

P34223W000_SEQ_PCT
SEQUENCE LISTING

<110> Monsanto Technology LLC
Baum, James A
Cerruti, Thomas
Flasinski, Stanislaw
Fu, Xiaoran
Howe, Arlene R
Salvador, Sara

<120> Lepidopteran-Active Cry1Da1 Amino Acid Sequence Variant Proteins

<130> P34223W000/0022270.00078

<150> US 62/064994

<151> 2014-10-16

<150> US 62/065017

<151> 2014-10-17

<160> 44

<170> PatentIn version 3.5

<210> 1

<211> 3498

<212> DNA

<213> Bacillus thuringiensis

<220>

<221> misc_feature

<222> (1)..(3498)

<223> Nucleotide sequence used for expression in a bacterial cell
encoding Cry1Da1.

<400> 1

atggaaataa ataatcaaaa ccaatgtgtg ccttacaatt gttaaagtaa tcctaaggag 60

ataatattag gcgaggaaag gctagaaaca gggaatactg tagcagacat ttcattaggg 120

cttattaatt ttctatattc taattttgta ccaggaggag gatttatagt aggtttacta 180

gaattaatat ggggatttat agggccttcg caatgggata ttttttagc tcaaattgag 240

caattgatta gtcaaagaat agaagaattt gctaggaatc aggcaatttc aagattggag 300

gggctaagca atctttataa ggtctatgtt agagcgttta gcgactggga gaaagatcct 360

P34223W000_SEQ_PCT

actaatcctg ctttaaggga agaaatgcgt atacaattta atgacatgaa tagtgctctc	420
ataacggcta ttccactttt tagagttcaa aattatgaag ttgctctttt atctgtatat	480
gttcaagccg caaacttaca tttatctatt ttaagggatg tttcagtttt cggagaaaga	540
tggggatatg atacagcgac tatcaataat cgctatagtg atctgactag ccttattcat	600
gtttatacta accatttgtgt ggatacgtat aatcagggat taaggcgttt ggaaggtcgt	660
tttcttagcg attggattgt atataatcgt ttccggagac aattgacaat ttcagtatta	720
gatattgttg cgttttttcc aaattatgat attagaacat atccaattca aacagctact	780
cagctaacga ggggaagtcta tctggattta ctttttatta atgaaaatct ttctcctgca	840
gcaagctatc caaccttttc agctgctgaa agtgctataa ttagaagtcc tcatttagta	900
gactttttta atagctttac catttataca gatagtctgg cacgttatgc atattggggga	960
gggcacttgg taaattcttt ccgcacagga accactacta atttgataag atccccctta	1020
tatggaaggg aaggaaatac agagcgcccc gtaactatta ccgcatcacc tagcgtacca	1080
atatttagaa cactttcata tattacaggc cttgacaatt caaatcctgt agctggaatc	1140
gagggagtgg aattccaaaa tactataagt agaagtatct atcgtaaaag cggccaata	1200
gattctttta gtgaattacc acctcaagat gccagcgat ctctgcaat tgggtatagt	1260
caccgtttat gccatgcaac attttttagaa cggattagtg gaccaagaat agcaggcacc	1320
gtattttctt ggacacaccg tagtgccagc cttactaacg aagtaagtcc atctagaatt	1380
acacaaattc catgggtaaa ggcgcatact cttgcatctg gtgcctccgt cattaaaggt	1440
cctggattta caggtggaga tattctgact aggaatagta tgggcgagct ggggacctta	1500
cgagtaacct tcacaggaag attaccacaa agttattata tacgtttccg ttatgcttcg	1560
gtagcaaata ggagtggtag atttagatat tcacagccac cttcgtagtg aatttcattt	1620
ccaaaaacta tggacgcagg tgaaccacta acatctcgtt cgttcgctca tacaacactc	1680
ttcactccaa taaccttttc acgagctcaa gaagaatttg atctatacat ccaatcgggt	1740
gtttatatag atcgaattga atttataccg gttactgcaa catttgaggc agaatatgat	1800

P34223W000_SEQ_PCT

ttagaaaagag cgcaaaaagg	ggtgaatgcc ctgtttacgt	ctacaaacca actagggcta	1860
aaaacagatg tgacggatta	tcatattgat caggatatcca	atctagttgc gtgtttatcg	1920
gatgaatttt gtctggatga	aaagagagaa ttgtccgaga	aagttaaaca tgcaaagcga	1980
ctcagtgatg agcgggaattt	acttcaagat ccaaacttca	gagggatcaa taggcaacca	2040
gaccgtggct ggagaggaag	tacggatatt actatccaag	gaggagatga cgtattcaaa	2100
gagaattacg ttacgctacc	gggtaccttt gatgagtgc	atccaacgta tttatatcaa	2160
aaaatagatg agtcgaaatt	aaaagcctat acccgttatc	aattaagagg gtatatcgaa	2220
gatagtcaag acttagaaat	ctatttaatt cgttacaatg	caaaacacga aatagtaa	2280
gtaccaggta caggaagttt	atggcctctt tctgtagaaa	atcaaattgg accttgtgga	2340
gaaccgaatc gatgcgcgcc	acaccttgaa tggaatcctg	atttactg ttcctgcaga	2400
gacggggaaa aatgtgcaca	tcattctcat catttctctt	tggacattga tgttggatgt	2460
acagacttaa atgaggactt	aggtgtatgg gtgatattca	agattaagac gcaagatggc	2520
cacgcacgac tagggaatct	agagtttctc gaagagaaac	cattattagg agaagcacta	2580
gctcgtgtga aaagagcgga	gaaaaaatgg agagacaaac	gcgaaacatt acaattggaa	2640
acaactatcg tttataaaga	ggcaaaaagaa tctgtagatg	ctttatttgt aaactctcaa	2700
tatgatagat tacaagcgga	tacgaacatc gcgatgattc	atgcggcaga taaacgcgtt	2760
catagaattc gagaagcgta	tctgccggag ctgtctgtga	ttccgggtgt caatgcggct	2820
atttttgaag aattagaaga	gcgtattttc actgcatttt	ccctatatga tgcgagaaat	2880
attattaaaa atggcgattt	caataatggc ttattatgct	ggaacgtgaa agggcatgta	2940
gaggtagaag aacaaaacaa	tcaccgttca gtcctggtta	tcccagaatg ggaggcagaa	3000
gtgtcacaag aggttcgtgt	ctgtccaggc cgtggctata	tccttcgtgt tacagcgtac	3060
aaagagggat atggagaagg	ttgcgtaacg atccatgaga	tcgagaacaa tacagacgaa	3120
ctgaaattca acaactgtgt	agaagaggaa gtatatccaa	acaacacggc aacgtgtatt	3180
aattatactg cgactcaaga	agaatatgag ggtacgtaca	cttctcgtaa tcgaggatat	3240

P34223W000_SEQ_PCT

gacgaagcct atggtaataa cccttccgta ccagctgatt atgcgtcagt ctatgaagaa 3300
 aaatcgtata cagatagacg aagagagaat ccttgtgaat ctaacagagg atatggagat 3360
 tacacaccac taccagctgg ttatgtaaca aaggaattag agtacttccc agagaccgat 3420
 aaggatatgga ttgagattgg agaaacagaa ggaacattca tcgtggacag cgtggaatta 3480
 ctccttatgg aggaatag 3498

<210> 2
 <211> 1165
 <212> PRT
 <213> Bacillus thuringiensis

<220>
 <221> MISC_FEATURE
 <222> (1)..(1165)
 <223> Amino acid sequence of the protein Cry1Da1.

<400> 2

Met Glu Ile Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu Ser
 1 5 10 15

Asn Pro Lys Glu Ile Ile Leu Gly Glu Glu Arg Leu Glu Thr Gly Asn
 20 25 30

Thr Val Ala Asp Ile Ser Leu Gly Leu Ile Asn Phe Leu Tyr Ser Asn
 35 40 45

Phe Val Pro Gly Gly Gly Phe Ile Val Gly Leu Leu Glu Leu Ile Trp
 50 55 60

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

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

P34223W000_SEQ_PCT

Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Lys Val Tyr Val Arg Ala
100 105 110

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

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

Pro Leu Phe Arg Val Gln Asn Tyr Glu Val Ala Leu Leu Ser Val Tyr
145 150 155 160

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

Phe Gly Glu Arg Trp Gly Tyr Asp Thr Ala Thr Ile Asn Asn Arg Tyr
180 185 190

Ser Asp Leu Thr Ser Leu Ile His Val Tyr Thr Asn His Cys Val Asp
195 200 205

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

Trp Ile Val Tyr Asn Arg Phe Arg Arg Gln Leu Thr Ile Ser Val Leu
225 230 235 240

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

Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro Phe
260 265 270

Ile Asn Glu Asn Leu Ser Pro Ala Ala Ser Tyr Pro Thr Phe Ser Ala
275 280 285

P34223W000_SEQ_PCT

Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu Asn
290 295 300

Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Tyr Ala Tyr Trp Gly
305 310 315 320

Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu Ile
325 330 335

Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val Thr
340 345 350

Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr Ile
355 360 365

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

Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro Ile
385 390 395 400

Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro Ala
405 410 415

Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg Ile
420 425 430

Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg Ser
435 440 445

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

Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys Gly
465 470 475 480

P34223W000_SEQ_PCT

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

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

Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr Phe
515 520 525

Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr Met
530 535 540

Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr Leu
545 550 555 560

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

Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Thr
580 585 590

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

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

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

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

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

P34223W000_SEQ_PCT

Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr
675 680 685

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
690 695 700

Thr Leu Pro Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
705 710 715 720

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
725 730 735

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
740 745 750

Asn Ala Lys His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp
755 760 765

Pro Leu Ser Val Glu Asn Gln Ile Gly Pro Cys Gly Glu Pro Asn Arg
770 775 780

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu His Cys Ser Cys Arg
785 790 795 800

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
805 810 815

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
820 825 830

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
835 840 845

Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys
850 855 860

P34223W000_SEQ_PCT

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Thr Leu Gln Leu Glu
865 870 875 880

Thr Thr Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
885 890 895

Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met
900 905 910

Ile His Ala Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu
915 920 925

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

Leu Glu Glu Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
945 950 955 960

Ile Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn Val
965 970 975

Lys Gly His Val Glu Val Glu Glu Gln Asn Asn His Arg Ser Val Leu
980 985 990

Val Ile Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys
995 1000 1005

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

Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr
1025 1030 1035

Asp Glu Leu Lys Phe Asn Asn Cys Val Glu Glu Glu Val Tyr Pro
1040 1045 1050

P34223W000_SEQ_PCT

Asn Asn Thr Val Thr Cys Ile Asn Tyr Thr Ala Thr Gln Glu Glu
1055 1060 1065

Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Glu Ala
1070 1075 1080

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

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

Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
1115 1120 1125

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

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

Glu Leu Leu Leu Met Glu Glu
1160 1165

<210> 3
<211> 3498
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence used for expression in a bacterial cell
encoding Cry1Da1_3.

<400> 3
atggaaataa ataatcaaaa ccaatgtgtg ccttacaatt gttaaagtaa tcctaaggag 60
ataatattag gcgaggaaag gctagaaaca gggaatactg tagcagacat ttcattaggg 120
cttattaatt ttctatattc taattttgta ccaggaggag gatttatagt aggtttacta 180

P34223W000_SEQ_PCT

gaattaatat ggggatttat agggccttcg caatgggata tttttttagc tcaaattgag	240
caattgatta gtcaaagaat agaagaatth gctaggaatc aggcaatttc aagattggag	300
gggctaagca atctttataa ggtctatgth agagcgttha gcgactggga gaaagatcct	360
actaatcctg ctttaaggga agaaatgcgt atacaattta atgacatgaa tagtgctctc	420
ataacggcta ttccactttt tagagttcaa aattatgaag ttgctctttt atctgtatat	480
gttcaagccg caaacttaca tttatctatt ttaagggatg tttcagtttt cggagaaaga	540
tggggatatg atacagcgac tatcaataat cgctatagtg atctgactag cttattcat	600
gtttatacta accattgtgt ggatacgtat aatcagggat taaggcgttt ggaaggctgt	660
tttcttagcg attggattgt atataatcgt ttccggagac aattgacaat ttcagtatta	720
gatattgttg cgttttttcc aaattatgat attagaacat atccaattca aacagctact	780
cagctaacga gggaagtcta tctggattta ctttttatta atgaaaatct ttctcctgca	840
gcaagctatc caaccttttc agctgctgaa agtgctataa ttagaagtcc tcatttagta	900
gactttttta atagctttac catttataca gatagtctgg cacgtagtgc atattgggga	960
gggcacttgg taaattcttt ccgcacagga accactacta atttgataag atcccctta	1020
tatggaaggg aaggaaatac agagcgcccc gtaactatta ccgcatcacc tagcgtacca	1080
atatttagaa cactttcata tattacaggc cttgacaatt caaatcctgt agctggaatc	1140
gagggagtgg aattccaaaa tactataagt agaagtatct atcgtaaaag cggccaata	1200
gattctttta gtgaattacc acctcaagat gccagcgtat ctctgcaat tgggtatagt	1260
caccgtttat gccatgcaac attttttagaa cggatttagtg gaccaagaat agcaggcacc	1320
gtatttttctt ggacacaccg tagtgccagc cctactaacg aagtaagtcc atctagaatt	1380
acacaaattc catgggtaaa ggcgcatact cttgcatctg gtgcctccgt cattaaaggt	1440
cctggattta caggtggaga tattctgact aggaatagta tgggcgagct ggggacctta	1500
cgagtaacct tcacaggaag attaccacaa agttattata tacgtttccg ttatgcttcg	1560
gtagcaaata ggagtgggtac atttagatat tcacagccac cttcgatatg aatttcattt	1620

P34223W000_SEQ_PCT

ccaaaaacta tggacgcagg tgaaccacta acatctcggt cggttcgctca tacaacactc	1680
ttcactccaa taaccttttc acgagctcaa gaagaatttg atctatacat ccaatcgggt	1740
gtttatatag atcgaattga atttataccg gttactgcaa catttgaggc agaatatgat	1800
ttagaaagag cgcaaaaggt ggtgaatgcc ctgtttacgt ctacaaacca actagggcta	1860
aaaacagatg tgacggatta tcatattgat caggatatcca atctagttgc gtgtttatcg	1920
gatgaatttt gtctggatga aaagagagaa ttgtccgaga aagttaaaca tgcaaagcga	1980
ctcagtgatg agcgggaattt acttcaagat ccaaacttca gagggatcaa taggcaacca	2040
gaccgtggct ggagaggaag tacggatatt actatccaag gaggagatga cgtattcaaa	2100
gagaattacg ttacgctacc gggtagcttt gatgagtgct atccaacgta tttatatcaa	2160
aaaatagatg agtcgaaatt aaaagcctat acccgttatc aattaagagg gtatatcgaa	2220
gatagtcaag acttagaaat ctatttaatt cgttacaatg caaaacacga aatagtaa	2280
gtaccaggta caggaagttt atggcctctt tctgtagaaa atcaaattgg accttggtga	2340
gaaccgaatc gatgcgcgcc acaccttgaa tggaatcctg atttacactg ttcctgcaga	2400
gacggggaaa aatgtgcaca tcattctcat ctttctctt tggacattga tgttgatgt	2460
acagacttaa atgaggactt aggtgtatgg gtgatattca agattaagac gcaagatggc	2520
cacgcacgac tagggaatct agagtttctc gaagagaaac cattattagg agaagcacta	2580
gctcgtgtga aaagagcgga gaaaaaatgg agagacaaac gcgaaacatt acaattggaa	2640
acaactatcg tttataaaga ggcaaaagaa tctgtagatg ctttatttgt aaactctcaa	2700
tatgatagat tacaagcgga tacgaacatc gcgatgattc atgcggcaga taaacgcgtt	2760
catagaattc gagaagcgta tctgccggag ctgtctgtga ttccgggtgt caatgcggct	2820
atttttgaag aattagaaga gcgtattttc actgcatttt ccctatatga tgcgagaaat	2880
attattaaaa atggcgattt caataatggc ttattatgct ggaacgtgaa agggcatgta	2940
gaggtagaag aacaaaacaa tcaccgttca gtcctgggta tcccagaatg ggaggcagaa	3000
gtgtcacaag aggttcgtgt ctgtccaggt cgtggctata tccttcgtgt tacagcgta	3060

P34223W000_SEQ_PCT

```

aaagagggat atggagaagg ttgcgtaacg atccatgaga tcgagaacaa tacagacgaa      3120
ctgaaattca acaactgtgt agaagaggaa gtatatccaa acaacacggg aacgtgtatt      3180
aattatactg cgactcaaga agaatatgag ggtacgtaca cttctcgtaa tcgaggatat      3240
gacgaagcct atggtaataa cccctccgta ccagctgatt atgcgtcagt ctatgaagaa      3300
aaatcgtata cagatagacg aagagagaat ccttgtgaat ctaacagagg atatggagat      3360
tacacaccac taccagctgg ttatgtaaca aaggaattag agtacttccc agagaccgat      3420
aaggatatga ttgagattgg agaaacagaa ggaacattca tcgtggacag cgtggaatta      3480
ctccttatgg aggaatag                                          3498

```

<210> 4
 <211> 1165
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of the engineered insecticidal protein
 Cry1Da1_3.

<400> 4

Met Glu Ile Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu Ser
 1 5 10 15

Asn Pro Lys Glu Ile Ile Leu Gly Glu Glu Arg Leu Glu Thr Gly Asn
 20 25 30

Thr Val Ala Asp Ile Ser Leu Gly Leu Ile Asn Phe Leu Tyr Ser Asn
 35 40 45

Phe Val Pro Gly Gly Gly Phe Ile Val Gly Leu Leu Glu Leu Ile Trp
 50 55 60

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

P34223W000_SEQ_PCT

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

Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Lys Val Tyr Val Arg Ala
100 105 110

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

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

Pro Leu Phe Arg Val Gln Asn Tyr Glu Val Ala Leu Leu Ser Val Tyr
145 150 155 160

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

Phe Gly Glu Arg Trp Gly Tyr Asp Thr Ala Thr Ile Asn Asn Arg Tyr
180 185 190

Ser Asp Leu Thr Ser Leu Ile His Val Tyr Thr Asn His Cys Val Asp
195 200 205

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

Trp Ile Val Tyr Asn Arg Phe Arg Arg Gln Leu Thr Ile Ser Val Leu
225 230 235 240

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

Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro Phe
260 265 270

P34223W000_SEQ_PCT

Ile Asn Glu Asn Leu Ser Pro Ala Ala Ser Tyr Pro Thr Phe Ser Ala
275 280 285

Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu Asn
290 295 300

Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Ser Ala Tyr Trp Gly
305 310 315 320

Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu Ile
325 330 335

Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val Thr
340 345 350

Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr Ile
355 360 365

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

Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro Ile
385 390 395 400

Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro Ala
405 410 415

Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg Ile
420 425 430

Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg Ser
435 440 445

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

P34223W000_SEQ_PCT

Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys Gly
465 470 475 480

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

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

Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr Phe
515 520 525

Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr Met
530 535 540

Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr Leu
545 550 555 560

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

Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Thr
580 585 590

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

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

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

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

P34223W000_SEQ_PCT

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

Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr
675 680 685

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
690 695 700

Thr Leu Pro Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
705 710 715 720

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
725 730 735

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
740 745 750

Asn Ala Lys His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp
755 760 765

Pro Leu Ser Val Glu Asn Gln Ile Gly Pro Cys Gly Glu Pro Asn Arg
770 775 780

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu His Cys Ser Cys Arg
785 790 795 800

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
805 810 815

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
820 825 830

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
835 840 845

P34223W000_SEQ_PCT

Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys
850 855 860

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Thr Leu Gln Leu Glu
865 870 875 880

Thr Thr Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
885 890 895

Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met
900 905 910

Ile His Ala Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu
915 920 925

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

Leu Glu Glu Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
945 950 955 960

Ile Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn Val
965 970 975

Lys Gly His Val Glu Val Glu Glu Gln Asn Asn His Arg Ser Val Leu
980 985 990

Val Ile Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys
995 1000 1005

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

Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr
1025 1030 1035

P34223W000_SEQ_PCT

Asp Glu Leu Lys Phe Asn Asn Cys Val Glu Glu Glu Val Tyr Pro
1040 1045 1050

Asn Asn Thr Val Thr Cys Ile Asn Tyr Thr Ala Thr Gln Glu Glu
1055 1060 1065

Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Glu Ala
1070 1075 1080

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

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

Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
1115 1120 1125

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

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

Glu Leu Leu Leu Met Glu Glu
1160 1165

<210> 5

<211> 3498

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence used for expression in a bacterial cell
encoding Cry1Da1_4.

<400> 5

atggaaataa ataatacaaaa ccaatgtgtg ccttacaatt gttaaagtaa tcctaaggag

60

P34223W000_SEQ_PCT

ataatattag gcgaggaaag gctagaaaca gggaatactg tagcagacat ttcattaggg	120
cttattaatt ttctatattc taattttgta ccaggaggag gatttatagt aggtttacta	180
gaattaatat ggggatttat agggccttcg caatgggata tttttttagc tcaaattgag	240
caattgatta gtcaaagaat agaagaattt gctaggaatc aggcaatttc aagattggag	300
gggctaagca atctttataa ggtctatgtt agagcgttta gcgactggga gaaagatcct	360
actaatcctg ctttaaggga agaaatgcgt atacaattta atgacatgaa tagtgctctc	420
ataacggcta ttccactttt tagagttcaa aattatgaag ttgctctttt atctgtatat	480
gttcaagccg caaacttaca tttatctatt ttaagggatg tttcagtttt cggagaaaga	540
tggggatatg atacagcgac tatcaataat cgctatagtg atctgactag ccttattcat	600
gtttatacta accattgtgt ggatacgtat aatcagggat taaggcgttt ggaaggtcgt	660
tttcttagcg attggattgt atataatcgt ttccggagac aattgacaat ttcagtatta	720
gatattgttg cgttttttcc aaattatgat attagaacat atccaattca aacagctact	780
cagctaacga gggaagtcta tctggattta ctttttatta atgaaaatct ttctcctgca	840
gcaagctatc caaccttttc agctgctgaa agtgctataa ttagaagtcc tcatttagta	900
gactttttta atagctttac catttataca gatagtctgg cacgttatgc atattgggga	960
gggcacttgg taaattcttt ccgcacagga accactacta atttgataag atccccctta	1020
tatggaaggg aaggaaatac agagcgcccc gtaactatta ccgcatcacc tagcgtacca	1080
atatttagaa cactttcata tattacaggc cttgacaatc gtaatcctgt agctggaatc	1140
gagggagtgg aattccaaaa tactataagt agaagtatct atcgtaaaaag cggccaata	1200
gattctttta gtgaattacc acctcaagat gccagcgtat ctctgcaat tgggtatagt	1260
caccgtttat gccatgcaac attttttagaa cggatttagtg gaccaagaat agcaggcacc	1320
gtattttctt ggacacaccg tagtgccagc cctactaacg aagtaagtcc atctagaatt	1380
acacaaattc catgggtaaa ggcgcatact cttgcatctg gtgcctccgt cattaaaggt	1440
cctggattta caggtggaga tattctgact aggaatagta tgggcgagct ggggacctta	1500

P34223W000_SEQ_PCT

cgagtaacct tcacaggaag attaccacaa agttattata tacgtttccg ttatgcttcg	1560
gtagcaaata ggagtgggtac atttagatat tcacagccac cttcgtatgg aatttcattt	1620
ccaaaaacta tggacgcagg tgaaccacta acatctcggt cgttcgctca tacaacactc	1680
ttcactccaa taaccttttc acgagctcaa gaagaatttg atctatacat ccaatcgggt	1740
gtttatatag atcgaattga atttataccg gttactgcaa catttgaggc agaatatgat	1800
ttagaaagag cgcaaaagggt ggtgaatgcc ctgtttacgt ctacaaacca actagggcta	1860
aaaacagatg tgacggatta tcatattgat caggatatca atctagttgc gtgtttatcg	1920
gatgaatttt gtctggatga aaagagagaa ttgtccgaga aagttaaaca tgcaaaagcga	1980
ctcagtgatg agcgggaattt acttcaagat ccaaacttca gagggatcaa taggcaacca	2040
gaccgtggct ggagaggaag tacggatatt actatccaag gaggagatga cgtattcaaa	2100
gagaattacg ttacgctacc gggtagcttt gatgagtgt atccaacgta tttatatcaa	2160
aaaatagatg agtcgaaatt aaaagcctat acccgttatc aattaagagg gtatatcgaa	2220
gatagtcaag acttagaaat ctatttaatt cgttacaatg caaaacacga aatagtaa	2280
gtaccaggta caggaagttt atggcctctt tctgtagaaa atcaaattgg accttggtga	2340
gaaccgaatc gatgcgcgcc acaccttgaa tggaatcctg atttacctg ttcctgcaga	2400
gacggggaaa aatgtgcaca tcattctcat catttctctt tggacattga tgttggtgt	2460
acagacttaa atgaggactt aggtgtatgg gtgatattca agattaagac gcaagatggc	2520
cacgcacgac tagggaatct agagtttctc gaagagaaac cattattagg agaagcacta	2580
gctcgtgtga aaagagcgga gaaaaaatgg agagacaaac gcgaaacatt acaattggaa	2640
acaactatcg tttataaaga ggcaaaagaa tctgtagatg ctttatttgt aaactctcaa	2700
tatgatagat tacaagcgga tacgaacatc gcgatgattc atgcggcaga taaacgcgtt	2760
catagaattc gagaagcgta tctgccggag ctgtctgtga ttccgggtgt caatgcggct	2820
atttttgaag aattagaaga gcgtattttc actgcatttt ccctatatga tgcgagaaat	2880
attattaaaa atggcgattt caataatggc ttattatgct ggaacgtgaa agggcatgta	2940

P34223W000_SEQ_PCT

gaggtagaag aacaaaaaca tcaccgttca gtcctgggta tcccagaatg ggaggcagaa 3000
 gtgtcacaag aggttcgtgt ctgtccagggt cgtgggtata tccttcgtgt tacagcgtag 3060
 aaagagggat atggagaagg ttgcgtaacg atccatgaga tcgagaacaa tacagacgaa 3120
 ctgaaattca acaactgtgt agaagaggaa gtatatccaa acaacacggg aacgtgtatt 3180
 aattatactg cgactcaaga agaatatgag ggtacgtaca cttctcgtaa tcgaggatat 3240
 gacgaagcct atggtaataa cccttccgta ccagctgatt atgcgtcagt ctatgaagaa 3300
 aaatcgtata cagatagacg aagagagaat ctttgtgaat ctaacagagg atatggagat 3360
 tacacaccac taccagctgg ttatgtaaca aaggaattag agtacttccc agagaccgat 3420
 aaggtatgga ttgagattgg agaaacagaa ggaacattca tcgtggacag cgtggaatta 3480
 ctccttatgg aggaatag 3498

<210> 6
 <211> 1165
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of the engineered insecticidal protein
 Cry1Da1_4.

