccca agctgccaat ttacatttgt tgttattaag agatgtatct 480
atttttggaa aagaatgggg attatcagct tcagaaattt caacatttta taaccgtcaa 540
gtcgaacgaa caagagatta ttccgaccat tgtgtaaaaat ggtataatac aggcctaaat 600
aacttgaggg gtacaaatgc caaaagttgg gttcggtata atcaatttcg taaagatatg 660
acattaatgg tattagattt agttgcgcta ttcccaagct atgatacact tgtatatcct 720
attaaaacca cttcacaact tacaagagaa gtatatacag acgcaattgg gaccgtgcat 780

ccgaatcaag cttttgcaag tacgacttgg tataataata atgcaccttc gttctctgcc	840
atagaggctg ctgttatccg aagtccacac ctacttgatt ttctagaaaa agttacaata	900
tacagcttat taagtcggtg gagtaatact cagtatatga atatgtgggg aggacataga	960
cttgaatccc gcccaatagg aggggcatta aatacctcaa cacaaggatc taccaatact	1020
tcgattaatc cagtaacatt acagttcacg tctcgagacg tttataggac tgaatcatgg	1080
gcagggctga atttatTTTT aactcaacct gttaatggag tacctagagt tgatttccat	1140
tggaaattcg tcacacatcc gatcgcctct gataatttct attatccagg gtatgctgga	1200
attgggacac aattacaaga ttcagaaaaat gaattaccac ctgaaacaac aggacagcca	1260
aattatgaat catatagtca tagattatct catataggac tcatttcagc atcacatgtg	1320
aaagcattgg tatattcttg gacgcatcgt agtgcagatc gtacaaatac aattgagcca	1380
aatagcatta caciaatacc attagtaaaa gcgttcaatc tttcttcagg tgccgctggt	1440
gtgagaggac caggatttac aggtggggat atccttcgaa gaacgaatac tggtacattt	1500
ggggatatac gagtaaatat taatccacca tttgcacaaa ggtatcgcgt aaggattcgc	1560
tatgcttcta ctacagattt acaattccat acgtcaatta acggtaaagc tattaatcaa	1620
ggtaattttt cagcaactat gaatagagga gaggacttag actataaaac ctttagaact	1680
gtaggcttta ccactccatt tagcttttca gatgtacaaa gtacattcac aataggtgct	1740
tggaaacttct cttcaggtaa cgaagtttat atagatagaa ttgaatttgt tccggtagaa	1800
gttacatatg gggcagaata tgattttgaa aaagcgcaag agaaggttac tgcactgttt	1860
acatctacga atccaagaga attaaaaata gatgtaacgg attatcatat tgaccaggta	1920
tcaaatttag tagagtctct attagacgaa ttctatcttg atgaaaagag agaattattc	1980
gagatagtta aatacgcgaa gcaactctat attgagcgta acatgtag	2028

<210> 9
 <211> 2028
 <212> ADN
 <213> Artificial

<220>
 <223> Una secuencia codificadora sintética que codifica la variante TIC2199_1 de SEQ ID NO:7 y es capaz de ser usada en una célula vegetal.

<400> 9

atgtctaagt acaagaacgt cgcacccttc gtctcggctt ctacgatcca gacgggcatt	60
ggcatcgccg ggaagatact cggcacactc gggtgtcccg tgcgtgggtca aatcgccctcg	120
ctctactcct tcatactcgg tgaactgtgg ccgaagggca agtcgcagtg ggaaatcttc	180
atggagcacg tggaggagat catcaaccag aagataagca cctacgcccg taacaaggcg	240
ctgagcgacc tccgtgggct gggcgatgcg ctggcggtgt accacgagtc gctggagtcg	300
tgggtggaga accgcaaca caccgcgcc cggtccgtgg tcaagaacca gtacattgcc	360
ctggagctga tgttcgtgca gaagctcccg tccttcgcgg tgtccggcga ggaagtcca	420
ctgttgccca tctacgcca agcagccaac ctgcacctcc ttctcctccg ggacgtcagc	480
atcttcggga aggagtgggg cctttcagcg tcagagattt caaccttcta caacaggcaa	540
gttgagcgca cgcgcgacta ctcggaccac tgcgtcaagt ggtacaacac cggcctcaac	600
aacctgcgtg gaacgaacgc caagagctgg gtccgctaca accagtttcg aaaggacatg	660
accctcatgg tgctggacct tgtggccttg ttcccgtcct acgacaccct cgtttatccg	720
attaagacta catctcaact taccgcgag gtttacacag acgcatagg gaccgtgcat	780
cctaaccagg cgttcgcata gacaacttgg tacaacaaca acgcgccctc gttctcagcc	840
atcgaggccg ccgtgatccg ttcaccgcac ctcctggact tcctggagaa ggttaccatc	900
tactccctct tgtctcgctg gagtaatact cagtacatga acatgtgggg aggacatcgc	960
ctcgaatctc gaccgattgg cggcgcgctt aacacatcca cacagggtc cacgaacacc	1020
agcatcaacc cggtgacgtt gcaattcact tcacgcgatg tctatcggac cgagagctgg	1080
gctggcctga acctgttcct aactcagccc gtgaacggtg tgcccagagt cgatttccac	1140
tggaaattcg tcaatcatcc catcgccagc gacaatttct actaccaggg ctacgccggt	1200
atcggcacac agcttcaaga ctccgagaac gaactgcctc ccgagactac tggccagccg	1260
aactacgaga gttactccca taggctttcg cacatcggcc taatctcagc ttcgatgtt	1320
aaagcactcg tgtactcatg gacacacaga agcgccgaca gaacgaacac cattgagcca	1380
aactctatca cgcagatccc gctgggttaag gcgttcaact tgtcgagcgg cgctgcggtc	1440
gtgcgcggac ctggattcac cgggtggcgac attctgcgcc gcaccaacac aggaaccttc	1500
ggcgacatcc ggggtgaacat caaccgcgcg ttgacacaac gctatcgcgt caggatacgg	1560
tacgcatcca cgacggacct ccagttccac accagcatca acgggaaggc tatcaaccag	1620

