

SEQUENCE LISTING

<110> Monsanto Technology LLC

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<120> Novel Chimeric Insecticidal Proteins Toxic or Inhibitory to
Lepidopteran Pests

<130> P34230W000/0022270.00098

<150> US 62/064989

<151> 2014-10-16

<160> 53

<170> PatentIn version 3.5

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<212> DNA

<213> Artificial

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<223> Recombinant nucleotide sequence used for expression in a
bacterial cell encoding TIC1100.

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

Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
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355 360 365

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370 375 380

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Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
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Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
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Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
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485 490 495

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645 650 655

Ile Asp Gln Val Ser Asn Leu Val Thr Tyr Leu Ser Asp Glu Phe Cys
660 665 670

Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg
675 680 685

Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Ser Asn Phe Lys Asp Ile
690 695 700

Asn Arg Gln Pro Glu Arg Gly Trp Gly Gly Ser Thr Gly Ile Thr Ile
705 710 715 720

Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Ser Gly
725 730 735

Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu
740 745 750

Ser Lys Leu Lys Ala Phe Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu
755 760 765

Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His
770 775 780

Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala
785 790 795 800

Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His
805 810 815

Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys
820 825 830

Cys Ala His His Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys
835 840 845

Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys
850 855 860

Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu
865 870 875 880

Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys
885 890 895

Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu Thr Asn Ile Val
900 905 910

Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln
915 920 925

Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile Ala Met Ile His Ala Ala
930 935 940

Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser
945 950 955 960

Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg
965 970 975

Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn
980 985 990

Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val Lys Gly His Val
995 1000 1005

Asp Val Glu Glu Gln Asn Asn Gln Arg Ser Val Leu Val Val Pro
1010 1015 1020

Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly
1025 1030 1035

Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly
1040 1045 1050

Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu
1055 1060 1065

Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Ile Tyr Pro Asn Asn
1070 1075 1080

Thr Val Thr Cys Asn Asp Tyr Thr Val Asn Gln Glu Glu Tyr Gly
1085 1090 1095

Gly Ala Tyr Thr Ser Arg Asn Arg Gly Tyr Asn Glu Ala Pro Ser
1100 1105 1110

Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr
1115 1120 1125

Asp Gly Arg Arg Glu Asn Pro Cys Glu Phe Asn Arg Gly Tyr Arg
1130 1135 1140

Asp Tyr Thr Pro Leu Pro Val Gly Tyr Val Thr Lys Glu Leu Glu
1145 1150 1155

Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr
1160 1165 1170

Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu
1175 1180 1185

Glu

<210> 5
<211> 3672
<212> DNA
<213> Artificial

<220>
<223> Recombinant nucleotide sequence used for expression in a
bacterial cell encoding TIC860.

<400> 5
atgacttcaa ataggaaaaa tgagaatgaa attataaatg ctttatcgat tccaacggta 60
tcgaatcctt ccacgcaaat gaatctatca ccagatgctc gtattgaaga tagcttgtgt 120
gtagccgagg tgaacaatat tgatccattt gttagcgcac caacagtcca aacgggtata 180

aacatagctg gtagaatatt gggcgtatta ggtgtgccgt ttgctggaca actagctagt	240
ttttatagtt ttcttgttgg ggaattatgg cctagtggca gagatccatg ggaaattttc	300
ctggaacatg tagaacaact tataagacaa caagtaacag aaaatactag gaatacggct	360
attgctcgat tagaaggtct aggaagaggc tatagatctt accagcaggc tcttgaaact	420
tggttagata accgaaatga tgcaagatca agaagcatta ttcttgagcg ctatgttgct	480
ttagaacttg acattactac tgctataccg cttttcagaa tacgaaatga agaagttcca	540
ttattaatgg tatatgctca agctgcaaat ttacacctat tattattgag agacgcatcc	600
ctttttggta gtgaatgggg gatggcatct tccgatgtta accaatatta ccaagaacaa	660
atcagatata cagaggaata ttctaaccat tgcgtacaat ggtataatac agggctaaat	720
aacttaagag ggacaaatgc tgaaagttgg ttgcggtata atcaattccg tagagaccta	780
acgttagggg tattagattt agtagcccta ttcccaagct atgatactcg cacttatcca	840
atcaatacga gtgctcagtt aacaagagaa atttatacag atccaattgg gagaacaaat	900
gcaccttcag gatttgcaag tacgaattgg ttaataata atgcaccatc gttttctgcc	960
atagaggctg ccattttcag gcctccgcat ctacttgatt ttccagaaca acttacaatt	1020
tacagtgcac caagccgttg gagtagcact caacatatga attattgggt gggacatagg	1080
cttaacttcc gcccaatagg agggacatta aatacctcaa cacaaggact tactaataat	1140
acttcaatta atcctgtaac attacagttt acgtctcgag acgtttatag aacagaatca	1200
aatgcaggga caaatatact atttactact cctgtgaatg gagtaccttg ggctagattt	1260
aattttataa accctcagaa tatttatgaa agaggcgcca ctacctacag tcaaccgtat	1320
cagggagttg ggattcaatt atttgattca gaaactgaat taccaccaga aacaacagaa	1380
cgaccaaatt atgaatcata tagtcataga ttatctcata taggactaat cataggaaac	1440
actttgagag caccagtcta ttcttgagcg catcgtagtg cagatcgtag gaatacgatt	1500
ggaccaaata gaattaatca aataccttta gtgaaaggat ttagagtttg ggggggcacc	1560
tctgtcatta caggaccagg atttacagga ggggatatcc ttcgaagaaa tacctttggt	1620
gattttgtat ctctacaagt caatattaat tcaccaatta cccaaagata ccgtttaaga	1680

tttcgttacg cttccagtag ggatgcacga gttatagtat taacaggagc ggcatccaca	1740
ggagtgggag gccaaagttag tgtaaatatg cctcttcaga aaactatgga aataggggag	1800
aacttaacat ctagaacatt tagatatacc gatttttagta atcctttttc atttagagct	1860
aatccagata taattgggat aagtgaacaa cctctatttg gtgcaggttc tattagtagc	1920
ggtgaacttt atatagataa aattgaaatt attctagcag atgcaacatt tgaagcagaa	1980
tctgatttag aaagagcgca gaaggcgggtg aatgcgctgt ttacgtctac aaaccaacta	2040
gggctaataaa caaatgtaac ggattatcat attgatcaag tgtccaattt agttacgtat	2100
ttatcggatg aattttgtct ggatgaaaag cgagaattgt ccgagaaagt caaacatgcg	2160
aagcgactca gtgatgaacg caatttactc caagattcaa atttcaaaga cattaatagg	2220
caaccagaac gtgggtgggg cggaagtaca gggattacca tccaaggagg ggatgacgta	2280
tttaaagaaa attacgtcac actatcaggt acctttgatg agtgctatcc aacatatttg	2340
tatcaaaaaa tcgatgaatc aaaattaaaa gcctttaccc gttatcaatt aagagggtat	2400
atcgaagata gtcaagactt agaaatctat ttaattcgct acaatgcaaa acatgaaaca	2460
gtaaatgtgc cagggtacggg ttccttatgg ccgctttcag cccaaagtcc aatcggaaag	2520
tgtggagagc cgaatcgatg cgcgccacac cttgaatgga atcctgactt agattgttcg	2580
tgtagggatg gagaaaagtg tgcccatcat tcgcatcatt tctccttaga cattgatgta	2640
ggatgtacag acttaaatga ggacctaggt gtatgggtga tctttaagat taagacgcaa	2700
gatgggcacg caagactagg gaatctagag tttctcgaag agaaaccatt agtaggagaa	2760
gcgctagctc gtgtgaaaag agcggagaaa aaatggagag acaaacgtga aaaattggaa	2820
tgggaaacaa atatcgttta taaagaggca aaagaatctg tagatgcttt atttgtaaac	2880
tctcaatatg atcaattaca agcggatacg aatattgcc a tgattcatgc ggcagataaa	2940
cgtgttcata gcattcgaga agcttatctg cctgagctgt ctgtgattcc ggggtgtcaat	3000
gcggctattt ttgaagaatt agaaggcggt attttcactg cattctccct atatgatgcg	3060
agaaatgtca ttaaaaaatgg tgattttaat aatggcttat cctgctggaa cgtgaaaggg	3120
catgtagatg tagaagaaca aaacaaccaa cgttcgggtcc ttgttggtcc ggaatgggaa	3180

gcagaagtgt cacaagaagt tcgtgtctgt ccgggtcgtg gctatatcct tcgtgtcaca	3240
gcgtacaagg agggatatgg agaaggttgc gtaaccattc atgagatcga gaacaatata	3300
gacgaactga agtttagcaa ctgcgtagaa gaggaaatct atccaaataa cacggtaacg	3360
tgtaatgatt atactgtaaa tcaagaagaa tacggagggtg cgtacacttc tcgtaatcga	3420
ggatataacg aagctccttc cgtaccagct gattatgcgt cagtctatga agaaaaatcg	3480
tatacagatg gacgaagaga gaatccttgt gaatttaaca gagggtatag ggattacacg	3540
ccactaccag ttggttatgt gacaaaagaa ttagaatact tcccagaaac cgataaggta	3600
tggattgaga ttggagaaac ggaaggaaca tttatcgtgg acagcgtgga attactcctt	3660
atggaggaat ag	3672

<210> 6
 <211> 3672
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC860.

<400> 6	
atgaccagca accggaagaa cgagaacgag atcatcaacg ccctgagcat cccgaccgtg	60
agcaacccta gcacccagat gaacctgagc cctgacgctc gcatcgagga ctccctctgc	120
gtggctgagg tgaacaacat cgacccgttc gtgtccgcct ccaccgtgca gaccggcatc	180
aacatcgcg gccgcatcct cggcgtgctc ggcggtgcct ttgcgggcca gctcgcctcc	240
ttctactcct tcctcgtggg agagctgtgg ccctccggcc gcgacccgtg ggagatcttc	300
ctggagcacg tggagcagct catccgccag caagtcaccg agaacacccg caacaccgcc	360
atcgcccgcc tggagggcct gggccgtggc taccgctcct accagcaagc cctggagacc	420
tggtctgaca accgcaacga cggccgtctc cgctccatca tcctggagcg ctacgtcgcc	480
ctggaactgg acatcaccac tgccatccca ctcttccgca tcaggaacga ggagggtgcct	540
ctgctgatgg tgtacgcca ggctgcgaac ctgcacctgc tgctgctgcg cgacgcaagc	600
ctgtttggct ccgagtgggg tatggcaagc tccgacgtca accagtacta ccaggagcag	660

atccgctaca ccgaggagta cagcaaccac tgcgtccagt ggtacaacac cggcttgaac	720
aatctcagag ggaccaacgc tgagagctgg ctgctgctaca accagttccg gcgggatctg	780
accctaggtg tcctggatct ggctgctctg ttcccagagct acgataccag gacgtaccct	840
atcaacacct ctgctcagct taccagggag atctacactg atcctatcgg taggactaac	900
gctcctagt gtttcgccag cactaactgg ttcaacaaca acgcgcctag tttctctgcc	960
atcgaggcgg cgatcttccg gcctcctcac ctctctgact tcccggagca gcttactatc	1020
tactctgcgt cttcgcggtg gtcttcgact cagcacatga actactgggt tggtcaccgg	1080
cttaacttcc gcccgattgg aggaactctt aacaccagta cgcaaggctt tacgaacaac	1140
acttccatca acccggttac gttgcagttc acgtctcggg acgtttaccg gacggagtcg	1200
aatgctggga cgaacatcct gttcacgaca ccggtgaatg gtgttccgtg ggcacgtttc	1260
aacttcatca acccgagaa catctacgag cgtggagcaa cgacatactc gcaaccatac	1320
caaggcgttg gcatccaact gtttgactcg gagacggaac tgccaccaga gacgacagaa	1380
cgtccgaatt acgagtcata ctacacaga ctatcacaca ttggactcat tatcggaac	1440
acactgagag caccagtgtat ctcatggaca catcggtcag cagatcgta gaacaccatc	1500
ggaccaatc ggatcaacca gatcccgctc gtgaagggtc tccgcgtgtg gggcggcacc	1560
tccgtcatca ccggtccggg cttcaccggc ggcgacatcc tccgccgcaa caccttcggc	1620
gacttcgtgt cactccaagt gaacatcaac agcccgatca cccagcgcta tcgcctccgc	1680
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cttagcgacg agttctgcct tgacgagaag cgtgagctga gcgagaagggt gaagcacgcc	2160

aagcgctctt	ccgacgagcg	caacctcctc	caggactcca	acttcaagga	catcaaccgc	2220
cagcccgagc	gcggtctgggg	cggtagcacc	ggcatcacca	tccagggcgg	tgacgatgtg	2280
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gtgaacgtgc	ccggcaccgg	ctccctctgg	ccgctctccg	cccagagccc	tatcggcaag	2520
tgctggcgagc	ccaaccgctg	cgctcctcac	ctggagtggg	accctgacct	cgactgctcc	2580
tgccgcgacg	gcgagaagtg	cgcccaccat	agccaccact	tctctctcga	catcgacgtg	2640
ggctgcaccg	acctcaacga	ggatctgggc	gtgtgggtga	tcttcaagat	caagaccag	2700
gacggccacg	ccaggctggg	caacctggag	ttcctggagg	agaagcctct	ggtgggtgag	2760
gccctggcca	gggtcaagag	ggctgagaag	aaatggaggg	acaagaggga	gaagctggag	2820
tgggagacca	acatcgtgta	caaggaggct	aaggagtccg	tggacgtctt	gttcgtcaac	2880
tctcagtacg	atcagctcca	ggctgacacc	aacatcgcta	tgatccacgc	tgcgataag	2940
agggtccact	ctatcaggga	ggcttacctg	cctgagcttt	ctgtcatccc	tggtgtcaac	3000
gcggcaatct	tcgaggaact	tgagggccgc	atcttcactg	cgttctcgct	ttacgatgcg	3060
cggaacgtca	ttaagaacgg	tgacttcaac	aatggctctt	cgctgtggaa	cgtaagggt	3120
catgtcgatg	tcgaggaaca	gaacaaccag	cggctcggcc	ttgtcgttcc	cgagtgggag	3180
gccgaggctt	cgcaagaggt	ccgggtctgc	cctgggcgcg	ggtacattct	tcgtgtcact	3240
gcgtacaagg	agggtctacg	cgagggtctg	gttactattc	atgagattga	gaacaatacg	3300
gatgagctta	agtttagtaa	ctgtgttgag	gaggagatct	acccgaacaa	tacggttacg	3360
tgcaatgatt	acacggtgaa	ccaggaggaa	tacggcggag	catacacctc	acgtaataga	3420
gggtacaatg	aggcaccgtc	agttccggca	gattatgcct	cagtttatga	ggagaagtcc	3480
tacacggatg	gaagacgcga	gaatccatgt	gagtttaata	gaggataccg	agactacaca	3540
ccactcccag	ttggatacgt	tacaaaggag	ttggaatact	tcccagaaac	agataaagtt	3600
tggatagaga	tcggagaaac	agaaggaacc	ttcatcgtgg	acagtgtaga	actgctgctg	3660

atggaagaat ga

3672

<210> 7

<211> 1223

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC860.

<400> 7

Met Thr Ser Asn Arg Lys Asn Glu Asn Glu Ile Ile Asn Ala Leu Ser
1 5 10 15

Ile Pro Thr Val Ser Asn Pro Ser Thr Gln Met Asn Leu Ser Pro Asp
20 25 30

Ala Arg Ile Glu Asp Ser Leu Cys Val Ala Glu Val Asn Asn Ile Asp
35 40 45

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

Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Leu Ala Ser
65 70 75 80

Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Ser Gly Arg Asp Pro
85 90 95

Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln Val
100 105 110

Thr Glu Asn Thr Arg Asn Thr Ala Ile Ala Arg Leu Glu Gly Leu Gly
115 120 125

Arg Gly Tyr Arg Ser Tyr Gln Gln Ala Leu Glu Thr Trp Leu Asp Asn
130 135 140

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

Leu Glu Leu Asp Ile Thr Thr Ala Ile Pro Leu Phe Arg Ile Arg Asn
165 170 175

Glu Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His
180 185 190

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

Ala Ser Ser Asp Val Asn Gln Tyr Tyr Gln Glu Gln Ile Arg Tyr Thr
210 215 220

Glu Glu Tyr Ser Asn His Cys Val Gln Trp Tyr Asn Thr Gly Leu Asn
225 230 235 240

Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln Phe
245 250 255

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

Ser Tyr Asp Thr Arg Thr Tyr Pro Ile Asn Thr Ser Ala Gln Leu Thr
275 280 285

Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser Gly
290 295 300

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

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

Gln Leu Thr Ile Tyr Ser Ala Ser Ser Arg Trp Ser Ser Thr Gln His
340 345 350

Met Asn Tyr Trp Val Gly His Arg Leu Asn Phe Arg Pro Ile Gly Gly
355 360 365

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

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

Asn Ala Gly Thr Asn Ile Leu Phe Thr Thr Pro Val Asn Gly Val Pro
405 410 415

Trp Ala Arg Phe Asn Phe Ile Asn Pro Gln Asn Ile Tyr Glu Arg Gly
420 425 430

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

Asp Ser Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn Tyr
450 455 460

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

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

Thr Asn Thr Ile Gly Pro Asn Arg Ile Asn Gln Ile Pro Leu Val Lys
500 505 510

Gly Phe Arg Val Trp Gly Gly Thr Ser Val Ile Thr Gly Pro Gly Phe
515 520 525

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

Leu Gln Val Asn Ile Asn Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg
545 550 555 560

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

Ala Ala Ser Thr Gly Val Gly Gly Gln Val Ser Val Asn Met Pro Leu
580 585 590

Gln Lys Thr Met Glu Ile Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg
595 600 605

Tyr Thr Asp Phe Ser Asn Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile
610 615 620

Ile Gly Ile Ser Glu Gln Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser
625 630 635 640

Gly Glu Leu Tyr Ile Asp Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr
645 650 655

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

Leu Phe Thr Ser Thr Asn Gln Leu Gly Leu Lys Thr Asn Val Thr Asp
675 680 685

Tyr His Ile Asp Gln Val Ser Asn Leu Val Thr Tyr Leu Ser Asp Glu
690 695 700

Phe Cys Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala
705 710 715 720

Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Ser Asn Phe Lys
725 730 735

Asp Ile Asn Arg Gln Pro Glu Arg Gly Trp Gly Gly Ser Thr Gly Ile
740 745 750

Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu
755 760 765

Ser Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile
770 775 780

Asp Glu Ser Lys Leu Lys Ala Phe Thr Arg Tyr Gln Leu Arg Gly Tyr
785 790 795 800

Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala
805 810 815

Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu
820 825 830

Ser Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala
835 840 845

Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly
850 855 860

Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile Asp Val
865 870 875 880

Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys
885 890 895

Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu
900 905 910

Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys Arg Ala
915 920 925

Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu Thr Asn
930 935 940

Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn
945 950 955 960

Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile Ala Met Ile His
965 970 975

Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu Pro Glu
980 985 990

Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu Leu Glu
995 1000 1005

Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn Val
1010 1015 1020

Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val
1025 1030 1035

Lys Gly His Val Asp Val Glu Glu Gln Asn Asn Gln Arg Ser Val
1040 1045 1050

Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg
1055 1060 1065

Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys
1070 1075 1080

Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn
1085 1090 1095

Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Ile
1100 1105 1110

Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Val Asn Gln
1115 1120 1125

Glu Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn Arg Gly Tyr Asn
1130 1135 1140

Glu Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu
1145 1150 1155

Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys Glu Phe Asn
1160 1165 1170

Arg Gly Tyr Arg Asp Tyr Thr Pro Leu Pro Val Gly Tyr Val Thr
1175 1180 1185

Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu
1190 1195 1200

Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
1205 1210 1215

Leu Leu Met Glu Glu
1220

<210> 8

<211> 3564

<212> DNA

<213> Artificial

<220>

<223> Recombinant nucleotide sequence used for expression in a
bacterial cell encoding TIC867.

<400> 8

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tcgaatcatt ccgcacaaat gaatctatca accgatgctc gtattgagga tagcttgtgt 120

atagccgagg ggaacaatat cgatccattht gttagcgcac caacagtcca aacgggtatt 180

aacatagctg gtagaatact aggtgtatta ggcgtaccgt ttgctggaca aatagctagt 240

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<211> 1187
<212> PRT
<213> Artificial

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<220>
<223> Amino acid sequence of the chimeric protein TIC867.