<400> 6

Met Glu Ile Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu Ser
 1 5 10 15

Asn Pro Lys Glu Ile Ile Leu Gly Glu Glu Arg Leu Glu Thr Gly Asn
 20 25 30

Thr Val Ala Asp Ile Ser Leu Gly Leu Ile Asn Phe Leu Tyr Ser Asn
 35 40 45

Phe Val Pro Gly Gly Gly Phe Ile Val Gly Leu Leu Glu Leu Ile Trp
 50 55 60

P34223W000_SEQ_PCT

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

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

Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Lys Val Tyr Val Arg Ala
100 105 110

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

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

Pro Leu Phe Arg Val Gln Asn Tyr Glu Val Ala Leu Leu Ser Val Tyr
145 150 155 160

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

Phe Gly Glu Arg Trp Gly Tyr Asp Thr Ala Thr Ile Asn Asn Arg Tyr
180 185 190

Ser Asp Leu Thr Ser Leu Ile His Val Tyr Thr Asn His Cys Val Asp
195 200 205

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

Trp Ile Val Tyr Asn Arg Phe Arg Arg Gln Leu Thr Ile Ser Val Leu
225 230 235 240

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

P34223W000_SEQ_PCT

Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro Phe
260 265 270

Ile Asn Glu Asn Leu Ser Pro Ala Ala Ser Tyr Pro Thr Phe Ser Ala
275 280 285

Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu Asn
290 295 300

Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Tyr Ala Tyr Trp Gly
305 310 315 320

Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu Ile
325 330 335

Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val Thr
340 345 350

Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr Ile
355 360 365

Thr Gly Leu Asp Asn Arg Asn Pro Val Ala Gly Ile Glu Gly Val Glu
370 375 380

Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro Ile
385 390 395 400

Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro Ala
405 410 415

Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg Ile
420 425 430

Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg Ser
435 440 445

P34223W000_SEQ_PCT

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

Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys Gly
465 470 475 480

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

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

Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr Phe
515 520 525

Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr Met
530 535 540

Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr Leu
545 550 555 560

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

Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Thr
580 585 590

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

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

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

P34223W000_SEQ_PCT

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

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

Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr
675 680 685

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
690 695 700

Thr Leu Pro Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
705 710 715 720

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
725 730 735

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
740 745 750

Asn Ala Lys His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp
755 760 765

Pro Leu Ser Val Glu Asn Gln Ile Gly Pro Cys Gly Glu Pro Asn Arg
770 775 780

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu His Cys Ser Cys Arg
785 790 795 800

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
805 810 815

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
820 825 830

P34223W000_SEQ_PCT

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
835 840 845

Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys
850 855 860

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Thr Leu Gln Leu Glu
865 870 875 880

Thr Thr Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
885 890 895

Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met
900 905 910

Ile His Ala Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu
915 920 925

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

Leu Glu Glu Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
945 950 955 960

Ile Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn Val
965 970 975

Lys Gly His Val Glu Val Glu Glu Gln Asn Asn His Arg Ser Val Leu
980 985 990

Val Ile Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys
995 1000 1005

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

P34223W000_SEQ_PCT

Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr
1025 1030 1035

Asp Glu Leu Lys Phe Asn Asn Cys Val Glu Glu Glu Val Tyr Pro
1040 1045 1050

Asn Asn Thr Val Thr Cys Ile Asn Tyr Thr Ala Thr Gln Glu Glu
1055 1060 1065

Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Glu Ala
1070 1075 1080

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

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

Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
1115 1120 1125

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

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

Glu Leu Leu Leu Met Glu Glu
1160 1165

<210> 7

<211> 3498

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence used for expression in a bacterial cell

P34223W000_SEQ_PCT

encoding Cry1Da1_5.

<400> 7

atggaaataa ataatcaaaa ccaatgtgtg ccttacaatt gtttaagtaa tcctaaggag	60
ataatattag gcgaggaaag gctagaaaca gggaatactg tagcagacat ttcattaggg	120
cttattaatt ttctatattc taattttgta ccaggaggag gatttatagt aggtttacta	180
gaattaatat ggggatttat agggccttcg caatgggata tttttttagc tcaaattgag	240
caattgatta gtcaaagaat agaagaattt gctaggaatc aggcaatttc aagattggag	300
gggctaagca atctttataa ggtctatgtt agagcgttta gcgactggga gaaagatcct	360
actaatcctg ctttaaggga agaaatgcgt atacaattta atgacatgaa tagtgctctc	420
ataacggcta ttccactttt tagagttcaa aattatgaag ttgctctttt atctgtatat	480
gttcaagccg caaacttaca tttatctatt ttaagggatg tttcagtttt cggagaaaga	540
tggggatatg atacagcgac tatcaataat cgctatagtg atctgactag ccttattcat	600
gtttatacta accatttgtgt ggatacgtat aatcagggat taaggcgttt ggaaggctgt	660
tttcttagcg attggattgt atataatcgt ttccggagac aattgacaat ttcagtatta	720
gatattgttg cgttttttcc aaattatgat attagaacat atccaattca aacagctact	780
cagctaacga ggggaagtcta tctggattta ctttttatta atgaaaatct ttctcctgca	840
gcaagctatc caaccttttc agctgctgaa agtgctataa ttagaagtcc tcatttagta	900
gactttttta atagctttac catttataca gatagtctgg cacgttctgc atattgggga	960
gggcacttgg taaattcttt ccgcacagga accactacta atttgataag atccccitta	1020
tatggaaggg aaggaaatac agagcgcccc gtaactatta ccgcatcacc tagcgtacca	1080
atatttagaa cactttcata tagaacaggc cttgacaatt caaatcctgt agctggaatc	1140
gaggagtggt aattccaaaa tactataagt agaagtatct atcgtaaaag cggccaata	1200
gattctttta gtgaattacc acctcaagat gccagcgtat ctctgcaat tgggtatagt	1260
caccgtttat gccatgcaac attttttagaa cggattagtg gaccaagaat agcaggcacc	1320
gtattttctt ggacacaccg tagtgccagc cttactaacg aagtaagtcc atctagaatt	1380

P34223W000_SEQ_PCT

acacaaaattc catgggtaaa ggcgcatact cttgcatctg gtgcctccgt cattaaaggt	1440
cctggatttta caggtggaga tattctgact aggaatagta tgggcgagct ggggacctta	1500
cgagtaacct tcacaggaag attaccacaa agttattata tacgtttccg ttatgcttcg	1560
gtagcaaaata ggagtggtag atttagatat tcacagccac cttcgtatgg aatttcattt	1620
ccaaaaacta tggacgcagg tgaaccacta acatctcggt cgttcgctca tacaacactc	1680
ttcactccaa taaccttttc acgagctcaa gaagaatttg atctatacat ccaatcgggt	1740
gtttatatag atcgaattga atttataccg gttactgcaa catttgaggc agaatatgat	1800
ttagaaaagag cgcaaaaggt ggtgaatgcc ctgtttacgt ctacaaacca actagggcta	1860
aaaacagatg tgacggatta tcatattgat caggatatcca atctagttgc gtgtttatcg	1920
gatgaatttt gtctggatga aaagagagaa ttgtccgaga aagttaaaca tgcaaagcga	1980
ctcagtgatg agcggaattt acttcaagat ccaaacttca gagggatcaa taggcaacca	2040
gaccgtggct ggagaggaag tacggatatt actatccaag gaggagatga cgtattcaaa	2100
gagaattacg ttacgctacc gggtagcttt gatgagtgc atccaacgta tttatatcaa	2160
aaaatagatg agtcgaaatt aaaagcctat acccgttatc aattaagagg gtatatcgaa	2220
gatagtcaag acttagaaat ctatttaatt cgttacaatg caaaacacga aatagtaa	2280
gtaccaggta caggaagttt atggcctctt tctgtagaaa atcaaattgg accttgatga	2340
gaaccgaatc gatgcgcgcc acaccttgaa tggaatcctg atttacctg ttcctgcaga	2400
gacggggaaa aatgtgcaca tcattctcat catttctctt tggacattga tgttgatgt	2460
acagacttaa atgaggactt aggtgtatgg gtgatattca agattaagac gcaagatggc	2520
cacgcacgac tagggaatct agagtttctc gaagagaaac cattattagg agaagcacta	2580
gctcgtgtga aaagagcgga gaaaaaatgg agagacaaac gcgaaacatt acaattggaa	2640
acaactatcg tttataaaga ggcaaaaagaa tctgtagatg ctttatttgt aaactctcaa	2700
tatgatagat tacaagcgga tacgaacatc gcgatgattc atgcggcaga taaacgcgtt	2760
catagaattc gagaagcgta tctgccggag ctgtctgtga ttccgggtgt caatgcggct	2820

P34223W000_SEQ_PCT

```

atTTTTgaag aattagaaga gcgtatTTTt actgcatttt ccctatatga tgcgagaaat      2880
attattaaaa atggcgattt caataatggc ttattatgct ggaacgtgaa agggcatgta      2940
gaggtagaag aacaaaacaa tcaccgttca gtcctgggta tcccagaatg ggaggcagaa      3000
gtgtcacaag aggttcgtgt ctgtccaggt cgtggctata tccttcgtgt tacagcgtac      3060
aaagagggat atggagaagg ttgcgtaacg atccatgaga tcgagaacaa tacagacgaa      3120
ctgaaattca acaactgtgt agaagaggaa gtatatccaa acaacacggg aacgtgtatt      3180
aattatactg cgactcaaga agaatatgag ggtacgtaca cttctcgtaa tcgaggatat      3240
gacgaagcct atggtaataa cccttccgta ccagctgatt atgcgtcagt ctatgaagaa      3300
aaatcgtata cagatagacg aagagagaat ccttgtgaat ctaacagagg atatggagat      3360
tacacaccac taccagctgg ttatgtaaca aaggaattag agtacttccc agagaccgat      3420
aaggtatgga ttgagattgg agaaacagaa ggaacattca tcgtggacag cgtggaatta      3480
ctccttatgg aggaatag                                     3498

```

<210> 8
 <211> 1165
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of the engineered insecticidal protein
 Cry1Da1_5.

<400> 8

```

Met Glu Ile Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu Ser
1           5           10          15

```

```

Asn Pro Lys Glu Ile Ile Leu Gly Glu Glu Arg Leu Glu Thr Gly Asn
20           25           30

```

```

Thr Val Ala Asp Ile Ser Leu Gly Leu Ile Asn Phe Leu Tyr Ser Asn
35           40           45

```

P34223W000_SEQ_PCT

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

P34223W000_SEQ_PCT

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

Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro Phe
260 265 270

Ile Asn Glu Asn Leu Ser Pro Ala Ala Ser Tyr Pro Thr Phe Ser Ala
275 280 285

Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu Asn
290 295 300

Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Ser Ala Tyr Trp Gly
305 310 315 320

Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu Ile
325 330 335

Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val Thr
340 345 350

Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr Arg
355 360 365

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

Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro Ile
385 390 395 400

Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro Ala
405 410 415

Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg Ile
420 425 430

P34223W000_SEQ_PCT

Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg Ser
435 440 445

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

Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys Gly
465 470 475 480

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

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

Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr Phe
515 520 525

Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr Met
530 535 540

Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr Leu
545 550 555 560

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

Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Thr
580 585 590

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

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

P34223W000_SEQ_PCT

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

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

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

Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr
675 680 685

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
690 695 700

Thr Leu Pro Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
705 710 715 720

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
725 730 735

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
740 745 750

Asn Ala Lys His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp
755 760 765

Pro Leu Ser Val Glu Asn Gln Ile Gly Pro Cys Gly Glu Pro Asn Arg
770 775 780

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu His Cys Ser Cys Arg
785 790 795 800

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
805 810 815

P34223W000_SEQ_PCT

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
820 825 830

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
835 840 845

Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys
850 855 860

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Thr Leu Gln Leu Glu
865 870 875 880

Thr Thr Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
885 890 895

Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met
900 905 910

Ile His Ala Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu
915 920 925

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

Leu Glu Glu Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
945 950 955 960

Ile Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn Val
965 970 975

Lys Gly His Val Glu Val Glu Glu Gln Asn Asn His Arg Ser Val Leu
980 985 990

Val Ile Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys
995 1000 1005

P34223W000_SEQ_PCT

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

Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr
1025 1030 1035

Asp Glu Leu Lys Phe Asn Asn Cys Val Glu Glu Glu Val Tyr Pro
1040 1045 1050

Asn Asn Thr Val Thr Cys Ile Asn Tyr Thr Ala Thr Gln Glu Glu
1055 1060 1065

Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Glu Ala
1070 1075 1080

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

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

Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
1115 1120 1125

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

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

Glu Leu Leu Leu Met Glu Glu
1160 1165

<210> 9
<211> 3498
<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence used for expression in a bacterial cell encoding Cry1Da1_6.

<400> 9

atggaaataa ataatcaaaa ccaatgtgtg ccttacaatt gtttaagtaa tcctaaggag	60
ataatattag gcgaggaaaag gctagaaaca gggaatactg tagcagacat ttcattaggg	120
cttattaatt ttctatattc taattttgta ccaggaggag gatttatagt aggtttacta	180
gaattaatat ggggatttat agggccttcg caatgggata ttttttagc tcaaattgag	240
caattgatta gtcaaagaat agaagaattt gctaggaatc aggcaatttc aagattggag	300
gggctaagca atctttataa ggtctatgtt agagcgttta gcgactggga gaaagatcct	360
actaatcctg ctttaaggga agaaatgcgt atacaattta atgacatgaa tagtgctctc	420
ataacggcta ttccactttt tagagttcaa aattatgaag ttgctctttt atctgtatat	480
gttcaagccg caaacttaca tttatctatt ttaagggatg tttcagtttt cggagaaaaga	540
tggggatatg atacagcgac tatcaataat cgctatagtg atctgactag ccttattcat	600
gtttatacta accattgtgt ggatacgtat aatcagggat taaggcgttt ggaaggctgt	660
tttcttagcg attggattgt atataatcgt ttccggagac aattgacaat ttcagtatta	720
gatattgttg cgttttttcc aaattatgat attagaacat atccaattca aacagctact	780
cagctaacga ggggaagtcta tctggattta ctttttatta atgaaaatct ttctcctgca	840
gcaaaaatc caaccttttc agctgctgaa agtgctataa ttagaagtcc tcatttagta	900
gactttttta atagctttac catttataca gatagtctgg cacgttctgc atattgggga	960
gggcacttgg taaattcttt ccgcacagga accactacta atttgataag atccccctta	1020
tatggaaggg aaggaaatac agagcgcccc gtaactatta ccgcatcacc tagcgtacca	1080
atatttagaa cactttcata tccaacaggc cttgacaatt caaatcctgt agctggaatc	1140
gagggagtgg aattccaaaa tactataagt agaagtatct atcgtaaaag cgggtccaata	1200
gattctttta gtgaattacc acctcaagat gccagcgtat ctctgcaat tgggtatagt	1260

P34223W000_SEQ_PCT

caccgtttat gccatgcaac attttttagaa cggattagtg gaccaagaat agcaggcacc	1320
gtatttttcctt ggacacaccg tagtgccagc cctactaacg aagtaagtcc atctagaatt	1380
acacaaattc catgggtaaa ggcgcatact cttgcatctg gtgcctccgt cattaaaggt	1440
cctggattta caggtggaga tattctgact aggaatagta tgggcgagct ggggacctta	1500
cgagtaacct tcacaggaag attaccacaa agttattata tacgtttccg ttatgcttcg	1560
gtagcaaata ggagtggtag atttagatat tcacagccac cttcgtagtg aatttcattt	1620
ccaaaaacta tggacgcagg tgaaccacta acatctcggt cgttcgctca tacaacactc	1680
ttcactccaa taaccttttc acgagctcaa gaagaatttg atctatacat ccaatcgggt	1740
gtttatatag atcgaattga atttataccg gttactgcaa catttgaggc agaatatgat	1800
ttagaaagag cgcaaaaggt ggtgaatgcc ctgtttacgt ctacaaacca actagggcta	1860
aaaacagatg tgacggatta tcatattgat caggatatcca atctagttgc gtgtttatcg	1920
gatgaatttt gtctggatga aaagagagaa ttgtccgaga aagttaaaca tgcaaagcga	1980
ctcagtgatg agcgggaattt acttcaagat ccaaacttca gagggatcaa taggcaacca	2040
gaccgtggct ggagaggaag tacggatatt actatccaag gagggatga cgtattcaaa	2100
gagaattacg ttacgctacc gggtagcttt gatgagtgt atccaacgta tttatatcaa	2160
aaaatagatg agtcgaaatt aaaagcctat acccgttatc aattaagagg gtatatcgaa	2220
gatagtcaag acttagaaat ctatttaatt cgttacaatg caaaacacga aatagtaa	2280
gtaccaggta caggaagttt atggcctctt tctgtagaaa atcaaattgg accttggtga	2340
gaaccgaatc gatgcgcgcc acaccttgaa tggaatcctg atttacactg ttcctgcaga	2400
gacggggaaa aatgtgcaca tcattctcat catttctctt tggacattga tgttggatgt	2460
acagacttaa atgaggactt aggtgtatgg gtgatattca agattaagac gcaagatggc	2520
cacgcacgac tagggaatct agagtttctc gaagagaaac cattattagg agaagcacta	2580
gctcgtgtga aaagagcgga gaaaaaatgg agagacaaac gcgaaacatt acaattggaa	2640
acaactatcg tttataaaga ggcaaaagaa tctgtagatg ctttatttgt aaactctcaa	2700

P34223W000_SEQ_PCT

tatgatagat tacaagcgga tacgaacatc gcgatgattc atgcggcaga taaacgcgtt	2760
catagaattc gagaagcgta tctgccggag ctgtctgtga ttccgggtgt caatgcggct	2820
atttttgaag aattagaaga gcgtattttc actgcatttt ccctatatga tgcgagaaat	2880
attattaaaa atggcgattt caataatggc ttattatgct ggaacgtgaa agggcatgta	2940
gaggtagaag aacaaaaaca tcaccgttca gtcctgggta tcccagaatg ggaggcagaa	3000
gtgtcacaag aggttcgtgt ctgtccaggc cgtggctata tccttcgtgt tacagcgtac	3060
aaagagggat atggagaagg ttgcgtaacg atccatgaga tcgagaacaa tacagacgaa	3120
ctgaaattca acaactgtgt agaagaggaa gtatatccaa acaacacggc aacgtgtatt	3180
aattatactg cgactcaaga agaatatgag ggtacgtaca cttctcgtaa tcgaggatat	3240
gacgaagcct atggtaataa cccttccgta ccagctgatt atgcgtcagt ctatgaagaa	3300
aaatcgtata cagatagacg aagagagaat ccttgtgaat ctaacagagg atatggagat	3360
tacacaccac taccagctgg ttatgtaaca aaggaattag agtacttccc agagaccgat	3420
aaggtatgga ttgagattgg agaaacagaa ggaacattca tcgtggacag cgtggaatta	3480
ctccttatgg aggaatag	3498

<210> 10

<211> 1165

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of the engineered insecticidal protein Cry1Da1_6.

<400> 10

Met	Glu	Ile	Asn	Asn	Gln	Asn	Gln	Cys	Val	Pro	Tyr	Asn	Cys	Leu	Ser
1				5				10						15	

Asn	Pro	Lys	Glu	Ile	Ile	Leu	Gly	Glu	Glu	Arg	Leu	Glu	Thr	Gly	Asn
			20					25					30		

P34223W000_SEQ_PCT

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

P34223W000_SEQ_PCT

Trp Ile Val Tyr Asn Arg Phe Arg Arg Gln Leu Thr Ile Ser Val Leu
225 230 235 240

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

Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro Phe
260 265 270

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

Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu Asn
290 295 300

Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Ser Ala Tyr Trp Gly
305 310 315 320

Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu Ile
325 330 335

Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val Thr
340 345 350

Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr Pro
355 360 365

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

Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro Ile
385 390 395 400

Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro Ala
405 410 415

P34223W000_SEQ_PCT

Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg Ile
420 425 430

Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg Ser
435 440 445

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

Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys Gly
465 470 475 480

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

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

Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr Phe
515 520 525

Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr Met
530 535 540

Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr Leu
545 550 555 560

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

Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Thr
580 585 590

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

P34223W000_SEQ_PCT

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

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

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

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

Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr
675 680 685

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
690 695 700

Thr Leu Pro Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
705 710 715 720

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
725 730 735

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
740 745 750

Asn Ala Lys His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp
755 760 765

Pro Leu Ser Val Glu Asn Gln Ile Gly Pro Cys Gly Glu Pro Asn Arg
770 775 780

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu His Cys Ser Cys Arg
785 790 795 800

P34223W000_SEQ_PCT

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
805 810 815

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
820 825 830

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
835 840 845

Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys
850 855 860

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Thr Leu Gln Leu Glu
865 870 875 880

Thr Thr Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
885 890 895

Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met
900 905 910

Ile His Ala Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu
915 920 925

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

Leu Glu Glu Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
945 950 955 960

Ile Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn Val
965 970 975

Lys Gly His Val Glu Val Glu Glu Gln Asn Asn His Arg Ser Val Leu
980 985 990

P34223W000_SEQ_PCT

Val Ile Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys
 995 1000 1005

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

Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr
 1025 1030 1035

Asp Glu Leu Lys Phe Asn Asn Cys Val Glu Glu Glu Val Tyr Pro
 1040 1045 1050

Asn Asn Thr Val Thr Cys Ile Asn Tyr Thr Ala Thr Gln Glu Glu
 1055 1060 1065

Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Glu Ala
 1070 1075 1080

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

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

Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 1115 1120 1125

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

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

Glu Leu Leu Leu Met Glu Glu
 1160 1165

P34223W000_SEQ_PCT

<210> 11
 <211> 3498
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence used for expression in a bacterial cell encoding Cry1Da1_7.