ggaaacttta gcgccacgat gaaccgtggt gaggacttgg actacaagac attccggacg 1680
 gtcggcttca cgacgccctt cagctttagc gacgtccagt ccaccttcac catcggagca 1740
 tggaacttca gtagcggcaa cgagggtgtac atcgaccgaa tcgagttcgt cccggttgag 1800
 gtgacctacg gagccgaata cgacttcgag aaggcacagg agaaggtgac tgctctgttt 1860
 acaagcacia atcctcggga actaaagatc gacgtcacag actaccacat cgaccaagtt 1920
 agcaacctcg tcgagagcct cctggacgag ttctatttgg acgagaagcg ggagctgttc 1980
 gagatcgtga aatacgccaa gcagttgtac atcgagcgta acatgtga 2028

<210> 10
 <211> 655
 <212> PRT
 <213> Artificial

<220>
 <223> Una secuencia de aminoácidos de una variante de TIC2199, TIC2199_2
 en la cual los 64 aminoácidos del extremo C también han sido removidos.

<400> 10

Met Lys Pro Lys Asn Gln Asn Met Tyr Gln Ser Leu Ser Ser Asn Val
 1 5 10 15

Thr Val Asp Lys Ile Ser Thr Asn Pro Leu Lys Asn Glu Thr Asp Ile
 20 25 30

Glu Leu Gln Asn Ile Asn His Glu Ala Cys Leu Lys Met Ser Lys Tyr
 35 40 45

Lys Asn Val Ala Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
 50 55 60

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

Gln Ile Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
 85 90 95

Gly Lys Ser Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
 100 105 110

Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Ser Asp Leu
115 120 125

Arg Gly Leu Gly Asp Ala Leu Ala Val Tyr His Glu Ser Leu Glu Ser
130 135 140

Trp Val Glu Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Asn
145 150 155 160

Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
165 170 175

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

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

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

Val Glu Arg Thr Arg Asp Tyr Ser Asp His Cys Val Lys Trp Tyr Asn
225 230 235 240

Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Lys Ser Trp Val Arg
245 250 255

Tyr Asn Gln Phe Arg Lys Asp Met Thr Leu Met Val Leu Asp Leu Val
260 265 270

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

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

Pro Asn Gln Ala Phe Ala Ser Thr Thr Trp Tyr Asn Asn Asn Ala Pro
305 310 315 320

Ser Phe Ser Ala Ile Glu Ala Ala Val Ile Arg Ser Pro His Leu Leu
325 330 335

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

Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Arg Leu Glu Ser Arg
355 360 365

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

Ser Ile Asn Pro Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg
385 390 395 400

Thr Glu Ser Trp Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn
405 410 415

Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile
420 425 430

Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile Gly Thr Gln
435 440 445

Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Thr Thr Gly Gln Pro
450 455 460

Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser
465 470 475 480

Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala
485 490 495

Asp Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu
500 505 510

Val Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro
515 520 525

Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe
530 535 540

Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg
545 550 555 560

Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser
565 570 575

Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn
580 585 590

Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr Val Gly Phe Thr
595 600 605

Thr Pro Phe Ser Phe Ser Asp Val Gln Ser Thr Phe Thr Ile Gly Ala
610 615 620

Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe
625 630 635 640

Val Pro Val Glu Val Thr Tyr Gly Ala Glu Tyr Asp Phe Glu Lys
645 650 655

<210> 11
<211> 1968
<212> ADN
<213> Artificial

<220>
<223> Una secuencia de ADN que codifica la variante TIC2199_2 de SEQ ID NO:10.