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<400> 10

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

Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Arg Gly Arg Asp Pro
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Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln Val
100 105 110

Thr Glu Asn Thr Arg Asp Thr Ala Leu Ala Arg Leu Gln Gly Leu Gly
115 120 125

Asn Ser Phe Arg Ala Tyr Gln Gln Ser Leu Glu Asp Trp Leu Glu Asn
130 135 140

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

Leu Glu Leu Asp Phe Leu Asn Ala Met Pro Leu Phe Ala Ile Arg Asn
165 170 175

Gln Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His
180 185 190

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

Gln Leu Thr Ile Phe Ser Val Leu Ser Arg Trp Ser Asn Thr Gln Tyr
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Met Asn Tyr Trp Val Gly His Arg Leu Glu Ser Arg Thr Ile Arg Gly
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Ser Leu Ser Thr Ser Thr His Gly Asn Thr Asn Thr Ser Ile Asn Pro
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Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu Ser Phe
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405 410 415

Ala Arg Phe Asn Trp Arg Asn Pro Leu Asn Ser Leu Arg Gly Ser Leu
420 425 430

Leu Tyr Thr Ile Gly Tyr Thr Gly Val Gly Thr Gln Leu Phe Asp Ser
435 440 445

Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn Tyr Glu Ser
450 455 460

Tyr Ser His Arg Leu Ser Asn Ile Arg Leu Ile Ser Gly Asn Thr Leu
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Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp Arg Thr Asn
485 490 495

Thr Ile Ser Ser Asp Ser Ile Thr Gln Ile Pro Leu Val Lys Ala His
500 505 510

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515 520 525

Gly Asp Ile Leu Arg Arg Thr Ser Gly Gly Pro Phe Ala Phe Ser Asn
530 535 540

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

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565 570 575

Arg Ile Phe Ala Gly Gln Phe Asp Lys Thr Met Asp Ala Gly Ala Pro
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Ser Gly Asn Glu Val Tyr Val Asp Arg Phe Glu Leu Ile Pro Val Thr
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660 665 670

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

Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys
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His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn
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Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr
725 730 735

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
740 745 750

Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
755 760 765

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
770 775 780

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
785 790 795 800

Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
805 810 815

Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Ala His His Ser His
820 825 830

His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp
835 840 845

Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala
850 855 860

Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu
865 870 875 880

Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg
885 890 895

Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu
900 905 910

Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala
915 920 925

Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser
930 935 940

Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn
945 950 955 960

Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser
965 970 975

Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly
980 985 990

Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn
995 1000 1005

Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val
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Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
1025 1030 1035

Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile
1040 1045 1050

His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys
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Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp
1070 1075 1080

Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg
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Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser Val Pro
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Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr Asp Gly
1115 1120 1125

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1130 1135 1140

Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe
1145 1150 1155

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<213> Artificial

<220>

<223> Recombinant nucleotide sequence used for expression in a bacterial cell encoding TIC867_20.

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<210> 12

<211> 3642

<212> DNA

<213> Artificial

<220>

<223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC867_20.

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gattatgcct cggtttatga ggagaagtcg tacacggata gacgacgcga gaatccatgt      3480
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ttggaatact tcccggaaac agataaagtt tggattgaaa tcggagaaac agaaggaaca      3600
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<211> 1213

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein variant TIC867_20.

<400> 13

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Ala Arg Ile Glu Asp Ser Leu Cys Ile Ala Glu Gly Asn Asn Ile Asp
35           40           45

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

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Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Ile Ala Ser
65           70           75           80

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Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Arg Gly Arg Asp Pro
85           90           95

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Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln Val
100          105          110

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Thr Glu Asn Thr Arg Asp Thr Ala Leu Ala Arg Leu Gln Gly Leu Gly
115 120 125

Asn Ser Phe Arg Ala Tyr Gln Gln Ser Leu Glu Asp Trp Leu Glu Asn
130 135 140

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

Leu Glu Leu Asp Phe Leu Asn Ala Met Pro Leu Phe Ala Ile Arg Asn
165 170 175

Gln Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His
180 185 190

Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe Gly Ser Glu Phe Gly Leu
195 200 205

Thr Ser Gln Glu Ile Gln Arg Tyr Tyr Glu Arg Gln Val Glu Lys Thr
210 215 220

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

Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln Phe
245 250 255

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

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

Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser Gly
290 295 300

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

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

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

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

Ser Leu Ser Thr Ser Thr His Gly Asn Thr Asn Thr Ser Ile Asn Pro
370 375 380

Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu Ser Phe
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Ala Gly Ile Asn Ile Leu Leu Thr Thr Pro Val Asn Gly Val Pro Trp
405 410 415

Ala Arg Phe Asn Trp Arg Asn Pro Leu Asn Ser Leu Arg Gly Ser Leu
420 425 430

Leu Tyr Thr Ile Gly Tyr Thr Gly Val Gly Thr Gln Leu Phe Asp Ser
435 440 445

Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn Tyr Glu Ser
450 455 460

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

Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp Arg Thr Asn
485 490 495

Thr Ile Ser Ser Asp Ser Ile Thr Gln Ile Pro Leu Val Lys Ala His
500 505 510

Thr Leu Gln Ser Gly Thr Thr Val Val Lys Gly Pro Gly Phe Thr Gly
515 520 525

Gly Asp Ile Leu Arg Arg Thr Ser Gly Gly Pro Phe Ala Phe Ser Asn
530 535 540

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

Tyr Ala Ser Thr Thr Asn Leu Arg Ile Tyr Val Thr Val Ala Gly Glu
565 570 575

Arg Ile Phe Ala Gly Gln Phe Asp Lys Thr Met Asp Ala Gly Ala Pro
580 585 590

Leu Thr Phe Gln Ser Phe Ser Tyr Ala Thr Ile Asn Thr Ala Phe Thr
595 600 605

Phe Pro Glu Arg Ser Ser Ser Leu Thr Val Gly Ala Asp Thr Phe Ser
610 615 620

Ser Gly Asn Glu Val Tyr Val Asp Arg Phe Glu Leu Ile Pro Val Thr
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Ala Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Val Val
645 650 655

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660 665 670

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

Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys
690 695 700

His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn
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Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr
725 730 735

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
740 745 750

Thr Leu Pro Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
755 760 765

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
770 775 780

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
785 790 795 800

Asn Ala Lys His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp
805 810 815

Pro Leu Ser Val Glu Asn Gln Ile Gly Pro Cys Gly Glu Pro Asn Arg
820 825 830

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu His Cys Ser Cys Arg
835 840 845

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
850 855 860

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
865 870 875 880

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
885 890 895

Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys
900 905 910

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Thr Leu Gln Leu Glu
915 920 925

Thr Thr Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
930 935 940

Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met
945 950 955 960

Ile His Ala Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu
965 970 975

Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu
980 985 990

Leu Glu Glu Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
995 1000 1005

Ile Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn
1010 1015 1020

Val Lys Gly His Val Glu Val Glu Glu Gln Asn Asn His Arg Ser
1025 1030 1035

Val Leu Val Ile Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val
1040 1045 1050

Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr
1055 1060 1065

Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu
1070 1075 1080

Asn Asn Thr Asp Glu Leu Lys Phe Asn Asn Cys Val Glu Glu Glu
1085 1090 1095

Val Tyr Pro Asn Asn Thr Val Thr Cys Ile Asn Tyr Thr Ala Thr
1100 1105 1110

Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr
1115 1120 1125

Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala
1130 1135 1140

Ser Val Tyr Glu Glu Lys Ser Tyr Thr Asp Arg Arg Arg Glu Asn
1145 1150 1155

Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro
1160 1165 1170

Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp
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Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val
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Asp Ser Val Glu Leu Leu Leu Met Glu Glu
1205 1210

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<211> 3690
<212> DNA
<213> Artificial

<220>
<223> Recombinant nucleotide sequence used for expression in a
bacterial cell encoding TIC867_21.

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<210> 15

<211> 3690

<212> DNA

<213> Artificial

<220>

<223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC867_21.

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tggctggaga accgagacga cgccagaacc cgctcagttc tgtacacaca gtacatcgcc	480
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cttctgatgg tgtacgcaca agcagcgaac ctccatctgc tcctgctgcg agacgcatct	600
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<210> 16
<211> 1229
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of the chimeric protein variant TIC867_21.

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Ile Pro Ala Val Ser Asn His Ser Ala Gln Met Asn Leu Ser Thr Asp
20 25 30

Ala Arg Ile Glu Asp Ser Leu Cys Ile Ala Glu Gly Asn Asn Ile Asp
35 40 45

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

Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Ile Ala Ser
65 70 75 80

Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Arg Gly Arg Asp Pro
85 90 95

Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln Val
100 105 110

Thr Glu Asn Thr Arg Asp Thr Ala Leu Ala Arg Leu Gln Gly Leu Gly
115 120 125

Asn Ser Phe Arg Ala Tyr Gln Gln Ser Leu Glu Asp Trp Leu Glu Asn
130 135 140

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

Leu Glu Leu Asp Phe Leu Asn Ala Met Pro Leu Phe Ala Ile Arg Asn
165 170 175

Gln Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His
180 185 190

Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe Gly Ser Glu Phe Gly Leu
195 200 205

Thr Ser Gln Glu Ile Gln Arg Tyr Tyr Glu Arg Gln Val Glu Lys Thr
210 215 220

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

Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln Phe
245 250 255

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

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

Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser Gly
290 295 300

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

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

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

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

Ser Leu Ser Thr Ser Thr His Gly Asn Thr Asn Thr Ser Ile Asn Pro
370 375 380

Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu Ser Phe
385 390 395 400

Ala Gly Ile Asn Ile Leu Leu Thr Thr Pro Val Asn Gly Val Pro Trp
405 410 415

Ala Arg Phe Asn Trp Arg Asn Pro Leu Asn Ser Leu Arg Gly Ser Leu
420 425 430

Leu Tyr Thr Ile Gly Tyr Thr Gly Val Gly Thr Gln Leu Phe Asp Ser
435 440 445

Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn Tyr Glu Ser
450 455 460

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

Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp Arg Thr Asn
485 490 495

Thr Ile Ser Ser Asp Ser Ile Thr Gln Ile Pro Leu Val Lys Ala His
500 505 510

Thr Leu Gln Ser Gly Thr Thr Val Val Lys Gly Pro Gly Phe Thr Gly
515 520 525

Gly Asp Ile Leu Arg Arg Thr Ser Gly Gly Pro Phe Ala Phe Ser Asn
530 535 540

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

Tyr Ala Ser Thr Thr Asn Leu Arg Ile Tyr Val Thr Val Ala Gly Glu
565 570 575

Arg Ile Phe Ala Gly Gln Phe Asp Lys Thr Met Asp Ala Gly Ala Pro
580 585 590

Leu Thr Phe Gln Ser Phe Ser Tyr Ala Thr Ile Asn Thr Ala Phe Thr
595 600 605

Phe Pro Glu Arg Ser Ser Ser Leu Thr Val Gly Ala Asp Thr Phe Ser
610 615 620

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

Ala Thr Gly Thr Thr Thr Tyr Glu Tyr Glu Glu Lys Gln Asn Leu Glu
645 650 655

Lys Ala Gln Lys Ala Leu Asn Ala Leu Phe Thr Asp Gly Thr Asn Gly
660 665 670

Tyr Leu Gln Met Asp Ala Thr Asp Tyr Asp Ile Asn Gln Thr Ala Asn
675 680 685

Leu Ile Glu Cys Val Ser Asp Glu Leu Tyr Ala Lys Glu Lys Ile Val
690 695 700

Leu Leu Asp Glu Val Lys Tyr Ala Lys Arg Leu Ser Ile Ser Arg Asn
705 710 715 720

Leu Leu Leu Asn Asp Asp Leu Glu Phe Ser Asp Gly Phe Gly Glu Asn
725 730 735

Gly Trp Thr Thr Ser Asp Asn Ile Ser Ile Gln Ala Asp Asn Pro Leu
740 745 750

Phe Lys Gly Asn Tyr Leu Lys Met Phe Gly Ala Arg Asp Ile Asp Gly
755 760 765

Thr Leu Phe Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Arg Leu
770 775 780

Lys Pro Tyr Thr Arg Tyr Arg Val Arg Gly Phe Val Gly Ser Ser Lys
785 790 795 800

Asn Leu Lys Leu Val Val Thr Arg Tyr Glu Lys Glu Ile Asp Ala Ile
805 810 815

Met Asn Val Pro Asn Asp Leu Ala His Met Gln Leu Asn Pro Ser Cys
820 825 830

Gly Asp Tyr Arg Cys Glu Ser Ser Ser Gln Phe Leu Val Asn Gln Val
835 840 845

His Pro Thr Pro Thr Ala Gly Tyr Ala Leu Asp Met Tyr Ala Cys Pro
850 855 860

Ser Ser Ser Asp Lys Lys His Ile Met Cys His Asp Arg His Pro Phe
865 870 875 880

Asp Phe His Ile Asp Thr Gly Glu Leu Asn Pro Asn Thr Asn Leu Gly
885 890 895

Ile Asp Val Leu Phe Lys Ile Ser Asn Pro Asn Gly Tyr Ala Thr Leu
900 905 910

Gly Asn Leu Glu Val Ile Glu Glu Gly Pro Leu Thr Asp Glu Ala Leu
915 920 925

Val His Val Lys Gln Lys Glu Lys Lys Trp Arg Gln His Met Glu Lys
930 935 940

Lys Arg Met Glu Thr Gln Gln Ala Tyr Asp Pro Ala Lys Gln Ala Val
945 950 955 960

Asp Ala Leu Phe Thr Asn Glu Gln Glu Leu Asp Tyr His Thr Thr Leu
965 970 975

Asp His Ile Gln Asn Ala Asp Gln Leu Val Gln Ala Ile Pro Tyr Val
980 985 990

His His Ala Trp Leu Pro Asp Ala Pro Gly Met Asn Tyr Asp Val Tyr
995 1000 1005

Gln Gly Leu Asn Ala Arg Ile Met Gln Ala Tyr Asn Leu Tyr Asp
1010 1015 1020

Ala Arg Asn Val Ile Ile Asn Gly Asp Phe Thr Gln Gly Leu Gln
1025 1030 1035

Gly Trp His Ala Thr Gly Lys Ala Ala Val Gln Gln Ile Asp Gly
1040 1045 1050

Ala Ser Val Leu Val Leu Ser Asn Trp Ser Ala Glu Val Ser Gln
1055 1060 1065

Asn Leu His Ala Gln Asp His His Gly Tyr Met Leu Arg Val Ile
1070 1075 1080

Ala Lys Lys Glu Gly Pro Gly Lys Gly Tyr Val Met Met Met Asp
1085 1090 1095

Phe Asn Gly Lys Gln Glu Thr Leu Thr Phe Thr Ser Cys Glu Glu
1100 1105 1110

Gly Tyr Ile Thr Lys Thr Ile Glu Val Phe Pro Glu Ser Asp Arg
1115 1120 1125

Ile Arg Ile Glu Met Gly Glu Thr Glu Gly Thr Phe Tyr Val Asp
1130 1135 1140

Ser Ile Glu Leu Leu Cys Met Gln Gly Tyr Ala Ser Asp Asn Asn
1145 1150 1155

Pro His Thr Gly Asn Met Tyr Glu Gln Ser Tyr Asn Gly Asn Tyr
1160 1165 1170

Asn Gln Asn Thr Ser Asp Val Tyr His Gln Gly Tyr Ile Asn Asn
1175 1180 1185

Tyr Asn Gln Asn Ser Ser Ser Met Tyr Asn Gln Asn Tyr Ile Asn
1190 1195 1200

Asn Asp Asp Leu His Ser Gly Cys Thr Cys Asn Gln Gly His Asn
1205 1210 1215

Ser Gly Cys Thr Cys Asn Gln Gly Tyr Asn Arg
1220 1225

<210> 17
<211> 3432
<212> DNA
<213> Artificial

<220>
<223> Recombinant nucleotide sequence used for expression in a
bacterial cell encoding TIC867_22.

<400> 17
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tcgaatcatt ccgcacaaat gaatctatca accgatgctc gtattgagga tagcttgtgt 120
atagccgagg ggaacaatat cgatccattt gttagcgcac caacagtcca aacgggtatt 180
aacatagctg gtagaataact aggtgtatta ggcgtaccgt ttgctggaca aatagctagt 240
ttttatagtt ttcttggttg tgaattatgg ccccgcgga gagatccttg ggaaattttc 300
ctagaacatg tcgaacaact tataagacaa caagtaacag aaaataactag ggatacggct 360
cttgctcgat tacaaggttt aggaaattcc tttagagcct atcaacagtc acttgaagat 420
tggctagaaa accgtgatga tgcaagaacg agaagtgttc tttataccca atatatagcc 480

ttagaacttg attttcttaa tgcgatgccg cttttcgcaa ttagaaacca agaagttcca	540
ttattaatgg tatatgctca agctgcaaat ttacacctat tattattgag agatgcctct	600
ctttttggta gtgaatttgg gcttacatcc caagaaattc aacgttatta tgagcgccaa	660
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gtgactgata atacgtatct aacaaaagaa gtggtattct attcacatac agaacacatg	3360
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acagaaaagt ag	3432

<210> 18
<211> 3432
<212> DNA
<213> Artificial

<220>

<223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC867_22.

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atcgccgagg gcaacaacat cgaccggttc gtgtctgcaa gcacgggtcca gaccggcatc	180
aacatcgcg ggcgcacatcct gggcgtgctc ggcgtgccct tcgcgggtca aatcgctct	240
ttctactcat tcctcgtggg cgagctgtgg ccgcgcggac gtgaccctgt ggaaatcttc	300
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 atacctggca tcaactacga gatctacaca gagttgtcca acagggtcca gcaagcgta 3000
 tacctctaca ccagccgcaa cgccgtccag aatggcgact tcaattccgg actagactcc 3060
 tggaacgcca cgggcgggagc tacggtgcaa caagacggca acacccactt cctcgtactt 3120
 agccactggg acgtcaagt gagtcagcaa ttccgggttc agccgaactg caagtacgtc 3180
 ctgcgcgtaa cggccgagaa ggttggaggc ggagacggct acgttaccat ccgcgacggc 3240
 gctcaccaca ccgagaaact gacgttcaac gcttgtgact acgacatcaa cggcacttac 3300
 gtgacggaca acacctacct gacgaaggag gtggtgttct attctcacac cgagcacatg 3360
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 actgagaagt ga 3432

<210> 19

<211> 1143

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein variant TIC867_22.

