

SEQUENCE LISTING

<110> Monsanto Technology LLC

Baum, James A
Cerruti, Thomas A
Dart, Crystal L
English, Leigh H
Flasinski, Stanislaw
Fu, Xiaoran
Guzov, Victor M
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Roberts, James K
Salvador, Sara A
Wang, Jinling

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

<130> P34230WO00/0022270.00098

<150> US 62/064989

<151> 2014-10-16

<160> 130

<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.

<400> 1

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<223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC1100.

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<211> 1189

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC1100.

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 20 25 30

Asn Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser

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355 360 365

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385 390 395 400

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

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

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530 535 540

Ser Thr Gly Val Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys
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Asp Phe Ser Asn Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly
580 585 590

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595 600 605

Leu Tyr Ile Asp Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu
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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 ataggaaaa tgagaatgaa attataaatg ctttatcgat tccaacggta 60
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 gtagccgagg tgaacaatat tgatccattt gtagcgcac caacagtcga aacgggtata 180
 aacatagctg gtagaatatt gggcgtatta ggtgtgccgt ttgctggaca actagctagt 240
 ttttatagtt ttctgttg ggaattatgg cctagtggca gagatccatg ggaaattttc 300
 ctggaacatg tagaacaact tataagacaa caagtaacag aaaatactag gaatacggct 360
 attgctcgat tagaagggtc aggaagaggc tatagatctt accagcaggc tcttgaaact 420
 tggtagata accgaaatga tgcaagatca agaagcatta ttctgagcg ctatgttgct 480
 ttagaacttg acattactac tgctataccg ctttcagaa tacgaaatga agaagttcca 540
 ttattaatgg tatatgctca agctgcaaata ttacacatat tattattgag agacgcaccc 600
 ctttttggtg gtgaatgggg gatggcatct tccgatgta accaatatta ccaagaacaa 660
 atcagatata cagaggaata ttctaaccat tgcgtacaat ggtataatac agggctaaat 720
 aacttaagag ggacaaatgc tgaaagtggg ttgcgggtata atcaattccg tagagaccta 780

acgttagggg tattagattt agtagcccta ttccaagct atgatactcg cacttatcca 840
 atcaatacga gtgctcagtt aacaagagaa atttatacag atccaattgg gagaacaaat 900
 gcaccttcag gatttgcaag tacgaattgg ttaataata atgcaccatc gtttctgcc 960
 atagaggctg ccatttcag gcctccgcat ctacttgatt ttccagaaca acttacaatt 1020
 tacagtgcac caagccgttg gagtagcact caacatatga attattgggt gggacatagg 1080
 cttacttcc gcccaatagg aggacatta aatacctcaa cacaaggact tactaataat 1140
 acttcaatta atcctgtaac attacagttt acgtctcgag acgtttatag aacagaatca 1200
 aatgcaggga caaatatact attactact cctgtgaatg gagtaccttg ggctagattt 1260
 aattttataa accctcagaa tatttatgaa agaggcgcca ctacctacag tcaaccgtat 1320
 caggggagttg ggattcaatt atttgattca gaaactgaat taccaccaga aacaacagaa 1380
 cgaccaaatt atgaatcata tagtcataga ttatctcata taggactaat cataggaaac 1440
 actttgagag caccagtcta ttctggacg catcgtagtg cagatcgtac gaatacgatt 1500
 ggaccaaata gaattaatca aataccttta gtgaaaggat ttagagtttg ggggggcacc 1560
 tctgtcatta caggaccagg atttacagga ggggatatcc ttcgaagaaa taccttgggt 1620
 gattttgtat ctctacaagt caatattaat tcaccaatta ccaaagata ccgtttaaga 1680
 ttctgttacg ctccagtag ggatgcacga gttatagtat taacaggagc ggcattccaca 1740
 ggagtgggag gccaaagtag tgtaaatatg cctctcaga aaactatgga aataggggag 1800
 aacttaacat ctagaacatt tagatatacc gattttagta atccttttc atttagagct 1860
 aatccagata taattgggat aagtgaacaa cctctatttg gtgcagggtc tattagtagc 1920
 ggtgaacttt atatagataa aattgaaatt attctagcag atgcaacatt tgaagcagaa 1980
 tctgatttag aaagagcgca gaaggcgggtg aatgcgctgt ttacgtctac aaaccaacta 2040
 gggctaaaaa caaatgtaac ggattatcat attgatcaag tgtccaattt agttacgtat 2100
 ttatcggatg aattttgtct ggatgaaaag cgagaattgt ccgagaaagt caaacatgcg 2160
 aagcgactca gtgatgaacg caatttactc caagattcaa attcaaaga cattaatagg 2220
 caaccagaac gtgggtgggg cggaagtaca gggattacca tccaaggagg ggatgacgta 2280
 tttaaagaaa attacgtcac actatcaggt acccttgatg agtgctatcc aacatatttg 2340
 tatcaaaaaa tcgatgaatc aaaattaaaa gcctttaccc gttatcaatt aagagggtat 2400

atcgaagata gtcaagactt agaaatctat ttaattcgct acaatgcaaa acatgaaaca 2460
 gttaaattgtc caggtagcggg ttccttatgg ccgctttcag cccaaagtcc aatcggaag 2520
 tgtggagagc cgaatcgatg cgcgccacac ctggaatgga atcctgactt agattgttcg 2580
 tgtagggatg gagaaaagtg tgcccatcat tcgcatcatt tctccttaga cattgatgta 2640
 ggatgtacag acttaaatga ggacctaggt gtatgggtga tcttaagat taagacgcaa 2700
 gatgggcacg caagactagg gaatctagag ttctcgaag agaaaccatt agtaggagaa 2760
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 cgtgttcata gcattcgaga agcttatctg cctgagctgt ctgtgattcc ggggtgcaat 3000
 gcggctattt ttgaagaatt agaagggcgt attttactg cattctccct atatgatgcg 3060
 agaaatgtca ttaaaatgg tgattttaat aatggcttat cctgctggaa cgtgaaaggg 3120
 catgtagatg tagaagaaca aaacaaccaa cgctcgttc ttgtgttc ggaatgggaa 3180
 gcagaagtgt cacaagaagt tcgtgtctgt ccgggtcgtg gctatattct tcgtgtcaca 3240
 gcgtacaagg agggatatgg agaaggtgc gtaaccattc atgagatcga gaacaataca 3300
 gacgaactga agtttagcaa ctgcgtagaa gaggaatct atccaaataa cacggtaacg 3360
 tgtaatgatt atactgtaaa tcaagaagaa tacggaggtg cgtacacttc tcgtaatcga 3420
 ggatataacg aagctccttc cgtaccagct gattatgcgt cagtctatga agaaaaatcg 3480
 tatacagatg gacgaagaga gaatccttgt gaatttaaca gaggttatag ggattacacg 3540
 ccactaccag ttggttatgt gacaaaagaa ttagaatact tcccagaaac cgataaggta 3600
 tggattgaga ttgagaaaac ggaaggaaca ttatcgtgg 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 gcaccagat gaacctgagc cctgacgctc gcatcgagga ctccctctgc 120
 gtggctgagg tgaacaacat cgaccggtc gtgtccgct ccaccgtgca gaccggcatc 180
 aacatcgcg gccgcatcct cggcgtgctc ggcggtgcct ttgcgggcca gctgcctcc 240
 ttctactcct tcctcgtggg agagctgtgg ccctccggcc gcgaccgtg ggagatcttc 300
 ctggagcacg tggagcagct catccgccag caagtcaccg agaacacccg caacaccgcc 360
 atgccccgcc tggagggcct gggccgtggc taccgtcct accagcaagc cctggagacc 420
 tggctcgaca accgcaacga cggcgctcc cgctccatca tcctggagcg ctacgtcgcc 480
 ctggaactgg acatcaccac tgccatcca ctctccga tcaggaacga ggaggtgcct 540
 ctgctgatgg tgtacgcca ggctgcaac ctgcacctgc tgctgctgcg cgacgcaagc 600
 ctgtttggct ccgagtgggg tatggcaagc tccgacgtca accagtacta ccaggagcag 660
 atccgctaca ccgaggagta cagcaaccac tgcgtccagt ggtacaacac cggctgaac 720
 aatctcagag ggaccaacgc tgagagctgg ctgcgtaca accagttccg gcgggatctg 780
 accctagggtg tcctggatct ggtcgtctg tccccgagct acgataccag gacgtaccct 840
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 cttacttcc gcccgattgg aggaactctt aacaccagta cgcaaggctt tacgaacaac 1140
 acttccatca acccggttac gttgcagttc acgtctcggg acgtttaccg gacggagtcg 1200
 aatgtggga cgaacatcct gttcacgaca ccggtgaatg gtgtccgtg ggcacgttc 1260
 aactcatca acccgagaa catctacgag cgtggagcaa cgacatactc gcaaccatac 1320
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 cgtccgaatt acgagtcata ctacacaga ctatcacaca ttggactcat tatcggaac 1440
 aactgagag caccagtgt ctatggaca catcggtcag cagatcgta gaacaccatc 1500
 ggaccaatc ggatcaacca gatcccgctc gtgaagggt tccgctgtg gggcggcacc 1560
 tccgtcatca ccggtccggg cttaccggc ggcgacatcc tccgccgaa cacctcggc 1620
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ttccgctacg cctcctcccg cgacgctaga gtgatcgtgc tcaccggagc ggcgtccaca 1740
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 aacctcacct ctgcacctt ccgctacacc gacttctcca atccgttctc cttcagagcc 1860
 aaccagaca tcacggcat ctccgagcag cctctctttg gcgctggctc catctctcc 1920
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 tgccgagc ccaaccgtg cgcgcctcac ctggagtga accctgacct cgactgctcc 2580
 tgccgagc gcgagaagt cgccaccat agccaccact tctctctga catcgacgtg 2640
 ggctgcaccg acctcaacga ggatctgggc gtgtgggtga tcttaagat caagaccag 2700
 gacggccacg ccaggctggg caacctggag ttctggagg agaagcctt ggtgggtgag 2760
 gccctggcca gggtaagag ggctgagaag aatggaggg acaagaggga gaagctggag 2820
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 agggctcact ctatcagga ggcttacctg cctgagctt ctgtcatccc tgggtgtaac 3000
 gcggaatct tcgaggaact tgaggccgc atcttactg cgttctgct ttacgatgcg 3060
 cggaacgtca ttaagaacgg tgactcaac aatggtctt cgtgctgga cgtcaagggt 3120
 catgtcgatg tcgaggaaca gaacaaccag cggtcggtcc ttgtcgtcc cgagtgggag 3180
 gccgaggtct cgcaagaggt ccgggtctgc cctgggcgcg ggtacattct tcgtgtcact 3240
 gcgtacaagg agggctacgg cgagggtgc gttactattc atgagattga gaacaatacg 3300

gatgagctta agtttagtaa ctgtgttgag gaggagatct acccgaacaa tacgggtacg 3360
 tgcaatgatt acacggtgaa ccaggaggaa tacggcggag catacacctc acgtaataga 3420
 ggggtacaatg aggcaccgtc agttccggca gattatgcct cagtttatga ggagaagtcc 3480
 tacacggatg gaagacgcga gaatccatgt gagttaata gaggataccg agactacaca 3540
 ccactcccag ttggatacgt taaaaggag ttggaatact tcccagaaac agataaagtt 3600
 tggatagaga tcggagaaac agaaggaacc tcatcgtgg 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 cgatccattt gttagcgcac caacagtcca aacgggtatt 180
aacatagctg gtagaatact aggtgtatta ggcgtaccgt ttgctggaca aatagctagt 240
ttttatagtt ttcttgttgg tgaattatgg ccccgcgcca gagatccttg ggaaatttc 300
ctagaacatg tcgaacaact tataagacaa caagtaacag aaaatactag ggatacggct 360
cttgctcgat tacaaggttt aggaaattcc ttagagcct atcaacagtc acttgaagat 420
tggctagaaa accgtgatga tgcaagaacg agaagtgttc ttataccca atatatagcc 480
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ttattaatgg tatatgctca agctgcaa atcacctat tattattgag agatgcctct 600
cttttggtg gtgaatttgg gcttacatcc caagaaattc aacgttatta tgagcgccaa 660
gtggaaaaaa cgagagaata ttctgattat tgcgcaagat ggtataatac gggtttaa 720
aatttgagag ggacaaatgc tgaaagtgg ttgcgatata atcaattccg tagagactta 780
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atagaggctg ccgttattag gcctccgcac ctacttgatt ttccagaaca gcttacaatt 1020
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cttgaatcgc gaacaataag ggggtcatta agtacctcga cacacggaaa taccaatact 1140

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 ggggattaca caccactacc agctggctat gtgacaaaag aattagagta ctcccagaa 3480
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 gaattacttc ttatggagga atag 3564

<210> 9
 <211> 3564
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC867.

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 atcgccgagg gcaacaacat cgacccgttc gtgtctgcaa gcacgggtcca gaccggcatc 180
 aacatcgcgg gccgcatacct gggcgtgctc ggcgtgccct tcgcgggtca aatgcctct 240
 ttctactcat tcctcgtggg cgagctgtgg ccgcgcggac gtgaccctgt ggaaatcttc 300
 ctggagcacg ttgagcagct catccggcag caagtgaccg agaacaccag ggacaccgca 360
 ctggcacggc tccagggcct tggcaacagc ttccgcgcct accagcagtc gctggaggac 420
 tggctggaga accgagacga cgccagaacc cgctcagttc tgtacacaca gtacatcgcc 480
 ctagagctgg acttctctaa cgctatgccg ctcttcgccca tccgtaacca ggaagtaccg 540

ctctgatgg tgtacgcaca agcagcgaac ctccatctgc tctgtgtcg agacgcatct 600
 ctgttcggca gtgagttcgg gctgacgagc caggagatcc agcgctacta cgagcgccaa 660
 gtggagaaga ctctgtagta cagcgactac tgcgcgcgct ggtacaacac gggcttgaac 720
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 gacgaactca agttctcga ttgcgtggag gaggaggtgt acccgaacaa tacggtgacg 3240
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 ggcgactaca ctctctccc ggccggatac gtcacaaagg agctggagta ttccagag 3480
 acggacaagg tgtggtcga aatcgagag acagaggga ccttcatcgt ggacagcgtg 3540
 gagctgctcc tcatggagga gtga 3564

<210> 10
 <211> 1187
 <212> PRT
 <213> Artificial
 <220>

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

<400> 10

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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 Phe Glu Ala Glu Ser Asp Leu Glu Arg Ala Gln Lys Ala Val

645	650	655
Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val		
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		
690	695	700
His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn		
705	710	715
		720
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
1010 1015 1020

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
1055 1060 1065

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
 1085 1090 1095

Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser Val Pro
 1100 1105 1110

Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr Asp Gly
 1115 1120 1125

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

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

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

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

<210> 11
 <211> 3642
 <212> DNA
 <213> Artificial

<220>
 <223> Recombinant nucleotide sequence used for expression in a
 bacterial cell encoding TIC867_20.

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 atagccgagg ggaacaatat cgatccattt gttagcgcac caacagtcca aacgggtatt 180
 aacatagctg gtagaatact aggtgtatta ggcgtaccgt ttgctggaca aatagctagt 240
 ttttatagtt ttctgttgg tgaattatgg ccccgcgga gagatccttg ggaaatttc 300
 ctagaacatg tcgaacaact tataagacaa caagtaacag aaaatactag ggatacggct 360
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 tggctagaaa accgtgatga tgcaagaacg agaagtgttc ttatacca atatatagcc 480

ttagaacttg attttcttaa tgcgatgccg ctttcgcaa ttagaaacca agaagttcca 540
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 cttttggta gtgaattgg gcttacatcc caagaaattc aacgttatta tgagcgccaa 660
 gtggaaaaaa cgagagaata ttctgattat tgcgcaagat ggtataatac gggtttaa at 720
 aatttgagag ggacaaatgc tgaagttgg ttgcgatata atcaattccg tagagactta 780
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<210> 12
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 <212> DNA

<213> Artificial

<220>

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

<400> 12

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 <211> 1213
 <212> PRT
 <213> Artificial

<220>
 <223> Amino acid sequence of the chimeric protein variant TIC867_20.

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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

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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		
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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 Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Val Val
 645 650 655

Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly Leu Lys Thr Asp Val
 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
705 710 715 720

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
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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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 1190 1195 1200

Asp Ser Val Glu Leu Leu Leu Met Glu Glu
 1205 1210

<210> 14
 <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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3690

<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
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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
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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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atagccgagg ggaacaatat cgatccattt gttagcgcac caacagtcca aacgggtatt    180
aacatagctg gtagaatact aggtgtatta ggcgtaccgt ttgctggaca aatagctagt    240
ttttatagtt ttctgttggt tgaattatgg ccccgcgcca gagatccttg ggaaattttc    300
ctagaacatg tcgaacaact tataagacaa caagtaacag aaaatactag ggatacggct    360
cttgctcgat tacaagggtt aggaaattcc ttagagcctt atcaacagtc acttgaagat    420
tggctagaaa accgtgatga tgcaagaacg agaagtgttc ttataccca atatatagcc    480
ttagaacttg attttcttaa tgcatgccg ctttcgcaa ttagaaacca agaagttcca    540
ttattaatgg tatatgctca agctgcaaata ttacacctat tattattgag agatgcctct    600
cttttggtg gtgaatttgg gcttacatcc caagaaattc aacgttatta tgagcgccaa    660
gtggaaaaaa cgagagaata ttctgattat tgcgcaagat ggtataatac gggtttaaat    720
aatttgagag ggacaaatgc tgaaagtggg ttgcgatata atcaattccg tagagactta    780
acgctaggag tattagatct agtggcacta ttccaagct atgacacgag tgtttatcca    840
atgaatacca gtgctcaatt aacaagagaa attatacag atccaattgg gagaacaaat    900
gcaccttcag gatttgcaag tacgaattgg ttaataata atgcaccatc gtttctgcc    960
atagaggctg ccgttattag gcctccgcat ctactgatt ttccagaaca gcttacaatt   1020
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cttgaatcgc gaacaataag ggggtcatta agtacctcga cacacggaaa taccaatact   1140
tctattaatc ctgtaacatt acagttcaca tctcgagacg ttatagaac agaattcatt   1200
gcagggataa atatacttct aactactcct gtgaatggag tacctgggc tagatttaat   1260
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aattatgaat cttacagtca tagattatct aatataagac taatacagg aaacacttgg   1440
agagcaccag tatattcttg gacgcaccgt agtgcagatc gtacaaatac cattagttca   1500
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gtgactgata atacgtatct aacaaaagaa gtggtattct attcacatac agaacacatg 3360
tgggtagagg taagtgaaac agaaggtgca ttcatatag atagtattga attcgttgaa 3420
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.

<400> 18
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tcaaaccact ccgcccagat gaacctctcc accgacgcga ggatcgagga ctccctctgc 120
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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

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 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	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	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
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Tyr Ser His Thr Glu His Met Trp Val Glu Val Ser Glu Thr Glu
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<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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<211> 1231

<212> PRT

<213> Artificial

<220>

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

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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

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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
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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
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<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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ccagcgggct acgtgacgct ggagctggaa tactttcccg agacagaaca agtgtggata 3600
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gagtaa 3666

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<211> 1221

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein variant TIC867_24.

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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
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
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			
1190	1195	1200	
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1220			
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<211> 3651			
<212> DNA			
<213> Artificial			
<220>			
<223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC867_25.			
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atcgccgagg gcaacaacat cgaccggtc gtgtctgcaa gcacggtcca gaccggcatc	180		
aacatcgcg gccgcatcct gggcgtgctc ggcgtgccct tcgcgggtca aatcgctct	240		
ttctactcat tcctcgtggg cgagctgtgg ccgcgcggac gtgaccctg ggaaatcttc	300		
ctggagcacg ttgagcagct catccggcag caagtgaccg agaacaccag ggacaccgca	360		
ctggcacggc tccagggcct tggcaacagc ttccgcgcct accagcagtc gctggaggac	420		

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 ctgttcggca gtgagttcgg gctgacgagc caggagatcc agcgctacta cgagcgccaa 660
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<211> 1216
<212> PRT
<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein variant TIC867_25.

<400> 25

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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

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

Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys
660 665 670

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

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atagccgagg ggaacaatat cgatccattt gttagcgcat caacagtcca aacgggtatt 180
 aacatagctg gtagaatact aggtgtatta ggcgtaccgt ttgctggaca aatagctagt 240
 tttatagtt ttctgttg tgaattatgg ccccgcgga gagatccttg ggaaatttc 300
 ctagaacatg tcgaacaact tataagacaa caagtaacag aaaatactag ggatacggct 360
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 tggctagaaa accgtgatga tgcaagaacg agaagtgttc ttataccca atatatagcc 480
 ttagaacttg attttctaa tgcgatgccg ctttcgcaa ttagaaacca agaagttcca 540
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<212> PRT

<213> Artificial

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

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 35 40 45

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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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

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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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260 265 270

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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

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

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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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Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp Arg Thr Asn
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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
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

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595 600 605

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625 630 635 640

Leu Tyr Ile Asp Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu
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675 680 685

Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser Asp Glu Phe Cys
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Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile

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770	775	780
Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu		
785	790	795
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Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His		
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Pro Ser Pro Ile Gly Lys Cys Ala His His Ser His His Phe Ser Leu		
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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
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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

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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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<213> Artificial

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

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<210> 30

<211> 1199

<212> PRT

<213> Artificial

<220>

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

<400> 30

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

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
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> 31

<211> 3678

<212> DNA

<213> Artificial

<220>

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

<400> 31

atgacttcaa ataggaaaaa tgagaatgaa attataaatg ctttatcgat tccagctgta 60

tcgaatcatt ccgcacaaat gaatctatca accgatgctc gtattgagga tagcttggtg 120

atagccgagg ggaacaatat cgatccattt gttagcgcac caacagtcca aacgggtatt 180

aacatagctg gtagaatact aggtgtatta ggcgtaccgt ttgctggaca aatagctagt 240

ttttatagtt ttctgttgga tgaattatgg ccccgcgcca gagatccttg ggaaattttc 300

ctagaacatg tcgaacaact tataagacaa caagtaacag aaaatactag ggatacggct 360

cttgctcgat tacaagggtt aggaaattcc ttagagcct atcaacagtc acttgaagat 420

tggctagaaa accgtgatga tgcaagaacg agaagtgttc ttataccca atatatagcc 480

ttagaacttg attttcttaa tgcgatgccg ctttcgcaa ttagaaacca agaagttcca 540

ttattaatgg tatatgctca agctgcaaatt tacacctat tattattgag agatgcctct 600

cttttggtg gtgaatttgg gcttacatcc caagaaattc aacgttatta tgagcgccaa 660

gtggaaaaaa cgagagaata ttctgattat tgcgcaagat ggtataatac ggggtttaa 720

aattgagag ggacaaatgc tgaagttgg ttgcgatata atcaattccg tagagactta 780

acgctaggag tattagatct agtggcacta ttccaagct atgacacgcg tgtttatcca 840

atgaatacca gtgctcaatt aacaagagaa atttatacag atccaattgg gagaacaaat 900
 gcaccttcag gatttgcaag tacgaattgg ttaataata atgcaccatc gtttctgcc 960
 atagaggctg ccgttattag gcctccgcat ctacttgatt ttccagaaca gcttacaatt 1020
 ttcagcgtat taagtcgatg gagtaatact caatatatga attactgggt gggacataga 1080
 ctggaatcgc gaacaataag ggggtcatta agtacctcga cacacggaaa taccaatact 1140
 tctattaatc ctgtaacatt acagttcaca tctcgagacg ttatagaac agaatactt 1200
 gcagggataa atatacttct aactactcct gtgaatggag taccttgggc tagatttaat 1260
 tggagaaatc ccctgaattc tcttagaggt agccttctct atactatagg gtatactgga 1320
 gtggggacac aactattga ttcagaaact gaattaccac cagaaacaac agaacgacca 1380
 aattatgaat ctacagtca tagattatct aatataagac taatatcagg aaacacttg 1440
 agagcaccag tatattcttg gacgcaccgt agtcagatc gtacaaatac cattagtca 1500
 gatagcatta atcaaatacc ttagtgaaa ggatttagag ttggggggg cacctctgtc 1560
 attacaggac caggatttac aggaggggat atccttcgaa gaaatacctt tgggtattt 1620
 gtatctctac aagtcaatat taattacca attacccaaa gataccgtt aagattcgt 1680
 tacgctcca gtagggatgc acgagtata gtattaacag gagcggcatc cacaggagt 1740
 ggaggccaag ttagtgtaaa tatgcctct cagaaaacta tggaaatagg ggagaactta 1800
 acatctagaa catttagata taccgattt agtaatcctt ttcatttag agctaatcca 1860
 gatataattg ggataagtga acaacctcta ttggtgcag gttctattag tagcggtgaa 1920
 ctttatatag ataaaattga aattattcta gcagatgcaa catttgaggc agaataatgat 1980
 ttagaaagag cgcaaaagggt ggtgaatgcc ctgtttacgt ctacaaacca actagggcta 2040
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 gatgaattt gtctggatga aaagagagaa ttgtccgaga aagttaaaca tgcaaagcga 2160
 ctcagtgatg agcgggaatt actcaagat ccaaactca gagggatcaa taggcaacca 2220
 gaccgtggct ggagaggaag tacggatatt actatccaag gaggagatga cgtattcaaa 2280
 gagaattacg ttacgtacc gggtaacctt gatgagtgc atccaacgta ttatatcaa 2340
 aaaatagatg agtcgaaatt aaaagcctat acccggtatc aattaagagg gtatatcgaa 2400
 gatagtcaag acttagaaat ctatttaatt cggtacaatg caaacacga aatagtaaat 2460

gtaccaggta caggaagttt atggcctctt tctgtagaaa atcaaattgg accttggtga 2520
 gaaccgaatc gatgcgcgcc acaccttgaa tggaatcctg atttacactg ttcctgcaga 2580
 gacggggaaa aatgtgcaca tcatttcat catttctctt tggacattga tgttgatgt 2640
 acagacttaa atgaggactt aggtgtatgg gtgatattca agattaagac gcaagatggc 2700
 cacgcacgac tagggaatct agagttctc gaagagaaac cattattagg agaagcacta 2760
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 attattaaaa atggcgattt caataatggc ttattatgct ggaacgtgaa agggcatgta 3120
 gaggtagaag aacaaaacaa tcaccgttca gtctgggtta tccagaatg ggaggcagaa 3180
 gtgtcacaag aggttcgtgt ctgtccaggt cgtggctata tccttcgtgt tacagcgtac 3240
 aaagagggat atggagaagg ttgcgtaacg atccatgaga tcgagaacaa tacagacgaa 3300
 ctgaaattca acaactgtgt agaagaggaa gtatatccaa acaacacggt aacgtgtatt 3360
 aattatactg cgactcaaga agaatatgag ggtacgtaca ctctcgtaa tcgaggatat 3420
 gacgaagcct atggaataa ccctccgta ccagctgatt atgcgtcagt ctatgaagaa 3480
 aaatcgata cagatagacg aagagagaat cttgtgaat ctaacagagg atatggagat 3540
 tacacaccac taccagctgg ttatgtaaca aaggaattag agtactccc agagaccgat 3600
 aaggtagga ttgagattgg agaaacagaa ggaacattca tcgtggacag cgtggaatta 3660
 ctcttatgg aggaatag 3678

<210> 32

<211> 3678

<212> DNA

<213> Artificial

<220>

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

<400> 32

atgacgagca accggaagaa cgagaacgag atcatcaacg ccctctcgat ccctgctgtt 60

tcaaaccact ccgcgcagat gaacctgtcc accgacgcgc gcatcgagga ctccctctgc 120
 atagccgagg gcaacaacat cgacccattc gtgtcggcca gcacgggtca gaccggcatc 180
 aacatcgcg gccgtatcct cggcgtctc ggtgtccat tcgccgtca gatcgctcc 240
 ttctactcgt tcctgtggg cgagctgtg cctcgcggc gtgaccgtg ggagatctc 300
 ctggagcatg tggagcagtt gatccggcag caagtcacgg agaacacccg cgatactgct 360
 ctggccaggc tacagggcct gggaaactcc ttctgggcat accagcagtc actggaggac 420
 tggttggaga acagggatga cgcgcaaca cgctcggtag tctacacca gtacatcgct 480
 ctggaactcg acttctgaa cgctatgccg ctgttcgcca tcaggaacca ggaagtcca 540
 ctcttatgg ttagcggcca ggccgcaac ttacatctgc tctgctgcg ggacgccagc 600
 ctgttcggct ccgagttcgg actcacatct caagaaatcc agcgttacta cgagcgccaa 660
 gtggagaaga cccgtgagta cagtgactac tgcgctcgat ggtacaacac agggctcaac 720
 aacctgcgcg gcaccaacgc tagtcatgg ctccgttaca accagttccg ccgcgacttg 780
 actttgggtg tctagacct ggtggcgcta ttcccgtctt acgacacag ggtgtacca 840
 atgaacta gcgcgcaact cacgcgggag atctacacag acccaatcgg ccggacgaac 900
 gcaccctccg gtttcgcatc cacgaattgg ttcaacaaca acgcaccctc ctctcggca 960
 atcgaggccg ccgtcatccg cctcctcac ctgctcgact ttccgagca gtcacgac 1020
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 ttggagagta ggacgatccg tggcagcttg agcaccagta cccacggcaa caccaacacc 1140
 tccatcaacc cagttacgt acagttcac agccgcgacg ttaccggac tagtcgttc 1200
 gcgggcatta acatccttct gacaacgcc gtcaacggcg tccgtgggc ccggtcaac 1260
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 gtcggcacc agctcttga cagtgaact gagctgccg ccgagaccac ggaacgccc 1380
 aactacgagt cctacagcca ccgcctgtcc aacatccggc tcattcttg caacacgtg 1440
 cgtgcgccg tgtactctg gacacaccg agcgccgacc ggaccaacac gatctctcc 1500
 gactccatta accagatccc gctcgtgaag ggctccgtg tgtgggtgg cacgagcgtc 1560
 atcaccggtc cgggcttac cgttgagac atactcggc gcaacactt cggcgacttc 1620
 gttcgttg aagtgaacat caactcgcc atcaccagc gttaccgtt gaggttccg 1680
 tacgttcaa gccgcgacg gagggtcatt gtcctgacc gagccgcgtc cacaggcgtg 1740

ggaggccaag tctcagtaa catgcctctc cagaagacga tggagatagg cgagaacttg 1800
 actagccgaa ccttccggta cactgatttc tcgaaccctt tctcattcag agcgaaccct 1860
 gacatcattg ggatctccga gcaaccgctg ttcggtgctg gctccatcag ctctggcgaa 1920
 ctgtacatcg acaagattga gatcatcctg gcggatgcga cgttcgaggc cgagtacgac 1980
 cttgagcgcg cccagaaggt ggtgaacgcc ctcttacta gcactaacca gctaggcctg 2040
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 gacggcgaga agtgcgcccc ccatagccac cacttctctc tggacatcga cgtgggctgc 2640
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 cacgccaggc tgggtaacct ggagttcctt gaggaagagc ctctgctggg tgaggccctg 2760
 gccaggggtca agaggggtga gaagaaatgg agggataaga gggagaccct gcagctggag 2820
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 atcttcgagg aacttgagga acggatcttc actgcgttta gtctttacga tgcgcggaac 3060
 atcatcaaga acggggactt caacaatggt ctgctgtgct ggaacgtcaa gggcatgctc 3120
 gaggtcgagg aacaaaacaa tcatcgtagt gtcctgtca ttctgagtg ggaggcggag 3180
 gtctctcaag aggtccgtgt ttgccgggg cggtgggtaca ttctctgtgt tactgcgtac 3240
 aaggaggggt acggggaggg gtgcgttact attcatgaga ttgagaacaa tactgatgag 3300
 ctttaagtca acaattgtgt tgaggaggag gtttaccga acaatactgt tacgtgcatc 3360

aactacacgg caacgcaaga ggaatacagag gggacgtaca cctcgcgtaa tagagggtat 3420
gatgaggcgt acggaacaaa cccgtcgggt ccagcagatt atgcctcgggt ttatgaggag 3480
aagtcgtaca cggatagacg acgcgagaat ccatgtgagt caaatcgagg atacggagat 3540
tacacaccat taccagcagg atacgttaca aaggagttgg aatacttccc ggaaacagat 3600
aaagtttggg ttgaaatcgg agaaacagaa ggaacattca tcgtcgactc agtagaattg 3660
ttgttgatgg aagaatga 3678

<210> 33

<211> 1225

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein variant TIC868_10.

<400> 33

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

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

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

Leu Asp Glu Lys Arg 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 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			
	805	810	815
Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Val			
	820	825	830
Glu Asn Gln Ile Gly Pro Cys Gly Glu Pro Asn Arg Cys Ala Pro His			
	835	840	845
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			
	900	905	910
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			
	945	950	955
		960	
Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met Ile His Ala Ala			
	965	970	975
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
1010 1015 1020

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

His Val Glu Val Glu Glu Gln Asn Asn His Arg Ser Val Leu Val
1040 1045 1050

Ile Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys
1055 1060 1065

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

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
1190 1195 1200

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

Glu Leu Leu Leu Met Glu Glu
 1220 1225

<210> 34
 <211> 3726
 <212> DNA
 <213> Artificial

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

<400> 34
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 atagccgagg ggaacaatat cgatccattt gttagcgcac caacagtcca aacgggtatt 180
 aacatagctg gtagaatact aggtgtatta ggcgtaccgt ttgctggaca aatagctagt 240
 ttttatagtt ttcttgttgg tgaattatgg ccccgcgcca gagatccttg ggaaatttc 300
 ctagaacatg tcgaacaact tataagacaa caagtaacag aaaatactag ggatacggct 360
 cttgctcgat tacaaggttt aggaaattcc ttagagcct atcaacagtc acttgaagat 420
 tggctagaaa accgtgatga tgcaagaacg agaagtgttc ttataccca atatatagcc 480
 ttagaacttg attttcttaa tgcgatgccg ctttcgcaa ttagaaacca agaagtcca 540
 ttattaatgg tatatgctca agctgcaaatt tacacctat tattattgag agatgcctct 600
 ctttttgta gtgaatttgg gcttacatcc caagaaattc aacgttatta tgagcgccaa 660
 gtggaaaaaa cgagagaata ttctgattat tgcgcaagat ggtataatac gggtttaaatt 720
 aatttgagag ggacaaatgc tgaaagtgg ttgcgatata atcaattccg tagagactta 780
 acgctaggag tattagatct agtggcacta ttccaagct atgacacgcg tgtttatcca 840
 atgaatacca gtgctcaatt aacaagagaa atttatacag atccaattgg gagaacaaat 900
 gcaccttcag gatttgcaag tacgaattgg ttaataata atgcaccatc gtttctgcc 960
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 ttcagcgtat taagtcgatg gagtaatact caatatatga attactgggt gggacataga 1080
 cttgaatcgc gaacaataag ggggtcatta agtacctcga cacacggaaa taccaatact 1140
 tctattaatc ctgtaacatt acagttcaca tctcgagacg ttatagaac agaattcatt 1200

gcagggataa atatacttct aactactcct gtgaatggag taccttgggc tagatttaat 1260
 tggagaaatc ccttgaattc tcttagaggt agccttctct atactatagg gtatactgga 1320
 gtggggacac aactatttga ttcagaaact gaattaccac cagaaacaac agaacgacca 1380
 aattatgaat ctacagtca tagattatct aatataagac taatatcagg aaacactttg 1440
 agagcaccag tatattcttg gacgcaccgt agtcagatc gtacaaatac cattagtca 1500
 gatagcatta atcaaatacc tttagtgaat ggatttagag ttgggggggg cacctctgtc 1560
 attacaggac caggatttac aggaggggat atccttcgaa gaaatacctt tgggtatttt 1620
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 tacgcttcca gtagggatgc acgagtata gtattaacag gagcggcatc cacaggagtg 1740
 ggaggccaag ttagtgtaaa tatgcctctt cagaaaacta tggaaatagg ggagaactta 1800
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 gatataattg ggataagtga acaacctcta tttggtgcag gttctattag tagcggtgaa 1920
 ctttatatag ataaaattga aattattcta gcagatgcaa caggaacgac aacctatgag 1980
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 gataatcccc ttttaagggt gaattattta aaaatgtttg gggcaagaga tattgatgga 2340
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 tacgctacat tagggaatct agaagtcatt gaagaaggac cactaacaga tgaagcattg 2820
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 caacaaatag atggagcttc agtattagti ctatcaaact ggagtgccga ggtatctcag 3240
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 tgtatgcaag gatatgctag cgataataac ccgcacacgg gtaatatgta tgagcaaagt 3540
 tataatggaa attataatca aaatactagc gatgtgtatc accaaggata tataaacaac 3600
 tataacaaa attctagtag tatgtataat caaaattata ttaacaatga tgacctgcat 3660
 tccggttgca catgtaacca agggcataac tctggctgta catgtaatca aggatataac 3720
 cgttag 3726

<210> 35
 <211> 3726
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC868_11.