<400> 11
atgaaaccaa agaatcaaaa tatgtatcaa agcttgtcta gcaatgtgac agttgataaa 60
atctctacaa atccactaaa aatgaaaca gatatagaat tacaaaatat taatcatgaa 120
gcttgtttaa aaatgtctaa gtataaaaat gtagcgccat ttgttagcgc atcaacaatt 180
caaacgggga ttggaattgc tggttaagatt cttggtactc taggtgttcc ttttgctgga 240
caaatagcta gcctctatag ttttatctta ggcgagcttt ggcctaaagg gaaaagtcaa 300
tgggaaatct ttatggaaca tgtagaagag attattaatc aaaaaatatc aacttatgca 360
agaaataaag ctctttcaga cttgagagga ttaggggatg ctttagccgt ctaccatgaa 420
tcgcttgaaa gttgggttga aaatcgtaat aacactcgag cgaggagtgt agtcaagaac 480
caatatatcg cattagaact gatgtttgtt caaaaactac cttcttttgc agtatctggt 540

gaggaagtac cattattacc gatatacgcc caagctgcca atttacattt gttgttatta	600
agagatgtat ctatTTTTGG aaaagaatgg ggattatcag cttcagaaat ttcaacattt	660
tataaccgtc aagtcgaacg aacaagagat tattccgacc attgtgtaaa atggtataat	720
acaggcctaa ataacttgag ggggtacaaat gccaaaagtt gggttcgtta taatcaattt	780
cgtaaagata tgacattaat ggtattagat ttagttgcgc tattcccaag ctatgataca	840
cttgtatatac ctattaaaac cacttcacaa cttacaagag aagtatatac agacgcaatt	900
gggaccgtgc atccgaatca agcttttgca agtacgactt ggtataataa taatgcacct	960
tcgttctctg ccatagaggc tgctgttatc cgaagtccac acctacttga ttttctagaa	1020
aaagttacaa tatacagctt attaagtcgg tggagtaata ctcagtatat gaatatgtgg	1080
ggaggacata gacttgaatc ccgccaata ggaggggcat taaatacctc aacacaagga	1140
tctaccaata cttcgattaa tccagtaaca ttacagttca cgtctcgaga cgtttatagg	1200
actgaatcat gggcagggtc gaatttattt ttaactcaac ctgttaatgg agtacctaga	1260
gttgatttcc attggaaatt cgtcacacat ccgatcgcat ctgataattt ctattatcca	1320
gggtatgctg gaattgggac acaattacaa gattcagaaa atgaattacc acctgaaaca	1380
acaggacagc caaattatga atcatatagt catagattat ctcatatagg actcatttca	1440
gcatcacatg tgaaagcatt ggtatatattc tggacgcac gtagtgcaga tcgtacaaat	1500
acaattgagc caaatagcat tacacaaata ccattagtaa aagcgttcaa tctttcttca	1560
ggtgccgctg ttgtgagagg accaggattt acaggtgggg atatccttcg aagaacgaat	1620
actggtacat ttggggatat acgagtaaatt attaatccac catttgcaca aaggtatcgc	1680
gtaaggattc gctatgcttc tactacagat ttacaattcc atacgtcaat taacggtaaa	1740
gctattaatc aaggtaattt ttcagcaact atgaatagag gagaggactt agactataaa	1800
acctttagaa ctgtaggctt taccactcca tttagctttt cagatgtaca aagtacattc	1860
acaataggtg cttggaactt ctcttcaggt aacgaagttt atatagatag aattgaattt	1920
gttccggtag aagttacata tggggcagaa tatgattttg aaaaatga	1968

<210> 12
 <211> 1968
 <212> ADN
 <213> Artificial

<220>

<223> Una secuencia codificadora sintética que codifica la variante
TIC2199_2 de SEQ ID NO:10 y es capaz de ser usada en una célula vegetal.

<400> 12

atgaagccca agaatcagaa catgtaccag tccctcagct cgaacgtcac cgtcgataag	60
attagcacca acccgctcaa gaatgagacc gacatcgaat tacagaacat taaccacgag	120
gcgtgcctca agatgtctaa gtacaagaac gtcgcaccct tcgtctcggc ttctacgata	180
cagacgggca ttggcatcgc cggaagata ctcggcacac tcggcgtccc gttcgctggt	240
caaatgcct cgctctactc cttcatactc ggtgaactgt ggccgaaggg caagtcgcag	300
tgggaaatct tcatggagca cgtggaggag atcatcaacc agaagataag cacctacgcc	360
cgtaacaagg cgctgagcga cctccgtggg ctgggcgatg cgctggcggg gtaccacgag	420
tcgctggagt cgtgggtgga gaaccgcaac aacaccgcg cccgggtccgt ggtcaagaac	480
cagtacattg ccctggagct gatgttcgtg cagaagctcc cgtccttcgc ggtgtccggc	540
gaggaagtgc cactgttgcc catctacgcc caagcagcca acctgcacct ctttctctc	600
cgggacgtca gcatcttcgg gaaggagtgg ggcctttcag cgtcagagat ttcaaccttc	660
tacaacaggc aagttgagcg cacgcgcgac tactcggacc actgcgtcaa gtggtacaac	720
accggcctca acaacctgcg tggaacgaac gccaaagact gggtccgcta caaccagttt	780
cgaaaggaca tgacctcat ggtgctggac cttgtggcct tgttcccgtc ctacgacacc	840
ctcgtttatc cgattaagac tacatctcaa cttaccgcg aggtttacac agacgccata	900
gggaccgtgc atcctaacca ggcgttcgca tcgacaactt ggtacaacaa caacgcgccc	960
tcgttctcag ccatcgaggc cgccgtgatc cgttcaccgc acctcctgga cttcctggag	1020
aaggttacca tctactccct cttgtctcgc tggagtaata ctacgtacat gaacatgtgg	1080
ggaggacatc gcctcgaatc tcgaccgatt ggcggcgcgc ttaacacatc cacacagggc	1140
tccacgaaca ccagcatcaa cccggtgacg ttgcaattca cttcacgcga tgtctatcgg	1200
accgagagct gggctggcct gaacctgttc ctaactcagc ccgtgaacgg tgtgcccaga	1260
gtcgatttcc actggaaatt cgtcactcat cccatcgcca gcgacaactt ctactacca	1320
ggctacgccg gtatcggcac acagcttcaa gactccgaga acgaactgcc tcccagagact	1380
actggccagc cgaactacga gagttactcc cataggcttt cgcacatcgg cctaattctca	1440