<400> 19

Met Thr Ser Asn Arg Lys Asn Glu Asn Glu Ile Ile Asn Ala Leu Ser
 1 5 10 15

Ile Pro Ala Val Ser Asn His Ser Ala Gln Met Asn Leu Ser Thr Asp
 20 25 30

Ala Arg Ile Glu Asp Ser Leu Cys Ile Ala Glu Gly Asn Asn Ile Asp
 35 40 45

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

Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Ile Ala Ser
65 70 75 80

Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Arg Gly Arg Asp Pro
85 90 95

Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln Val
100 105 110

Thr Glu Asn Thr Arg Asp Thr Ala Leu Ala Arg Leu Gln Gly Leu Gly
115 120 125

Asn Ser Phe Arg Ala Tyr Gln Gln Ser Leu Glu Asp Trp Leu Glu Asn
130 135 140

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

Leu Glu Leu Asp Phe Leu Asn Ala Met Pro Leu Phe Ala Ile Arg Asn
165 170 175

Gln Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His
180 185 190

Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe Gly Ser Glu Phe Gly Leu
195 200 205

Thr Ser Gln Glu Ile Gln Arg Tyr Tyr Glu Arg Gln Val Glu Lys Thr
210 215 220

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

Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln Phe
245 250 255

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

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

Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser Gly
290 295 300

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

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

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

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

Ser Leu Ser Thr Ser Thr His Gly Asn Thr Asn Thr Ser Ile Asn Pro
370 375 380

Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu Ser Phe
385 390 395 400

Ala Gly Ile Asn Ile Leu Leu Thr Thr Pro Val Asn Gly Val Pro Trp
405 410 415

Ala Arg Phe Asn Trp Arg Asn Pro Leu Asn Ser Leu Arg Gly Ser Leu
420 425 430

Leu Tyr Thr Ile Gly Tyr Thr Gly Val Gly Thr Gln Leu Phe Asp Ser
435 440 445

Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn Tyr Glu Ser
450 455 460

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

Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp Arg Thr Asn
485 490 495

Thr Ile Ser Ser Asp Ser Ile Thr Gln Ile Pro Leu Val Lys Ala His
500 505 510

Thr Leu Gln Ser Gly Thr Thr Val Val Lys Gly Pro Gly Phe Thr Gly
515 520 525

Gly Asp Ile Leu Arg Arg Thr Ser Gly Gly Pro Phe Ala Phe Ser Asn
530 535 540

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

Tyr Ala Ser Thr Thr Asn Leu Arg Ile Tyr Val Thr Val Ala Gly Glu
565 570 575

Arg Ile Phe Ala Gly Gln Phe Asp Lys Thr Met Asp Ala Gly Ala Pro
580 585 590

Leu Thr Phe Gln Ser Phe Ser Tyr Ala Thr Ile Asn Thr Ala Phe Thr
595 600 605

Phe Pro Glu Arg Ser Ser Ser Leu Thr Val Gly Ala Asp Thr Phe Ser
610 615 620

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

Ala Thr Asn Pro Thr Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys
645 650 655

Lys Ala Val Ala Ser Leu Phe Thr Arg Thr Arg Asp Gly Leu Gln Val
660 665 670

Asn Val Thr Asp Tyr Gln Val Asp Gln Ala Ala Asn Leu Val Ser Cys
675 680 685

Leu Ser Asp Glu Gln Tyr Gly His Asp Lys Lys Met Leu Leu Glu Ala
690 695 700

Val Arg Ala Ala Lys Arg Leu Ser Arg Glu Arg Asn Leu Leu Gln Asp
705 710 715 720

Pro Asp Phe Asn Thr Ile Asn Ser Thr Glu Glu Asn Gly Trp Lys Ala
725 730 735

Ser Asn Gly Val Thr Ile Ser Glu Gly Gly Pro Phe Tyr Lys Gly Arg
740 745 750

Ala Leu Gln Leu Ala Ser Ala Arg Glu Asn Tyr Pro Thr Tyr Ile Tyr
755 760 765

Gln Lys Val Asn Ala Ser Glu Leu Lys Pro Tyr Thr Arg Tyr Arg Leu
770 775 780

Asp Gly Phe Val Lys Ser Ser Gln Asp Leu Glu Ile Asp Leu Ile His
785 790 795 800

His His Lys Val His Leu Val Lys Asn Val Pro Asp Asn Leu Val Ser
805 810 815

Asp Thr Tyr Ser Asp Gly Ser Cys Ser Gly Met Asn Arg Cys Glu Glu
820 825 830

Gln Gln Met Val Asn Ala Gln Leu Glu Thr Glu His His His Pro Met
835 840 845

Asp Cys Cys Glu Ala Ala Gln Thr His Glu Phe Ser Ser Tyr Ile Asn
850 855 860

Thr Gly Asp Leu Asn Ser Ser Val Asp Gln Gly Ile Trp Val Val Leu
865 870 875 880

Lys Val Arg Thr Thr Asp Gly Tyr Ala Thr Leu Gly Asn Leu Glu Leu
885 890 895

Val Glu Val Gly Pro Leu Ser Gly Glu Ser Leu Glu Arg Glu Gln Arg
900 905 910

Asp Asn Ala Lys Trp Ser Ala Glu Leu Gly Arg Lys Arg Ala Glu Thr
915 920 925

Asp Arg Val Tyr Gln Asp Ala Lys Gln Ser Ile Asn His Leu Phe Val
930 935 940

Asp Tyr Gln Asp Gln Gln Leu Asn Pro Glu Ile Gly Met Ala Asp Ile
945 950 955 960

Ile Asp Ala Gln Asn Leu Val Ala Ser Ile Ser Asp Val Tyr Ser Asp
965 970 975

Ala Val Leu Gln Ile Pro Gly Ile Asn Tyr Glu Ile Tyr Thr Glu Leu
980 985 990

Ser Asn Arg Leu Gln Gln Ala Ser Tyr Leu Tyr Thr Ser Arg Asn Ala
995 1000 1005

Val Gln Asn Gly Asp Phe Asn Ser Gly Leu Asp Ser Trp Asn Ala
1010 1015 1020

Thr Gly Gly Ala Thr Val Gln Gln Asp Gly Asn Thr His Phe Leu
1025 1030 1035

Val Leu Ser His Trp Asp Ala Gln Val Ser Gln Gln Phe Arg Val
1040 1045 1050

Gln Pro Asn Cys Lys Tyr Val Leu Arg Val Thr Ala Glu Lys Val
 1055 1060 1065

Gly Gly Gly Asp Gly Tyr Val Thr Ile Arg Asp Gly Ala His His
 1070 1075 1080

Thr Glu Lys Leu Thr Phe Asn Ala Cys Asp Tyr Asp Ile Asn Gly
 1085 1090 1095

Thr Tyr Val Thr Asp Asn Thr Tyr Leu Thr Lys Glu Val Val Phe
 1100 1105 1110

Tyr Ser His Thr Glu His Met Trp Val Glu Val Ser Glu Thr Glu
 1115 1120 1125

Gly Ala Phe His Ile Asp Ser Ile Glu Phe Val Glu Thr Glu Lys
 1130 1135 1140

<210> 20

<211> 3696

<212> DNA

<213> Artificial

<220>

<223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC867_23.

<400> 20

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atcgccgagg gcaacaacat cgacccgttc gtgtctgcaa gcacgggtcca gaccggcatc	180
aacatcgcg ggcgcacatcct gggcgtgctc ggcgtgccct tcgcgggtca aatgcctct	240
ttctactcat tcctcgtggg cgagctgtgg ccgcgcggac gtgacccgtg ggaaatcttc	300
ctggagcacg ttgagcagct catccggcag caagtgaccg agaacaccag ggacaccgca	360
ctggcacggc tccagggcct tggcaacagc ttccgcgcct accagcagtc gctggaggac	420

tggctggaga accgagacga cgccagaacc cgctcagttc tgtacacaca gtacatcgcc	480
ctagagctgg acttcctcaa cgctatgccg ctcttcgcca tccgtaacca ggaagtaccg	540
cttctgatgg tgtacgcaca agcagcgaac ctccatctgc tcctgctgcg agacgcatct	600
ctgttcggca gtgagttcgg gctgacgagc caggagatcc agcgctacta cgagcgccaa	660
gtggagaaga ctcgtgagta cagcgactac tgcgcgcgct ggtacaacac gggcttgaac	720
aaccttcgcg ggacaaacgc cgaatcctgg cttcgctaca accagttccg ccgcgacctc	780
acgctgggtg tgctggacct ggctgcgctc ttcccgctct acgacacacg ggtgtaccca	840
atgaacacga gcgcacagct caccctgtgag atctacacag atcccatcgg ccgcaccaac	900
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gactcgatca cccagatccc gctgggtgaag gctcacacgc ttcagtcggg caccacagtc	1560
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gcaatctcac tttatgacgc gaggaatgtg gtcaagaacg gtgacttcaa caacggcttg	3120
gcgtgttgga acgttaaagg gcacgtggat gtacaacagt cacaccacag aagtgtcttg	3180
gtcatcccgg agtgggaggc ggaagtgagc caggccgtcc gggctctgcc tgggcgcggt	3240
tacatcctcc gcgtgacagc gtacaaggag ggctacggtg agggctgcgt gacgatccac	3300
gagattgaga acaacacgga cgagcttaag ttcaagaact gcgaggagga ggaagtgtac	3360
ccgacagaca ccggcacctg caacgactac accgcccacc aagggaccgc cgctgcaac	3420

agccgcaacg cgggctatga agatgcgtac gaggttgata ccaccgcctc agtgaactac	3480
aaaccgactt atgaggagga gacatacacg gacgtcaggc gcgacaacca ttgtgagtac	3540
gaccgtggct acgtgaacta tccgccgggtg ccagcgggct acatgacgaa ggagctagaa	3600
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<210> 21
 <211> 1231
 <212> PRT
 <213> Artificial

<220>
 <223> Amino acid sequence of the chimeric protein variant TIC867_23.

<400> 21

Met Thr Ser Asn Arg Lys Asn Glu Asn Glu Ile Ile Asn Ala Leu Ser
1 5 10 15

Ile Pro Ala Val Ser Asn His Ser Ala Gln Met Asn Leu Ser Thr Asp
20 25 30

Ala Arg Ile Glu Asp Ser Leu Cys Ile Ala Glu Gly Asn Asn Ile Asp
35 40 45

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

Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Ile Ala Ser
65 70 75 80

Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Arg Gly Arg Asp Pro
85 90 95

Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln Val
100 105 110

Thr Glu Asn Thr Arg Asp Thr Ala Leu Ala Arg Leu Gln Gly Leu Gly

115

120

125

Asn Ser Phe Arg Ala Tyr Gln Gln Ser Leu Glu Asp Trp Leu Glu Asn
 130 135 140

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

Leu Glu Leu Asp Phe Leu Asn Ala Met Pro Leu Phe Ala Ile Arg Asn
 165 170 175

Gln Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His
 180 185 190

Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe Gly Ser Glu Phe Gly Leu
 195 200 205

Thr Ser Gln Glu Ile Gln Arg Tyr Tyr Glu Arg Gln Val Glu Lys Thr
 210 215 220

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

Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln Phe
 245 250 255

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

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

Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser Gly
 290 295 300

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

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

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

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

Ser Leu Ser Thr Ser Thr His Gly Asn Thr Asn Thr Ser Ile Asn Pro
370 375 380

Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu Ser Phe
385 390 395 400

Ala Gly Ile Asn Ile Leu Leu Thr Thr Pro Val Asn Gly Val Pro Trp
405 410 415

Ala Arg Phe Asn Trp Arg Asn Pro Leu Asn Ser Leu Arg Gly Ser Leu
420 425 430

Leu Tyr Thr Ile Gly Tyr Thr Gly Val Gly Thr Gln Leu Phe Asp Ser
435 440 445

Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn Tyr Glu Ser
450 455 460

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

Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp Arg Thr Asn
485 490 495

Thr Ile Ser Ser Asp Ser Ile Thr Gln Ile Pro Leu Val Lys Ala His
500 505 510

Thr Leu Gln Ser Gly Thr Thr Val Val Lys Gly Pro Gly Phe Thr Gly

515

520

525

Gly Asp Ile Leu Arg Arg Thr Ser Gly Gly Pro Phe Ala Phe Ser Asn
 530 535 540

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

Tyr Ala Ser Thr Thr Asn Leu Arg Ile Tyr Val Thr Val Ala Gly Glu
 565 570 575

Arg Ile Phe Ala Gly Gln Phe Asp Lys Thr Met Asp Ala Gly Ala Pro
 580 585 590

Leu Thr Phe Gln Ser Phe Ser Tyr Ala Thr Ile Asn Thr Ala Phe Thr
 595 600 605

Phe Pro Glu Arg Ser Ser Ser Leu Thr Val Gly Ala Asp Thr Phe Ser
 610 615 620

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

Ala Thr Thr Ala Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln
 645 650 655

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

Thr Gly Val Thr Asp Tyr His Ile Asp Glu Val Ser Asn Leu Val Ala
 675 680 685

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

Lys Val Lys Tyr Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln
 705 710 715 720

Asp Pro Asn Phe Thr Ser Ile Asn Lys Gln Pro Asp Phe Ile Ser Thr
725 730 735

Asn Glu Gln Ser Asn Phe Thr Ser Ile His Glu Gln Ser Glu His Gly
740 745 750

Trp Trp Gly Ser Glu Asn Ile Thr Ile Gln Glu Gly Asn Asp Val Phe
755 760 765

Lys Glu Asn Tyr Val Ile Leu Pro Gly Thr Phe Asn Glu Cys Tyr Pro
770 775 780

Thr Tyr Leu Tyr Gln Lys Ile Gly Glu Ala Glu Leu Lys Ala Tyr Thr
785 790 795 800

Arg Tyr Gln Leu Ser Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile
805 810 815

Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Leu Asp Val Pro Gly
820 825 830

Thr Glu Ser Val Trp Pro Leu Ser Val Glu Ser Pro Ile Gly Arg Cys
835 840 845

Gly Glu Pro Asn Arg Cys Ala Pro His Phe Glu Trp Asn Pro Asp Leu
850 855 860

Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His
865 870 875 880

Phe Ser Leu Asp Ile Asp Val Gly Cys Ile Asp Leu His Glu Asn Leu
885 890 895

Gly Val Trp Val Val Phe Lys Ile Lys Thr Gln Glu Gly His Ala Arg
900 905 910

Leu Gly Asn Leu Glu Phe Ile Glu Glu Lys Pro Leu Leu Gly Glu Ala

915

920

925

Leu Ser Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu
 930 935 940

Lys Leu Gln Leu Glu Thr Lys Arg Val Tyr Thr Glu Ala Lys Glu Ala
 945 950 955 960

Val Asp Ala Leu Phe Val Asp Ser Gln Tyr Asp Arg Leu Gln Ala Asp
 965 970 975

Thr Asn Ile Gly Met Ile His Ala Ala Asp Lys Leu Val His Arg Ile
 980 985 990

Arg Glu Ala Tyr Leu Ser Glu Leu Ser Val Ile Pro Gly Val Asn Ala
 995 1000 1005

Glu Ile Phe Glu Glu Leu Glu Gly Arg Ile Ile Thr Ala Ile Ser
 1010 1015 1020

Leu Tyr Asp Ala Arg Asn Val Val Lys Asn Gly Asp Phe Asn Asn
 1025 1030 1035

Gly Leu Ala Cys Trp Asn Val Lys Gly His Val Asp Val Gln Gln
 1040 1045 1050

Ser His His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu
 1055 1060 1065

Val Ser Gln Ala Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu
 1070 1075 1080

Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr
 1085 1090 1095

Ile His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Lys Asn
 1100 1105 1110

Cys Glu Glu Glu Glu Val Tyr Pro Thr Asp Thr Gly Thr Cys Asn
1115 1120 1125

Asp Tyr Thr Ala His Gln Gly Thr Ala Ala Cys Asn Ser Arg Asn
1130 1135 1140

Ala Gly Tyr Glu Asp Ala Tyr Glu Val Asp Thr Thr Ala Ser Val
1145 1150 1155

Asn Tyr Lys Pro Thr Tyr Glu Glu Glu Thr Tyr Thr Asp Val Arg
1160 1165 1170

Arg Asp Asn His Cys Glu Tyr Asp Arg Gly Tyr Val Asn Tyr Pro
1175 1180 1185

Pro Val Pro Ala Gly Tyr Met Thr Lys Glu Leu Glu Tyr Phe Pro
1190 1195 1200

Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Lys
1205 1210 1215

Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
1220 1225 1230

<210> 22
<211> 3666
<212> DNA
<213> Artificial

<220>
<223> Synthetic nucleotide sequence designed for expression in a plant
cell encoding TIC867_24.

<400> 22
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atcgccgagg gcaacaacat cgacccgttc gtgtctgcaa gcacgggtcca gaccggcatc 180
aacatcgcg ggcgcacatcct gggcgtgctc ggcgtgccct tcgcgggtca aatgcctct 240

ttctactcat tcctcgtggg cgagctgtgg ccgcgcggac gtgacccgtg ggaaatcttc	300
ctggagcacg ttgagcagct catccggcag caagtgaccg agaacaccag ggacaccgca	360
ctggcacggc tccagggcct tggcaacagc ttccgcgcct accagcagtc gctggaggac	420
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ctagagagcc ggaccatccg tggcagtctc tcaacctcga cccacggcaa cacgaacacg	1140
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gctggcatta acattctgtt gaccactccg gtgaacggcg tcccttgggc ccgcttcaac	1260
tggaggaatc ctctgaactc actgcgcggc agccttctct aactatcgg ctacaccggc	1320
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 <213> Artificial

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Ile Pro Ala Val Ser Asn His Ser Ala Gln Met Asn Leu Ser Thr Asp
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Ala Arg Ile Glu Asp Ser Leu Cys Ile Ala Glu Gly Asn Asn Ile Asp
 35 40 45

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

Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Ile Ala Ser
 65 70 75 80

Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Arg Gly Arg Asp Pro
 85 90 95

Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln Val
100 105 110

Thr Glu Asn Thr Arg Asp Thr Ala Leu Ala Arg Leu Gln Gly Leu Gly
115 120 125

Asn Ser Phe Arg Ala Tyr Gln Gln Ser Leu Glu Asp Trp Leu Glu Asn
130 135 140

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

Leu Glu Leu Asp Phe Leu Asn Ala Met Pro Leu Phe Ala Ile Arg Asn
165 170 175

Gln Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His
180 185 190

Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe Gly Ser Glu Phe Gly Leu
195 200 205

Thr Ser Gln Glu Ile Gln Arg Tyr Tyr Glu Arg Gln Val Glu Lys Thr
210 215 220

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

Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln Phe
245 250 255

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

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

Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser Gly
290 295 300

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

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

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

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

Ser Leu Ser Thr Ser Thr His Gly Asn Thr Asn Thr Ser Ile Asn Pro
370 375 380

Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu Ser Phe
385 390 395 400

Ala Gly Ile Asn Ile Leu Leu Thr Thr Pro Val Asn Gly Val Pro Trp
405 410 415

Ala Arg Phe Asn Trp Arg Asn Pro Leu Asn Ser Leu Arg Gly Ser Leu
420 425 430

Leu Tyr Thr Ile Gly Tyr Thr Gly Val Gly Thr Gln Leu Phe Asp Ser
435 440 445

Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn Tyr Glu Ser
450 455 460

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

Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp Arg Thr Asn
485 490 495

Thr Ile Ser Ser Asp Ser Ile Thr Gln Ile Pro Leu Val Lys Ala His
500 505 510

Thr Leu Gln Ser Gly Thr Thr Val Val Lys Gly Pro Gly Phe Thr Gly
515 520 525

Gly Asp Ile Leu Arg Arg Thr Ser Gly Gly Pro Phe Ala Phe Ser Asn
530 535 540

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

Tyr Ala Ser Thr Thr Asn Leu Arg Ile Tyr Val Thr Val Ala Gly Glu
565 570 575

Arg Ile Phe Ala Gly Gln Phe Asp Lys Thr Met Asp Ala Gly Ala Pro
580 585 590

Leu Thr Phe Gln Ser Phe Ser Tyr Ala Thr Ile Asn Thr Ala Phe Thr
595 600 605

Phe Pro Glu Arg Ser Ser Ser Leu Thr Val Gly Ala Asp Thr Phe Ser
610 615 620

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

Ala Thr Thr Ala Thr Phe Glu Ala Glu Ser Asp Leu Glu Arg Ala Arg
645 650 655

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

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

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

Glu Val Lys Tyr Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln
705 710 715 720

Asp Pro Thr Phe Thr Ser Ile Ser Gly Gln Thr Asp Arg Gly Trp Ile
725 730 735

Gly Ser Thr Gly Ile Ser Ile Gln Gly Gly Asp Asp Ile Phe Lys Glu
740 745 750

Asn Tyr Val Arg Leu Pro Gly Thr Val Asp Glu Cys Tyr Pro Thr Tyr
755 760 765

Leu Tyr Gln Lys Ile Asp Glu Ser Gln Leu Lys Ser Tyr Thr Arg Tyr
770 775 780

Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu
785 790 795 800

Ile Arg Tyr Asn Ala Lys His Glu Thr Leu Ser Val Pro Gly Thr Glu
805 810 815

Ser Pro Trp Pro Ser Ser Gly Val Tyr Pro Ser Gly Arg Cys Gly Glu
820 825 830

Pro Asn Arg Cys Ala Pro Arg Ile Glu Trp Asn Pro Asp Leu Asp Cys
835 840 845

Ser Cys Arg Tyr Gly Glu Lys Cys Val His His Ser His His Phe Ser
850 855 860

Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val
865 870 875 880

Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Lys Leu Gly
885 890 895

Asn Leu Glu Phe Ile Glu Glu Lys Pro Leu Leu Gly Lys Ala Leu Ser
900 905 910

Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Tyr Glu Lys Leu
915 920 925

Gln Leu Glu Thr Lys Arg Val Tyr Thr Glu Ala Lys Glu Ser Val Asp
930 935 940

Ala Leu Phe Val Asp Ser Gln Tyr Asp Lys Leu Gln Ala Asn Thr Asn
945 950 955 960

Ile Gly Ile Ile His Gly Ala Asp Lys Gln Val His Arg Ile Arg Glu
965 970 975

Pro Tyr Leu Ser Glu Leu Pro Val Ile Pro Ser Ile Asn Ala Ala Ile
980 985 990

Phe Glu Glu Leu Glu Gly His Ile Phe Lys Ala Tyr Ser Leu Tyr Asp
995 1000 1005

Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser
1010 1015 1020

Cys Trp Asn Val Lys Gly His Val Asp Val Gln Gln Asn His His
1025 1030 1035

Arg Ser Val Leu Val Leu Ser Glu Trp Glu Ala Glu Val Ser Gln
1040 1045 1050

Lys Val Arg Val Cys Pro Asp Arg Gly Tyr Ile Leu Arg Val Thr
1055 1060 1065

Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu
1070 1075 1080

Phe Glu Asp Asn Thr Asp Val Leu Lys Phe Arg Asn Phe Val Glu
1085 1090 1095

Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr
1100 1105 1110

Thr Asn Gln Ser Ala Glu Gly Ser Thr Asp Ala Cys Asn Ser Tyr
1115 1120 1125

Asn Arg Gly Tyr Glu Asp Gly Tyr Glu Asn Arg Tyr Glu Pro Asn
1130 1135 1140

Pro Ser Ala Pro Val Asn Tyr Thr Pro Thr Tyr Glu Glu Gly Met
1145 1150 1155

Tyr Thr Asp Thr Gln Gly Tyr Asn His Cys Val Ser Asp Arg Gly
1160 1165 1170

Tyr Arg Asn His Thr Pro Leu Pro Ala Gly Tyr Val Thr Leu Glu
1175 1180 1185

Leu Glu Tyr Phe Pro Glu Thr Glu Gln Val Trp Ile Glu Ile Gly
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Glu Thr Glu Gly Thr Phe Ile Val Gly Ser Val Glu Leu Leu Leu
1205 1210 1215

Met Glu Glu
1220

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<211> 3651
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<213> Artificial

<220>
<223> Synthetic nucleotide sequence designed for expression in a plant
cell encoding TIC867_25.