<400> 35
 atgacgagca accggaagaa cgagaacgag atcatcaacg ccctctcgat ccctgctgtt 60
 taaaccact ccgcgcatg gaacctgtcc accgacgcgc gcatcgagga ctccctctgc 120
 atagccgagg gcaacaacat cgaccattc gtgtcggcca gcacgggtca gaccggcatc 180
 aacatcgcg gccgtatcct cggcgtctc ggtgtccat tcgccgtca gatcgcttc 240
 ttctactcgt tcctgtggg cgagctgtg cctcgcggtc gtgaccgtg ggagatctc 300
 ctggagcatg tggagcagtt gatccggcag caagtcacgg agaacaccg cgatactgct 360
 ctggccaggc tacagggcct gggaaactcc ttccggcat accagcagtc actggaggac 420

tgggtggaga acagggatga cgcgcggaaca cgctcggtac tctacacca gtacatcgct 480
 ctggaactcg acttctgaa cgctatgccg ctgttcgcca tcaggaacca ggaagtcca 540
 ctcttatgg tgtacgcca ggccgccaac ttacatctgc tcctgctgcg ggacgccagc 600
 ctgttcggct ccgagttcgg actcacatct caagaaatcc agcgttacta cgagcgccaa 660
 gtggagaaga cccgtgagta cagtactac tgcgctcgat ggtacaacac agggctcaac 720
 aacctgcgcg gcaccaacgc tgagtcatgg ctccgttaca accagttccg ccgcgacttg 780
 actttgggtg tctagacct ggtggcgcta ttccgtctt acgacacag ggtgtacca 840
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 gcaccctccg gtttcgcatc cacgaattgg ttcaacaaca acgcaccctc ttctcggca 960
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 ttggagagta ggacgatccg tggcagcttg agcaccagta cccacggcaa caccaacacc 1140
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 gactccatta accagatccc gctcgtgaag ggctccgtg tgtggggtg cacgagcgtc 1560
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 tacaaccaga acagcagcag catgtacaac cagaactaca tcaacaacga tgactgcac 3660
 tcgggttgca cctgcaacca gggtcacaac agtgggtgca cgtgcaacca gggatacaac 3720

cgttga

3726

<210> 36

<211> 1241

<212> PRT

<213> Artificial

<220>

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

<400> 36

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
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
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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atagccgagg ggaacaatat cgatccattt gttagcgcac caacagtcca aacgggtatt    180
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<211> 3468

<212> DNA

<213> Artificial

<220>

<223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC868_12.

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<211> 1155

<212> PRT

<213> Artificial

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<223> Amino acid sequence of the chimeric protein variant TIC868_12.

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

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740 745 750

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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
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His Ile Asp Ser Ile Glu Phe Val Glu Thr Glu Lys
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 <211> 3732
 <212> DNA
 <213> Artificial

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 <223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC868_13.

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 gaaatcttcg aggaactgga gggccgcatt atcacggcaa tctcacttta tgacgcgagg 3120
 aatgtggtca agaacggtga cttcaacaac ggcttggcgt gttggaacgt taaagggcac 3180
 gtggatgtac aacagtcaca ccacagaagt gtcttggta tcccggagtg ggaggcgga 3240
 gtgagccagg ccgtccgggt ctgccctggg cgcggttaca tcctccgctg gacagcgtac 3300
 aaggagggct acggtgaggg ctgctgacg atccacgaga ttgagaacaa cacggacgag 3360
 cttagtca agaactgcga ggaggaggaa gtgtaccga cagacaccgg cacctgcaac 3420
 gactacaccg cccaccaagg gaccgccgcc tgcaacagcc gcaacgcggg ctatgaagat 3480
 gcgtacgagg ttgataccac cgcctcagtg aactacaaac cgacttatga ggaggagaca 3540
 tacacggacg tcaggcgcga caaccattgt gactacgacc gtggctacgt gaactatccg 3600
 ccggtgccag cgggctacat gacgaaggag ctagaatact tcctgagac ggacaaggtg 3660
 tggattgaaa tcggcgagac cgagggcaag ttatcgtgg attctgtcga gctgctgcta 3720
 atggaggagt ag 3732

<210> 41

<211> 1243

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein variant TIC868_13.

<400> 41

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 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.

<400> 42
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 tcaaaccact ccgcgcagat gaacctgtcc accgacgcgc gcatcgagga ctccctctgc 120
 atagccgagg gcaacaacat cgaccattc gtgtcggcca gcacggttca gaccggcatc 180
 aacatcgcg ggcgtatcct cggcgtctc ggtgtcccat tcgccggtca gatcgcgctc 240
 ttctactcgt tcctgtggg cgagctgtgg cctcgcggtc gtgaccctg ggagatctc 300
 ctggagcatg tggagcagtt gatccggcag caagtcacgg agaacaccg cgatactgct 360
 ctggccaggc tacagggcct gggaaactcc ttctgggcat accagcagtc actggaggac 420
 tggttggaga acagggatga cgcgcaaca cgctcggtac tctacacca gtacatcgct 480

ctcgaaactcg acttcttgaa cgctatgccg ctgttcgccca tcaggaacca ggaagttcca 540
 ctcttatgg tgtacgcca ggccgccaac ttacatctgc tctgctgcg ggacgccagc 600
 ctgttcggct ccgagttcgg actcacatct caagaaatcc agcgttacta cgagcgccaa 660
 gtggagaaga cccgtgagta cagtgactac tgcgctcgat ggtacaacac agggctcaac 720
 aacctgcgcg gcaccaacgc tgagtcattg ctccgttaca accagttccg ccgcgacttg 780
 actttgggtg tcttagacct ggtggcgcta ttccgtctt acgacacacg ggtgtacca 840
 atgaacacta gcgcgcaact cacgcgggag atctacacag acccaatcgg ccggacgaac 900
 gcaccctccg gtttcgcatc cacgaattgg ttcaacaaca acgcaccctc cttctcgga 960
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 ttggagagta ggacgatccg tggcagcttg agcaccagta cccacggcaa caccaacacc 1140
 tccatcaacc cagttacgct acagttcacg agccgcgacg ttaccggac tgagtcgttc 1200
 gcgggcatta acatccttct gacaacgccc gtcaacggcg tcccgtaggc ccggttcaac 1260
 tggcgtaacc cgttgaactc cctgcgcggg tcattgtct acaccatcgg gtacacgggc 1320
 gtcggcacc agctcttga cagtgaact gagctgccgc ccgagaccac ggaacgcccg 1380
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 cgtgcgccg tgtactcctg gacacaccgc agcgccgacc ggaccaacac gatctcttc 1500
 gactccatta accagatccc gctcgtgaag ggctccgtg tgtggggtg cacgagcgtc 1560
 atcaccggtc cgggcttcac cgttgagac atactgcggc gcaacactt cggcgacttc 1620
 gtttcgtgc aagtgaacat caactcgccg atcaccagc gttaccgtct gaggttccgc 1680
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caggacgggc acgcgaaact aggaaacctg gagttcatcg aggagaagcc actcctcggc 2760
aaggcacttt ccaggggtcaa gcggggccgag aagaaatgga gggacaagta cgagaaactc 2820
cagctcgaac caaagcgggt gtacacggag gcaaaggaat ccgtggacgc cctgttcgtg 2880
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aacgcggcga tcttcgagga actggagggc cacatcttca aggcgtattc tctgtacgac 3060
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gcggaggtgt ccagaaggt gcgcgtgtgc ccggtatcgc gctacatctt gagggtgaca 3240
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gatgtcctga aattccgtaa ctctcgcgag gaggaggctt atccaacaa caccgtgacc 3360
tgcaacgact acacgaccaa tcagtcggct gagggcagta ccgatgcctg caacagctac 3420
aaccgtggtt acgaagatgg atacgagaac cgctacgagc ccaatcctc ggctcccgtg 3480
aattacactc ccacgtacga ggagggcatg tacactgaca ctcagggcta caaccattgc 3540
gtcagcgacc gtggctaccg caaccacacg ccgctcccag cgggctacgt gacgctggag 3600
ctggaatact tcccagagac agaacaagtg tggatagaga tcggcgagac cgagggcaca 3660
ttcatcgtgg gctctgtgga attgctctc atggaggagt aa 3702

<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
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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
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
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

<210> 44

<211> 3687

<212> DNA

<213> Artificial

<220>

<223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC868_15.

<400> 44

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tcaaaccact ccgcgcagat gaacctgtcc accgacgcgc gcatcgagga ctccctctgc 120

atagccgagg gcaacaacat cgaccattc gtgtcggcca gcacggttca gaccggcatc 180

aacatcgcgg gccgtatcct cggcgtctc ggtgtccat tcgccggtca gatcgcgctc 240

ttctactcgt tccttggtgg cgagctgtgg cctcgcggtc gtgacccgtg ggagatcttc 300
 ctggagcatg tggagcagtt gatccggcag caagtcacgg agaacacccg cgatactgct 360
 ctggccaggc tacagggcct gggaaactcc ttccgggcat accagcagtc actggaggac 420
 tggttggaga acagggatga cgcgcgaaca cgctcggtag tctacacca gtacatcgct 480
 ctcgaactcg acttctgaa cgctatgccg ctgttcgcca tcaggaacca ggaagttcca 540
 ctcttatgg tgtacgcca ggccgccaac ttacatctgc tctgctgcg ggacgccagc 600
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 gtggagaaga cccgtgagta cagtactac tgcgctcgat ggtacaacac agggctcaac 720
 aacctgcgcg gcaccaacgc tgagtcattg ctccgttaca accagttccg ccgcgacttg 780
 actttgggtg tcctagacct ggtggcgcta ttccgtctt acgacacacg ggtgtacca 840
 atgaacacta gcgcgcaact cacgcgggag atctacacag acccaatcgg ccggacgaac 900
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cagggctatg acgaagccta tgggaacaac ccgtcgggtc ctgctgacta tgcgtcggtc 3480
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tatggtgact acacgccgct accggcgggc tatgtaacga aagacctgga atactcccg 3600
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gtagagctgc tgctcatgga ggagtga 3687

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<211> 1228
<212> PRT
<213> Artificial

<220>
<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	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	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
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Asp Ser	Val Glu Leu Leu Leu	Met Glu Glu
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<210> 46
<211> 3600
<212> DNA
<213> Artificial

<220>

<223> Synthetic nucleotide sequence designed for expression in a plant cell encoding TIC868_29.

<400> 46

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atagccgagg gcaacaacat cgaccattc gtgtcggcca gcacgggtca gaccggcatc    180
aacatcgcgg gccgtatcct cggcgctctc ggtgtcccat tcgccggtca gatcgcgctc    240
tttactcgt tccttgtagg cgagctgtgg cctcgcggtc gtgaccctg ggagatctc    300
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ttggagagta ggacgatccg tggcagcttg agcaccagta cccacggcaa caccaacacc    1140
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gcgggcatta acatccttct gacaacgcc gtcaacggcg tccgtgggc ccggttcaac    1260
tggcgtaacc cgttgaaact cctgcgctgg tcattgtct acaccatcgg gtacacgggc    1320
gtcggcacc agctcttca cagtgaact gagctgccgc ccgagaccac ggaacgcccg    1380
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<210> 47

<211> 1199

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein variant TIC868_29.

<400> 47

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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 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
 atggagataa ataatcagaa gcaatgcata ccatataatt gcttaagtaa tcctgaggaa 60
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 cttttgcaat ttctttgaa taactttgtt ccagggggag gctttatttc aggattagtt 180
 gataaaatat ggggggcttt gagaccatct gaatgggact tatttcttgc acagattgaa 240
 cgggtgattg atcaaagaat agaagcaaca gtaagagcaa aagcaatcac tgaattagaa 300
 ggattagggga gaaattatca aatatacgct gaagcattta aagaatggga atcagatcct 360
 gataacgaag cggctaaaag tagagtaatt gatcgcttgc gtatacttga tggcttaatt 420
 gaagcaaata tcccttcatt tcggataatt ggatttgaag tgccactttt atcggtttat 480
 gttcaagcag ctaatctaca tctcgctcta ttgagagatt ctgttatttt tggagagaga 540
 tggggattga cgacaaaaaa tgtcaatgat atctataata gacaaattag agaaattcat 600
 gaatatagca atcattgcgt agatacgat aacacagaac tagaacgtct agggtttaga 660
 tctatagcgc agtggagaat atataatcag tttagaagag aactaacact aactgtatta 720
 gatattgtcg ctctttccc gaactatgac agtagactgt atccgatcca aacttttct 780
 caattgacaa gagaaattgt tacatcccca gtaagcgaat ttattatgg tgttattaat 840
 agtggtaata taattggtac tcttactgaa cagcagataa ggcgaccaca tcttatggac 900
 ttcttaact ccatgatcat gtatacatca gataatagac gggaacatta ttggtcagga 960
 cttgaaatga cggcttattt tacaggattt gcaggagctc aagtgtcatt cccttagtc 1020
 gggactagag gggagtcagc tccaccatta actgtagaa gtgttaatga tggaatttat 1080
 agaatattat cggcaccgtt ttattcagcg cctttctag gcaccattgt attgggaagt 1140
 cgtggagaaa aatttgattt tgcgcttaat aatatttcac ctccgccatc tacaatatac 1200

agacatcctg gaacagtaga ttcactagtc agtataccgc cacaggataa tagcgtacca 1260
 ccgcacaggg gatctagtca tcgattaagt catgttacaa tgcgcgcaag tcccctata 1320
 ttccattgga cgcatcgcag cgcaaccact acaaatacaa ttaatccaaa tgctattatc 1380
 caaataccac tagtaaaagc attaacctt cattcagggtg ccactgttgt tagaggacca 1440
 gggtttacag gtggagatct cttacgaaga acgaatactg gtacatttgc agacataaga 1500
 gtcaatgttc cttcatcact attttccaa agatatcgcg taaggattcg ttatgcttct 1560
 actaccgatt tacaatttt cacgagaatt aatggaactt ctgttaatca aggtaatttc 1620
 tcaaaaacga tggatagagg ggataaactg aaatctgaaa actttagaac tgccggattt 1680
 agtactcctt ttagattttc aaatttcaa agtacattca cgttgggtac tcaggctttt 1740
 tcaaatacagg aagtttatat agatagaatt gaattgtcc cggcagaagt aacattcgag 1800
 gcagaatctg atttagaaag agcacaaaag gcggtgaatg agctgtttac ttctccaat 1860
 caaatcgggt taaaaacaga tgtgacggat tatcatattg atcaagtatc caatttagtt 1920
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 catgcgaagc gacttagtga tgagcggaat ttacttcaag atccaaactt tagagggatc 2040
 aatagacaac tagaccgtgg ctggagagga agtacggata ttaccatcca aggaggcgat 2100
 gacgtattca aagagaatta cgttacgcta ttgggtacct ttgatgagtg ctatccaacg 2160
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 attgtttata aagaggcaaa agaactgtga gatgctttat ttgtaaactc tcaatatgat 2640
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 aaaaatggtg atttaataa tggcttatcc tgctggaacg tgaaagggca ttagatgta 2880

gaagaacaaa acaaccaccg ttcggtcctt gttgttcgg aatgggaagc agaagtgta 2940
 caagaagttc gtgtctgtcc gggtcgtggc tatatcctc gtgtcacagc gtacaaggag 3000
 ggatatggag aaggttcgt aaccattcat gagatcgaga acaatacaga cgaactgaag 3060
 ttagcaact gtgtagaaga ggaagtatat ccaaacaaca cggtaacgtg taatgattat 3120
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 gcctatgaaa gcaattctc tgtaccagct gattatgcat cagcctatga agaaaaagca 3240
 tatacatgac gacgaagaga caatccttgt gaatctaaca gaggatatgg ggattacaca 3300
 ccactaccag ctggctatgt gacaaaagaa ttagagtact tcccagaaac cgataaggta 3360
 tggattgaga tcggagaaac ggaaggaaca ttcacgtgg 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

atggagataa acaaccagaa gcagtcatt ccgtacaact gcctcagcaa cccggaggag 60
 gtgtctgtgg acggcgagcg tctctccca gacatcgacc cactggaggt cagcctgagc 120
 ctctccagt tctctctcaa taacttcgtg ccaggcggcg gcttcattc cggcctggtg 180
 gacaagatct ggggcgcact ccggccaagt gaggggatc tgttctggc ccaaatcgag 240
 cgctgatcg accagaggat cgaggcgacg gtccgcgcca aggcgataac cgagctggag 300
 ggctcggtc gcaactacca gatctacgca gaggcgttca aggagtggga gagcgaccg 360
 gacaacgagg cggccaagtc tcgggtgatt gaccgcttc gcatcctga cggcctcatc 420
 gaagccaaca tcccttctt ccgatcata ggcttcgaag tccgctcct cagcgtgtac 480
 gtgcaagcgg ccaatctcca ctcgcttg ctccgtgaca gcgtcatctt tggcgagaga 540
 tggggcctga cgacgaagaa cgtgaacgac atctacaaca ggcagatccg agagattcac 600
 gagtacagca accactcgt ggacacatac aacacggagc tggagcggct cggctccgc 660
 tcaatcgctc agtggcggat ctacaaccag ttccgccgag agctgaccct caccgtgctc 720

gacatcgtcg cattgtttcc caattacgac tcacgcctct acccaatcca gactttcagc 780
cagctcacac gcgagattgt gaccagcccc gtgtcagagt tctactacgg cgatcatcaac 840
tcaggcaaca tcacggggac actgactgaa cagcagatca gacgtccgca ctgatggac 900
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agaatactgt cggctccctt ctacagtgcg ccgttctcgc gcaccatcgt cctcgggtca 1140
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tcgacaccgt tcagattcag caactccag agcacttca cgctgggcac acaggcgttc 1740
tccaaccagg aggtgtacat cgaccgcac gagttcgtgc ctgctgaggt taccttcgag 1800
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cagatcggtc tcaagaccga cgtcactgac tatcacattg accaagtcag caacctgggt 1920
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cacgcaaagc gcttgagcga cgagcgcaac ctctccagg acccgaattt ccgtggtatc 2040
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gatgtgtca aggagaatta tgttacgctg ctcggtacgt tcgacgagtg ctatcccacg 2160
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 aagaacggcg acttcaacaa cggctcttcc tgttgaacg tgaagggcca cgtggatgtc 2880
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 ggctacggcg aaggctgctg 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 gacggcgcg caatccctgc gagagtaacc gtggatacgg agattacacg 3300
 ccgctacccg ctggctacgt cactaaggaa ctggagtact tcccagagac ggacaagggtg 3360
 tggatcga aa tcggcgagac agagggcacg ttcacgtgg 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
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
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
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 gaaatattaa atgaagaaag aagtactggc agattaccgt tagatatatc cttatcgctt 120
 acacgtttcc ttttgagtga attgttcca ggtgtgggag ttgcgtttgg attatttgat 180
 ttaatatggg gttttataac tccttctgat tggagcttat ttctttaca gattgaacaa 240
 ttgattgagc aaagaataga aacattggaa aggaaccggg caattactac attacgaggg 300
 ttagcagata gctatgaaat ttatattgaa gcactaagag agtggaagc aaatcctaata 360
 aatgcacaat taagggaaga tgtgcgtatt cgatttgcta atacagacga cgctttaata 420
 acagcaataa ataattttac acttacaagt ttgaaatcc ctctttatc ggtctatgtt 480
 caagcggcga atttacattt atcactatta agagacgctg tatcgtttgg gcaggggttg 540
 ggactggata tagctactgt taataatcat tataatagat taataaatct tattcataga 600
 tatacgaaac attgtttgga cacatacaat caaggattag aaaacttaag aggtactaat 660
 actcgacaat gggcaagatt caatcagttt aggagagatt taacacttac tgtattagat 720
 atcgttgctc ttttccgaa ctacgatgtt agaacatac caattcaaac gtcacccaa 780
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gtagcatttc aacaaactgg tacgaaccac acccgaacat ttagaaatag tgggaccata 1200
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 gtcgttaaag gaccaggatt tacaggagga gatattcttc gaagaacttc acctggccag 1500
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 cgttatcaat taagagggtat ttcgaagat agtcaagact tagaaatcta ttaattcgc 2280
 tacaatgcaa aacatgaaac agtaaattgt ccaggtagcg gttccttatg gccgcttca 2340
 gcccaaagtc caatcggaag gtgtggagag ccgaatcgat gcgcgccaca ccttgaatgg 2400
 aatcctgact tagattgttc gtgtagggtat ggagaaaagt gtgccatca ttcgcatcat 2460
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 gaaaaacat tagtaggaga agcgctagct cgtgtgaaaa gagcggagaa aaaatggaga 2640
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tctgtgattc cgggtgtcaa tgcggctatt tttgaagaat tagaagggcg tattttact 2880
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agaggggtata gggattacac gccactacca gttgggtatg 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
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accgcttcc tccttagtga gttcgtgcc ggctgtggcg tggccttcgg cctcttcgac 180
ctcatctggg gcttcatcac tccttcgac tggtcctct tcctcctca gattgagcaa 240
ctgatcgagc agcgcatcga gaccctgag cgcaaccgcg ccatcaccac tctcagaggt 300
ctgccgact cctacgaaat ctacatcgag gcactccgtg agtgggaggc caaccgaaac 360
aatgcccagc tccgcgagga cgtgaggatc agattcgcca acaccgacga tgccctcatc 420
accgccatca acaatttcac cctcacctcc ttcgagatcc ctcttctgtc tgtgtacgtt 480
caagctgcta accttcacct ttcctcctg cgcgacgccg tgagcttcgg ccagggtcgtg 540
ggcctcgaca tcgccaccgt gaacaatcac tacaaccgcc tcatcaacct catccaccgc 600

tacaccaagc actgccttga cacctacaac cagggccttg agaacctccg tggcaccaac 660
 acccgccagt gggcccgtt caaccagttc cgagagacc tcacctcac cgtgctcgac 720
 atcgtggcac tcttccaaa ctacgacgtg cgtacctacc ctatccagac ctccagccag 780
 ctaccaggg aaatctacac ctccagcgtg atcgaggact ctctgtgtc cgccaacatc 840
 cctaacggct tcaaccgcgc cgagttcggc gtgcgccctc ctacctcat ggacttcatg 900
 aactccctct tcgtactgc cgagaccgtg cgctcccaga ccgtgtggg cggtcacctc 960
 gtgtccagcc gtaacaccgc tggcaacagg atcaacttc cgtctacgg cgtgttcaac 1020
 ccaggcgggtg ccatctggat cgccgatgaa gacctcgtc ctttctaccg taccctgtcc 1080
 gacctgtgt tcgtgcgtg cggttcggc aacctcact acgtgctggg cctgcgtggc 1140
 gtggccttc agcaaaccgg caccaaccac accaggacgt tccgtaactc cggcaccatc 1200
 gacagtcttg acgagatccc tccgcaagac aactccgggtg caccttgga cgactactcc 1260
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 atcagcactc tgagggtgaa catcactgct ccgctgagcc agcggtacag ggtcagaatc 1560
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 gtcagtaacc tggtcacgta cctgtctgac gagttctgtc ttgacgagaa gcgggagctg 1980
 tctgagaagg tcaagcacgc taagcggctg tctgacgagc ggaacctgct tcaagacagt 2040
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 gagtgctatc caacgtacct ttaccagaag attgacgagt cgaagctgaa ggcttcact 2220

cgttaccagc ttcgtgggta cattgaggac tcgcaagacc tcgaaatcta cctcattcgt 2280
 tacaacgcta agcacgagac tgtcaacgct cctgggtacgg gtagtctttg gccgctttct 2340
 gctcagtcgc cgattggcaa gtgtggcgag ccgaaccgtt gcgctcctca cttggagtgg 2400
 aacccgatc tcgattgctc gtgccgtgac ggtgagaagt gcgcgcacca tagtcatcac 2460
 tttagccttg acattgatgt cggttgcacg gatcttaacg aggatcttgg agtctgggtg 2520
 attttcaaga tcaaaactca ggatgggcac gcgcgtcttg ggaatcttga gttctggag 2580
 gagaagccac ttgtcgggta ggcgcttgcg cgtgtcaagc gtgcggagaa gaaatggcgt 2640
 gataagcgtg agaagtggga 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 aagaaatggt attaagaatg gagatttcaa caatgggttg 2940
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 ttggtgttac cagagtggga ggcagagggt tcacaagagg tgagagtttg cccaggcaga 3060
 ggctacatct tgagagttac agcatacaaa gagggatacg gcgagggatg tgttacaatc 3120
 cacgaaatcg agaacaatac cgatgagcta aagtttcaa 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 attcatcgtt 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

<210> 54

<211> 3588

<212> DNA

<213> Artificial

<220>

<223> Chimeric coding sequence encoding TIC713

<400> 54

atggataaca atccgaacat caatgaatgc attccttata attgtttaag taaccctgaa 60

gtagaagtat taggtggaga aagaatagaa actgggtaca cccaatcga tatttccttg 120

tcgctaacgc aatttcttt gagtgaattt gttcccgggtg ctggatttgt gtaggacta 180

gttgatataa tatggggaat tttgggtccc tctcaatggg acgcatttct tgtacaaatt 240

gaacagttaa ttaaccaaag aatagaagaa ttcgctagga accaagccat ttctagatta 300

gaaggactaa gcaatcttta tcaaatttac gcagaatctt ttagagagtg ggaagcagat 360

cctactaatc cagcattaag agaagagatg cgtattcaat tcaatgacat gaacagtgcc 420

cttacaaccg ctattcctct tttggcagtt caaaattatc aagttcctct ttatcagta 480

tatgttcaag ctgcaaattt acatttatca gtttgagag atgtttcagt gtttgacaa 540

aggtggggat ttgatgccgc gactatcaat agtcgttata atgatttaac taggcttatt 600

ggcaactata cagattatgc tgtacgtggt tacaatacgg gattagaacg tgtatgggga 660

ccggattcta gagattgggt aaggataat caatttagaa gagaattaac actaactgta 720

ttagatatcg ttgctctgtt cccgaattat gatagtagaa gatatccaat tcgaacagtt 780

tccaattaa caagagaaat ttatacaaac ccagtattag aaaatttga tggtagttt 840
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 aacagtataa ccatctatac ggatgctcat aggggttatt attattggtc agggcatcaa 960
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 tacagaaaaa gcggaacggt agattcgctg gatgaaatac cgccacagaa taacaacgtg 1260
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 cgtagaacia atacgggtac atttgagat atacgattaa atattaatgt gccattatcc 1560
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 caaagcacat tcacattggg tgctcagagt tttcaaac aggaagtta tatagataga 1800
 gtcgaattg ttccagcaga ggtaacatt gaggcagaat atgattaga aagagcacia 1860
 aaggcggta atgctctgt tacttctaca aatccaagaa gattgaaaac agatgtgaca 1920
 gattatcata ttgaccaagt gtccaatag gtggcatgtt tatcagatga attttgctg 1980
 gatgagaagc gagaattatt tgagaaagt aaatatgca agcgactcag tgatgaaaga 2040
 aacttactcc aagatccaaa cttcacattc atcagtgggc aattaagttt cgcattcatc 2100
 gatggacaat caaactccc ctctattaat gagctatctg aacatggatg gtggggaagt 2160
 gcgaatgta ccattcagga aggaatgac gtatttaaag agaattacgt cactaccg 2220
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tggccgcttt cagttgaaag cccaatcgga aggtgctggag aaccaaactg atgctgcacca 2460
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 ccggggcgtg gctatattct tcgtgtcaca gcgtacaaag agggatatgg agagggtctg 3180
 gtaacgatcc atgaaatcga gaacaataca gacgaactaa aatttaaaaa ctgtgaagaa 3240
 gaggaagtgt atccaacgga tacaggaacg tgtaatgatt atactgcaca ccaaggtaca 3300
 gcagcatgta attcccgtaa tgctggatat gaggatgcat atgaagttga tactacagca 3360
 tctgttaatt acaaaccgac ttatgaagaa gaaacgtata cagatgtacg aagagataat 3420
 cattgtgaat atgacagagg gtatgtgaat tatccaccag taccagctgg ttatgtgaca 3480
 aaagaattag aatacttccc agaaacagat acagtatgga ttgagattgg agaaacggaa 3540
 ggaaagttta ttgtagatag cgtggaacta ctctcatgg aagaatag 3588

<210> 55

<211> 1195

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC713.

<400> 55

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu

1

5

10

15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
20 25 30

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

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

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

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110

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

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140

Ile Pro Leu Leu Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160

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

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240

Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285

Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
450 455 460

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

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

Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe Gly Asp Ile Arg
500 505 510

Leu Asn Ile Asn Val Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
515 520 525

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

Thr Val Asn Ile Gly Asn Phe Ser Arg Thr Met Asn Arg Gly Asp Asn
545 550 555 560

Leu Glu Tyr Arg Ser Phe Arg Thr Ala Gly Phe Ser Thr Pro Phe Asn
565 570 575

Phe Leu Asn Ala Gln Ser Thr Phe Thr Leu Gly Ala Gln Ser Phe Ser
580 585 590

Asn Gln Glu Val Tyr Ile Asp Arg Val Glu Phe Val Pro Ala Glu Val
595 600 605

Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val Asn
610 615 620

Ala Leu Phe Thr Ser Thr Asn Pro Arg Arg Leu Lys Thr Asp Val Thr
625 630 635 640

Asp Tyr His Ile Asp Gln Val Ser Asn Met Val Ala Cys Leu Ser Asp
645 650 655

Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Phe Glu Lys Val Lys Tyr
660 665 670

Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe

675	680	685			
Thr Phe Ile Ser Gly Gln Leu Ser Phe Ala Ser Ile Asp Gly Gln Ser					
690	695	700			
Asn Phe Pro Ser Ile Asn Glu Leu Ser Glu His Gly Trp Trp Gly Ser					
705	710	715	720		
Ala Asn Val Thr Ile Gln Glu Gly Asn Asp Val Phe Lys Glu Asn Tyr					
	725	730	735		
Val Thr Leu Pro Gly Thr Phe Asn Glu Cys Tyr Pro Asn Tyr Leu Tyr					
	740	745	750		
Gln Lys Ile Gly Glu Ser Glu Leu Lys Ala Tyr Thr Arg Tyr Gln Leu					
	755	760	765		
Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg					
	770	775	780		
Tyr Asn Ala Lys His Glu Thr Leu Asp Val Pro Gly Thr Asp Ser Leu					
785	790	795	800		
Trp Pro Leu Ser Val Glu Ser Pro Ile Gly Arg Cys Gly Glu Pro Asn					
	805	810	815		
Arg Cys Ala Pro His Phe Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys					
	820	825	830		
Arg Asp Gly Glu Arg Cys Ala His His Ser His His Phe Thr Leu Asp					
	835	840	845		
Ile Asp Val Gly Cys Thr Asp Leu His Glu Asn Leu Gly Val Trp Val					
	850	855	860		
Val Phe Lys Ile Lys Thr Gln Glu Gly Tyr Ala Arg Leu Gly Asn Leu					
865	870	875	880		
Glu Phe Ile Glu Glu Lys Pro Leu Ile Gly Glu Ala Leu Ser Arg Val					
	885	890	895		

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

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

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

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

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

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

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

Val Lys Gly His Val Asp Val Gln Gln Ser His His Arg Ser Asp
1010 1015 1020

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

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

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

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

Tyr Pro Thr Asp Thr Gly Thr Cys Asn Asp Tyr Thr Ala His Gln
1085 1090 1095

Gly Thr Ala Ala Cys Asn Ser Arg Asn Ala Gly Tyr Glu Asp Ala
1100 1105 1110

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

Glu Glu Glu Thr Tyr Thr Asp Val Arg Arg Asp Asn His Cys Glu
 1130 1135 1140

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

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

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

Glu Leu Leu Leu Met Glu Glu
 1190 1195

<210> 56
 <211> 3531
 <212> DNA
 <213> Artificial

<220>
 <223> Chimeric coding sequence encoding TIC843.

<400> 56
 atggataaca atccgaacat caatgaatgc attccttata attgtttaag taaccctgaa 60
 gtagaagtat taggtggaga aagaatagaa actgggtaca cccaatcga ttttccttg 120
 tcgctaacgc aatttcttt gagtgaattt gttcccgggtg ctggatttgt gtaggacta 180
 gttgatataa tatggggaat ttttggccc tctcaatggg acgcatttct tgtacaaatt 240
 gaacagttaa ttaaccaaag aatagaagaa ttcgctagga accaagccat ttctagatta 300
 gaaggactaa gcaatcttta tcaaatttac gcagaatctt ttagagagtg ggaagcagat 360
 cctactaatc cagcattaag agaagagatg cgtattcaat tcaatgacat gaacagtgcc 420
 cttacaaccg ctattcctct ttggcagtt caaaattatc aagttcctct ttatcagta 480
 tatgttcaag ctgcaaattt acatttatca gtttgagag atgtttcagt gtttgacaa 540
 aggtggggat ttgatccgc gactatcaat agtcgttata atgatttaac taggcttatt 600
 ggcaactata cagattatgc tgtacgtggt tacaatacgg gattagaacg tgtatgggga 660

ccggattcta gagattgggt aaggataat caatttagaa gagaattaac actaactgta 720
 ttagatatcg ttgctctgtt cccgaattat gatagtagaa gatatccaat tcgaacagtt 780
 tccaattaa caagagaaat ttatacaaac ccagtattag aaaatttga tggtagttt 840
 cgaggctcgg ctcagggcat agaaagaagt attaggagtc cacatttgat ggatatactt 900
 aacagtataa ccatctatac ggatgctcat aggggttatt attattggtc agggcatcaa 960
 ataatggctt ctctgtcgg ttttcgggg ccagaattca cgttccgct atatggaacc 1020
 atgggaaatg cagctccaca acaacgtatt gttgctcaac taggtcaggg cgtgtataga 1080
 acattatcgt ccactttata tagaagacct ttaatatag ggataaataa tcaacaacta 1140
 tctgttcttg acgggacaga atttgcttat ggaacctct caaatttgcc atccgctgta 1200
 tacagaaaaa gcggaacggg agattcgctg gatgaaatac cgccacagaa taacaacgtg 1260
 ccacctaggc aaggatttag tcatcgatta agccatgtt caatgttctg ttcaggcttt 1320
 agtaatagta gtgtaagtat aataagagct cctatgttct cttggataga tcgtagtgt 1380
 gaatttaata atacgattgg accaaataga attacacaaa taccattggg aaaagcactg 1440
 aatcttcatt cagggtgtac tgtgttgga gggccaggat ttacaggtgg ggatatacctt 1500
 cgtagaacia atacgggtac atttgagat atacgattaa atattaatgt gccattatcc 1560
 caaagataac gcgtaaggat tcgttatgct tctactacag atttacaatt ttcacgaga 1620
 attaatggaa ccactgttaa tattggtaat ttctcaagaa ctatgaatag gggggataat 1680
 ttagaatata gaagtttag aactgcagga ttagtactc ctttaattt tttaaagcc 1740
 caaagcacat tcacattggg tgctcagagt tttcaaac aggaagtta tatagataga 1800
 gtcgaatttg ttccagcaga ggtaacatt gaggcagaat atgatttaga aagagcgcag 1860
 aaggcgggta atgcgctgtt tacgtctaca aaccaactag ggctaaaaac aaatgtaacg 1920
 gattatcata ttgatcaagt gtccaattta gttacgtatt tatcggatga atttgtctg 1980
 gatgaaaagc gagaattgtc cgagaaagtc aaacatgcga agcgactcag tgatgaacgc 2040
 aatttactcc aagattcaaa ttcaaagac attaataggc aaccagaacg tgggtggggc 2100
 ggaagtacag ggattacat ccaaggaggg gatgacgtat ttaaagaaaa ttacgtcaca 2160
 ctatcaggta ctttgatga gtgctatcca acatattgt atcaaaaaat cgatgaatca 2220
 aaattaaaag ctttaccg ttatcaatta agagggtata tcgaagatag tcaagactta 2280

gaaatctatt taattcgcta caatgcaaaa catgaaacag taaatgtgcc aggtacgggt 2340
 tccttatggc cgcttcagc ccaaagtcca atcggaaggt gtggagagcc gaatcgatgc 2400
 ggcgcacacc tgaatggaa tcctgactta gattgttcgt gtagggatgg agaaaagtgt 2460
 gcccatcatt cgcatcattt ctccttagac attgatgtag gatgtacaga cttaaagtag 2520
 gacctagggtg tatgggtgat cttaagatt aagacgcaag atgggcacgc aagactaggg 2580
 aatctagagt ttctgaaga gaaaccatta gtaggagaag cgctagctcg tgtgaaaaga 2640
 gcggagaaaa aatggagaga caaacgtgaa aaattggaat gggaaacaaa tatcgtttat 2700
 aaagaggcaa agaactctgt agatgcttta ttgtaaact ctcaatatga tcaattacaa 2760
 gcggatacga atattgcat gattcatgcg gcagataaac gtgtcatag cattcgagaa 2820
 gcttatctgc ctgagctgct tgtgattccg ggtgtcaatg cggctatatt tgaagaatta 2880
 gaagggcgta ttttactgc attctcccta tatgatgcga gaaatgtcat taaaaatggt 2940
 gattttaata atggcttacc ctgctggaac gtgaaagggc atgtagatgt agaagaacaa 3000
 aacaaccaac gttcggctct tgtgttccg gaatgggaag cagaagtgtc acaagaagtt 3060
 cgtgtctgct cgggtcgtgg ctatattcct cgtgtcacag cgtacaagga gggatatgga 3120
 gaaggttgcg taaccattca tgagatcgag aacaatacag acgaactgaa gtttagcaac 3180
 tgcgtagaag aggaaatcta tccaaataac acggtaacgt gtaatgatta tactgtaaat 3240
 caagaagaat acggaggtgc gtacacttct cgtaatcgag gatataacga agctccttcc 3300
 gtaccagctg attatgcgtc agtctatgaa gaaaaatcgt atacagatgg acgaagagag 3360
 aatccttggt aatttaacag agggatatagg gattacacgc cactaccagt tggttatgtg 3420
 acaaaagaat tagaatactt cccagaaacc gataaggtat ggattgagat tggagaaacg 3480
 gaaggaacat ttatcgtgga cagcgtggaa ttactcctta tggaggaata g 3531

<210> 57

<211> 1176

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC843.