<400> 11
 atggaaataa ataatcaaaa ccaatgtgtg ccttacaatt gttaaagtaa tcctaaggag 60
 ataatatag gcgaggaaag gctagaaaca gggaatactg tagcagacat ttcattaggg 120
 cttattaatt ttctatattc taattttgta ccaggaggag gatttatagt aggtttacta 180
 gaattaatat ggggatttat agggccttcg caatgggata tttttttagc tcaaattgag 240
 caattgatta gtcaaagaat agaagaattt gctaggaatc aggcaatttc aagattggag 300
 gggctaagca atctttataa ggtctatgtt agagcgttta gcgactggga gaaagatcct 360
 actaatcctg ctttaaggga agaaatgcgt atacaattta atgacatgaa tagtgctctc 420
 ataacggcta ttccactttt tagagttcaa aattatgaag ttgctctttt atctgtatat 480
 gttcaagccg caaacttaca tttatctatt ttaagggatg tttcagtttt cggagaaaga 540
 tggggatatg atacagcgac tatcaataat cgctatagtg atctgactag cttattcat 600
 gtttatacta accattgtgt ggatacgtat aatcagggat taaggcgttt ggaaggctcg 660
 tttcttagcg attggattgt atataatcgt ttccggagac aattgacaat ttcagtatta 720
 gatattgttg cgttttttcc aaattatgat attagaacat atccaattca aacagctact 780
 cagctaacga gggaagtcta tctggattta ctttttatta atgaaaatct ttctcctgca 840
 gcagtatatc caaccttttc agctgctgaa agtgctataa ttagaagtcc tcatttagta 900
 gactttttaa atagctttac catttataca gatagtctgg cacgttctgc atattgggga 960
 gggcacttgg taaattcttt ccgcacagga accactacta atttgataag atccccitta 1020
 tatggaaggg aaggaaatac agagcgcccc gtaactatta ccgcatcacc tagcgtagca 1080
 atatttagaa cactttcata tccaacaggc cttgacaatt caaatcctgt agctggaatc 1140

P34223W000_SEQ_PCT

gagggagtgg aattccaaaa tactataagt agaagtatct atcgtaaaag cggccaata	1200
gattctttta gtgaattacc acctcaagat gccagcgtat ctcctgcaat tgggtatagt	1260
caccgtttat gccatgcaac attttttagaa cggattagtg gaccaagaat agcaggcacc	1320
gtattttctt ggacacaccg tagtgccagc cctactaacg aagtaagtcc atctagaatt	1380
acacaaattc catgggtaaa ggcgcatact cttgcatctg gtgcctccgt cattaaaggt	1440
cctggattta caggtggaga tattctgact aggaatagta tgggcgagct ggggacctta	1500
cgagtaacct tcacaggaag attaccacaa agttattata tacgtttccg ttatgcttcg	1560
gtagcaaata ggagtggtag atttagatat tcacagccac cttcgtatgg aatttcattt	1620
ccaaaaacta tggacgcagg tgaaccacta acatctcggt cggtcgctca tacaacactc	1680
ttcactccaa taaccttttc acgagctcaa gaagaatttg atctatacat ccaatcgggt	1740
gtttatatag atcgaattga atttataccg gttactgcaa catttgaggc agaatatgat	1800
ttagaaaagag cgcaaaaggt ggtgaatgcc ctgtttacgt ctacaaacca actagggcta	1860
aaaacagatg tgacggatta tcatattgat caggtatcca atctagttgc gtgtttatcg	1920
gatgaatttt gtctggatga aaagagagaa ttgtccgaga aagttaaaca tgcaaagcga	1980
ctcagtgatg agcgggaattt acttcaagat ccaaacttca gagggatcaa taggcaacca	2040
gaccgtggct ggagaggaag tacggatatt actatccaag gagggatga cgtattcaaa	2100
gagaattacg ttacgctacc gggtagcttt gatgagtgc atccaacgta tttatatcaa	2160
aaaatagatg agtcgaaatt aaaagcctat acccgttatc aattaagagg gtatatcgaa	2220
gatagtcaag acttagaaat ctatttaatt cgttacaatg caaaacacga aatagtaa	2280
gtaccaggta caggaagttt atggcctctt tctgtagaaa atcaaattgg accttgatga	2340
gaaccgaatc gatgcgcgcc acaccttgaa tggaatcctg atttacactg ttcctgcaga	2400
gacggggaaa aatgtgcaca tcattctcat catttctctt tggacattga tgttgatgt	2460
acagacttaa atgaggactt aggtgtatgg gtgatattca agattaagac gcaagatggc	2520
cacgcacgac tagggaatct agagtttctc gaagagaaac cattattagg agaagcacta	2580

P34223W000_SEQ_PCT

gctcgtgtga aaagagcggg gaaaaaatgg agagacaaac gcgaaacatt acaattggaa	2640
acaactatcg tttataaaga ggcaaaagaa tctgtagatg ctttatttgt aaactctcaa	2700
tatgatatagat tacaagcggg tacgaacatc gcgatgattc atgcggcaga taaacgcggt	2760
catagaattc gagaagcgta tctgccggag ctgtctgtga ttccgggtgt caatgcggct	2820
atTTTTgaag aattagaaga gcgtatTTTt actgcatttt ccctatatga tgcgagaaat	2880
attattaaaa atggcgattt caataatggc ttattatgct ggaacgtgaa agggcatgta	2940
gaggtagaag aacaaaacaa tcaccgttca gtcctgggta tcccagaatg ggaggcagaa	3000
gtgtcacaag aggttcgtgt ctgtccagggt cgtggctata tccttcgtgt tacagcgta	3060
aaagaggggat atggagaagg ttgcgtaacg atccatgaga tcgagaacaa tacagacgaa	3120
ctgaaattca acaactgtgt agaagaggaa gtatatccaa acaacacggg aacgtgtatt	3180
aattatactg cgactcaaga agaatatgag ggtacgtaca cttctcgtaa tcgaggatat	3240
gacgaagcct atggtaataa ccttccgta ccagctgatt atgcgtcagt ctatgaagaa	3300
aaatcgtata cagatagacg aagagagaat ctttgtgaat ctaacagagg atatggagat	3360
tacacaccac taccagctgg ttatgtaaca aaggaattag agtacttccc agagaccgat	3420
aaggatatgga ttgagattgg agaaacagaa ggaacattca tcgtggacag cgtggaatta	3480
ctccttatgg aggaatag	3498

<210> 12
 <211> 1165
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Amino acid sequence of the engineered insecticidal protein
 Cry1Da1_7.

<400> 12

Met	Glu	Ile	Asn	Asn	Gln	Asn	Gln	Cys	Val	Pro	Tyr	Asn	Cys	Leu	Ser
1				5					10					15	

P34223W000_SEQ_PCT

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

P34223W000_SEQ_PCT

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

Trp Ile Val Tyr Asn Arg Phe Arg Arg Gln Leu Thr Ile Ser Val Leu
225 230 235 240

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

Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro Phe
260 265 270

Ile Asn Glu Asn Leu Ser Pro Ala Ala Val Tyr Pro Thr Phe Ser Ala
275 280 285

Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu Asn
290 295 300

Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Ser Ala Tyr Trp Gly
305 310 315 320

Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu Ile
325 330 335

Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val Thr
340 345 350

Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr Pro
355 360 365

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

Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro Ile
385 390 395 400

P34223W000_SEQ_PCT

Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro Ala
405 410 415

Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg Ile
420 425 430

Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg Ser
435 440 445

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

Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys Gly
465 470 475 480

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

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

Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr Phe
515 520 525

Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr Met
530 535 540

Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr Leu
545 550 555 560

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

Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Thr
580 585 590

P34223W000_SEQ_PCT

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

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

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

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

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

Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr
675 680 685

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
690 695 700

Thr Leu Pro Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
705 710 715 720

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
725 730 735

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
740 745 750

Asn Ala Lys His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp
755 760 765

Pro Leu Ser Val Glu Asn Gln Ile Gly Pro Cys Gly Glu Pro Asn Arg
770 775 780

P34223W000_SEQ_PCT

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu His Cys Ser Cys Arg
785 790 795 800

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
805 810 815

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
820 825 830

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
835 840 845

Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys
850 855 860

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Thr Leu Gln Leu Glu
865 870 875 880

Thr Thr Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
885 890 895

Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met
900 905 910

Ile His Ala Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu
915 920 925

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

Leu Glu Glu Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
945 950 955 960

Ile Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn Val
965 970 975

P34223W000_SEQ_PCT

Lys Gly His Val Glu Val Glu Glu Gln Asn Asn His Arg Ser Val Leu
 980 985 990

Val Ile Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys
 995 1000 1005

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

Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr
 1025 1030 1035

Asp Glu Leu Lys Phe Asn Asn Cys Val Glu Glu Glu Val Tyr Pro
 1040 1045 1050

Asn Asn Thr Val Thr Cys Ile Asn Tyr Thr Ala Thr Gln Glu Glu
 1055 1060 1065

Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Glu Ala
 1070 1075 1080

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

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

Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 1115 1120 1125

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

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

P34223W000_SEQ_PCT

Glu Leu Leu Leu Met Glu Glu
1160 1165

<210> 13
<211> 3420
<212> DNA
<213> Artificial sequence

<220>
<223> Nucleotide sequence used for expression in a bacterial cell encoding TIC844.

<400> 13
atggagatca acaaccagaa ccagtgcgtc ccgtacaact gcctgagcaa ccctaaggag 60
atcatcctgg gtgaggaacg cctggagacc ggcaacaccg tagccgacat tagcctgggc 120
ctcatcaact tcctctacag caacttcgtg cccggcggtg gcttcatcgt gggcctcctg 180
gagcttatct ggggcttcat cggcccgctc cagtgggaca tcttcctcgc ccagatcgag 240
caactgatca gccagcggat cgaggagttc gctaggaacc aggccatctc ccgcctggag 300
ggactctcca acctctacaa ggtgtacgtg cgcgcggttca gcgactggga gaaggacccg 360
accaaccggg ccctccgca ggaaatgcgt atccagttca acgatatgaa ctcggccctc 420
atcaccgcca tcccgtctt ccgctgcag aactacgagg tggccctcct gtccgtgtac 480
gttcaagccg ccaacctcca cctctccatc ctccgcgacg tgagcgtgtt cggcgagcgc 540
tggggctacg acaccgccac catcaacaac cgctactccg acctcacctc cctcatccac 600
gtttacacca accactgcgt ggacacgtac aaccagggcc tccgccgctt ggagggccgc 660
ttcctctccg actggatcgt gtacaaccgc ttccgccgcc agctcaccat ctccgtcctg 720
gacatcgtcg ctttctttcc caactacgac atccgcacct accctatcca gaccgccacc 780
cagctcacc gcgagggtcta cctcgacctc ccgttcatca acgagaacct cagcccggcc 840
gccagctacc cgaccttctc cgccgtgag tccgccatca ttgcagccc gcacctcgtg 900
gacttcctca actccttcac catctacacc gactccctcg cccgctacgc ctactggggc 960
ggtcacctcg tgaactcctt ccgcaccggc accactacca acctcatccg cagcccgtc 1020

P34223W000_SEQ_PCT

tacggccg	cg	agggaacac	cgagcgcccc	gtgaccatca	ccgccagccc	gagcgtgccc	1080
atcttccg	ca	ccctcagcta	catcaccggc	ctggacaaca	gcaaccctgt	ggcgggcatc	1140
gagggcgt	gg	agttccagaa	caccatctcc	aggagcatct	accgcaagag	cggccctatc	1200
gacagctt	ca	gcgagctgcc	tcctcaggac	gccagcgtga	gccctgccat	cggctacagc	1260
cacaggct	gt	gccacgccac	cttcctggag	cgcatcagcg	gccctcgcat	cgcgggcacc	1320
gtgttctc	gt	ggacccaccg	cagcgctctt	cctacgaacg	aggtgtctcc	tagtcgcatc	1380
accagatcc	cttgggtcaa	ggccccacacc	ctggctagt	gcgctagtgt	catcaagggc		1440
cctggctt	ca	ccggtgggtga	catcctgacc	aggaactcta	tgggcgagct	gggcactctg	1500
agggtcact	tt	tcactggccg	cctgcctcag	tcttactaca	tccgcttccg	ctacgctagt	1560
gtcgctaacc	gctctggtac	tttccgctac	tctcagcctc	cgtcttacgg	tatctctttc		1620
cctaagacta	tggacgctgg	tgagcctctg	accagtagga	gcttcgctca	cactactctg		1680
ttcactccta	tcactttctc	tagggctcag	gaggagtctg	acctgtacat	ccagtctggt		1740
gtgtacatcg	acaggatcga	gttcatcccc	gtgaccgcca	cgttcgaggc	cgagtacgac		1800
cttgagcgcg	cccagaaggc	tgtcaatgag	ctcttcacgt	ccagcaatca	gatcggcctg		1860
aagaccgacg	tcactgacta	ccacatcgac	caagtctcca	acctcgtgga	gtgcctctcc		1920
gatgagttct	gcctcgacga	gaagaaggag	ctgtccgaga	aggtgaagca	tgccaagcgt		1980
ctcagcgacg	agaggaatct	cctccaggac	cccaatttcc	gcggcatcaa	caggcagctc		2040
gaccgcggct	ggcgcggcag	caccgacatc	acgatccagg	gcggcgacga	tgtgttcaag		2100
gagaactacg	tgactctcct	gggcactttc	gacgagtgt	accctaccta	cttgtaccag		2160
aagatcgatg	agtccaagct	caaggcttac	actcgctacc	agctccgcgg	ctacatcgaa		2220
gacagccaag	acctcgagat	ttacctgatc	cgctacaacg	ccaagcacga	gaccgtcaac		2280
gtgcccggta	ctggttccct	ctggccgctg	agcgcccca	gcccgatcgg	caagtgtgcc		2340
caccacagcc	accacttctc	cttgacatc	gatgtgggct	gcaccgacct	gaacgaggac		2400
ctcggagtct	gggtcatctt	caagatcaag	acccaggacg	gccacgcgcg	cctgggcaac		2460

P34223W000_SEQ_PCT

ctggagttcc tcgaggagaa gcccctggtc ggtgaggctc tggccagggt caagagggct	2520
gagaagaagt ggaggggacaa gcgcgagaag ctcgagtggg agaccaacat cgttttacaag	2580
gaggccaagg agagcgtcga cgccctgttc gtgaactccc agtacgaccg cctgcaggcc	2640
gacaccaaca tcgcatgat ccacgctgcc gacaagaggg tgcacagcat tcgagaggcc	2700
tacctgcctg agctgtccgt gatccctggg gtgaacgctg ccatctttga ggagctggag	2760
ggccgcatct ttaccgcatt ctccctgtac gacgcccga acgtgatcaa gaacggtgac	2820
ttcaacaatg gcctcagctg ctggaacgtc aaggggccacg tggacgtcga ggaacagaac	2880
aaccaccgct ccgtcctggg cgtcccagag tgggaggctg aggtctccca agaggtccgc	2940
gtctgcccag gccgcggcta cattctcagg gtcaccgctt acaaggaggg ctacggtgag	3000
ggctgtgtga ccatccacga gatcgagaac aacaccgacg agcttaagtt ctccaactgc	3060
gtggaggagg aggtgtaccc aaacaacacc gttacttgca acgactacac cgccaccag	3120
gaggagtacg agggcaccta cacttccagg aacaggggct acgatgggtgc ctacgagagc	3180
aacagcagcg ttcctgctga ctacgcttcc gcctacgagg agaaggccta cacggatggc	3240
cgcagggaca acccttgca gagcaaccgc ggctacggcg actacactcc cctgcccgcc	3300
ggctacgtta ccaaggagct ggagtacttc ccggagactg acaagggtgtg gatcgagatc	3360
ggcgagaccg agggcacctt catcgtggac agcgtggagc tgctcctgat ggaggagtag	3420

<210> 14

<211> 1139

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of the chimeric protein TIC844.

<400> 14

Met	Glu	Ile	Asn	Asn	Gln	Asn	Gln	Cys	Val	Pro	Tyr	Asn	Cys	Leu	Ser
1				5				10						15	

P34223W000_SEQ_PCT

Asn Pro Lys Glu Ile Ile Leu Gly Glu Glu Arg Leu Glu Thr Gly Asn
20 25 30

Thr Val Ala Asp Ile Ser Leu Gly Leu Ile Asn Phe Leu Tyr Ser Asn
35 40 45

Phe Val Pro Gly Gly Gly Phe Ile Val Gly Leu Leu Glu Leu Ile Trp
50 55 60

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

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

Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Lys Val Tyr Val Arg Ala
100 105 110

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

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

Pro Leu Phe Arg Val Gln Asn Tyr Glu Val Ala Leu Leu Ser Val Tyr
145 150 155 160

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

Phe Gly Glu Arg Trp Gly Tyr Asp Thr Ala Thr Ile Asn Asn Arg Tyr
180 185 190

Ser Asp Leu Thr Ser Leu Ile His Val Tyr Thr Asn His Cys Val Asp
195 200 205

P34223W000_SEQ_PCT

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

Trp Ile Val Tyr Asn Arg Phe Arg Arg Gln Leu Thr Ile Ser Val Leu
225 230 235 240

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

Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro Phe
260 265 270

Ile Asn Glu Asn Leu Ser Pro Ala Ala Ser Tyr Pro Thr Phe Ser Ala
275 280 285

Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu Asn
290 295 300

Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Tyr Ala Tyr Trp Gly
305 310 315 320

Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu Ile
325 330 335

Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val Thr
340 345 350

Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr Ile
355 360 365

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

Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro Ile
385 390 395 400

P34223W000_SEQ_PCT

Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro Ala
405 410 415

Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg Ile
420 425 430

Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg Ser
435 440 445

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

Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys Gly
465 470 475 480

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

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

Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr Phe
515 520 525

Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr Met
530 535 540

Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr Leu
545 550 555 560

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

Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Thr
580 585 590

P34223W000_SEQ_PCT

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

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val
610 615 620

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

Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys
645 650 655

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

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr
675 680 685

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
690 695 700

Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
705 710 715 720

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
725 730 735

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
740 745 750

Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
755 760 765

Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Ala His His Ser His
770 775 780

P34223W000_SEQ_PCT

His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp
785 790 795 800

Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala
805 810 815

Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu
820 825 830

Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg
835 840 845

Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu
850 855 860

Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala
865 870 875 880

Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser
885 890 895

Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn
900 905 910

Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser
915 920 925

Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly
930 935 940

Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn
945 950 955 960

Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser
965 970 975

P34223W000_SEQ_PCT

Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr
 980 985 990

Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile
 995 1000 1005

Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu
 1010 1015 1020

Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Ala
 1025 1030 1035

Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly
 1040 1045 1050

Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser Val Pro Ala Asp Tyr
 1055 1060 1065

Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr Asp Gly Arg Arg Asp
 1070 1075 1080

Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu
 1085 1090 1095

Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr
 1100 1105 1110

Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile
 1115 1120 1125

Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
 1130 1135

<210> 15
 <211> 3420
 <212> DNA
 <213> Artificial sequence

P34223W000_SEQ_PCT

<220>

<223> Nucleotide sequence used for expression in a bacterial cell encoding TIC844_2.

<400> 15

atggaaataa ataatcaaaa ccaatgtgtg ccttacaatt gttaaagtaa tcctaaggag	60
ataatattag gcgaggaaaag gctagaaaca gggaatactg tagcagacat ttcattaggg	120
cttattaatt ttctatattc taattttgta ccaggaggag gatttatagt aggtttacta	180
gaattaatat ggggatttat agggccttcg caatgggata tttttttagc tcaaattgag	240
caattgatta gtcaaagaat agaagaattt gctaggaatc aggcaatttc aagattggag	300
gggctaagca atctttataa ggtctatgtt agagcgttta gcgactggga gaaagatcct	360
actaatcctg ctttaaggga agaaatgcgt atacaattta atgacatgaa tagtgctctc	420
ataacggcta ttccactttt tagagttcaa aattatgaag ttgctctttt atctgtatat	480
gttcaagccg caaacttaca tttatctatt ttaagggatg tttcagtttt cggagaaaaga	540
tggggatatg atacagcgac tatcaataat cgctatagtg atctgactag ccttattcat	600
gtttatacta accattgtgt ggatacgtat aatcagggat taaggcgttt ggaaggctcgt	660
tttcttagcg attggattgt atataatcgt ttccggagac aattgacaat ttcagtatta	720
gatattgttg cgttttttcc aaattatgat attagaacat atccaattca aacagctact	780
cagctaacga gggaagtcta tctggattta ctttttatta atgaaaatct ttctcctgca	840
gcaagctatc caaccttttc agctgctgaa agtgctataa ttagaagtcc tcatttagta	900
gactttttta atagctttac catttataca gatagtctgg cacgttctgc atattgggga	960
gggcacttgg taaattcttt ccgcacagga accactacta atttgataag atccccttta	1020
tatggaaggg aaggaaatac agagcgcccc gtaactatta ccgcatcacc tagcgtacca	1080
atatttagaa cactttcata tattacaggc cttgacaatt cacatcctgt agctggaatc	1140
gagggagtgg aattccaaaa tactataagt agaagtatct atcgtaaaaag cgggtccaata	1200
gattctttta gtgaattacc acctcaagat gccagcgtat ctcctgcaat tgggtatagt	1260

P34223W000_SEQ_PCT

caccgtttat gccatgcaac attttttagaa cggttaagtg gaccaagaat agcaggcacc	1320
gtattttctt ggacacaccg tagtgccagc cctactaacg aagtaagtcc atctagaatt	1380
acacaaattc catgggtaaa ggcgcatact cttgcatctg gtgcctccgt cattaaaggt	1440
cctggattta caggtggaga tattctgact aggaatagta tgggcgagct ggggacctta	1500
cgagtaacct tcacaggaag attaccacaa agttattata tacgtttccg ttatgcttcg	1560
gtagcaaata ggagtggtag atttagatat tcacagccac cttcgatatg aatttcattt	1620
ccaaaaacta tggacgcagg tgaaccacta acatctcggt cgttcgctca tacaacactc	1680
ttcactccaa taaccttttc acgagctcaa gaagaatttg atctatacat ccaatcgggt	1740
gtttatatag atcgaattga atttataccg gttactgcaa catttgaggc agaatatgat	1800
ttagaaagag cacaaaaggc ggtgaatgag ctgtttactt cttccaatca aatcgggtta	1860
aaaacagatg tgacggatta tcatattgat caagtatcca atttagttga gtgtttatct	1920
gatgaatttt gtctggatga aaaaaaagaa ttgtccgaga aagtcaaaca tgcgaagcga	1980
cttagtgatg agcgggaattt acttcaagat ccaaacttta gagggatcaa tagacaacta	2040
gaccgtggct ggagaggaag tacggatatt accatccaag gaggcgatga cgtattcaaa	2100
gagaattacg ttacgctatt gggtaccttt gatgagtgt atccaacgta tttatatcaa	2160
aaaatagatg agtcgaaatt aaaagcctat acccggtacc aattaagagg gtatatcgaa	2220
gatagtcaag acttagaaat ctatttaatt cgctacaatg ccaaacacga aacagtaa	2280
gtgccaggta cgggttcctt atggccgctt tcagcccaa gtccaatcgg aaaatgtgcc	2340
catcattccc atcatttctc cttggacatt gatgttggat gtacagactt aaatgaggac	2400
ttaggtgtat gggatgatatt caagattaag acgcaagatg gccatgcaag actaggaaat	2460
ctagaatttc tcgaagagaa accattagta ggagaagcac tagctcgtgt gaaaagagcg	2520
gagaaaaaat ggagagacaa acgtgaaaaa ttggaatggg aaacaaatat tgtttataaa	2580
gaggcaaaaag aatctgtaga tgctttatct gttaaactctc aatatgatag attacaagcg	2640
gataccaaca tcgcatgat tcatgcggca gataaacgcg ttcatagcat tcgagaagct	2700

P34223W000_SEQ_PCT

tatctgcctg agctgtctgt gattccgggt gtcaatgcgg ctatTTTTga agaattagaa	2760
gggcgtatTT tCactgcatt ctccctatat gatgcgagaa atgtcattaa aaatgggtgat	2820
TTtaataatg gcttatcctg ctggaacgtg aaagggcatg tagatgtaga agaacaaaac	2880
aaccaccgtt cggtccttgt tgttccggaa tgggaagcag aagtgtcaca agaagttcgt	2940
gtctgtccgg gtcgtggcta tatccttcgt gtcacagcgt acaaggaggg atatggagaa	3000
ggttgcgtaa ccattcatga gatcgagaac aatacagacg aactgaagtt tagcaactgt	3060
gtagaagagg aagtatatcc aaacaacacg gtaacgtgta atgattatac tgcgactcaa	3120
gaagaatatg agggtagcta cacttctcgt aatcgaggat atgacggagc ctatgaaagc	3180
aattcttctg taccagctga ttatgcatca gcctatgaag aaaaagcata tacagatgga	3240
cgaagagaca atccttgtga atctaacaga ggatatgggg attacacacc actaccagct	3300
ggctatgtga caaaagaatt agagtacttc ccagaaaccg ataaggtatg gattgagatc	3360
ggagaaacgg aaggaacatt catcgtggac agcgtggaat tacttcttat ggaggaatag	3420

<210> 16

<211> 1139

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of the engineered insecticidal chimeric protein TIC844_2.