gcttcgcatg ttaaagcact cgtgtactca tggacacaca gaagcgccga cagaacgaac 1500
accattgagc caaactctat cacgcagatc ccgctgggta aggcgttcaa cttgtcgagc 1560
ggcgtgcggt tcgtgcgcgg acctggattc accggtggcg acattctgcg ccgcaccaac 1620
acaggaacct tcggcgacat ccgggtgaac atcaaccgc cgtttgcaca acgctatcgc 1680
gtcaggatac ggtacgcac cagcagggac ctccagttcc acaccagcat caacgggaag 1740
gctatcaacc agggaaactt tagcgccacg atgaaccgtg gtgaggactt ggactacaag 1800
acattccgga cggtcggctt cagcagccc ttacagcttta gcgacgtcca gtccaccttc 1860
accatcggag catggaactt cagtagcggc aacgaggtgt acatcgaccg aatcgagttc 1920
gtcccgggtg aggtgaccta cggagccgaa tacgacttcg agaagtga 1968

<210> 13
<211> 674
<212> PRT
<213> Artificial

<220>
<223> Una secuencia de aminoácidos de la variante TIC2199_1 a la que se le ha eliminado la metionina inicial y se utiliza para unirla de forma operativa a un péptido de tránsito del cloroplasto.

<400> 13

Ser Lys Tyr Lys Asn Val Ala Pro Phe Val Ser Ala Ser Thr Ile Gln
1 5 10 15

Thr Gly Ile Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro
20 25 30

Phe Ala Gly Gln Ile Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu
35 40 45

Trp Pro Lys Gly Lys Ser Gln Trp Glu Ile Phe Met Glu His Val Glu
50 55 60

Glu Ile Ile Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu
65 70 75 80

Ser Asp Leu Arg Gly Leu Gly Asp Ala Leu Ala Val Tyr His Glu Ser
85 90 95

Leu Glu Ser Trp Val Glu Asn Arg Asn Asn Thr Arg Ala Arg Ser Val
100 105 110

Val Lys Asn Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu
115 120 125

Pro Ser Phe Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr
130 135 140

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

Phe Gly Lys Glu Trp Gly Leu Ser Ala Ser Glu Ile Ser Thr Phe Tyr
165 170 175

Asn Arg Gln Val Glu Arg Thr Arg Asp Tyr Ser Asp His Cys Val Lys
180 185 190

Trp Tyr Asn Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Lys Ser
195 200 205

Trp Val Arg Tyr Asn Gln Phe Arg Lys Asp Met Thr Leu Met Val Leu
210 215 220

Asp Leu Val Ala Leu Phe Pro Ser Tyr Asp Thr Leu Val Tyr Pro Ile
225 230 235 240

Lys Thr Thr Ser Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly
245 250 255

Thr Val His Pro Asn Gln Ala Phe Ala Ser Thr Thr Trp Tyr Asn Asn
260 265 270

Asn Ala Pro Ser Phe Ser Ala Ile Glu Ala Ala Val Ile Arg Ser Pro
275 280 285

His Leu Leu Asp Phe Leu Glu Lys Val Thr Ile Tyr Ser Leu Leu Ser
290 295 300

Arg Trp Ser Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Arg Leu

305		310		315		320
Glu Ser Arg Pro	Ile Gly Gly Ala Leu Asn Thr Ser Thr Gln Gly Ser					
	325			330		335
Thr Asn Thr Ser	Ile Asn Pro Val Thr Leu Gln Phe Thr Ser Arg Asp					
	340		345			350
Val Tyr Arg Thr	Glu Ser Trp Ala Gly Leu Asn Leu Phe Leu Thr Gln					
	355		360			365
Pro Val Asn Gly	Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr					
	370		375			380
His Pro Ile Ala	Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile					
	385		390		395	400
Gly Thr Gln Leu	Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Thr Thr					
	405		410			415
Gly Gln Pro Asn	Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly					
	420		425			430
Leu Ile Ser Ala	Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His					
	435		440			445
Arg Ser Ala Asp	Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln					
	450		455			460
Ile Pro Leu Val	Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val					
	465		470		475	480
Arg Gly Pro Gly	Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr					
	485		490			495
Gly Thr Phe Gly	Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln					
	500		505			510
Arg Tyr Arg Val	Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe					
	515		520			525