<400> 57

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
 1 5 10 15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
20 25 30

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

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

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

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110

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

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140

Ile Pro Leu Leu Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160

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

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val

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

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
450 455 460

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

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

Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe Gly Asp Ile Arg
500 505 510

Leu Asn Ile Asn Val Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
515 520 525

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

Thr Val Asn Ile Gly Asn Phe Ser Arg Thr Met Asn Arg Gly Asp Asn
545 550 555 560

Leu Glu Tyr Arg Ser Phe Arg Thr Ala Gly Phe Ser Thr Pro Phe Asn
565 570 575

Phe Leu Asn Ala Gln Ser Thr Phe Thr Leu Gly Ala Gln Ser Phe Ser
580 585 590

Asn Gln Glu Val Tyr Ile Asp Arg Val Glu Phe Val Pro Ala Glu Val
595 600 605

Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val Asn
610 615 620

Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly Leu Lys Thr Asn Val Thr
625 630 635 640

Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Thr Tyr Leu Ser Asp
645 650 655

Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys His
660 665 670

Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Ser Asn Phe
675 680 685

Lys Asp Ile Asn Arg Gln Pro Glu Arg Gly Trp Gly Gly Ser Thr Gly
690 695 700

Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr
705 710 715 720

Leu Ser Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys
725 730 735

Ile Asp Glu Ser Lys Leu Lys Ala Phe Thr Arg Tyr Gln Leu Arg Gly
740 745 750

Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn
755 760 765

Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro
770 775 780

Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys
785 790 795 800

Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp
805 810 815

Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile Asp
820 825 830

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

Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe
850 855 860

Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys Arg
865 870 875 880

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

Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val
900 905 910

Asn Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile Ala Met Ile
915 920 925

His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu Pro
930 935 940

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

Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn Val
965 970 975

Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val Lys
980 985 990

Gly His Val Asp Val Glu Glu Gln Asn Asn Gln Arg Ser Val Leu Val
995 1000 1005

Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys
1010 1015 1020

Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly
1025 1030 1035

Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr
1040 1045 1050

Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Ile Tyr Pro
1055 1060 1065

Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Val Asn Gln Glu Glu
1070 1075 1080

Tyr Gly Gly Ala Tyr Thr Ser Arg Asn Arg Gly Tyr Asn Glu Ala
1085 1090 1095

Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys Ser

1100	1105	1110
Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys Glu Phe Asn Arg Gly		
1115	1120	1125

Tyr Arg Asp Tyr Thr Pro Leu Pro Val Gly Tyr Val Thr Lys Glu
1130 1135 1140

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

Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu
1160 1165 1170

Met Glu Glu
1175

<210> 58
 <211> 3501
 <212> DNA
 <213> Artificial

<220>
 <223> Chimeric coding sequence encoding TIC862.

<400> 58
 atggataaca atccgaacat caatgaatgc attccttata attgtttaag taaccctgaa 60
 gtagaagtat taggtggaga aagaatagaa actgggtaca cccaatcga tatttccttg 120
 tcgctaacgc aatttcttt gagtgaattt gttcccgggtg ctggatttgt gtaggacta 180
 gttgatataa tatggggaat ttttggccc tctcaatggg acgcatttct tgtacaaatt 240
 gaacagttaa ttaaccaaag aatagaagaa ttcgctagga accaagccat ttctagatta 300
 gaaggactaa gcaatcttta tcaaatttac gcagaatctt ttagagagtg ggaagcagat 360
 cctactaatc cagcattaag agaagagatg cgtattcaat tcaatgacat gaacagtgcc 420
 ctacaaccg ctattcctct ttggcagtt caaaattatc aagttcctct ttatcagta 480
 tatgttcaag ctgcaaattt acatttatca gtttgagag atgtttcagt gtttgacaa 540
 aggtggggat ttgatccgc gactatcaat agtcgttata atgatttaac taggcttatt 600
 ggcaactata cagattatgc tgtacgtgg tacaatacgg gattagaacg tgtatgggga 660
 ccggattcta gagattgggt aaggataat caatttagaa gagaattaac actaactgta 720

ttagatatcg ttgctctgtt cccgaattat gatagtagaa gatatccaat tcgaacagtt 780
 tccaattaa caagagaaat ttatacaaac ccagtattag aaaatttga tggtagttt 840
 cgaggctcgg ctcaaggcat agaaagaagt attaggagtc cacattgat ggatatatta 900
 aacagtataa ccatctatac ggatgctcat aggggttatt attattggtc agggcatcaa 960
 ataatggctt ctctgtcgg ttttcgggg ccagaattca cgttccgct atatggaacc 1020
 atgggaaatg cagctccaca acaacgtatt gttgctcaac taggtcaggg cgtgtataga 1080
 acattatcgt ccactttata tagaagacct ttaatatag ggataaataa tcaacaacta 1140
 tctgttcttg acgggacaga atttgcttat ggaacctct caaattgcc atccgctgta 1200
 tacagaaaaa gcggaacggt agattcgctg gatgaaatac cgccacagaa taacaacgtg 1260
 ccacctaggc aaggatttag tcatcgatta agccatgtt caatgttcg ttcaggcttt 1320
 agtaatagta gtgtaagtat aataagagct cctatgttct ctggatata tcgtagtgt 1380
 gaatttaata atataattgc atcggatagt attactcaaa tccctgcagt gaagggaaac 1440
 tttctttta atggttctgt aatttcagga ccaggattta ctggtgggga ctagttaga 1500
 tgtacgaatg gatctggatt aactttatat gttacaccgg caccggactt gacgtattct 1560
 aaaacatata aaattcgaat tcgttatgct tctacatctc aggtgagatt tggaattgac 1620
 ttaggcagtt acactcatag tatttcgtat ttcgataaaa cgatggataa aggaaatata 1680
 ttaacgtata attcatttaa ttatcaagt gtcagcagac caattgaaat atcaggaggg 1740
 aataaaatcg gggatccgt cggaggtatt ggctctgggg atgaagtta tatagacaaa 1800
 atcgaattta ttccaatgga aagagcgcag aaggcgggtga atgcgctgtt tacgtctaca 1860
 aaccaactag ggctaaaaac aaatgtaacg gattatcata ttgatcaagt gtccaattta 1920
 gttacgtatt tatcggatga atttgtctg gatgaaaagc gagaattgtc cgagaaagtc 1980
 aaacatgca agcgactcag tgatgaacgc aatttactcc aagattcaaa ttcaaagac 2040
 attaataggc aaccagaacg tgggtggggc ggaagtacag ggattaccat ccaaggaggg 2100
 gatgacgtat taaagaaaa ttacgtcaca ctatcaggta ctttgatga gtgctatcca 2160
 acatatttgt atcaaaaaat cgatgaatca aaattaaaag cctttaccg ttatcaatta 2220
 agaggggtata tcgaagatag tcaagactta gaaatctatt taattcgcta caatgcaaaa 2280
 catgaaacag taaatgtgcc aggtacgggt tccttatggc cgcttcagc ccaaagtcca 2340

atcggaaagt gtggagagcc gaatcgatgc gcgccacacc ttgaatggaa tcctgactta 2400
 gattgttcgt gtagggatgg agaaaagtgt gccatcatt cgcattcatt ctccttagac 2460
 attgatgtag gatgtacaga cttaaatgag gacctagggt tatgggtgat cttaagatt 2520
 aagacgcaag atgggcacgc aagactaggg aatctagagt ttctgaaga aaaaccatta 2580
 gtaggagaag cgctagctcg tgtgaaaaga gcggagaaaa aatggagaga caaacgtgaa 2640
 aaattggaat gggaaacaaa tatcgtttat aaagaggcaa aagaatctgt agatgcttta 2700
 ttgtaaact ctcaatatga tcaattacaa gcggatacga atattgcat gattcatgcg 2760
 gcagataaac gtgttcatac cattcgagaa gcttatctgc ctgagctgtc tgtgattccg 2820
 ggtgtcaatg cggctatfff tgaagaatta gaaggcgta tttcactgc attctcccta 2880
 tatgatgcga gaaatgtcat taaaaatggg gattttaata atggcttatt ctgctggaac 2940
 gtgaaagggc atgtagatgt agaagaacaa aacaaccaac gtgcggcctt tgtgttcg 3000
 gaatgggaag cagaagtgtc acaagaagtt cgtgtctgtc cgggtcgtgg ctatcctt 3060
 cgtgtcacag cgtacaagga gggatatgga gaagggtgag taaccattca tgagatcgag 3120
 aacaatacag acgaactgaa gtttagcaac tgcgtagagg aggaaatcta tccaataac 3180
 acggtaacgt gtaatgatta tactgtaaat caagaagaat acggaggtgc gtacacttct 3240
 cgtaatcgag gatataacga agctccttcc gtaccagctg attatgcgtc agtctatgaa 3300
 gaaaaatcgt atacagatgg acgtagagag aatccttgtg aatttaacag agggatatagg 3360
 gattacacgc cactaccagt tggttatgtg aaaaaagaat tagaatactt cccagaaacc 3420
 gataaggat ggattgagat tggagaaacg gaaggaacat ttatcgtgga cagcgtggaa 3480
 ttactccta tggaggaata a 3501

<210> 59

<211> 1166

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC862.

<400> 59

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu

1

5

10

15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
20 25 30

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

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

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

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110

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

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140

Ile Pro Leu Leu Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160

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

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240

Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285

Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
450 455 460

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

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

Asp Leu Val Arg Cys Thr Asn Gly Ser Gly Leu Thr Leu Tyr Val Thr
500 505 510

Pro Ala Pro Asp Leu Thr Tyr Ser Lys Thr Tyr Lys Ile Arg Ile Arg
515 520 525

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

Thr His Ser Ile Ser Tyr Phe Asp Lys Thr Met Asp Lys Gly Asn Thr
545 550 555 560

Leu Thr Tyr Asn Ser Phe Asn Leu Ser Ser Val Ser Arg Pro Ile Glu
565 570 575

Ile Ser Gly Gly Asn Lys Ile Gly Val Ser Val Gly Gly Ile Gly Ser
580 585 590

Gly Asp Glu Val Tyr Ile Asp Lys Ile Glu Phe Ile Pro Met Glu Arg
595 600 605

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

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

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

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

Leu Gln Asp Ser Asn Phe Lys Asp Ile Asn Arg Gln Pro Glu Arg Gly

Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Gln Leu Gln Ala Asp
900 905 910

Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser Ile
915 920 925

Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala
930 935 940

Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu
945 950 955 960

Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu
965 970 975

Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn Asn
980 985 990

Gln Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln
995 1000 1005

Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr
1010 1015 1020

Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu
1025 1030 1035

Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
1040 1045 1050

Glu Glu Ile Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr
1055 1060 1065

Val Asn Gln Glu Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn Arg
1070 1075 1080

Gly Tyr Asn Glu Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser Val
1085 1090 1095

Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
1100 1105 1110

Glu Phe Asn Arg Gly Tyr Arg Asp Tyr Thr Pro Leu Pro Val Gly
 1115 1120 1125

Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val
 1130 1135 1140

Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser
 1145 1150 1155

Val Glu Leu Leu Leu Met Glu Glu
 1160 1165

<210> 60

<211> 3549

<212> DNA

<213> Artificial

<220>

<223> Chimeric coding sequence encoding TIC1099.

<400> 60

atggataaca atccgaacat caatgaatgc attccttata attgtttaag taaccctgaa 60

gtagaagtat taggtggaga aagaatagaa actggttaca cccaatcga tatttccttg 120

tgcctaacgc aatttctttt gagtgaattt gttcccgggtg ctggatttgt gtaggacta 180

gttgatataa tatggggaat ttttgggtccc tctcaatggg acgcatttct tgtacaaatt 240

gaacagttaa ttaaccaaag aatagaagaa ttcgctagga accaagccat ttctagatta 300

gaaggactaa gcaatcttta tcaaatttac gcagaatctt ttagagagtg ggaagcagat 360

cctactaatc cagcattaag agaagagatg cgtattcaat tcaatgacat gaacagtgcc 420

cttacaaccg ctattcctct tttggcagtt caaaattatc aagttcctct ttatcagta 480

tatgttcaag ctgcaaattt acatttatca gttttgagag atgtttcagt gtttgacaa 540

aggtggggat ttgatgccgc gactatcaat agtcgttata atgatttaac taggcttatt 600

ggcaactata cagattatgc tgtacgttg tacaatacgg gattagaacg tgtatgggga 660

ccggattcta gagattgggt aaggataat caatttagaa gagaattaac actaactgta 720

ttagatatcg ttgctctgtt cccgaattat gatagtagaa gatatccaat tcgaacagtt 780

tccaattaa caagagaaat ttatacaaac ccagtattag aaaatttga tggtagtttt 840

cgaggctcgg ctcagggcat agaaagaagt attaggagtc cacatttgat ggatatactt 900

aacagtataa ccatctatac ggatgctcat aggggttatt attattggtc agggcatcaa 960
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 gaatttaata atataattgc atcggatagt attacacaat taccattggt aaaggcatct 1440
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 caaagatatc gcgtaagagt tcgttttgct tcatcaggaa atttcagcat aaggatactg 1620
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 tcggatgaat ttgtctgga tgaaaagcga gaattgtccg agaaagtcaa acatgcgaag 2040
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 aatgtgccag gtacgggttc ctatggccg ctttcagccc aaagtccaat cggaaagtgt 2400
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tgtacagact taaatgagga cctaggtgta tgggtgatct ttaagattaa gacgcaagat 2580
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 gaaacaaata tcgtttataa agaggcaaaa gaatctgtag atgctttatt tgtaaactct 2760
 caatatgatac aattacaagc ggatacgaat attgccatga ttcattgcggc agataaacgt 2820
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 gtagatgtag aagaacaaaa caaccaacgt tcggctcttg ttgtccgga atgggaagca 3060
 gaagtgtcac aagaagttcg tgtctgtccg ggtcgtggct atatccttcg tgcacagcg 3120
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 gaactgaagt ttagcaactg cgtagaggag gaaatctatc caaataacac ggtaacgtgt 3240
 aatgattata ctgtaaatac agaagaatac ggaggtgcgt acacttctcg taatcgagga 3300
 tataacgaag ctcttccgt accagctgat tatgcgtcag tctatgaaga aaaatcgtat 3360
 acagatggac gtagagagaa tccttgtgaa ttaacagag ggtataggga ttacacgcca 3420
 ctaccagttg gttatgtgac aaaagaatta gaatacttcc cagaaaccga taaggtatgg 3480
 attgagattg gagaaacgga aggaacattt atcgtggaca gcgtggaatt actccttatg 3540
 gaggaataa 3549

<210> 61

<211> 1182

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC1099.

<400> 61

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
 1 5 10 15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
 20 25 30

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

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

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

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110

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

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140

Ile Pro Leu Leu Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160

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

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240

Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285

Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Trp Ser Gly His Gln
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
450 455 460

Ile Ile Ala Ser Asp Ser Ile Thr Gln Leu Pro Leu Val Lys Ala Ser
465 470 475 480

Ala Pro Val Ser Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly
485 490 495

Gly Gly Ile Leu Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg
500 505 510

Val Thr Val Asn Ser Pro Leu Thr Gln Arg Tyr Arg Val Arg Val Arg
515 520 525

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

Ser Ile Ala Tyr Gln Arg Phe Gly Ser Thr Met Asn Arg Gly Gln Glu
545 550 555 560

Leu Thr Tyr Glu Ser Phe Val Thr Ser Glu Phe Thr Thr Asn Gln Ser
565 570 575

Asp Leu Pro Phe Thr Phe Thr Gln Ala Gln Glu Asn Leu Thr Ile Leu
580 585 590

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

Ile Ile Pro Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Arg
610 615 620

Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly
625 630 635 640

Leu Lys Thr Asn Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu
645 650 655

Val Thr Tyr Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu
660 665 670

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

Leu Gln Asp Ser Asn Phe Lys Asp Ile Asn Arg Gln Pro Glu Arg Gly

690	695	700	
Trp Gly Gly Ser Thr Gly Ile Thr Ile Gln Gly Gly Asp Asp Val Phe			
705	710	715	720
Lys Glu Asn Tyr Val Thr Leu Ser Gly Thr Phe Asp Glu Cys Tyr Pro			
	725	730	735
Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Phe Thr			
	740	745	750
Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile			
	755	760	765
Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly			
	770	775	780
Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys			
	785	790	795
Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu			
	805	810	815
Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His			
	820	825	830
Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu			
	835	840	845
Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg			
	850	855	860
Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala			
	865	870	875
Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu			
	885	890	895
Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser			
	900	905	910

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

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

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

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

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

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

Gln Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser
1010 1015 1020

Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val
1025 1030 1035

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

Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val
1055 1060 1065

Glu Glu Glu Ile Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr
1070 1075 1080

Thr Val Asn Gln Glu Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn
1085 1090 1095

Arg Gly Tyr Asn Glu Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser
1100 1105 1110

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

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

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

Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp
 1160 1165 1170

Ser Val Glu Leu Leu Leu Met Glu Glu
 1175 1180

<210> 62

<211> 3549

<212> DNA

<213> Artificial

<220>

<223> Chimeric coding sequence encoding TIC1099 T507E.

<400> 62

atggataaca atccgaacat caatgaatgc attccttata attgtttaag taaccctgaa 60
 gtagaagtat taggtggaga aagaatagaa actggttaca cccaatcga tatttccttg 120
 tgcctaacgc aatttctttt gagtgaattt gttcccgggtg ctggatttgt gtaggacta 180
 gttgatataa tatggggaat ttttggtccc tctcaatggg acgcatttct tgtacaaatt 240
 gaacagttaa ttaaccaaag aatagaagaa ttcgctagga accaagccat ttctagatta 300
 gaaggactaa gcaatcttta tcaaatttac gcagaatctt ttagagagtg ggaagcagat 360
 cctactaatc cagcattaag agaagagatg cgtattcaat tcaatgacat gaacagtgcc 420
 cttaacaaccg ctattcctct ttggcagtt caaaattatc aagttcctct ttatcagta 480
 tatgttcaag ctgcaaattt acatttatca gtttgagag atgtttcagt gtttgacaa 540
 aggtggggat ttgatgccgc gactatcaat agtcgttata atgatttaac taggcttatt 600
 ggcaactata cagattatgc tgtacgctgg tacaatacgg gattagaacg tgtatgggga 660
 ccggattcta gagattgggt aaggataat caatttagaa gagaattaac actaactgta 720
 ttagatatcg ttgctctgtt cccgaattat gatagtagaa gatatccaat tcgaacagtt 780
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aacagtataa ccatctatac ggatgctcat aggggttatt attattggtc agggcatcaa 960
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 ctaaaaacaa atgtaacgga ttatcatatt gatcaagtgt ccaatttagt tacgtattta 1980
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 tataacgaag ctcttccgt accagctgat tatgcgtcag tctatgaaga aaaatcgtat 3360
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 ctaccagttg gttatgtgac aaaagaatta gaatacttcc cagaaaccga taaggtatgg 3480
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 gaggaataa 3549

<210> 63

<211> 1182

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC1099 T507E.

<400> 63

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
 1 5 10 15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
 20 25 30

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

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

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

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110

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

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140

Ile Pro Leu Leu Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160

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

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240

Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285

Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Trp Ser Gly His Gln
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
450 455 460

Ile Ile Ala Ser Asp Ser Ile Thr Gln Leu Pro Leu Val Lys Ala Ser
465 470 475 480

Ala Pro Val Ser Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly
485 490 495

Gly Gly Ile Leu Arg Arg Thr Thr Asn Gly Glu Phe Gly Thr Leu Arg
500 505 510

Val Thr Val Asn Ser Pro Leu Thr Gln Arg Tyr Arg Val Arg Val Arg
515 520 525

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

Ser Ile Ala Tyr Gln Arg Phe Gly Ser Thr Met Asn Arg Gly Gln Glu
545 550 555 560

Leu Thr Tyr Glu Ser Phe Val Thr Ser Glu Phe Thr Thr Asn Gln Ser
565 570 575

Asp Leu Pro Phe Thr Phe Thr Gln Ala Gln Glu Asn Leu Thr Ile Leu
580 585 590

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

Ile Ile Pro Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Arg
610 615 620

Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly
625 630 635 640

Leu Lys Thr Asn Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu
645 650 655

Val Thr Tyr Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu
660 665 670

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

Leu Gln Asp Ser Asn Phe Lys Asp Ile Asn Arg Gln Pro Glu Arg Gly

690	695	700	
Trp Gly Gly Ser Thr Gly Ile Thr Ile Gln Gly Gly Asp Asp Val Phe			
705	710	715	720
Lys Glu Asn Tyr Val Thr Leu Ser Gly Thr Phe Asp Glu Cys Tyr Pro			
	725	730	735
Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Phe Thr			
	740	745	750
Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile			
	755	760	765
Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly			
	770	775	780
Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys			
	785	790	795
Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu			
	805	810	815
Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His			
	820	825	830
Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu			
	835	840	845
Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg			
	850	855	860
Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala			
	865	870	875
Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu			
	885	890	895
Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser			
	900	905	910

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

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

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

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

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

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

Gln Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser
1010 1015 1020

Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val
1025 1030 1035

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

Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val
1055 1060 1065

Glu Glu Glu Ile Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr
1070 1075 1080

Thr Val Asn Gln Glu Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn
1085 1090 1095

Arg Gly Tyr Asn Glu Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser
1100 1105 1110

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

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

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

Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp
 1160 1165 1170

Ser Val Glu Leu Leu Leu Met Glu Glu
 1175 1180

<210> 64

<211> 3549

<212> DNA

<213> Artificial

<220>

<223> Chimeric coding sequence encoding TIC1099 R522K.

<400> 64

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 gtagaagtat taggtggaga aagaatagaa actggttaca cccaatcga tatttccttg 120
 tcgctaacgc aatttctttt gagtgaattt gttcccgggtg ctggatttgt gttaggacta 180
 gttgatataa tatggggaat ttttggccc tctcaatggg acgcatttct tgtacaaatt 240
 gaacagttaa ttaaccaaag aatagaagaa ttcgctagga accaagccat ttctagatta 300
 gaaggactaa gcaatcttta tcaaatttac gcagaatctt ttagagagtg ggaagcagat 360
 cctactaatc cagcattaag agaagagatg cgtattcaat tcaatgacat gaacagtgcc 420
 cttaacaaccg ctattcctct tttggcagtt caaaattatc aagttcctct ttatcagta 480
 tatgttcaag ctgcaaattt acatttatca gtttgagag atgtttcagt gtttgacaa 540
 aggtggggat ttgatgccgc gactatcaat agtcgttata atgatttaac taggcttatt 600
 ggcaactata cagattatgc tgtacgctgg tacaatacgg gattagaacg tgtatgggga 660
 ccggattcta gagattgggt aaggataat caatttagaa gagaattaac actaactgta 720
 ttagatatcg ttgctctgtt cccgaattat gatagtagaa gatatccaat tcgaacagtt 780
 tccaattaa caagagaaat ttatacaaac ccagtattag aaaatttga tggtagtttt 840
 cgaggctcgg ctcagggcat agaaagaagt attaggagtc cacatttgat ggatatactt 900

aacagtataa ccatctatac ggatgctcat aggggttatt attattggtc agggcatcaa 960
 ataatggctt ctctgtcgg ttttcgggg ccagaattca cgttccgct atatggaacc 1020
 atgggaaatg cagctccaca acaacgtatt gttgctcaac taggtcaggg cgtgtataga 1080
 acattatcgt ccactttata tagaagacct ttaatatag ggataaataa tcaacaacta 1140
 tctgttcttg acgggacaga atttgcttat ggaacctcct caaatttgcc atccgctgta 1200
 tacagaaaaa gcggaacggt agattcgctg gatgaaatac cgccacagaa taacaacgtg 1260
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 agtaatagta gtgtaagtat aataagagct cctatgttct ctggataca tcgtagtgt 1380
 gaatttaata atataattgc atcggatagt attacacaat taccattggt aaaggcatct 1440
 gcacctgttt cgggtactac ggtcttaaaa ggtccaggat ttacaggagg gggataactc 1500
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 cgtggaaata cctctatagc ttatcaaaga ttggggagta caatgaacag aggacaggaa 1680
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 gaatatttta tagatagaat tgaaatcatc cctgtgaacc cggcacgaga agcagaagag 1860
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 ctaaaaacaa atgtaacgga ttatcatatt gatcaagtgt ccaatttagt tacgtattta 1980
 tcggatgaat ttgtctgga tgaaaagcga gaattgtccg agaaagtcaa acatgcgaag 2040
 cgactcagt atgaacgcaa ttactcaa gattcaaatt tcaaagacat taataggcaa 2100
 ccagaacgtg ggtggggcgg aagtacaggg attaccatcc aaggagggga tgacgtattt 2160
 aaagaaaatt acgtcacact atcaggtacc ttgatgagt gctatccaac atattgtat 2220
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 aatgtgccag gtacgggttc ctatggccg ctttcagccc aaagtccaat cggaaagtgt 2400
 ggagagccga atcgatgcgc gccacacctt gaatggaatc ctgacttaga ttgtcgtgt 2460
 agggatggag aaaagtgtgc ccatcattcg catcatttct ccttagacat tgatgtagga 2520

tgtacagact taaatgagga cctaggtgta tgggtgatct ttaagattaa gacgcaagat 2580
 gggcacgcaa gactagggaa tctagagttt ctcgaagaaa aaccattagt aggagaagcg 2640
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 gaaacaaata tcgtttataa agaggcaaaa gaatctgtag atgctttatt tgtaaactct 2760
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 gttcatagca ttcgagaagc ttatctgcct gagctgtctg tgattccggg tgtcaatgcg 2880
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 aatgtcatta aaaatggtga tttaataat ggcttacct gctggaacgt gaaagggcat 3000
 gtagatgtag aagaacaaaa caaccaacgt tcggctcttg ttgtccgga atgggaagca 3060
 gaagtgtcac aagaagttcg tgtctgtccg ggtcgtggct atatccttcg tgcacagcg 3120
 tacaaggagg gatattggaga aggttgcgta accattcatg agatcgagaa caatacagac 3180
 gaactgaagt ttagcaactg cgtagaggag gaaatctatc caataacac ggtaacgtgt 3240
 aatgattata ctgtaaatca agaagaatac ggaggtgcgt acacttctcg taatcgagga 3300
 tataacgaag ctcttccgt accagctgat tatgcgtcag tctatgaaga aaaatcgtat 3360
 acagatggac gtagagagaa tccttgtgaa ttaacagag ggtataggga ttacacgcca 3420
 ctaccagttg gttatgtgac aaaagaatta gaatacttc cagaaaccga taaggtatgg 3480
 attgagattg gagaaacgga aggaacattt atcgtggaca gcgtggaatt actcctatg 3540
 gaggaataa 3549

<210> 65

<211> 1182

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC1099 R522K.

<400> 65

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
 1 5 10 15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
 20 25 30

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

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

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

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110

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

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140

Ile Pro Leu Leu Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160

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

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240

Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285

Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Trp Ser Gly His Gln
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
450 455 460

Ile Ile Ala Ser Asp Ser Ile Thr Gln Leu Pro Leu Val Lys Ala Ser
465 470 475 480

Ala Pro Val Ser Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly
485 490 495

Gly Gly Ile Leu Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg
500 505 510

Val Thr Val Asn Ser Pro Leu Thr Gln Lys Tyr Arg Val Arg Val Arg
515 520 525

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

Ser Ile Ala Tyr Gln Arg Phe Gly Ser Thr Met Asn Arg Gly Gln Glu
545 550 555 560

Leu Thr Tyr Glu Ser Phe Val Thr Ser Glu Phe Thr Thr Asn Gln Ser
565 570 575

Asp Leu Pro Phe Thr Phe Thr Gln Ala Gln Glu Asn Leu Thr Ile Leu
580 585 590

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

Ile Ile Pro Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Arg
610 615 620

Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly
625 630 635 640

Leu Lys Thr Asn Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu
645 650 655

Val Thr Tyr Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu
660 665 670

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

Leu Gln Asp Ser Asn Phe Lys Asp Ile Asn Arg Gln Pro Glu Arg Gly

690	695	700	
Trp Gly Gly Ser Thr Gly Ile Thr Ile Gln Gly Gly Asp Asp Val Phe			
705	710	715	720
Lys Glu Asn Tyr Val Thr Leu Ser Gly Thr Phe Asp Glu Cys Tyr Pro			
	725	730	735
Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Phe Thr			
	740	745	750
Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile			
	755	760	765
Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly			
	770	775	780
Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys			
	785	790	795
Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu			
	805	810	815
Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His			
	820	825	830
Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu			
	835	840	845
Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg			
	850	855	860
Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala			
	865	870	875
Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu			
	885	890	895
Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser			
	900	905	910

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

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

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

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

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

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

Gln Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser
1010 1015 1020

Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val
1025 1030 1035

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

Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val
1055 1060 1065

Glu Glu Glu Ile Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr
1070 1075 1080

Thr Val Asn Gln Glu Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn
1085 1090 1095

Arg Gly Tyr Asn Glu Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser
1100 1105 1110

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

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

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

Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp
 1160 1165 1170

Ser Val Glu Leu Leu Leu Met Glu Glu
 1175 1180

<210> 66

<211> 3549

<212> DNA

<213> Artificial

<220>

<223> Chimeric coding sequence encoding TIC1099 K490S.

<400> 66

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 tcgctaacgc aatttctttt gagtgaattt gttcccgggtg ctggatttgt gttaggacta 180
 gttgatataa tatggggaat ttttgggtccc tctcaatggg acgcatttct tgtacaaatt 240
 gaacagttaa ttaaccaaag aatagaagaa ttcgctagga accaagccat ttctagatta 300
 gaaggactaa gcaatcttta tcaaatttac gcagaatctt ttagagagtg ggaagcagat 360
 cctactaatc cagcattaag agaagagatg cgtattcaat tcaatgacat gaacagtgcc 420
 cttacaaccg ctattcctct tttggcagtt caaaattatc aagttcctct ttatcagta 480
 tatgttcaag ctgcaaattt acatttatca gttttgagag atgtttcagt gtttgacaa 540
 aggtggggat ttgatgccgc gactatcaat agtcgttata atgatttaac taggcttatt 600
 ggcaactata cagattatgc tgtacgctgg tacaatacgg gattagaacg tgtatgggga 660
 ccggattcta gagattgggt aaggataat caatttagaa gagaattaac actaactgta 720
 ttagatatcg ttgctctgtt cccgaattat gatagtagaa gatatccaat tcgaacagtt 780
 tccaattaa caagagaaat ttatacaaac ccagtattag aaaatttga tggtagtttt 840
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 ccacctaggc aaggatttag tcatcgatta agccatgttt caatgttctg ttcaggcttt 1320
 agtaatagta gtgtaagtat aataagagct cctatgttct ctgggataca tcgtagtgtc 1380
 gaatttaata atataattgc atcggatagt attacacaat taccattggt aaaggcatct 1440
 gcacctgttt cgggtactac ggtcttatca ggtccaggat ttacaggagg ggggtatactc 1500
 cgaagaacaa ctaatggcac atttgaacg ttaagagtaa cagttaattc accattaaca 1560
 caaagatatc gcgtaagagt tcgttttgct tcatcaggaa atttcagcat aaggatactg 1620
 cgtggaaata cctctatagc ttatcaaaga ttggggagta caatgaacag aggacaggaa 1680
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 aatgtgccag gtacgggttc ctatggccg ctttcagccc aaagtccaat cggaaagtgt 2400
 ggagagccga atcgatgcgc gccacacctt gaatggaatc ctgacttaga ttgtcgtgt 2460
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 gctatttttg aagaattaga agggcgtatt ttactgcat tctccctata tgatgcgaga 2940
 aatgtcatta aaaatggtga tttaataat ggcttattct gctggaacgt gaaagggcat 3000
 gtagatgtag aagaacaaaa caaccaacgt tcggctcttg ttgtccgga atgggaagca 3060
 gaagtgtcac aagaagttcg tgtctgtccg ggtcgtggct atatccttcg tgcacagcg 3120
 tacaaggagg gatattggaga aggttgcgta accattcatg agatcgagaa caatacagac 3180
 gaactgaagt ttagcaactg cgtagaggag gaaatctatc caaataacac ggtaacgtgt 3240
 aatgattata ctgtaaatac agaagaatac ggaggtgcgt acacttctcg taatcgagga 3300
 tataacgaag ctcttccgt accagctgat tatgcgtcag tctatgaaga aaaatcgtat 3360
 acagatggac gtagagagaa tccttgtgaa ttaacagag ggtataggga ttacacgcca 3420
 ctaccagttg gttatgtgac aaaagaatta gaatacttcc cagaaaccga taaggtatgg 3480
 attgagattg gagaaacgga aggaacattt atcgtggaca gcgtggaatt actccttatg 3540
 gaggaataa 3549

<210> 67

<211> 1182

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC1099 K490S.

<400> 67

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
 1 5 10 15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
 20 25 30

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

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

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

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110

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

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140

Ile Pro Leu Leu Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160

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

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240

Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285

Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Trp Ser Gly His Gln
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
450 455 460

Ile Ile Ala Ser Asp Ser Ile Thr Gln Leu Pro Leu Val Lys Ala Ser
465 470 475 480

Ala Pro Val Ser Gly Thr Thr Val Leu Ser Gly Pro Gly Phe Thr Gly
485 490 495

Gly Gly Ile Leu Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg
500 505 510

Val Thr Val Asn Ser Pro Leu Thr Gln Arg Tyr Arg Val Arg Val Arg
515 520 525

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

Ser Ile Ala Tyr Gln Arg Phe Gly Ser Thr Met Asn Arg Gly Gln Glu
545 550 555 560

Leu Thr Tyr Glu Ser Phe Val Thr Ser Glu Phe Thr Thr Asn Gln Ser
565 570 575

Asp Leu Pro Phe Thr Phe Thr Gln Ala Gln Glu Asn Leu Thr Ile Leu
580 585 590

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

Ile Ile Pro Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Arg
610 615 620

Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly
625 630 635 640

Leu Lys Thr Asn Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu
645 650 655

Val Thr Tyr Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu
660 665 670

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

Leu Gln Asp Ser Asn Phe Lys Asp Ile Asn Arg Gln Pro Glu Arg Gly

690	695	700	
Trp Gly Gly Ser Thr Gly Ile Thr Ile Gln Gly Gly Asp Asp Val Phe			
705	710	715	720
Lys Glu Asn Tyr Val Thr Leu Ser Gly Thr Phe Asp Glu Cys Tyr Pro			
	725	730	735
Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Phe Thr			
	740	745	750
Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile			
	755	760	765
Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly			
	770	775	780
Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys			
	785	790	795
Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu			
	805	810	815
Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His			
	820	825	830
Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu			
	835	840	845
Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg			
	850	855	860
Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala			
	865	870	875
Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu			
	885	890	895
Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser			
	900	905	910

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

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

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

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

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

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

Gln Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser
1010 1015 1020

Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val
1025 1030 1035

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

Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val
1055 1060 1065

Glu Glu Glu Ile Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr
1070 1075 1080

Thr Val Asn Gln Glu Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn
1085 1090 1095

Arg Gly Tyr Asn Glu Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser
1100 1105 1110

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

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

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

Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp
 1160 1165 1170

Ser Val Glu Leu Leu Leu Met Glu Glu
 1175 1180

<210> 68

<211> 3549

<212> DNA

<213> Artificial

<220>

<223> Chimeric coding sequence encoding TIC1099 T562R.

<400> 68

atggataaca atccgaacat caatgaatgc attccttata attgtttaag taaccctgaa 60
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 tcgctaacgc aatttctttt gagtgaattt gttcccgggtg ctggatttgt gttaggacta 180
 gttgatataa tatggggaat ttttggccc tctcaatggg acgcatttct tgtacaaatt 240
 gaacagttaa ttaaccaaag aatagaagaa ttcgctagga accaagccat ttctagatta 300
 gaaggactaa gcaatcttta tcaaatttac gcagaatctt ttagagagtg ggaagcagat 360
 cctactaatc cagcattaag agaagagatg cgtattcaat tcaatgacat gaacagtgcc 420
 cttaacaaccg ctattcctct tttggcagtt caaaattatc aagttcctct ttatcagta 480
 tatgttcaag ctgcaaattt acatttatca gtttgagag atgtttcagt gtttgacaa 540
 aggtggggat ttgatgccgc gactatcaat agtcgttata atgatttaac taggcttatt 600
 ggcaactata cagattatgc tgtacgctgg tacaatacgg gattagaacg tgtatgggga 660
 ccggattcta gagattgggt aaggataat caatttagaa gagaattaac actaactgta 720
 ttagatatcg ttgctctgtt cccgaattat gatagtagaa gatatccaat tcgaacagtt 780
 tccaattaa caagagaaat ttatacaaac ccagtattag aaaatttga tggtagtttt 840
 cgaggctcgg ctcagggcat agaaagaagt attaggagtc cacatttgat ggatatactt 900

aacagtataa ccatctatac ggatgctcat aggggttatt attattggtc agggcatcaa 960
 ataatggctt ctctgtcgg ttttcgggg ccagaattca cgttccgct atatggaacc 1020
 atgggaaatg cagctccaca acaacgtatt gttgctcaac taggtcaggg cgtgtataga 1080
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 tctgttcttg acgggacaga atttgcttat ggaacctct caaatttgcc atccgctgta 1200
 tacagaaaaa gcggaacggt agattcgctg gatgaaatac cgccacagaa taacaacgtg 1260
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 agtaatagta gtgtaagtat aataagagct cctatgttct ctggataca tcgtagtgtc 1380
 gaatttaata atataattgc atcgatagt attacacaat taccattggt aaaggcatct 1440
 gcacctgttt cgggtactac ggtcttaaaa ggtccaggat ttacaggagg gggatatactc 1500
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 cgtggaaata cctctatagc ttatcaaaga ttggggagta caatgaacag aggacaggaa 1680
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 gatttagaaa gagcgcagaa ggcgggtgaat gcgctgttta cgtctacaaa ccaactaggg 1920
 ctaaaaacaa atgtaacgga ttatcatatt gatcaagtgt ccaatttagt tacgtattta 1980
 tcggatgaat ttgtctgga tgaaaagcga gaattgtccg agaaagtcaa acatgcgaag 2040
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 ccagaacgtg ggtggggcgg aagtacaggg attaccatcc aaggagggga tgacgtattt 2160
 aaagaaaatt acgtcacact atcaggtacc ttgatgagt gctatccaac atattgtat 2220
 caaaaaatcg atgaatcaaa attaaaagcc ttaccctgt atcaattaag aggttatatc 2280
 gaagatagtc aagacttaga aatctattta attcgctaca atgcaaaaca tgaaacagta 2340
 aatgtgccag gtacgggttc ctatggccg ctttcagccc aaagtccaat cggaaagtgt 2400
 ggagagccga atcgatgcgc gccacacctt gaatggaatc ctgacttaga ttgtcgtgt 2460
 agggatggag aaaagtgtgc ccatcattcg catcatttct ccttagacat tgatgtagga 2520

tgtacagact taaatgagga cctaggtgta tgggtgatct ttaagattaa gacgcaagat 2580
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 ctagctcgtg tgaaaagagc ggagaaaaaa tggagagaca aacgtgaaaa attggaatgg 2700
 gaaacaaata tcgtttataa agaggcaaaa gaatctgtag atgctttatt tgtaaactct 2760
 caatatgatac aattacaagc ggatacgaat attgcatga ttcattgcggc agataaacgt 2820
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 gaactgaagt ttagcaactg cgtagaggag gaaatctatc caaataacac ggtaacgtgt 3240
 aatgattata ctgtaaatca agaagaatac ggaggtgcgt acacttctcg taatcgagga 3300
 tataacgaag ctcttccgt accagctgat tatgcgtcag tctatgaaga aaaatcgtat 3360
 acagatggac gtagagagaa tccttgtgaa ttaacagag ggtataggga ttacacgcca 3420
 ctaccagttg gttatgtgac aaaagaatta gaatacttcc cagaaaccga taaggtatgg 3480
 attgagattg gagaaacgga aggaacattt atcgtggaca gcgtggaatt actccttatg 3540
 gaggaataa 3549

<210> 69

<211> 1182

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC1099 T526R.