<400> 16

Met	Glu	Ile	Asn	Asn	Gln	Asn	Gln	Cys	Val	Pro	Tyr	Asn	Cys	Leu	Ser
1				5				10						15	

Asn	Pro	Lys	Glu	Ile	Ile	Leu	Gly	Glu	Glu	Arg	Leu	Glu	Thr	Gly	Asn
			20					25					30		

Thr	Val	Ala	Asp	Ile	Ser	Leu	Gly	Leu	Ile	Asn	Phe	Leu	Tyr	Ser	Asn
		35					40					45			

P34223W000_SEQ_PCT

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

P34223W000_SEQ_PCT

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

Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro Phe
260 265 270

Ile Asn Glu Asn Leu Ser Pro Ala Ala Ser Tyr Pro Thr Phe Ser Ala
275 280 285

Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu Asn
290 295 300

Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Ser Ala Tyr Trp Gly
305 310 315 320

Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu Ile
325 330 335

Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val Thr
340 345 350

Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr Ile
355 360 365

Thr Gly Leu Asp Asn Ser His Pro Val Ala Gly Ile Glu Gly Val Glu
370 375 380

Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro Ile
385 390 395 400

Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro Ala
405 410 415

Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg Leu
420 425 430

P34223W000_SEQ_PCT

Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg Ser
435 440 445

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

Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys Gly
465 470 475 480

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

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

Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr Phe
515 520 525

Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr Met
530 535 540

Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr Leu
545 550 555 560

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

Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Thr
580 585 590

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

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val
610 615 620

P34223W000_SEQ_PCT

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

Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys
645 650 655

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

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr
675 680 685

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
690 695 700

Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
705 710 715 720

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
725 730 735

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
740 745 750

Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
755 760 765

Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Ala His His Ser His
770 775 780

His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp
785 790 795 800

Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala
805 810 815

P34223W000_SEQ_PCT

Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu
820 825 830

Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg
835 840 845

Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu
850 855 860

Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala
865 870 875 880

Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser
885 890 895

Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn
900 905 910

Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser
915 920 925

Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly
930 935 940

Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn
945 950 955 960

Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser
965 970 975

Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr
980 985 990

Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile
995 1000 1005

P34223W000_SEQ_PCT

Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu
1010 1015 1020

Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Ala
1025 1030 1035

Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly
1040 1045 1050

Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser Val Pro Ala Asp Tyr
1055 1060 1065

Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr Asp Gly Arg Arg Asp
1070 1075 1080

Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu
1085 1090 1095

Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr
1100 1105 1110

Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile
1115 1120 1125

Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
1130 1135

<210> 17

<211> 3420

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleotide sequence used for expression in a bacterial cell encoding TIC844_4.

<400> 17

atggaaataa ataatcaaaa ccaatgtgtg ccttacaatt gtttaagtaa tcctaaggag

60

P34223W000_SEQ_PCT

ataatattag gcgaggaaag gctagaaaca gggaatactg tagcagacat ttcattaggg	120
cttattaatt ttctatattc taattttgta ccaggaggag gatttatagt aggtttacta	180
gaattaatat ggggatttat agggccttcg caatgggata tttttttagc tcaaattgag	240
caattgatta gtcaaagaat agaagaattt gctaggaatc aggcaatttc aagattggag	300
gggctaagca atctttataa ggtctatgtt agagcgttta gcgactggga gaaagatcct	360
actaatcctg ctttaaggga agaaatgcgt atacaattta atgacatgaa tagtgctctc	420
ataacggcta ttccactttt tagagttcaa aattatgaag ttgctctttt atctgtatat	480
gttcaagccg caaacttaca tttatctatt ttaagggatg tttcagtttt cggagaaaga	540
tggggatatg atacagcgac tatcaataat cgctatagtg atctgactag cttattcat	600
gtttatacta accattgtgt ggatacgtat aatcagggat taaggcgttt ggaaggtcgt	660
tttcttagcg attggattgt atataatcgt ttccggagac aattgacaat ttcagtatta	720
gatattgttg cgttttttcc aaattatgat attagaacat atccaattca aacagctact	780
cagctaacga gggaagtcta tctggattta ctttttatta atgaaaatct ttctcctgca	840
gcaagctatc caaccttttc agctgctgaa agtgctataa ttagaagtcc tcatttagta	900
gactttttta atagctttac catttataca gatagtctgg cacgtagtgc atattgggga	960
gggcacttgg taaattcttt ccgcacagga accactacta atttgataag atccccitta	1020
tatggaaggg aaggaaatac agagcgcccc gtaactatta ccgcatcacc tagcgtacca	1080
atatttagaa cactttcata tattacaggc cttgacaatt caaatcctgt agctggaatc	1140
gagggagtgg aattccaaaa tactataagt agaagtatct atcgtaaaag cggccaata	1200
gattctttta gtgaattacc acctcaagat gccagcgtat ctctgcaat tgggtatagt	1260
caccgtttat gccatgcaac attttttagaa cggatttagtg gaccaagaat agcaggcacc	1320
gtattttctt ggacacaccg tagtgccagc cctactaacg aagtaagtcc atctagaatt	1380
acacaaattc catgggtaaa ggcgcatact cttgcatctg gtgcctccgt cattaaaggt	1440
cctggattta caggtggaga tattctgact aggaatagta tgggcgagct ggggacctta	1500

P34223W000_SEQ_PCT

cgagtaacct tcacaggaag attaccacaa agttattata tacgtttccg ttatgcttcg	1560
gtagcaaata ggagtgggtac atttagatat tcacagccac cttcgtatgg aatttcattt	1620
ccaaaaacta tggacgcagg tgaaccacta acatctcggt cgttcgctca tacaacactc	1680
ttcactccaa taaccttttc acgagctcaa gaagaatttg atctatacat ccaatcgggt	1740
gtttatatag atcgaattga atttataccg gttactgcaa catttgaggc agaatatgat	1800
ttagaaaagag cacaaaaggc ggtgaatgag ctgtttactt cttccaatca aatcgggtta	1860
aaaacagatg tgacggatta tcatattgat caagtatcca atttagttga gtgtttatct	1920
gatgaatttt gtctggatga aaaaaaagaa ttgtccgaga aagtcaaaca tgcgaagcga	1980
cttagtgatg agcgggaattt acttcaagat ccaaacttta gagggatcaa tagacaacta	2040
gaccgtggct ggagaggaag tacggatatt accatccaag gaggcgatga cgtattcaaa	2100
gagaattacg ttacgctatt gggtagcttt gatgagtgt atccaacgta tttatatcaa	2160
aaaatagatg agtcgaaatt aaaagcctat acccggtacc aattaagagg gtatatcgaa	2220
gatagtcaag acttagaaat ctatttaatt cgctacaatg ccaaacacga aacagtaaat	2280
gtgccaggta cgggttcctt atggccgctt tcagcccca gtccaatcgg aaaatgtgcc	2340
catcattccc atcatttctc cttggacatt gatgttggat gtacagactt aaatgaggac	2400
ttaggtgtat ggggtgatatt caagattaag acgcaagatg gccatgcaag actaggaaat	2460
ctagaatttc tcgaagagaa accattagta ggagaagcac tagctcgtgt gaaaagagcg	2520
gagaaaaaat ggagagacaa acgtgaaaaa ttggaatggg aaacaaatat tgtttataaa	2580
gaggcaaaaag aatctgtaga tgctttattt gtaaaactctc aatatgatag attacaagcg	2640
gataccaaca tcgcgatgat tcatgcggca gataaacgcg ttcatagcat tcgagaagct	2700
tatctgcctg agctgtctgt gattccgggt gtcaatgcgg ctatttttga agaattagaa	2760
gggcgtattt tctactgcatt ctccctatat gatgcgagaa atgtcattaa aaatggtgat	2820
tttaataatg gcttatcctg ctggaacgtg aaagggcatg tagatgtaga agaacaaaac	2880
aaccaccgtt cggctccttgt tggtccggaa tgggaagcag aagtgtcaca agaagttcgt	2940

P34223W000_SEQ_PCT

gtctgtccgg gtcgtggcta tatccttcgt gtcacagcgt acaaggaggg atatggagaa 3000
 ggttgcgtaa ccattcatga gatcgagaac aatacagacg aactgaagtt tagcaactgt 3060
 gtagaagagg aagtatatcc aaacaacacg gtaacgtgta atgattatac tgcgactcaa 3120
 gaagaatatg aggggtacgta cacttctcgt aatcgaggat atgacggagc ctatgaaagc 3180
 aattcttctg taccagctga ttatgcatca gcctatgaag aaaaagcata tacagatgga 3240
 cgaagagaca atccttgtga atctaacaga ggatatggggg attacacacc actaccagct 3300
 ggctatgtga caaaagaatt agagtacttc ccagaaaccg ataaggtatg gattgagatc 3360
 ggagaaacgg aaggaacatt catcgtggac agcgtggaat tacttcttat ggaggaatag 3420

<210> 18

<211> 1139

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of the engineered insecticidal chimeric protein TIC844_4.

<400> 18

Met Glu Ile Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu Ser
 1 5 10 15

Asn Pro Lys Glu Ile Ile Leu Gly Glu Glu Arg Leu Glu Thr Gly Asn
 20 25 30

Thr Val Ala Asp Ile Ser Leu Gly Leu Ile Asn Phe Leu Tyr Ser Asn
 35 40 45

Phe Val Pro Gly Gly Gly Phe Ile Val Gly Leu Leu Glu Leu Ile Trp
 50 55 60

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

P34223W000_SEQ_PCT

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

Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Lys Val Tyr Val Arg Ala
100 105 110

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

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

Pro Leu Phe Arg Val Gln Asn Tyr Glu Val Ala Leu Leu Ser Val Tyr
145 150 155 160

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

Phe Gly Glu Arg Trp Gly Tyr Asp Thr Ala Thr Ile Asn Asn Arg Tyr
180 185 190

Ser Asp Leu Thr Ser Leu Ile His Val Tyr Thr Asn His Cys Val Asp
195 200 205

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

Trp Ile Val Tyr Asn Arg Phe Arg Arg Gln Leu Thr Ile Ser Val Leu
225 230 235 240

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

Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro Phe
260 265 270

P34223W000_SEQ_PCT

Ile Asn Glu Asn Leu Ser Pro Ala Ala Ser Tyr Pro Thr Phe Ser Ala
 275 280 285

Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu Asn
 290 295 300

Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Ser Ala Tyr Trp Gly
 305 310 315 320

Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu Ile
 325 330 335

Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val Thr
 340 345 350

Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr Ile
 355 360 365

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

Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro Ile
 385 390 395 400

Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro Ala
 405 410 415

Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg Ile
 420 425 430

Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg Ser
 435 440 445

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

P34223W000_SEQ_PCT

Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys Gly
465 470 475 480

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

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

Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr Phe
515 520 525

Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr Met
530 535 540

Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr Leu
545 550 555 560

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

Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Thr
580 585 590

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

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val
610 615 620

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

Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys
645 650 655

P34223W000_SEQ_PCT

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

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr
675 680 685

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
690 695 700

Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
705 710 715 720

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
725 730 735

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
740 745 750

Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
755 760 765

Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Ala His His Ser His
770 775 780

His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp
785 790 795 800

Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala
805 810 815

Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu
820 825 830

Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg
835 840 845

P34223W000_SEQ_PCT

Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu
850 855 860

Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala
865 870 875 880

Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser
885 890 895

Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn
900 905 910

Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser
915 920 925

Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly
930 935 940

Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn
945 950 955 960

Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser
965 970 975

Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr
980 985 990

Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile
995 1000 1005

Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu
1010 1015 1020

Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Ala
1025 1030 1035

P34223W000_SEQ_PCT

Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly
1040 1045 1050

Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser Val Pro Ala Asp Tyr
1055 1060 1065

Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr Asp Gly Arg Arg Asp
1070 1075 1080

Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu
1085 1090 1095

Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr
1100 1105 1110

Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile
1115 1120 1125

Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
1130 1135

<210> 19
<211> 3420
<212> DNA
<213> Artificial sequence

<220>
<223> Nucleotide sequence used for expression in a bacterial cell
encoding TIC844_5.

<400> 19
atggaaataa ataatcaaaa ccaatgtgtg ccttacaatt gttaaagtaa tcctaaggag 60
ataatattag gcgaggaaag gctagaaaca gggaatactg tagcagacat ttcattaggg 120
cttattaatt ttctatattc taattttgta ccaggaggag gatttatagt aggtttacta 180
gaattaatat ggggatttat agggccttcg caatgggata tttttttagc tcaaattgag 240
caattgatta gtcaaagaat agaagaattt gctaggaatc aggcaatttc aagattggag 300

P34223W000_SEQ_PCT

gggctaagca atctttataa ggtctatggt agagcggtta gcgactggga gaaagatcct	360
actaatcctg ctttaaggga agaaatgcgt atacaattta atgacatgaa tagtgctctc	420
ataacggcta ttccactttt tagagttcaa aattatgaag ttgctctttt atctgtatat	480
gttcaagccg caaacttaca tttatctatt ttaagggatg tttcagtttt cggagaaaga	540
tggggatatg atacagcgac tatcaataat cgctatagtg atctgactag cttattcat	600
gtttatacta accatttgtgt ggatacgtat aatcagggat taaggcgttt ggaaggctgt	660
tttcttagcg attggattgt atataatcgt ttccggagac aattgacaat ttcagtatta	720
gatattgttg cgttttttcc aaattatgat attagaacat atccaattca aacagctact	780
cagctaacga gggaagtcta tctggattta ctttttatta atgaaaatct ttctcctgca	840
gcaaaatatc caaccttttc agctgctgaa agtgctataa ttagaagtcc tcatttagta	900
gactttttaa atagctttac catttataca gatagtctgg cacgttctgc atattgggga	960
gggcacttgg taaattcttt ccgcacagga accactacta atttgataag atccccitta	1020
tatggaaggg aaggaaatac agagcgcccc gtaactatta ccgcatcacc tagcgtacca	1080
atatttagaa cactttcata tccaacaggc cttgacaatt caaatcctgt agctggaatc	1140
gagggagtgg aattccaaaa tactataagt agaagtatct atcgtaaaag cggccaata	1200
gattctttta gtgaattacc acctcaagat gccagcgat ctcttgcaat tgggtatagt	1260
caccgtttat gccatgcaac attttttagaa cggattagtg gaccaagaat agcaggcacc	1320
gtattttctt ggacacaccg tagtgccagc cttactaacg aagtaagtcc atctagaatt	1380
acacaaattc catgggtaaa ggcgcatact cttgcatctg gtgcctccgt cattaaaggt	1440
cctggattta cagggtggaga tattctgact aggaatagta tgggcgagct ggggacctta	1500
cgagtaacct tcacaggaag attaccacaa agttattata tacgtttccg ttatgcttcg	1560
gtagcaaata ggagtggtag atttagatat tcacagccac cttcgtagtg aatttcattt	1620
ccaaaaacta tggacgcagg tgaaccacta acatctcgtt cggttcgtca tacaacactc	1680
ttcactccaa taaccttttc acgagctcaa gaagaatttg atctatacat ccaatcgggt	1740

P34223W000_SEQ_PCT

gtttatatag atcgaattga atttataccg gttactgcaa catttgaggc agaatatgat	1800
ttagaaaagag cacaaaaaggc ggtgaatgag ctgtttactt cttccaatca aatcgggtta	1860
aaaacagatg tgacggatta tcatattgat caagtatcca atttagttga gtgtttatct	1920
gatgaatfff gtctggatga aaaaaaagaa ttgtccgaga aagtcaaaca tgcgaagcga	1980
cttagtgatg agcgggaatff acttcaagat ccaaacttta gagggatcaa tagacaacta	2040
gaccgtggct ggagaggaag tacggatatt accatccaag gaggcgatga cgtattcaaa	2100
gagaattacg ttacgctatt gggtagctff gatgagtgc tccaacgta tttatatcaa	2160
aaaatagatg agtcgaaatt aaaagcctat acccgttacc aattaagagg gtatatcgaa	2220
gatagtcaag acttagaaat ctattttaatt cgctacaatg ccaaacacga aacagtaa	2280
gtgccaggta cgggttcctt atggccgctt tcagcccca gtccaatcgg aaaatgtgcc	2340
catcattccc atcatttctc cttggacatt gatgttggat gtacagactt aaatgaggac	2400
ttaggtgtat gggatgatatt caagattaag acgcaagatg gccatgcaag actaggaa	2460
ctagaatffc tcgaagagaa accattagta ggagaagcac tagctcgtgt gaaaagagcg	2520
gagaaaaaat ggagagacaa acgtgaaaaa ttggaatggg aaacaaatat tgtttataaa	2580
gaggcaaaaag aatctgtaga tgctttatff gtaaactctc aatatgatag attacaagcg	2640
gataccaaca tcgcgatgat tcatgcggca gataaacgcg ttcatagcat tcgagaagct	2700
tatctgcctg agctgtctgt gattccgggt gtcaatgcgg ctatffffga agaattagaa	2760
gggcgtatff tactgcatt ctccctatat gatgcgagaa atgtcattaa aaatggtgat	2820
tttaataatg gcttatcctg ctggaacgtg aaaggcatg tagatgtaga agaacaaaac	2880
aaccaccgtt cggtccttgt tgttccggaa tgggaagcag aagtgtcaca agaagttcgt	2940
gtctgtccgg gtcgtggcta tatccttcgt gtcacagcgt acaaggaggg atatggagaa	3000
ggttgcgtaa ccattcatga gatcgagaac aatacagacg aactgaagtt tagcaactgt	3060
gtagaagagg aagtatatcc aaacaacacg gtaacgtgta atgattatac tgcgactcaa	3120
gaagaatatg agggtagcta cacttctcgt aatcgaggat atgacggagc ctatgaaagc	3180

P34223W000_SEQ_PCT

aattcttctg taccagctga ttatgcatca gcctatgaag aaaaagcata tacagatgga 3240
cgaagagaca atccttgtga atctaacaga ggatatgggg attacacacc actaccagct 3300
ggctatgtga caaaagaatt agagtacttc ccagaaaccg ataaggtatg gattgagatc 3360
ggagaaacgg aaggaacatt catcgtggac agcgtggaat tacttcttat ggaggaatag 3420

<210> 20

<211> 1139

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of the engineered insecticidal chimeric protein TIC844_5.

<400> 20

Met Glu Ile Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu Ser
1 5 10 15

Asn Pro Lys Glu Ile Ile Leu Gly Glu Glu Arg Leu Glu Thr Gly Asn
20 25 30

Thr Val Ala Asp Ile Ser Leu Gly Leu Ile Asn Phe Leu Tyr Ser Asn
35 40 45

Phe Val Pro Gly Gly Gly Phe Ile Val Gly Leu Leu Glu Leu Ile Trp
50 55 60

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

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

Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Lys Val Tyr Val Arg Ala
100 105 110

P34223W000_SEQ_PCT

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

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

Pro Leu Phe Arg Val Gln Asn Tyr Glu Val Ala Leu Leu Ser Val Tyr
145 150 155 160

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

Phe Gly Glu Arg Trp Gly Tyr Asp Thr Ala Thr Ile Asn Asn Arg Tyr
180 185 190

Ser Asp Leu Thr Ser Leu Ile His Val Tyr Thr Asn His Cys Val Asp
195 200 205

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

Trp Ile Val Tyr Asn Arg Phe Arg Arg Gln Leu Thr Ile Ser Val Leu
225 230 235 240

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

Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro Phe
260 265 270

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

Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu Asn
290 295 300

P34223W000_SEQ_PCT

Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Ser Ala Tyr Trp Gly
305 310 315 320

Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu Ile
325 330 335

Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val Thr
340 345 350

Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr Pro
355 360 365

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

Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro Ile
385 390 395 400

Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro Ala
405 410 415

Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg Ile
420 425 430

Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg Ser
435 440 445

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

Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys Gly
465 470 475 480

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

P34223W000_SEQ_PCT

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

Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr Phe
515 520 525

Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr Met
530 535 540

Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr Leu
545 550 555 560

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

Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Thr
580 585 590

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

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val
610 615 620

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

Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys
645 650 655

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

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr
675 680 685

P34223W000_SEQ_PCT

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
690 695 700

Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
705 710 715 720

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
725 730 735

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
740 745 750

Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
755 760 765

Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Ala His His Ser His
770 775 780

His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp
785 790 795 800

Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala
805 810 815

Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu
820 825 830

Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg
835 840 845

Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu
850 855 860

Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala
865 870 875 880

P34223W000_SEQ_PCT

Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser
885 890 895

Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn
900 905 910

Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser
915 920 925

Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly
930 935 940

Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn
945 950 955 960

Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser
965 970 975

Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr
980 985 990

Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile
995 1000 1005

Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu
1010 1015 1020

Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Ala
1025 1030 1035

Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly
1040 1045 1050

Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser Val Pro Ala Asp Tyr
1055 1060 1065

P34223W000_SEQ_PCT

Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr Asp Gly Arg Arg Asp
1070 1075 1080

Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu
1085 1090 1095

Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr
1100 1105 1110

Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile
1115 1120 1125

Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
1130 1135

<210> 21
<211> 3420
<212> DNA
<213> Artificial sequence

<220>
<223> Nucleotide sequence used for expression in a bacterial cell
encoding TIC844_6.