His Thr Ser Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala
530 535 540

Thr Met Asn Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr Val
545 550 555 560

Gly Phe Thr Thr Pro Phe Ser Phe Ser Asp Val Gln Ser Thr Phe Thr
565 570 575

Ile Gly Ala Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg
580 585 590

Ile Glu Phe Val Pro Val Glu Val Thr Tyr Gly Ala Glu Tyr Asp Phe
595 600 605

Glu Lys Ala Gln Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro
610 615 620

Arg Glu Leu Lys Ile Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser
625 630 635 640

Asn Leu Val Glu Ser Leu Leu Asp Glu Phe Tyr Leu Asp Glu Lys Arg
645 650 655

Glu Leu Phe Glu Ile Val Lys Tyr Ala Lys Gln Leu Tyr Ile Glu Arg
660 665 670

Asn Met

<210> 14
<211> 2025
<212> ADN
<213> Artificial

<220>
<223> Una secuencia codificadora sintética que codifica la variante
TIC2199_1 a la cual se le ha eliminado el codón de metionina inicial
y se utiliza para unirla de forma operativa a un péptido de tránsito
del cloroplasto y es capaz de ser utilizada en una célula vegetal.

<400> 14
tctaagtaca agaacgtcgc acccttcgtc tcggcttcta cgatccagac gggcattggc 60

atcgccggga agatactcgg cacactcggc gtcccgttcg ctggtcaa	at	cgcc	cgctc	120
tactccttca tactcgggtga actgtggccg aagggaagt cgagtg	ga	aatctt	catg	180
gagcacgtgg aggagatcat caaccagaag ataagcacct acgccc	gtaa	caaggc	gctg	240
agcgacctcc gtgggctggg cgatgcgctg gcggtgtacc acgagtc	gct	ggagtc	gctg	300
gtggagaacc gcaacaacac ccgcgcccgg tccgtggtca agaacc	agta	cattgc	cctg	360
gagctgatgt tcgtgcagaa gctcccgtcc ttcgcggtgt ccggcg	agga	agtgcc	actg	420
ttgcccattc acgccaagc agccaacctg cacctccttc tcctcc	ggga	cgtcag	catc	480
ttcggaagg agtggggcct ttcagcgtca gagatttcaa ctttcta	caa	caggca	agtt	540
gagcgcacgc gcgactactc ggaccactgc gtcaagtgggt acaac	accgg	cctcaaca	ac	600
ctgctgggaa cgaacgcaa gagctgggtc cgctacaacc agtttc	gaaa	ggacat	gacc	660
ctcatggtgc tggaccttgt ggccttggtc ccgtcctacg acacc	ctgt	ttatcc	gatt	720
aagactacat ctcaacttac ccgcgagggt tacacagacg ccatag	ggac	cgtgca	tcct	780
aaccaggcgt tcgcatcgac aacttggtac aacaacaacg cgccct	cgtt	ctcagcc	atc	840
gaggccgccg tgatccgttc accgcacctc ctggacttcc tggaga	aggt	taccat	ctac	900
tccctcttgt ctcgctggag taatactcag tacatgaaca tgtggg	gagg	acatgc	cctc	960
gaatctcgac cgattggcgg cgcgcttaac acatccacac agggct	ccac	gaacacc	agc	1020
atcaaccggg tgacgttgca attcacttca cgcgatgtct atcgg	accga	gagctggg	ct	1080
ggcctgaacc tgttcctaac tcagcccgtg aacggtgtgc ccagag	tcga	tttccact	gg	1140
aaattcgtca ctcatcccat cgccagcgac aacttctact acccag	gcta	cgccgg	tatc	1200
ggcacacagc ttcaagactc cgagaacgaa ctgcctcccg agact	actgg	ccagccga	ac	1260
tacgagagtt actcccatag gctttcgcac atcggcctaa tctcag	cttc	gcatgt	taaa	1320
gcactcgtgt actcatggac acacagaagc gccgacagaa cgaac	accat	tgagccaa	ac	1380
tctatcacgc agatcccgtt ggttaaggcg ttcaacttgt cgagcg	gcgc	tgcggtc	gtg	1440
cgcggacctg gattcaccgg tggcgacatt ctgcgccgca ccaaca	cagg	aaccttc	ggc	1500
gacatccggg tgaacatcaa cccgccgttt gcacaacgct atcgc	gtcag	gatacg	gtac	1560
gcatccacga cggacctcca gttccacacc agcatcaacg ggaagg	ctat	caaccagg	ga	1620
aactttagcg ccacgatgaa ccgtggtgag gacttggact acaaga	catt	ccggac	ggtc	1680

```

ggcttcacga cgcccttcag ctttagcgac gtccagtcca ccttcaccat cggagcatgg      1740
aacttcagta gcggcaacga ggtgtacatc gaccgaatcg agttcgtccc ggttgagggtg      1800
acctacggag ccgaatacga cttcgagaag gcacaggaga aggtgactgc tctgtttaca      1860
agcacaaatc ctcgggaact aaagatcgac gtcacagact accacatcga ccaagttagc      1920
aacctcgtcg agagcctcct ggacgagttc tatttggacg agaagcggga gctgttcgag      1980
atcgtgaaat acgccaagca gttgtacatc gagcgtaaca tgtga                        2025