<400> 24

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<400> 25

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

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

Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser Gly
290 295 300

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

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

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

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

Ser Leu Ser Thr Ser Thr His Gly Asn Thr Asn Thr Ser Ile Asn Pro
370 375 380

Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu Ser Phe
385 390 395 400

Ala Gly Ile Asn Ile Leu Leu Thr Thr Pro Val Asn Gly Val Pro Trp
405 410 415

Ala Arg Phe Asn Trp Arg Asn Pro Leu Asn Ser Leu Arg Gly Ser Leu
420 425 430

Leu Tyr Thr Ile Gly Tyr Thr Gly Val Gly Thr Gln Leu Phe Asp Ser
435 440 445

Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn Tyr Glu Ser
450 455 460

Tyr Ser His Arg Leu Ser Asn Ile Arg Leu Ile Ser Gly Asn Thr Leu

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

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

Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln
705 710 715 720

Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg
725 730 735

Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu
740 745 750

Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu Cys Tyr Pro Thr Tyr
755 760 765

Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr
770 775 780

Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu
785 790 795 800

Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn Val Pro Gly Thr Gly
805 810 815

Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu
820 825 830

Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys
835 840 845

Ser Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His Phe Thr
850 855 860

Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val

865		870		875		880
Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly						
	885			890		895
Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala						
	900			905		910
Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu						
	915			920		925
Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp						
	930			935		940
Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Val Asp Thr Asn						
945		950		955		960
Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Arg Ile Arg Glu						
	965			970		975
Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile						
	980			985		990
Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Tyr Ser Leu Tyr Asp						
	995			1000		1005
Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Leu						
	1010			1015		1020
Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn Asn						
	1025			1030		1035
His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu Val Ser						
	1040			1045		1050
Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val						
	1055			1060		1065

Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
1070 1075 1080

Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val
1085 1090 1095

Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr
1100 1105 1110

Thr Gly Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn
1115 1120 1125

Gln Gly Tyr Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala
1130 1135 1140

Asp Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg
1145 1150 1155

Arg Glu Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr
1160 1165 1170

Pro Leu Pro Ala Gly Tyr Val Thr Lys Asp Leu Glu Tyr Phe Pro
1175 1180 1185

Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr
1190 1195 1200

Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
1205 1210 1215

<210> 26

<211> 3600

<212> DNA

<213> Artificial

<220>

<223> Recombinant nucleotide sequence used for expression in a
bacterial cell encoding TIC868.

<400> 26

atgacttcaa ataggaaaaa tgagaatgaa attataaatg ctttatcgat tccagctgta	60
tcgaatcatt cgcacaaaat gaatctatca accgatgctc gtattgagga tagcttgtgt	120
atagccgagg ggaacaatat cgatccattt gttagcgcac caacagtcca aacgggtatt	180
aacatagctg gtagaatact aggtgtatta ggcgtagcgt ttgctggaca aatagctagt	240
ttttatagtt ttcttggttg tgaattatgg ccccgaggca gagatccttg ggaaattttc	300
ctagaacatg tcgaacaact tataagacaa caagtaacag aaaatactag ggatacggct	360
cttgctcgat tacaaggttt aggaaattcc tttagagcct atcaacagtc acttgaagat	420
tggctagaaa accgtgatga tgcaagaacg agaagtgttc ttataacca atatatagcc	480
ttagaacttg attttcttaa tgcgatgccg cttttcgcaa ttagaaacca agaagttcca	540
ttattaatgg tatatgctca agctgcaaat ttacacctat tattattgag agatgcctct	600
ctttttggta gtgaatttgg gcttacatcc caagaaattc aacgttatta tgagcgccaa	660
gtggaaaaaaa cgagagaata ttctgattat tgcgcaagat ggtataatac gggtttaaat	720
aatttgagag ggacaaatgc tgaaagttag ttgcgatata atcaattccg tagagactta	780
acgctaggag tattagatct agtggcacta ttccaagct atgacacgcg tgtttatcca	840
atgaatacca gtgctcaatt aacaagagaa atttatacag atccaattgg gagaacaaat	900
gcaccttcag gatttgcaag tacgaattgg ttaataata atgcaccatc gttttctgcc	960
atagaggctg ccgttattag gcctccgcat ctacttgatt ttccagaaca gcttacaatt	1020
ttcagcgtat taagtcgatg gagtaatact caatatatga attactgggt gggacataga	1080
cttgaatcgc gaacaataag ggggtcatta agtacctcga cacacggaaa taccaatact	1140
tctattaatc ctgtaacatt acagttcaca tctcgagacg tttatagaac agaatcattt	1200
gcagggataa atatacttct aactactcct gtgaatggag taccttgggc tagatttaat	1260
tggagaaatc ccctgaattc tcttagaggt agccttctct atactatagg gtatactgga	1320
gtggggacac aactatttga ttcagaaact gaattaccac cagaaacaac agaacgacca	1380
aattatgaat cttacagtca tagattatct aatataagac taatatcagg aaacactttg	1440
agagcaccag tatattcttg gacgcaccgt agtgcagatc gtacaaatac cattagttca	1500

gatagcatta atcaaatacc tttagtgtaaa ggatttagag tttggggggg cacctctgtc	1560
attacaggac caggatttac aggaggggat atccttcgaa gaaatacctt tggtgatttt	1620
gtatctctac aagtcaatat taattcacca attacccaaa gataccgttt aagatttcgt	1680
tacgcttcca gtagggatgc acgagttata gtattaacag gagcggcatc cacaggagtg	1740
ggaggccaag ttagtgtaaa tatgcctctt cagaaaaacta tggaaatagg ggagaactta	1800
acatctagaa catttagata taccgatttt agtaatcctt tttcatttag agctaatacca	1860
gatataattg ggataagtga acaacctcta tttgggtgcag gttctattag tagcggtgaa	1920
ctttatatag ataaaaattga aattattcta gcagatgcaa catttgaagc agaatctgat	1980
ttagaaaagag cacaaaaggc ggtgaatgag ctgtttactt cttccaatca aatcgggtta	2040
aaaacagatg tgacggatta tcatattgat caagtatcca atttagttga gtgtttatct	2100
gatgaatttt gtctggatga aaaaaaagaa ttgtccgaga aagtcaaaca tgcgaagcga	2160
cttagtgatg agcgggaattt acttcaagat ccaaacttta gagggatcaa tagacaacta	2220
gaccgtggct ggagaggaag tacggatatt accatccaag gaggcgatga cgtattcaaa	2280
gagaattacg ttacgctatt gggtagcttt gatgagtgtc atccaacgta tttatatcaa	2340
aaaatagatg agtcgaaatt aaaagcctat acccgttacc aattaagagg gtatatcgaa	2400
gatagtcaag acttagaaat ctatttaatt cgctacaatg ccaaacacga aacagtaa	2460
gtgccaggta cgggttcctt atggccgctt tcagcccca gtccaatcgg aaaatgtgcc	2520
catcattccc atcatttctc cttggacatt gatgttggat gtacagactt aaatgaggac	2580
ttaggtgtat gggatgatatt caagattaag acgcaagatg gccatgcaag actaggaa	2640
ctagaatttc tcgaagagaa accattagta ggagaagcac tagctcgtgt gaaaagagcg	2700
gagaaaaaat ggagagacaa acgtgaaaaa ttggaatggg aaacaaatat tgtttataaa	2760
gaggcaaaaag aatctgtaga tgctttatct gttaaactctc aatatgatag attacaagcg	2820
gataccaaca tcgcgatgat tcatgcggca gataaacgcg ttcatagcat tcgagaagct	2880
tatctgcctg agctgtctgt gattccgggt gtcaatgcgg ctatTTTTTga agaattagaa	2940
gggcgtatTTT tactgcatt ctccctatat gatgcgagaa atgtcattaa aaatggtgat	3000

tttaataatg gcttatcctg ctggaacgtg aaagggcatg tagatgtaga agaacaaaac	3060
aaccaccgtt cggctccttgt tgttccggaa tgggaagcag aagtgtcaca agaagttcgt	3120
gtctgtccgg gtcgtggcta tatccttcgt gtcacagcgt acaaggaggg atatggagaa	3180
ggttgcgtaa ccattcatga gatcgagaac aatacagacg aactgaagtt tagcaactgt	3240
gtagaagagg aagtatatcc aaacaacacg gtaacgtgta atgattatac tgcgactcaa	3300
gaagaatatg aggggtacgta cacttctcgt aatcgaggat atgacggagc ctatgaaagc	3360
aattcttctg taccagctga ttatgcatca gcctatgaag aaaaagcata tacagatgga	3420
cgaagagaca atccttgtga atctaacaga ggatatgggg attacacacc actaccagct	3480
ggctatgtga caaaagaatt agagtacttc ccagaaaccg ataaggtatg gattgagatc	3540
ggagaaacgg aaggaacatt catcgtggac agcgtggaat tacttcttat ggaggaatag	3600

<210> 27
 <211> 3600
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC868.

<400> 27	
atgacgagca accggaagaa cgagaacgag atcatcaacg ccctctcgat ccctgctgtt	60
tcaaaccact ccgcgcagat gaacctgtcc accgacgcgc gcatcgagga ctccctctgc	120
atagccgagg gcaacaacat cgaccattc gtgtcggcca gcacggttca gaccggcatc	180
aacatcgcgg gccgtatcct cggcgtcctc ggtgtcccat tcgccggtca gatcgcgctc	240
ttctactcgt tccttgtggg cgagctgtgg cctcgcggtc gtgacccgtg ggagatcttc	300
ctggagcatg tggagcagtt gatccggcag caagtcacgg agaacacccg cgatactgct	360
ctggccaggc tacagggcct gggaaactcc tttcgggcat accagcagtc actggaggac	420
tggttggaga acagggatga cgcgcaaca cgctcggtac tctacacca gtacatcgct	480
ctcgaactcg acttcctgaa cgctatgccg ctgttcgcca tcaggaacca ggaagttcca	540

ctccttatgg tgtacgcca ggccgccaac ttacatctgc tcctgctgcg ggacgccagc	600
ctgttcgggt ccgagttcgg actcacatct caagaaatcc agcgttacta cgagcgccaa	660
gtggagaaga cccgtgagta cagtgactac tgcgctcgat ggtacaacac agggctcaac	720
aacctgcgcg gcaccaacgc tgagtcattg ctccgttaca accagttccg ccgcgacttg	780
actttgggtg tcctagacct ggtggcgcta ttcccgctt acgacacacg ggtgtacca	840
atgaacacta gcgcgcaact cacgcgggag atctacacag acccaatcgg ccggacgaac	900
gcaccctccg gtttcgcatt cacgaattgg ttcaacaaca acgcaccctc cttctcggca	960
atcgaggccg ccgtcattcc cctcctcac ctgctcgact ttcccagca gctcacgatt	1020
ttctccgtgc tctcacgtg gtccaacaca cagtacatga actactgggt cgggcaccga	1080
ttggagagta ggacgatccg tggcagcttg agcaccagta cccacggcaa caccaacacc	1140
tccatcaacc cagttacgt acagttcacg agccgcgacg tttaccggac tgagtcgttc	1200
gcgggcatta acatccttct gacaacgccc gtcaacggcg tcccgtgggc ccggttcaac	1260
tggcgtaacc cgttgaactc cctgcgcggg tcattgctct acaccatcgg gtacacgggc	1320
gtcggcacc agctcttcga cagtgaact gagctgccgc ccgagaccac ggaacgcccg	1380
aactacgagt cctacagcca ccgcctgtcc aacatccggc tcatctctgg caacacgtg	1440
cgtgcgccg tgtactcctg gacacaccgc agcgccgacc ggaccaacac gatctcttcc	1500
gactccatta accagatccc gctcgtgaag ggcttccgtg tgtgggggtg cacgagcgtc	1560
atcaccggtc cgggcttcac cggaggagac atactgcggc gcaaaccttt cggcgacttc	1620
gtttcgttg aagtgaacat caactcgccg atcaccagc gttaccgtct gaggttccgc	1680
tacgcttcaa gccgcgacgc gagggtcatt gtcctgaccg gagccgcgtc cacaggcgtg	1740
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actagccgaa ctttccggt cactgatttc tcgaaccctt tctcattcag agcgaaccct	1860
gacatcatt ggatctccga gcaaccgctg ttcgggtgct gctccatcag ctctggcgaa	1920
ctgtacatcg acaagattga gatcatcctg gcggatgcga cgttcgaggc cgagtctgac	1980
ctggagcggg ctcaagaagg tgtcaacgaa ctgttcacca gcagcaacca gattgggctc	2040

aagaccgacg tcacggacta tcacattgac caagtgtcca accttgtgga gtgcctgtcc	2100
gacgagttct gcctcgacga gaagaaggag ctgtccgaga aggtcaaaca cgcgaagcgt	2160
ctgagtgacg agcgggaattt gctccaggac ccgaacttcc gtggcatcaa ccgccagctc	2220
gaccgtgggtt ggcgcgggag tacagacatc accatccagg gaggcgacga tgtgttcaag	2280
gagaactatg tgacgtgct cgggactttc gacgaatgct acccgacgta tctctaccag	2340
aagatagacg agagtaaatt gaaggcgta acccgctacc agcttcgcgg gtacatcgag	2400
gatagtcagg acctggaaat ctacctgatc cgatacaacg ccaagcacga gacagtgaac	2460
gtgccaggca cgggctcact ttggccattg agcgctccct ctccaatcgg aaagtgcgct	2520
caccactcgc accacttctc tctggacatc gacgtgggct gcaccgacct caacgaggac	2580
ctgggtgtct gggttatctt caagattaag acccaggacg gacatgcccc cctcggcaac	2640
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gagaagaaat ggcgagacaa gcgggagaag ctggagtggg agaccaacat cgtgtacaag	2760
gaggccaagg agtcagtgga cgcactcttc gtcaacagcc agtacgaccg cctccaggct	2820
gacaccaaca tcgccatgat ccacgcggct gacaagcggg tccacagcat ccgtgaggcg	2880
tacctgcccc agctgtcagt gatccctggg gtgaacgcgg cgatcttcga ggaactggag	2940
ggccgcatct tcacagcatt cagcctgtac gatgccagga atgttattaa gaacggtgac	3000
ttcaacaacg ggctgagttg ctggaacgtc aagggccatg tggacgtcga ggagcagaac	3060
aaccaccggt ccgtgctggt cgtgccggag tgggaggcag aggtgagcca ggagggtccgc	3120
gtctgccctg gtcgcggcta catcctccgt gtgactgcgt acaaggaagg ctacggtgaa	3180
ggctgcgtga ctatccacga gatcgagaac aacaccgacg agctcaagtt ctcgaactgt	3240
gtggaggagg aggtgtaccc gaacaacacc gttacttgca acgactacac tgccacgcaa	3300
gaggagtacg agggcactta cacttcccgg aatcgcggct atgatggcgc gtacgagtcc	3360
aacagcagcg tgcctgcgga ttatgcgtcc gcttacgagg agaaggcgta caccgacgga	3420
cggagggaca acccttgcca gtccaaccgt ggctacggtg actacactcc gctgccccgcc	3480
gggtacgtca ccaaggagct ggagtacttc ccggagaccg acaaagtctg gatcgagatc	3540

ggcgagacgg agggcacttt catcgtggac tcggtcgagc tgctactgat ggaggagtga 3600

<210> 28
<211> 1199
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of the chimeric protein TIC868.

<400> 28

Met Thr Ser Asn Arg Lys Asn Glu Asn Glu Ile Ile Asn Ala Leu Ser
1 5 10 15

Ile Pro Ala Val Ser Asn His Ser Ala Gln Met Asn Leu Ser Thr Asp
20 25 30

Ala Arg Ile Glu Asp Ser Leu Cys Ile Ala Glu Gly Asn Asn Ile Asp
35 40 45

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

Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Ile Ala Ser
65 70 75 80

Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Arg Gly Arg Asp Pro
85 90 95

Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln Val
100 105 110

Thr Glu Asn Thr Arg Asp Thr Ala Leu Ala Arg Leu Gln Gly Leu Gly
115 120 125

Asn Ser Phe Arg Ala Tyr Gln Gln Ser Leu Glu Asp Trp Leu Glu Asn
130 135 140

Arg Asp Asp Ala Arg Thr Arg Ser Val Leu Tyr Thr Gln Tyr Ile Ala

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

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

Ser Leu Ser Thr Ser Thr His Gly Asn Thr Asn Thr Ser Ile Asn Pro
370 375 380

Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu Ser Phe
385 390 395 400

Ala Gly Ile Asn Ile Leu Leu Thr Thr Pro Val Asn Gly Val Pro Trp
405 410 415

Ala Arg Phe Asn Trp Arg Asn Pro Leu Asn Ser Leu Arg Gly Ser Leu
420 425 430

Leu Tyr Thr Ile Gly Tyr Thr Gly Val Gly Thr Gln Leu Phe Asp Ser
435 440 445

Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn Tyr Glu Ser
450 455 460

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

Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp Arg Thr Asn
485 490 495

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

Arg Val Trp Gly Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly
515 520 525

Gly Asp Ile Leu Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln
530 535 540

Val Asn Ile Asn Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg

545		550		555		560									
Tyr	Ala	Ser	Ser	Arg	Asp	Ala	Arg	Val	Ile	Val	Leu	Thr	Gly	Ala	Ala
				565					570					575	
Ser	Thr	Gly	Val	Gly	Gly	Gln	Val	Ser	Val	Asn	Met	Pro	Leu	Gln	Lys
			580					585					590		
Thr	Met	Glu	Ile	Gly	Glu	Asn	Leu	Thr	Ser	Arg	Thr	Phe	Arg	Tyr	Thr
		595					600					605			
Asp	Phe	Ser	Asn	Pro	Phe	Ser	Phe	Arg	Ala	Asn	Pro	Asp	Ile	Ile	Gly
	610						615				620				
Ile	Ser	Glu	Gln	Pro	Leu	Phe	Gly	Ala	Gly	Ser	Ile	Ser	Ser	Gly	Glu
625					630					635					640
Leu	Tyr	Ile	Asp	Lys	Ile	Glu	Ile	Ile	Leu	Ala	Asp	Ala	Thr	Phe	Glu
				645					650					655	
Ala	Glu	Ser	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val	Asn	Glu	Leu	Phe
			660					665					670		
Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val	Thr	Asp	Tyr	His
			675				680					685			
Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser	Asp	Glu	Phe	Cys
	690					695					700				
Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys	His	Ala	Lys	Arg
705					710					715					720
Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	Phe	Arg	Gly	Ile
				725					730					735	
Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	Asp	Ile	Thr	Ile
			740					745					750		

Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Leu Gly
755 760 765

Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu
770 775 780

Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu
785 790 795 800

Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His
805 810 815

Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala
820 825 830

Pro Ser Pro Ile Gly Lys Cys Ala His His Ser His His Phe Ser Leu
835 840 845

Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp
850 855 860

Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn
865 870 875 880

Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg
885 890 895

Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu
900 905 910

Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala
915 920 925

Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile
930 935 940

Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala

945	950	955	960
Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe	965	970	975
Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala	980	985	990
Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp	995	1000	1005
Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg	1010	1015	1020
Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu	1025	1030	1035
Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala	1040	1045	1050
Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile	1055	1060	1065
Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu	1070	1075	1080
Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Ala	1085	1090	1095
Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly	1100	1105	1110
Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser Val Pro Ala Asp Tyr	1115	1120	1125
Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr Asp Gly Arg Arg Asp	1130	1135	1140

Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu
 1145 1150 1155

Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr
 1160 1165 1170

Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile
 1175 1180 1185

Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
 1190 1195

<210> 29

<211> 3600

<212> DNA

<213> Artificial

<220>

<223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC868_9.

<400> 29

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<212> PRT

<213> Artificial

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<223> Amino acid sequence of the chimeric protein variant TIC868_9.