<400> 21
atggaaataa ataatcaaaa ccaatgtgtg cttacaatt gttaaagtaa tcctaaggag 60
ataatattag gcgaggaaag gctagaaaca gggaatactg tagcagacat ttcattaggg 120
cttattaatt ttctatattc taattttgta ccaggaggag gatttatagt aggtttacta 180
gaattaatat ggggatttat agggccttcg caatgggata tttttttagc tcaaattgag 240
caattgatta gtcaaagaat agaagaattt gctaggaatc aggcaatttc aagattggag 300
gggctaagca atctttataa ggtctatggt agagcgttta gcgactggga gaaagatcct 360
actaatcctg ctttaaggga agaaatgcgt atacaattta atgacatgaa tagtgctctc 420
ataacggcta ttccactttt tagagttcaa aattatgaag ttgctctttt atctgtatat 480
gttcaagccg caaacttaca tttatctatt ttaagggatg tttcagtttt cggagaaaga 540

P34223W000_SEQ_PCT

tggggatatg atacagcgac tatcaataat cgctatagtg atctgactag ccttattcat	600
gtttatacta accattgtgt ggatacgtat aatcagggat taaggcgttt ggaaggctgt	660
tttcttagcg attggattgt atataatcgt ttccggagac aattgacaat ttcagtatta	720
gatattgttg cgttttttcc aaattatgat attagaacat atccaattca aacagctact	780
cagctaacga ggggaagtcta tctggattta ctttttatta atgaaaatct ttctcctgca	840
gcaagctatc caaccttttc agctgctgaa agtgctataa ttagaagtcc tcatttagta	900
gactttttta atagctttac catttataca gatagtctgg cacgttatgc atattgggga	960
gggcacttgg taaattcttt ccgcacagga accactacta atttgataag atccccitta	1020
tatggaaggg aaggaaatac agagcgcccc gtaactatta ccgcatcacc tagcgtagca	1080
atatttagaa cactttcata tattacaggc cttgacaatc gtaatcctgt agctggaatc	1140
gagggagtgg aattccaaaa tactataagt agaagtatct atcgtaaaag cggccaata	1200
gattctttta gtgaattacc acctcaagat gccagcgtat ctctgcaat tgggtatagt	1260
caccgtttat gccatgcaac attttttagaa cggatttagtg gaccaagaat agcaggcacc	1320
gtattttctt ggacacaccg tagtgccagc cttactaacg aagtaagtcc atctagaatt	1380
acacaaattc catgggtaaa ggcgcatact cttgcatctg gtgcctccgt cattaaaggt	1440
cctggattta caggtggaga tattctgact aggaatagta tgggcgagct ggggacctta	1500
cgagtaacct tcacaggaag attaccacaa agttattata tacgtttccg ttatgcttcg	1560
gtagcaaata ggagtggtag atttagatat tcacagccac cttcgtagtg aatttcattt	1620
ccaaaaacta tggacgcagg tgaaccacta acatctcgtt cgttcgctca tacaacactc	1680
ttcactccaa taaccttttc acgagctcaa gaagaatttg atctatacat ccaatcgggt	1740
gtttatatag atcgaattga atttataccg gttactgcaa catttgaggc agaatatgat	1800
ttagaaagag cacaaaaggc ggtgaatgag ctgtttactt cttccaatca aatcgggtta	1860
aaaacagatg tgacggatta tcatattgat caagtatcca atttagttga gtgtttatct	1920
gatgaatttt gtctggatga aaaaaaagaa ttgtccgaga aagtcaaaca tgcgaagcga	1980

P34223W000_SEQ_PCT

cttagtgatg agcgggaatth acttcaagat ccaaacttta gagggatcaa tagacaacta	2040
gaccgtggct ggagaggaag tacggatatt accatccaag gaggcgatga cgtattcaaa	2100
gagaattacg ttacgctatt gggtagcttt gatgagtgct atccaacgta tttatatcaa	2160
aaaatagatg agtcgaaatt aaaagcctat acccgttacc aattaagagg gtatatcgaa	2220
gatagtcaag acttagaaat ctatttaatt cgctacaatg ccaaacacga aacagtaa	2280
gtgccaggta cgggttcctt atggccgctt tcagcccca gtccaatcgg aaaatgtgcc	2340
catcattccc atcatttctc cttggacatt gatgttggat gtacagactt aaatgaggac	2400
ttaggtgtat gggtagatatt caagattaag acgcaagatg gccatgcaag actaggaa	2460
ctagaatttc tcgaagagaa accattagta ggagaagcac tagctcgtgt gaaaagagcg	2520
gagaaaaaat ggagagacaa acgtgaaaaa ttggaatggg aaacaaatat tgtttataaa	2580
gaggcaaaag aatctgtaga tgctttatth gtaaactctc aatatgatag attacaagcg	2640
gataccaaca tcgcatgat tcatgcggca gataaacgcg ttcatagcat tcgagaagct	2700
tatctgcctg agctgtctgt gattccgggt gtcaatgcgg ctatthttga agaattagaa	2760
gggcgtatth tcatgcat ctccctatat gatgcgagaa atgtcattaa aaatggtgat	2820
thtaataatg gcttatcctg ctggaacgtg aaaggcatg tagatgtaga agaacaaaac	2880
aaccaccgtt cggctcctgt tgttccggaa tgggaagcag aagtgtcaca agaagttcgt	2940
gtctgtccgg gtcgtggcta tatccttcgt gtcacagcgt acaaggaggg atatggagaa	3000
ggttgcgtaa ccattcatga gatcgagaac aatacagacg aactgaagtt tagcaactgt	3060
gtagaagagg aagtatatcc aaacaacacg gtaacgtgta atgattatac tgcgactcaa	3120
gaagaatatg agggtagcta cacttctcgt aatcgaggat atgacggagc ctatgaaagc	3180
aattcttctg taccagctga ttatgcatca gcctatgaag aaaaagcata tacagatgga	3240
cgaagagaca atccttgatga atctaacaga ggatatgggg attacacacc actaccagct	3300
ggctatgtga caaaagaatt agagtacttc ccagaaaccg ataaggatatg gattgagatc	3360
ggagaaacgg aaggaacatt catcgtggac agcgtggaat tacttcttat ggaggaatag	3420

P34223W000_SEQ_PCT

<210> 22
 <211> 1139
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Amino acid sequence of the engineered insecticidal chimeric protein TIC844_6.

<400> 22

Met Glu Ile Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu Ser
 1 5 10 15

Asn Pro Lys Glu Ile Ile Leu Gly Glu Glu Arg Leu Glu Thr Gly Asn
 20 25 30

Thr Val Ala Asp Ile Ser Leu Gly Leu Ile Asn Phe Leu Tyr Ser Asn
 35 40 45

Phe Val Pro Gly Gly Gly Phe Ile Val Gly Leu Leu Glu Leu Ile Trp
 50 55 60

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

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

Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Lys Val Tyr Val Arg Ala
 100 105 110

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

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

P34223W000_SEQ_PCT

Pro Leu Phe Arg Val Gln Asn Tyr Glu Val Ala Leu Leu Ser Val Tyr
145 150 155 160

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

Phe Gly Glu Arg Trp Gly Tyr Asp Thr Ala Thr Ile Asn Asn Arg Tyr
180 185 190

Ser Asp Leu Thr Ser Leu Ile His Val Tyr Thr Asn His Cys Val Asp
195 200 205

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

Trp Ile Val Tyr Asn Arg Phe Arg Arg Gln Leu Thr Ile Ser Val Leu
225 230 235 240

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

Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro Phe
260 265 270

Ile Asn Glu Asn Leu Ser Pro Ala Ala Ser Tyr Pro Thr Phe Ser Ala
275 280 285

Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu Asn
290 295 300

Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Tyr Ala Tyr Trp Gly
305 310 315 320

Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu Ile
325 330 335

P34223W000_SEQ_PCT

Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val Thr
340 345 350

Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr Ile
355 360 365

Thr Gly Leu Asp Asn Arg Asn Pro Val Ala Gly Ile Glu Gly Val Glu
370 375 380

Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro Ile
385 390 395 400

Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro Ala
405 410 415

Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg Ile
420 425 430

Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg Ser
435 440 445

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

Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys Gly
465 470 475 480

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

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

Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr Phe
515 520 525

P34223W000_SEQ_PCT

Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr Met
530 535 540

Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr Leu
545 550 555 560

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

Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Thr
580 585 590

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

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val
610 615 620

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

Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys
645 650 655

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

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr
675 680 685

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
690 695 700

Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
705 710 715 720

P34223W000_SEQ_PCT

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
725 730 735

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
740 745 750

Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
755 760 765

Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Ala His His Ser His
770 775 780

His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp
785 790 795 800

Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala
805 810 815

Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu
820 825 830

Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg
835 840 845

Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu
850 855 860

Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala
865 870 875 880

Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser
885 890 895

Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn
900 905 910

P34223W000_SEQ_PCT

Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser
915 920 925

Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly
930 935 940

Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn
945 950 955 960

Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser
965 970 975

Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr
980 985 990

Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile
995 1000 1005

Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu
1010 1015 1020

Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Ala
1025 1030 1035

Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly
1040 1045 1050

Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser Val Pro Ala Asp Tyr
1055 1060 1065

Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr Asp Gly Arg Arg Asp
1070 1075 1080

Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu
1085 1090 1095

P34223W000_SEQ_PCT

Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr
1100 1105 1110

Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile
1115 1120 1125

Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
1130 1135

<210> 23

<211> 3420

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleotide sequence used for expression in a bacterial cell encoding TIC844_7.

<400> 23

atggaaataa ataatcaaaa ccaatgtgtg ccttacaatt gtttaagtaa tcctaaggag	60
ataatattag gcgaggaaaag gctagaaaca gggaatactg tagcagacat ttcattaggg	120
cttattaatt ttctatattc taattttgta ccaggaggag gatttatagt aggtttacta	180
gaattaatat ggggatttat agggccttcg caatgggata tttttttagc tcaaattgag	240
caattgatta gtcaaagaat agaagaattt gctaggaatc aggcaatttc aagattggag	300
gggctaagca atctttataa ggtctatggt agagcgttta gcgactggga gaaagatcct	360
actaatcctg ctttaaggga agaaatgcgt atacaattta atgacatgaa tagtgctctc	420
ataacggcta ttccactttt tagagttcaa aattatgaag ttgctctttt atctgtatat	480
gttcaagccg caaacttaca tttatctatt ttaagggatg tttcagtttt cggagaaaga	540
tggggatatg atacagcgac tatcaataat cgctatagtg atctgactag ccttattcat	600
gtttatacta accattgtgt ggatacgtat aatcagggat taaggcgttt ggaaggctgt	660
tttcttagcg attggattgt atataatcgt ttccggagac aattgacaat ttcagtatta	720
gatattgttg cgttttttcc aaattatgat attagaacat atccaattca aacagctact	780

P34223W000_SEQ_PCT

cagctaacga ggggaagtcta tctggattta ccttttatta atgaaaatct ttctcctgca	840
gcaagctatc caaccttttc agctgctgaa agtgctataa ttagaagtcc tcatttagta	900
gacttttttaa atagcttttac catttataca gatagtctgg cacgttctgc atattggggga	960
gggcacttgg taaattcttt ccgcacagga accactacta atttgataag atccccctta	1020
tatggaaggg aaggaaatac agagcgcccc gtaactatta ccgcatcacc tagcgtacca	1080
atatttagaa cactttcata tagaacaggc cttgacaatt caaatcctgt agctggaatc	1140
gagggagtgg aattccaaaa tactataagt agaagtatct atcgtaaaag cggccaata	1200
gattctttta gtgaattacc acctcaagat gccagcgtat ctctgcaat tgggtatagt	1260
caccgtttat gccatgcaac attttttagaa cggatttagt gaccaagaat agcaggcacc	1320
gtattttctt ggacacaccg tagtgccagc cttactaacg aagtaagtcc atctagaatt	1380
acacaaattc catgggtaaa ggcgcatact cttgcatctg gtgcctccgt cattaaaggt	1440
cctggattta caggtggaga tattctgact aggaatagta tgggcgagct ggggacctta	1500
cgagtaacct tcacaggaag attaccacaa agttattata tacgtttccg ttatgcttcg	1560
gtagcaaata ggagtggtag atttagatat tcacagccac cttcgtagtg aatttcattt	1620
ccaaaaacta tggacgcagg tgaaccacta acatctcgtt cgttcgctca tacaacactc	1680
ttcactccaa taaccttttc acgagctcaa gaagaatttg atctatacat ccaatcgggt	1740
gtttatatag atcgaattga atttataccg gttactgcaa catttgaggc agaatatgat	1800
ttagaaagag cacaaaaggc ggtgaatgag ctgtttactt cttccaatca aatcgggtta	1860
aaaacagatg tgacggatta tcatattgat caagtatcca atttagttga gtgtttatct	1920
gatgaatttt gtctggatga aaaaaaagaa ttgtccgaga aagtcaaaca tgcaagcga	1980
cttagtgatg agcgggaattt acttcaagat ccaaacttta gagggatcaa tagacaacta	2040
gaccgtggct ggagaggaag tacggatatt accatccaag gaggcgatga cgtattcaaa	2100
gagaattacg ttacgctatt gggtagcttt gatgagtgtc atccaacgta tttatatcaa	2160
aaaatagatg agtcgaaatt aaaagcctat acccggttacc aattaagagg gtatatcgaa	2220

P34223W000_SEQ_PCT

gatagtcaag acttagaaat ctattttaatt cgctacaatg ccaaacacga aacagtaa	2280
gtgccaggta cgggttcctt atggccgctt tcagcccaa gtccaatcgg aaaatgtgcc	2340
catcattccc atcatttctc cttggacatt gatgttggat gtacagactt aaatgaggac	2400
ttaggtgtat ggggtgatatt caagattaag acgcaagatg gccatgcaag actaggaa	2460
ctagaatttc tcgaagagaa accattagta ggagaagcac tagctcgtgt gaaaagagcg	2520
gagaaaaaat ggagagacaa acgtgaaaaa ttggaatggg aaacaaatat tgtttataaa	2580
gaggcaaaag aatctgtaga tgctttattt gtaaactctc aatatgatag attacaagcg	2640
gataccaaca tcgcatgat tcatgcggca gataaacgcg ttcatagcat tcgagaagct	2700
tatctgcctg agctgtctgt gattccgggt gtcaatgcgg ctatttttga agaattagaa	2760
gggcgtattt tcaactgcatt ctccctatat gatgcgagaa atgtcattaa aaatggtgat	2820
tttaataatg gcttatcctg ctggaacgtg aaagggcatg tagatgtaga agaacaaaac	2880
aaccaccgtt cggtccttgt tgttccggaa tgggaagcag aagtgtcaca agaagttcgt	2940
gtctgtccgg gtcgtggcta tatccttcgt gtcacagcgt acaaggaggg atatggagaa	3000
ggttgcgtaa ccattcatga gatcgagaac aatacagacg aactgaagtt tagcaactgt	3060
gtagaagagg aagtatatcc aaacaacacg gtaacgtgta atgattatac tgcgactcaa	3120
gaagaatatg agggtagcgt cacttctcgt aatcgaggat atgacggagc ctatgaaagc	3180
aattcttctg taccagctga ttatgcatca gcctatgaag aaaaagcata tacagatgga	3240
cgaagagaca atccttgtga atctaacaga ggatatgggg attacacacc actaccagct	3300
ggctatgtga caaaagaatt agagtacttc ccagaaaccg ataaggtatg gattgagatc	3360
ggagaaacgg aaggaacatt catcgtggac agcgtggaat tacttcttat ggaggaatag	3420

<210> 24

<211> 1139

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of the engineered insecticidal chimeric

P34223W000_SEQ_PCT

protein TIC844_7.

<400> 24

Met Glu Ile Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu Ser
1 5 10 15

Asn Pro Lys Glu Ile Ile Leu Gly Glu Glu Arg Leu Glu Thr Gly Asn
20 25 30

Thr Val Ala Asp Ile Ser Leu Gly Leu Ile Asn Phe Leu Tyr Ser Asn
35 40 45

Phe Val Pro Gly Gly Gly Phe Ile Val Gly Leu Leu Glu Leu Ile Trp
50 55 60

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

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

Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Lys Val Tyr Val Arg Ala
100 105 110

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

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

Pro Leu Phe Arg Val Gln Asn Tyr Glu Val Ala Leu Leu Ser Val Tyr
145 150 155 160

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

P34223W000_SEQ_PCT

Phe Gly Glu Arg Trp Gly Tyr Asp Thr Ala Thr Ile Asn Asn Arg Tyr
180 185 190

Ser Asp Leu Thr Ser Leu Ile His Val Tyr Thr Asn His Cys Val Asp
195 200 205

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

Trp Ile Val Tyr Asn Arg Phe Arg Arg Gln Leu Thr Ile Ser Val Leu
225 230 235 240

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

Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro Phe
260 265 270

Ile Asn Glu Asn Leu Ser Pro Ala Ala Ser Tyr Pro Thr Phe Ser Ala
275 280 285

Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu Asn
290 295 300

Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Ser Ala Tyr Trp Gly
305 310 315 320

Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu Ile
325 330 335

Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val Thr
340 345 350

Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr Arg
355 360 365

P34223W000_SEQ_PCT

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

Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro Ile
385 390 395 400

Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro Ala
405 410 415

Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg Ile
420 425 430

Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg Ser
435 440 445

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

Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys Gly
465 470 475 480

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

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

Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr Phe
515 520 525

Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr Met
530 535 540

Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr Leu
545 550 555 560

P34223W000_SEQ_PCT

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

Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Thr
580 585 590

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

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val
610 615 620

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

Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys
645 650 655

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

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr
675 680 685

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
690 695 700

Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
705 710 715 720

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
725 730 735

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
740 745 750

P34223W000_SEQ_PCT

Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
755 760 765

Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Ala His His Ser His
770 775 780

His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp
785 790 795 800

Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala
805 810 815

Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu
820 825 830

Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg
835 840 845

Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu
850 855 860

Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala
865 870 875 880

Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser
885 890 895

Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn
900 905 910

Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser
915 920 925

Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly
930 935 940

P34223W000_SEQ_PCT

Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn
945 950 955 960

Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser
965 970 975

Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr
980 985 990

Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile
995 1000 1005

Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu
1010 1015 1020

Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Ala
1025 1030 1035

Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly
1040 1045 1050

Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser Val Pro Ala Asp Tyr
1055 1060 1065

Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr Asp Gly Arg Arg Asp
1070 1075 1080

Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu
1085 1090 1095

Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr
1100 1105 1110

Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile
1115 1120 1125

P34223W000_SEQ_PCT

Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
1130 1135

<210> 25
<211> 3420
<212> DNA
<213> Artificial sequence

<220>
<223> Nucleotide sequence used for expression in a bacterial cell encoding TIC844_8.

<400> 25
atggaaataa ataatcaaaa ccaatgtgtg ccttacaatt gttaaagtaa tcctaaggag 60
ataatattag gcgaggaaag gctagaaaca gggaatactg tagcagacat ttcattaggg 120
cttattaatt ttctatattc taattttgta ccaggaggag gatttatagt aggtttacta 180
gaattaatat ggggatttat agggccttcg caatgggata ttttttttagc tcaaattgag 240
caattgatta gtcaaagaat agaagaattt gctaggaatc aggcaatttc aagattggag 300
gggctaagca atctttataa ggtctatgtt agagcgttta gcgactggga gaaagatcct 360
actaatcctg cttaaaggga agaaatgcgt atacaattta atgacatgaa tagtgctctc 420
ataacggcta ttccactttt tagagttcaa aattatgaag ttgctctttt atctgtatat 480
gttcaagccg caaacttaca tttatctatt ttaagggatg tttcagtttt cggagaaaga 540
tggggatatg atacagcgac tatcaataat cgctatagtg atctgactag ccttattcat 600
gtttatacta accattgtgt ggatacgtat aatcagggat taaggcgttt ggaaggctcgt 660
tttcttagcg attggattgt atataatcgt ttccggagac aattgacaat ttcagtatta 720
gatattgttg cgttttttcc aaattatgat attagaacat atccaattca aacagctact 780
cagctaacga gggaagtcta tctggattta ccttttatta atgaaaatct ttctcctgca 840
gcagtatatc caaccttttc agctgctgaa agtgctataa ttagaagtcc tcatttagta 900
gactttttta atagctttac catttataca gatagtctgg cacgttctgc atattgggga 960
gggcacttgg taaattcttt ccgcacagga accactacta atttgataag atccccctta 1020

P34223W000_SEQ_PCT

tatggaaggg aaggaaatac agagcgcccc gtaactatta ccgcatcacc tagcgtacca	1080
atatttagaa cactttcata tccaacaggc cttgacaatt caaatcctgt agctggaatc	1140
gagggagtg aattccaaaa tactataagt agaagtatct atcgtaaaag cgggtccaata	1200
gattctttta gtgaattacc acctcaagat gccagcgtat ctcttgcaat tgggtatagt	1260
caccgtttat gccatgcaac attttttagaa cggattagtg gaccaagaat agcaggcacc	1320
gtatttttctt ggacacaccg tagtgccagc cctactaacg aagtaagtcc atctagaatt	1380
acacaaattc catgggtaaa ggcgcatact cttgcatctg gtgcctccgt cattaaaggt	1440
cctggattta caggtggaga tattctgact aggaatagta tgggcgagct ggggacctta	1500
cgagtaacct tcacaggaag attaccacaa agttattata tacgtttccg ttatgcttcg	1560
gtagcaaata ggagtggtag atttagatat tcacagccac cttcgtatgg aatttcattt	1620
ccaaaaacta tggacgcagg tgaaccacta acatctcggt cgttcgctca tacaacactc	1680
ttcactccaa taaccttttc acgagctcaa gaagaatttg atctatacat ccaatcgggt	1740
gtttatatag atcgaattga atttataccg gttactgcaa catttgaggc agaatatgat	1800
ttagaaagag cacaaaaggc ggtgaatgag ctgtttactt cttccaatca aatcgggtta	1860
aaaacagatg tgacggatta tcatattgat caagtatcca atttagttga gtgtttatct	1920
gatgaatttt gtctggatga aaaaaaagaa ttgtccgaga aagtcaaaca tgcgaagcga	1980
cttagtgatg agcgggaattt acttcaagat ccaaacttta gagggatcaa tagacaacta	2040
gaccgtggct ggagaggaag tacggatatt accatccaag gaggcgatga cgtattcaaa	2100
gagaattacg ttacgctatt gggtagcttt gatgagtgt atccaacgta tttatatcaa	2160
aaaatagatg agtcgaaatt aaaagcctat acccgttacc aattaagagg gtatatcgaa	2220
gatagtcaag acttagaaat ctatttaatt cgctacaatg ccaaacacga aacagtaa	2280
gtgccaggta cgggttcctt atggccgctt tcagcccaa gtccaatcgg aaaatgtgcc	2340
catcattccc atcatttctc cttggacatt gatgttggat gtacagactt aaatgaggac	2400
ttaggtgtat gggatgatatt caagattaag acgcaagatg gccatgcaag actaggaa	2460

P34223W000_SEQ_PCT

ctagaatttc tcgaagagaa accattagta ggagaagcac tagctcgtgt gaaaagagcg	2520
gagaaaaaat ggagagacaa acgtgaaaaa ttggaatggg aaacaaatat tgtttataaa	2580
gaggcaaaag aatctgtaga tgctttatct gtaaactctc aatatgatag attacaagcg	2640
gataccaaca tcgcatgat tcatgcggca gataaacgcg ttcatacat tcgagaagct	2700
tatctgcctg agctgtctgt gattccgggt gtcaatgcgg ctatctttga agaattagaa	2760
gggcgtatct tcaactgcatt ctccctatat gatgcgagaa atgtcattaa aaatggtgat	2820
tttaataatg gcttatcctg ctggaacgtg aaagggcatg tagatgtaga agaacaaaac	2880
aaccaccgtt cggtccttgt tggtccggaa tgggaagcag aagtgtcaca agaagttcgt	2940
gtctgtccgg gtcgtggcta tatccttcgt gtcacagcgt acaaggaggg atatggagaa	3000
ggttgcgtaa ccattcatga gatcgagaac aatacagacg aactgaagtt tagcaactgt	3060
gtagaagagg aagtatatcc aaacaacacg gtaacgtgta atgattatac tgcgactcaa	3120
gaagaatatg agggtagta cacttctcgt aatcgaggat atgacggagc ctatgaaagc	3180
aattcttctg taccagctga ttatgcatca gcctatgaag aaaaagcata tacagatgga	3240
cgaagagaca atccttgtga atctaacaga ggatatgggg attacacacc actaccagct	3300
ggctatgtga caaaagaatt agagtacttc ccagaaaccg ataaggtatg gattgagatc	3360
ggagaaacgg aaggaacatt catcgtggac agcgtggaat tacttcttat ggaggaatag	3420

<210> 26

<211> 1139

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of the engineered insecticidal chimeric protein TIC844_8.

<400> 26

Met	Glu	Ile	Asn	Asn	Gln	Asn	Gln	Cys	Val	Pro	Tyr	Asn	Cys	Leu	Ser
1				5				10						15	

P34223W000_SEQ_PCT

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

P34223W000_SEQ_PCT

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

Trp Ile Val Tyr Asn Arg Phe Arg Arg Gln Leu Thr Ile Ser Val Leu
225 230 235 240

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

Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro Phe
260 265 270

Ile Asn Glu Asn Leu Ser Pro Ala Ala Val Tyr Pro Thr Phe Ser Ala
275 280 285

Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu Asn
290 295 300

Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Ser Ala Tyr Trp Gly
305 310 315 320

Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu Ile
325 330 335

Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val Thr
340 345 350

Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr Pro
355 360 365

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

Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro Ile
385 390 395 400

P34223W000_SEQ_PCT

Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro Ala
405 410 415

Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg Ile
420 425 430

Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg Ser
435 440 445

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

Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys Gly
465 470 475 480

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

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

Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr Phe
515 520 525

Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr Met
530 535 540

Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr Leu
545 550 555 560

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

Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Thr
580 585 590

P34223W000_SEQ_PCT

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

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val
610 615 620

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

Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys
645 650 655

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

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr
675 680 685

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
690 695 700

Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
705 710 715 720

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
725 730 735

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
740 745 750

Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
755 760 765

Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Ala His His Ser His
770 775 780

P34223W000_SEQ_PCT

His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp
785 790 795 800

Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala
805 810 815

Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu
820 825 830

Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg
835 840 845

Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu
850 855 860

Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala
865 870 875 880

Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser
885 890 895

Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn
900 905 910

Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser
915 920 925

Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly
930 935 940

Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn
945 950 955 960

Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser
965 970 975

P34223W000_SEQ_PCT

Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr
 980 985 990

Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile
 995 1000 1005

Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu
 1010 1015 1020

Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Ala
 1025 1030 1035

Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly
 1040 1045 1050

Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser Val Pro Ala Asp Tyr
 1055 1060 1065

Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr Asp Gly Arg Arg Asp
 1070 1075 1080

Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu
 1085 1090 1095

Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr
 1100 1105 1110

Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile
 1115 1120 1125

Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
 1130 1135

<210> 27
 <211> 3498
 <212> DNA
 <213> Artificial sequence

P34223W000_SEQ_PCT

<220>

<223> Synthetic DNA sequence designed for plant expression encoding Cry1Da1.