```

<210> 15
 <211> 654
 <212> PRT
 <213> Artificial

<220>
 <223> Una secuencia de aminoácidos de la variante TIC2199_2 a la cual se le ha eliminado la metionina inicial y se utiliza para unirla de forma operativa a un péptido de tránsito del cloroplasto.

<400> 15

```

Lys Pro Lys Asn Gln Asn Met Tyr Gln Ser Leu Ser Ser Asn Val Thr
1          5          10          15

```

```

Val Asp Lys Ile Ser Thr Asn Pro Leu Lys Asn Glu Thr Asp Ile Glu
          20          25          30

```

```

Leu Gln Asn Ile Asn His Glu Ala Cys Leu Lys Met Ser Lys Tyr Lys
          35          40          45

```

```

Asn Val Ala Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile Gly
          50          55          60

```

```

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

```

```

Ile Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys Gly
          85          90          95

```

```

Lys Ser Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile Asn
          100          105          110

```

Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Ser Asp Leu Arg
115 120 125

Gly Leu Gly Asp Ala Leu Ala Val Tyr His Glu Ser Leu Glu Ser Trp
130 135 140

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

Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe Ala
165 170 175

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

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

Trp Gly Leu Ser Ala Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln Val
210 215 220

Glu Arg Thr Arg Asp Tyr Ser Asp His Cys Val Lys Trp Tyr Asn Thr
225 230 235 240

Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Lys Ser Trp Val Arg Tyr
245 250 255

Asn Gln Phe Arg Lys Asp Met Thr Leu Met Val Leu Asp Leu Val Ala
260 265 270

Leu Phe Pro Ser Tyr Asp Thr Leu Val Tyr Pro Ile Lys Thr Thr Ser
275 280 285

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

Asn Gln Ala Phe Ala Ser Thr Thr Trp Tyr Asn Asn Asn Ala Pro Ser
305 310 315 320

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

Phe Leu Glu Lys Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser Asn
340 345 350

Thr Gln Tyr Met Asn Met Trp Gly Gly His Arg Leu Glu Ser Arg Pro
355 360 365

Ile Gly Gly Ala Leu Asn Thr Ser Thr Gln Gly Ser Thr Asn Thr Ser
370 375 380

Ile Asn Pro Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr
385 390 395 400

Glu Ser Trp Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn Gly
405 410 415

Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile Ala
420 425 430

Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile Gly Thr Gln Leu
435 440 445

Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Thr Thr Gly Gln Pro Asn
450 455 460

Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser Ala
465 470 475 480

Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala Asp
485 490 495

Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu Val
500 505 510

Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro Gly
515 520 525

Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe Gly
530 535 540

Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg Val
 545 550 555 560

Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser Ile
 565 570 575

Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn Arg
 580 585 590

Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr Val Gly Phe Thr Thr
 595 600 605

Pro Phe Ser Phe Ser Asp Val Gln Ser Thr Phe Thr Ile Gly Ala Trp
 610 615 620

Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val
 625 630 635 640

Pro Val Glu Val Thr Tyr Gly Ala Glu Tyr Asp Phe Glu Lys
 645 650

<210> 16
 <211> 1965
 <212> ADN
 <213> Artificial

<220>
 <223> Una secuencia codificadora sintética que codifica la variante TIC2199_2 a la cual se le ha eliminado el codón de metionina inicial y se utiliza para unirla de forma operativa a un péptido de tránsito del cloroplasto y es capaz de ser utilizada en una célula vegetal.

<400> 16
 aagcccaaga atcagaacat gtaccagtcc ctacagctcga acgtcaccgt cgataagatt 60
 agcaccaacc cgctcaagaa tgagaccgac atcgaattac agaacattaa ccacgaggcg 120
 tgcctcaaga tgtctaagta caagaacgtc gcacccttcg tctcggcttc tacgatccag 180
 acggggcattg gcatcgccgg gaagatactc ggcacactcg gcgtcccggt cgctgggtcaa 240
 atcgcttcgc tctactcctt catactcggg gaactgtggc cgaagggcaa gtcgcagtgg 300
 gaaatcttca tggagcacgt ggaggagatc atcaaccaga agataagcac ctacgcccgt 360
 aacaaggcgc tgagcgacct ccgtgggctg ggcgatgcgc tggcggtgta ccacgagtcg 420