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Ile Pro Ala Val Ser Asn His Ser Ala Gln Met Asn Leu Ser Thr Asp
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Ala Arg Ile Glu Asp Ser Leu Cys Ile Ala Glu Gly Asn Asn Ile Asp
35 40 45

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

Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Ile Ala Ser
65 70 75 80

Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Arg Gly Arg Asp Pro
85 90 95

Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln Val
100 105 110

Thr Glu Asn Thr Arg Asp Thr Ala Leu Ala Arg Leu Gln Gly Leu Gly
115 120 125

Asn Ser Phe Arg Ala Tyr Gln Gln Ser Leu Glu Asp Trp Leu Glu Asn
130 135 140

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

Leu Glu Leu Asp Phe Leu Asn Ala Met Pro Leu Phe Ala Ile Arg Asn
165 170 175

Gln Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His
180 185 190

Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe Gly Ser Glu Phe Gly Leu
195 200 205

Thr Ser Gln Glu Ile Gln Arg Tyr Tyr Glu Arg Gln Val Glu Lys Thr
210 215 220

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

Ser Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln Phe
245 250 255

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

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

Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser Gly
290 295 300

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

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

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

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

Ser Leu Ser Thr Ser Thr His Gly Asn Thr Asn Thr Ser Ile Asn Pro
370 375 380

Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu Ser Gln
385 390 395 400

Ala Gly Ile Asn Ile Leu Met Thr Thr Pro Val Asn Gly Val Pro Trp
405 410 415

Ala Arg Phe Asn Trp Arg Asn Pro Lys Asn Ser Leu Arg Gly Ser Leu
420 425 430

Leu Tyr Thr Ile Gly Tyr Thr Gly Val Gly Thr Gln Leu Phe Asp Ser
435 440 445

Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn Tyr Glu Ser
450 455 460

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

Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp Arg Thr Asn
485 490 495

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

Arg Val Trp Gly Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly
515 520 525

Gly Asp Ile Leu Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln
530 535 540

Val Asn Ile Asn Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg
545 550 555 560

Tyr Ala Ser Ser Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala
565 570 575

Ser Thr Gly Val Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys
580 585 590

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595 600 605

Asp Phe Ser Asn Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly
610 615 620

Ile Ser Glu Gln Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu
625 630 635 640

Leu Tyr Ile Asp Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu
645 650 655

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660 665 670

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

Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser Asp Glu Phe Cys
690 695 700

Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg
705 710 715 720

Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile
725 730 735

Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile
740 745 750

Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Leu Gly
755 760 765

Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu
770 775 780

Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu
785 790 795 800

Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His
805 810 815

Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala
820 825 830

Pro Ser Pro Ile Gly Lys Cys Ala His His Ser His His Phe Ser Leu
835 840 845

Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp
850 855 860

Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn
865 870 875 880

Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg
885 890 895

Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu
900 905 910

Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala
915 920 925

Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile
930 935 940

Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala
945 950 955 960

Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe
965 970 975

Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala
980 985 990

Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp
995 1000 1005

Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg
1010 1015 1020

Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu
1025 1030 1035

Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala
1040 1045 1050

Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile
1055 1060 1065

Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu
1070 1075 1080

Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Ala
1085 1090 1095

Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly
1100 1105 1110

Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser Val Pro Ala Asp Tyr
1115 1120 1125

Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr Asp Gly Arg Arg Asp
1130 1135 1140

Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu
1145 1150 1155

Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr
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Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile
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Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
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 <212> DNA
 <213> Artificial

<220>
 <223> Recombinant nucleotide sequence used for expression in a
 bacterial cell encoding TIC868_10.

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<210> 32
 <211> 3678
 <212> DNA

<213> Artificial

<220>

<223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC868_10.

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Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Ile Ala Ser
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Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Arg Gly Arg Asp Pro
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Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln Val
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Thr Glu Asn Thr Arg Asp Thr Ala Leu Ala Arg Leu Gln Gly Leu Gly
115 120 125

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

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

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Gln Leu Thr Ile Phe Ser Val Leu Ser Arg Trp Ser Asn Thr Gln Tyr
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Met Asn Tyr Trp Val Gly His Arg Leu Glu Ser Arg Thr Ile Arg Gly
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Ala Arg Phe Asn Trp Arg Asn Pro Leu Asn Ser Leu Arg Gly Ser Leu
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Leu Tyr Thr Ile Gly Tyr Thr Gly Val Gly Thr Gln Leu Phe Asp Ser
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Tyr Ser His Arg Leu Ser Asn Ile Arg Leu Ile Ser Gly Asn Thr Leu
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Arg Val Trp Gly Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly
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Gly Asp Ile Leu Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln
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Val Asn Ile Asn Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg
545 550 555 560

Tyr Ala Ser Ser Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala
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580 585 590

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675 680 685

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690 695 700

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Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile
725 730 735

Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile
740 745 750

Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly
755 760 765

Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu
770 775 780

Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu
785 790 795 800

Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His
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820 825 830

Glu Asn Gln Ile Gly Pro Cys Gly Glu Pro Asn Arg Cys Ala Pro His
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Leu Glu Trp Asn Pro Asp Leu His Cys Ser Cys Arg Asp Gly Glu Lys
850 855 860

Cys Ala His His Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys
865 870 875 880

Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys
885 890 895

Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu
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Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys
915 920 925

Lys Trp Arg Asp Lys Arg Glu Thr Leu Gln Leu Glu Thr Thr Ile Val
930 935 940

Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln
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Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met Ile His Ala Ala
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Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser
980 985 990

Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Glu Arg
995 1000 1005

Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn Ile Ile Lys
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Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn Val Lys Gly
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His Val Glu Val Glu Glu Gln Asn Asn His Arg Ser Val Leu Val
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Ile Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys
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Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly
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Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr
1085 1090 1095

Asp Glu Leu Lys Phe Asn Asn Cys Val Glu Glu Glu Val Tyr Pro
1100 1105 1110

Asn Asn Thr Val Thr Cys Ile Asn Tyr Thr Ala Thr Gln Glu Glu
1115 1120 1125

Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Glu Ala
1130 1135 1140

Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr
1145 1150 1155

Glu Glu Lys Ser Tyr Thr Asp Arg Arg Arg Glu Asn Pro Cys Glu
1160 1165 1170

Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
1175 1180 1185

Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp
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Glu Leu Leu Leu Met Glu Glu
1220 1225

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<213> Artificial

<220>
<223> Recombinant nucleotide sequence used for expression in a
bacterial cell encoding TIC868_11.

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<211> 3726

<212> DNA

<213> Artificial

<220>

<223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC868_11.

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<212> PRT

<213> Artificial

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<223> Amino acid sequence of the chimeric protein variant TIC868_11.

<400> 36

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

Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Arg Gly Arg Asp Pro
85 90 95

Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln Val
100 105 110

Thr Glu Asn Thr Arg Asp Thr Ala Leu Ala Arg Leu Gln Gly Leu Gly
115 120 125

Asn Ser Phe Arg Ala Tyr Gln Gln Ser Leu Glu Asp Trp Leu Glu Asn
130 135 140

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

Leu Glu Leu Asp Phe Leu Asn Ala Met Pro Leu Phe Ala Ile Arg Asn
165 170 175

Gln Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His
180 185 190

Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe Gly Ser Glu Phe Gly Leu
195 200 205

Thr Ser Gln Glu Ile Gln Arg Tyr Tyr Glu Arg Gln Val Glu Lys Thr
210 215 220

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

Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln Phe
245 250 255

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

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

Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser Gly
290 295 300

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

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

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

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

Ser Leu Ser Thr Ser Thr His Gly Asn Thr Asn Thr Ser Ile Asn Pro
370 375 380

Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu Ser Phe
385 390 395 400

Ala Gly Ile Asn Ile Leu Leu Thr Thr Pro Val Asn Gly Val Pro Trp
405 410 415

Ala Arg Phe Asn Trp Arg Asn Pro Leu Asn Ser Leu Arg Gly Ser Leu
420 425 430

Leu Tyr Thr Ile Gly Tyr Thr Gly Val Gly Thr Gln Leu Phe Asp Ser
435 440 445

Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn Tyr Glu Ser
450 455 460

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

Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp Arg Thr Asn
485 490 495

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

Arg Val Trp Gly Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly
515 520 525

Gly Asp Ile Leu Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln
530 535 540

Val Asn Ile Asn Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg
545 550 555 560

Tyr Ala Ser Ser Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala
565 570 575

Ser Thr Gly Val Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys
580 585 590

Thr Met Glu Ile Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr
595 600 605

Asp Phe Ser Asn Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly
610 615 620

Ile Ser Glu Gln Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu
625 630 635 640

Leu Tyr Ile Asp Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Gly Thr
645 650 655

Thr Thr Tyr Glu Tyr Glu Glu Lys Gln Asn Leu Glu Lys Ala Gln Lys
660 665 670

Ala Leu Asn Ala Leu Phe Thr Asp Gly Thr Asn Gly Tyr Leu Gln Met
675 680 685

Asp Ala Thr Asp Tyr Asp Ile Asn Gln Thr Ala Asn Leu Ile Glu Cys
690 695 700

Val Ser Asp Glu Leu Tyr Ala Lys Glu Lys Ile Val Leu Leu Asp Glu
705 710 715 720

Val Lys Tyr Ala Lys Arg Leu Ser Ile Ser Arg Asn Leu Leu Leu Asn
725 730 735

Asp Asp Leu Glu Phe Ser Asp Gly Phe Gly Glu Asn Gly Trp Thr Thr
740 745 750

Ser Asp Asn Ile Ser Ile Gln Ala Asp Asn Pro Leu Phe Lys Gly Asn
755 760 765

Tyr Leu Lys Met Phe Gly Ala Arg Asp Ile Asp Gly Thr Leu Phe Pro
770 775 780

Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Arg Leu Lys Pro Tyr Thr
785 790 795 800

Arg Tyr Arg Val Arg Gly Phe Val Gly Ser Ser Lys Asn Leu Lys Leu
805 810 815

Val Val Thr Arg Tyr Glu Lys Glu Ile Asp Ala Ile Met Asn Val Pro
820 825 830

Asn Asp Leu Ala His Met Gln Leu Asn Pro Ser Cys Gly Asp Tyr Arg
835 840 845

Cys Glu Ser Ser Ser Gln Phe Leu Val Asn Gln Val His Pro Thr Pro
850 855 860

Thr Ala Gly Tyr Ala Leu Asp Met Tyr Ala Cys Pro Ser Ser Ser Asp
865 870 875 880

Lys Lys His Ile Met Cys His Asp Arg His Pro Phe Asp Phe His Ile
885 890 895

Asp Thr Gly Glu Leu Asn Pro Asn Thr Asn Leu Gly Ile Asp Val Leu
900 905 910

Phe Lys Ile Ser Asn Pro Asn Gly Tyr Ala Thr Leu Gly Asn Leu Glu
915 920 925

Val Ile Glu Glu Gly Pro Leu Thr Asp Glu Ala Leu Val His Val Lys
930 935 940

Gln Lys Glu Lys Lys Trp Arg Gln His Met Glu Lys Lys Arg Met Glu
945 950 955 960

Thr Gln Gln Ala Tyr Asp Pro Ala Lys Gln Ala Val Asp Ala Leu Phe
965 970 975

Thr Asn Glu Gln Glu Leu Asp Tyr His Thr Thr Leu Asp His Ile Gln
980 985 990

Asn Ala Asp Gln Leu Val Gln Ala Ile Pro Tyr Val His His Ala Trp
995 1000 1005

Leu Pro Asp Ala Pro Gly Met Asn Tyr Asp Val Tyr Gln Gly Leu
1010 1015 1020

Asn Ala Arg Ile Met Gln Ala Tyr Asn Leu Tyr Asp Ala Arg Asn
1025 1030 1035

Val Ile Ile Asn Gly Asp Phe Thr Gln Gly Leu Gln Gly Trp His
1040 1045 1050

Ala Thr Gly Lys Ala Ala Val Gln Gln Ile Asp Gly Ala Ser Val
1055 1060 1065

Leu Val Leu Ser Asn Trp Ser Ala Glu Val Ser Gln Asn Leu His
1070 1075 1080

Ala Gln Asp His His Gly Tyr Met Leu Arg Val Ile Ala Lys Lys
1085 1090 1095

Glu Gly Pro Gly Lys Gly Tyr Val Met Met Met Asp Phe Asn Gly
1100 1105 1110

Lys Gln Glu Thr Leu Thr Phe Thr Ser Cys Glu Glu Gly Tyr Ile
1115 1120 1125

Thr Lys Thr Ile Glu Val Phe Pro Glu Ser Asp Arg Ile Arg Ile
1130 1135 1140

Glu Met Gly Glu Thr Glu Gly Thr Phe Tyr Val Asp Ser Ile Glu
1145 1150 1155

Leu Leu Cys Met Gln Gly Tyr Ala Ser Asp Asn Asn Pro His Thr
1160 1165 1170

Gly Asn Met Tyr Glu Gln Ser Tyr Asn Gly Asn Tyr Asn Gln Asn
1175 1180 1185

Thr Ser Asp Val Tyr His Gln Gly Tyr Ile Asn Asn Tyr Asn Gln
1190 1195 1200

Asn Ser Ser Ser Met Tyr Asn Gln Asn Tyr Ile Asn Asn Asp Asp
1205 1210 1215

Leu His Ser Gly Cys Thr Cys Asn Gln Gly His Asn Ser Gly Cys
1220 1225 1230

Thr Cys Asn Gln Gly Tyr Asn Arg
1235 1240

<210> 37
<211> 3468
<212> DNA
<213> Artificial

<220>
<223> Recombinant nucleotide sequence used for expression in a
bacterial cell encoding TIC868_12.

<400> 37
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tcgaatcatt ccgcacaaat gaatctatca accgatgctc gtattgagga tagcttgtgt 120
atagccgagg ggaacaatat cgatccattt gttagcgcac caacagtcca aacgggtatt 180
aacatagctg gtagaatact aggtgtatta ggcgtagcgt ttgctggaca aatagctagt 240
ttttatagtt ttcttggttg tgaattatgg ccccgaggca gagatccttg ggaaattttc 300
ctagaacatg tcgaacaact tataagacaa caagtaacag aaaataactag ggatacggct 360
cttgctcgat tacaagggtt aggaaattcc tttagagcct atcaacagtc acttgaagat 420
tggctagaaa accgtgatga tgcaagaacg agaagtgttc ttatatacca atatatagcc 480
ttagaacttg attttcttaa tgcgatgccg cttttcgcaa ttagaaacca agaagttcca 540
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ctttttggta gtgaatttgg gcttacatcc caagaaattc aacgttatta tgagcgccaa 660
gtggaaaaaa cgagagaata ttctgattat tgcgcaagat ggtataatac gggtttaaata 720
aatgtgagag ggacaaatgc tgaaagttag ttgcgatata atcaattccg tagagactta 780
acgctaggag tattagatct agtggcacta ttccaagct atgacacgcg tgtttatcca 840
atgaatacca gtgctcaatt aacaagagaa atttatacag atccaattgg gagaacaaat 900
gcaccttcag gatttgcaag tacgaattgg ttaataata atgcaccatc gttttctgcc 960
atagaggctg ccgttattag gcctccgcat ctacttgatt ttccagaaca gcttacaatt 1020
ttcagcgtat taagtcgatg gagtaatact caatatatga attactgggt gggacataga 1080

cttgaatcgc gaacaataag ggggtcatta agtacctcga cacacggaaa taccaatact	1140
tctattaatc ctgtaacatt acagttcaca tctcgagacg tttatagaac agaatcattt	1200
gcagggataa atatacttct aactactcct gtgaatggag taccttgggc tagatttaat	1260
tggagaaatc ccctgaattc tcttagaggt agccttctct atactatagg gtatactgga	1320
gtggggacac aactatttga ttcagaaact gaattaccac cagaaacaac agaacgacca	1380
aattatgaat cttacagtca tagattatct aatataagac taatatcagg aaacactttg	1440
agagcaccag tatattcttg gacgcaccgt agtgcagatc gtacaaatac cattagttca	1500
gatagcatta atcaaatacc tttagtgaag ggatttagag tttggggggg cacctctgtc	1560
attacaggac caggatttac aggaggggat atccttcgaa gaaatacctt tgggtgattt	1620
gtatctctac aagtcaatat taattcacca attacccaaa gataccgttt aagatttcgt	1680
tacgcttcca gtagggatgc acgagttata gtattaacag gagcggcatc cacaggagt	1740
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gatataattg ggataagtga acaacctcta tttggtgcag gttctattag tagcggtgaa	1920
ctttatatag ataaaattga aattattcta gcagatgcaa caaatccgac gcgagaggcg	1980
gaagaggatc tagaagcagc gaagaaaagcg gtggcgagct tgtttacacg tacaagggac	2040
ggattacaag taaatgtgac agattatcaa gtcgatcaag cggcaaattt agtgtcatgc	2100
ttatcagatg aacaatatgg gcatgacaaa aagatgttat tggaagcggg aagagcggca	2160
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acagaagaaa atggatggaa agcaagtaac ggcgttacta ttagcgaggg cgggccattc	2280
tataaaggcc gtgcgcttca gctagcaagc gcaagagaaa attacccaac atacatttat	2340
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aagagtagtc aagatttaga aattgatctc attcaccatc ataaagtcca tctcgtgaaa	2460
aatgtaccag ataatttagt atccgatact tactcggatg gttcttgagc tggaatgaat	2520
cgatgtgagg aacaacagat ggtaaatgcg caactggaaa cagaacatca tcatccgatg	2580

gattgctgtg aagcggctca aacacatgag ttttcttcct atattaatac aggcgatcta	2640
aattcaagtg tagatcaagg catttgggtt gtattgaaag ttcgaacaac cgatgggtat	2700
gcgacgctag gaaatcttga attggtagag gtcggaccgt tatcgggtga atctctagaa	2760
cgtgaacaaa gggataatgc gaaatggagt gcagagctag gaagaaagcg tgcagaaaca	2820
gatcgcgtgt atcaagatgc caaacaatcc atcaatcatt tatttgtgga ttatcaagat	2880
caacaattaa atccagaaat agggatggca gatattattg acgctcaaaa tcttgtcgca	2940
tcaatttcag atgtgtatag cgatgcagta ctgcaaatcc ctggaattaa ctatgagatt	3000
tacacagagc tatccaatcg cttacaacaa gcatcgtatc tgtatacgtc tcgaaatgcg	3060
gtgcaaaatg gggacttta cagcgggtcta gatagttgga atgcaacagg gggggctacg	3120
gtacaacagg atggcaatac gcatttctta gttctttctc attgggatgc acaagtttct	3180
caacaattta gagtgcagcc gaattgtaaa tatgtattac gtgtaacagc agagaaagta	3240
ggcggcggag acggatacgt gacaatccgg gatggtgctc atcatacaga aaagcttaca	3300
tttaatgcat gtgattatga tataaatggc acgtacgtga ctgataatac gtatctaaca	3360
aaagaagtgg tattctattc acatacagaa cacatgtggg tagaggtaag tgaaacagaa	3420
ggtgcatttc atatagatag tattgaattc gttgaaacag aaaagtag	3468

<210> 38

<211> 3468

<212> DNA

<213> Artificial

<220>

<223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC868_12.

<400> 38

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atagccgagg gcaacaacat cgaccattc gtgtcggcca gcacggttca gaccggcatc	180
aacatcgcg ggcgtatcct cggcgtcctc ggtgtcccat tcgccggtca gatcgcgtcc	240
ttctactcgt tccttgtggg cgagctgtgg cctcgcggtc gtgaccggtg ggagatcttc	300

ctggagcatg tggagcagtt gatccggcag caagtcacgg agaacacccg cgatactgct	360
ctggccaggc tacagggcct gggaaactcc tttcgggcat accagcagtc actggaggac	420
tggttggaga acagggatga cgcgcgaaca cgctcggtag tctacaccca gtacatcgct	480
ctcgaactcg acttcctgaa cgctatgccg ctgttcgcca tcaggaacca ggaagttcca	540
ctccttatgg tgtacgcca ggccgccaac ttacatctgc tcctgctgcg ggacgccagc	600
ctgttcggct ccgagttcgg actcacatct caagaaatcc agcgttacta cgagcgccaa	660
gtggagaaga cccgtgagta cagtgactac tgcgctcgat ggtacaacac agggctcaac	720
aacctgcgcg gcaccaacgc tgagtcatgg ctccgttaca accagttccg ccgcgacttg	780
actttgggtg tcctagacct ggtggcgcta ttcccgctt acgacacacg ggtgtacca	840
atgaacacta gcgcgcaact cacgcgggag atctacacag acccaatcgg ccggacgaac	900
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aactacgagt cctacagcca ccgcctgtcc aacatccggc tcatctctgg caacacgctg	1440
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gactccatta accagatccc gctcgtgaag ggcttccgtg tgtgggggtgg cacgagcgtc	1560
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tacacagagt tgtccaacag gctccagcaa gcgtcatacc tctacaccag ccgcaacgcc	3060
gtccagaatg gcgacttcaa ttccggacta gactcctgga acgccacggg cggagctacg	3120
gtgcaacaag acggcaacac ccacttcctc gtacttagcc actgggacgc tcaagtgagt	3180
cagcaattcc gggttcagcc gaactgcaag tacgtcctgc gcgtaacggc cgagaagggt	3240
ggaggcggag acggctacgt taccatccgc gacggcgctc accacaccga gaaactgacg	3300

ttcaacgctt gtgactacga catcaacggc acttacgtga cggacaacac ctacctgacg 3360
aaggagggtgg tgttctattc tcacaccgag cacatgtggg ttgaggtcag cgagaccgag 3420
ggagccttcc acattgacag catcgagttc gtggagactg agaagtga 3468

<210> 39
<211> 1155
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of the chimeric protein variant TIC868_12.