<400> 27

atggagatca acaaccagaa ccagtgcgtc ccgtacaact gcctgagcaa ccctaaggag	60
atcatcctgg gtgaggaacg cctggagacc ggcaacaccg tagccgacat tagcctgggc	120
ctcatcaact tcctctacag caacttcgtg cccggcggtg gcttcatcgt gggcctcctg	180
gagcttatct ggggcttcat cggcccgtcc cagtgggaca tcttcctcgc ccagatcgag	240
caactgatca gccagcggat cgaggagttc gctaggaacc aggccatctc ccgcctggag	300
ggactctcca acctctacaa ggtgtacgtg cgcgcggttca gcgactggga gaaggacccg	360
accaacccgg ccctccgcga ggaaatgcgt atccagttca acgatatgaa ctcggccctc	420
atcaccgcca tcccgtctt ccgcgtgcag aactacgagg tggccctcct gtccgtgtac	480
gttcaagccg ccaacctcca cctctccatc ctccgcgacg tgagcgtgtt cggcgagcgc	540
tggggctacg acaccgccac catcaacaac cgctactccg acctcacctc cctcatccac	600
gtttacacca accactgcgt ggacacgtac aaccagggcc tccgccgcct ggagggccgc	660
ttcctctccg actggatcgt gtacaaccgc ttccgccgcc agctcaccat ctccgtcctg	720
gacatcgtcg ctttctttcc caactacgac atccgcacct accctatcca gaccgccacc	780
cagctcaccg gcgagggtcta cctcgacctc ccgttcatca acgagaacct cagcccggcc	840
gccagctacc cgaccttctc cgccgctgag tccgccatca ttgcagccc gcacctcgtg	900
gacttcctca actccttcac catctacacc gactccctcg cccgctacgc ctactggggc	960
ggtcacctcg tgaactcctt ccgcaccggc accactacca acctcatccg cagcccgtc	1020
tacggccgcg agggcaacac cgagcgcccg gtgacctca ccgccagccc gagcgtgccc	1080
atcttccgca ccctcagcta catcaccggc ctggacaaca gcaaccctgt ggcgggcatc	1140
gagggcgtgg agttccagaa caccatctcc aggagcatct accgcaagag cggccctatc	1200
gacagcttca gcgagctgcc tcctcaggac gccagcgtga gccctgccat cggctacagc	1260

P34223W000_SEQ_PCT

cacaggctgt gccacgccac cttcctggag cgcatcagcg gccctcgcat cgcgggcacc	1320
gtgttctcgt ggacccaccg cagcgcctct cctacgaacg aggtgtctcc tagtcgcatc	1380
accagatcc cttgggtcaa ggcccacacc ctggctagtgt gcgctagtgt catcaagggc	1440
cctggcttca ccggtggtga catcctgacc aggaactcta tgggcgagct gggcactctg	1500
agggtcactt tctactggccg cctgcctcag tcttactaca tccgcttccg ctacgctagt	1560
gtcgctaacc gctctggtac tttccgctac tctcagcctc cgtcttacgg tatctctttc	1620
cctaagacta tggacgctgg tgagcctctg accagtagga gcttcgctca cactactctg	1680
ttcactccta tcactttctc tagggctcag gaggagtctg acctgtacat ccagtctggt	1740
gtgtacatcg acaggatcga gttcatcccc gtgaccgcca cgttcgaggc cgagtacgac	1800
cttgagcgcg ccagaaggt ggtgaacgcc ctcttcacta gcactaacca gctaggcctg	1860
aagactgacg tgaccgacta ccacatcgac caagtgagca acctagtggc ctgcctctcc	1920
gacgagttct gcctcgacga gaagcgcgag ctgtccgaga aggtgaagca cgccaagcgc	1980
ctctccgacg agcgcaacct gctccaggac cccaacttca ggggcatcaa caggcagccc	2040
gaccgcggct ggcgcggtc caccgacatc accatccagg gcggtgacga cgtattcaag	2100
gagaactacg ttaccctccc cggcaccttc gacgagtgtt accccaccta cctctaccag	2160
aagatcgacg agtccaagct gaaggcctac acccgctacc agctccgcgg ctacatcgag	2220
gactcccagg acctggaaat ctacctcatc cgctacaacg ccaagcacga gatcgtgaac	2280
gtgcctggca ccggcagcct ctggcctctc agcgtggaga accagatcgg cccttgcggc	2340
gagcctaacc gctgcgcccc tcacctcgag tggaaccctg acctccactg ctcgtgcagg	2400
gacggcgaga agtgcgcccc ccatagccac cacttctctc tggacatcga cgtgggctgc	2460
accgacctga acgaggacct gggcgtgtgg gttatcttca agatcaagac ccaggacggt	2520
cacgccaggc tgggtaacct ggagttcctt gaggaaaagc ctctgctggg tgaggccctg	2580
gccaggggtca agagggtga gaagaaatgg agggataaga gggagaccct gcagctggag	2640
accactatcg tctacaagga ggctaaggag tctgtcgatg ctctgttcgt caactctcag	2700

P34223W000_SEQ_PCT

tacgatagac tgcaagctga taccaacatc gctatgatcc acgctgcgga taagcgggtc	2760
caccggatcc gggaggctta ccttccggag ctttctgtca tcccgggtgt caacgctgcg	2820
atcttcgagg aacttgagga acggatcttc actgcgttta gtctttacga tgcgcggaac	2880
atcatcaaga acgggggactt caacaatggt ctgctgtgct ggaacgtcaa gggatcatgtc	2940
gaggctcagg aacaaaaaca tcatcgtagt gtccttgtca ttcctgagtg ggaggcggag	3000
gtctctcaag aggtccgtgt ttgcccgggg cgtgggtaca ttcttcgtgt tactgcgtac	3060
aaggaggggt acgggggaggg gtgcgttact attcatgaga ttgagaacaa tactgatgag	3120
cttaagttca acaatttgtt tgaggaggag gtttaccga acaatactgt tacgtgcatc	3180
aactacacgg caacgcaaga ggaatacgag gggacgtaca cctcgcgtaa tagagggtat	3240
gatgaggcgt acggaaacaa cccgtcgggt ccagcagatt atgcctcggg ttatgaggag	3300
aagtcgtaca cggatagacg acgcgagaat ccatgtgagt caaatcgagg atacggagat	3360
tacacaccat taccagcagg atacgttaca aaggagttag aatacttccc ggaaacagat	3420
aaagtttggg ttgaaatcgg agaaacagaa ggaacattca tcgtcgactc agtagaattg	3480
ttgttgatgg aagaatga	3498

<210> 28
 <211> 1165
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Amino acid sequence of Cry1Da1 encoded by a synthetic DNA sequence.

<400> 28

Met	Glu	Ile	Asn	Asn	Gln	Asn	Gln	Cys	Val	Pro	Tyr	Asn	Cys	Leu	Ser
1				5				10						15	

Asn	Pro	Lys	Glu	Ile	Ile	Leu	Gly	Glu	Glu	Arg	Leu	Glu	Thr	Gly	Asn
			20					25					30		

P34223W000_SEQ_PCT

Thr Val Ala Asp Ile Ser Leu Gly Leu Ile Asn Phe Leu Tyr Ser Asn
35 40 45

Phe Val Pro Gly Gly Gly Phe Ile Val Gly Leu Leu Glu Leu Ile Trp
50 55 60

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

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

Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Lys Val Tyr Val Arg Ala
100 105 110

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

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

Pro Leu Phe Arg Val Gln Asn Tyr Glu Val Ala Leu Leu Ser Val Tyr
145 150 155 160

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

Phe Gly Glu Arg Trp Gly Tyr Asp Thr Ala Thr Ile Asn Asn Arg Tyr
180 185 190

Ser Asp Leu Thr Ser Leu Ile His Val Tyr Thr Asn His Cys Val Asp
195 200 205

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

P34223W000_SEQ_PCT

Trp Ile Val Tyr Asn Arg Phe Arg Arg Gln Leu Thr Ile Ser Val Leu
225 230 235 240

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

Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro Phe
260 265 270

Ile Asn Glu Asn Leu Ser Pro Ala Ala Ser Tyr Pro Thr Phe Ser Ala
275 280 285

Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu Asn
290 295 300

Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Tyr Ala Tyr Trp Gly
305 310 315 320

Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu Ile
325 330 335

Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val Thr
340 345 350

Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr Ile
355 360 365

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

Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro Ile
385 390 395 400

Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro Ala
405 410 415

P34223W000_SEQ_PCT

Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg Ile
420 425 430

Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg Ser
435 440 445

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

Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys Gly
465 470 475 480

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

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

Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr Phe
515 520 525

Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr Met
530 535 540

Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr Leu
545 550 555 560

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

Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Thr
580 585 590

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

P34223W000_SEQ_PCT

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

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

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

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

Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr
675 680 685

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
690 695 700

Thr Leu Pro Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
705 710 715 720

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
725 730 735

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
740 745 750

Asn Ala Lys His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp
755 760 765

Pro Leu Ser Val Glu Asn Gln Ile Gly Pro Cys Gly Glu Pro Asn Arg
770 775 780

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu His Cys Ser Cys Arg
785 790 795 800

P34223W000_SEQ_PCT

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
805 810 815

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
820 825 830

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
835 840 845

Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys
850 855 860

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Thr Leu Gln Leu Glu
865 870 875 880

Thr Thr Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
885 890 895

Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met
900 905 910

Ile His Ala Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu
915 920 925

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

Leu Glu Glu Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
945 950 955 960

Ile Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn Val
965 970 975

Lys Gly His Val Glu Val Glu Glu Gln Asn Asn His Arg Ser Val Leu
980 985 990

P34223W000_SEQ_PCT

Val Ile Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys
 995 1000 1005

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

Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr
 1025 1030 1035

Asp Glu Leu Lys Phe Asn Asn Cys Val Glu Glu Glu Val Tyr Pro
 1040 1045 1050

Asn Asn Thr Val Thr Cys Ile Asn Tyr Thr Ala Thr Gln Glu Glu
 1055 1060 1065

Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Glu Ala
 1070 1075 1080

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

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

Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 1115 1120 1125

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

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

Glu Leu Leu Leu Met Glu Glu
 1160 1165

P34223W000_SEQ_PCT

<210> 29
 <211> 3501
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic DNA sequence designed for plant expression encoding
 Cry1Da1 with an additional Alanine residue inserted at position
 2.

<400> 29
 atggctgaga tcaacaacca gaaccagtgc gtcccgtaga actgcctgag caaccctaag 60
 gagatcatcc tgggtgagga acgcctggag accggcaaca ccgtagccga cattagcctg 120
 ggccatcatca acttcctcta cagcaacttc gtgcccggcg gtggcttcat cgtgggcctc 180
 ctggagctta tctggggcctt catcggtccc tcccagtgag acatcttcct cgcccagatc 240
 gagcaactga tcagccagcg gatcgaggag ttgcttagga accaggccat ctcccgctg 300
 gagggactct ccaacctcta caaggtgtac gtgcgcgctg tcagcgactg ggagaaggac 360
 ccgaccaacc cggccctccg cgaggaaatg cgtatccagt tcaacgatat gaactcggcc 420
 ctcatcaccg ccatcccgct cttccgcgtg cagaactacg aggtggccct cctgtccgtg 480
 tacgttcaag ccgccaacct ccacctctcc atcctccgcg acgtgagcgt gttcggcgag 540
 cgctggggct acgacaccgc caccatcaac aaccgtact ccgacctac ctccctcatc 600
 cacgtttaca ccaaccactg cgtggacacg tacaaccagg gcctccgccc cctggagggc 660
 cgcttcctct ccgactggat cgtgtacaac cgcttccgcc gccagctcac catctccgtc 720
 ctggacatcg tcgccttctt tcccaactac gacatccgca cctaccctat ccagaccgcc 780
 acccagctca ccgcgagggt ctacctgac ctcccgttca tcaacgagaa cctcagcccg 840
 gccgccagct acccgacctt ctccgccgct gagtccgcca tcattcgag cccgcacctc 900
 gtggacttcc tcaactcctt caccatctac accgactccc tcgcccgtta cgcctactgg 960
 ggcggtcacc tcgtgaactc cttccgcacc ggaccacta ccaacctcat ccgagccccg 1020
 ctctacggcc gcgagggcaa caccgagcgc ccggtgacca tcaccgccag cccgagcgtg 1080
 cccatcttcc gcacctcag ctacatcacc ggcttggaac acagcaaccc tgtggcgggc 1140

P34223W000_SEQ_PCT

atcgagggcg tggagttcca gaacaccatc tccaggagca tctaccgcaa gagcggccct	1200
atcgacagct tcagcgagct gcctcctcag gacgccagcg tgagccctgc catcggctac	1260
agccacaggc tgtgccacgc caccttcctg gagcgcatca gcggccctcg catcgcgggc	1320
accgtgttct cgtggacca cgcagcgcc tctcctacga acgagggtgc tcctagtcgc	1380
atcacccaga tcccttgggt caaggccac accctggcta gtggcgctag tgtcatcaag	1440
ggccctggct tcaccggtgg tgacatcctg accaggaact ctatgggcga gctgggcact	1500
ctgaggggtca ctttactgg ccgcctgcct cagtcttact acatccgctt ccgctacgct	1560
agtgtcgcta accgctctgg tactttccgc tactctcagc ctccgtctta cggtatctct	1620
ttccctaaga ctatggacgc tggtgagcct ctgaccagta ggagcttcgc tcacactact	1680
ctgttcactc ctatcacttt ctctagggct caggaggagt tcgacctgta catccagtct	1740
ggtgtgtaca tcgacaggat cgagttcatc cccgtgaccg ccacgttcga ggccgagtac	1800
gaccttgagc gcgcccagaa ggtggtgaac gccctcttca ctagcactaa ccagctaggc	1860
ctgaagactg acgtgaccga ctaccacatc gaccaagtga gcaacctagt ggccctgcctc	1920
tccgacgagt tctgcctcga cgagaagcgc gagctgtccg agaagggtgaa gcacgccaag	1980
cgctctccg acgagcgcaa cctgctccag gaccccaact tcaggggcat caacaggcag	2040
cccgaccgcg gctggcgcggt cccaccgac atcaccatcc agggcggtga cgacgtattc	2100
aaggagaact acgttacct ccccggcacc ttcgacgagt gttacccac ctacctctac	2160
cagaagatcg acgagtcaa gctgaaggcc tacacccgct accagctccg cggctacatc	2220
gaggactccc aggacctgga aatctacctc atccgctaca acgccaagca cgagatcgtg	2280
aacgtgcctg gcaccggcag cctctggcct ctcagcgtgg agaaccagat cggcccttgc	2340
ggcgagccta accgctgcgc cctcacctc gagtggaacc ctgacctca ctgctcgtgc	2400
agggacggcg agaagtgcgc ccaccatagc caccacttct ctctggacat cgacgtgggc	2460
tgcaccgacc tgaacgagga cctgggcgtg tgggttatct tcaagatcaa gacccaggac	2520
ggtcacgcca ggctgggtaa cctggagttc cttgaggaaa agcctctgct gggtgaggcc	2580

P34223W000_SEQ_PCT

ctggccaggg tcaagagggc tgagaagaaa tggagggata agagggagac cctgcagctg	2640
gagaccacta tcgtctacaa ggaggctaag gagtctgtcg atgctctgtt cgtcaactct	2700
cagtacgata gactgcaagc tgataccaac atcgctatga tccacgctgc ggataagcgg	2760
gtccaccgga tccgggaggc ttaccttccg gagctttctg tcatcccggg tgtcaacgct	2820
gcgatcttcg aggaacttga ggaacggatc ttcactgcgt ttagtcttta cgatgcgcgg	2880
aacatcatca agaacgggga cttcaacaat ggtctgctgt gctggaacgt caagggtcat	2940
gtcgaggctc aggaacaaaa caatcatcgt agtgtccttg tcattcctga gtgggagggc	3000
gaggtctctc aagagggtccg tgtttgcccc gggcgtgggt acattcttcg tgttactgcg	3060
tacaaggagg ggtacgggga ggggtgctgt actattcatg agattgagaa caatactgat	3120
gagcttaagt tcaacaattg tgttgaggag gaggtttacc cgaacaatac tgttacgtgc	3180
atcaactaca cggcaacgca agaggaatac gaggggacgt acacctcgcg taatagaggg	3240
tatgatgagg cgtacggaaa caaccgctc gttccagcag attatgcctc ggtttatgag	3300
gagaagtcgt acacggatag acgacgcgag aatccatgtg agtcaaatac aggatacggg	3360
gattacacac cattaccagc aggatacgtt acaaaggagt tggaataactt cccggaaaca	3420
gataaagttt ggattgaaat cggagaaaca gaaggaacat tcatcgtcga ctcagtagaa	3480
ttgttggtga tggaagaatg a	3501

<210> 30

<211> 1166

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of Cry1Da1 encoded by a synthetic DNA sequence wherein an additional Alanine residue has been inserted at position 2.

<400> 30

Met	Ala	Glu	Ile	Asn	Asn	Gln	Asn	Gln	Cys	Val	Pro	Tyr	Asn	Cys	Leu
1				5				10						15	

P34223W000_SEQ_PCT

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

Asn Thr Val Ala Asp Ile Ser Leu Gly Leu Ile Asn Phe Leu Tyr Ser
35 40 45

Asn Phe Val Pro Gly Gly Gly Phe Ile Val Gly Leu Leu Glu Leu Ile
50 55 60

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

Glu Gln Leu Ile Ser 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 Lys Val Tyr Val Arg
100 105 110

Ala Phe Ser Asp Trp Glu Lys 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 Ile Thr Ala
130 135 140

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

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

Val Phe Gly Glu Arg Trp Gly Tyr Asp Thr Ala Thr Ile Asn Asn Arg
180 185 190

Tyr Ser Asp Leu Thr Ser Leu Ile His Val Tyr Thr Asn His Cys Val
195 200 205

P34223W000_SEQ_PCT

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

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

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

Ile Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro
260 265 270

Phe Ile Asn Glu Asn Leu Ser Pro Ala Ala Ser Tyr Pro Thr Phe Ser
275 280 285

Ala Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu
290 295 300

Asn Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Tyr Ala Tyr Trp
305 310 315 320

Gly Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu
325 330 335

Ile Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val
340 345 350

Thr Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr
355 360 365

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

Glu Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro
385 390 395 400

P34223W000_SEQ_PCT

Ile Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro
 405 410 415

Ala Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg
 420 425 430

Ile Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg
 435 440 445

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

Pro Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys
 465 470 475 480

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

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

Tyr Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr
 515 520 525

Phe Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr
 530 535 540

Met Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr
 545 550 555 560

Leu Phe Thr Pro Ile Thr Phe Ser Arg Ala Gln Glu Glu Phe Asp Leu
 565 570 575

Tyr Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val
 580 585 590

P34223W000_SEQ_PCT

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

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

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

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

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

Asn Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser
675 680 685

Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr
690 695 700

Val Thr Leu Pro Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr
705 710 715 720

Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu
725 730 735

Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg
740 745 750

Tyr Asn Ala Lys His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu
755 760 765

Trp Pro Leu Ser Val Glu Asn Gln Ile Gly Pro Cys Gly Glu Pro Asn
770 775 780

P34223W000_SEQ_PCT

Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu His Cys Ser Cys
785 790 795 800

Arg Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp
805 810 815

Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val
820 825 830

Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu
835 840 845

Glu Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val
850 855 860

Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Thr Leu Gln Leu
865 870 875 880

Glu Thr Thr Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu
885 890 895

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

Met Ile His Ala Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr
915 920 925

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

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

Asn Ile Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn
965 970 975

P34223W000_SEQ_PCT

Val Lys Gly His Val Glu Val Glu Glu Gln Asn Asn His Arg Ser Val
 980 985 990

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

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

Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn
 1025 1030 1035

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

Pro Asn Asn Thr Val Thr Cys Ile Asn Tyr Thr Ala Thr Gln Glu
 1055 1060 1065

Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Glu
 1070 1075 1080

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

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

Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala 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

P34223W000_SEQ_PCT

Val Glu Leu Leu Leu Met Glu Glu
1160 1165

<210> 31
<211> 3501
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic DNA sequence designed for plant expression encoding
Cry1Da1_3 with an additional Alanine residue inserted at position
2.

<400> 31
atggctgaga tcaacaacca gaaccagtgc gtcccgtaga actgcctgag caaccctaag 60
gagatcatcc tgggtgagga acgcctggag accggcaaca ccgtagccga cattagcctg 120
ggcctcatca acttcctcta cagcaacttc gtgcccggcg gtggcttcat cgtgggcctc 180
ctggagctta tctggggctt catcggtccc tcccagtggg acatcttcct cgcccagatc 240
gagcaactga tcagccagcg gatcgaggag ttcgctagga accaggccat ctcccgctg 300
gagggactct ccaacctcta caaggtgtac gtgcgcgcgt tcagcgactg ggagaaggac 360
ccgaccaacc cggccctccg cgaggaaatg cgtatccagt tcaacgatat gaactcggcc 420
ctcatcaccg ccatcccgct cttccgcgtg cagaactacg aggtggccct cctgtccgtg 480
tacgttcaag ccgccaacct ccacctctcc atcctccgcg acgtgagcgt gttcggcgag 540
cgctggggct acgacaccgc caccatcaac aaccgtact ccgacctac ctccctcatc 600
cacgtttaca ccaaccactg cgtggacacg tacaaccagg gcctccgccg cctggagggc 660
cgcttcctct ccgactggat cgtgtacaac cgcttccgcc gccagctcac catctccgtc 720
ctggacatcg tcgccttctt tccaactac gacatccgca cctaccctat ccagaccgcc 780
accagctca cccgcgagggt ctacctgac ctccgttca tcaacgagaa cctcagcccg 840
gccgccagct acccgacctt ctccgccgct gagtccgcca tcattcgag cccgcacctc 900
gtggacttcc tcaactcctt caccatctac accgactccc tcgcccgcag cgcctactgg 960

P34223W000_SEQ_PCT

ggcggtcacc tcgtgaactc cttccgcacc ggcaccacta ccaacctcat ccgcagcccg	1020
ctctacggcc gcgagggcaa caccgagcgc ccggtgacca tcaccgccag cccgagcgtg	1080
cccatcttcc gcaccctcag ctacatcacc ggccctggaca acagcaaccc tgtggcgggc	1140
atcgagggcg tggagttcca gaacaccatc tccaggagca tctaccgcaa gagcggccct	1200
atcgacagct tcagcgagct gcctcctcag gacgccagcg tgagccctgc catcggctac	1260
agccacaggc tgtgccacgc caccttcctg gagcgcacatca gcggccctcg catcgcgggc	1320
accgtgttct cgtggacca cgcagcgc tctcctacga acgaggtgtc tcctagtcgc	1380
atcaccacaga tcccttgggt caaggccac accctggcta gtggcgctag tgtcatcaag	1440
ggccctggct tcaccgggtg tgacatcctg accaggaact ctatgggcga gctgggcact	1500
ctgaggggtca ctttactgg ccgcctgcct cagtcttact acatccgctt ccgctacgct	1560
agtgtcgcta accgctctgg tactttccgc tactctcagc ctccgtctta cggatatctt	1620
ttccctaaga ctatggacgc tggtagacct ctgaccagta ggagcttcgc tcacactact	1680
ctgttcactc ctatcacttt ctctagggct caggaggagt tcgacctgta catccagtct	1740
ggtgtgtaca tcgacaggat cgagttcatc cccgtgaccg ccacgttcga ggccgagtac	1800
gaccttgagc gcgcccagaa ggtggtgaac gccctcttca ctagcactaa ccagctaggc	1860
ctgaagactg acgtgaccga ctaccacatc gaccaagtga gcaacctagt ggccctgcctc	1920
tccgacgagt tctgcctcga cgagaagcgc gagctgtccg agaagggtgaa gcacgccaag	1980
cgctctccg acgagcgcaa cctgctccag gaccccaact tcaggggcat caacaggcag	2040
cccgaccgcg gctggcgcg ctccaccgac atcaccatcc agggcggtga cgacgtattc	2100
aaggagaact acgttaccct ccccggcacc ttcgacgagt gttacccac ctacctctac	2160
cagaagatcg acgagtccaa gctgaaggcc tacacccgct accagctccg cggctacatc	2220
gaggactccc aggacctgga aatctacctc atccgtaca acgccaagca cgagatcgtg	2280
aacgtgcctg gcaccggcag cctctggcct ctgagcgtgg agaaccagat cggcccttgc	2340
ggcgagccta accgctgcgc ccctcacctc gagtggaaacc ctgacctcca ctgctcgtgc	2400

P34223W000_SEQ_PCT

agggacggcg agaagtgcgc ccaccatagc caccacttct ctctggacat cgacgtgggc	2460
tgcaccgacc tgaacgagga cctgggcgtg tgggttatct tcaagatcaa gacccaggac	2520
ggtcacgcca ggctgggtaa cctggagttc cttgaggaaa agcctctgct ggggtgaggcc	2580
ctggccaggg tcaagagggc tgagaagaaa tggagggata agagggagac cctgcagctg	2640
gagaccacta tcgtctacaa ggaggctaag gagtctgtcg atgctctgtt cgtcaactct	2700
cagtacgata gactgcaagc tgataccaac atcgctatga tccacgctgc ggataagcgg	2760
gtccaccgga tccgggaggc ttaccttccg gagctttctg tcatcccggg tgtcaacgct	2820
gcgatcttcg aggaacttga ggaacggatc ttactgctg ttagtcttta cgatgcgcgg	2880
aacatcatca agaacgggga cttcaacaat ggtctgctgt gctggaacgt caagggtcat	2940
gtcgaggctc aggaacaaaa caatcatcgt agtgtccttg tcattcctga gtgggaggcg	3000
gaggtctctc aagaggtccg tgtttgcccg gggcgtgggt acattcttcg tgttactgcg	3060
tacaaggagg ggtacgggga ggggtgctgt actattcatg agattgagaa caatactgat	3120
gagcttaagt tcaacaattg tgttgaggag gaggtttacc cgaacaatac tgttacgtgc	3180
atcaactaca cggcaacgca agaggaatac ggggggacgt acacctcgcg taatagaggg	3240
tatgatgagg cgtacggaaa caaccgctc gttccagcag attatgcctc ggtttatgag	3300
gagaagtcgt acacggatag acgacgcgag aatccatgtg agtcaaatcg aggatacggg	3360
gattacacac cattaccagc aggatacgtt acaaaggagt tggaatactt cccggaaaca	3420
gataaagttt ggattgaaat cggagaaaca gaaggaacat tcatcgtcga ctcagtagaa	3480
ttgttggtga tggaagaatg a	3501

<210> 32

<211> 1166

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of the engineered insecticidal protein Cry1Da1_3 encoded by a synthetic DNA sequence wherein an

P34223W000_SEQ_PCT

additional Alanine residue has been inserted at position 2.