ctggagtcgt gggaggagaa ccgcaacaac acccgcgccc ggtccgtggt caagaaccag	480
tacattgccc tggagctgat gttcgtgcag aagctcccgt ccttcgagggt gtccggcgag	540
gaagtgccac tgttgcccat ctacgcccac gcagccaacc tgcacctcct tctcctccgg	600
gacgtcagca tcttcgggaa ggagtggggc ctttcagcgt cagagatttc aaccttctac	660
aacaggcaag ttgagcgac gcgcgactac tcggaccact gcgtcaagt gtacaacacc	720
ggcctcaaca acctgcgtgg aacgaacgcc aagagctggg tccgctacaa ccagtttcga	780
aaggacatga ccctcatggt gctggacctt gtggccttgt tcccgtccta cgacaccctc	840
gtttatccga ttaagactac atctcaactt acccgcgagg ttacacaga cgccataggg	900
accgtgcatc ctaaccaggc gttcgcacg acaacttggt acaacaaca cgcgccctcg	960
ttctcagcca tcgaggccgc cgtgatccgt tcaccgcacc tcctggactt cctggagaag	1020
gttaccatct actccctctt gtctcgctgg agtaatactc agtacatgaa catgtgggga	1080
ggacatcgcc tcgaatctcg accgattggc ggcgcgctta acacatccac acagggctcc	1140
acgaacacca gcatcaacc ggtgacgtt caattcactt cacgcgatgt ctatcggacc	1200
gagagctggg ctggcctgaa cctgttccta actcagcccg tgaacgggtgt gccagagtc	1260
gatttccact ggaaattcgt cactcatccc atcgccagcg acaacttcta ctaccaggc	1320
tacgccggtg tcggcacaca gtttcaagac tccgagaacg aactgcctcc cgagactact	1380
ggccagccga actacgagag ttactcccat aggctttcgc acatcggcct aatctcagct	1440
tcgcatgtta aagcactcgt gtactcatgg acacacagaa gcgccgacag aacgaacacc	1500
attgagccaa actctatcac gcagatccc ctggttaagg cgttcaactt gtcgagcggc	1560
gctgcggtcg tgcgcggacc tggattcacc ggtggcgaca ttctgcgccg caccaacaca	1620
ggaaccttcg gcgacatccg ggtgaacatc aacccgccgt ttgcacaacg ctatcgcgtc	1680
aggatacggg acgcatccac gacggacctc cagttccaca ccagcatcaa cgggaaggct	1740
atcaaccagg gaaactttag cgccacgatg aaccgtggtg aggacttgga ctacaagaca	1800
ttccggacgg tcggcttcac gacgcccttc agcttttagcg acgtccagtc caccttcacc	1860
atcggagcat ggaacttcag tagcggcaac gaggtgtaca tcgaccgaat cgagttcgtc	1920
ccggttgagg tgacctacgg agccgaatac gacttcgaga agtga	1965

<210> 17
<211> 610
<212> PRT
<213> Artificial

<220>

<223> Una secuencia de aminoácidos de la variante de TIC2199_3 a la cual se le ha eliminado la metionina inicial y se utiliza para unirle de forma operativa a un péptido de tránsito del cloroplasto.

<400> 17

Ser Lys Tyr Lys Asn Val Ala Pro Phe Val Ser Ala Ser Thr Ile Gln
1 5 10 15

Thr Gly Ile Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro
20 25 30

Phe Ala Gly Gln Ile Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu
35 40 45

Trp Pro Lys Gly Lys Ser Gln Trp Glu Ile Phe Met Glu His Val Glu
50 55 60

Glu Ile Ile Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu
65 70 75 80

Ser Asp Leu Arg Gly Leu Gly Asp Ala Leu Ala Val Tyr His Glu Ser
85 90 95

Leu Glu Ser Trp Val Glu Asn Arg Asn Asn Thr Arg Ala Arg Ser Val
100 105 110

Val Lys Asn Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu
115 120 125

Pro Ser Phe Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr
130 135 140

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

Phe Gly Lys Glu Trp Gly Leu Ser Ala Ser Glu Ile Ser Thr Phe Tyr
165 170 175

Asn Arg Gln Val Glu Arg Thr Arg Asp Tyr Ser Asp His Cys Val Lys
180 185 190

Trp Tyr Asn Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Lys Ser
195 200 205

Trp Val Arg Tyr Asn Gln Phe Arg Lys Asp Met Thr Leu Met Val Leu
210 215 220

Asp Leu Val Ala Leu Phe Pro Ser Tyr Asp Thr Leu Val Tyr Pro Ile
225 230 235 240

Lys Thr Thr Ser Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly
245 250 255

Thr Val His Pro Asn Gln Ala Phe Ala Ser Thr Thr Trp Tyr Asn Asn
260 265 270

Asn Ala Pro Ser Phe Ser Ala Ile Glu Ala Ala Val Ile Arg Ser Pro
275 280 285

His Leu Leu Asp Phe Leu Glu Lys Val Thr Ile Tyr Ser Leu Leu Ser
290 295 300

Arg Trp Ser Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Arg Leu
305 310 315 320