<400> 39

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Ile Pro Ala Val Ser Asn His Ser Ala Gln Met Asn Leu Ser Thr Asp
20 25 30

Ala Arg Ile Glu Asp Ser Leu Cys Ile Ala Glu Gly Asn Asn Ile Asp
35 40 45

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

Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Ile Ala Ser
65 70 75 80

Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Arg Gly Arg Asp Pro
85 90 95

Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln Val
100 105 110

Thr Glu Asn Thr Arg Asp Thr Ala Leu Ala Arg Leu Gln Gly Leu Gly
115 120 125

Asn Ser Phe Arg Ala Tyr Gln Gln Ser Leu Glu Asp Trp Leu Glu Asn
130 135 140

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

Leu Glu Leu Asp Phe Leu Asn Ala Met Pro Leu Phe Ala Ile Arg Asn
165 170 175

Gln Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His
180 185 190

Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe Gly Ser Glu Phe Gly Leu
195 200 205

Thr Ser Gln Glu Ile Gln Arg Tyr Tyr Glu Arg Gln Val Glu Lys Thr
210 215 220

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

Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln Phe
245 250 255

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

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

Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser Gly
290 295 300

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

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

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

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

Ser Leu Ser Thr Ser Thr His Gly Asn Thr Asn Thr Ser Ile Asn Pro
370 375 380

Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu Ser Phe
385 390 395 400

Ala Gly Ile Asn Ile Leu Leu Thr Thr Pro Val Asn Gly Val Pro Trp
405 410 415

Ala Arg Phe Asn Trp Arg Asn Pro Leu Asn Ser Leu Arg Gly Ser Leu
420 425 430

Leu Tyr Thr Ile Gly Tyr Thr Gly Val Gly Thr Gln Leu Phe Asp Ser
435 440 445

Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn Tyr Glu Ser
450 455 460

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

Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp Arg Thr Asn
485 490 495

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

Arg Val Trp Gly Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly
515 520 525

Gly Asp Ile Leu Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln
530 535 540

Val Asn Ile Asn Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg
545 550 555 560

Tyr Ala Ser Ser Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala
565 570 575

Ser Thr Gly Val Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys
580 585 590

Thr Met Glu Ile Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr
595 600 605

Asp Phe Ser Asn Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly
610 615 620

Ile Ser Glu Gln Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu
625 630 635 640

Leu Tyr Ile Asp Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Asn Pro
645 650 655

Thr Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys Ala Val Ala
660 665 670

Ser Leu Phe Thr Arg Thr Arg Asp Gly Leu Gln Val Asn Val Thr Asp
675 680 685

Tyr Gln Val Asp Gln Ala Ala Asn Leu Val Ser Cys Leu Ser Asp Glu
690 695 700

Gln Tyr Gly His Asp Lys Lys Met Leu Leu Glu Ala Val Arg Ala Ala
705 710 715 720

Lys Arg Leu Ser Arg Glu Arg Asn Leu Leu Gln Asp Pro Asp Phe Asn
725 730 735

Thr Ile Asn Ser Thr Glu Glu Asn Gly Trp Lys Ala Ser Asn Gly Val
740 745 750

Thr Ile Ser Glu Gly Gly Pro Phe Tyr Lys Gly Arg Ala Leu Gln Leu
755 760 765

Ala Ser Ala Arg Glu Asn Tyr Pro Thr Tyr Ile Tyr Gln Lys Val Asn
770 775 780

Ala Ser Glu Leu Lys Pro Tyr Thr Arg Tyr Arg Leu Asp Gly Phe Val
785 790 795 800

Lys Ser Ser Gln Asp Leu Glu Ile Asp Leu Ile His His His Lys Val
805 810 815

His Leu Val Lys Asn Val Pro Asp Asn Leu Val Ser Asp Thr Tyr Ser
820 825 830

Asp Gly Ser Cys Ser Gly Met Asn Arg Cys Glu Glu Gln Gln Met Val
835 840 845

Asn Ala Gln Leu Glu Thr Glu His His His Pro Met Asp Cys Cys Glu
850 855 860

Ala Ala Gln Thr His Glu Phe Ser Ser Tyr Ile Asn Thr Gly Asp Leu
865 870 875 880

Asn Ser Ser Val Asp Gln Gly Ile Trp Val Val Leu Lys Val Arg Thr
885 890 895

Thr Asp Gly Tyr Ala Thr Leu Gly Asn Leu Glu Leu Val Glu Val Gly
900 905 910

Pro Leu Ser Gly Glu Ser Leu Glu Arg Glu Gln Arg Asp Asn Ala Lys
915 920 925

Trp Ser Ala Glu Leu Gly Arg Lys Arg Ala Glu Thr Asp Arg Val Tyr
930 935 940

Gln Asp Ala Lys Gln Ser Ile Asn His Leu Phe Val Asp Tyr Gln Asp
945 950 955 960

Gln Gln Leu Asn Pro Glu Ile Gly Met Ala Asp Ile Ile Asp Ala Gln
965 970 975

Asn Leu Val Ala Ser Ile Ser Asp Val Tyr Ser Asp Ala Val Leu Gln
980 985 990

Ile Pro Gly Ile Asn Tyr Glu Ile Tyr Thr Glu Leu Ser Asn Arg Leu
995 1000 1005

Gln Gln Ala Ser Tyr Leu Tyr Thr Ser Arg Asn Ala Val Gln Asn
1010 1015 1020

Gly Asp Phe Asn Ser Gly Leu Asp Ser Trp Asn Ala Thr Gly Gly
1025 1030 1035

Ala Thr Val Gln Gln Asp Gly Asn Thr His Phe Leu Val Leu Ser
1040 1045 1050

His Trp Asp Ala Gln Val Ser Gln Gln Phe Arg Val Gln Pro Asn
1055 1060 1065

Cys Lys Tyr Val Leu Arg Val Thr Ala Glu Lys Val Gly Gly Gly
1070 1075 1080

Asp Gly Tyr Val Thr Ile Arg Asp Gly Ala His His Thr Glu Lys
1085 1090 1095

Leu Thr Phe Asn Ala Cys Asp Tyr Asp Ile Asn Gly Thr Tyr Val
1100 1105 1110

Thr Asp Asn Thr Tyr Leu Thr Lys Glu Val Val Phe Tyr Ser His
1115 1120 1125

Thr Glu His Met Trp Val Glu Val Ser Glu Thr Glu Gly Ala Phe
1130 1135 1140

His Ile Asp Ser Ile Glu Phe Val Glu Thr Glu Lys
1145 1150 1155

<210> 40
<211> 3732
<212> DNA
<213> Artificial

<220>
<223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC868_13.

<400> 40
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aacatcgcgg gccgtatcct cggcgtcctc ggtgtcccat tcgccggtca gatcgcgctc 240
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gtgagccagg ccgtccgggt ctgccctggg cgcggttaca tcctccgcgt gacagcgtag	3300
aaggagggtc acggtgaggg ctgcgtgacg atccacgaga ttgagaacaa cacggacgag	3360
cttaagttca agaactgcga ggaggaggaa gtgtacccga cagacaccgg cacctgcaac	3420
gactacaccg cccaccaagg gaccgccgcc tgcaacagcc gcaacgcggg ctatgaagat	3480
gcgtacgagg ttgataccac cgcctcagtg aactacaaac cgacttatga ggaggagaca	3540
tacacggacg tcaggcgcga caaccattgt gagtacgacc gtggctacgt gaactatccg	3600
ccggtgccag cgggctacat gacgaaggag ctagaatact tccctgagac ggacaaggtg	3660
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atggaggagt ag	3732

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 <211> 1243
 <212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein variant TIC868_13.

<400> 41

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Ala Arg Ile Glu Asp Ser Leu Cys Ile Ala Glu Gly Asn Asn Ile Asp
35 40 45

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

Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Ile Ala Ser
65 70 75 80

Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Arg Gly Arg Asp Pro
85 90 95

Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln Val
100 105 110

Thr Glu Asn Thr Arg Asp Thr Ala Leu Ala Arg Leu Gln Gly Leu Gly
115 120 125

Asn Ser Phe Arg Ala Tyr Gln Gln Ser Leu Glu Asp Trp Leu Glu Asn
130 135 140

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

Leu Glu Leu Asp Phe Leu Asn Ala Met Pro Leu Phe Ala Ile Arg Asn
165 170 175

Gln Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His
180 185 190

Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe Gly Ser Glu Phe Gly Leu
195 200 205

Thr Ser Gln Glu Ile Gln Arg Tyr Tyr Glu Arg Gln Val Glu Lys Thr
210 215 220

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

Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln Phe
245 250 255

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

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

Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser Gly
290 295 300

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

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

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

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

Ser Leu Ser Thr Ser Thr His Gly Asn Thr Asn Thr Ser Ile Asn Pro

370

375

380

Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu Ser Phe
 385 390 395 400

Ala Gly Ile Asn Ile Leu Leu Thr Thr Pro Val Asn Gly Val Pro Trp
 405 410 415

Ala Arg Phe Asn Trp Arg Asn Pro Leu Asn Ser Leu Arg Gly Ser Leu
 420 425 430

Leu Tyr Thr Ile Gly Tyr Thr Gly Val Gly Thr Gln Leu Phe Asp Ser
 435 440 445

Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn Tyr Glu Ser
 450 455 460

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

Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp Arg Thr Asn
 485 490 495

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

Arg Val Trp Gly Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly
 515 520 525

Gly Asp Ile Leu Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln
 530 535 540

Val Asn Ile Asn Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg
 545 550 555 560

Tyr Ala Ser Ser Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala
 565 570 575

Ser Thr Gly Val Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys
580 585 590

Thr Met Glu Ile Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr
595 600 605

Asp Phe Ser Asn Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly
610 615 620

Ile Ser Glu Gln Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu
625 630 635 640

Leu Tyr Ile Asp Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Thr Ala
645 650 655

Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Glu Ala Val Asn
660 665 670

Ala Leu Phe Thr Asn Thr Asn Pro Arg Arg Leu Lys Thr Gly Val Thr
675 680 685

Asp Tyr His Ile Asp Glu Val Ser Asn Leu Val Ala Cys Leu Ser Asp
690 695 700

Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Leu Glu Lys Val Lys Tyr
705 710 715 720

Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe
725 730 735

Thr Ser Ile Asn Lys Gln Pro Asp Phe Ile Ser Thr Asn Glu Gln Ser
740 745 750

Asn Phe Thr Ser Ile His Glu Gln Ser Glu His Gly Trp Trp Gly Ser
755 760 765

Glu Asn Ile Thr Ile Gln Glu Gly Asn Asp Val Phe Lys Glu Asn Tyr

770

775

780

Val Ile Leu Pro Gly Thr Phe Asn Glu Cys Tyr Pro Thr Tyr Leu Tyr
 785 790 795 800

Gln Lys Ile Gly Glu Ala Glu Leu Lys Ala Tyr Thr Arg Tyr Gln Leu
 805 810 815

Ser Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg
 820 825 830

Tyr Asn Ala Lys His Glu Thr Leu Asp Val Pro Gly Thr Glu Ser Val
 835 840 845

Trp Pro Leu Ser Val Glu Ser Pro Ile Gly Arg Cys Gly Glu Pro Asn
 850 855 860

Arg Cys Ala Pro His Phe Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys
 865 870 875 880

Arg Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp
 885 890 895

Ile Asp Val Gly Cys Ile Asp Leu His Glu Asn Leu Gly Val Trp Val
 900 905 910

Val Phe Lys Ile Lys Thr Gln Glu Gly His Ala Arg Leu Gly Asn Leu
 915 920 925

Glu Phe Ile Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ser Arg Val
 930 935 940

Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Gln Leu
 945 950 955 960

Glu Thr Lys Arg Val Tyr Thr Glu Ala Lys Glu Ala Val Asp Ala Leu
 965 970 975

Phe Val Asp Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Gly
980 985 990

Met Ile His Ala Ala Asp Lys Leu Val His Arg Ile Arg Glu Ala Tyr
995 1000 1005

Leu Ser Glu Leu Ser Val Ile Pro Gly Val Asn Ala Glu Ile Phe
1010 1015 1020

Glu Glu Leu Glu Gly Arg Ile Ile Thr Ala Ile Ser Leu Tyr Asp
1025 1030 1035

Ala Arg Asn Val Val Lys Asn Gly Asp Phe Asn Asn Gly Leu Ala
1040 1045 1050

Cys Trp Asn Val Lys Gly His Val Asp Val Gln Gln Ser His His
1055 1060 1065

Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu Val Ser Gln
1070 1075 1080

Ala Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr
1085 1090 1095

Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu
1100 1105 1110

Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Lys Asn Cys Glu Glu
1115 1120 1125

Glu Glu Val Tyr Pro Thr Asp Thr Gly Thr Cys Asn Asp Tyr Thr
1130 1135 1140

Ala His Gln Gly Thr Ala Ala Cys Asn Ser Arg Asn Ala Gly Tyr
1145 1150 1155

Glu Asp Ala Tyr Glu Val Asp Thr Thr Ala Ser Val Asn Tyr Lys

1160

1165

1170

Pro Thr Tyr Glu Glu Glu Thr Tyr Thr Asp Val Arg Arg Asp Asn
 1175 1180 1185

His Cys Glu Tyr Asp Arg Gly Tyr Val Asn Tyr Pro Pro Val Pro
 1190 1195 1200

Ala Gly Tyr Met Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp
 1205 1210 1215

Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Lys Phe Ile Val
 1220 1225 1230

Asp Ser Val Glu Leu Leu Leu Met Glu Glu
 1235 1240

<210> 42
 <211> 3702
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC868_14.

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 aacatcgcg ggcgtatcct cggcgtcctc ggtgtcccat tcgccggtca gatcgcgctcc 240
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aaccgtgggt acgaagatgg atacgagaac cgctacgagc ccaatccttc ggctcccgtg	3480
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 ctggaatact ttcccagagac agaacaagtg tggatagaga tcggcgagac cgagggcaca 3660
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<210> 43
 <211> 1200
 <212> PRT
 <213> Artificial

<220>
 <223> Amino acid sequence of the chimeric protein variant TIC868_14.

<400> 43

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Ile Pro Ala Val Ser Asn His Ser Ala Gln Met Asn Leu Ser Thr Asp
 20 25 30

Ala Arg Ile Glu Asp Ser Leu Cys Ile Ala Glu Gly Asn Asn Ile Asp
 35 40 45

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

Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Ile Ala Ser
 65 70 75 80

Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Arg Gly Arg Asp Pro
 85 90 95

Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln Val
 100 105 110

Thr Glu Asn Thr Arg Asp Thr Ala Leu Ala Arg Leu Gln Gly Leu Gly
 115 120 125

Asn Ser Phe Arg Ala Tyr Gln Gln Ser Leu Glu Asp Trp Leu Glu Asn
130 135 140

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

Leu Glu Leu Asp Phe Leu Asn Ala Met Pro Leu Phe Ala Ile Arg Asn
165 170 175

Gln Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His
180 185 190

Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe Gly Ser Glu Phe Gly Leu
195 200 205

Thr Ser Gln Glu Ile Gln Arg Tyr Tyr Glu Arg Gln Val Glu Lys Thr
210 215 220

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

Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln Phe
245 250 255

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

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

Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser Gly
290 295 300

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

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

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

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

Ser Leu Ser Thr Ser Thr His Gly Asn Thr Asn Thr Ser Ile Asn Pro
370 375 380

Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu Ser Phe
385 390 395 400

Ala Gly Ile Asn Ile Leu Leu Thr Thr Pro Val Asn Gly Val Pro Trp
405 410 415

Ala Arg Phe Asn Trp Arg Asn Pro Leu Asn Ser Leu Arg Gly Ser Leu
420 425 430

Leu Tyr Thr Ile Gly Tyr Thr Gly Val Gly Thr Gln Leu Phe Asp Ser
435 440 445

Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn Tyr Glu Ser
450 455 460

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

Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp Arg Thr Asn
485 490 495

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

Arg Val Trp Gly Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly
515 520 525

Gly Asp Ile Leu Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln
530 535 540

Val Asn Ile Asn Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg
545 550 555 560

Tyr Ala Ser Ser Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala
565 570 575

Ser Thr Gly Val Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys
580 585 590

Thr Met Glu Ile Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr
595 600 605

Asp Phe Ser Asn Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly
610 615 620

Ile Ser Glu Gln Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu
625 630 635 640

Leu Tyr Ile Asp Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Thr Ala
645 650 655

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

Ala Leu Phe Thr Ser Thr Asn Pro Arg Gly Leu Lys Thr Asp Val Thr
675 680 685

Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser Asp
690 695 700

Glu Phe Cys Leu Asp Lys Lys Arg Glu Leu Leu Glu Glu Val Lys Tyr
705 710 715 720

Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Thr Phe
725 730 735

Thr Ser Ile Ser Gly Gln Thr Asp Arg Gly Trp Ile Gly Ser Thr Gly
740 745 750

Ile Ser Ile Gln Gly Gly Asp Asp Ile Phe Lys Glu Asn Tyr Val Arg
755 760 765

Leu Pro Gly Thr Val Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys
770 775 780

Ile Asp Glu Ser Gln Leu Lys Ser Tyr Thr Arg Tyr Gln Leu Arg Gly
785 790 795 800

Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn
805 810 815

Ala Lys His Glu Thr Leu Ser Val Pro Gly Thr Glu Ser Pro Trp Pro
820 825 830

Ser Ser Gly Val Tyr Pro Ser Gly Arg Cys Gly Glu Pro Asn Arg Cys
835 840 845

Ala Pro Arg Ile Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg Tyr
850 855 860

Gly Glu Lys Cys Val His His Ser His His Phe Ser Leu Asp Ile Asp
865 870 875 880

Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile Phe
885 890 895

Lys Ile Lys Thr Gln Asp Gly His Ala Lys Leu Gly Asn Leu Glu Phe
900 905 910

Ile Glu Glu Lys Pro Leu Leu Gly Lys Ala Leu Ser Arg Val Lys Arg
915 920 925

Ala Glu Lys Lys Trp Arg Asp Lys Tyr Glu Lys Leu Gln Leu Glu Thr
930 935 940

Lys Arg Val Tyr Thr Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val
945 950 955 960

Asp Ser Gln Tyr Asp Lys Leu Gln Ala Asn Thr Asn Ile Gly Ile Ile
965 970 975

His Gly Ala Asp Lys Gln Val His Arg Ile Arg Glu Pro Tyr Leu Ser
980 985 990

Glu Leu Pro Val Ile Pro Ser Ile Asn Ala Ala Ile Phe Glu Glu Leu
995 1000 1005

Glu Gly His Ile Phe Lys Ala Tyr Ser Leu Tyr Asp Ala Arg Asn
1010 1015 1020

Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn
1025 1030 1035

Val Lys Gly His Val Asp Val Gln Gln Asn His His Arg Ser Val
1040 1045 1050

Leu Val Leu Ser Glu Trp Glu Ala Glu Val Ser Gln Lys Val Arg
1055 1060 1065

Val Cys Pro Asp Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys
1070 1075 1080

Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Phe Glu Asp
1085 1090 1095

Asn Thr Asp Val Leu Lys Phe Arg Asn Phe Val Glu Glu Glu Val
1100 1105 1110

Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Thr Asn Gln
1115 1120 1125

Ser Ala Glu Gly Ser Thr Asp Ala Cys Asn Ser Tyr Asn Arg Gly
1130 1135 1140

Tyr Glu Asp Gly Tyr Glu Asn Arg Tyr Glu Pro Asn Pro Ser Ala
1145 1150 1155

Pro Val Asn Tyr Thr Pro Thr Tyr Glu Glu Gly Met Tyr Thr Asp
1160 1165 1170

Thr Gln Gly Tyr Asn His Cys Val Ser Asp Arg Gly Tyr Arg Asn
1175 1180 1185

His Thr Pro Leu Pro Ala Gly Tyr Val Thr Leu Glu
1190 1195 1200

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<211> 3687
<212> DNA
<213> Artificial

<220>
<223> Synthetic nucleotide sequence designed for expression in a plant
cell encoding TIC868_15.