<400> 32

Met Ala Glu Ile Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu
1 5 10 15

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

Asn Thr Val Ala Asp Ile Ser Leu Gly Leu Ile Asn Phe Leu Tyr Ser
35 40 45

Asn Phe Val Pro Gly Gly Gly Phe Ile Val Gly Leu Leu Glu Leu Ile
50 55 60

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

Glu Gln Leu Ile Ser 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 Lys Val Tyr Val Arg
100 105 110

Ala Phe Ser Asp Trp Glu Lys 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 Ile Thr Ala
130 135 140

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

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

P34223W000_SEQ_PCT

Val Phe Gly Glu Arg Trp Gly Tyr Asp Thr Ala Thr Ile Asn Asn Arg
180 185 190

Tyr Ser Asp Leu Thr Ser Leu Ile His Val Tyr Thr Asn His Cys Val
195 200 205

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

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

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

Ile Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro
260 265 270

Phe Ile Asn Glu Asn Leu Ser Pro Ala Ala Ser Tyr Pro Thr Phe Ser
275 280 285

Ala Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu
290 295 300

Asn Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Ser Ala Tyr Trp
305 310 315 320

Gly Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu
325 330 335

Ile Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val
340 345 350

Thr Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr
355 360 365

P34223W000_SEQ_PCT

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

Glu Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro
385 390 395 400

Ile Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro
405 410 415

Ala Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg
420 425 430

Ile Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg
435 440 445

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

Pro Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys
465 470 475 480

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

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

Tyr Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr
515 520 525

Phe Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr
530 535 540

Met Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr
545 550 555 560

P34223W000_SEQ_PCT

Leu Phe Thr Pro Ile Thr Phe Ser Arg Ala Gln Glu Glu Phe Asp Leu
565 570 575

Tyr Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val
580 585 590

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

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

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

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

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

Asn Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser
675 680 685

Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr
690 695 700

Val Thr Leu Pro Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr
705 710 715 720

Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu
725 730 735

Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg
740 745 750

P34223W000_SEQ_PCT

Tyr Asn Ala Lys His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu
755 760 765

Trp Pro Leu Ser Val Glu Asn Gln Ile Gly Pro Cys Gly Glu Pro Asn
770 775 780

Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu His Cys Ser Cys
785 790 795 800

Arg Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp
805 810 815

Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val
820 825 830

Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu
835 840 845

Glu Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val
850 855 860

Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Thr Leu Gln Leu
865 870 875 880

Glu Thr Thr Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu
885 890 895

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

Met Ile His Ala Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr
915 920 925

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

P34223W000_SEQ_PCT

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

Asn Ile Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn
965 970 975

Val Lys Gly His Val Glu Val Glu Glu Gln Asn Asn His Arg Ser Val
980 985 990

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

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

Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn
1025 1030 1035

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

Pro Asn Asn Thr Val Thr Cys Ile Asn Tyr Thr Ala Thr Gln Glu
1055 1060 1065

Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Glu
1070 1075 1080

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

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

Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly
1115 1120 1125

P34223W000_SEQ_PCT

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> 33

<211> 3501

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic DNA sequence designed for plant expression encoding
Cry1Da1_4 with an additional Alanine residue inserted at position
2.

<400> 33

atggctgaga tcaacaacca gaaccagtgc gtcccgtaga actgcctgag caaccctaag	60
gagatcatcc tgggtgagga acgcctggag accggcaaca ccgtagccga cattagcctg	120
ggcctcatca acttcctcta cagcaacttc gtgcccggcg gtggcttcat cgtgggcctc	180
ctggagctta tctggggctt catcgccccg tcccagtggg acatcttcct cgcccagatc	240
gagcaactga tcagccagcg gatcgaggag ttcgctagga accaggccat ctcccgcctg	300
gagggactct ccaacctcta caaggtgtac gtgcgcgctg tcagcgactg ggagaaggac	360
ccgaccaacc cggccctccg cgaggaaatg cgtatccagt tcaacgatat gaactcggcc	420
ctcatcaccg ccatcccgtt cttccgcgtg cagaactacg aggtggccct cctgtccgtg	480
tacgttcaag ccgccaacct ccacctctcc atcctccgcg acgtgagcgt gttcggcgag	540
cgctggggct acgacaccgc caccatcaac aaccgtact ccgacctcac ctccctcatc	600
cacgtttaca ccaaccactg cgtggacacg tacaaccagg gcctccgccg cctggagggc	660
cgcttcctct ccgactggat cgtgtacaac cgcttcgcc gccagctcac catctccgtc	720
ctggacatcg tcgccttctt tcccaactac gacatccgca cctaccctat ccagaccgcc	780

P34223W000_SEQ_PCT

accagctca cccgcgaggt ctacctcgac ctcccgttca tcaacgagaa cctcagccccg	840
gccgccagct acccgacctt ctccgccgct gagtccgcca tcattcgcag cccgcacctc	900
gtggacttcc tcaactcctt caccatctac accgactccc tcgcccgcta cgcctactgg	960
ggcggtcacc tcgtgaactc cttccgcacc ggcaccacta ccaacctcat ccgcagccccg	1020
ctctacggcc gcgagggcaa caccgagcgc ccggtgacca tcaccgccag cccgagcgtg	1080
cccatcttcc gcaccctcag ctacatcacc ggcctggaca acaggaaccc tgtggcgggc	1140
atcgagggcg tggagttcca gaacaccatc tccaggagca tctaccgcaa gagcggccct	1200
atcgacagct tcagcgagct gcctcctcag gacgccagcg tgagccctgc catcggctac	1260
agccacaggc tgtgccacgc caccttcctg gagcgcacatc gcggccctcg catcgcgggc	1320
accgtgttct cgtggacca cccgagcgc tctcctacga acgaggtgtc tcctagtcgc	1380
atcacccaga tcccttgggt caaggccac accctggcta gtggcgctag tgtcatcaag	1440
ggccctggct tcaccggtgg tgacatcctg accaggaact ctatgggcga gctgggcact	1500
ctgaggggtca ctttacttgg ccgcctgcct cagtcttact acatccgctt ccgctacgct	1560
agtgtcgcta accgctctgg tactttccgc tactctcagc ctccgtctta cggatatctt	1620
ttccctaaga ctatggacgc tggtagcct ctgaccagta ggagcttcgc tcacactact	1680
ctgttcactc ctatcacttt ctctagggct caggaggagt tcgacctgta catccagtct	1740
ggtgtgtaca tcgacaggat cgagttcatc cccgtgaccg ccacgttcga ggccgagtac	1800
gaccttgagc gcgcccagaa ggtgggtgaac gccctcttca ctagcactaa ccagctaggc	1860
ctgaagactg acgtgaccga ctaccacatc gaccaagtga gcaacctagt ggcctgcctc	1920
tccgacgagt tctgcctcga cgagaagcgc gagctgtccg agaagggtgaa gcacgccaag	1980
cgcctctccg acgagcgcaa cctgctccag gaccccaact tcaggggcat caacaggcag	2040
cccgaccgcg gctggcgcgg ctccaccgac atcaccatcc agggcgggtga cgacgtattc	2100
aaggagaact acgttaccct ccccggcacc ttcgacgagt gttacccac ctacctctac	2160
cagaagatcg acgagtcaa gctgaaggcc tacacccgct accagctccg cggctacatc	2220

P34223W000_SEQ_PCT

gaggactccc aggacctgga aatctacctc atccgctaca acgccaagca cgagatcgtg	2280
aacgtgcctg gcaccggcag cctctggcct ctcagcgtgg agaaccagat cggcccttgc	2340
ggcgagccta accgctgcgc ccctcacctc gagtgggaacc ctgacctcca ctgctcgtgc	2400
agggacggcg agaagtgcgc ccaccatagc caccacttct ctctggacat cgacgtgggc	2460
tgcaccgacc tgaacgagga cctgggcgtg tgggttatct tcaagatcaa gacccaggac	2520
ggtcacgcca ggctgggtaa cctggagttc cttgaggaaa agcctctgct gggtgaggcc	2580
ctggccaggg tcaagagggc tgagaagaaa tggagggata agagggagac cctgcagctg	2640
gagaccacta tcgtctacaa ggaggctaag gagtctgtcg atgctctgtt cgtcaactct	2700
cagtacgata gactgcaagc tgataccaac atcgctatga tccacgctgc ggataagcgg	2760
gtccaccgga tccgggaggc ttaccttccg gagctttctg tcatcccggg tgtcaacgct	2820
gcgatcttcg aggaacttga ggaacggatc ttcactgcgt ttagtcttta cgatgcgcgg	2880
aacatcatca agaacgggga cttcaacaat ggtctgctgt gctggaacgt caagggtcat	2940
gtcgaggctc aggaacaaaa caatcatcgt agtgtccttg tcattcctga gtgggaggcg	3000
gaggctcttc aagaggctcg tgtttgcccg gggcgtgggt acattcttcg tgttactgcg	3060
tacaaggagg ggtacgggga ggggtgcgtt actattcatg agattgagaa caatactgat	3120
gagcttaagt tcaacaattg tgttgaggag gaggtttacc cgaacaatac tgttacgtgc	3180
atcaactaca cggcaacgca agaggaatac gaggggacgt acacctcgcg taatagaggg	3240
tatgatgagg cgtacggaaa caaccgctc gttccagcag attatgcctc ggtttatgag	3300
gagaagtcgt acacggatag acgacgcgag aatccatgtg agtcaaatcg aggatacggg	3360
gattacacac cattaccagc aggatacgtt acaaaggagt tggaatactt cccggaaaca	3420
gataaagttt ggattgaaat cggagaaaca gaaggaacat tcatcgtcga ctcagtagaa	3480
ttgttgttga tggaagaatg a	3501

<210> 34

<211> 1166

P34223W000_SEQ_PCT

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of the engineered insecticidal protein Cry1Da1_4 encoded by a synthetic DNA sequence wherein an additional Alanine residue has been inserted at position 2.

<400> 34

Met Ala Glu Ile Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu
1 5 10 15

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

Asn Thr Val Ala Asp Ile Ser Leu Gly Leu Ile Asn Phe Leu Tyr Ser
35 40 45

Asn Phe Val Pro Gly Gly Gly Phe Ile Val Gly Leu Leu Glu Leu Ile
50 55 60

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

Glu Gln Leu Ile Ser 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 Lys Val Tyr Val Arg
100 105 110

Ala Phe Ser Asp Trp Glu Lys 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 Ile Thr Ala
130 135 140

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

P34223W000_SEQ_PCT

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

Val Phe Gly Glu Arg Trp Gly Tyr Asp Thr Ala Thr Ile Asn Asn Arg
180 185 190

Tyr Ser Asp Leu Thr Ser Leu Ile His Val Tyr Thr Asn His Cys Val
195 200 205

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

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

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

Ile Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro
260 265 270

Phe Ile Asn Glu Asn Leu Ser Pro Ala Ala Ser Tyr Pro Thr Phe Ser
275 280 285

Ala Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu
290 295 300

Asn Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Tyr Ala Tyr Trp
305 310 315 320

Gly Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu
325 330 335

Ile Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val
340 345 350

P34223W000_SEQ_PCT

Thr Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr
355 360 365

Ile Thr Gly Leu Asp Asn Arg Asn Pro Val Ala Gly Ile Glu Gly Val
370 375 380

Glu Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro
385 390 395 400

Ile Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro
405 410 415

Ala Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg
420 425 430

Ile Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg
435 440 445

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

Pro Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys
465 470 475 480

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

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

Tyr Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr
515 520 525

Phe Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr
530 535 540

P34223W000_SEQ_PCT

Met Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr
545 550 555 560

Leu Phe Thr Pro Ile Thr Phe Ser Arg Ala Gln Glu Glu Phe Asp Leu
565 570 575

Tyr Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val
580 585 590

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

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

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

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

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

Asn Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser
675 680 685

Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr
690 695 700

Val Thr Leu Pro Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr
705 710 715 720

Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu
725 730 735

P34223W000_SEQ_PCT

Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg
740 745 750

Tyr Asn Ala Lys His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu
755 760 765

Trp Pro Leu Ser Val Glu Asn Gln Ile Gly Pro Cys Gly Glu Pro Asn
770 775 780

Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu His Cys Ser Cys
785 790 795 800

Arg Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp
805 810 815

Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val
820 825 830

Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu
835 840 845

Glu Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val
850 855 860

Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Thr Leu Gln Leu
865 870 875 880

Glu Thr Thr Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu
885 890 895

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

Met Ile His Ala Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr
915 920 925

P34223W000_SEQ_PCT

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

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

Asn Ile Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn
965 970 975

Val Lys Gly His Val Glu Val Glu Glu Gln Asn Asn His Arg Ser Val
980 985 990

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

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

Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn
1025 1030 1035

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

Pro Asn Asn Thr Val Thr Cys Ile Asn Tyr Thr Ala Thr Gln Glu
1055 1060 1065

Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Glu
1070 1075 1080

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

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

P34223W000_SEQ_PCT

Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala 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> 35
<211> 3501
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic DNA sequence designed for plant expression encoding
Cry1Da1_5 with an additional Alanine residue inserted at position
2.

<400> 35
atggctgaga tcaacaacca gaaccagtgc gtcccgtaga actgcctgag caaccctaag 60
gagatcatcc tgggtgagga acgcctggag accggcaaca ccgtagccga cattagcctg 120
ggcctcatca acttcttcta cagcaacttc gtgcccggcg gtggcttcat cgtgggcctc 180
ctggagctta tctggggctt catcggtccc tcccagtggg acatcttcct cgcccagatc 240
gagcaactga tcagccagcg gatcgaggag ttcgctagga accaggccat ctcccgcctg 300
gagggactct ccaacctcta caaggtgtac gtgcgcgcgt tcagcgactg ggagaaggac 360
ccgaccaacc cggccctccg cgaggaaatg cgtatccagt tcaacgatat gaactcggcc 420
ctcatcaccg ccatcccgtt cttccgcgtg cagaactacg aggtggccct cctgtccgtg 480
tacgttcaag ccgccaacct ccacctctcc atcctccgcg acgtgagcgt gttcggcgag 540
cgctgggggt acgacaccgc caccatcaac aaccgtact ccgacctcac ctccctcatc 600

P34223W000_SEQ_PCT

cacgtttaca ccaaccactg cgtggacacg tacaaccagg gcctccgccg cctggagggc	660
cgcttcctct ccgactggat cgtgtacaac cgcttccgcc gccagctcac catctccgtc	720
ctggacatcg tcgccttctt tcccaactac gacatccgca cctaccctat ccagaccgcc	780
accagctca cccgcgaggt ctacctgac ctcccggttca tcaacgagaa cctcagccc	840
gccgccagct acccgacctt ctccgccgt gagtccgcc tcatctgcag cccgcacctc	900
gtggacttcc tcaactcctt caccatctac accgactccc tcgcccgcag cgcctactgg	960
ggcggtcacc tcgtgaactc cttccgcacc ggcaccacta ccaacctcat ccgcagccc	1020
ctctacggcc gcgaggga caccgagcgc ccggtgacca tcaccgccag cccgagcgtg	1080
cccatcttcc gcacctcag ctaccgcacc ggcttgga acagcaaccc tgtggcgggc	1140
atcgagggcg tggagttcca gaacaccatc tccaggagca tctaccgcaa gagcggccct	1200
atcgacagct tcagcgagct gcctcctcag gacgccagcg tgagccctgc catcggctac	1260
agccacaggc tgtgccacgc caccttcctg gagcgcacat gcggccctcg catcgcgggc	1320
accgtgttct cgtggaccca ccgcagcgcc tctcctacga acgaggtgtc tcctagtcgc	1380
atcaccaga tcccttgggt caaggccac accctggcta gtggcgctag tgtcatcaag	1440
ggccctggct tcaccgggtg tgacatcctg accaggaact ctatgggcga gctgggcact	1500
ctgaggggtca ctttacttgg ccgcctgcct cagtcttact acatccgctt ccgctacgct	1560
agtgtcgcta accgctctgg tactttccgc tactctcagc ctccgtctta cggatatctt	1620
ttccctaaga ctatggacgc tggtgagcct ctgaccagta ggagcttcgc tcacactact	1680
ctgttcactc ctatcacttt ctctagggct caggaggagt tcgacctgta catccagtct	1740
ggtgtgtaca tcgacaggat cgagttcatc cccgtgaccg ccacgttcga ggccgagtac	1800
gaccttgagc gcgcccagaa ggtggtgaac gccctcttca ctagcactaa ccagctaggc	1860
ctgaagactg acgtgaccga ctaccacatc gaccaagtga gcaacctagt ggctgcctc	1920
tccgacgagt tctgcctcga cgagaagcgc gagctgtccg agaaggtgaa gcacgccaag	1980
cgctctccg acgagcgcaa cctgctccag gaccccaact tcaggggcat caacaggcag	2040

P34223W000_SEQ_PCT

cccgaccgcg gctggcgcg gctccaccgac atcaccatcc agggcggtga cgacgtattc	2100
aaggagaact acgttaccct ccccggcacc ttcgacgagt gttacccac ctacctctac	2160
cagaagatcg acgagtccaa gctgaaggcc tacacccgct accagctccg cggctacatc	2220
gaggactccc aggacctgga aatctacctc atccgctaca acgccaagca cgagatcgtg	2280
aacgtgcctg gcaccggcag cctctggcct ctcagcgtgg agaaccagat cggcccttgc	2340
ggcgagccta accgctgcgc ccctcacctc gagtgggaacc ctgacctcca ctgctcgtgc	2400
agggacggcg agaagtgcgc ccaccatagc caccacttct ctctggacat cgacgtgggc	2460
tgcaccgacc tgaacgagga cctgggcgtg tgggttatct tcaagatcaa gaccaggac	2520
ggtcacgcca ggctgggtaa cctggagttc cttgaggaaa agcctctgct gggtgaggcc	2580
ctggccaggg tcaagagggc tgagaagaaa tggagggata agagggagac cctgcagctg	2640
gagaccacta tcgtctacaa ggaggctaag gagtctgtcg atgctctgtt cgtcaactct	2700
cagtacgata gactgcaagc tgataccaac atcgctatga tccacgctgc ggataagcgg	2760
gtccaccgga tccgggaggc ttaccttccg gagctttctg tcatcccggg tgtcaacgct	2820
gcgatcttcg aggaacttga ggaacggatc ttcactgcgt ttagtcttta cgatgcgcgg	2880
aacatcatca agaacgggga cttcaacaat ggtctgctgt gctggaacgt caagggtcat	2940
gtcgaggctg aggaacaaaa caatcatcgt agtgtccttg tcattcctga gtgggaggcg	3000
gaggctctctc aagaggctcg tgtttgcccg gggcgtgggt acattcttcg tgttactgcg	3060
tacaaggagg ggtacgggga ggggtgcgtt actattcatg agattgagaa caatactgat	3120
gagcttaagt tcaacaattg tgttgaggag gaggtttacc cgaacaatac tgttacgtgc	3180
atcaactaca cggcaacgca agaggaatac gaggggacgt acacctcgcg taatagaggg	3240
tatgatgagg cgtacggaaa caaccgctcg gttccagcag attatgcctc ggtttatgag	3300
gagaagtcgt acacggatag acgacgcgag aatccatgtg agtcaaactc aggatacgg	3360
gattacacac cattaccagc aggatacgtt acaaaggagt tggaatactt cccggaaaca	3420
gataaagttt ggattgaaat cggagaaaca gaaggaacat tcatcgtcga ctcagtagaa	3480

ttgtttgtga tggaagaatg a

3501

<210> 36

<211> 1166

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of the engineered insecticidal protein
Cry1Da1_5 encoded by a synthetic DNA sequence wherein an
additional Alanine residue has been inserted at position 2.

<400> 36

Met Ala Glu Ile Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu
1 5 10 15

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

Asn Thr Val Ala Asp Ile Ser Leu Gly Leu Ile Asn Phe Leu Tyr Ser
35 40 45

Asn Phe Val Pro Gly Gly Gly Phe Ile Val Gly Leu Leu Glu Leu Ile
50 55 60

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

Glu Gln Leu Ile Ser 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 Lys Val Tyr Val Arg
100 105 110

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

P34223W000_SEQ_PCT

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

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

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

Val Phe Gly Glu Arg Trp Gly Tyr Asp Thr Ala Thr Ile Asn Asn Arg
180 185 190

Tyr Ser Asp Leu Thr Ser Leu Ile His Val Tyr Thr Asn His Cys Val
195 200 205

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

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

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

Ile Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro
260 265 270

Phe Ile Asn Glu Asn Leu Ser Pro Ala Ala Ser Tyr Pro Thr Phe Ser
275 280 285

Ala Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu
290 295 300

Asn Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Ser Ala Tyr Trp
305 310 315 320

P34223W000_SEQ_PCT

Gly Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu
325 330 335

Ile Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val
340 345 350

Thr Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr
355 360 365

Arg Thr Gly Leu Asp Asn Ser Asn Pro Val Ala Gly Ile Glu Gly Val
370 375 380

Glu Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro
385 390 395 400

Ile Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro
405 410 415

Ala Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg
420 425 430

Ile Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg
435 440 445

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

Pro Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys
465 470 475 480

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

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

P34223W000_SEQ_PCT

Tyr Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr
515 520 525

Phe Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr
530 535 540

Met Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr
545 550 555 560

Leu Phe Thr Pro Ile Thr Phe Ser Arg Ala Gln Glu Glu Phe Asp Leu
565 570 575

Tyr Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val
580 585 590

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

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

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

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

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

Asn Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser
675 680 685

Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr
690 695 700

P34223W000_SEQ_PCT

Val Thr Leu Pro Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr
705 710 715 720

Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu
725 730 735

Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg
740 745 750

Tyr Asn Ala Lys His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu
755 760 765

Trp Pro Leu Ser Val Glu Asn Gln Ile Gly Pro Cys Gly Glu Pro Asn
770 775 780

Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu His Cys Ser Cys
785 790 795 800

Arg Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp
805 810 815

Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val
820 825 830

Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu
835 840 845

Glu Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val
850 855 860

Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Thr Leu Gln Leu
865 870 875 880

Glu Thr Thr Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu
885 890 895

P34223W000_SEQ_PCT

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

Met Ile His Ala Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr
915 920 925

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

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

Asn Ile Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn
965 970 975

Val Lys Gly His Val Glu Val Glu Glu Gln Asn Asn His Arg Ser Val
980 985 990

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

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

Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn
1025 1030 1035

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

Pro Asn Asn Thr Val Thr Cys Ile Asn Tyr Thr Ala Thr Gln Glu
1055 1060 1065

Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Glu
1070 1075 1080

P34223W000_SEQ_PCT

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

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

Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala 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> 37
<211> 3501
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic DNA sequence designed for plant expression encoding
Cry1Da1_6 with an additional Alanine residue inserted at position
2.