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

Thr Asn Thr Ser Ile Asn Pro Val Thr Leu Gln Phe Thr Ser Arg Asp
340 345 350

Val Tyr Arg Thr Glu Ser Trp Ala Gly Leu Asn Leu Phe Leu Thr Gln
355 360 365

Pro Val Asn Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr
370 375 380

His Pro Ile Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile
385 390 395 400

Gly Thr Gln Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Thr Thr
405 410 415

Gly Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly
420 425 430

Leu Ile Ser Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His
435 440 445

Arg Ser Ala Asp Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln
450 455 460

Ile Pro Leu Val Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val
465 470 475 480

Arg Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr
485 490 495

Gly Thr Phe Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln
500 505 510

Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe
515 520 525

His Thr Ser Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala
530 535 540

Thr Met Asn Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr Val
545 550 555 560

Gly Phe Thr Thr Pro Phe Ser Phe Ser Asp Val Gln Ser Thr Phe Thr
565 570 575

Ile Gly Ala Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg
580 585 590

Ile Glu Phe Val Pro Val Glu Val Thr Tyr Gly Ala Glu Tyr Asp Phe
595 600 605

Glu Lys
610

<210> 18
<211> 1833
<212> ADN
<213> Artificial

<220>
<223> Una secuencia codificadora sintética que codifica la variante TIC2199_3 a la cual se le ha eliminado el codón de metionina inicial y se utiliza para unirla de forma operativa al péptido de tránsito del cloroplasto y es capaz de ser utilizada en una célula vegetal.

<400> 18
tctaagtaca agaacgtcgc acccttcgtc tcggcttcta cgatccagac gggcattggc 60
atgccggga agatactcgg cacactcggc gtcccgttcg ctggtcaa atcgctcgtc 120
tactccttca tactcgggtga actgtggccg aagggaagtc cgagtgaggga aatcttcatg 180
gagcacgtgg aggagatcat caaccagaag ataagcacct acgcccgtaa caaggcgtg 240
agcgacctcc gtgggctggg cgatgcgctg gcgggtgtacc acgagtcgct ggagtcgtgg 300
gtggagaacc gcaacaacac ccgcgcccgg tccgtgggtca agaaccagta cattgccctg 360
gagctgatgt tcgtgcagaa gctcccgtcc ttgcggtgtt ccggcgagga agtgccactg 420
ttgcccattc acgccaagc agccaacctg cacctccttc tcctccggga cgtcagcatc 480
ttcgggaagg agtggggcct ttcagcgtca gagatttcaa ctttctacaa caggcaagtt 540
gagcgcacgc gcgactactc ggaccactgc gtcaagtggc acaacaccgg cctcaacaac 600
ctgcgtggaa cgaacgcaa gagctgggtc cgctacaacc agtttcgaaa ggacatgacc 660
ctcatggtgc tggaccttgt ggccttggtc ccgtcctacg acaccctcgt ttatccgatt 720
aagactacat ctcaacttac ccgcgaggtt tacacagacg ccatagggac cgtgcatcct 780
aaccaggcgt tcgcatcgac aacttggtac aacaacaacg cgccctcgtt ctgagccatc 840
gaggccgccg tgatccgttc accgcacctc ctggacttcc tggagaaggt taccatctac 900
tccctcttgt ctcgctggag taatactcag tacatgaaca tgtggggagg acatcgcctc 960
gaatctcgac cgattggcgg cgcgcttaac acatccacac agggctccac gaacaccagc 1020
atcaaccggg tgacgttgca attcacttca cgcgatgtct atcggaccga gagctgggct 1080

ggcctgaacc tggtcctaac tcagcccgtg aacggtgtgc ccagagtcga tttccactgg	1140
aaattcgtca ctcatcccat cgccagcgac aacttctact acccaggcta cgccggtatc	1200
ggcacacagc ttcaagactc cgagaacgaa ctgcctcccg agactactgg ccagccgaac	1260
tacgagagtt actcccatag gctttcgcac atcggcctaa tctcagcttc gcatgtttaa	1320
gcactcgtgt actcatggac acacagaagc gccgacagaa cgaacaccat tgagccaaac	1380
tctatcacgc agatcccgtt gggttaaggcg ttcaacttgt cgagcggcgc tgcggtcgtg	1440
cgcggacctg gattcaccgg tggcgacatt ctgcgccga ccaacacagg aaccttcggc	1500
gacatccggg tgaacatcaa cccgccgttt gcacaacgt atcgcgtcag gatacggtac	1560
gcatccacga cggacctcca gttccacacc agcatcaacg ggaaggctat caaccaggga	1620
aacttttagcg ccacgatgaa ccgtggtgag gacttggact acaagacatt ccggacggtc	1680
ggcttcacga cgcccttcag ctttagcgac gtccagtcca ccttcaccat cggagcatgg	1740
aacttcagta gcggcaacga ggtgtacatc gaccgaatcg agttcgtccc ggttgaggtg	1800
acctacggag ccgaatacga cttcgagaag tga	1833