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gcccgcaatg tcattaagaa tggcgacttc aacaatggct tactatgctg gaatgtcaaa	3120
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gaggccgaag tcagccagga agtccgcgtc tgtccagggc gcgggtacat cctgcgggtc	3240
accgcctaca aagagggata cggcgagggg tgtgtcacca tacacgagat agaggacaat	3300
accgacgaac tcaagttcag caattgtgtc gaggaggaag tctatcccaa caataccgta	3360
acctgcaaca actacaccgg aaccaggag gagtatgaag ggacgtacac ctcgcggaac	3420
cagggctatg acgaagccta tgggaacaac ccgtcggtgc ctgctgacta tgcgtcggtc	3480
tatgaggaga aatcgtacac ggacgggcgg cgggagaatc cgtgtgagtc gaatcgcggg	3540

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gagacggaca	aagtatggat	agagataggc	gagacggagg	gaacgttcat	cgtggactcg	3660
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<212>	PRT
<213>	Artificial

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<223> Amino acid sequence of the chimeric protein variant TIC868 15.

<400> 45

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Ile Pro Ala Val Ser Asn His Ser Ala Gln Met Asn Leu Ser Thr Asp
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Ala Arg Ile Glu Asp Ser Leu Cys Ile Ala Glu Gly Asn Asn Ile Asp
35 40 45

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

Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Ile Ala Ser
65 70 75 80

Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Arg Gly Arg Asp Pro
85 90 95

Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln Val
100 105 110

Thr Glu Asn Thr Arg Asp Thr Ala Leu Ala Arg Leu Gln Gly Leu Gly
115 120 125

Asn Ser Phe Arg Ala Tyr Gln Gln Ser Leu Glu Asp Trp Leu Glu Asn

130

135

140

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

Leu Glu Leu Asp Phe Leu Asn Ala Met Pro Leu Phe Ala Ile Arg Asn
 165 170 175

Gln Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His
 180 185 190

Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe Gly Ser Glu Phe Gly Leu
 195 200 205

Thr Ser Gln Glu Ile Gln Arg Tyr Tyr Glu Arg Gln Val Glu Lys Thr
 210 215 220

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

Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln Phe
 245 250 255

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

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

Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser Gly
 290 295 300

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

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

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

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

Ser Leu Ser Thr Ser Thr His Gly Asn Thr Asn Thr Ser Ile Asn Pro
370 375 380

Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu Ser Phe
385 390 395 400

Ala Gly Ile Asn Ile Leu Leu Thr Thr Pro Val Asn Gly Val Pro Trp
405 410 415

Ala Arg Phe Asn Trp Arg Asn Pro Leu Asn Ser Leu Arg Gly Ser Leu
420 425 430

Leu Tyr Thr Ile Gly Tyr Thr Gly Val Gly Thr Gln Leu Phe Asp Ser
435 440 445

Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn Tyr Glu Ser
450 455 460

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

Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp Arg Thr Asn
485 490 495

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

Arg Val Trp Gly Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly
515 520 525

Gly Asp Ile Leu Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln

530

535

540

Val Asn Ile Asn Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg
 545 550 555 560

Tyr Ala Ser Ser Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala
 565 570 575

Ser Thr Gly Val Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys
 580 585 590

Thr Met Glu Ile Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr
 595 600 605

Asp Phe Ser Asn Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly
 610 615 620

Ile Ser Glu Gln Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu
 625 630 635 640

Leu Tyr Ile Asp Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Asp Ala
 645 650 655

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

Ala Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val Thr
 675 680 685

Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Asp Cys Leu Ser Asp
 690 695 700

Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys His
 705 710 715 720

Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe
 725 730 735

Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr Asp
740 745 750

Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr
755 760 765

Leu Pro Gly Thr Val Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys
770 775 780

Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Glu Leu Arg Gly
785 790 795 800

Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn
805 810 815

Ala Lys His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro
820 825 830

Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys
835 840 845

Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp
850 855 860

Gly Glu Lys Cys Ala His His Ser His His Phe Thr Leu Asp Ile Asp
865 870 875 880

Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile Phe
885 890 895

Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe
900 905 910

Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys Arg
915 920 925

Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Gln Leu Glu Thr

930

935

940

Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val
 945 950 955 960

Asn Ser Gln Tyr Asp Arg Leu Gln Val Asp Thr Asn Ile Ala Met Ile
 965 970 975

His Ala Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu Pro
 980 985 990

Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu Leu
 995 1000 1005

Glu Gly Arg Ile Phe Thr Ala Tyr Ser Leu Tyr Asp Ala Arg Asn
 1010 1015 1020

Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn
 1025 1030 1035

Val Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser
 1040 1045 1050

Val Leu Val Ile Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val
 1055 1060 1065

Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr
 1070 1075 1080

Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu
 1085 1090 1095

Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu
 1100 1105 1110

Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly Thr
 1115 1120 1125

Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
1130 1135 1140

Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala
1145 1150 1155

Ser Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn
1160 1165 1170

Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro
1175 1180 1185

Ala Gly Tyr Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp
1190 1195 1200

Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val
1205 1210 1215

Asp Ser Val Glu Leu Leu Leu Met Glu Glu
1220 1225

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<211> 3600
<212> DNA
<213> Artificial

<220>
<223> Synthetic nucleotide sequence designed for expression in a plant
cell encoding TIC868_29.

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ctggagttcc ttgaggagaa gcctctcgtg ggcgaggccc tcgctcgtgt gaagcgcgcc	2700
gagaagaaat ggcgagacaa gcgggagaag ctggagtggg agaccaacat cgtgtacaag	2760
gaggccaagg agtcagtgga cgcactcttc gtcaacagcc agtacgaccg cctccaggct	2820
gacaccaaca tcgccatgat ccacgcggct gacaagcggg tccacagcat ccgtgaggcg	2880
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ggccgcatct tcacagcatt cagcctgtac gatgccagga atgttattaa gaacggtgac	3000
ttcaacaacg ggctgagttg ctggaacgtc aagggccatg tggacgtcga ggagcagaac	3060
aaccaccggt ccgtgctggt cgtgccggag tgggaggcag aggtgagcca ggaggtccgc	3120
gtctgccctg gtcgcggcta catcctccgt gtgactgcgt acaaggaagg ctacggtgaa	3180
ggctgcgtga ctatccacga gatcgagaac aacaccgacg agctcaagtt ctcgaactgt	3240
gtggaggagg aggtgtaccc gaacaacacc gttacttgca acgactacac tgccacgcaa	3300
gaggagtacg agggcactta cacttcccgg aatcgcggct atgatggcgc gtacgagtcc	3360

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aacagcagcg tgcctgcgga ttatgcgtcc gcttacgagg agaaggcgta caccgacgga      3420
cggaggggaca acccttgcga gtccaaccgt ggctacgggtg actacactcc gctgcccgcc      3480
gggtacgtca ccaaggagct ggagtacttc ccggagaccg acaaagtctg gatcgagatc      3540
ggcgagacgg agggcacttt catcgtggac tcggtcgagc tgctactgat ggaggagtga      3600

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<210> 47
<211> 1199
<212> PRT
<213> Artificial

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<220>
<223> Amino acid sequence of the chimeric protein variant TIC868_29.

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<400> 47

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Met Thr Ser Asn Arg Lys Asn Glu Asn Glu Ile Ile Asn Ala Leu Ser
1           5           10           15

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Ile Pro Ala Val Ser Asn His Ser Ala Gln Met Asn Leu Ser Thr Asp
          20           25           30

```

```

Ala Arg Ile Glu Asp Ser Leu Cys Ile Ala Glu Gly Asn Asn Ile Asp
          35           40           45

```

```

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

```

```

Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Ile Ala Ser
65           70           75           80

```

```

Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Arg Gly Arg Asp Pro
          85           90           95

```

```

Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln Val
          100          105          110

```

```

Thr Glu Asn Thr Arg Asp Thr Ala Leu Ala Arg Leu Gln Gly Leu Gly
          115          120          125

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Asn Ser Phe Arg Ala Tyr Gln Tyr Ser Leu Glu Asp Trp Leu Glu Asn
130 135 140

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

Leu Glu Leu Asp Phe Leu Asn Ala Met Pro Leu Phe Ala Ile Arg Asn
165 170 175

Gln Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His
180 185 190

Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe Gly Ser Glu Phe Gly Leu
195 200 205

Thr Ser Gln Glu Ile Gln Arg Tyr Tyr Glu Arg Gln Val Glu Lys Thr
210 215 220

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

Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln Phe
245 250 255

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

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

Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser Gly
290 295 300

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

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

Gln Leu Thr Ile Phe Ser Gln Leu Ser Arg Trp Ser His Thr Gln Tyr
340 345 350

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

Ser Leu Ser Thr Ser Thr His Gly Asn Thr Asn Thr Ser Ile Asn Pro
370 375 380

Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu Ser Phe
385 390 395 400

Ala Gly Ile Asn Ile Leu Leu Thr Thr Pro Val Asn Gly Val Pro Trp
405 410 415

Ala Arg Phe Asn Trp Arg Asn Pro Leu Asn Ser Leu Arg Gly Ser Leu
420 425 430

Leu Tyr Thr Ile Gly Tyr Thr Gly Val Gly Thr Gln Leu Phe Asp Ser
435 440 445

Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn Tyr Glu Ser
450 455 460

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

Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp Arg Thr Asn
485 490 495

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

Arg Val Trp Gly Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly
515 520 525

Gly Asp Ile Leu Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln
530 535 540

Val Asn Ile Asn Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg
545 550 555 560

Tyr Ala Ser Ser Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala
565 570 575

Ser Thr Gly Val Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys
580 585 590

Thr Met Glu Ile Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr
595 600 605

Asp Phe Ser Asn Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly
610 615 620

Ile Ser Glu Gln Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu
625 630 635 640

Leu Tyr Ile Asp Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu
645 650 655

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

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

Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser Asp Glu Phe Cys
690 695 700

Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg
705 710 715 720

Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile
725 730 735

Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile
740 745 750

Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Leu Gly
755 760 765

Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu
770 775 780

Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu
785 790 795 800

Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His
805 810 815

Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala
820 825 830

Pro Ser Pro Ile Gly Lys Cys Ala His His Ser His His Phe Ser Leu
835 840 845

Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp
850 855 860

Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn
865 870 875 880

Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg
885 890 895

Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu
900 905 910

Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala
915 920 925

Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile
930 935 940

Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala
945 950 955 960

Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe
965 970 975

Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala
980 985 990

Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp
995 1000 1005

Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg
1010 1015 1020

Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu
1025 1030 1035

Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala
1040 1045 1050

Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile
1055 1060 1065

Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu
1070 1075 1080

Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Ala
1085 1090 1095

Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly
1100 1105 1110

Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser Val Pro Ala Asp Tyr
1115 1120 1125

Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr Asp Gly Arg Arg Asp
1130 1135 1140

Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu
1145 1150 1155

Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr
1160 1165 1170

Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile
1175 1180 1185

Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
1190 1195

<210> 48
<211> 3432
<212> DNA
<213> Artificial

<220>
<223> Recombinant nucleotide sequence used for expression in a
bacterial cell encoding TIC869.

<400> 48
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cttttgcaat ttcttttgaa taactttggt ccagggggag gctttatttc aggattagtt 180
gataaaatat ggggggcttt gagaccatct gaatgggact tatttcttgc acagattgaa 240
cggttgattg atcaaagaat agaagcaaca gtaagagcaa aagcaatcac tgaattagaa 300
ggattagga gaaattatca aatatacgct gaagcattta aagaatggga atcagatcct 360
gataacgaag cggctaaaag tagagtaatt gatcgctttc gtatacttga tgggtctaatt 420
gaagcaaata tcccttcatt tcggataatt ggatttgaag tgccactttt atcggtttat 480

gttcaagcag ctaatctaca tctcgctcta ttgagagatt ctgttatTTTt tggagagaga	540
tggggattga cgacaaaaaa tgtcaatgat atctataata gacaaattag agaaattcat	600
gaatatagca atcattgcgt agatacgtat aacacagaac tagaacgtct agggTTtaga	660
tctatagcgc agtggagaat atataatcag tttagaagag aactaacact aactgtatta	720
gatattgtcg ctctTTTccc gaactatgac agtagactgt atccgatcca aactTTTtct	780
caattgacaa gagaaattgt tacatcccca gtaagcgaat tttattatgg tgttattaat	840
agtggtaata taattggtac tcttactgaa cagcagataa ggcgaccaca tcttatggac	900
ttctTTaact ccatgatcat gtatacatca gataatagac gggaacatta ttggtcagga	960
cttgaaatga cggcttattt tacaggattt gcaggagctc aagtgtcatt ccctTTtagtc	1020
gggactagag gggagtcagc tccaccatta actgttagaa gtgttaatga tggaatttat	1080
agaatattat cggcaccgtt ttattcagcg cctTTTctag gcaccattgt attgggaagt	1140
cgtggagaaa aatttgattt tgcgcttaat aatTTTcac ctccgccatc tacaatatac	1200
agacatcctg gaacagtaga ttcactagtc agtataccgc cacaggataa tagcgtacca	1260
ccgcacaggg gatctagtca tcgattaagt catgttaca tgcgcgcaag ttccctata	1320
ttccattgga cgcatcgag cgcaaccact acaaatacaa ttaatccaaa tgctattatc	1380
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gtcaatgttc cttcatcact atTTTccaa agatatcgcg taaggattcg ttatgcttct	1560
actaccgatt tacaattTTTt cacgagaatt aatggaactt ctgttaatca aggtaatttc	1620
tcaaaaacga tggatagagg ggataaactg aaatctgaaa actTTtagaac tgccggattt	1680
agtactcctt ttagattTTTt aaattTTcaa agtacattca cgTTgggtac tcaggctTTTt	1740
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caaatcgggt taaaaacaga tgtgacggat tatcatattg atcaagtatc caatttagtt	1920
gagtgtttat ctgatgaatt ttgtctggat gaaaaaaaag aattgtccga gaaagtcaaa	1980

catgcgaagc gacttagtga tgagcgggaat ttacttcaag atccaaactt tagagggatc	2040
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gacgtattca aagagaatta cgttacgcta ttgggtacct ttgatgagtg ctatccaacg	2160
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caagaagttc gtgtctgtcc gggtcgtggc tatatccttc gtgtcacagc gtacaaggag	3000
ggatatggag aaggttgcgt aaccattcat gagatcgaga acaatacaga cgaactgaag	3060
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actgcgactc aagaagaata tgagggtacg tacacttctc gtaatcgagg atatgacgga	3180
gcctatgaaa gcaattcttc tgtaccagct gattatgcat cagcctatga agaaaaagca	3240
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ccactaccag ctggctatgt gacaaaagaa ttagagtact tcccagaaac cgataaggta	3360
tggattgaga tcggagaaac ggaaggaaca ttcatcgtgg acagcgtgga attacttctt	3420
atggaggaat ag	3432

<210> 49
<211> 3432
<212> DNA
<213> Artificial

<220>

<223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC869.

<400> 49

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ctcctccagt tcctcctcaa taacttcgtg ccaggcggcg gcttcatctc cggcctggtg	180
gacaagatct ggggcgcact ccggccaagt gagtgggatac tggttcctggc ccaaatacgag	240
cgcctgatcg accagaggat cgaggcgacg gtccgcgcca aggcgataac cgagctggag	300
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gacaacgagg cggccaagtc tcgggtgatt gaccgcttcc gcatcctcga cggcctcatc	420
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gacatcgctc cattgtttcc caattacgac tcacgcctct acccaatcca gactttcagc	780
cagctcacac gcgagattgt gaccagcccc gtgtcagagt tctactacgg cgtcatcaac	840
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ggaactcgtg gcgagtcagc tcctccgcta actgtgcgat ctgtcaacga cgggatctac	1080
agaatactgt cggctccctt ctacagtgcg ccgttcctcg gcaccatcgt cctcggctca	1140
cgtggtgaga agttcgactt cgcactgaac aacattagcc cgccgcctag tacaatctac	1200

aggcaccctg gcaccgtgga ctacttggtt tcgatcccg cacaagacaa cagtgtgccg	1260
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gatgtgttca aggagaatta tggtacgctg ctcggtacgt tcgacgagtg ctatcccacg	2160
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cgtctccagg ccgacaccaa catcgccatg atccacgccg ctgacaaacg agttcattcc	2700

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 aagaacggcg acttcaacaa cggctctctcc tgttggaaacg tgaagggcca cgtggatgtc 2880
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 ggctacggcg aaggctgcgt tactattcac gagattgaga acaataccga cgaactcaag 3060
 ttctccaact gtgtcgagga ggaggtgtac ccgaacaaca ccgtgacgtg caacgactac 3120
 accgcgacac aggaggaata cgagggcacc tacaccagcc gcaaccgagg ctacgacgga 3180
 gcgtacgaga gcaactcgtc cgtgcccgt gattacgcga gtgcgtacga ggagaaggct 3240
 tacaccgacg gacggcgcga caatccctgc gagagtaacc gtggatacgg agattacacg 3300
 ccgctacccg ctggctacgt cactaaggaa ctggagtact tcccagagac ggacaagggtg 3360
 tggatcga aa tcggcgagac agagggcacg ttcatcgtgg actccgtgga gctgctgctg 3420
 atggaggagt ga 3432

<210> 50
 <211> 1143
 <212> PRT
 <213> Artificial

<220>
 <223> Amino acid sequence of the chimeric protein TIC869.

<400> 50

Met	Glu	Ile	Asn	Asn	Gln	Lys	Gln	Cys	Ile	Pro	Tyr	Asn	Cys	Leu	Ser
1				5				10						15	

Asn	Pro	Glu	Glu	Val	Leu	Leu	Asp	Gly	Glu	Arg	Ile	Leu	Pro	Asp	Ile
		20						25					30		

Asp	Pro	Leu	Glu	Val	Ser	Leu	Ser	Leu	Leu	Gln	Phe	Leu	Leu	Asn	Asn
		35						40					45		

Phe Val Pro Gly Gly Gly Phe Ile Ser Gly Leu Val Asp Lys Ile Trp
50 55 60

Gly Ala Leu Arg Pro Ser Glu Trp Asp Leu Phe Leu Ala Gln Ile Glu
65 70 75 80

Arg Leu Ile Asp Gln Arg Ile Glu Ala Thr Val Arg Ala Lys Ala Ile
85 90 95

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

Phe Lys Glu Trp Glu Ser Asp Pro Asp Asn Glu Ala Ala Lys Ser Arg
115 120 125

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

Pro Ser Phe Arg Ile Ile Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
145 150 155 160

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

Phe Gly Glu Arg Trp Gly Leu Thr Thr Lys Asn Val Asn Asp Ile Tyr
180 185 190

Asn Arg Gln Ile Arg Glu Ile His Glu Tyr Ser Asn His Cys Val Asp
195 200 205

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

Trp Arg Ile Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val Leu
225 230 235 240

Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Leu Tyr Pro Ile
245 250 255

Gln Thr Phe Ser Gln Leu Thr Arg Glu Ile Val Thr Ser Pro Val Ser
260 265 270

Glu Phe Tyr Tyr Gly Val Ile Asn Ser Gly Asn Ile Ile Gly Thr Leu
275 280 285

Thr Glu Gln Gln Ile Arg Arg Pro His Leu Met Asp Phe Phe Asn Ser
290 295 300

Met Ile Met Tyr Thr Ser Asp Asn Arg Arg Glu His Tyr Trp Ser Gly
305 310 315 320

Leu Glu Met Thr Ala Tyr Phe Thr Gly Phe Ala Gly Ala Gln Val Ser
325 330 335

Phe Pro Leu Val Gly Thr Arg Gly Glu Ser Ala Pro Pro Leu Thr Val
340 345 350

Arg Ser Val Asn Asp Gly Ile Tyr Arg Ile Leu Ser Ala Pro Phe Tyr
355 360 365

Ser Ala Pro Phe Leu Gly Thr Ile Val Leu Gly Ser Arg Gly Glu Lys
370 375 380

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

Arg His Pro Gly Thr Val Asp Ser Leu Val Ser Ile Pro Pro Gln Asp
405 410 415

Asn Ser Val Pro Pro His Arg Gly Ser Ser His Arg Leu Ser His Val
420 425 430

Thr Met Arg Ala Ser Ser Pro Ile Phe His Trp Thr His Arg Ser Ala
435 440 445

Thr Thr Thr Asn Thr Ile Asn Pro Asn Ala Ile Ile Gln Ile Pro Leu
450 455 460

Val Lys Ala Phe Asn Leu His Ser Gly Ala Thr Val Val Arg Gly Pro
465 470 475 480

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

Ala Asp Ile Arg Val Asn Val Pro Ser Ser Leu Phe Ser Gln Arg Tyr
500 505 510

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

Arg Ile Asn Gly Thr Ser Val Asn Gln Gly Asn Phe Ser Lys Thr Met
530 535 540

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

Ser Thr Pro Phe Arg Phe Ser Asn Phe Gln Ser Thr Phe Thr Leu Gly
565 570 575

Thr Gln Ala Phe Ser Asn Gln Glu Val Tyr Ile Asp Arg Ile Glu Phe
580 585 590

Val Pro Ala Glu Val Thr Phe Glu Ala Glu Ser Asp Leu Glu Arg Ala
595 600 605

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

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

Glu Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser
645 650 655

Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu
660 665 670

Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp
675 680 685

Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys
690 695 700

Glu Asn Tyr Val Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr
705 710 715 720

Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg
725 730 735

Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr
740 745 750

Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr
755 760 765

Gly Ser Leu Trp Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Ala
770 775 780

His His Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp
785 790 795 800

Leu Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln
805 810 815

Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro
820 825 830

Leu Val Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp
835 840 845

Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys
850 855 860

Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp
865 870 875 880

Arg Leu Gln Ala Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys
885 890 895

Arg Val His Ser Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile
900 905 910

Pro Gly Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe
915 920 925

Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp
930 935 940

Phe Asn Asn Gly Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val
945 950 955 960

Glu Glu Gln Asn Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu
965 970 975

Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile
980 985 990

Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr
995 1000 1005

Ile His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn
1010 1015 1020

Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn
1025 1030 1035

Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser
1040 1045 1050

Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser Val
 1055 1060 1065

Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr Asp
 1070 1075 1080

Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp
 1085 1090 1095

Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr
 1100 1105 1110

Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu
 1115 1120 1125

Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
 1130 1135 1140

<210> 51
 <211> 3513
 <212> DNA
 <213> Artificial

<220>
 <223> Recombinant nucleotide sequence used for expression in a
 bacterial cell encoding TIC836.