<400> 69

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Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
 20 25 30

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

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

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

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110

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

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140

Ile Pro Leu Leu Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160

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

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240

Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285

Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Trp Ser Gly His Gln
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
450 455 460

Ile Ile Ala Ser Asp Ser Ile Thr Gln Leu Pro Leu Val Lys Ala Ser
465 470 475 480

Ala Pro Val Ser Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly
485 490 495

Gly Gly Ile Leu Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg
500 505 510

Val Thr Val Asn Ser Pro Leu Thr Gln Arg Tyr Arg Val Arg Val Arg
515 520 525

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

Ser Ile Ala Tyr Gln Arg Phe Gly Ser Thr Met Asn Arg Gly Gln Glu
545 550 555 560

Leu Arg Tyr Glu Ser Phe Val Thr Ser Glu Phe Thr Thr Asn Gln Ser
565 570 575

Asp Leu Pro Phe Thr Phe Thr Gln Ala Gln Glu Asn Leu Thr Ile Leu
580 585 590

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

Ile Ile Pro Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Arg
610 615 620

Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly
625 630 635 640

Leu Lys Thr Asn Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu
645 650 655

Val Thr Tyr Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu
660 665 670

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

Leu Gln Asp Ser Asn Phe Lys Asp Ile Asn Arg Gln Pro Glu Arg Gly

690	695	700	
Trp Gly Gly Ser Thr Gly Ile Thr Ile Gln Gly Gly Asp Asp Val Phe			
705	710	715	720
Lys Glu Asn Tyr Val Thr Leu Ser Gly Thr Phe Asp Glu Cys Tyr Pro			
	725	730	735
Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Phe Thr			
	740	745	750
Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile			
	755	760	765
Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly			
	770	775	780
Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys			
	785	790	795
Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu			
	805	810	815
Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His			
	820	825	830
Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu			
	835	840	845
Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg			
	850	855	860
Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala			
	865	870	875
Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu			
	885	890	895
Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser			
	900	905	910

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

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

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

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

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

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

Gln Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser
1010 1015 1020

Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val
1025 1030 1035

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

Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val
1055 1060 1065

Glu Glu Glu Ile Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr
1070 1075 1080

Thr Val Asn Gln Glu Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn
1085 1090 1095

Arg Gly Tyr Asn Glu Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser
1100 1105 1110

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

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

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

Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp
 1160 1165 1170

Ser Val Glu Leu Leu Leu Met Glu Glu
 1175 1180

<210> 70

<211> 3549

<212> DNA

<213> Artificial

<220>

<223> Chimeric coding sequence encoding TIC1099 S553R.

<400> 70

atggataaca atccgaacat caatgaatgc attccttata attgtttaag taaccctgaa 60

gtagaagtat taggtggaga aagaatagaa actggttaca cccaatcga tatttccttg 120

tgcctaacgc aatttctttt gagtgaattt gttcccgggtg ctggatttgt gtaggacta 180

gttgatataa tatggggaat ttttggccc tctcaatggg acgcatttct tgtacaaatt 240

gaacagttaa ttaaccaaag aatagaagaa ttcgctagga accaagccat ttctagatta 300

gaaggactaa gcaatcttta tcaaatttac gcagaatctt ttagagagtg ggaagcagat 360

cctactaatc cagcattaag agaagagatg cgtattcaat tcaatgacat gaacagtgcc 420

cttacaaccg ctattcctct tttggcagtt caaaattatc aagttcctct ttatcagta 480

tatgttcaag ctgcaaattt acatttatca gtttgagag atgtttcagt gtttgacaa 540

aggtggggat ttgatgccgc gactatcaat agtcgttata atgatttaac taggcttatt 600

ggcaactata cagattatgc tgtacgctgg tacaatacgg gattagaacg tgtatgggga 660

ccggattcta gagattgggt aaggataat caatttagaa gagaattaac actaactgta 720

ttagatatcg ttgctctgtt cccgaattat gatagtagaa gatatccaat tcgaacagtt 780

tccaattaa caagagaaat ttatacaaac ccagtattag aaaatttga tggtagtttt 840

cgaggctcgg ctcagggcat agaaagaagt attaggagtc cacatttgat ggatatactt 900

aacagtataa ccatctatac ggatgctcat aggggttatt attattggtc agggcatcaa 960
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 tctgttcttg acgggacaga atttgcttat ggaacctcct caaatttgcc atccgctgta 1200
 tacagaaaaa gcggaacggt agattcgctg gatgaaatac cgccacagaa taacaacgtg 1260
 ccacctaggc aaggatttag tcatcgatta agccatgttt caatgtttcg ttcaggcttt 1320
 agtaatagta gtgtaagtat aataagagct cctatgttct ctgggataca tcgtagtgtc 1380
 gaatttaata atataattgc atcggatagt attacacaat taccattggt aaaggcatct 1440
 gcacctgttt cgggtactac ggtcttaaaa ggtccaggat ttacaggagg gggatatactc 1500
 cgaagaacaa ctaatggcac atttgaacg ttaagagtaa cagttaattc accattaaca 1560
 caaagatatc gcgtaagagt tcgttttgct tcatcaggaa atttcagcat aaggatactg 1620
 cgtggaaata cctctatagc ttatcaaaga ttggggcgta caatgaacag aggacaggaa 1680
 ctaacttacg aatcatttgt cacaagttag ttactacta atcagagcga tctgcctttt 1740
 acatttacac aagctcaaga aaatttaaca atccttgtag aagggttag caccggtagt 1800
 gaatatttta tagatagaat tgaaatcatc cctgtgaacc cggcacgaga agcagaagag 1860
 gatttagaaa gagcgcagaa ggcgggtgaat gcgctgttta cgtctacaaa ccaactaggg 1920
 ctaaaaacaa atgtaacgga ttatcatatt gatcaagtgt ccaatttagt tacgtattta 1980
 tcggatgaat ttgtctgga tgaaaagcga gaattgtccg agaaagtcaa acatgcgaag 2040
 cgactcagtg atgaacgcaa ttactcaa gattcaaatt tcaaagacat taataggcaa 2100
 ccagaacgtg ggtggggcgg aagtacaggg attaccatcc aaggagggga tgacgtattt 2160
 aaagaaaatt acgtcacact atcagggtacc ttgatgagt gctatccaac atatttgtat 2220
 caaaaaatcg atgaatcaaa attaaaagcc ttaccctgt atcaattaag aggttatatc 2280
 gaagatagtc aagacttaga aatctattta attcgctaca atgcaaaaca tgaaacagta 2340
 aatgtgccag gtacgggttc ctatggccg ctttcagccc aaagtccaat cggaaagtgt 2400
 ggagagccga atcgatgcgc gccacacctt gaatggaatc ctgacttaga ttgtcgtgt 2460
 agggatggag aaaagtgtgc ccatcattcg catcatttct ccttagacat tgatgtagga 2520

tgtacagact taaatgagga cctaggtgta tgggtgatct ttaagattaa gacgcaagat 2580
 gggcacgcaa gactagggaa tctagagttt ctcgaagaaa aaccattagt aggagaagcg 2640
 ctagctcgtg tgaaaagagc ggagaaaaaa tggagagaca aacgtgaaaa attggaatgg 2700
 gaaacaaata tcgtttataa agaggcaaaa gaatctgtag atgctttatt tgtaaactct 2760
 caatatgatac aattacaagc ggatacgaat attgccatga ttcattgcggc agataaacgt 2820
 gttcatagca ttcgagaagc ttatctgcct gagctgtctg tgattccggg tgtcaatgcg 2880
 gctatttttg aagaattaga agggcgtatt ttcactgcat tctccctata tgatgcgaga 2940
 aatgtcatta aaaatggtga tttaataat ggcttatcct gctggaacgt gaaagggcat 3000
 gtagatgtag aagaacaaaa caaccaacgt tcggctcttg ttgtccgga atgggaagca 3060
 gaagtgtcac aagaagttcg tgtctgtccg ggctgtggct atatccttcg tgcacagcg 3120
 tacaaggagg gatattggaga aggttgcgta accattcatg agatcgagaa caatacagac 3180
 gaactgaagt ttagcaactg cgtagaggag gaaatctatc caaataacac ggtaacgtgt 3240
 aatgattata ctgtaaatca agaagaatac ggaggtgcgt acacttctcg taatcgagga 3300
 tataacgaag ctcttccgt accagctgat tatgcgtcag tctatgaaga aaaatcgtat 3360
 acagatggac gtagagagaa tccttgtgaa ttaacagag ggtataggga ttacacgcca 3420
 ctaccagttg gttatgtgac aaaagaatta gaatacttcc cagaaaccga taaggtatgg 3480
 attgagattg gagaaacgga aggaacattt atcgtggaca gcgtggaatt actcctatg 3540
 gaggaataa 3549

<210> 71

<211> 1182

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC1099 S553R.

<400> 71

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
 1 5 10 15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
 20 25 30

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

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

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

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110

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

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140

Ile Pro Leu Leu Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160

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

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240

Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285

Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Trp Ser Gly His Gln
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
450 455 460

Ile Ile Ala Ser Asp Ser Ile Thr Gln Leu Pro Leu Val Lys Ala Ser
465 470 475 480

Ala Pro Val Ser Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly
485 490 495

Gly Gly Ile Leu Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg
500 505 510

Val Thr Val Asn Ser Pro Leu Thr Gln Arg Tyr Arg Val Arg Val Arg
515 520 525

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

Ser Ile Ala Tyr Gln Arg Phe Gly Arg Thr Met Asn Arg Gly Gln Glu
545 550 555 560

Leu Thr Tyr Glu Ser Phe Val Thr Ser Glu Phe Thr Thr Asn Gln Ser
565 570 575

Asp Leu Pro Phe Thr Phe Thr Gln Ala Gln Glu Asn Leu Thr Ile Leu
580 585 590

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

Ile Ile Pro Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Arg
610 615 620

Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly
625 630 635 640

Leu Lys Thr Asn Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu
645 650 655

Val Thr Tyr Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu
660 665 670

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

Leu Gln Asp Ser Asn Phe Lys Asp Ile Asn Arg Gln Pro Glu Arg Gly

690	695	700	
Trp Gly Gly Ser Thr Gly Ile Thr Ile Gln Gly Gly Asp Asp Val Phe			
705	710	715	720
Lys Glu Asn Tyr Val Thr Leu Ser Gly Thr Phe Asp Glu Cys Tyr Pro			
	725	730	735
Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Phe Thr			
	740	745	750
Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile			
	755	760	765
Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly			
	770	775	780
Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys			
	785	790	795
Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu			
	805	810	815
Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His			
	820	825	830
Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu			
	835	840	845
Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg			
	850	855	860
Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala			
	865	870	875
Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu			
	885	890	895
Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser			
	900	905	910

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

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

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

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

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

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

Gln Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser
1010 1015 1020

Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val
1025 1030 1035

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

Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val
1055 1060 1065

Glu Glu Glu Ile Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr
1070 1075 1080

Thr Val Asn Gln Glu Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn
1085 1090 1095

Arg Gly Tyr Asn Glu Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser
1100 1105 1110

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

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

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

Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp
 1160 1165 1170

Ser Val Glu Leu Leu Leu Met Glu Glu
 1175 1180

<210> 72

<211> 3549

<212> DNA

<213> Artificial

<220>

<223> Chimeric coding sequence encoding TIC1099 G498D.

<400> 72

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 gtagaagtat taggtggaga aagaatagaa actggttaca cccaatcga tatttccttg 120
 tcgctaacgc aatttctttt gagtgaattt gttcccgggtg ctggatttgt gttaggacta 180
 gttgatataa tatggggaat ttttggccc tctcaatggg acgcatttct tgtacaaatt 240
 gaacagttaa ttaaccaaag aatagaagaa ttcgctagga accaagccat ttctagatta 300
 gaaggactaa gcaatcttta tcaaatttac gcagaatctt ttagagagtg ggaagcagat 360
 cctactaatc cagcattaag agaagagatg cgtattcaat tcaatgacat gaacagtgcc 420
 cttaacaaccg ctattcctct tttggcagtt caaaattatc aagttcctct ttatcagta 480
 tatgttcaag ctgcaaattt acatttatca gtttgagag atgtttcagt gtttgacaa 540
 aggtggggat ttgatgccgc gactatcaat agtcgttata atgatttaac taggcttatt 600
 ggcaactata cagattatgc tgtacgctgg tacaatacgg gattagaacg tgtatgggga 660
 ccggattcta gagattgggt aaggataat caatttagaa gagaattaac actaactgta 720
 ttagatatcg ttgctctgtt cccgaattat gatagtagaa gatatccaat tcgaacagtt 780
 tccaattaa caagagaaat ttatacaaac ccagtattag aaaatttga tggtagtttt 840
 cgaggctcgg ctcagggcat agaaagaagt attaggagtc cacatttgat ggatatactt 900

aacagtataa ccatctatac ggatgctcat aggggttatt attattggtc agggcatcaa 960
 ataatggctt ctctgtcgg ttttcgggg ccagaattca cgttccgct atatggaacc 1020
 atgggaaatg cagctccaca acaacgtatt gttgctcaac taggtcaggg cgtgtataga 1080
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 tctgttcttg acgggacaga atttgcttat ggaacctcct caaatttgcc atccgctgta 1200
 tacagaaaaa gcggaacggg agattcgctg gatgaaatac cgccacagaa taacaacgtg 1260
 ccacctaggc aaggatttag tcatcgatta agccatgttt caatgttctg ttcaggcttt 1320
 agtaatagta gtgtaagtat aataagagct cctatgttct ctgggataca tcgtagtgtc 1380
 gaatttaata atataattgc atcggatagt attacacaat taccattggt aaaggcatct 1440
 gcacctgttt cgggtactac ggtcttaaaa ggtccaggat ttacaggagg ggatatactc 1500
 cgaagaacaa ctaatggcac atttgaacg ttaagagtaa cagttaattc accattaaca 1560
 caaagatatc gcgtaagagt tcgttttgct tcatcaggaa atttcagcat aaggatactg 1620
 cgtggaaata cctctatagc ttatcaaaga ttggggagta caatgaacag aggacaggaa 1680
 ctaacttacg aatcatttgt cacaagttag ttactacta atcagagcga tctgcctttt 1740
 acatttacac aagctcaaga aaatttaaca atccttgtag aagggttag caccggtagt 1800
 gaatatttta tagatagaat tgaaatcatc cctgtgaacc cggcacgaga agcagaagag 1860
 gatttagaaa gagcgcagaa ggcgggtgaat gcgctgttta cgtctacaaa ccaactaggg 1920
 ctaaaaacaa atgtaacgga ttatcatatt gatcaagtgt ccaatttagt tacgtattta 1980
 tcggatgaat ttgtctgga tgaaaagcga gaattgtccg agaaagtcaa acatgcgaag 2040
 cgactcagtg atgaacgcaa ttactccaa gattcaaatt tcaaagacat taataggcaa 2100
 ccagaacgtg ggtggggcgg aagtacaggg attaccatcc aaggagggga tgacgtattt 2160
 aaagaaaatt acgtcacact atcaggtacc ttgatgagt gctatccaac atattgtat 2220
 caaaaaatcg atgaatcaaa attaaaagcc ttaccctgt atcaattaag aggttatatc 2280
 gaagatagtc aagacttaga aatctattta attcgctaca atgcaaaaca tgaaacagta 2340
 aatgtgccag gtacgggttc ctatggccg ctttcagccc aaagtccaat cggaaagtgt 2400
 ggagagccga atcgatgcgc gccacacctt gaatggaatc ctgacttaga ttgtcgtgt 2460
 agggatggag aaaagtgtgc ccatcattcg catcatttct ccttagacat tgatgtagga 2520

tgtacagact taaatgagga cctaggtgta tgggtgatct ttaagattaa gacgcaagat 2580
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 gaaacaaata tcgtttataa agaggcaaaa gaatctgtag atgctttatt tgtaaactct 2760
 caatatgatac aattacaagc ggatacgaat attgccatga ttcattgcggc agataaacgt 2820
 gttcatagca ttcgagaagc ttatctgcct gagctgtctg tgattccggg tgtcaatgcg 2880
 gctatttttg aagaattaga agggcgtatt ttcactgcat tctccctata tgatgcgaga 2940
 aatgtcatta aaaatggtga tttaataat ggcttatcct gctggaacgt gaaagggcat 3000
 gtagatgtag aagaacaaaa caaccaacgt tcggctcttg ttgtccgga atgggaagca 3060
 gaagtgtcac aagaagttcg tgtctgtccg ggtcgtggct atatccttcg tgcacagcg 3120
 tacaaggagg gatattggaga aggttgcgta accattcatg agatcgagaa caatacagac 3180
 gaactgaagt ttagcaactg cgtagaggag gaaatctatc caaataacac ggtaacgtgt 3240
 aatgattata ctgtaaatac agaagaatac ggaggtgcgt acacttctcg taatcgagga 3300
 tataacgaag ctcttccgt accagctgat tatgcgtcag tctatgaaga aaaatcgtat 3360
 acagatggac gtagagagaa tccttgtgaa tttaacagag ggtataggga ttacacgcca 3420
 ctaccagttg gttatgtgac aaaagaatta gaatacttcc cagaaaccga taaggtatgg 3480
 attgagattg gagaaacgga aggaacattt atcgtggaca gcgtggaatt actccttatg 3540
 gaggaataa 3549

<210> 73

<211> 1182

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC1099 G498D.

<400> 73

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
 1 5 10 15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
 20 25 30

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

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

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

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110

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

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140

Ile Pro Leu Leu Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160

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

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240

Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285

Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Trp Ser Gly His Gln
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
450 455 460

Ile Ile Ala Ser Asp Ser Ile Thr Gln Leu Pro Leu Val Lys Ala Ser
465 470 475 480

Ala Pro Val Ser Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly
485 490 495

Gly Asp Ile Leu Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg
500 505 510

Val Thr Val Asn Ser Pro Leu Thr Gln Arg Tyr Arg Val Arg Val Arg
515 520 525

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

Ser Ile Ala Tyr Gln Arg Phe Gly Ser Thr Met Asn Arg Gly Gln Glu
545 550 555 560

Leu Thr Tyr Glu Ser Phe Val Thr Ser Glu Phe Thr Thr Asn Gln Ser
565 570 575

Asp Leu Pro Phe Thr Phe Thr Gln Ala Gln Glu Asn Leu Thr Ile Leu
580 585 590

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

Ile Ile Pro Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Arg
610 615 620

Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly
625 630 635 640

Leu Lys Thr Asn Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu
645 650 655

Val Thr Tyr Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu
660 665 670

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

Leu Gln Asp Ser Asn Phe Lys Asp Ile Asn Arg Gln Pro Glu Arg Gly

690	695	700	
Trp Gly Gly Ser Thr Gly Ile Thr Ile Gln Gly Gly Asp Asp Val Phe			
705	710	715	720
Lys Glu Asn Tyr Val Thr Leu Ser Gly Thr Phe Asp Glu Cys Tyr Pro			
	725	730	735
Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Phe Thr			
	740	745	750
Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile			
	755	760	765
Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly			
	770	775	780
Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys			
	785	790	795
Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu			
	805	810	815
Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His			
	820	825	830
Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu			
	835	840	845
Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg			
	850	855	860
Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala			
	865	870	875
Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu			
	885	890	895
Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser			
	900	905	910

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

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

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

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

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

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

Gln Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser
1010 1015 1020

Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val
1025 1030 1035

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

Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val
1055 1060 1065

Glu Glu Glu Ile Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr
1070 1075 1080

Thr Val Asn Gln Glu Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn
1085 1090 1095

Arg Gly Tyr Asn Glu Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser
1100 1105 1110

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

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

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

Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp
 1160 1165 1170

Ser Val Glu Leu Leu Leu Met Glu Glu
 1175 1180

<210> 74

<211> 3549

<212> DNA

<213> Artificial

<220>

<223> Chimeric coding sequence encoding TIC1099 K490A.

<400> 74

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 tcgctaacgc aatttctttt gagtgaattt gttcccgggtg ctggatttgt gtaggacta 180
 gttgatataa tatggggaat ttttggccc tctcaatggg acgcatttct tgtacaaatt 240
 gaacagttaa ttaaccaaag aatagaagaa ttcgctagga accaagccat ttctagatta 300
 gaaggactaa gcaatcttta tcaaatttac gcagaatctt ttagagagtg ggaagcagat 360
 cctactaatc cagcattaag agaagagatg cgtattcaat tcaatgacat gaacagtgcc 420
 cttaacaaccg ctattcctct tttggcagtt caaaattatc aagttcctct ttatcagta 480
 tatgttcaag ctgcaaattt acatttatca gtttgagag atgtttcagt gtttgacaa 540
 aggtggggat ttgatgccgc gactatcaat agtcgttata atgatttaac taggcttatt 600
 ggcaactata cagattatgc tgtacgctgg tacaatacgg gattagaacg tgtatgggga 660
 ccggattcta gagattgggt aaggataat caatttagaa gagaattaac actaactgta 720
 ttagatatcg ttgctctgtt cccgaattat gatagtagaa gatatccaat tcgaacagtt 780
 tccaattaa caagagaaat ttatacaaac ccagtattag aaaatttga tggtagtttt 840
 cgaggctcgg ctcagggcat agaaagaagt attaggagtc cacatttgat ggatatactt 900

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 atgggaaatg cagctccaca acaacgtatt gttgctcaac taggtcaggg cgtgtataga 1080
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 acagatggac gtagagagaa tccttgtgaa ttaacagag ggtataggga ttacacgcca 3420
 ctaccagttg gttatgtgac aaaagaatta gaatacttcc cagaaaccga taaggtatgg 3480
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 gaggaataa 3549

<210> 75

<211> 1182

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC1099 K490A.

<400> 75

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

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

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

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

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110

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

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140

Ile Pro Leu Leu Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160

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

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240

Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285

Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Trp Ser Gly His Gln
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
450 455 460

Ile Ile Ala Ser Asp Ser Ile Thr Gln Leu Pro Leu Val Lys Ala Ser
465 470 475 480

Ala Pro Val Ser Gly Thr Thr Val Leu Ala Gly Pro Gly Phe Thr Gly
485 490 495

Gly Gly Ile Leu Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg
500 505 510

Val Thr Val Asn Ser Pro Leu Thr Gln Arg Tyr Arg Val Arg Val Arg
515 520 525

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

Ser Ile Ala Tyr Gln Arg Phe Gly Ser Thr Met Asn Arg Gly Gln Glu
545 550 555 560

Leu Thr Tyr Glu Ser Phe Val Thr Ser Glu Phe Thr Thr Asn Gln Ser
565 570 575

Asp Leu Pro Phe Thr Phe Thr Gln Ala Gln Glu Asn Leu Thr Ile Leu
580 585 590

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

Ile Ile Pro Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Arg
610 615 620

Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly
625 630 635 640

Leu Lys Thr Asn Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu
645 650 655

Val Thr Tyr Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu
660 665 670

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

Leu Gln Asp Ser Asn Phe Lys Asp Ile Asn Arg Gln Pro Glu Arg Gly

690	695	700	
Trp Gly Gly Ser Thr Gly Ile Thr Ile Gln Gly Gly Asp Asp Val Phe			
705	710	715	720
Lys Glu Asn Tyr Val Thr Leu Ser Gly Thr Phe Asp Glu Cys Tyr Pro			
	725	730	735
Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Phe Thr			
	740	745	750
Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile			
	755	760	765
Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly			
	770	775	780
Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys			
	785	790	795
Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu			
	805	810	815
Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His			
	820	825	830
Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu			
	835	840	845
Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg			
	850	855	860
Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala			
	865	870	875
Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu			
	885	890	895
Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser			
	900	905	910

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

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

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

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

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

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

Gln Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser
1010 1015 1020

Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val
1025 1030 1035

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

Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val
1055 1060 1065

Glu Glu Glu Ile Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr
1070 1075 1080

Thr Val Asn Gln Glu Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn
1085 1090 1095

Arg Gly Tyr Asn Glu Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser
1100 1105 1110

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

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

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

Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp
 1160 1165 1170

Ser Val Glu Leu Leu Leu Met Glu Glu
 1175 1180

<210> 76

<211> 3549

<212> DNA

<213> Artificial

<220>

<223> Chimeric coding sequence encoding TIC1099 E564A.

<400> 76

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 gttgatataa tatgggggaat ttttgggtccc tctcaatggg acgcatttct tgtacaaatt 240
 gaacagttaa ttaaccaaag aatagaagaa ttcgctagga accaagccat ttctagatta 300
 gaaggactaa gcaatcttta tcaaatttac gcagaatctt ttagagagtg ggaagcagat 360
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 tatgttcaag ctgcaaattt acatttatca gtttgagag atgtttcagt gtttgacaa 540
 aggtggggat ttgatgccgc gactatcaat agtcgttata atgatttaac taggcttatt 600
 ggcaactata cagattatgc tgtacgctgg tacaatacgg gattagaacg tgtatgggga 660
 ccggattcta gagattgggt aaggataat caatttagaa gagaattaac actaactgta 720
 ttagatatcg ttgctctgtt cccgaattat gatagtagaa gatatccaat tcgaacagtt 780
 tccaattaa caagagaaat ttatacaaac ccagtattag aaaatttga tggtagtttt 840
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aacagtataa ccatctatac ggatgctcat aggggttatt attattggtc agggcatcaa 960
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 gaggaataa 3549

<210> 77

<211> 1182

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC1099 E564A.

<400> 77

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Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
 20 25 30

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

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

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

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110

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

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140

Ile Pro Leu Leu Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160

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

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240

Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285

Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Trp Ser Gly His Gln
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
450 455 460

Ile Ile Ala Ser Asp Ser Ile Thr Gln Leu Pro Leu Val Lys Ala Ser
465 470 475 480

Ala Pro Val Ser Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly
485 490 495

Gly Gly Ile Leu Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg
500 505 510

Val Thr Val Asn Ser Pro Leu Thr Gln Arg Tyr Arg Val Arg Val Arg
515 520 525

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

Ser Ile Ala Tyr Gln Arg Phe Gly Ser Thr Met Asn Arg Gly Gln Glu
545 550 555 560

Leu Thr Tyr Ala Ser Phe Val Thr Ser Glu Phe Thr Thr Asn Gln Ser
565 570 575

Asp Leu Pro Phe Thr Phe Thr Gln Ala Gln Glu Asn Leu Thr Ile Leu
580 585 590

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

Ile Ile Pro Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Arg
610 615 620

Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly
625 630 635 640

Leu Lys Thr Asn Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu
645 650 655

Val Thr Tyr Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu
660 665 670

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

Leu Gln Asp Ser Asn Phe Lys Asp Ile Asn Arg Gln Pro Glu Arg Gly

690	695	700	
Trp Gly Gly Ser Thr Gly Ile Thr Ile Gln Gly Gly Asp Asp Val Phe			
705	710	715	720
Lys Glu Asn Tyr Val Thr Leu Ser Gly Thr Phe Asp Glu Cys Tyr Pro			
	725	730	735
Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Phe Thr			
	740	745	750
Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile			
	755	760	765
Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly			
	770	775	780
Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys			
	785	790	795
Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu			
	805	810	815
Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His			
	820	825	830
Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu			
	835	840	845
Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg			
	850	855	860
Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala			
	865	870	875
Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu			
	885	890	895
Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser			
	900	905	910

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

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

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

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

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

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

Gln Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser
1010 1015 1020

Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val
1025 1030 1035

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

Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val
1055 1060 1065

Glu Glu Glu Ile Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr
1070 1075 1080

Thr Val Asn Gln Glu Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn
1085 1090 1095

Arg Gly Tyr Asn Glu Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser
1100 1105 1110

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

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

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

Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp
 1160 1165 1170

Ser Val Glu Leu Leu Leu Met Glu Glu
 1175 1180

<210> 78

<211> 3534

<212> DNA

<213> Artificial

<220>

<223> Chimeric coding sequence encoding TIC1103.

<400> 78

atggataaca atccgaacat caatgaatgc attccttata attgtttaag taaccctgaa 60
 gtagaagtat taggtggaga aagaatagaa actggttaca cccaatcga tatttccttg 120
 tcgctaacgc aatttctttt gagtgaattt gttcccgggtg ctggatttgt gtaggacta 180
 gttgatataa tatggggaat ttttggccc tctcaatggg acgcatttct tgtacaaatt 240
 gaacagttaa ttaaccaaag aatagaagaa ttcgctagga accaagccat ttctagatta 300
 gaaggactaa gcaatcttta tcaaatttac gcagaatctt ttagagagtg ggaagcagat 360
 cctactaatc cagcattaag agaagagatg cgtattcaat tcaatgacat gaacagtgcc 420
 cttacaaccg ctattcctct tttggcagtt caaaattatc aagttcctct tttatcagta 480
 tatgttcaag ctgcaaattt acatttatca gttttgagag atgtttcagt gtttgacaa 540
 aggtggggat ttgatgccgc gactatcaat agtcgttata atgatttaac taggcttatt 600
 ggcaactata cagattatgc tgtacgctgg tacaatacgg gattagaacg tgtatgggga 660
 ccggattcta gagattgggt aaggataat caatttagaa gagaattaac actaactgta 720
 ttagatatcg ttgctctgtt cccgaattat gatagtagaa gatatccaat tcgaacagtt 780
 tccaattaa caagagaaat ttatacaaac ccagtattag aaaatttga tggtagtttt 840
 cgaggctcgg ctcagggcat agaaagaagt attaggagtc cacatttgat ggatatactt 900

aacagtataa ccatctatac ggatgctcat aggggttatt attattggtc agggcatcaa 960
 ataatggctt ctctgtcgg ttttcgggg ccagaattca cgttccgct atatggaacc 1020
 atgggaaatg cagctccaca acaacgtatt gttgctcaac taggtcaggg cgtgtataga 1080
 acattatcgt ccactttata tagaagacct ttaatatag ggataaataa tcaacaacta 1140
 tctgttcttg acgggacaga atttgcttat ggaacctcct caaatttgcc atccgctgta 1200
 tacagaaaaa gcggaacggg agattcgctg gatgaaatac cgccacagaa taacaacgtg 1260
 ccacctaggc aaggatttag tcatcgatta agccatgttt caatgtttcg ttcaggcttt 1320
 agtaatagta gtgtaagtat aataagagct cctatgttct ctgggataca tcgtagtgtc 1380
 gaatttaata atataattgc atcggatagt attactcaac tacccatggt aaaggcaaatt 1440
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 agaagaacaa gtgttggcag agtaggaaat ttaagggtta acgtaaatgg accattaaca 1560
 caacgataac ttgtaagaat tcgttatgct tctacaactg atctagactt ttacgtctat 1620
 cgtggaggta ccactgtaag taattataga ttaacaaaa caatgaataa gggagcttct 1680
 ttaacttacg acatttttaa attgcaagt tttctaccc cttcacatt taaaaaaca 1740
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 aggattgaag tcattccagt aggtacgaca tatgaagcgg aaacggattt agaaagagcg 1860
 cagaaggcgg tgaatgcgct gtttacgtct acaaccaac tagggctaaa acaaatgta 1920
 acggattatc atattgatca agtgtccat ttagttacgt atttatcgga tgaatttgt 1980
 ctggatgaaa agcgagaatt gtccgagaaa gtcaaactg cgaagcgact cagtgatgaa 2040
 cgcaatttac tccaagattc aaatttcaa gacattaata ggcaaccaga acgtgggtgg 2100
 ggcggaagta cagggttac catccaagga ggggatgacg tatttaaaga aaattacgtc 2160
 acactatcag gtaccttga tgagtgtat ccaacatatt tgtatcaaaa aatcgatgaa 2220
 tcaaaattaa aagcctttac ccgttatcaa ttaagagggt atatcgaaga tagtcaagac 2280
 ttagaaatct atttaattcg ctacaatgca aaacatgaaa cagtaaatgt gccaggtagc 2340
 ggttccttat ggccgcttc agcccaaagt ccaatcgga agtgtggaga gccgaatcga 2400
 tgcgcgccac acctgaatg gaatcctgac ttagattgtt cgtgtaggga tggagaaaag 2460
 tgtgccatc attcgcatca tttctccta gacattgat taggatgtac agactaaat 2520

gaggacctag gtgtatgggt gatctttaag attaagacgc aagatgggca cgcaagacta 2580
 gggaatctag agtttctcga agaaaaacca ttagtaggag aagcgctagc tcgtgtgaaa 2640
 agagcggaga aaaaatggag agacaaacgt gaaaaattgg aatgggaaac aaatatcggt 2700
 tataaagagg caaaagaatc ttagatgctt ttattgttaa actctcaata tgatcaatta 2760
 caagcggata cgaatattgc catgattcat gcggcagata aacgtgttca tagcattcga 2820
 gaagcttatt tgcctgagct gtctgtgatt ccgggtgtca atgcggctat tttgaagaa 2880
 ttagaagggc gtattttcac tgcattctcc ctatatgatg cgagaaatgt cattaataat 2940
 ggtgatttta ataatggctt atcctgctgg aacgtgaaag ggcatgtaga tgtagaagaa 3000
 caaaacaacc aacgttcggt cctgtgtgtt ccggaatggg aagcagaagt gtcacaagaa 3060
 gttcgtgtct gtccgggtcg tggctatatc cttcgtgtca cagcgtacaa ggagggatat 3120
 ggagaagggt gcgtaacatc tcatgagatc gagaacaata cagacgaact gaagtttagc 3180
 aactgcgtag aggaggaaat ctatccaaat aacacggtaa cgtgtaatga ttactactga 3240
 aatcaagaag aatacggagg tgcgtacact tctcgtaatc gaggatataa cgaagctcct 3300
 tccgtaccag ctgattatgc gtcagtctat gaagaaaaat cgtatacaga tggacgtaga 3360
 gagaatcctt gtgaatttaa cagagggtat agggattaca cgccactacc agttggttat 3420
 gtgacaaaag aattagaata ctcccagaa accgataagg tatggattga gattggagaa 3480
 acggaaggaa catttatcgt ggacagcgtg gaattactcc ttatggagga ataa 3534

<210> 79

<211> 1177

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC1103.

<400> 79

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu

1 5 10 15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly

20 25 30

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser

35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

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

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110

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

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140

Ile Pro Leu Leu Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160

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

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240

Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
245 250 255

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

260	265	270
Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu		
275	280	285
Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr		
290	295	300
Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln		
305	310	315 320
Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro		
325	330	335
Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala		
340	345	350
Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg		
355	360	365
Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp		
370	375	380
Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val		
385	390	395 400
Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln		
405	410	415
Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His		
420	425	430
Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile		
435	440	445
Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn		
450	455	460
Ile Ile Ala Ser Asp Ser Ile Thr Gln Leu Pro Met Val Lys Ala Asn		
465	470	475 480

Ala Leu Leu Ser Gly Thr Ser Val Ile Lys Gly Pro Gly Ser Thr Gly
485 490 495

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

Val Asn Val Asn Gly Pro Leu Thr Gln Arg Tyr Leu Val Arg Ile Arg
515 520 525

Tyr Ala Ser Thr Thr Asp Leu Asp Phe Tyr Val Tyr Arg Gly Gly Thr
530 535 540

Thr Val Ser Asn Tyr Arg Phe Asn Lys Thr Met Asn Lys Gly Ala Ser
545 550 555 560

Leu Thr Tyr Asp Ile Phe Lys Phe Ala Ser Phe Ser Thr Pro Phe Thr
565 570 575

Phe Thr Lys Thr Gln Asp Glu Leu Gly Ile Ser Ile Gln Asn Phe Ser
580 585 590

Ser Gly Glu Glu Val Tyr Ile Asp Arg Ile Glu Val Ile Pro Val Gly
595 600 605

Thr Thr Tyr Glu Ala Glu Thr Asp Leu Glu Arg Ala Gln Lys Ala Val
610 615 620

Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly Leu Lys Thr Asn Val
625 630 635 640

Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Thr Tyr Leu Ser
645 650 655

Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys
660 665 670

His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Ser Asn
675 680 685

Phe Lys Asp Ile Asn Arg Gln Pro Glu Arg Gly Trp Gly Gly Ser Thr
690 695 700

Gly Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
705 710 715 720

Thr Leu Ser Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
725 730 735

Lys Ile Asp Glu Ser Lys Leu Lys Ala Phe Thr Arg Tyr Gln Leu Arg
740 745 750

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
755 760 765

Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
770 775 780

Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg
785 790 795 800

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg
805 810 815

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
820 825 830

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
835 840 845

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
850 855 860

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

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

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

Val Asn Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile Ala Met
915 920 925

Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu
930 935 940

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

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

Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val
980 985 990

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

Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val
1010 1015 1020

Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu
1025 1030 1035

Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn
1040 1045 1050

Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Ile Tyr
1055 1060 1065

Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Val Asn Gln Glu
1070 1075 1080

Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn Arg Gly Tyr Asn Glu
1085 1090 1095

Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys
1100 1105 1110

Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys Glu Phe Asn Arg
1115 1120 1125

Gly Tyr Arg Asp Tyr Thr Pro Leu Pro Val Gly Tyr Val Thr Lys

1130	1135	1140
Glu Leu	Glu Tyr Phe Pro Glu	Thr Asp Lys Val Trp Ile Glu Ile
1145	1150	1155
Gly Glu	Thr Glu Gly Thr Phe Ile Val Asp Ser Val	Glu Leu Leu
1160	1165	1170
Leu Met	Glu Glu	
1175		

<210> 80
 <211> 3597
 <212> DNA
 <213> Artificial

<220>
 <223> Chimeric coding sequence encoding TIC1101.

<400> 80
 atgaaaaaca gtatcaaatt atcagaactt tggatttca atgaaagaaa atggaggtat 60
 tttatggaga tagtgaataa tcagaatcaa tgcgtgcctt ataattgtt gaataatccc 120
 gaaatcgaat tattagaagg cggaagaata tcagttggta atacccaat tgatatttct 180
 ctttcgctta ctacgtttct tttagtgaa ttgtcccag gtgcgggggt tgtattagga 240
 ttaattgatt taatatgggg attgtaggt ccttccaat gggacgcatt tcttgctcaa 300
 gtggaacagt taattaacca aagaatagca gaagctgtaa gaaatacagc aattcaggaa 360
 ttagagggaa tggcacgggt ttatagaacc tatgctactg ctttgctga gtgggaaaaa 420
 gctcctgatg acccagagct aagagaagca ctacgtacac aatttacagc aactgagact 480
 tatataagtg gaagaatac cgtttaaaa attcaaactt ttgaagtaca gctgttatca 540
 gtgtttgcc aagctgcaaa ttacattta tctttattaa gagacgtgt gtttttggg 600
 caaagatggg gttttcaac gacaaccgta aataattact acaatgatt aacagaaggg 660
 attagtagct atacagatta tgctgtacgc tggtaacaata cgggattaga acgtgtatgg 720
 ggaccggatt ctatagattg ggtaagggt aatcaattta gaagagaatt aactactaact 780
 gtattagata tcgtgtctct gtcccgaat tatgatagta gaagatatcc aattcgaaca 840
 gtttccaat taacaagaga aatttataca aaccagat tagaaaaatt tgatgtagt 900
 ttcgaggct cggctcagg catagaaaga agtattagga gtccacatt gatggatata 960

ctaacagta taaccatcta tacggatgct cataggggtt attattattg gtcagggcat 1020
 caaataatgg ctctcctgt cggttttcg gggccagaat tcacgtttcc gctatatgga 1080
 accatgggaa atgcagctcc acaacaacgt attgttgctc aactaggta gggcgtgtat 1140
 agaacattat cgtccacttt atatagaaga cctttaata tagggataaa taatcaacaa 1200
 ctatctgttc ttgacgggac agaatttgct tatggaacct cctcaaattt gccatccgct 1260
 gtatacagaa aaagcgggac ggtagattcg ctggatgaaa taccgccaca gaataacaac 1320
 gtgccaccta ggcaaggatt tagtcatcga ttaagccatg ttcaatggt tcgttcaggc 1380
 ttagtaata gtagtgaag tataataaga gctcctatgt tctcttgat acatcgtagt 1440
 gctgaattta ataataat tgcacggat agtattactc aactacccat ggtaaaggca 1500
 aatgctttac ttcaggtagc ttccgtgata aagggtcctg gatctacagg gggagatata 1560
 ttaagaagaa caagtgttg cagagtagga aattttaagg ttaacgtaaa tggaccatta 1620
 acacaacgat atcttgaag aattcgttat gcttctacaa ctgatctaga ctttacgctc 1680
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 acacaagatg aattaggaat atctatacaa aactttagta gcggtgaaga agtgtatata 1860
 gacaggattg aagtcattcc agtaggtacg acatatgaag cggaacgga ttagaaaga 1920
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 gtaacggatt atcatattga tcaagtgtcc aatttagtta cgtatttatc ggatgaattt 2040
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 gaacgcaatt tactccaaga ttcaaatttc aaagacatta ataggcaacc agaacgtggg 2160
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 gtcacactat caggtagctt tgatgagtgc tatccaacat atttgatca aaaaatcgat 2280
 gaatcaaaat taaaagcctt taccggttat caattaagag ggtatatcga agatagtaa 2340
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 acgggttctt tatggccgct ttacgcccac agtccaatcg gaaagtgtgg agagccgaat 2460
 cgatgcgcgc cacaccttga atggaatcct gacttagatt gttcgtgtag ggatggagaa 2520
 aagtgtgcc atcattcgca tcatttctcc ttagacattg atgtaggatg tacagactta 2580

aatgaggacc taggtgtatg ggtgatcttt aagattaaga cgcaagatgg gcacgcaaga 2640
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gaacaaaaca accaacgttc ggtccttggt gttccggaat gggaagcaga agtgtcacia 3120
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gtaaatcaag aagaatacgg aggtgcgtac acttctcgta atcgaggata taacgaagct 3360
ccttccgtac cagctgatta tgcgtcagtc tatgaagaaa aatcgtatac agatggacga 3420
agagagaatc cttgtgaatt taacagaggg tatagggatt acacgccact accagttggt 3480
tatgtgacaa aagaattaga atactccca gaaaccgata aggtatggat tgagattgga 3540
gaaacggaag gaacatttat cgtggacagc gtggaattac tccttatgga ggaatag 3597

<210> 81

<211> 1198

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC1101.

<400> 81

Met Lys Asn Ser Ile Lys Leu Ser Glu Leu Trp Tyr Phe Asn Glu Arg
1 5 10 15

Lys Trp Arg Tyr Phe Met Glu Ile Val Asn Asn Gln Asn Gln Cys Val
20 25 30

Pro Tyr Asn Cys Leu Asn Asn Pro Glu Ile Glu Ile Leu Glu Gly Gly
35 40 45

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

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

Leu Ile Asp Leu Ile Trp Gly Phe Val Gly Pro Ser Gln Trp Asp Ala
85 90 95

Phe Leu Ala Gln Val Glu Gln Leu Ile Asn Gln Arg Ile Ala Glu Ala
100 105 110

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

Arg Thr Tyr Ala Thr Ala Phe Ala Glu Trp Glu Lys Ala Pro Asp Asp
130 135 140

Pro Glu Leu Arg Glu Ala Leu Arg Thr Gln Phe Thr Ala Thr Glu Thr
145 150 155 160

Tyr Ile Ser Gly Arg Ile Ser Val Leu Lys Ile Gln Thr Phe Glu Val
165 170 175

Gln Leu Leu Ser Val Phe Ala Gln Ala Ala Asn Leu His Leu Ser Leu
180 185 190

Leu Arg Asp Val Val Phe Phe Gly Gln Arg Trp Gly Phe Ser Thr Thr
195 200 205

Thr Val Asn Asn Tyr Tyr Asn Asp Leu Thr Glu Gly Ile Ser Thr Tyr
210 215 220

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

Gly Pro Asp Ser Arg Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu
245 250 255

Leu Thr Leu Thr Val Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp

260	265	270
Ser Arg Arg Tyr Pro Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile		
275	280	285
Tyr Thr Asn Pro Val Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser		
290	295	300
Ala Gln Gly Ile Glu Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile		
305	310	315
320		
Leu Asn Ser Ile Thr Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr		
325	330	335
Trp Ser Gly His Gln Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro		
340	345	350
Glu Phe Thr Phe Pro Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln		
355	360	365
Gln Arg Ile Val Ala Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser		
370	375	380
Ser Thr Leu Tyr Arg Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln		
385	390	395
400		
Leu Ser Val Leu Asp Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn		
405	410	415
Leu Pro Ser Ala Val Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp		
420	425	430
Glu Ile Pro Pro Gln Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser		
435	440	445
His Arg Leu Ser His Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser		
450	455	460
Ser Val Ser Ile Ile Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser		
465	470	475
480		

Ala Glu Phe Asn Asn Ile Ile Ala Ser Asp Ser Ile Thr Gln Leu Pro
485 490 495

Met Val Lys Ala Asn Ala Leu Leu Ser Gly Thr Ser Val Ile Lys Gly
500 505 510

Pro Gly Ser Thr Gly Gly Asp Ile Leu Arg Arg Thr Ser Val Gly Arg
515 520 525

Val Gly Asn Phe Lys Val Asn Val Asn Gly Pro Leu Thr Gln Arg Tyr
530 535 540

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

Tyr Arg Gly Gly Thr Thr Val Ser Asn Tyr Arg Phe Asn Lys Thr Met
565 570 575

Asn Lys Gly Ala Ser Leu Thr Tyr Asp Ile Phe Lys Phe Ala Ser Phe
580 585 590

Ser Thr Pro Phe Thr Phe Thr Lys Thr Gln Asp Glu Leu Gly Ile Ser
595 600 605

Ile Gln Asn Phe Ser Ser Gly Glu Glu Val Tyr Ile Asp Arg Ile Glu
610 615 620

Val Ile Pro Val Gly Thr Thr Tyr Glu Ala Glu Thr Asp Leu Glu Arg
625 630 635 640

Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly
645 650 655

Leu Lys Thr Asn Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu
660 665 670

Val Thr Tyr Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu
675 680 685

Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu
690 695 700

Leu Gln Asp Ser Asn Phe Lys Asp Ile Asn Arg Gln Pro Glu Arg Gly
705 710 715 720

Trp Gly Gly Ser Thr Gly Ile Thr Ile Gln Gly Gly Asp Asp Val Phe
725 730 735

Lys Glu Asn Tyr Val Thr Leu Ser Gly Thr Phe Asp Glu Cys Tyr Pro
740 745 750

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

Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile
770 775 780

Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly
785 790 795 800

Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys
805 810 815

Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu
820 825 830

Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His
835 840 845

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

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

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

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

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

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

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

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

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

Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu
995 1000 1005

Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn
1010 1015 1020

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

Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
1040 1045 1050

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

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

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

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

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

Ser Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn

1130	1135	1140
Pro Cys	Glu Phe Asn Arg Gly	Tyr Arg Asp Tyr Thr Pro Leu Pro
1145	1150	1155
Val Gly	Tyr Val Thr Lys Glu	Leu Glu Tyr Phe Pro Glu Thr Asp
1160	1165	1170
Lys Val	Trp Ile Glu Ile Gly	Glu Thr Glu Gly Thr Phe Ile Val
1175	1180	1185
Asp Ser	Val Glu Leu Leu Leu	Met Glu Glu
1190	1195	

<210> 82
 <211> 3573
 <212> DNA
 <213> Artificial

<220>
 <223> Chimeric coding sequence encoding TIC845.

<400> 82
 atgacttcaa ataggaaaaa tgagaatgaa attataaatg ctttatcgat tccaacggta 60
 tcgaatcctt ccacgcaaata gaatttatca ccagatgctc gtattgaaga tagcttgtgt 120
 gtagccgagg tgaacaatat tgatccattt gttagcgcac caacagtcca aacgggtata 180
 aacatagctg gtagaatatt gggcgtatta ggtgtgccgt ttgctggaca actagctagt 240
 ttttatagtt ttctgttgg ggaattatgg cctagtggca gagatccatg ggaaattttc 300
 ctggaacatg tagaacaact tataagacaa caagtaacag aaaatactag gaatacggct 360
 attgctcgat tagaagggtc aggaagaggc tatagatctt accagcaggc tcttgaaact 420
 tggtagata accgaaatga tgcaagatca agaagcatta ttctgagcg ctatgttgct 480
 ttagaacttg acattactac tgctataccg ctttcagaa tacgaaatga agaagttcca 540
 ttattaatgg tatatgctca agctgcaaata ttacacctat tattattgag agacgcatcc 600
 ctttttggtg gtgaatgggg gatggcatct tccgatgta accaatatta ccaagaacaa 660
 atcagatata cagaggaata ttctaaccat tgcgtacaat ggtataatac agggctaaat 720
 aacttaagag ggacaaatgc tgaaagtggg ttgcgggtata atcaattccg tagagaccta 780
 acgttagggg tattagattt agtagcccta ttccaagct atgatactcg cacttatcca 840

atcaatacga gtgctcagtt aacaagagaa atttatacag atccaattgg gagaacaaat 900
 gcaccttcag gatttgcaag tacgaattgg ttaataata atgcaccatc gtttctgcc 960
 atagaggctg ccatttcag gcctccgcat ctacttgatt ttccagaaca acttacaatt 1020
 tacagtgcac caagccgttg gagtagcact caacatatga attattgggt gggacatagg 1080
 cttacttcc gcccaatagg aggacatta 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
 caggaggttg ggattcaatt atttgattca gaaactgaat taccaccaga aacaacagaa 1380
 cgaccaaatt atgaatcata tagtcataga ttatctcata taggactaat cataggaaac 1440
 actttgagag caccagtcta ttcttgacg catcgtagtg cagatcgtag gaacataatt 1500
 gcatcggata gtattactca aatccctgca gtgaaggga actttcttt taatggttct 1560
 gtaatttcag gaccaggatt tactggtggg gacttagtta gattaaatag tagtggaat 1620
 aacattcaga atagagggtta tattgaagtt ccaattcact tccatcgac atctaccaga 1680
 tatcgagttc gtgtacggtta tgcttctgta acccggattc acctcaacgt taattggggt 1740
 aattcatcca tttttccaa tacagtacca gctacagcta cgtcattaga taatctacaa 1800
 tcaagtgatt ttggttatt tgaaagtgcc aatgcttta catcttcatt aggtaataa 1860
 gtaggtgta gaaattttag tgggactgca ggagtataa tagacagatt tgaatttatt 1920
 ccagttactg caacactcga ggctgaatat aatctggaaa gagcacaaaa ggcggtgaat 1980
 gagctgttta ctcttccaa tcaaatcggg ttaaaaacag atgtgacgga ttatcatatt 2040
 gatcaagtat ccaatttagt tgagtgttta tctgatgaat ttgtctgga tgaaaaaaaa 2100
 gaattgtccg agaaagtcaa acatgcgaag cgacttagtg atgagcggaa ttacttcaa 2160
 gatccaaact ttagagggat caatagacaa ctgaccgtg gctggagagg aagtacggat 2220
 attacatcc aaggaggcga tgacgtattc aaagagaatt acgttacgct attgggtacc 2280
 ttgatgagt gctatccaac gtatttatat caaaaaatag atgagtcgaa attaaaagcc 2340
 tataccggtt accaattaag agggatatc gaagatagtc aagacttaga aatctattta 2400
 attcgctaca atgccaaaca cgaaacagta aatgtgccag gtacgggttc ctatggccg 2460

ctttcagccc caagtccaat cggaaaatgt gccatcatt cccatcattt ctccttgac 2520
 attgatgttg gatgtacaga cttaaatgag gacttaggtg tatgggtgat attcaagatt 2580
 aagacgcaag atggccatgc aagactagga aatctagaat ttctcgaaga gaaaccatta 2640
 gtaggagaag cactagctcg tgtgaaaaga gcggagaaaa aatggagaga caaacgtgaa 2700
 aaattggaat gggaaacaaa tattgtttat aaagaggcaa aagaatctgt agatgcttta 2760
 ttgtaaact ctcaatatga tagattacaa gcggatacca acatcgcgat gattcatgcg 2820
 gcagataaac gcgttcatag cattcgagaa gcttatctgc ctgagctgtc tgtgattccg 2880
 ggtgtcaatg cggctathtt tgaagaatta gaagggcgta tttcactgc attctcccta 2940
 tatgatcgga gaaatgtcat taaaaatggt gattttaata atggcttacc ctgctggaac 3000
 gtgaaagggc atgtagatgt agaagaacaa aacaaccacc gttcggctct tgtgttccg 3060
 gaatgggaag cagaagtgtc acaagaagtt cgtgtctgtc cgggtcgtgg ctatcctt 3120
 cgtgtcacag cgtacaagga gggatatgga gaaggttgcg taaccattca tgagatcgag 3180
 aacaatacag acgaactgaa gtttagcaac tgtgtagaag aggaagtata tccaaacaac 3240
 acggtaacgt gtaatgatta tactgcgact caagaagaat atgagggtag gtacacttct 3300
 cgtaatcgag gatatgacgg agcctatgaa agcaattctt ctgtaccagc tgattatgca 3360
 tcagcctatg aagaaaaagc atatacagat ggacgaagag acaatccttg tgaatctaac 3420
 agaggatatg gggattacac accactacca gctggctatg tgacaaaaga attagagtag 3480
 ttcccagaaa ccgataaggt atggattgag atcgagaaaa cggaaggaaac attcatcgtg 3540
 gacagcgtgg aattacttct tatggaggaa tag 3573

<210> 83

<211> 1190

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC845.

<400> 83

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

Gly Asn Phe Leu Phe Asn Gly Ser Val Ile Ser Gly Pro Gly Phe Thr
515 520 525

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

Arg Gly Tyr Ile Glu Val Pro Ile His Phe Pro Ser Thr Ser Thr Arg
545 550 555 560

Tyr Arg Val Arg Val Arg Tyr Ala Ser Val Thr Pro Ile His Leu Asn
565 570 575

Val Asn Trp Gly Asn Ser Ser Ile Phe Ser Asn Thr Val Pro Ala Thr
580 585 590

Ala Thr Ser Leu Asp Asn Leu Gln Ser Ser Asp Phe Gly Tyr Phe Glu
595 600 605

Ser Ala Asn Ala Phe Thr Ser Ser Leu Gly Asn Ile Val Gly Val Arg
610 615 620

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

Pro Val Thr Ala Thr Leu Glu Ala Glu Tyr Asn Leu Glu Arg Ala Gln
645 650 655

Lys Ala Val Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile 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 Glu Lys Lys 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 Leu 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 Leu Gly Thr Phe 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

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 Val Asn Val Pro Gly Thr Gly
805 810 815

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

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

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

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

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

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

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

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

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

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

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

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

Glu Gln Asn Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu
1010 1015 1020

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

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

Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe
1055 1060 1065

Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr
1070 1075 1080

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

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

Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr

1115	1120	1125
Thr Asp	Gly Arg Arg Asp Asn	Pro Cys Glu Ser Asn Arg Gly Tyr
1130	1135	1140
Gly Asp	Tyr Thr Pro Leu Pro	Ala Gly Tyr Val Thr Lys Glu Leu
1145	1150	1155
Glu Tyr	Phe Pro Glu Thr Asp	Lys Val Trp Ile Glu Ile Gly Glu
1160	1165	1170
Thr Glu	Gly Thr Phe Ile Val	Asp Ser Val Glu Leu Leu Leu Met
1175	1180	1185
Glu Glu		
1190		

<210> 84
 <211> 3567
 <212> DNA
 <213> Artificial

<220>
 <223> Chimeric coding sequence encoding TIC846.

<400> 84
 atgacttcaa ataggaaaa tgagaatgaa attataaatg ctttatcgat tccaacggta 60
 tcgaatcctt ccacgcaaata gaatctatca ccagatgctc gtattgaaga tagcttgtgt 120
 gtagccgagg tgaacaatat tgatccattt gtagcgcac caacagtcca aacgggtata 180
 aacatagctg gtagaatatt gggcgtatta ggtgtgccgt ttgctggaca actagctagt 240
 ttttatagtt ttctgttgg ggaattatgg cctagtggca gagatccatg ggaaattttc 300
 ctggaacatg tagaacaact tataagacaa caagtaacag aaaatactag gaatacggct 360
 attgctcgat tagaaggctt aggaagaggc tatagatctt accagcaggc tcttgaaact 420
 tggtagata accgaaatga tgcaagatca agaagcatta ttctgagcg ctatgttgct 480
 ttagaacttg acattactac tgctataccg ctttcagaa tacgaaatga agaagtcca 540
 ttattaatgg tatatgctca agctgcaaata ttacacatat tattattgag agacgcatcc 600
 ctttttggtg gtgaatgggg gatggcatct tccgatgtta accaatatta ccaagaacaa 660
 atcagatata cagaggaata ttctaaccat tgcgtacaat ggtataatac agggctaaat 720

aacttaagag ggacaaatgc tgaaagtgg ttgcggtata atcaattccg tagagaccta 780
acgtagggg tattagattt agtagcccta ttccaagct atgatactcg cacttatcca 840
atcaatacga gtgctcagtt aacaagagaa atttatacag atccaattgg gagaacaaat 900
gcaccttcag gatttgcaag tacgaattgg ttaataata atgcaccatc gtttctgcc 960
atagaggctg ccatttcag gcctccgcat ctactgatt ttccagaaca acttacaatt 1020
tacagtgcac caagccgttg gagtagcact caacatatga attattgggt gggacatagg 1080
cttaactcc gcccaatagg agggacatta aatacctcaa cacaaggact tactaataat 1140
acttcaatta atcctgtaac attacagttt acgtctcgag acgtttatag aacagaatca 1200
aatgcaggga caaatatact attactact 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 ttcttgacg catcgtagt cagatcgtaac gaatacgatt 1500
ggaccaaata gaattacaca aataccattg gtaaaagcac tgaatcttca ttcaggtgtt 1560
actgtgttg gagggccagg atttacaggt ggagatatcc ttcgaagaac gaatactggc 1620
acatttgag atatgagagt aaatattact gggccattat cccaaagata tcgtgtaaga 1680
attcgctatg ctctacgac agatttaca ttttcacga gaatcaatgg aacttctgta 1740
aatcaaggta atttcaaag aactatgaat agaggggata atttagaatc tggaaacttt 1800
aggactgcag gatttagtac gccttttagt tttcaaagtg cgcaaagtac attcacattg 1860
ggtagtcagg cttttcaaa tcaggaagtt tatatagatc gaattgaatt tgtcccgga 1920
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aactttagag ggatcaatag acaactagac cgtggctgga gaggaagtac ggatattacc 2220
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gagtgctatc caacgtattt atatcaaaaa atagatgagt cgaaattaaa agcctatacc 2340

cgttaccaat taagagggtat tatcgaagat agtcaagact tagaaatcta ttttaattcgc 2400
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 gggcatgtag atgtagaaga acaaaacaac caccgttcgg tccttggtgt tccggaatgg 3060
 gaagcagaag tgtcacaaga agttcgtgtc tgtccgggtc gtggctatat ccttcgtgtc 3120
 acagcgtaca aggaggggata tggagaagggt tgcgtaacca ttcattgagat cgagaacaat 3180
 acagacgaac tgaagtttag caactgtgta gaagaggaag tatatccaaa caacacggta 3240
 acgtgtaatg attatactgc gactcaagaa gaatatgagg gtacgtacac ttctcgtaat 3300
 cgaggatatg acggagccta tgaaagcaat tcttctgtac cagctgatta tgcattcagcc 3360
 tatgaagaaa aagcatatac agatggacga agagacaatc cttgtgaatc taacagagga 3420
 tatggggatt acacaccact accagctggc tatgtgacaa aagaattaga gtacttccca 3480
 gaaaccgata aggtatggat tgagatcgga gaaacggaag gaacattcat cgtggacagc 3540
 gtggaattac ttcttatgga ggaatag 3567

<210> 85
 <211> 1188
 <212> PRT
 <213> Artificial

<220>
 <223> Amino acid sequence of the chimeric protein TIC846.

<220>
 <221> MISC_FEATURE
 <222> (1)..(1188)

<223> Amino acid sequence of the chimeric protein TIC846.

<400> 85

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 Thr Gln Ile Pro Leu Val Lys
500 505 510

Ala Leu Asn Leu His Ser Gly Val Thr Val Val Gly Gly Pro Gly Phe
515 520 525

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

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

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

Gly Thr Ser Val Asn Gln Gly Asn Phe Gln Arg Thr Met Asn Arg Gly
580 585 590

Asp Asn Leu Glu Ser Gly Asn Phe Arg Thr Ala Gly Phe Ser Thr Pro
595 600 605

Phe Ser Phe Ser Asn Ala Gln Ser Thr Phe Thr Leu Gly Thr Gln Ala
610 615 620

Phe Ser Asn Gln Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala
625 630 635 640

Glu Val Thr Phe Glu Ala Glu Ser Asp Leu Glu Arg Ala Gln Lys Ala

645	650	655
Val Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp		
660	665	670
Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu		
675	680	685
Ser Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val		
690	695	700
Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro		
705	710	715
720		
Asn Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser		
725	730	735
Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr		
740	745	750
Val Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr		
755	760	765
Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu		
770	775	780
Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg		
785	790	795
800		
Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu		
805	810	815
Trp Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Ala His His Ser		
820	825	830
His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu		
835	840	845
Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His		
850	855	860

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

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

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

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

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

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

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

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

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

Asn Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu
 1010 1015 1020

Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu
 1025 1030 1035

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

Ile His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn
 1055 1060 1065

Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn
 1070 1075 1080

Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser
 1085 1090 1095

Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser Val
 1100 1105 1110

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

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

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

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

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

<210> 86

<211> 3570

<212> DNA

<213> Artificial

<220>

<223> Chimeric coding sequence encoding TIC858.

<400> 86

atgacttcaa ataggaaaa 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 ttctgttgg ggaattatgg cctagtggca gagatccatg ggaaatttc 300

ctggaacatg tagaacaact tataagacaa caagtaacag aaaatactag gaatacggct 360

attgctcgat tagaaggctt aggaagaggg tatagatctt accagcaggc tcttgaaact 420

tggttagata accgaaatga tgcaagatca agaagcatta ttctgagcg ctatgttgct 480

ttagaacttg acattactac tgctataccg ctttcagaa tacgaaatga agaagttcca 540

ttattaatgg tatatgctca agctgcaaatt tacacctat tattattgag agacgcatcc 600
 ctttttggtg gtgaatgggg gatggcatct tccgatgta accaatatta ccaagaacaa 660
 atcagatata cagaggaata ttctaacctat tgcgtacaat ggtataatac agggctaaat 720
 aacttaagag ggacaaatgc tgaaagtgg ttgcggtata atcaattccg tagagaccta 780
 acgtagggg tattagattt agtagcccta ttccaagct atgatactcg cacttatcca 840
 atcaatacga gtgctcagtt aacaagagaa atttatacag atccaattgg gagaacaaat 900
 gcaccttcag gatttgcaag tacgaattgg ttaataata atgcaccatc gtttctgcc 960
 atagaggctg ccatttcag gcctccgcat ctacttgatt ttccagaaca acttacaatt 1020
 tacagtgcac caagccgttg gagtagcact caacatatga attattgggt gggacatagg 1080
 ctttaactcc 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 ttctggacg catcgtagtg cagatcgtaac gaatacgtt 1500
 ggaccaaata gaattacca aatcccaatg gtaaaagcat ccgaacttc tcaaggtacc 1560
 actgttgta gaggaccagg atttactggt ggggatattc ttcgaagaac gaatactggt 1620
 ggattggac cgataagagt aactgttaac ggaccattaa cacaagata tcgtatagga 1680
 ttccgctatg cttcaactgt agattttgat ttctttgat cacgtggagg tactactgta 1740
 aataatttta gattcctacg tacaatgaac agtggagacg aactaaaata cggaatttt 1800
 gtgagacgtg ctttactac acctttact ttacacaaa ttcaagatat aattcgaacg 1860
 tctattcaag gccttagtg aaatggggaa gtgtatatag ataaaattga aattattcca 1920
 gttactgcaa ccttcgaagc agaatatgat ttagaaagag cacaaaaggc ggtgaatgag 1980
 ctgtttactt cttccaatca aatcgggtta aaaacagatg tgacggatta tcatattgat 2040
 caagtatcca atttagttga gtgttatct gatgaatttt gtctggatga aaaaaagaa 2100
 ttgtccgaga aagtcaaaca tgcaagcga cttagtgtg agcggaattt acttcaagat 2160

ccaaacttta gagggatcaa tagacaacta gaccgtggct ggagaggaag tacggatatt 2220
 accatccaag gaggcgatga cgtattcaaa gagaattacg ttacgctatt gggtagcttt 2280
 gatgagtgt atccaacgta ttatatcaa aaaatagatg agtcgaaatt aaaagcctat 2340
 acccgttacc aattaagagg gtatatcgaa gatagtcaag actagaaat ctatttaatt 2400
 cgctacaatg ccaaacacga aacagtaaatt gtgccaggta cgggttcctt atggccgctt 2460
 tcagcccaaa gtccaatcgg aaaatgtgcc catcattccc atcatttctc cttggacatt 2520
 gatgttggat gtacagactt aaatgaggac ttaggtgtat ggggtgatatt caagattaag 2580
 acgcaagatg gccatgcaag actaggaaat ctagaatttc tcgaagagaa accattagta 2640
 ggagaagcac tagctcgtgt gaaaagagcg gagaaaaaat ggagagacaa acgtgaaaaa 2700
 ttggaatggg aaacaaatat tgtttataaa gaggcaaaag aatctgtaga tgctttattt 2760
 gtaaactctc aatatgatag attacaagcg gataccaaca tcgcgatgat tcatgcggca 2820
 gataaacgcg tcatagcat tcgagaagct tatctgcctg agctgtctgt gattccgggt 2880
 gtcaatgcgg ctattttga agaattagaa gggcgtattt tactgcatt ctccctatat 2940
 gatgcgagaa atgtcattaa aaatggtgat ttaataatg gcttatcctg ctggaacgtg 3000
 aaagggcatg tagatgtaga agaacaaaac aaccaccgtt cggtccttgt tgtccggaa 3060
 tgggaagcag aagtgtcaca agaagttcgt gtctgtccgg gtcgtggcta tacccttctg 3120
 gtcacagcgt acaaggaggg atatggagaa ggttgcgtaa ccattcatga gatcgagaac 3180
 aatacagacg aactgaagtt tagcaactgt gtagaagagg aagtatatcc aaacaacacg 3240
 gtaacgtgta atgattatac tgcgactcaa gaagaatatg agggtagcga cacttctcgt 3300
 aatcgaggat atgacggagc ctatgaaagc aattcttctg taccagctga ttatgcatca 3360
 gcctatgaag aaaaagcata tacagatgga cgaagagaca atccttgtga atctaacaga 3420
 ggatatgggg attacacacc actaccagct ggctatgtga caaaagaatt agagtacttc 3480
 ccagaaaccg ataaggtatg gattgagatc ggagaaacgg aaggaacatt catcgtggac 3540
 agcgtggaat tacttcttat ggaggaatag 3570

<210> 87
 <211> 1189
 <212> PRT
 <213> Artificial
 <220>

<223> Amino acid sequence of the chimeric protein TIC858.

<400> 87

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 Thr Gln Ile Pro Met Val Lys
500 505 510

Ala Ser Glu Leu Pro Gln Gly Thr Thr Val Val Arg Gly Pro Gly Phe
515 520 525

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

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

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

Gly Thr Thr Val Asn Asn Phe Arg Phe Leu Arg Thr Met Asn Ser Gly
580 585 590

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

Phe Thr Phe Thr Gln Ile Gln Asp Ile Ile Arg Thr Ser Ile Gln Gly
610 615 620

Leu Ser Gly Asn Gly Glu Val Tyr Ile Asp Lys Ile Glu Ile Ile Pro
625 630 635 640

Val Thr Ala Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys

645	650	655
Ala Val Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr		
660	665	670
Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys		
675	680	685
Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys		
690	695	700
Val Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp		
705	710	715
Pro Asn Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly		
725	730	735
Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn		
740	745	750
Tyr Val Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu		
755	760	765
Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln		
770	775	780
Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile		
785	790	795
Arg Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser		
805	810	815
Leu Trp Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Ala His His		
820	825	830
Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn		
835	840	845
Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly		
850	855	860

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

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

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

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

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

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

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

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

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

Gln Asn Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala
1010 1015 1020

Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile
1025 1030 1035

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

Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser
1055 1060 1065

Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys
1070 1075 1080

Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr
 1085 1090 1095

Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser
 1100 1105 1110

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

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

Asp Tyr Thr Pro Leu Pro Ala 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> 88
 <211> 3570
 <212> DNA
 <213> Artificial

<220>
 <223> Chimeric coding sequence encoding TIC865.

<400> 88
 atgactcaa ataggaaaaa tgagaatgaa attataaatg ccttatcgat tccagctgta 60
 tcgaatcatt ccgcacaaat ggatctatcg ctatgatgctc gtattgagga ttctttgtgt 120
 atagccgagg ggaataatat caatccactt gttagcgcac caacagtcca aacgggtata 180
 aacatagctg gtagaatatt gggcgtatta ggtgtgccgt ttgctggaca actagctagt 240
 ttttatagtt ttctgttgg ggaattatgg cctagtggca gagatccatg ggaaatttc 300
 ctggaacatg tagaacaact tataagacaa caagtaacag aaaatactag gaatacggct 360
 attgctcgat tagaagggtct aggaagaggc tatagatctt accagcaggc tcttgaaact 420

tggtagata accgaaatga tgcaagatca agaagcatta ttcttgagcg ctatgttgct 480
 ttagaacttg acattactac tgctataccg ctttcagaa tacgaaatga agaagttcca 540
 ttattaatgg tatatgctca agctgcaa atacacctat tattattgag agacgcatcc 600
 ctttttgta gtgaatgggg gatggcatct tccgatgta accaatatta ccaagaacaa 660
 atcagatata cagaggaata ttctaaccat tgcgtacaat ggtataatac agggctaaat 720
 aacttaagag ggacaaatgc tgaaagtgg ttgcgggata atcaattccg tagagaccta 780
 acgttagggg tattagattt agtagcccta ttccaagct atgatactcg cacttatcca 840
 atcaatacga gtgctcagtt aacaagagaa attatacag atccaattgg gagaacaaat 900
 gcaccttcag gatttgcaag tacgaattgg ttaataata atgcaccatc gtttctgcc 960
 atagaggctg ccatttcag gcctccgcat ctactgatt ttccagaaca acttacaatt 1020
 tacagtgcac caagccgttg gagtagcact caacatatga attattgggt gggacatagg 1080
 ctttaactcc gcccaatagg agggacatta aatacctcaa cacaaggact tactaataat 1140
 acttcaatta atcctgtaac attacagttt acgtctcgtg acgtttatag aacagaatca 1200
 aatgcaggga caaatatact attactact cctgtgaatg gagtacctg ggctagattt 1260
 aattttataa accctcagaa tatttatgaa agaggcgcca ctacctacag tcaaccgtat 1320
 caggaggttg ggattcaatt attgattca gaaactgaat taccaccaga aacaacagaa 1380
 cgaccaaatt atgaatcata tagtcataga ttatctcata taggactaat cataggaaac 1440
 acttgagag caccagtcta ttctggacg catcgtagt cagatcgta gaacacaatt 1500
 gatccggaga ggattactca aataccattg gtaaaagcac atacactca gtcaggact 1560
 actgttgtaa gagggcccg gtttacggga ggagatatc ttcgacgaac aagtggagga 1620
 ccatttgctt atactattgt taatataaat gggcaattac ccaaaggta tcgtgcaaga 1680
 atacgctatg cctctactac aaatctaaga atttacgtaa cggttgcagg tgaacggatt 1740
 ttgctggc aatttaacaa aacaatggat accggtgacc cattaacatt ccaatcttt 1800
 agttacgcaa ctattaatac agctttaca ttccaatga gccagagtag ttccacagta 1860
 ggtgctgata ctttagttc agggaaatgaa gtttatatag acagattga attgattcca 1920
 gttactgcaa cattgaagc agaatatgat ttagaaagag cacaaaaggc ggtgaatgag 1980
 ctgttactt ctccaatca aatcgggtta aaaacagatg tgacggatta tcatattgat 2040

caagtatcca atttagttga gtgtttatct gatgaatctt gtctggatga aaaaaaagaa 2100
 ttgtccgaga aagtcaaaca tgcaagcga ctagtgatg agcggaattt acttcaagat 2160
 ccaaacttta gagggatcaa tagacaacta gaccgtggct ggagaggaag tacggatatt 2220
 accatccaag gaggcgatga cgtattcaaa gagaattacg ttacgctatt gggtagcttt 2280
 gatgagtgtc atccaacgta ttatatcaa aaaatagatg agtcgaaatt aaaagcctat 2340
 acccgttacc aattaagagg gtatatcgaa gatagtcaag acttagaaat ctatttaatt 2400
 cgctacaatg ccaaacacga aacagtaaat gtgccaggta cgggttcctt atggccgctt 2460
 tcagcccaa gtccaatcgg aaaatgtgcc catcattccc atcatttctc ctggacatt 2520
 gatgttggat gtacagactt aaatgaggac ttaggtgtat gggatgatt caagattaag 2580
 acgcaagatg gccatgcaag actaggaaat ctagaatttc tcgaagagaa accattagta 2640
 ggagaagcac tagctcgtgt gaaaagagcg gagaaaaaat ggagagacaa acgtgaaaaa 2700
 ttggaatggg aaacaaatat tgtttataaa gaggcaaaag aatctgtaga tgctttattt 2760
 gtaaactctc aatatgatag attacaagcg gataccaaca tcgcatgat tcatgcggca 2820
 gataaacgcg tcatagcat tcgagaagct tatctgcctg agctgtctgt gattccgggt 2880
 gtcaatgcgg ctattttga agaattagaa gggcgtattt tctactgcatt ctcctatat 2940
 gatgcgagaa atgtcattaa aaatggtgat ttaataatg gcttatcctg ctggaacgtg 3000
 aaagggcatg tagatgtaga agaacaaaac aaccaccgtt cggtccttgt tgtccggaa 3060
 tgggaagcag aagtgcaca agaagttcgt gtctgtccgg gtcgtggcta taccctcgt 3120
 gtcacagcgt acaaggaggg atatggagaa ggttgcgtaa ccattcatga gatcgagaac 3180
 aatacagacg aactgaagt tagcaactgt gtagaagagg aagtatatcc aaacaacacg 3240
 gtaacgtgta atgattatac tgcgactcaa gaagaatatg agggtagcga cacttctcgt 3300
 aatcaggat atgacggagc ctatgaaagc aattctctg taccagctga ttatcatca 3360
 gcctatgaag aaaaagcata tacagatgga cgaagagaca atccttgtga atctaacaga 3420
 ggatatgggg attacacacc actaccagct ggctatgtga caaaagaatt agagtacttc 3480
 ccagaaaccg ataaggtatg gattgagatc ggagaaacgg aaggaacatt catcgtggac 3540
 agcgtggaat tacttcttat ggaggaatag 3570

<210> 89

<211> 1189

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC865.