<400> 51
 atggagaata atattcaaaa tcaatgcgta ccttacaatt gtttaaataa tcctgaagta 60
 gaaatattaa atgaagaaag aagtactggc agattaccgt tagatatatc cttatcgctt 120
 acacgtttcc ttttgagtga atttgttcca ggtgtgggag ttgcgtttgg attatttgat 180
 ttaatatggg gttttataac tccttctgat tggagcttat ttcttttaca gattgaacaa 240
 ttgattgagc aaagaataga aacattggaa aggaaccggg caattactac attacgaggg 300
 ttagcagata gctatgaaat ttatattgaa gcactaagag agtggggaagc aaatcctaata 360
 aatgcacaat taagggaaga tgtgcgtatt cgatttgcta atacagacga cgctttaata 420

acagcaataa ataatttttac acttacaagt tttgaaatcc ctctttttatc ggtctatggt	480
caagcggcga atttacattt atcactatta agagacgctg tatcgtttgg gcagggttgg	540
ggactggata tagctactgt taataatcat tataatagat taataaatct tattcataga	600
tatacgaaac attgttttga cacatacaat caaggattag aaaacttaag aggtactaat	660
actcgacaat gggcaagatt caatcagttt aggagagatt taacacttac tgtattagat	720
atcgttgctc tttttccgaa ctacgatggt agaacatatc caattcaaac gtcattccaa	780
ttaacaaggg aaattttatac aagttcagta attgaggatt ctccagtttc tgctaataata	840
cctaattggtt ttaatagggc ggaattttga gttagaccgc cccatcttat ggactttatg	900
aattctttgt ttgtaactgc agagactggt agaagtcaaa ctgtgtgggg aggacactta	960
gtagttcac gaaatacggc tggtaaccgt ataaatttcc ctagttacgg ggtcttcaat	1020
cctggtggcg ccatttggat tgcagatgag gatccacgtc ctttttatcg gacattatca	1080
gacctgttt ttgtccgagg aggatttggg aatcctcatt atgtactggg gcttagggga	1140
gtagcatttc aacaaactgg tacgaaccac acccgaacat ttagaaatag tgggaccata	1200
gattctctag atgaaatccc acctcaggat aatagtgggg caccttggaa tgattatagt	1260
catgtattaa atcatgttac atttgtacga tggccagggt agatttcagg aagtgattca	1320
tggagagctc caatgttttc ttggacgcac cgtagtgcaa cccctacaaa tacaattgat	1380
ccggagagga ttacacaaat acctttaaca aaatctacta atcttggctc tggaacttct	1440
gtcgttaaag gaccaggatt tacaggagga gatattcttc gaagaacttc acctggccag	1500
atttcaacct taagagtaaa tattactgca ccattatcac aaagatatcg ggtaagaatt	1560
cgctacgctt ctaccacaaa tttacaattc catacatcaa ttgacggaag acctattaat	1620
caggggaatt tttcagcaac tatgagtagt gggagtaatt tacagtccgg aagctttagg	1680
actgtaggtt ttactactcc gttaaacttt tcaaattggat caagtgtatt tacgttaagt	1740
gctcatgtct tcaattcagg caatgaagtt tatatagatc gaattgaatt tgttccggca	1800
gaagtaacct ttgaggcaga atatgattta gaaagagcgc agaaggcggg gaatgcgctg	1860
tttacgtcta caaaccaact agggctaata acaaatgtaa cggattatca tattgatcaa	1920

gtgtccaatt tagttacgta tttatcggat gaatthttgtc tggatgaaaa gcgagaattg	1980
tccgagaaaag tcaaacatgc gaagcgactc agtgatgaac gcaatthtact ccaagattca	2040
aatthtcaaag acattaatag gcaaccagaa cgtgggtggg gcggaagtac agggattacc	2100
atccaaggag gggatgacgt atttaaagaa aattacgtca cactatcagg tacctthtgat	2160
gagtgcatac caacatatht gtatcaaaaa atcgatgaat caaaatthaa agcctthtacc	2220
cgttatcaat taagagggtat tatcgaagat agtcaagact tagaaatcta tthaatcgc	2280
tacaatgcaa aacatgaaac agtaaattgt ccaggtagcg gttccttatg gccgctthca	2340
gccccaaagtc caatcggaat gtgtggagag ccgaatcgat gcgcgccaca ccttgaatgg	2400
aatcctgact tagattgttc gtgtagggtat ggagaaaagt gtgccccatca ttcgcatcat	2460
ttctccttag acattgatgt aggatgtaca gactthaaatg aggacctagg tgtatgggtg	2520
atctthtaaga ttaagacgca agatgggcac gcaagactag ggaatctaga gthtctcgaa	2580
gaaaaaccat tagtaggaga agcgctagct cgtgtgaaaa gagcggagaa aaaatggaga	2640
gacaaacgtg aaaaattgga atgggaaaca aatatcgtht ataaagaggc aaaagaatct	2700
gtagatgctt tathttgtaa ctctcaatat gatcaattac aagcggatac gaatattgcc	2760
atgattcatg cggcagataa acgtgttcat agcattcgag aagcttatct gcctgagctg	2820
tctgtgattc cgggtgtcaa tgcggctatt thtgaagaat tagaaggcg tathttcact	2880
gcattctccc tatatgatgc gagaaatgtc attaaaaatg gtgattthta taatggctta	2940
tcctgctgga acgtgaaagg gcatgtagat gtagaagaac aaaacaacca acgttcggtc	3000
cttgthgttc cggaatggga agcagaagtg tcacaagaag ttcgtgtctg tccgggtcgt	3060
ggctatatcc thtctgtcac agcgtacaag gagggatatg gagaaggthg cgtaaccatt	3120
catgagatcg agaacaatac agacgaactg aagthttagca actgcgtaga ggaggaaatc	3180
tatccaaata acacggtaac gtgtaatgat tatactgtaa atcaagaaga atacggaggt	3240
gcgtacactt ctcgtaatcg aggatataac gaagctcctt ccgtaccagc tgattatgcg	3300
tcagtctatg aagaaaaatc gtatacagat ggacgtagag agaatccttg tgaattthaa	3360
agagggtata gggattacac gccactacca gthtggthtat tgacaaaaga attagaatac	3420

ttcccagaaa ccgataaggt atggattgag attggagaaa cggaaggaac atttatcgtg	3480
gacagcgtgg aattactcct tatggaggaa taa	3513

<210> 52
 <211> 3513
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC836.

<400> 52	
atggagaaca acatccagaa ccagtgcgtg ccctacaact gcctgaacaa ccctgaggtt	60
gagatcctga acgaggagcg tagcaccggt aggctcccg tagacatctc cctgagcctg	120
acccgcttcc tccttagtga gttcgtgccc ggcggtggcg tggccttcgg cctcttcgac	180
ctcatctggg gcttcatcac tccttccgac tggtcctct tcctccttca gattgagcaa	240
ctgatcgagc agcgcatcga gacccttgag cgcaaccgcg ccatcaccac tctcagaggt	300
ctcgccgact cctacgaaat ctacatcgag gcactccgtg agtgggaggc caacccgaac	360
aatgcccagc tccgagagga cgtgaggatc agattcgcca acaccgacga tgccctcatc	420
accgccatca acaatttcac cctcacctcc ttcgagatcc ctcttctgtc tgtgtacgtt	480
caagctgcta accttcacct ttccctcctg cgcgacgccg tgagcttcgg ccagggctgg	540
ggcctcgaca tcgccaccgt gaacaatcac tacaaccgcc tcatcaacct catccaccgc	600
tacaccaagc actgccttga cacctacaac cagggccttg agaacctccg tggcaccaac	660
acccgccagt gggcccgtt caaccagttc cgagagagacc tcaccctcac cgtgctcgac	720
atcgtggcac tcttcccaaa ctacgacgtg cgtacctacc ctatccagac ctccagccag	780
ctcaccaggg aaatctacac ctccagcgtg atcgaggact ctctgtgtc cgccaacatc	840
cctaacggct tcaaccgcgc cgagttcggc gtgcgccctc ctcacctcat ggacttcatg	900
aactccctct tcgtcactgc cgagaccgtg cgctcccaga ccgtgtgggg cggtcacctc	960
gtgtccagcc gtaacaccgc tggcaacagg atcaacttcc cgtcctacgg cgtgttcaac	1020
ccaggcgggtg ccatctggat cgccgatgaa gaccctcgtc ctttctaccg taccctgtcc	1080

gacctgtgt tcgtgcgtgg cggtttcggc aaccctcact acgtgctggg cctgcgtggc	1140
gtggccttcc agcaaaccgg caccaaccac accaggacgt tccgtaactc cggcaccatc	1200
gacagtcttg acgagatccc tccgcaagac aactccgggtg caccttggaa cgactactcc	1260
cacgtgctga accacgtgac cttcgtgagg tggcctggcg aaatctccgg ctccgactcc	1320
tggagggctc ctatgttcag ttggaccacac aggagcgcta cgcctacca caccatcgac	1380
cctgagcgta tcactcagat ccctctgact aagagcacta acctgggcag cggcactagc	1440
gtggtcaagg gccctggctt cactggcggg gacatcctga ggcggactag ccctggccag	1500
atcagcactc tgagggtgaa catcactgct ccgctgagcc agcggttacag ggtcagaatc	1560
cgttacgctt ctactactaa ccttcagttc cacactagca tcgacggccg tccgatcaac	1620
cagggcaact tctctgctac tatgagttct ggcagtaacc tccagtctgg tagtttccgg	1680
actgtcgggt tcaactagcc gttcaacttc tccaacggta gttctgtctt cactctgtct	1740
gctcacgtgt tcaactctgg caacgagggtg tacatcgacc ggatcgagtt cgtccctgct	1800
gaggtgacgt tcgaggccga gtacgacctg gagcgggctc agaaggctgt caacgctctg	1860
ttcacttcta ctaaccagct tggtttgaag actaacgtga ccgactacca cattgatcaa	1920
gtcagtaacc tggtcacgta cctgtctgac gagttctgtc ttgacgagaa gcgggagctg	1980
tctgagaagg tcaagcacgc taagcggctg tctgacgagc ggaacctgct tcaagacagt	2040
aacttcaagg acattaaccg ccagcctgag cgtggttggg gaggggccac ggggtattacg	2100
attcaaggag gtgacgatgt ctttaaggag aactatgtga cgctttcggg tacgtttgat	2160
gagtgtatc caacgtacct ttaccagaag attgacgagt cgaagctgaa ggctttcact	2220
cgttaccagc ttcgtgggta cattgaggac tcgcaagacc tcgaaatcta cctcattcgt	2280
tacaacgcta agcacgagac tgtcaacgtc cctgggtacgg gtagtctttg gccgctttct	2340
gctcagtcgc cgattggcaa gtgtggcgag ccgaaccgtt gcgctcctca cttggagtg	2400
aacccggatc tcgattgctc gtgccgtgac ggtgagaagt gcgcgcacca tagtcatcac	2460
tttagccttg acattgatgt cggttgcacg gatcttaacg aggatcttgg agtctgggtg	2520
atthtcaaga tcaaaactca ggatgggcac gcgcgtcttg ggaatcttga gttcctggag	2580

gagaagccac ttgtcgggtga ggcgcttgcg cgtgtcaagc gtgcggagaa gaaatggcgt 2640
gataagcgtg agaagttgga gtgggagacg aacatcgtgt acaaggaggc gaaggagtcg 2700
gtcgatgcgt tgtttgtcaa tagtcaatac gatcaattgc aagcggatac gaacatcgca 2760
atgattcatg cggcagataa gcgtgtccat tcgattcgtg aggcgtactt gccagagttg 2820
tcggtcatcc caggagttaa tgcggcaatc tttgaggaat tggagggcag aatcttcacg 2880
gcgttctcgt tgtacgatgc aagaaatggtt attaagaatg gagatttcaa caatgggttg 2940
tcatgctgga atgttaaggg tcacgttgat gttgaagaac agaacaacca gagatcagtg 3000
ttggttgtag cagagtggga ggcagagggtt tcacaagagg tgagagtttg cccaggcaga 3060
ggctacatct tgagagttac agcatacaaa gagggatacg gcgagggatg tgttacaatc 3120
cacgaaatcg agaacaatac cgatgagcta aagttctcaa attgtgttga ggaggagatc 3180
taccgaaca acacggttac ttgtaatgat tacacagtga accaggagga gtatggtggt 3240
gcatacacat caagaaatag aggctacaat gaagcaccat cagttccagc agattatgcc 3300
tcagtttatg aggagaagtc atacacagat ggacgacgtg agaatccatg tgagttcaat 3360
cgaggatacc gagattacac accactacca gttggatacg ttacaaagga actagaatac 3420
ttcccagaaa cagataaagt atggatagag atcggagaaa cagaaggaac attcatcggt 3480
gattcagtag aactactact tatggaagaa tga 3513

<210> 53
<211> 1170
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of the chimeric protein TIC836.

<400> 53

Met Glu Asn Asn Ile Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu Asn
1 5 10 15

Asn Pro Glu Val Glu Ile Leu Asn Glu Glu Arg Ser Thr Gly Arg Leu
20 25 30

Pro Leu Asp Ile Ser Leu Ser Leu Thr Arg Phe Leu Leu Ser Glu Phe
35 40 45

Val Pro Gly Val Gly Val Ala Phe Gly Leu Phe Asp Leu Ile Trp Gly
50 55 60

Phe Ile Thr Pro Ser Asp Trp Ser Leu Phe Leu Leu Gln Ile Glu Gln
65 70 75 80

Leu Ile Glu Gln Arg Ile Glu Thr Leu Glu Arg Asn Arg Ala Ile Thr
85 90 95

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

Arg Glu Trp Glu Ala Asn Pro Asn Asn Ala Gln Leu Arg Glu Asp Val
115 120 125

Arg Ile Arg Phe Ala Asn Thr Asp Asp Ala Leu Ile Thr Ala Ile Asn
130 135 140

Asn Phe Thr Leu Thr Ser Phe Glu Ile Pro Leu Leu Ser Val Tyr Val
145 150 155 160

Gln Ala Ala Asn Leu His Leu Ser Leu Leu Arg Asp Ala Val Ser Phe
165 170 175

Gly Gln Gly Trp Gly Leu Asp Ile Ala Thr Val Asn Asn His Tyr Asn
180 185 190

Arg Leu Ile Asn Leu Ile His Arg Tyr Thr Lys His Cys Leu Asp Thr
195 200 205

Tyr Asn Gln Gly Leu Glu Asn Leu Arg Gly Thr Asn Thr Arg Gln Trp
210 215 220

Ala Arg Phe Asn Gln Phe Arg Arg Asp Leu Thr Leu Thr Val Leu Asp
225 230 235 240

Ile Val Ala Leu Phe Pro Asn Tyr Asp Val Arg Thr Tyr Pro Ile Gln
245 250 255

Thr Ser Ser Gln Leu Thr Arg Glu Ile Tyr Thr Ser Ser Val Ile Glu
260 265 270

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

Phe Gly Val Arg Pro Pro His Leu Met Asp Phe Met Asn Ser Leu Phe
290 295 300

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

Val Ser Ser Arg Asn Thr Ala Gly Asn Arg Ile Asn Phe Pro Ser Tyr
325 330 335

Gly Val Phe Asn Pro Gly Gly Ala Ile Trp Ile Ala Asp Glu Asp Pro
340 345 350

Arg Pro Phe Tyr Arg Thr Leu Ser Asp Pro Val Phe Val Arg Gly Gly
355 360 365

Phe Gly Asn Pro His Tyr Val Leu Gly Leu Arg Gly Val Ala Phe Gln
370 375 380

Gln Thr Gly Thr Asn His Thr Arg Thr Phe Arg Asn Ser Gly Thr Ile
385 390 395 400

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

Asn Asp Tyr Ser His Val Leu Asn His Val Thr Phe Val Arg Trp Pro
420 425 430

Gly Glu Ile Ser Gly Ser Asp Ser Trp Arg Ala Pro Met Phe Ser Trp
435 440 445

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

Thr Gln Ile Pro Leu Thr Lys Ser Thr Asn Leu Gly Ser Gly Thr Ser
465 470 475 480

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

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

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

Gln Phe His Thr Ser Ile Asp Gly Arg Pro Ile Asn Gln Gly Asn Phe
530 535 540

Ser Ala Thr Met Ser Ser Gly Ser Asn Leu Gln Ser Gly Ser Phe Arg
545 550 555 560

Thr Val Gly Phe Thr Thr Pro Phe Asn Phe Ser Asn Gly Ser Ser Val
565 570 575

Phe Thr Leu Ser Ala His Val Phe Asn Ser Gly Asn Glu Val Tyr Ile
580 585 590

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

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

Asn Gln Leu Gly Leu Lys Thr Asn Val Thr Asp Tyr His Ile Asp Gln
625 630 635 640

Val Ser Asn Leu Val Thr Tyr Leu Ser Asp Glu Phe Cys Leu Asp Glu
645 650 655

Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp
660 665 670

Glu Arg Asn Leu Leu Gln Asp Ser Asn Phe Lys Asp Ile Asn Arg Gln
675 680 685

Pro Glu Arg Gly Trp Gly Gly Ser Thr Gly Ile Thr Ile Gln Gly Gly
690 695 700

Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Ser Gly Thr Phe Asp
705 710 715 720

Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu
725 730 735

Lys Ala Phe Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln
740 745 750

Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val
755 760 765

Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro
770 775 780

Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp
785 790 795 800

Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His
805 810 815

His Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu
820 825 830

Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp
835 840 845

Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu
850 855 860

Val Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg
865 870 875 880

Asp Lys Arg Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu
885 890 895

Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Gln
900 905 910

Leu Gln Ala Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg
915 920 925

Val His Ser Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro
930 935 940

Gly Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr
945 950 955 960

Ala Phe Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe
965 970 975

Asn Asn Gly Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu
980 985 990

Glu Gln Asn Asn Gln Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala
995 1000 1005

Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile
1010 1015 1020

Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val
1025 1030 1035

Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser
1040 1045 1050

Asn Cys Val Glu Glu Glu Ile Tyr Pro Asn Asn Thr Val Thr Cys
1055 1060 1065

Asn Asp Tyr Thr Val Asn Gln Glu Glu Tyr Gly Gly Ala Tyr Thr
1070 1075 1080

Ser Arg Asn Arg Gly Tyr Asn Glu Ala Pro Ser Val Pro Ala Asp
1085 1090 1095

Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg
1100 1105 1110

Glu Asn Pro Cys Glu Phe Asn Arg Gly Tyr Arg Asp Tyr Thr Pro
1115 1120 1125

Leu Pro Val Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu
1130 1135 1140

Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe
1145 1150 1155

Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
1160 1165 1170