<400> 89

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 Asp Leu Ser Leu Asp
20 25 30

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

Pro Leu 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 Asp Pro Glu Arg Ile Thr Gln Ile Pro Leu Val Lys
500 505 510

Ala His Thr Leu Gln Ser Gly Thr Thr Val Val Arg Gly Pro Gly Phe
515 520 525

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

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

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

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

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

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

Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Phe Glu Leu Ile Pro

625	630	635	640
Val Thr Ala Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys			
	645	650	655
Ala Val Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr			
	660	665	670
Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys			
	675	680	685
Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys			
	690	695	700
Val Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp			
705	710	715	720
Pro Asn Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly			
	725	730	735
Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn			
	740	745	750
Tyr Val Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu			
	755	760	765
Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln			
	770	775	780
Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile			
785	790	795	800
Arg Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser			
	805	810	815
Leu Trp Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Ala His His			
	820	825	830
Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn			
	835	840	845

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

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

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

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

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

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

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

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

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

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

Gln Asn Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala
1010 1015 1020

Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile
1025 1030 1035

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

Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser
1055 1060 1065

Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys
 1070 1075 1080

Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr
 1085 1090 1095

Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser
 1100 1105 1110

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

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

Asp Tyr Thr Pro Leu Pro Ala 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> 90

<211> 3564

<212> DNA

<213> Artificial

<220>

<223> Chimeric coding sequence encoding TIC866.

<400> 90

atgactcaa ataggaaaa tgagaatgaa attataaatg cttatcgat tccagctgta 60

tcgaatcatt ccgcacaaat gaatctatca accgatgctc gtattgagga tagcttgtgt 120

atagccgagg ggaacaatat cgatccattt gttagcgcac caacagtcca aacgggtatt 180

aacatagctg gtagaatact aggtgtatta ggcgtaccgt ttgctggaca aatagctagt 240

ttttatagtt ttctgttggt tgaattatgg cccgcgggca gagatccttg ggaaattttc 300

ctagaacatg tcgaacaact tataagacaa caagtaacag aaaatactag ggatacggct 360
 ctgctcgat tacaagggtt aggaaattcc ttagagcct atcaacagtc actgaagat 420
 tggctagaaa accgtgatga tgcaagaacg agaagtgttc ttataccca atatatagcc 480
 ttagaacttg attttcttaa tgcgatgccg ctttcgcaa ttagaaacca agaagttcca 540
 ttattaatgg tatatgctca agctgcaa atcacctat tattattgag agatgcctct 600
 cttttggta gtgaattgg gcttacatcc caagaaattc aacgttatta tgagcgccaa 660
 gtggaaaaaa cgagagaata ttctgattat tgcgcaagat ggtataatac gggtttaaat 720
 aattgagag ggacaaatgc tgaagttgg ttgcatata atcaattccg tagagactta 780
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 gcaccttcag gatttgcaag tacgaattgg ttaataata atgcaccatc gtttctgcc 960
 atagaggctg ccgttattag gcctccgcat ctactgatt ttccagaaca gcttacaatt 1020
 ttcagcgtat taagtcgatg gagtaatact caatatatga attactgggt gggacataga 1080
 ctgaatcgc gaacaataag ggggtcatta agtacctcga cacacggaaa taccaatact 1140
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 gcagggataa atatactct aactactcct gtgaatggag tacctgggc tagatttaatt 1260
 tggagaaatc ccctgaattc tcttagaggt agccttctct atactatagg gtatactgga 1320
 gtggggacac aactattga ttcagaaact gaattaccac cagaacaac agaacgacca 1380
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 gatagcatta ctcaaatacc attggtaaaa gcacatacac ttcagtcagg tactactgtt 1560
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 gcttatacta ttgtaatat aaatgggcaa ttacccaaa ggtatcgtgc aagaatacgc 1680
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 ggtcaattta acaaaacaat ggataccggt gaccattaa cattccaatc ttttagttac 1800
 gcaactatta atacagctt tacattccca atgagccaga gtagttcac agtaggtgct 1860
 gatacttta gttcaggga tgaagttat atagacagat ttgaattgat tccagttact 1920

gcaacatttg aagcagaata tgatttagaa agagcacaaa aggcggtgaa tgagctgttt 1980
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aatgccaaac acgaaacagt aaatgtgcca ggtacgggtt ctttatggcc gcttcagcc 2460
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gaagaaaaag catatacaga tggacgaaga gacaatcctt gtgaatctaa cagaggatat 3420
ggggattaca caccactacc agctggctat gtgacaaaag aattagagta ctcccagaa 3480
accgataagg tatggattga gatcggagaa acggaaggaa cattcatcgt ggacagcgtg 3540
gaattacttc ttatggagga atag 3564

<210> 91
<211> 1187
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of the chimeric protein TIC866.

<400> 91

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 Arg Gly Pro Gly Phe Thr Gly
515 520 525

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

Val Asn Ile Asn Gly Gln Leu Pro 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 Asn Lys Thr Met Asp Thr Gly Asp 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 Met Ser Gln Ser Ser Phe Thr Val Gly Ala Asp Thr Phe Ser

610	615	620	
Ser Gly Asn Glu Val Tyr Ile Asp Arg Phe Glu Leu Ile Pro Val Thr			
625	630	635	640
Ala Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val			
645	650	655	
Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val			
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			
690	695	700	
His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn			
705	710	715	720
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
1010 1015 1020

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
 1055 1060 1065

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
 1085 1090 1095

Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser Val Pro
 1100 1105 1110

Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr Asp Gly
 1115 1120 1125

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

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

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

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

<210> 92

<211> 3525

<212> DNA

<213> Artificial

<220>

<223> Chimeric coding sequence encoding TIC838.

<400> 92

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cttggtcagt ttctggatc taactttgta ccagggggag gatttttagt tggattaata 180

gattttgtat ggggaatagt tggcccttct caatgggatg catttctagt acaaattgaa 240

caattaatta atgaaagaat agctgaattt gctaggaatg ctgctattgc taatttagaa 300

ggattaggaa acaatttcaa tatatatgtg gaagcattta aagaatggga agaagatcct 360
 aataatccag caaccaggac cagagtaatt gatcgcttgc gtatacttga tgggctactt 420
 gaaagggaca ttccttcgtt tgcaatttct ggatttgaag taccctttt atccgtttat 480
 gctcaagcgg ccaatctgca tctagctata ttaagagatt ctgtaattt tggagaaaga 540
 tggggattga caacgataaa tgtcaatgaa aactataata gactaattag gcatattgat 600
 gaatatgctg atcactgtgc aaatacgtat aatcggggat taaataatt accgaaatct 660
 acgtatcaag attggataac atataatcga ttacggagag acttaacatt gactgtatta 720
 gatatcgccg ctttcttcc aaactatgac aataggagat atccaattca gtcagttggt 780
 caactaaca gggaaattta tacggacca ttaattact ttaatccaca gttacagtct 840
 gtagtcaat tacctactt taacgttatg gaaagcaacg caattagaac tcctcattta 900
 ttgatgtat tgaataatct tacaatttt acagattggt ttagtgttg acgcaactt 960
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 ttaatttac gtggtgtga aggagtagaa ttctacac cttaaatac ctttacgtat 1200
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 aatatagtag gtgttagaaa tttagtggg actgcaggag tgataataga cagattgaa 1800
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 gtgaatgcgc tgttacgtc tacaaccaa ctagggctaa aaacaaatgt aacggattat 1920

catattgatc aagtgtccaa ttagttacg tatttatcgg atgaatttg tctggatgaa 1980
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caacgttcgg tcctgttgt tccggaatgg gaagcagaag tgcacaaga agttcgtgtc 3060
tgtccgggtc gtggctatat ccttcgtgtc acagcgtaca aggagggata tggagaaggt 3120
tgcgtaacca ttcatgagat cgagaacaat acagacgaac tgaagtttag caactgcgta 3180
gaggaggaaa tctatccaaa taacacggta acgtgtaatg attatactgt aaatcaagaa 3240
gaatacggag gtgcgtacac ttctgtaat cgaggatata acgaagctcc ttccgtacca 3300
gctgattatg cgtcagtcta tgaagaaaaa tcgtatacag atggacgtag agagaatcct 3360
tgtgaattta acagagggtg tagggattac acgccactac cagttggta tgtgacaaaa 3420
gaattagaat acttcccaga aaccgataag gtatggattg agattggaga aacggaagga 3480
acatttatcg tggacagcgt ggaattactc cttatggagg aatag 3525

<210> 93
<211> 1174
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of the chimeric protein TIC838.

<400> 93

Met Glu Glu Asn Asn Gln Asn 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 Ser Thr Gly Asn
20 25 30

Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
35 40 45

Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
50 55 60

Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
65 70 75 80

Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
85 90 95

Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
100 105 110

Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg
115 120 125

Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
130 135 140

Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
145 150 155 160

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

Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr

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

Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp
405 410 415

Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala
420 425 430

Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Pro Val
435 440 445

Phe Ser Trp Thr His Arg Ser Ala Thr Asp Arg Asn Ile Ile Ala Ser
450 455 460

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

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

Leu Asn Ser Ser Gly Asn Asn Ile Gln Asn Arg Gly Tyr Ile Glu Val
500 505 510

Pro Ile His Phe Pro Ser Thr Ser Thr Arg Tyr Arg Val Arg Val Arg
515 520 525

Tyr Ala Ser Val Thr Pro Ile His Leu Asn Val Asn Trp Gly Asn Ser
530 535 540

Ser Ile Phe Ser Asn Thr Val Pro Ala Thr Ala Thr Ser Leu Asp Asn
545 550 555 560

Leu Gln Ser Ser Asp Phe Gly Tyr Phe Glu Ser Ala Asn Ala Phe Thr
565 570 575

Ser Ser Leu Gly Asn Ile Val Gly Val Arg Asn Phe Ser Gly Thr Ala
580 585 590

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

Glu Ala Glu Tyr Asn Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu
610 615 620

Phe Thr Ser Thr Asn Gln Leu Gly Leu Lys Thr Asn Val Thr Asp Tyr
625 630 635 640

His Ile Asp Gln Val Ser Asn Leu Val Thr Tyr Leu Ser Asp Glu Phe
 645 650 655

Cys Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys
 660 665 670

Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Ser Asn Phe Lys Asp
 675 680 685

Ile Asn Arg Gln Pro Glu Arg Gly Trp Gly Gly Ser Thr Gly Ile Thr
 690 695 700

Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Ser
705 710 715 720

Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp
 725 730 735

Glu Ser Lys Leu Lys Ala Phe Thr Arg Tyr Gln Leu Arg Gly Tyr Ile
 740 745 750

Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys
 755 760 765

His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser
 770 775 780

Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro
785 790 795 800

His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu
 805 810 815

Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile Asp Val Gly
 820 825 830

Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile
 835 840 845

Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu
850 855 860

Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu
865 870 875 880

Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu Thr Asn Ile
885 890 895

Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser
900 905 910

Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile Ala Met Ile His Ala
915 920 925

Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu Pro Glu Leu
930 935 940

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

Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys
965 970 975

Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val Lys Gly His
980 985 990

Val Asp Val Glu Glu Gln Asn Asn Gln Arg Ser Val Leu Val Val Pro
995 1000 1005

Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly
1010 1015 1020

Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly
1025 1030 1035

Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu
1040 1045 1050

Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Ile Tyr Pro Asn Asn

1055	1060	1065
Thr Val	Thr Cys Asn Asp Tyr	Thr Val Asn Gln Glu Glu Tyr Gly
1070	1075	1080
Gly Ala	Tyr Thr Ser Arg Asn	Arg Gly Tyr Asn Glu Ala Pro Ser
1085	1090	1095
Val Pro	Ala Asp Tyr Ala Ser	Val Tyr Glu Glu Lys Ser Tyr Thr
1100	1105	1110
Asp Gly	Arg Arg Glu Asn Pro	Cys Glu Phe Asn Arg Gly Tyr Arg
1115	1120	1125
Asp Tyr	Thr Pro Leu Pro Val	Gly Tyr Val Thr Lys Glu Leu Glu
1130	1135	1140
Tyr Phe	Pro Glu Thr Asp Lys	Val Trp Ile Glu Ile Gly Glu Thr
1145	1150	1155
Glu Gly	Thr Phe Ile Val Asp	Ser Val Glu Leu Leu Leu Met Glu
1160	1165	1170
Glu		

<210> 94
 <211> 3558
 <212> DNA
 <213> Artificial

<220>
 <223> Chimeric coding sequence encoding TIC839.

<400> 94
 atggaggaaa ataatcaaaa tcaatgcata ccttacaatt gtttaagtaa tctgaagaa 60
 gtacttttgg atggagaacg gatatcaact ggtaattcat caattgatat ttctctgtca 120
 cttgttcagt ttctggatc taactttgta ccagggggag gatttttagt tggattaata 180
 gattttgtat ggggaatagt tggcccttct caatgggatg catttctagt acaaattgaa 240
 caattaatta atgaaagaat agctgaattt gctaggaatg ctgctattgc taatttagaa 300
 ggattaggaa acaatttcaa tatatatgtg gaagcattta aagaatggga agaagatcct 360

aataatccag caaccaggac cagagtaatt gatcgcttc gtatactga tgggctactt 420
gaaagggaca ttccttcgtt tgcaatttct ggatttgaag taccctttt atccgtttat 480
gctcaagcgg ccaatctgca tctagctata ttaagagatt ctgtaattt tggagaaaga 540
tggggattga caacgataaa tgtcaatgaa aactataata gactaattag gcatattgat 600
gaatatgctg atcactgtgc aaatacgtat aatcggggat taaataattt accgaaatct 660
acgtatcaag attggataac atataatcga ttacggagag acttaacatt gactgtatta 720
gatatcgccg ctttctttcc aaactatgac aataggagat atccaattca gtcagttggt 780
caactaaciaa gggaaattta tacggacca ttaattactt ttaatccaca gttacagtct 840
gtagctcaat tacctacttt taacgttatg gaaagcaacg caattagaac tcctcattta 900
tttgatgtat tgaataatct tacaattttt acagattggt ttagtggtgg acgcaactt 960
tattggggag gacatcgagt aatatctaac cgtataggag gaggtaacat aacatctcct 1020
atatatggaa gggaggcgaa tcaggagcct ccaagatctt ttacttttaa tgggcctgtt 1080
ttaggactt tatcaaatcc tacttttaga ctttacagc aacctggcc agcgccacca 1140
ttaatttac gtggtgttga aggagtagaa tttctacac cttaaataag ctttacgtat 1200
cgaggaaggg gtacggttga ttcttaact gagttaccgc ctgaggataa tagtgtgcct 1260
cctcggaag gatatagtca tcgtttatgt catgcaactt ttgtcaaag atctggaacc 1320
ccattttta caactgggcc agtattttct tggacgcac gtagtgtac tgatcgaaat 1380
acaattgatc cagagagaat taatcaaata ccttagtga aaggatttag agttggggg 1440
ggcacctctg tcattacagg accaggattt acaggagggg ataccttcg aagaaatacc 1500
tttggtgatt ttgtatctct acaagtcaat attaatcac caattacca aagataccgt 1560
ttaagatttc gttacgctc cagtagggat gcacgagtta tagtattaac aggagcggca 1620
tccacaggag tgggaggcca agttagtga aatatgcctc tccagaaaac tatggaaata 1680
ggggagaact taacatctag aacatttaga tataccgatt ttagtaatcc ttttcattt 1740
agagctaac cagatataat tgggataagt gaacaacctc tatttggtgc aggttctatt 1800
agtagcgtg aactttatat agataaaatt gaaattattc ctgttactgc aacactcgag 1860
gctgaatata atctagaaag agcgcagaag gcggtgaatg cgctgtttac gtctacaaac 1920
caactagggc taaaaacaaa tgtaacggat tatcatattg atcaagtgc caatttagtt 1980

acgtatttat cggatgaatt ttgtctggat gaaaagcgag aattgtccga gaaagtcaaa 2040
 catgcgaagc gactcagtga tgaacgcaat ttactccaag attcaaattt caaagacatt 2100
 aataggcaac cagaacgtgg gtggggcgga agtacaggga ttaccatcca aggaggggat 2160
 gacgtattta aagaaaatta cgtcacacta tcagggtacct ttgatgagtg ctatccaaca 2220
 tatttgtatc aaaaaatcga tgaatcaaaa ttaaagcct ttaccggtta tcaattaaga 2280
 gggatatatc aagatagtca agacttagaa atctatttaa ttcgtacaa tgcaaaacat 2340
 gaaacagtaa atgtgccagg tacgggttcc ttatggccgc tttcagccca aagtccaatc 2400
 ggaaagtgtg gagagccgaa tcgatgcgcg ccacaccttg aatggaatcc tgacttagat 2460
 tgttcgtgta gggatggaga aaagtgtgcc catcattcgc atcatttctc cttagacatt 2520
 gatgtaggat gtacagactt aaatgaggac ctagggtgat gggatgatct taagattaag 2580
 acgcaagatg ggcacgcaag actaggggaat ctagagtctc tcgaagaaaa accattagta 2640
 ggagaagcgc tagctcgtgt gaaaagagcg gagaaaaaat ggagagacaa acgtgaaaaa 2700
 ttggaatggg aaacaaatat cgtttataaa gaggcaaaag aatctgtaga tgctttattt 2760
 gtaaactctc aatatgatca attacaagcg gatacgaata ttgccatgat tcatgcggca 2820
 gataaacgtg ttcatagcat tcgagaagct tatctgcctg agctgtctgt gattccgggt 2880
 gtcaatgcgg ctattttga agaattagaa gggcgatttt tctactgcatt ctcctatat 2940
 gatgcgagaa atgtcattaa aaatggtgat ttaataatg gcttatcctg ctggaacgtg 3000
 aaagggcatg tagatgtaga agaacaaaac aaccaacgtt cggtcctgt tgttccggaa 3060
 tgggaagcag aagtgtcaca agaagttcgt gtctgtccgg gtcgtggcta tatcctcgt 3120
 gtcacagcgt acaaggaggg atatggagaa ggttgcgtaa ccattcatga gatcgagaac 3180
 aatacagacg aactgaagt tagcaactgc gtagaggagg aaatctatcc aaataacacg 3240
 gtaacgtgta atgattatac tgtaaataca gaagaatacg gaggtgcgta cacttctcgt 3300
 aatcgaggat ataacgaagc tccttccgta ccagctgatt atgcgtcagt ctatgaagaa 3360
 aaatcgata cagatggacg tagagagaat ccttgtgaat ttaacagagg gtatagggat 3420
 tacacgccac taccagttgg ttatgtgaca aaagaattag aatacttccc agaaaccgat 3480
 aaggatatga ttgagattgg agaaacggaa ggaacattta tcgtggacag cgtggaatta 3540
 ctcttatgg aggaatag 3558

<210> 95
<211> 1185
<212> PRT
<213> ARtificial

<220>

<223> Amino acid sequence of the chimeric protein TIC839.

<400> 95

Met Glu Glu Asn Asn Gln Asn 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 Ser Thr Gly Asn
20 25 30

Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
35 40 45

Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
50 55 60

Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
65 70 75 80

Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
85 90 95

Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
100 105 110

Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg
115 120 125

Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
130 135 140

Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
145 150 155 160

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

Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr

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

Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp
405 410 415

Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala
420 425 430

Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Pro Val
435 440 445

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

Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly
465 470 475 480

Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu
485 490 495

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

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

Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val
530 535 540

Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile
545 550 555 560

Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn
565 570 575

Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln
580 585 590

Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp
595 600 605

Lys Ile Glu Ile Ile Pro Val Thr Ala Thr Leu Glu Ala Glu Tyr Asn
610 615 620

Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Thr Asn
625 630 635 640

Gln Leu Gly Leu Lys Thr Asn Val Thr Asp Tyr His Ile Asp Gln Val
645 650 655

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

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

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

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

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

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

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

Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val Asn
770 775 780

Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile
785 790 795 800

Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn
805 810 815

Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His
820 825 830

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

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

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

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

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

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

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

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

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

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

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

Gln Asn Asn Gln Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala
1010 1015 1020

Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile
1025 1030 1035

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

Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser

1055	1060	1065
Asn Cys Val Glu Glu Glu Ile Tyr Pro Asn Asn Thr Val Thr Cys		
1070	1075	1080
Asn Asp Tyr Thr Val Asn Gln Glu Glu Tyr Gly Gly Ala Tyr Thr		
1085	1090	1095
Ser Arg Asn Arg Gly Tyr Asn Glu Ala Pro Ser Val Pro Ala Asp		
1100	1105	1110
Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg		
1115	1120	1125
Glu Asn Pro Cys Glu Phe Asn Arg Gly Tyr Arg Asp Tyr Thr Pro		
1130	1135	1140
Leu Pro Val Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu		
1145	1150	1155
Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe		
1160	1165	1170
Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu		
1175	1180	1185

<210> 96
 <211> 3519
 <212> DNA
 <213> Artificial

<220>
 <223> Chimeric coding sequence encoding TIC841.

<400> 96
 atggaggaaa ataatcaaaa tcaatgcata ccttacaatt gtttaagtaa tcctgaagaa 60
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 cttgttcagt ttctggatc taactttgta ccagggggag gatttttagt tggattaata 180
 gattttgtat ggggaatagt tggcccttct caatgggatg catttctagt acaaattgaa 240
 caattaatta atgaaagaat agctgaattt gctaggaatg ctgctattgc taatttagaa 300
 ggattaggaa acaatttcaa tatatatgtg gaagcattta aagaatggga agaagatcct 360

aataatccag caaccaggac cagagtaatt gatcgcttc gtatactga tgggctactt 420
gaaagggaca ttccttcgtt tgcaatttct ggatttgaag taccctttt atccgtttat 480
gctcaagcgg ccaatctgca tctagctata ttaagagatt ctgtaattt tggagaaaga 540
tggggattga caacgataaa tgtcaatgaa aactataata gactaattag gcatattgat 600
gaatatgctg atcactgtgc aaatacgtat aatcggggat taaataattt accgaaatct 660
acgtatcaag attggataac atataatcga ttacggagag acttaacatt gactgtatta 720
gatatcgccg ctttctttcc aaactatgac aataggagat atccaattca gtcagttggt 780
caactaaciaa gggaaattta tacggacca ttaattactt ttaatccaca gttacagtct 840
gtagctcaat tacctacttt taacgttatg gaaagcaacg caattagaac tcctcattta 900
tttgatgtat taaataatct tacaattttt acagattggt ttagtgttg acgcaactt 960
tattggggag gacatcgagt aatatctaac cgtataggag gaggtaacat aacatctcct 1020
atatatggaa gggaggcgaa tcaggagcct ccaagatctt ttactttta tgggcctgtt 1080
ttaggactt tatcaaatcc tacttttaga ctttacagc aacctggcc agcgccacca 1140
ttaatttac gtggtgttga aggagtagaa tttctacac ctttaaataag ctttacgtat 1200
cgaggaaggg gtacggttga ttcttaact gagttaccgc ctgaggataa tagtgtgcct 1260
cctcggaag gatatagtca tcgtttatgt catgcaactt ttgtcaaag atctggaacc 1320
ccattttta caactgggcc agtattttct tggacgcac gtagtgtac tgatcgaaat 1380
acaattgatc cagagagaat taatcaaata ccttagtga aaggatttag agttggggg 1440
ggcacctctg tcattacagg accaggattt acaggagggg ataccttag aagaacgaat 1500
actggcacat ttgcagatat gagagtaaatt attactgggc cattatccca aagatatcgt 1560
gtaagaattc gctatgcttc tacgacagat ttacaattt tcacgagaat caatggaact 1620
tctgtaaatc aaggtaattt ccaaagaact atgaatagag gggataattt agaacttgga 1680
aacttagga ctgcaggatt tagtacgcct ttagttttt caaatgcgca aagtacattc 1740
acattgggta ctcaggcttt ttcaaatacag gaagttata tagatcgaat tgaattgtc 1800
ccggcagaag taacattcga ggcagaatct gatttagaaa gagcgagaa ggcggtgaat 1860
gcgctgttta cgtctacaaa ccaactaggg ctaaaaacia atgtaacgga ttatcatatt 1920
gatcaagtgt ccaatttagt tacgtattta tcggatgaat ttgtctgga tgaaaagcga 1980

gaattgtccg agaaagtcaa acatgcgaag cgactcagtg atgaacgcaa ttactcaa 2040
 gattcaaatt tcaaagacat taataggcaa ccagaacgtg ggtggggcgg aagtacaggg 2100
 attaccatcc aaggagggga tgacgtattt aaagaaaatt acgtcacact atcaggtacc 2160
 ttgatgagt gctatccaac atatttgtat caaaaaatcg atgaatcaaa attaaaagcc 2220
 ttacccggt atcaattaag agggatatc gaagatagtc aagacttaga aatctattta 2280
 attcgctaca atgcaaaaca tgaaacagta aatgtgccag gtacgggttc cttatggccg 2340
 cttcagccc aaagtccaat cggaagtgt ggagagccga atcgatgcgc gccacacctt 2400
 gaatggaatc ctgacttaga ttgtctgtg agggatggag aaaagtgtgc ccatcattcg 2460
 catcatttct ccttagacat tgatgtagga tgtacagact taaatgagga ctaggtgta 2520
 tgggtgatct ttaagattaa gacgcaagat gggcacgcaa gactagggaa tctagagttt 2580
 ctggaagaaa aaccattagt aggagaagcg ctagctcgtg tgaaaagagc ggagaaaaaa 2640
 tggagagaca aacgtgaaaa attggaatgg gaaacaaata tcgtttataa agaggcaaaa 2700
 gaatctgtag atgctttatt tgtaactct caatatgac aattacaagc ggatacgaat 2760
 attgccatga ttcatgcggc agataaacgt gttcatagca ttcgagaagc ttatctgcct 2820
 gagctgtctg tgattccggg tgcaatgcg gctattttg aagaattaga agggcgtatt 2880
 ttcactgcat tctccctata tgatgcgaga aatgtcatta aaaatggtga tttaataat 2940
 ggcttatcct gctggaacgt gaaagggcat gtagatgtag aagaacaaaa caaccaacgt 3000
 tcggtccttg ttgtccgga atgggaagca gaagtgtcac aagaagttcg tgtctgtccg 3060
 ggtcgtggct atatccttcg tgcacagcg tacaaggagg gatatggaga aggttcgta 3120
 accattcatg agatcgagaa caatacagac gaactgaagt ttagcaactg ctagaggag 3180
 gaaatctatc caaataacac ggtaacgtgt aatgattata ctgtaaatca agaagaatac 3240
 ggaggtgcgt acacttctcg taatcgagga tataacgaag ctcttccgt accagctgat 3300
 tatgcgtcag tctatgaaga aaaatcgtat acagatggac gtagagagaa tcctgtgaa 3360
 ttaacagag ggtataggga ttacacgcca ctaccagttg gttatgtgac aaaagaatta 3420
 gaatactcc cagaaaccga taaggtatgg attgagattg gagaaacgga aggaacattt 3480
 atcgtggaca gctggaatt actccttatg gaggaataa 3519

<210> 97

<211> 1172

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC841.

<400> 97

Met Glu Glu Asn Asn Gln Asn 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 Ser Thr Gly Asn
20 25 30

Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
35 40 45

Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
50 55 60

Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
65 70 75 80

Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
85 90 95

Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
100 105 110

Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg
115 120 125

Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
130 135 140

Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
145 150 155 160

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

Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr
180 185 190

Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn
195 200 205

Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp
210 215 220

Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu
225 230 235 240

Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile
245 250 255

Gln Ser Val Gly Gln Leu Thr Arg Glu Ile Tyr Thr Asp Pro Leu Ile
260 265 270

Thr Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn
275 280 285

Val Met Glu Ser Asn Ala Ile Arg Thr Pro His Leu Phe Asp Val Leu
290 295 300

Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe
305 310 315 320

Tyr Trp Gly Gly His Arg Val Ile Ser Asn Arg Ile Gly Gly Gly Asn
325 330 335

Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg
340 345 350

Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr
355 360 365

Phe Arg Pro Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg
370 375 380

Gly Val Glu Gly Val Glu Phe Ser Thr Pro Leu Asn Ser Phe Thr Tyr
385 390 395 400

Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp
405 410 415

Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala
420 425 430

Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Pro Val
435 440 445

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

Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly
465 470 475 480

Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu
485 490 495

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

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

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

Gly Asn Phe Gln Arg Thr Met Asn Arg Gly Asp Asn Leu Glu Ser Gly
545 550 555 560

Asn Phe Arg Thr Ala Gly Phe Ser Thr Pro Phe Ser Phe Ser Asn Ala
565 570 575

Gln Ser Thr Phe Thr Leu Gly Thr Gln Ala Phe Ser Asn Gln Glu Val
580 585 590

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

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

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

625	630	635	640
Asp Gln Val Ser Asn Leu Val Thr Tyr Leu Ser Asp Glu Phe Cys Leu			
	645	650	655
Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu			
	660	665	670
Ser Asp Glu Arg Asn Leu Leu Gln Asp Ser Asn Phe Lys Asp Ile Asn			
	675	680	685
Arg Gln Pro Glu Arg Gly Trp Gly Gly Ser Thr Gly Ile Thr Ile Gln			
	690	695	700
Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Ser Gly Thr			
705	710	715	720
Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser			
	725	730	735
Lys Leu Lys Ala Phe Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp			
	740	745	750
Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu			
	755	760	765
Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln			
	770	775	780
Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu			
785	790	795	800
Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys			
	805	810	815
Ala His His Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr			
	820	825	830
Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr			
	835	840	845

Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys
850 855 860

Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys
865 870 875 880

Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr
885 890 895

Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr
900 905 910

Asp Gln Leu Gln Ala Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp
915 920 925

Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val
930 935 940

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

Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly
965 970 975

Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val Lys Gly His Val Asp
980 985 990

Val Glu Glu Gln Asn Asn Gln Arg Ser Val Leu Val Val Pro Glu Trp
995 1000 1005

Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly
1010 1015 1020

Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly
1025 1030 1035

Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys
1040 1045 1050

Phe Ser Asn Cys Val Glu Glu Glu Ile Tyr Pro Asn Asn Thr Val
1055 1060 1065

Thr Cys Asn Asp Tyr Thr Val Asn Gln Glu Glu Tyr Gly Gly Ala
 1070 1075 1080

Tyr Thr Ser Arg Asn Arg Gly Tyr Asn Glu Ala Pro Ser Val Pro
 1085 1090 1095

Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly
 1100 1105 1110

Arg Arg Glu Asn Pro Cys Glu Phe Asn Arg Gly Tyr Arg Asp Tyr
 1115 1120 1125

Thr Pro Leu Pro Val Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe
 1130 1135 1140

Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly
 1145 1150 1155

Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
 1160 1165 1170

<210> 98
 <211> 3516
 <212> DNA
 <213> Artificial

<220>
 <223> Chimeric coding sequence encoding TIC842.

<400> 98
 atggcagaga ataatttca aaatcaatgc gtaccttaca attgtttaa taatcctgaa 60
 gtagaaatat taaatgaaga aagaagtact ggcagattac cgtagatat atccttatcg 120
 ctacacgtt tcctttgag tgaattgtt ccagggtgg gagtgcgtt tggattatt 180
 gattaatat ggggtttat aactcctct gattggagct tatttcttt acagattgaa 240
 caattgattg agcaaagaat agaaacattg gaaaggaacc gggcaattac tacattacga 300
 gggtagcag atagctatga aatttatatt gaagcactaa gagagtggga agcaaattcct 360
 aataatgcac aattaaggga agatgtcgt attcgatttg ctaatacaga cgacgcttta 420
 ataacagcaa taaataattt tacacttaca agtttgaaa tccctcttt atcgggtctat 480
 gttcaagcgg cgaatttaca ttatcacta ttaagagacg ctgtatcgt tgggcagggt 540

tggggactgg atatagctac tgtaataat cattataata gattaataaa tcttattcat 600
 agatatacga aacattgttt ggacacatac aatcaaggat tagaaaactt aagaggtact 660
 aatactcgac aatgggcaag attcaatcag ttaggagag atttaacgct aactgtatta 720
 gatatcgttg ctcttttcc gaactacgat gtagaacat atccaattca aacgtcatcc 780
 caattaacaa gggaaattta tacaagttca gtaattgagg atttccagt ttctgctaata 840
 atacctaata gtttaataag ggcggaattt ggagtagac cgccccatct tatggacttt 900
 atgaattctt tgttgtaac tgcagagact gtagaagtc aaactgtgtg gggaggacac 960
 ttagtagtt cacgaaatac ggctggaac cgtataaatt tccctagta cggggtcttc 1020
 aatcctggtg gcgccatttg gattgcagat gaggatccac gtcctttta tcggacatta 1080
 tcagatcctg ttttgtccg aggaggattt gggaatcctc attatgtact ggggcttagg 1140
 ggagtagcat ttcaacaaac tggtagaac cacacccgaa catttagaaa tagtgggacc 1200
 atagattctc tagatgaaat cccacctcag gataatagt gggcaccttg gaatgattat 1260
 agtcatgtat taaatcatgt tacatttgta cgatggccag gtgagatttc aggaagtgtat 1320
 tcatggagag ctccaatgtt ttctggacg caccgtagtg caaccctac aaatacaatt 1380
 gatccggaga ggattactca aataccattg gtaaaagcac atacacttca gtcaggtact 1440
 actgttgtaa gagggcccg gtttacggga ggagatattc ttcgacgaac aagtggagga 1500
 ccatttgctt atactattgt taatataaat gggcaattac ccaaaggta tcgtgcaaga 1560
 atacgctatg cctctactac aaatctaaga atttacgtaa cggttgcagg tgaacggatt 1620
 ttgtctggtc aatttaacaa aacaatggat accggtgacc cattaacatt ccaatcttt 1680
 agttacgcaa ctattaatac agcttttaca ttccaatga gccagagtag tttcacagta 1740
 ggtgctgata ctttagttc agggaatgaa gtttatatag acagatttga attgattcca 1800
 gttactgcaa catttgaagc agaatatgat ttagaaagag cacaaaaggc ggtgaatgcg 1860
 ctgtttactt ctataacca aatagggata aaaacagatg tgacggatta tcatattgat 1920
 caagtatcca atttagtgga ttgttatca gatgaattt gtctggatga aaagcgagaa 1980
 ttgtccgaga aagtcaaaca tgcgaagcga ctcagtgtg agcggaattt acttcaagat 2040
 ccaaacttca aaggcatcaa taggcaacta gaccgtggtt ggagaggaag tacggatatt 2100
 accatccaaa gaggagatga cgtattcaaa gaaaattatg tcacactacc aggtaccttt 2160

gatgagtgt atccaacata ttgtatcaa aaaatcgatg aatcaaaatt aaaagccttt 2220
accggtatc aattaagagg gtatatcgaa gatagtcaag acttagaaat ctatttaatt 2280
cgctacaatg caaaacatga aacagttaa gtgccaggta cgggttcctt atggccgctt 2340
tcagcccaaa gtccaatcgg aaagtgtgga gagccgaatc gatgcgcgcc acacctgaa 2400
tggaatcctg acttagattg ttcgtgtagg gatggagaaa agtgtgcca tcattcgcac 2460
catttctcct tagacattga ttaggatgt acagacttaa atgaggacct aggtgtatgg 2520
gtgatcttta agattaagac gcaagatggg cacgcaagac tagggaatct agagtttctc 2580
gaagagaaac cattagtagg agaagcgcta gctcgtgtga aaagagcgga gaaaaaatgg 2640
agagacaaac gtgaaaaatt ggaatgggaa acaaatatcg ttataaaga ggcaaaagaa 2700
tctgtatagc ctttattgt aaactctcaa tatgatcaat tacaagcgga tacgaatatt 2760
gccatgattc atgcggcaga taaacgtgtt catagcattc gagaagctta tctgcctgag 2820
ctgtctgtga ttccgggtgt caatgcggct attttgaag aattagaagg gcgtattttc 2880
actgcattct ccctatatga tgcgagaaat gtcattaaaa atgggtgatt taataatggc 2940
ttatcctgct ggaacgtgaa agggcatgta gatgtagaag aacaaaacaa ccaacgttcg 3000
gtcctgttg ttccggaatg ggaagcagaa gtgtcacaag aagttcgtgt ctgtccgggt 3060
cgtggctata tcctcgtgt cacagcgtac aaggagggat atggagaagg ttgcgtaacc 3120
attcatgaga tcgagaacaa tacagacgaa ctgaagtta gcaactgcgt agaagaggaa 3180
atctatccaa ataacacggt aacgtgtaat gattatactg taaatcaaga agaatacga 3240
ggtgcgtaca ctctcgtaa tcgaggatat aacgaagctc ctccgtacc agctgattat 3300
gcgtcagtct atgaagaaaa atcgatatac gatggacgaa gagagaatcc ttgtgaattt 3360
aacagagggg atagggatta cagccacta ccagttgggt atgtgacaaa agaattagaa 3420
tactcccag aaaccgataa ggtatggatt gagattggag aaacggaagg aacattatc 3480
gtggacagcg tggaattact cttatggag gaataa 3516

<210> 99

<211> 1171

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC842.

<400> 99

Met Ala Glu Asn Asn Ile Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu
1 5 10 15

Asn Asn Pro Glu Val Glu Ile Leu Asn Glu Glu Arg Ser Thr Gly Arg
20 25 30

Leu Pro Leu Asp Ile Ser Leu Ser Leu Thr Arg Phe Leu Leu Ser Glu
35 40 45

Phe Val Pro Gly Val Gly Val Ala Phe Gly Leu Phe Asp Leu Ile Trp
50 55 60

Gly Phe Ile Thr Pro Ser Asp Trp Ser Leu Phe Leu Leu Gln Ile Glu
65 70 75 80

Gln Leu Ile Glu Gln Arg Ile Glu Thr Leu Glu Arg Asn Arg Ala Ile
85 90 95

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

Leu Arg Glu Trp Glu Ala Asn Pro Asn Asn Ala Gln Leu Arg Glu Asp
115 120 125

Val Arg Ile Arg Phe Ala Asn Thr Asp Asp Ala Leu Ile Thr Ala Ile
130 135 140

Asn Asn Phe Thr Leu Thr Ser Phe Glu Ile Pro Leu Leu Ser Val Tyr
145 150 155 160

Val Gln Ala Ala Asn Leu His Leu Ser Leu Leu Arg Asp Ala Val Ser
165 170 175

Phe Gly Gln Gly Trp Gly Leu Asp Ile Ala Thr Val Asn Asn His Tyr
180 185 190

Asn Arg Leu Ile Asn Leu Ile His Arg Tyr Thr Lys His Cys Leu Asp
195 200 205

Thr Tyr Asn Gln Gly Leu Glu Asn Leu Arg Gly Thr Asn Thr Arg Gln

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

Pro Gly Glu Ile Ser Gly Ser Asp Ser Trp Arg Ala Pro Met Phe Ser
435 440 445

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

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

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

Thr Ser Gly Gly Pro Phe Ala Tyr Thr Ile Val Asn Ile Asn Gly Gln
500 505 510

Leu Pro Gln Arg Tyr Arg Ala Arg Ile Arg Tyr Ala Ser Thr Thr Asn
515 520 525

Leu Arg Ile Tyr Val Thr Val Ala Gly Glu Arg Ile Phe Ala Gly Gln
530 535 540

Phe Asn Lys Thr Met Asp Thr Gly Asp Pro Leu Thr Phe Gln Ser Phe
545 550 555 560

Ser Tyr Ala Thr Ile Asn Thr Ala Phe Thr Phe Pro Met Ser Gln Ser
565 570 575

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

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

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

Ile Asn Gln Ile Gly Ile Lys Thr Asp Val Thr Asp Tyr His Ile Asp
625 630 635 640

Gln Val Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp
645 650 655

Glu Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser
660 665 670

Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Lys Gly Ile Asn Arg
675 680 685

Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Arg
690 695 700

Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe
705 710 715 720

Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys
725 730 735

Leu Lys Ala Phe Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser
740 745 750

Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr
755 760 765

Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser
770 775 780

Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu
785 790 795 800

Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala
805 810 815

His His Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp
820 825 830

Leu Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln
835 840 845

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

Leu Val Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp
865 870 875 880

Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys
885 890 895

Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp
900 905 910

Gln Leu Gln Ala Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys
915 920 925

Arg Val His Ser Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile
930 935 940

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

Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp
965 970 975

Phe Asn Asn Gly Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val
980 985 990

Glu Glu Gln Asn Asn Gln Arg Ser Val Leu Val Val Pro Glu Trp Glu
995 1000 1005

Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr
1010 1015 1020

Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys
1025 1030 1035

Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe
1040 1045 1050

Ser Asn Cys Val Glu Glu Glu Ile Tyr Pro Asn Asn Thr Val Thr
1055 1060 1065

Cys Asn Asp Tyr Thr Val Asn Gln Glu Glu Tyr Gly Gly Ala Tyr
1070 1075 1080

Thr Ser Arg Asn Arg Gly Tyr Asn Glu Ala Pro Ser Val Pro Ala

1085	1090	1095
Asp Tyr	Ala Ser Val Tyr Glu	Glu Lys Ser Tyr Thr Asp Gly Arg
1100	1105	1110
Arg Glu	Asn Pro Cys Glu Phe	Asn Arg Gly Tyr Arg Asp Tyr Thr
1115	1120	1125
Pro Leu	Pro Val Gly Tyr Val	Thr Lys Glu Leu Glu Tyr Phe Pro
1130	1135	1140
Glu Thr	Asp Lys Val Trp Ile	Glu Ile Gly Glu Thr Glu Gly Thr
1145	1150	1155
Phe Ile	Val Asp Ser Val Glu	Leu Leu Leu Met Glu Glu
1160	1165	1170

<210> 100
 <211> 3444
 <212> DNA
 <213> Artificial

<220>
 <223> Chimeric coding sequence encoding TIC850.

<400> 100
 atggagaata atatcaaaa tcaatgcgta ccttacaatt gtttaaataa tcctgaagta 60
 gaaatattaa atgaagaaag aagtactggc agattaccgt tagatatac cttatcgctt 120
 acacgtttcc tttgagtga attgttcca ggtgtgggag ttgcgtttgg attattgat 180
 ttaatatggg gtttataac tccttctgat tggagcttat ttctttaca gattgaacaa 240
 ttgattgagc aaagaataga aacattggaa aggaaccggg caattactac attacgaggg 300
 ttagcagata gctatgaaat ttatattgaa gcactaagag agtgggaagc aaatcctaata 360
 aatgcacaat taagggaaga tgtgcgtatt cgatttgcta atacagacga cgctttaata 420
 acagcaataa ataattttac acttacaagt ttgaaatcc ctctttatc ggtctatgtt 480
 caagcggcga atttacattt atcactatta agagacgctg tatcgtttgg gcaggggttg 540
 ggactggata tagctactgt taataatcat tataatagat taataaatct tattcataga 600
 tatacgaaac attgtttgga cacatacaat caaggattag aaaacttaag aggtactaat 660
 actcgacaat gggcaagatt caatcagttt aggagagatt taacgctaac tgtattagat 720

atcgttgctc ttttccgaa ctacgatgtt agaacatac caattcaaac gtcacccaa 780
 ttaacaaggg aaatttatac aagttcagta attgaggatt ctccagttc tgctaata 840
 cctaattggtt ttaatagggc ggaatttga gttagaccgc cccatcttat ggactttatg 900
 aattctttgt ttgtaactgc agagactgtt agaagtcaaa ctgtgtgggg aggacactta 960
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 cctggtggcg ccatttggat tgcagatgag gatccacgtc cttttatcg gacattatca 1080
 gatcctgttt ttgtccgagg aggatttggg aatcctcatt atgtactggg gcttagggga 1140
 gtagcatttc acaaaactgg tacgaaccac acccgaacat ttagaaatag tgggaccata 1200
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 ttagaggga tcaatagaca actagaccgt ggctggagag gaagtacgga tattaccatc 2100
 caaggaggcg atgacgtatt caaagagaat tacgttacgc tattgggtac ctttgatgag 2160
 tgctatcaa cgtatttata tcaaaaaata gatgagtcga aattaaagc ctataccgt 2220
 taccaattaa gagggatat cgaagatagt caagacttag aaatctattt aattcgctac 2280
 aatgccaaac acgaaacagt aaatgtgcca ggtacgggtt cttatggcc gcttcagcc 2340

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 gatggccatg caagactagg aaatctagaa ttctcgaag agaaaccatt agtaggagaa 2520
 gcactagctc gtgtgaaaag agcggagaaa aaatggagag acaaacgtga aaaattggaa 2580
 tgggaaacaa atattgttta taaagaggca aaagaatctg tagatgcttt atttgtaaac 2640
 tctcaatatg atagattaca agcggatacc aacatcgca tgattcatgc ggcagataaa 2700
 cgcggtcata gcattcgaga agcttatctg cctgagctgt ctgtgattcc ggggtgcaat 2760
 gcggctattt ttgaagaatt agaagggcgt atttctactg cattctccct atatgatgcg 2820
 agaaatgtca ttaaaaatgg tgattttaat aatggcttat cctgctggaa cgtgaaaggg 2880
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 gcagaagtgt cacaagaagt tcgtgtctgt ccgggtcgtg gctatatcct tcgtgtcaca 3000
 gcgtacaagg agggatatgg agaaggttgc gtaaccattc atgagatcga gaacaataca 3060
 gacgaactga agtttagcaa ctgtgtagaa gaggaagtat atccaaacaa cacggtaacg 3120
 tgtaatgatt atactcgcac tcaagaagaa tatgagggta cgtacacttc tcgtaatcga 3180
 ggatatgacg gagcctatga aagcaattct tctgtaccag ctgattatgc atcagcctat 3240
 gaagaaaaag catatacaga tggacgaaga gacaatcctt gtgaatctaa cagaggatat 3300
 ggggattaca caccactacc agctggctat gtgacaaaag aattagagta ctcccagaa 3360
 accgataagg tatggattga gatcggagaa acggaaggaa cattcatcgt ggacagcgtg 3420
 gaattacttc ttatggagga atag 3444

<210> 101

<211> 1147

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC850.

<220>

<221> MISC_FEATURE

<222> (1)..(1147)

<223> Amino acid sequence of the chimeric protein TIC850.

<400> 101

Met Glu Asn Asn Ile Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu Asn
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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 Val Lys Ala His Thr Leu Gln Ser Gly Thr Thr
465 470 475 480

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

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

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

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

Gln Arg Thr Met Asn Arg Gly Asp Asn Leu Glu Ser Gly Asn Phe Arg
545 550 555 560

Thr Ala Gly Phe Ser Thr Pro Phe Ser Phe Ser Asn Ala Gln Ser Thr
565 570 575

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

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

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

Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val
625 630 635 640

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

Lys Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu

660	665	670
Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Leu		
675	680	685
Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp		
690	695	700
Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Leu Gly Thr Phe Asp Glu		
705	710	715
		720
Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys		
725	730	735
Ala Tyr Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp		
740	745	750
Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val Asn		
755	760	765
Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Pro Ser Pro Ile		
770	775	780
Gly Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile Asp Val		
785	790	795
		800
Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys		
805	810	815
Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu		
820	825	830
Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys Arg Ala		
835	840	845
Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu Thr Asn		
850	855	860
Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn		
865	870	875
		880

Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met Ile His
885 890 895

Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu Pro Glu
900 905 910

Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu Leu Glu
915 920 925

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

Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val Lys Gly
945 950 955 960

His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu Val Val
965 970 975

Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly
980 985 990

Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu
995 1000 1005

Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu Leu
1010 1015 1020

Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr
1025 1030 1035

Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly
1040 1045 1050

Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser
1055 1060 1065

Asn Ser Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys
1070 1075 1080

Ala Tyr Thr Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg
1085 1090 1095

Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys
 1100 1105 1110

Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile
 1115 1120 1125

Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu
 1130 1135 1140

Leu Met Glu Glu
 1145

<210> 102

<211> 3447

<212> DNA

<213> Artificial

<220>

<223> Chimeric coding sequence encoding TIC859.

<400> 102

atggagaata atattcaaaa tcaatgcgta cctacaatt gtttaaataa tcctgaagta 60
 gaaatattaa atgaagaaag aagtactggc agattaccgt tagatatatc cttatcgctt 120
 acacgtttcc ttttgagtga attgttcca ggtgtgggag ttgcgtttgg attattgat 180
 ttaatatggg gttttataac tccttctgat tggagcttat ttctttaca gattgaacaa 240
 ttgattgagc aaagaataga aacattggaa aggaaccggg caattactac attacgaggg 300
 ttagcagata gctatgaaat ttatattgaa gcactaagag agtgggaagc aaatcctaata 360
 aatgcacaat taaggggaaga tgtgcgtatt cgatttgcta atacagacga cgctttaata 420
 acagcaataa ataattttac acttacaagt ttgaaatcc ctcttttacc ggtctatgtt 480
 caagcggcga atttacattt atcactatta agagacgctg tatcgtttgg gcagggttgg 540
 ggactggata tagctactgt taataatcat tataatagat taataaatct tattcataga 600
 tatacgaaac attgtttgga cacatacaat caaggattag aaaacttaag aggtactaat 660
 actcgacaat gggcaagatt caatcagttt aggagagatt taacgctaac tgtattagat 720
 atcgttgctc ttttccgaa ctacgatgtt agaacataac caattcaaac gtcacccaa 780
 ttaacaaggg aaatttatac aagttcagta attgaggatt ctccagtttc tgctaataata 840
 cctaattggtt ttaatagggc ggaatttggg gttagaccgc cccatcttat ggactttatg 900

aattcttgt ttgtaactgc agagactgtt agaagtcaaa ctgtgtgggg aggacactta 960
gtagttcac gaaatacggc tggtaaccgt ataaattcc ctagttacgg ggtcttcaat 1020
cctggtggcg ccatttggat tgcagatgag gatccacgtc cttttatcg gacattatca 1080
gatcctgttt ttgtccgagg aggatttggg aatcctcatt atgtactggg gcttagggga 1140
gtagcatttc aacaaactgg tacgaaccac acccgaacat ttagaaatag tgggaccata 1200
gattctctag atgaaatccc acctcaggat aatagtgggg caccttgga tgattatagt 1260
catgtattaa atcatgttac attgtacga tggccagggt agatttcagg aagtattca 1320
tggagagctc caatgtttc ttggacgcac cgtagtgcaa cccctacaaa cgaagttcgt 1380
gtatctagaa ttacacaatt accgatgggt aaggcgcata cgcttcatgc gggagctact 1440
gttgtagag gaccaggatt tacaggagga gatatactcc gaagaactac ttcaggctca 1500
ttgggggata tgagaataac aaattttca agttcatcat cgaggtatcg tgtaagaata 1560
cgttatgctt ctactacaga ttacaattt ttcttgagt ttggaggaa cctgtcaat 1620
gtagccgatt tccgaaaac catagataga ggggaaaact tagaatatgg aagcttaga 1680
acggcagggt ttactacccc ttttagttt gtaagtcaa caaataatt cacattaggt 1740
gttcagagt ttcttcagg taacgagatt ttgtagatc gaattgaatt tgtccggca 1800
gatgcaacct ttgaggcaga atatgattta gaaagagcac aaaaggcggg gaatgagctg 1860
ttacttctt ccaatcaaat cgggttaaaa acagatgtga cggattatca tattgatcaa 1920
gtatccaatt tagttgagt ttatctgat gaatttgtc tggatgaaaa aaaagaattg 1980
tccgagaaag taaacatgc gaagcgact agtgatgagc ggaatttact tcaagatcca 2040
aacttagag ggaatcaatg acaactagac cgtggctgga gaggaagtac ggatattacc 2100
atccaaggag gcatgacgt attcaaagag aattacgtta cgctattggg tacctttgat 2160
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cgttaccaat taagagggt tatcgaagat agtcaagact tagaaatcta ttaattcgc 2280
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caagatggcc atgcaagact aggaaatcta gaatttctg aagagaaacc attagtagga 2520

gaagcactag ctcgtgtgaa aagagcggag aaaaaatgga gagacaaacg tgaaaaattg 2580
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 aactctcaat atgatatgatt acaagcggat accaaccatcg cgatgattca tgcggcagat 2700
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 aatgcggcta ttttgaaga attagaaggg cgtattttca ctgcattctc cctatatgat 2820
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 acagcgtaca aggagggata tggagaaggt tgcgtaacca ttcagagat cgagaacaat 3060
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 cgaggatatg acggagccta tgaaagcaat tcttctgtac cagctgatta tgcacagacc 3240
 tatgaagaaa aagcatatac agatggacga agagacaatc cttgtgaatc taacagagga 3300
 tatggggatt acacaccact accagctggc tatgtgacaa aagaattaga gtactccca 3360
 gaaaccgata aggtatggat tgagatcgga gaaacggaag gaacattcat cgtggacagc 3420
 gtggaattac ttcttatgga ggaatag 3447

<210> 103

<211> 1148

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC859.

<400> 103

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 Glu Val Arg Val Ser Arg Ile
450 455 460

Thr Gln Leu Pro Met Val Lys Ala His Thr Leu His Ala Gly Ala Thr
465 470 475 480

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

Thr Ser Gly Ser Phe Gly Asp Met Arg Ile Thr Asn Phe Ser Ser Ser
500 505 510

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

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

Pro Lys Thr Ile Asp Arg Gly Glu Asn Leu Glu Tyr Gly Ser Phe Arg
545 550 555 560

Thr Ala Gly Phe Thr Thr Pro Phe Ser Phe Val Ser Ser Thr Asn Asn
565 570 575

Phe Thr Leu Gly Val Gln Ser Val Ser Ser Gly Asn Glu Ile Phe Val
580 585 590

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

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

Asn Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln
625 630 635 640

Val Ser Asn Leu Val Glu Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu
645 650 655

Lys Lys Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp
660 665 670

Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln
675 680 685

Leu Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly
690 695 700

Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Leu 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 Tyr 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 Pro Ser Pro			
	770	775	780
Ile Gly Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile Asp			
	785	790	795
			800
Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile Phe			
	805	810	815
Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe			
	820	825	830
Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys Arg			
	835	840	845
Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu Thr			
	850	855	860
Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val			
	865	870	875
			880
Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met Ile			
	885	890	895
His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu Pro			
	900	905	910
Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu Leu			
	915	920	925

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

Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val Lys
945 950 955 960

Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu Val
965 970 975

Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro
980 985 990

Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly
995 1000 1005

Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu
1010 1015 1020

Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn
1025 1030 1035

Thr Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu
1040 1045 1050

Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu
1055 1060 1065

Ser Asn Ser Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu
1070 1075 1080

Lys Ala Tyr Thr Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn
1085 1090 1095

Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr
1100 1105 1110

Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu
1115 1120 1125

Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
1130 1135 1140

Leu Leu Met Glu Glu
1145

<210> 104
<211> 3612
<212> DNA
<213> Artificial

<220>
<223> Chimeric coding sequence encoding TIC861.

<400> 104
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atctctacgg attcactaaa aaatgaaaca gatatagaat tacaaaacat taatcatgaa 120
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caatatatcg cattagaatt gatgttcgtt cagaaactac ctcttttgc agtgtctgga 540
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tataaccgtc aagtcgaacg agcaggagat tattccgacc attgtgtgaa atggtatagt 720
acagggtctaa ataacttgag gggtaaaaat gccgaaagct gggttcgta taatcaattt 780
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actgaatcat tggcagggct gaatctattt ttaactcaac ctgttaatgg agtacctagg 1260

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 ggaaaatgtg cccatcattc ccatcattc tccttgaca ttgatgttg atgtacagac 2580
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 aaaaatgggtg attttaataa tggcttatcc tgctggaacg tgaaagggca ttagatgta 3060
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 ttagcaact gtgtagaaga ggaagtatat ccaaacaaca cggtaacgtg taatgattat 3300
 actgcgactc aagaagaata tgagggtacg tacacttctc gtaatcgagg atatgacgga 3360
 gcctatgaaa gcaattcttc tgtaccagct gattatgcat cagcctatga agaaaaagca 3420
 tatacagatg gacgaagaga caatccttgt gaatctaaca gaggatatgg ggattacaca 3480
 ccactaccag ctggctatgt gacaaaagaa ttagagtact tcccagaaac cgataaggta 3540
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<210> 105
 <211> 1203
 <212> PRT
 <213> Artificial

<220>
 <223> Amino acid sequence of the chimeric protein TIC861.

<400> 105

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

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

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

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

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

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

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

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

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

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

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

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

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

Val Glu Arg Ala Gly Asp Tyr Ser Asp His Cys Val Lys Trp Tyr Ser
225 230 235 240

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

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

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

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

290	295	300	
Pro Asn Ala Ser Phe Ala Ser Thr Thr Trp Tyr Asn Asn Asn Ala Pro			
305	310	315	320
Ser Phe Ser Thr Ile Glu Ser Ala Val Val Arg Asn Pro His Leu Leu			
	325	330	335
Asp Phe Leu Glu Gln Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser			
	340	345	350
Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Arg Leu Glu Phe Arg			
	355	360	365
Thr Ile Gly Gly Met Leu Asn Thr Ser Thr Gln Gly Ser Thr Asn Thr			
	370	375	380
Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg			
385	390	395	400
Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn			
	405	410	415
Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile			
	420	425	430
Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile Gly Thr Gln			
	435	440	445
Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Thr Thr Gly Gln Pro			
	450	455	460
Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser			
465	470	475	480
Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala			
	485	490	495
Asp Arg Thr Asn Thr Ile Asp Pro Glu Arg Ile Asn Gln Ile Pro Leu			
	500	505	510

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

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

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

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

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

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

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

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

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

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

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

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

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

His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn
725 730 735

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

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

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

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

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

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

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

His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp
850 855 860

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

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

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

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

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

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

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

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

Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly
995 1000 1005

Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln
1010 1015 1020

Asn Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu
1025 1030 1035

Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu
1040 1045 1050

Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr
1055 1060 1065

Ile His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn
1070 1075 1080

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

Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser
1100 1105 1110

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

Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr Asp
1130 1135 1140

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

Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr

1160 1165 1170

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

Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
1190 1195 1200

<210> 106
<211> 3432
<212> DNA
<213> Artificial

<220>
<223> Chimeric coding sequence encoding TIC848.

<400> 106
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gtacttttgg atggggagag gatattacct gatatcgatc cactcgaagt ttctttgtcg 120

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gataaaatat ggggggcttt gagaccatct gaatgggact tatttcttgc acagattgaa 240

cgggtgattg atcaaagaat agaagcaaca gtaagagcaa aagcaatcac tgaattagaa 300

ggattaggga gaaattatca aatatacgct gaagcattta agaatggga atcagatcct 360

gataacgaag cggctaaaag tagagtaatt gatcgctttc gtatacttga tggcttaatt 420

gaagcaaata tcccttcatt tcggataatt ggatttgaag tgccactttt atcggtttat 480

gttcaagcag ctaatctaca tctcgctcta ttgagagatt ctgttatttt tggagagaga 540

tggggattga cgacaaaaaa tgtcaatgat atctataata gacaaattag agaaattcat 600

gaatatagca atcattgcgt agatacgtat aacacagaac tagaacgtct aggggttaga 660

tctatagcgc agtggagaat atataatcag tttagaagag aactaacact aactgtatta 720

gatattgtcg ctcttttccc gaactatgac agtagactgt atccgatcca aacttttct 780

caattgacaa gagaaattgt tacatcccca gtaagcgaat ttattatgg tgttattaat 840

agtggtaata taattggtac tcttactgaa cagcagataa ggcgaccaca tcttatggac 900

ttctttaact ccatgatcat gtatacatca gataatagac gggaacatta ttggtcagga 960

cttgaaatga cggcttattt tacaggattt gcaggagctc aagtgtcatt cccttagtc 1020

gggactagag gggagtcagc tccaccatta actgttagaa gtgttaatga tggaatttat 1080

agaatattat cggcaccgtt ttattcagcg ccttttctag gcaccattgt attgggaagt 1140
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 actgcgactc aagaagaata tgagggtacg tacacttctc gtaatcgagg atatgacgga 3180
 gcctatgaaa gcaattcttc tgtaccagct gattatgcat cagcctatga agaaaaagca 3240
 tatacagatg gacgaagaga caatccttgt gaatctaaca gaggatatgg ggattacaca 3300
 ccactaccag ctggctatgt gacaaaagaa ttagagtact tcccagaaac cgataaggta 3360
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 atggaggaat ag 3432

<210> 107
 <211> 1143
 <212> PRT
 <213> Artificial

<220>
 <223> Amino acid sequence of the chimeric protein TIC848.

<400> 107

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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 Ser Thr Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro			
465	470	475	480
Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile			
	485	490	495
Ser Thr Leu Arg Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg			
	500	505	510

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

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

Ser Gly Ser Asn Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr
545 550 555 560

Thr Pro Phe Asn Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala
565 570 575

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

Val Pro Ala Glu Val Thr Phe Glu Ala Glu Tyr 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> 108
<211> 3429
<212> DNA
<213> Artificial

<220>

<223> Chimeric coding sequence encoding TIC849.

<400> 108

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ctttgcaat ttctttgaa taactttgtt ccagggggag gctttattc aggattagt 180
gataaaatat ggggggcttt gagaccatct gaatgggact tatttctgc acagattgaa 240
cgggtgattg atcaaagaat agaagcaaca gtaagagcaa aagcaatcac tgaattagaa 300
ggattaggga gaaattatca aatatacgct gaagcattta aagaatggga atcagatcct 360
gataacgaag cggctaaaag tagagtaatt gatcgcttc gtatactga tggcttaatt 420
gaagcaaata tcccttcatt tcggataatt ggatttgaag tgccacttt atcggttat 480
gttcaagcag ctaatctaca tctcgctcta ttgagagatt ctgtatttt tggagagaga 540
tggggattga cgacaaaaaa tgtcaatgat atctataata gacaaattag agaaattcat 600
gaatatagca atcattgcgt agatacgat aacacagaac tagaacgtct aggggttaga 660
tctatagcgc agtggagaat atataatcag tttagaagag aactaacact aactgtatta 720
gatattgtcg ctctttccc gaactatgac agtagactgt atccgatcca aacttttct 780
caattgacaa gagaaattgt tacatcccca gtaagcgaat ttattatgg tgttattaat 840
agtggtaata taattggtac tcttactgaa cagcagataa ggcgaccaca tcttatggac 900
ttcttaact ccatgatcat gtatacatca gataatagac gggaacatta ttggtcagga 960
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gggactagag gggagtcagc tccaccatta actgtagaa gtgttaatga tggaatttat 1080
agaatattat cggcaccgtt ttattcagcg cctttctag gcaccattgt attgggaagt 1140
cgtggagaaa aatttgattt tgcgcttaat aatatttcac ctccgccatc tacaatatac 1200
agacatcctg gaacagtaga ttactagtc agtataccgc cacaggataa tagcgtacca 1260
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gggtttacag gtggagatat ccttcgtaga acaaatacgg gtacatttg agatatacga 1500
ttaaatatta atgtgccatt atcccaaaga tatcgcgtaa ggattcgta tgcttctact 1560

acagatttac aatttttcac gagaattaat ggaaccactg ttaatattgg taatttctca 1620
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 actccttta attttttaa tgcccaaagc acattcacat tgggtgctca gagttttca 1740
 aatcaggaag tttatataga tagagtcgaa tttgtccag cagaggtaac atttgaggca 1800
 gaatatgatt tagaaagagc acaaaaggcg gtgaatgagc tgtttacttc ttccaatcaa 1860
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 tgtttatctg atgaatttg tctggatgaa aaaaaagaat tgtccgagaa agtcaaacaat 1980
 gcgaagcgac ttagtgatga gcggaattta cttcaagatc caaacttag agggatcaat 2040
 agacaactag accgtggctg gagaggaagt acggatatta ccatccaagg aggcgatgac 2100
 gtattcaaag agaattacgt tacgctattg ggtaccttg atgagtgcta tccaacgtat 2160
 ttatatcaa aaatagatga gtcgaaatta aaagcctata cccgttacca attaagaggg 2220
 tatatcgaag atagtcaaga cttagaaatc tatttaattc gctacaatgc caaacacgaa 2280
 acagtaaatg tgccaggtag gggtcctta tggccgctt cagccccaag tccaatcgga 2340
 aaatgtgccc atcattcca tcatttctc ttggacattg atgttgatg tacagactta 2400
 aatgaggact taggtgtatg ggtgatattc aagattaaga cgcaagatgg ccatgcaaga 2460
 ctaggaaatc tagaatttct cgaagagaaa ccattagtag gagaagcact agctcgtgtg 2520
 aaaagagcgg agaaaaaatg gagagacaaa cgtgaaaaat tggaatggga aacaaatatt 2580
 gttataaag aggcaaaaga atctgtagat gctttattg taaacttca atatgataga 2640
 ttacaagcgg ataccaacat cgcatgatt catgcggcag ataaacgcgt tcatagcatt 2700
 cgagaagctt atctgcctga gctgtctgtg attccgggtg tcaatgcggc tatttttgaa 2760
 gaattagaag ggcgtatttt cactgcattc tccctatatg atgcgagaaa tgcattaaa 2820
 aatggtgatt ttaataatgg cttatcctgc tggaacgtga aagggcattg agatgtagaa 2880
 gaacaaaaca accaccgttc ggtcctgtt gttccggaat gggaagcaga agtgtcaca 2940
 gaagtcgtg tctgtccggg tctgtgctat atccttcgtg tcacagcgta caaggaggga 3000
 tatggagaag gtgcgtaac cattcatgag atcgagaaca atacagacga actgaagttt 3060
 agcaactgtg tagaagagga agtatatcca aacaacacgg taactgttaa tgattatact 3120
 gcgactcaag aagaatatga gggtagctac acttctcgta atcgaggata tgacggagcc 3180

tatgaaagca attcttctgt accagctgat tatgcatcag cctatgaaga aaaagcatat 3240
acagatggac gaagagacaa tccttgtaa tctaacagag gatatgggga ttacacacca 3300
ctaccagctg gctatgtgac aaaagaatta gagtacttcc cagaaaccga taaggatatg 3360
attgagatcg gagaaacgga aggaacattc atcgtggaca gcgtggaatt acttcttatg 3420
gaggaatag 3429

<210> 109
<211> 1142
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of the chimeric protein TIC849.

<400> 109

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
370	375	380	Thr	Ile	Val
			Leu	Gly	Ser
			Arg	Gly	Glu
			Lys		
Phe	Asp	Phe	Ala	Leu	Asn
385	390	395	400	Ile	Ser
			Pro	Pro	Pro
			Ser	Thr	Ile
			Tyr		
Arg	His	Pro	Gly	Thr	Val
405	410	415	Asp	Ser	Leu
			Val	Ser	Ile
			Pro	Pro	Gln
			Asp		
Asn	Ser	Val	Pro	Pro	His
420	425	430	Arg	Gly	Ser
			Ser	Ser	His
			Arg	Leu	Ser
			His	Val	
Thr	Met	Arg	Ala	Ser	Ser
435	440	445	Pro	Ile	Phe
			His	Trp	Thr
			His	Arg	Ser
			Ala		
Thr	Thr	Thr	Asn	Thr	Ile
450	455	460	Asn	Pro	Asn
			Ala	Ile	Ile
			Gln	Ile	Pro
			Leu		
Val	Lys	Ala	Phe	Asn	Leu
465	470	475	480	His	Ser
			Gly	Ala	Thr
			Val	Val	Arg
			Gly	Pro	
Gly	Phe	Thr	Gly	Gly	Asp
485	490	495	Ile	Leu	Arg
			Arg	Thr	Asn
			Thr	Gly	Thr
			Phe		
Gly	Asp	Ile	Arg	Leu	Asn
500	505	510	Ile	Asn	Val
			Pro	Leu	Ser
			Gln	Arg	Tyr
			Arg		
Val	Arg	Ile	Arg	Tyr	Ala
515	520	525	Ser	Thr	Thr
			Asp	Leu	Gln
			Phe	Phe	Thr
			Arg		
Ile	Asn	Gly	Thr	Thr	Val
530	535	540	Asn	Ile	Gly
			Asn	Phe	Ser
			Arg	Thr	Met
			Asn		
Arg	Gly	Asp	Asn	Leu	Glu
545	550	555	560	Tyr	Arg
			Ser	Phe	Arg
			Thr	Ala	Gly
			Phe	Ser	
Thr	Pro	Phe	Asn	Phe	Leu
565	570	575	Asn	Ala	Gln
			Ser	Thr	Phe
			Thr	Leu	Gly
			Ala		

Gln Ser Phe Ser Asn Gln Glu Val Tyr Ile Asp Arg Val Glu Phe Val
580 585 590

Pro Ala Glu Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln
595 600 605

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

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

Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu
645 650 655

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

Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg
675 680 685

Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu
690 695 700

Asn Tyr Val Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr
705 710 715 720

Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr
725 730 735

Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu
740 745 750

Ile Arg Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly
755 760 765

Ser Leu Trp Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Ala His
770 775 780

His Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu
785 790 795 800

Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp
805 810 815

Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu
820 825 830

Val Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg
835 840 845

Asp Lys Arg Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu
850 855 860

Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg
865 870 875 880

Leu Gln Ala Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg
885 890 895

Val His Ser Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro
900 905 910

Gly Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr
915 920 925

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

Asn Asn Gly Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu
945 950 955 960

Glu Gln Asn Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala
965 970 975

Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu
980 985 990

Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile
995 1000 1005

His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys
1010 1015 1020

Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp
 1025 1030 1035

Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg
 1040 1045 1050

Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser Val Pro
 1055 1060 1065

Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr Asp Gly
 1070 1075 1080

Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr
 1085 1090 1095

Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe
 1100 1105 1110

Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly
 1115 1120 1125

Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
 1130 1135 1140

<210> 110
 <211> 3570
 <212> DNA
 <213> Artificial

<220>
 <223> Chimeric coding sequence encoding TIC847.

<400> 110
 atgactcaa ataggaaaa tgagaatgaa attataaatg cttatcgat tccaacggta 60
 tcgaatcctt ccacgcaa ataatctatca ccagatgctc gtattgaaga tagcttgtgt 120
 gtagccgagg tgaacaatat tgatccattt gttagcgc atcaacagtcca aacgggtata 180
 aacatagctg gtagaatatt gggcgtatta ggtgtgccgt ttgctggaca actagctagt 240
 ttttatagtt ttctgttg ggaattatgg cctagtggca gagatccatg ggaaatttc 300
 ctggaacatg tagaacaact tataagacaa caagtaacag aaaatactag gaatacggct 360

attgctcgat tagaaggctct aggaagagggc tatagatctt accagcagggc tcttgaaact 420
 tggtagata accgaaatga tgcaagatca agaagcatta ttcttgagcg ctatgttgct 480
 ttagaacttg acattactac tgctataccg ctttcagaa tacgaaatga agaagttcca 540
 ttattaatgg tatatgctca agctgcaaatt ttacacctat tattattgag agacgcatcc 600
 ctttttgga gtgaatgggg gatggcatct tccgatgta accaatatta ccaagaacaa 660
 atcagatata cagaggaata ttctaaccat tgcgtacaat ggtataatac agggctaaat 720
 aacttaagag ggacaaatgc tgaaagtgg ttgcgggata atcaattccg tagagaccta 780
 acgttagggg tattagattt agtagcccta ttccaagct atgatactcg cacttatcca 840
 atcaatacga gtgctcagtt aacaagagaa attatacag atccaattgg gagaacaaat 900
 gcaccttcag gatttgcaag tacgaattgg ttaataata atgcaccatc gtttctgcc 960
 atagaggctg ccatttcag gcctccgcat ctactgatt ttccagaaca acttacaatt 1020
 tacagtgcac caagccgttg gagtagcact caacatatga attattgggt gggacatagg 1080
 cttacttcc gcccaatagg agggacatta aatactcaa cacaaggact tactaataat 1140
 acttcaatta atcctgtaac attacagttt acgtctcgag acgtttatag aacagaatca 1200
 aatgcaggga caaatatact attactact cctgtgaatg gagtaccttg ggctagattt 1260
 aattttataa accctcagaa tatttatgaa agaggcgcca ctacctacag tcaaccgtat 1320
 caggaggttg ggattcaatt attgattca gaaactgaat taccaccaga aacaacagaa 1380
 cgaccaaatt atgaatcata tagtcataga ttatctcata taggactaat cataggaaac 1440
 actttgagag caccagtcta ttcttgacg catcgtagtg cagatcgtag gaatacgatt 1500
 ggaccaaata gaattacaca aataccattg gtaaaggcgc ataccctcca atcgggtacc 1560
 actgtagtaa aagggccagg gtttacagga ggggatatcc tccgtcgaac aagtggagga 1620
 ccatttgctt ttagtaatgt taatctagat ttaacttgt cacaaaggta tcgtgctaga 1680
 attcgttatg cctctactac taacctaaga atttacgtaa cggttgacagg tgaacgaatt 1740
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 agttacgcaa ctattaatac agctttaca ttccagaaa gatcgagcag ctgactgta 1860
 ggtgccgata cgtttagttc aggtaatgaa gtttatgtag atagattga attaattcca 1920
 gttactgcaa ccttcgagggc agaactctgat ttgaaagag cacaaaaggc ggtgaatgag 1980
 ctgtttactt cttccaatca aatcgggtta aaaacagatg tgacggatta tcatattgat 2040

caagtatcca atttagttga gtgtttatct gatgaatfff gtctggatga aaaaaaagaa 2100
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 cgctacaatg ccaaacacga aacagtaaat gtgccaggta cgggttcctt atggccgctt 2460
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 acgcaagatg gccatgcaag actaggaaat ctagaatttc tcgaagagaa accattagta 2640
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 gtaaactctc aatatgatag attacaagcg gataccaaca tcgcatgat tcatgcggca 2820
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 gtcaatgcgg ctattttga agaattagaa gggcgtattt tactgcatt ctccctatat 2940
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 aaagggcatg tagatgtaga agaacaaaac aaccaccgtt cggtccttgt tgtccggaa 3060
 tgggaagcag aagtgtcaca agaagttcgt gtctgtccgg gtcgtggcta taccctcgt 3120
 gtcacagcgt acaaggagg atatggagaa ggttgcgtaa ccattcatga gatcgagaac 3180
 aatacagacg aactgaagt tagcaactgt gtagaagagg aagtatatcc aaacaacacg 3240
 gtaacgtgta atgattatac tgcgactcaa gaagaatatg agggtagta cacttctcgt 3300
 aatcgaggat atgacggagc ctatgaaagc aattcttctg taccagctga ttatgcatca 3360
 gcctatgaag aaaaagcata tacagatgga cgaagagaca atccttgtga atctaacaga 3420
 ggatatgggg attacacacc actaccagct ggctatgtga caaaagaatt agagtacttc 3480
 ccagaaaccg ataaggtatg gattgagatc ggagaaacgg aaggaacatt catcgtggac 3540
 agcgtggaat tacttcttat ggaggaatag 3570

<210> 111

<211> 1189
<212> PRT
<213> Artificial

<220>

<223> Amino acid sequence of the chimeric protein TIC847.

<400> 111

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
420	425	430
Phe	Asn	Phe
Ile	Asn	Pro
Gln	Asn	Ile
Tyr	Glu	Arg
Gly		
Ala	Thr	Thr
435	440	445
Tyr	Ser	Gln
Pro	Tyr	Gln
Gly	Val	Gly
Ile	Gln	Leu
Phe		
Asp	Ser	Glu
450	455	460
Thr	Glu	Leu
Pro	Pro	Glu
Thr	Thr	Glu
Arg	Pro	Asn
Tyr		
Glu	Ser	Tyr
465	470	475
Ser	His	Arg
Leu	Ser	His
Ile	Gly	Leu
Ile	Ile	Gly
Asn		
Thr	Leu	Arg
485	490	495
Ala	Pro	Val
Tyr	Ser	Trp
Thr	His	Arg
Ser	Ala	Asp
Arg		
Thr	Asn	Thr
500	505	510
Ile	Gly	Pro
Asn	Arg	Ile
Thr	Gln	Ile
Pro	Leu	Val
Lys		
Ala	His	Thr
515	520	525
Leu	Gln	Ser
Gly	Thr	Thr
Val	Val	Lys
Gly	Pro	Gly
Phe		
Thr	Gly	Gly
530	535	540
Asp	Ile	Leu
Arg	Arg	Thr
Ser	Gly	Gly
Pro	Phe	Ala
Phe		
Ser	Asn	Val
545	550	555
Asn	Leu	Asp
Phe	Asn	Leu
Ser	Gln	Arg
Tyr	Arg	Ala
Arg		
Ile	Arg	Tyr
565	570	575
Ala	Ser	Thr
Thr	Thr	Asn
Leu	Arg	Ile
Tyr	Val	Thr
Val	Ala	
Gly	Glu	Arg
580	585	590
Ile	Phe	Ala
Gly	Gln	Phe
Asp	Lys	Thr
Met	Asp	Ala
Gly		
Ala	Pro	Leu
595	600	605
Thr	Phe	Gln
Ser	Phe	Ser
Tyr	Ala	Thr
Ile	Asn	Thr
Ala		
Phe	Thr	Phe
610	615	620
Pro	Glu	Arg
Ser	Ser	Ser
Leu	Thr	Val
Gly	Ala	Asp
Thr		

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

Val Thr Ala Thr Phe Glu Ala Glu Ser Asp Leu Glu Arg Ala Gln Lys
 645 650 655

Ala Val Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr
 660 665 670

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gln Asn Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala
1010 1015 1020

Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile
1025 1030 1035

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

Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser
1055 1060 1065

Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys
 1070 1075 1080

Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr
 1085 1090 1095

Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser
 1100 1105 1110

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

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

Asp Tyr Thr Pro Leu Pro Ala 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> 112

<211> 3588

<212> DNA

<213> Artificial

<220>

<223> Synthetic DNA sequence for expression in plants encoding TIC713.

<400> 112

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gtggaggtgc taggtggcga gcgcatcgaa acgggttaca cgccgattga catctccctg 120

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gttgacatca tctgggggat cttcgggtccc tccaatggg atgcgttct ggtgcagatc 240

gagcagctta tcaaccagcg gatcgaagag ttcgctagga accaggccat cagccgcctc 300
gaagggtctca gcaacctcta tcaaattctac gctgagtcct tccgcgagtg ggaggcggaac 360
cccaccaacc ctgccctccg cgaggaaatg cgtatccaat tcaatgacat gaacagcgcc 420
ctgaccacgg cgatcccgt gctggccgtc cagaactacc aggtccccct gctcagcgtc 480
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cattgtgagt atgatcgagg gtatgtaaat tatccaccag ttccagccgg gtatgtcaca 3480
aaggaactag aatactttcc agaaacagat acagtatgga tagagatcgg agaaacagaa 3540

ggaaagtca tagtggaactc agtagaacta ttactgatgg aagaatga 3588

<210> 113

<211> 3588

<212> DNA

<213> Artificial

<220>

<223> Synthetic DNA sequence for expression in plants encoding TIC713.

<400> 113

atggataaca acccaaacat caacgaatgc attccgtaca actgcctgag caaccctgag 60
gtggagggtgc taggtggcga gcgcatcgaa acgggttaca cgccgattga catctccctg 120
tccctcacc agttctcct tagcgagttc gtgccgggcg cggtttcgt gctgggcctc 180
gttgacatca tctgggggat ctcgggtccc tccaatggg atgcgttct ggtgcagatc 240
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gaagggtcga gcaacctcta tcaaactac gctgagtcct tccgagagtg ggaggcggac 360
cccaccaacc ctgccctccg cgaggaaatg cgtatccaat tcaatgacat gaacagcgcc 420
ctgaccacgg cgatcccgt gctggccgtc cagaactacc aggtccccct gctcagcgtc 480
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 tcagttaatt acaagccaac atacgaagaa gaaacataca cagatgttcg acgagataat 3420
 cattgtgagt atgatcgagg gtatgtaaat tatccaccag ttccagccgg gtatgtcaca 3480
 aaggaactag aatactttcc agaaacagat acagtatgga tagagatcgg agaaacagaa 3540
 ggaaagttca tagtggactc agtagaacta ttactgatgg aagaatag 3588

<210> 114

<211> 3531

<212> DNA

<213> Artificial

<220>

<223> Synthetic DNA sequence for expression in plants encoding TIC843.

<400> 114

atggataaca acccaaacat caacgaatgc attccgtaca actgcctgag caaccctgag 60
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 gttgacatca tctgggggat ctcgggtccc tccaatggg atgcgttctt ggtgcagatc 240
 gagcagctta tcaaccagcg gatcgaagag ttcgctagga accaggccat cagccgcctc 300
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 ctgaccacgg cgatcccgt gctggccgtc cagaactacc aggtccccct gctcagcgtc 480
 tacgtccagg ccgctaacct ccacctcagc gtgctgcgcg acgtctccgt ctcggccag 540
 aggtgggggt tcgacgcggc gacgatcaac agccgctaca acgacctgac ccggctgatc 600
 gggaactaca cggactacgc tgtccggtgg tacaacaccg gcctggagcg cgtgtgggga 660
 ccagactccc gtgactgggt ccggtacaac cagttccgta gggaactcac tctgacggtc 720

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 aaccctgcg agttcaaccg gggttacagg gattacacgc ctctgccgt tggctatgtc 3420
 actaaggagc tggagtattt cccggagact gataaagtct ggatcgagat cggggagact 3480
 gaagggactt tcacgtcga ttccgtggag ctgcttctga tggaggagt a 3531

<210> 115

<211> 3501

<212> DNA

<213> Artificial

<220>

<223> Synthetic DNA sequence for expression in plants encoding TIC862.

<400> 115

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3501

<210> 116

<211> 3549

<212> DNA

<213> Artificial

<220>

<223> Synthetic DNA sequence for expression in plants encoding TIC1099.

<400> 116

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gaggagtga 3549

<210> 117
<211> 3534
<212> DNA
<213> Artificial

<220>
<223> Synthetic DNA sequence for expression in plants encoding TIC1103.

<400> 117
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<210> 118

<211> 3573

<212> DNA

<213> Artificial

<220>

<223> Synthetic DNA sequence for expression in plants encoding TIC845.

<400> 118

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gtggctgagg tgaacaacat cgacccgttc gtgtccgcct ccaccgtgca gaccggcatc 180
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 gagtgggaag ctgaggtcag ccaagaagtc agggctctgcc ctggtcgcg ctacatctc 3120
 agggtgaccg cctacaagga agggatggt gaaggggtgtg tcacgatcca tgagattgag 3180
 aacaacacgg acgaactcaa gttcagcaac tgcgtcgagg aggaggtcta tccgaacaac 3240
 acggtcacct gcaacgacta cactgccact caggaggagt acgagggaac ctacactagc 3300
 cgcaaccgtg gctacgatgg agcctacgag tccaactcct ccgttcccgc tgactacgca 3360
 agcgcctacg aggagaaggc gtacacggac gggcggcgcg acaaccctg cgagtccaat 3420

cgtggctacg gtgactacac tccgctccc gctgggtacg tgaccaagga acttgagtac 3480
 ttccctgaga ccgacaaggt ctggatcgag ataggtgaga ccgaaggcac gttcatcggt 3540
 gactccgtcg aactgctgct catggaggag tga 3573

<210> 119
 <211> 3567
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic DNA sequence for expression in plants encoding TIC846.

<400> 119
 atgaccagca accggaagaa cgagaacgag atcatcaacg ccctgagcat cccgaccgtg 60
 agcaacccta gcaccagat gaacctgagc cctgacgctc gcatcgagga ctccctctgc 120
 gtggctgagg tgaacaacat cgaccggtc gtgtccgcct ccaccgtgca gaccggcatc 180
 aacatcgcg ggcgcatcct cggcgtgctc ggcggtgccct ttgcggggcca gctcgctcc 240
 ttctactcct tctcgtggg agagctgtgg ccctccggcc gcgaccgtg ggagatcttc 300
 ctggagcacg tggagcagct catccgccag caagtcaccg agaacacccg caacaccgcc 360
 atgccccgcc tggagggcct gggccgtggc taccgtcct accagcaagc cctggagacc 420
 tggctcgaca accgcaacga cgcccgctcc cgctccatca tctggagcg ctacgtcgcc 480
 ctggaactgg acatcaccac tgccatccca ctctccgca tcaggaacga ggaggtgcct 540
 ctgctgatgg tgtacgcca ggctgcgaac ctgcacctgc tgctgctgcg cgacgcaagc 600
 ctgtttggct ccgagtgggg tatggcaagc tccgacgtca accagtacta ccaggagcag 660
 atccgctaca ccgaggagta cagcaaccac tgcgtccagt ggtacaacac cggctctgaac 720
 aatctcagag ggaccaacgc tgagagctgg ctgcgtaca accagttccg gcgggatctg 780
 accctaggtg tctggatct ggtcgtctg tcccgagct acgataccag gacgtaccct 840
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 gctcctagt gtttcgccag cactaactgg ttcaacaaca acgcgctag ttctctgcc 960
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 tactctcgt cttcgcggtg gtctcgact cagcacatga actactgggt tggtcaccgg 1080
 cttacttcc gcccgattgg aggaactctt aacaccagta cgcaaggtct tacgaacaac 1140
 acttccatca acccggttac gttgcagttc acgtctcggg acgtttaccg gacggagtcg 1200

aatgctggga cgaacatcct gttcacgaca ccggtgaatg gtgttccgtg ggcacgtttc 1260
aactcatca acccgagaa catctacgag cgtggagcaa cgacatactc gcaaccatac 1320
caaggcgttg gcatccaact gtttgactcg gagacggaac tgccaccaga gacgacagaa 1380
cgtccgaatt acgagtcata ctacacaga ctatcacaca ttggactcat tatcggaaac 1440
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ggtccaacc gcatcactca gatcccgctc gtgaaggcac tgaacctgca cagcggagt 1560
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gcgccgagcc ctatcgaaa gtgtgcgcac cactccacc acttcagctt ggacatcgac 2520
gtgggttgca cggacctcaa cgaagacctg ggtgtctggg tgatctcaa gatcaagacg 2580
caagacggac acgcgagact cggcaatctg gagttcttg aggagaagcc tctggtcggc 2640
gaagctctcg ccagggtgaa gcgcgccgag aagaagtggc gcgacaagcg ggagaagctg 2700
gagtgggaga cgaacatcgt gtacaaggag gccaaggagt ccgtggacgc cctctttgtg 2760
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aagcgcgtgc actccatcag ggaggcgtat ctccctgaac tcagcgtgat tcctggcgtg 2880
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gccaggaacg tcataaaga cggagacttc aacaacgggc tgcctgctg gaacgtcaaa 3000
ggcacgttg acgtggagga gcagaacaac catcgcagcg tcctcgtcgt ccctgagtgg 3060
gaagctgagg tcagccaaga agtcagggtc tgccttggtc gcggctacat cctcagggtg 3120
accgcctaca aggaagggtg tgggaagggt tgtgtcacga tccatgagat tgagaacaac 3180
acggacgaac tcaagttcag caactgcgtc gaggaggagg tctatccgaa caacacggtc 3240
acctgaacg actacactgc cactcaggag gactacgagg gaacctacac tagccgcaac 3300
cgtggctacg atggagccta cgagtccaac tcctccgttc ccgtgacta cgcaagcgcc 3360
tacgaggaga aggcgtacac ggacggggcg cgcgacaacc cgtgcgagtc caatcgtggc 3420
tacggtgact acactccgct tcccgtggt tacgtgacca aggaactga gtacttcct 3480
gagaccgaca aggtctggat cgagataggt gagaccgaag gcacgttcac cgttgactcc 3540
gtcgaactgc tgctcatgga ggagtga 3567

<210> 120
<211> 3570
<212> DNA
<213> Artificial

<220>
<223> Synthetic DNA sequence for expression in plants encoding TIC858.

<400> 120
atgaccagca accggaagaa cgagaacgag atcatcaacg ccctgagcat cccgaccgtg 60
agcaacccta gcaccagat gaacctgagc cctgacgctc gcacgagga ctccctctgc 120
gtggctgagg tgaacaacat cgaccggtc gtgtccgcct ccaccgtgca gaccggcatc 180
aacatcgcg gccgcatcct cggcgtgctc ggctgcccct ttgcgggcca gctgcctcc 240
tttactcct tcctcgtggg agagctgtgg ccctccggcc gcgaccgtg ggagatcttc 300
ctggagcacg tggagcagct catccgccag caagtcaccg agaacacccg caacaccgcc 360
atgccccgcc tggagggcct gggccgtggc taccgtcct accagcaagc cctggagacc 420
tggctcgaca accgcaacga cgcccgctcc cgctccatca tcctggagcg ctacgtcgcc 480
ctggaactgg acatcaccac tgccatccca ctctccgca tcaggaacga ggagggtcct 540
ctgctgatgg tgtacgcca ggctgcgaac ctgcacctgc tgctgctgcg cgacgcaagc 600

ctgtttggct ccgagtgggg tatggcaagc tccgacgtca accagtacta ccaggagcag 660
 atccgctaca ccgaggagta cagcaaccac tgcgtccagt ggtacaacac cggctctgaac 720
 aatctcagag ggaccaacgc tgagagctgg ctgcgctaca accagttccg gcgggatctg 780
 accctagggtg tcttggatct ggtcgtctg ttcccgagct acgataccag gacgtaccct 840
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 gtcctagtgt gtttcgccag cactaactgg ttcaacaaca acgcgccctag tttctctgcc 960
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 aatgtctggga cgaacatcct gttcacgaca ccggtgaatg gtgttccgtg ggcacgtttc 1260
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 cgtccgaatt acgagtcata ctacacaga ctatcacaca ttggactcat tatcggaaac 1440
 aactgagag caccagtgt ccatggaca catcggtcag cagatcgtac gaacaccatc 1500
 ggtccgaacc gcatcactca gatccctatg gtcaaggctt ccgaacttc tcaaggaacc 1560
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 ggcttcggcc cgattcgtgt gacagtcaat ggtccgctga cccaacgcta tcgcataggc 1680
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 gtgactgcga ctttgaagc agagtacgat ctgagcgtg ccagaaggc agtgaatgag 1980
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 cgctacaacg cgaagcacga gactgtcaac gtgcccggca ctggcagcct gtggccgctc 2460
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 gacgtgggtt gcacggacct caacgaagac ctgggtgtct ggggtgatct caagatcaag 2580
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 gtgaccgcct acaaggaagg gtatggtgaa ggggtgtgtca cgatccatga gattgagaac 3180
 aacacggacg aactcaagtt cagcaactgc gtcgaggagg aggtctatcc gaacaacacg 3240
 gtcacctgca acgactacac tgccactcag gaggagtacg agggaaaccta cactagccgc 3300
 aaccgtggct acgatggagc ctacgagtcc aactcctccg ttcccgtga ctacgcaagc 3360
 gcctacgagg agaaggcgta cacggacggg cggcgcgaca acccgtgcga gtccaatcgt 3420
 ggctacgggt actacactcc gcttcccgtg ggttacgtga ccaaggaact tgagtacttc 3480
 cctgagaccg acaaggctg gatcgagata ggtgagaccg aaggcacgtt catcggtgac 3540
 tccgtcgaac tgctgctcat ggaggagtga 3570

<210> 121

<211> 3564

<212> DNA

<213> Artificial

<220>

<223> Synthetic DNA sequence for expression in plants encoding TIC866.

<400> 121

atgacgtcca accggaagaa cgagaacgag atcatcaacg cgctgtcaat cccggcggtg 60
tccaaccact cggcccagat gaacctgtcc acggacgcca ggatcgagga cagcctctgc 120
atcgccgagg gcaacaacat tgacccgttc gtagcgcca gcaccgtcca gaccggcatt 180
aacatcgcg gccgcacatc cggcggtctg ggcgtcccgt tcgcgggcca gatcgctca 240
ttctacagct tcttggtggg agagctgtgg ccgctgtggc gcgaccgtg ggagatcttc 300
ctggagcacg tggagcagct catcaggcag caagtcaccg agaacacacg agacaccgca 360
ttggcgcggc tccagggcct gggcaactca ttccgcgct accagcagag cctggaggac 420
tggctggaga accgagacga cgcgcgcact cgctccgtcc tgtacacgca gtacatcgcc 480
cttgagctgg acttctcaa cgcatgcca ctgttcgcca tccggaacca ggagtgccg 540
ctcctcatgg tgtacgtca ggctgccaac ctccacctgc tgctgctgcg ggacgcatcc 600
ctgttcgggt cggagttcgg cctgacctcc caggagattc agcgctacta cgagcggcaa 660
gtggagaaga caagggagta cagtgattat tgcgcccgt ggtacaacac cgggttgaac 720
aacttgcgag gcaccaacgc ggagtcattg ctccgtaca atcagttccg gcgagacctc 780
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gcgggcatta acattctgct cactactccg gtcaacgggt tcccggtggc ccgcttcaac 1260
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cgagcgccgg tgtactctg gaccacaga tcagcagacc ggaccaacac tatctgtcc 1500
gactccatca cccagatccc tctcgtgaag gctcacacc ttacagcgg gacgaccgtg 1560
gtgcgcgggc cgggcttcac cggtggcgac atctcgcgac gtactccgg cggtcattc 1620

gcatacaciaa tcgtgaacat caacggacag ctcccgagc gttaccgggc caggataaga 1680
 tacgccagca caacgaacct ccggatctac gtgaccgtgg ctggcgaacg gatctttgct 1740
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 ggctgcaccg acctaaatga ggacttgggt gtctgggtta tctcaagat caagaccag 2580
 gacgggcacg ctgctcttgg caacttggag ttctggagg agaagccgct ggtcggcgag 2640
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 gcgtacaagg agggctacgg cgaaggatgc gttaccatcc acgagattga gaacaatac 3180
 gacgagctta agtttagca ctgctggag gaggagggtg acccgaataa cacggtgacc 3240
 tgcaacgact acacggccac ccaaggaggaa tacgaaggca cctacaccag ccgaaccgt 3300

ggctacgacg gtgcctacga gagcaacagc tccgtgcccg ctgactacgc ttcggcctac 3360
 gaggagaagg cgtacactga cggcagacgc gacaaccctt gcgagagcaa cagaggctac 3420
 ggtgactaca cgccgctccc ggctggctac gtcaccaagg aactggagta cttcccggag 3480
 accgacaagg tgtgtagata gataggcgag accgagggca ctttcacgt cgtatagcgtc 3540
 gagcttcttc tgatggagga gtga 3564

<210> 122
 <211> 3525
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic DNA sequence for expression in plants encoding TIC838.

<400> 122
 atggaggaga acaaccagaa ccagtgcac cgtacaact gcctgagcaa ccctgaggag 60
 gtgtcctag acggtgagcg catctccacc ggcaactcta gcatcgacat ctccctgagc 120
 ctatgacagt tcctagttag caacttcgtg cccggcggtg gcttcctcgt gggcctcatc 180
 gacttcgtgt ggggcatcgt gggcccgtcc cagtgggacg ccttcctcgt gcagatcgag 240
 cagctcatca acgagcgcat cgccgagttc gcccgaacg ccgctatcgc caacctggag 300
 ggctcggca acaatttcaa catctacgtg gaggcggtca aggagtggga ggaagacccg 360
 aacaatcccg ccacccgcac ccgctgacg gaccgcttc gcatcctcga cggcctcctg 420
 gagcgcgaca tcccgtcctt cgccatctcc ggcttcgagg tgccgctcct gtccgtgtac 480
 gccaggccg ctaacctcca cctcgccatc ctccgcgact ccgtgatctt cggcgagcgc 540
 tggggcctca ccaatatcaa cgtgaacgag aactacaacc gcctcatccg ccacatcgac 600
 gtagtacgtg accactgcgc caacacctac aacagggggc tcaacaatct gccaagtcc 660
 acctaccagg actggatcac ctacaacagg ctgaggcgcg acctgaccct gaccgtgctg 720
 gacatcgctg cgttctccc gaactacgac aacaggcgct acccatcca gagcgtcggc 780
 cagctcacca gggagatcta caccgatccg ctcatcacct tcaacctca gctccagtcc 840
 gtcgctcagc tcctacctt caacgtcatg gagtccaacg ctatccgcac ccctcacctg 900
 ttcgatgtcc tgaacaatct taccatctt accgattggg tctccgtcgg caggaacttc 960
 tactggggcg gtcacagggg cattagcaac aggatcggcg gtggcaacat taccagccct 1020

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 ttcaaccttc ggggtgtcga ggggtgtcag ttacgactc cgcttaacag cttcacttac 1200
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 gggaacaaca tccagaacag aggctacatt gaagtccaa tccacttccc atctacgagc 1560
 acgcgctatc gcgtagagt tcgatacgca tcggttacac caatccacct gaatgttaat 1620
 tggggaaatt catcaatct ctcgaacaca gttccagcaa cagcaacatc attagacaat 1680
 ttgcaatcat cagatttcgg atacttcgaa tcggcaaacg cattcacatc gtcgttgggc 1740
 aacatcgtag gactacgcaa ctctcgggc accgccggcg tgatcattga ccgcttcgag 1800
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 cacatcgacc aagtgagtaa tctcgttacc tacctgtcgg acgagtctg cctggatgag 1980
 aagaggggaac tgtctgagaa agtgaagcac gcaaagcgcc tctcgatga gaggaacctc 2040
 ctccaggatt ccaacttcaa ggacatcaac cggcagccgg aaagaggctg gggtggtcc 2100
 accggcatta ctatccaggg cggcgacgat gtgttaagg agaactacgt cacacttca 2160
 ggcactttcg acgagtgtta cccgacgtac ctgtaccaga agattgatga gtccaagctg 2220
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 gagtttctt aggaaaagcc gctcgtaggt gaggcgctcg ccagggtaaa gcgcgcggag 2640
 aagaagtga gggataagcg tgagaaactt gaatgggaga caaacatcgt ctacaaggaa 2700

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 aacaatggcc tgagctgctg gaatgtgaag ggtcatgtgg atgtcgaaga gcagaacaat 3000
 cagcgttctg tgctcgtggt ccccgaatgg gaagctgagg ttccaaga agtgagagtg 3060
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 gagctggagt attcccgga gactgataaa gtctggatcg agatcgggga gactgaaggg 3480
 actttcatcg tcgattccgt ggagctgctt ctgatggagg agtga 3525

<210> 123

<211> 3519

<212> DNA

<213> Artificial

<220>

<223> Synthetic DNA sequence for expression in plants encoding TIC841.

<400> 123

atggaggaga acaaccagaa ccagtgcac ccgtacaact gcctgagcaa ccctgaggag 60
 gtgctcctag acggtgagcg catctccacc ggcaactcta gcatcgacat ctccctgagc 120
 ctatgacagt tctagttag caacttcgtg cccggcgggtg gcttcctcgt gggcctcatc 180
 gacttcgtgt ggggcatcgt gggcccgtcc cagtgggacg ccttcctcgt gcagatcgag 240
 cagctcatca acgagcgcat cgccgagttc gcccgcaacg ccgctatcgc caacctggag 300
 ggctcggca acaatttcaa catctacgtg gaggcgttca aggagtggga ggaagacccg 360
 aacaatcccg ccacccgcac ccgctgacg gaccgcttcc gcatcctcga cggcctcctg 420
 gagcgcgaca tcccgtcctt cgccatctcc ggcttcgagg tgccgctcct gtccgtgtac 480

gccagggcg ctaacctcca cctcgccatc ctccgcgact cctgatctt cggcgagcgc 540
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 gagtacgctg accactgcgc caacacctac aacagggggcc tcaacaatct gcccaggtcc 660
 acctaccagg actggatcac ctacaacagg ctgaggcgcg acctgaccct gaccgtgctg 720
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 cagctcacca gggagatcta caccgatccg ctcatcacct tcaacctca gtcacgtcc 840
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 ttcgatgtcc tgaacaatct taccatctt accgattggt tctccgctgg caggaacttc 960
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 atcaccatcc agggcggtga cgatgtgtt aaggagaact acgtgaccct ctccggcacc 2160

ttcgacgagt gctacccgac ctacctctac cagaagatcg acgagtccaa gctcaaggcg 2220
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 tcggtccttg tcgttccga gtgggaggcc gaggtctcgc aagaggccg ggtctgccct 3060
 gggcgcgggg acattcttcg tgtactgcg tacaaggagg gctacggcga gggctgcgtt 3120
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 gagatctacc cgaacaatac ggttacgtgc aatgattaca cggtaacca ggaggaatac 3240
 ggcggagcat acacctcacg taatagaggg tacaatgagg caccgtcagt tccggcagat 3300
 tatgcctcag ttatgagga gaagtcctac acggatggaa gacgcgagaa tccatgtgag 3360
 ttaatagag gataccgaga ctacacacca ctcccagttg gatacgttac aaaggagttg 3420
 gaatacttc cagaaacaga taaagtttg atagagatcg gagaaacaga aggaaccttc 3480
 atcgtggaca gtgtagaact gctgctgatg gaagaatga 3519

<210> 124

<211> 3516

<212> DNA

<213> Artificial

<220>

<223> Synthetic DNA sequence for expression in plants encoding TIC842.

<400> 124

atggctgaga acaacatcca gaaccagtgc gtgccctaca actgcctgaa caaccctgag 60
gtggagatcc tgaacgagga gcgtagcacc ggtaggctcc cgctagacat ctccctgagc 120
ctgacccgct tcctccttag cgagttcgtg cccggcgtgg gcgtggcctt cggcctcttc 180
gacctcatct ggggcttcat cacgccgtcc gactgggtccc tcttctcct ccagatcgag 240
cagctcatcg agcagcgcat cgagaccctg gagcgcaacc gcgccatcac cactctgcgc 300
ggcctcgccg actcctacga aatctacatc gagggcctcc gcgagtggga ggccaacccg 360
aacaatgccc agctccgcga ggacgtgcgg attcgcttcg ccaacaccga cgatgccctc 420
atcaccgcca tcaacaactt caccctcacc tccttcgaga tccgctgct cagcgtgtac 480
gtgcaagccg ctaacctcca cctctccctc ctgcgcgacg ccgtgagctt cggccagggc 540
tggggcctcg acatcgccac cgtgaacaat cactacaacc gcctcatcaa cctcatccac 600
cgctacacca agcactgcct cgacacctac aaccagggcc tggagaacct gcgcggcacc 660
aacacccgcc agtggggccg ctcaaccag ttccgccgag acctcacct caccgtgctc 720
gacatcgtag cctgttccc taactacgac gtccgcacct acccgatcca gacctcagc 780
cagctcacga gggaaatcta cacctcagc gtgatcgagg acagcccggg gtccgccaac 840
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ttcgccgggc agttcaacaa gacgatggac actggtgacc cgctgacttt ccagtctttc 1680
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 gtgttggtcg taccagagtg ggaggcagag gttcacaag aggtgagagt ctgccaggg 3060
 cgccgctaca tcttgagagt taccgctac aaggagggat acggcgaggg atgtgtgaca 3120
 attcacgaaa tcgagaacaa cacagacgag ctaaagtctt caaactgtgt cgaggaagaa 3180
 atctacccga ataacacagt cacatgcaat gattacacag tgaaccagga agaatacgga 3240

ggagcataca catcacgcaa tagaggatac aatgaagcac caagcgttcc agcagactac 3300
 gcctcagtgt acgaggagaa gtcatacaca gacggacgaa gggagaatcc atgtgagttc 3360
 aatcgaggat accgagatta cacaccactt ccagttggat acgttaccaa ggaactcgaa 3420
 tacttcccag aaacagacaa agtgtggatc gaaatcggcg aaaccgaagg cacattcatc 3480
 gtggactcag tcgaactgct gctgatggag gagtga 3516

<210> 125
 <211> 3444
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic DNA sequence for expression in plants encoding TIC850.

<400> 125
 atggagaaca acatccagaa ccagtgcgtg ccctacaact gcctgaacaa ccctgagggt 60
 gagatcctga acgaggagcg tagcaccggt aggcctccgc tagacatctc cctgagcctg 120
 acccgcttcc tccttagtga gttcgtgccc ggcgtgggcg tggccttcgg cctcttcgac 180
 ctcatctggg gcttcatcac tcctccgac tggctcctct tcctccttca gattgagcaa 240
 ctgatcgagc agcgcatcga gacccttgag cgcaaccgcg ccatcaccac tctcagaggt 300
 ctcgccgact cctacgaaat ctacatcgag gcactccgtg agtgggagggc caaccggaac 360
 aatgcccagc tccgcgagga cgtgaggatc agattcgcca acaccgacga tgccctcatc 420
 accgcatca acaattcac cctcacctcc ttcgagatcc ctcttctgtc tgtgtacgtt 480
 caagctgcta accttcacct ttcctcctg cgcgacgccg tgagcttcgg ccagggtctg 540
 ggcctcgaca tcgccaccgt gaacaatcac tacaaccgcc tcatcaacct catccaccgc 600
 tacaccaagc actgccttga cacctacaac cagggccttg agaacctccg tggcaccaac 660
 accgcccagt gggcccgtt caaccagttc cgcagagacc tcacctcac cgtgctcgac 720
 atcgtggcac tcttccaaa ctacgacgtg cgtacctacc ctatccagac ctccagccag 780
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 aactccctct tcgtactgc cgagaccgtg cgtcccaga ccgtgtgggg cggtcacctc 960
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cagggaact tccaacgac gatgaaccgt ggtgacaacc tggagtccgg gaacttccga 1680
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 gacgaactca agttcagcaa ctgcgtcgag gaggaggtct atccgaacaa cacggtcacc 3120
 tgcaacgact aactgccac tcaggaggag tacgagggaa cctacactag ccgcaaccgt 3180
 ggctacgatg gaggctacga gtccaactcc tccgttcccg ctgactacgc aagcgcctac 3240
 gaggagaagg cgtacacgga cgggcggcgc gacaaccgt gcgagtcaa tcgtggctac 3300
 ggtgactaca ctccgcttcc cgctgggtac gtgaccaagg aacttgagta cttccctgag 3360
 accgacaagg tctggatcga gatagggtgag accgaaggca cgttcacgtg tgactccgtc 3420
 gaactgctgc tcatggagga gtga 3444

<210> 126
 <211> 3447
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic DNA sequence for expression in plants encoding TIC859.

<400> 126
 atggagaaca acatccagaa ccagtgcgtg ccctacaact gcctgaacaa ccctgaggtt 60
 gagatcctga acgaggagcg tagcaccggt aggtcccccg tagacatctc cctgagcctg 120
 acccgcttcc tccttagtga gttcgtgccc ggcgtgggcg tggccttcgg cctcttcgac 180
 ctcatctggg gttcatcac tccttcgac tggtcctct tctccttca gattgagcaa 240
 ctgatcgagc agcgcatcga gacccttgag cgcaaccgcg ccatcaccac tctcagaggt 300
 ctgcccgact cctacgaaat ctacatcgag gcactccgtg agtgggaggg caaccggaac 360
 aatgcccagc tccgcgagga cgtgaggatc agattcgcca acaccgacga tgcctcatc 420
 accgccatca acaatttcac cctcacctcc ttcgagatcc ctcttctgtc tgtgtacgtt 480
 caagctgcta acctcacct ttcctcctg cgcgacgccg tgagcttcgg ccagggctgg 540
 ggctcgaca tcgccaccgt gaacaatcac tacaaccgcc tcatcaacct catccaccgc 600

tacaccaagc actgccttga cacctacaac cagggccttg agaacctccg tggcaccaac 660
 acccgccagt gggcccgtt caaccagttc cgagagacc tcacctcac cgtgctcgac 720
 atcgtggcac tcttccaaa ctacgacgtg cgtacctacc ctatccagac ctccagccag 780
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 ccaggcgggt ccatctggat cgccgatgaa gacctcgtc ctttctaccg taccctgtcc 1080
 gacctgtgt tcgtgcgtg cggttcggc aacctcact acgtgctggg cctgcgtggc 1140
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 cacgtgctga accacgtgac ctctgtagg tggcctggcg aaatctccg ctccgactcc 1320
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 gtcgaactgc tgctcatgga ggagtga 3447

<210> 127
 <211> 3612
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic DNA sequence for expression in plants encoding TIC861.

<400> 127
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 atcagcactg actccctcaa gaacgagact gacatcgagc ttcagaacat caaccacgag 120

gactgcctca agatcagcga gtacgagaac gtggaaccct tcgtgagcgc ctccaccatc 180
cagaccggca tctccattgc cgggaagatc ctcggcaccc tcggcgtagc cttcgcgggc 240
caagtggcct cccttactc cttcatcctc ggcgaaactgt ggcccaaagg caagaaccag 300
tgggagatct tcatggagca cgtggaggag atcatcaacc agaagatcag cacctatgcc 360
cgcaacaagg ccctcaccga cctcaagggc ctcggcgacg ccctcgccgt gtaccacgag 420
tcctggagt cctgggtcgg caaccgcaag aacaccgcg cccgctccgt ggtgaagtcc 480
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gaggagggtc cgtcctgcc catctacgcc caggccgcta acctccacct cctgctcctg 600
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 ggaaagtgtg cgcaccactc ccaccactc agcttgaca tcgacgtggg ttgcacggac 2580
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 aagaacggag acttaacaa cgggctgtcc tgctggaacg tcaaaggta cgttgacgtg 3060
 gaggagcaga acaaccatcg cagcgtctc gtcgtccctg agtgggaagc tgaggtcagc 3120
 caagaagtca gggctgccc tggcgcggc tacatctca gggtgaccgc ctacaaggaa 3180
 gggatatggtg aaggggtgtg cacgatccat gagattgaga acaacacgga cgaactcaag 3240
 ttcagcaact gcgtcgagga ggaggtctat ccgaacaaca cggtcacctg caacgactac 3300
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 gcctacgagt ccaactcctc cgttcccgt gactacgcaa gcgcctacga ggagaaggcg 3420

tacacggacg ggcggcgcgga caaccctgtc gagtccaatc gtggctacgg tgactacact 3480
 ccgcttcccg ctggttacgt gaccaaggaa cttgagtact tccctgagac cgacaaggtc 3540
 tggatcgaga taggtgagac cgaaggcacg ttcacgttg actccgtcga actgctgctc 3600
 atggaggagt ga 3612

<210> 128
 <211> 3432
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic DNA sequence for expression in plants encoding TIC848.

<400> 128
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 gtgtccttag acggtgagcg catcctccct gacatcgacc cgctggaggt gagcctgagc 120
 ctctccagt tctgtctgaa caacttcgtg cccggcggtg gcttcatctc cgggctcgtg 180
 gacaagatct ggggcgcgct ccgcccgtcc gagtgggatc tcttctcgc ccagatcgag 240
 cgcctcatcg accagcgcac cgaggccacc gtgcgcgcca aggccatcac cgagctggag 300
 ggctgggccc gcaactacca aatctacgcc gaggcgttca aggagtggga gtccgacccg 360
 gacaacgagg ccgctaagtc ccgctgacg gaccgcttcc gcatcctcga cggcctcatc 420
 gaggccaaca tcccgtcctt ccgcatcatt ggcttcgagg tgccgtgct gtccgtgtac 480
 gtgaagccg ctaacctcca cctcgccctc ctgcgcgact ccgtgatctt cggcgagcgc 540
 tggggcctca ccactaagaa cgtgaacgac atctacaacc gccagatccg cgagatccac 600
 gaatactcca accactgcgt ggacacctac aacaccgagc tggagcgcct cggcttccgc 660
 tccatgccc agtggcgcac ctacaaccag ttcgcccgcg agctgaccct gaccgtcctg 720
 gacatcgtgg ccctgttccc gaactacgac agccgcctct acccgatcca gaccttctcc 780
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 gcctacgagt ccaactcctc cgttcccgtg gactacgcaa gcgcctacga ggagaaggcg 3240
 tacacggacg ggcggcgaga caaccgtgc gagtccaatc gtggctacgg tgactacact 3300
 ccgcttcccg ctggttacgt gaccaaggaa cttgagtact tccctgagac cgacaaggtc 3360
 tggatcgaga taggtgagac cgaaggcacg ttcacgttg actccgtcga actgctgctc 3420
 atggaggagt ga 3432

<210> 129
 <211> 3429
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic DNA sequence for expression in plants encoding TIC849.

<400> 129
 atggagatca acaaccagaa gcagtgcac ccgtacaact gcctgagcaa ccctgaggag 60
 gtgctcctag acgggtgagc catcctccct gacatcgacc cgctggaggt gagcctgagc 120
 ctctccagt tctgtctgaa caacttcgtg cccggcggtg gcttcatctc cgggctcgtg 180
 gacaagatct ggggcgcgct ccgcccgtcc gaggggatc tcttctcgc ccagatcgag 240
 cgcctcatcg accagcgcac cgaggccacc gtgcgcgcca aggccatcac cgagctggag 300
 ggctgggccc gcaactacca aatctacgcc gaggcgttca aggagtggga gtccgacccg 360
 gacaacgagg ccgctaagtc ccgctgacg gaccgcttc gcatcctcga cggcctcatc 420
 gaggccaaac tccgctcctt ccgcatcatt ggcttcgagg tgccgctgct gtccgtgtac 480
 gtgcaagccg ctaacctcca cctcgccctc ctgcgcgact ccgtgatctt cggcgagcgc 540
 tggggcctca ccactaagaa cgtgaacgac atctacaacc gccagatccg cgagatccac 600

gaatactcca accactgcgt ggacacctac aacaccgagc tggagcgcct cggcttccgc 660
 tccatcgccc agtggcgcat ctacaaccag ttccgccgcg agctgaccct gaccgtcctg 720
 gacatcgtgg cctgttccc gaactacgac agccgcctct acccgatcca gaccttctcc 780
 cagctcaccg gcgagatcgt gaccagcccg gtgtccgagt tctactatgg cgatcatcaac 840
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 cttcccgctg gttacgtgac caaggaactt gagtacttcc ctgagaccga caaggtctgg 3360
 atcgagatag gtgagaccga aggcacgttc atcgttgact ccgtcgaact gctgctcatg 3420
 gaggagtga 3429

<210> 130

<211> 3570

<212> DNA

<213> Artificial

<220>

<223> Synthetic DNA sequence for expression in plants encoding TIC847.

<400> 130

atgaccagca accggaagaa cgagaacgag atcatcaacg ccctgagcat cccgaccgtg 60

agcaacccta gcaccagat gaacctgagc cctgacgctc gcatcgagga ctccctctgc 120

gtggctgagg tgaacaacat cgacccgttc gtgtccgcct ccaccgtgca gaccggcatc 180
 aacatcgcg ggcgcacatcct cggcgtgctc ggcggtgcct ttgcggggcca gctcgcctcc 240
 ttctactcct tcctcgtggg agagctgtgg ccctccggcc gcgacccgtg ggagatcttc 300
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