<400> 37
atggctgaga tcaacaacca gaaccagtgc gtcccgtaca actgcctgag caaccctaag 60
gagatcatcc tgggtgagga acgcctggag accggcaaca ccgtagccga cattagcctg 120
ggcctcatca acttcctcta cagcaacttc gtgcccggcg gtggcttcat cgtgggcctc 180
ctggagctta tctggggctt catcgggccg tccagtgagg acatcttcct cgccagatc 240
gagcaactga tcagccagcg gatcgaggag ttcgctagga accaggccat ctccgcctg 300
gagggactct ccaacctcta caaggtgtac gtgcgcgctg tcagcgactg ggagaaggac 360
ccgaccaacc cggccctccg cgaggaaatg cgtatccagt tcaacgatat gaactcggcc 420

P34223W000_SEQ_PCT

ctcatcaccg ccatcccgt cttccgcgtg cagaactacg aggtggccct cctgtccgtg	480
tacgttcaag ccgccaacct ccacctctcc atcctccgcg acgtgagcgt gttcggcgag	540
cgctgggggt acgacaccgc caccatcaac aaccgctact ccgacctcac ctccctcatc	600
cacgtttaca ccaaccactg cgtggacacg tacaaccagg gcctccgccg cctggagggc	660
cgcttcctct ccgactggat cgtgtacaac cgcttccgcc gccagctcac catctccgtc	720
ctggacatcg tcgccttctt tcccaactac gacatccgca cctaccctat ccagaccgcc	780
accagctca cccgcgaggt ctacctgac ctcccgttca tcaacgagaa cctcagcccg	840
gccgccaagt acccgacctt ctccgccgt gagtccgcca tcattcgag cccgcacctc	900
gtggacttcc tcaactcctt caccatctac accgactccc tcgcccgcag cgctactgg	960
ggcggtcacc tcgtgaactc cttccgcacc ggcaccacta ccaacctcat ccgcagcccg	1020
ctctacggcc gcgagggcaa caccgagcgc ccggtgacca tcaccgccag cccgagcgtg	1080
cccatcttcc gcaccctcag ctacccccacc ggcctggaca acagcaaccc tgtggcgggc	1140
atcgagggcg tggagttcca gaacaccatc tccaggagca tctaccgcaa gagcggccct	1200
atcgacagct tcagcgagct gcctcctcag gacgccagcg tgagccctgc catcggctac	1260
agccacaggc tgtgccacgc caccttcctg gagcgcacga gcggccctcg catcgcgggc	1320
accgtgttct cgtggaccca ccgcagcgcc tctcctacga acgaggtgtc tcctagtcgc	1380
atcaccaga tcccttgggt caaggccac accctggcta gtggcgctag tgtcatcaag	1440
ggccctggct tcaccggtgg tgacatcctg accaggaact ctatgggcga gctgggcact	1500
ctgaggggtca ctttactgg ccgcctgcct cagtcttact acatccgctt ccgctacgct	1560
agtgtcgcta accgctctgg tactttccgc tactctcagc ctccgtctta cggtatctct	1620
ttccctaaga ctatggacgc tggtagcct ctgaccagta ggagcttcgc tcacactact	1680
ctgttcactc ctatcacttt ctctagggct caggaggagt tcgacctgta catccagtct	1740
ggtgtgtaca tcgacaggat cgagttcatc cccgtgaccg ccacgttcga ggccgagtac	1800
gaccttgagc gcgcccagaa ggtggtgaac gccctcttca ctagcactaa ccagctaggc	1860

P34223W000_SEQ_PCT

ctgaagactg acgtgaccga ctaccacatc gaccaagtga gcaacctagt ggctgcctc	1920
tccgacgagt tctgcctcga cgagaagcgc gagctgtccg agaaggtgaa gcacgccaag	1980
cgcctctccg acgagcgcaa cctgctccag gaccccaact tcaggggcat caacaggcag	2040
cccgaccgcg gctggcgagg ctccaccgac atcaccatcc agggcgggtga cgacgtattc	2100
aaggagaact acgttaccct ccccggcacc ttcgacgagt gttacccac ctaccttac	2160
cagaagatcg acgagtccaa gctgaaggcc tacacccgct accagctccg cggctacatc	2220
gaggactccc aggacctgga aatctacctc atccgctaca acgccaagca cgagatcgtg	2280
aacgtgcctg gcaccggcag cctctggcct ctgacgtgg agaaccagat cggcccttgc	2340
ggcgagccta accgctgcgc cctcacctc gagtgggaacc ctgacctca ctgctcgtgc	2400
agggacggcg agaagtgcgc ccaccatagc caccacttct ctctggacat cgacgtgggc	2460
tgcaccgacc tgaacgagga cctgggcgtg tgggttatct tcaagatcaa gaccaggac	2520
ggtcacgcca ggctgggtaa cctggagttc cttgaggaaa agcctctgct gggtagggcc	2580
ctggccaggg tcaagagggc tgagaagaaa tggagggata agagggagac cctgcagctg	2640
gagaccacta tcgtctacaa ggaggctaag gagtctgtcg atgctctgtt cgtcaactct	2700
cagtacgata gactgcaagc tgataccaac atcgctatga tccacgtgc ggataagcgg	2760
gtccaccgga tccgggaggc ttaccttccg gagctttctg tcatcccggg tgtcaacgct	2820
gcgatcttcg aggaacttga ggaacggatc ttactgcgt ttagtcttta cgatgcgcgg	2880
aacatcatca agaacgggga cttcaacaat ggtctgctgt gctggaacgt caagggtcat	2940
gtcgaggctc aggaacaaaa caatcatcgt agtgccttg tcattcctga gtgggaggcg	3000
gaggctcttc aagaggtccg tgtttgcccg gggcgtgggt acattcttcg tgttactgcg	3060
tacaaggagg ggtacgggga ggggtgcgtt actattcatg agattgagaa caatactgat	3120
gagcttaagt tcaacaattg tgttgaggag gaggtttacc cgaacaatac tgttacgtgc	3180
atcaactaca cggcaacgca agaggaatac gaggggacgt acacctcgcg taatagaggg	3240
tatgatgagg cgtacggaaa caaccgctc gttccagcag attatgcctc ggtttatgag	3300

P34223W000_SEQ_PCT

gagaagtcgt acacggatag acgacgag aatccatgtg agtcaaatcg aggatacggg 3360
gattacacac cattaccagc aggatacgtt acaaaggagt tggaatactt cccggaaaca 3420
gataaagttt ggattgaaat cggagaaaca gaaggaacat tcatcgtcga cttagtagaa 3480
ttgttgttga tggaagaatg a 3501

<210> 38
<211> 1166
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of the engineered insecticidal protein
Cry1Da1_6 encoded by a synthetic DNA sequence wherein an
additional Alanine residue has been inserted at position 2.

<400> 38

Met Ala Glu Ile Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu
1 5 10 15

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

Asn Thr Val Ala Asp Ile Ser Leu Gly Leu Ile Asn Phe Leu Tyr Ser
35 40 45

Asn Phe Val Pro Gly Gly Gly Phe Ile Val Gly Leu Leu Glu Leu Ile
50 55 60

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

Glu Gln Leu Ile Ser 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 Lys Val Tyr Val Arg
100 105 110

P34223W000_SEQ_PCT

Ala Phe Ser Asp Trp Glu Lys 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 Ile Thr Ala
130 135 140

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

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

Val Phe Gly Glu Arg Trp Gly Tyr Asp Thr Ala Thr Ile Asn Asn Arg
180 185 190

Tyr Ser Asp Leu Thr Ser Leu Ile His Val Tyr Thr Asn His Cys Val
195 200 205

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

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

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

Ile Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro
260 265 270

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

Ala Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu
290 295 300

P34223W000_SEQ_PCT

Asn Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Ser Ala Tyr Trp
305 310 315 320

Gly Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu
325 330 335

Ile Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val
340 345 350

Thr Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr
355 360 365

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

Glu Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro
385 390 395 400

Ile Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro
405 410 415

Ala Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg
420 425 430

Ile Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg
435 440 445

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

Pro Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys
465 470 475 480

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

P34223W000_SEQ_PCT

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

Tyr Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr
515 520 525

Phe Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr
530 535 540

Met Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr
545 550 555 560

Leu Phe Thr Pro Ile Thr Phe Ser Arg Ala Gln Glu Glu Phe Asp Leu
565 570 575

Tyr Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val
580 585 590

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

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

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

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

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

Asn Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser
675 680 685

P34223W000_SEQ_PCT

Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr
690 695 700

Val Thr Leu Pro Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr
705 710 715 720

Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu
725 730 735

Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg
740 745 750

Tyr Asn Ala Lys His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu
755 760 765

Trp Pro Leu Ser Val Glu Asn Gln Ile Gly Pro Cys Gly Glu Pro Asn
770 775 780

Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu His Cys Ser Cys
785 790 795 800

Arg Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp
805 810 815

Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val
820 825 830

Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu
835 840 845

Glu Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val
850 855 860

Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Thr Leu Gln Leu
865 870 875 880

P34223W000_SEQ_PCT

Glu Thr Thr Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu
885 890 895

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

Met Ile His Ala Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr
915 920 925

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

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

Asn Ile Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn
965 970 975

Val Lys Gly His Val Glu Val Glu Glu Gln Asn Asn His Arg Ser Val
980 985 990

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

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

Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn
1025 1030 1035

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

Pro Asn Asn Thr Val Thr Cys Ile Asn Tyr Thr Ala Thr Gln Glu
1055 1060 1065

P34223W000_SEQ_PCT

Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Glu
1070 1075 1080

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

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

Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala 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> 39
<211> 3501
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic DNA sequence designed for plant expression encoding
Cry1Da1_7 with an additional Alanine residue inserted at position
2.

<400> 39
atggctgaga tcaacaacca gaaccagtgc gtcccgtaga actgcctgag caaccctaag 60
gagatcatcc tgggtgagga acgcctggag accggcaaca ccgtagccga cattagcctg 120
ggcctcatca acttcctcta cagcaacttc gtgcccggcg gtggcttcat cgtgggcctc 180
ctggagctta tctggggcctt catcggtccc tcccagtggg acatcttcct cgcccagatc 240

P34223W000_SEQ_PCT

gagcaactga tcagccagcg gatcgaggag ttcgctagga accaggccat ctcccgctg	300
gagggactct ccaacctcta caaggtgtac gtgcgcgcgt tcagcgactg ggagaaggac	360
ccgaccaacc cggccctccg cgaggaaatg cgtatccagt tcaacgatat gaactcggcc	420
ctcatcaccg ccatcccgtt cttccgcgtg cagaactacg aggtggccct cctgtccgtg	480
tacgttcaag ccgccaacct ccacctctcc atcctccgcg acgtgagcgt gttcggcgag	540
cgctggggct acgacaccgc caccatcaac aaccgctact ccgacctcac ctccctcatc	600
cacgtttaca ccaaccactg cgtggacacg tacaaccagg gcctccgccg cctggagggc	660
cgcttcctct ccgactggat cgtgtacaac cgcttcgcc gccagctcac catctccgtc	720
ctggacatcg tcgccttctt tcccaactac gacatccgca cctaccctat ccagaccgcc	780
accagctca cccgcgaggt ctacctgac ctcccgttca tcaacgagaa cctcagcccg	840
gccgccgtct acccgacctt ctccgccgt gagtccgcca tcattcgag cccgcacctc	900
gtggacttcc tcaactcctt caccatctac accgactccc tcgcccgcag cgcctactgg	960
ggcggtcacc tcgtgaactc cttccgcacc ggcaccacta ccaacctcat ccgcagcccg	1020
ctctacggcc gcgagggcaa caccgagcgc ccggtgacca tcaccgccag cccgagcgtg	1080
cccatcttcc gcacctcag ctaccccacc ggcttggaac acagcaaccc tgtggcgggc	1140
atcgagggcg tggagttcca gaacaccatc tccaggagca tctaccgcaa gagcggccct	1200
atcgacagct tcagcgagct gcctcctcag gacgccagcg tgagccctgc catcggctac	1260
agccacaggc tgtgccacgc caccttcctg gagcgcacga gcggccctcg catcgcgggc	1320
accgtgttct cgtggaccca ccgcagcgcc tctcctacga acgaggtgtc tcctagtgcg	1380
atcacccaga tcccttgggt caaggccac accctggcta gtggcgctag tgtcatcaag	1440
ggccctggct tcaccggtgg tgacatcctg accaggaact ctatgggcga gctgggcact	1500
ctgaggggtca ctttactg cgcctgcct cagtcttact acatccgctt ccgtacgct	1560
agtgtcgcta accgctctgg tactttccgc tactctcagc ctccgtctta cggatatctt	1620
ttccctaaga ctatggacgc tggtagcct ctgaccagta ggagcttcgc tcacactact	1680

P34223W000_SEQ_PCT

ctgttcactc ctatcacttt ctctagggct caggaggagt tcgacctgta catccagtct	1740
ggtgtgtaca tcgacaggat cgagttcatc cccgtgaccg ccacgttcga ggccgagtac	1800
gaccttgagc gcgcccagaa ggtggtgaac gccctcttca ctagcactaa ccagctaggc	1860
ctgaagactg acgtgaccga ctaccacatc gaccaagtga gcaacctagt ggctgcctc	1920
tccgacgagt tctgcctcga cgagaagcgc gagctgtccg agaagggtgaa gcacgccaag	1980
cgcctctccg acgagcgcaa cctgctccag gaccccaact tcaggggcat caacaggcag	2040
cccgaccgcg gctggcgagg ctccaccgac atcaccatcc agggcggtga cgacgtattc	2100
aaggagaact acgttaccct ccccggcacc ttcgacgagt gttacccac ctacctctac	2160
cagaagatcg acgagtccaa gctgaaggcc tacacccgct accagctccg cggctacatc	2220
gaggactccc aggacctgga aatctacctc atccgctaca acgccaagca cgagatcgtg	2280
aacgtgcctg gcaccggcag cctctggcct ctcagcgtgg agaaccagat cggcccttgc	2340
ggcgagccta accgctgcgc cctcacctc gagtggaacc ctgacctcca ctgctcgtgc	2400
agggacggcg agaagtgcgc ccaccatagc caccacttct ctctggacat cgacgtgggc	2460
tgcaccgacc tgaacgagga cctgggcgtg tgggttatct tcaagatcaa gaccaggac	2520
ggtcacgcca ggctgggtaa cctggagttc cttgaggaaa agcctctgct gggtgaggcc	2580
ctggccaggg tcaagagggc tgagaagaaa tggagggata agagggagac cctgcagctg	2640
gagaccacta tcgtctacaa ggaggctaag gagtctgtcg atgctctgtt cgtcaactct	2700
cagtacgata gactgcaagc tgataccaac atcgctatga tccacgctgc ggataagcgg	2760
gtccaccgga tccgggaggc ttaccttccg gagctttctg tcatcccggg tgtcaacgct	2820
gcgatcttcg aggaacttga ggaacggatc ttcactgcgt ttagtcttta cgatgcgcgg	2880
aacatcatca agaacgggga cttcaacaat ggtctgctgt gctggaacgt caagggtcat	2940
gtcgaggtcg aggaacaaaa caatcatcgt agtgccttg tcattcctga gtgggaggcg	3000
gaggtctctc aagaggctcg tgtttgcccg gggcgtgggt acattcttcg tgttactgcg	3060
tacaaggagg ggtacgggga ggggtgcgtt actattcatg agattgagaa caatactgat	3120

P34223W000_SEQ_PCT

gagcttaagt tcaacaattg tggtgaggag gaggtttacc cgaacaatac tgttacgtgc 3180
atcaactaca cggcaacgca agaggaatac gagggggacgt acacctcgcg taatagaggg 3240
tatgatgagg cgtacggaaa caacccgtcg gttccagcag attatgcctc ggtttatgag 3300
gagaagtcgt acacggatag acgacgcgag aatccatgtg agtcaaatcg aggatacggg 3360
gattacacac cattaccagc aggatacgtt acaaaggagt tggaatactt cccggaaaca 3420
gataaagttt ggattgaaat cggagaaaca gaaggaacat tcatcgtcga ctcagtagaa 3480
ttgttgttga tggaagaatg a 3501

<210> 40
<211> 1166
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of the engineered insecticidal protein
Cry1Da1_7 encoded by a synthetic DNA sequence wherein an
additional Alanine residue has been inserted at position 2.

<400> 40

Met Ala Glu Ile Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu
1 5 10 15

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

Asn Thr Val Ala Asp Ile Ser Leu Gly Leu Ile Asn Phe Leu Tyr Ser
35 40 45

Asn Phe Val Pro Gly Gly Gly Phe Ile Val Gly Leu Leu Glu Leu Ile
50 55 60

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

P34223W000_SEQ_PCT

Glu Gln Leu Ile Ser 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 Lys Val Tyr Val Arg
100 105 110

Ala Phe Ser Asp Trp Glu Lys 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 Ile Thr Ala
130 135 140

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

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

Val Phe Gly Glu Arg Trp Gly Tyr Asp Thr Ala Thr Ile Asn Asn Arg
180 185 190

Tyr Ser Asp Leu Thr Ser Leu Ile His Val Tyr Thr Asn His Cys Val
195 200 205

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

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

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

Ile Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro
260 265 270

P34223W000_SEQ_PCT

Phe Ile Asn Glu Asn Leu Ser Pro Ala Ala Val Tyr Pro Thr Phe Ser
 275 280 285

Ala Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu
 290 295 300

Asn Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Ser Ala Tyr Trp
 305 310 315 320

Gly Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu
 325 330 335

Ile Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val
 340 345 350

Thr Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr
 355 360 365

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

Glu Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro
 385 390 395 400

Ile Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro
 405 410 415

Ala Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg
 420 425 430

Ile Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg
 435 440 445

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

P34223W000_SEQ_PCT

Pro Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys
465 470 475 480

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

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

Tyr Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr
515 520 525

Phe Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr
530 535 540

Met Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr
545 550 555 560

Leu Phe Thr Pro Ile Thr Phe Ser Arg Ala Gln Glu Glu Phe Asp Leu
565 570 575

Tyr Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val
580 585 590

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

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

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

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

P34223W000_SEQ_PCT

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

Asn Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser
675 680 685

Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr
690 695 700

Val Thr Leu Pro Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr
705 710 715 720

Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu
725 730 735

Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg
740 745 750

Tyr Asn Ala Lys His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu
755 760 765

Trp Pro Leu Ser Val Glu Asn Gln Ile Gly Pro Cys Gly Glu Pro Asn
770 775 780

Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu His Cys Ser Cys
785 790 795 800

Arg Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp
805 810 815

Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val
820 825 830

Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu
835 840 845

P34223W000_SEQ_PCT

Glu Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val
850 855 860

Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Thr Leu Gln Leu
865 870 875 880

Glu Thr Thr Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu
885 890 895

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

Met Ile His Ala Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr
915 920 925

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

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

Asn Ile Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn
965 970 975

Val Lys Gly His Val Glu Val Glu Glu Gln Asn Asn His Arg Ser Val
980 985 990

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

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

Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn
1025 1030 1035

P34223W000_SEQ_PCT

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

Pro Asn Asn Thr Val Thr Cys Ile Asn Tyr Thr Ala Thr Gln Glu
1055 1060 1065

Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Glu
1070 1075 1080

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

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

Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala 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> 41

<211> 3423

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic DNA sequence designed for plant expression encoding
TIC844 with an additional Alanine residue inserted at position 2.

<400> 41

atggctgaga tcaacaacca gaaccagtgc gtcccgtaga actgcctgag caaccctaag

60

P34223W000_SEQ_PCT

gagatcatcc tgggtgagga acgcctggag accggcaaca ccgtagccga cattagcctg	120
ggcctcatca acttcctcta cagcaacttc gtgcccggcg gtggcttcat cgtgggcctc	180
ctggagctta tctggggcctt catcggccccg tcccagtgagg acatcttcct cgcccagatc	240
gagcaactga tcagccagcg gatcaggagg ttcgctagga accaggccat ctcccgctg	300
gagggactct ccaacctcta caaggtgtac gtgcgcgcgt tcagcgactg ggagaaggac	360
ccgaccaacc cggccctccg cgaggaaatg cgtatccagt tcaacgatat gaactcggcc	420
ctcatcaccg ccatcccgct cttccgcgtg cagaactacg aggtggccct cctgtccgtg	480
tacgttcaag ccgccaacct ccacctctcc atcctccgcg acgtgagcgt gttcggcgag	540
cgctgggggct acgacaccgc caccatcaac aaccgctact ccgacctcac ctccctcatc	600
cacgtttaca ccaaccactg cgtggacacg tacaaccagg gcctccgccg cctggagggc	660
cgcttcctct ccgactggat cgtgtacaac cgcttcgcc gccagctcac catctccgtc	720
ctggacatcg tcgccttctt tcccaactac gacatccgca cctaccctat ccagaccgcc	780
accagctca ccgcgagggt ctacctgac ctcccgttca tcaacgagaa cctcagcccg	840
gccgccagct acccgacctt ctccgccgct gagtccgcca tcattcgag cccgcacctc	900
gtggacttcc tcaactcctt caccatctac accgactccc tcgcccgcta cgcctactgg	960
ggcggtcacc tcgtgaactc cttccgcacc ggaccacta ccaacctcat ccgcagcccg	1020
ctctacggcc gcgagggcaa caccgagcgc ccggtgacca tcaccgccag cccgagcgtg	1080
cccatcttcc gcacctcag ctacatcacc ggcttgga acagcaaccc tgtggcgggc	1140
atcgagggcg tggagttcca gaacaccatc tccaggagca tctaccgaa gagcggccct	1200
atcgacagct tcagcgagct gcctcctcag gacgccagcg tgagccctgc catcggctac	1260
agccacaggc tgtgccacgc caccttcctg gagcgcacga gcggccctcg catcgcgggc	1320
accgtgttct cgtggacca ccgcagcgc tctcctacga acgaggtgtc tcctagtcgc	1380
atcaccaga tcccttgggt caaggccac accctggcta gtggcgctag tgtcatcaag	1440
ggccctggct tcaccggtgg tgacatcctg accaggaact ctatgggcga gctgggcact	1500

P34223W000_SEQ_PCT

ctgagggtca ctttacttgg ccgcctgcct cagtcttact acatccgctt ccgctacgct	1560
agtgtcgcta accgctctgg tactttccgc tactctcagc ctccgtctta cggtatctct	1620
ttccctaaga ctatggacgc tggtagcct ctgaccagta ggagcttcgc tcacactact	1680
ctgttcactc ctatcacttt ctctagggct caggaggagt tcgacctgta catccagtct	1740
gggtgtgtaca tcgacaggat cgagttcatc cccgtgaccg ccacgttcga ggccgagtac	1800
gaccttgagc gcgcccagaa ggctgtcaat gagctcttca cgtccagcaa tcagatcggc	1860
ctgaagaccg acgtcactga ctaccacatc gaccaagtct ccaacctcgt ggagtgcctc	1920
tccgatgagt tctgcctcga cgagaagaag gagctgtccg agaaggtgaa gcatgccaaag	1980
cgtctcagcg acgagaggaa tctcctccag gaccccaatt tccgcggcat caacaggcag	2040
ctcgaccgcg gctggcgcg gaggaccgac atcacgatcc agggcgggcga cgatgtgttc	2100
aaggagaact acgtgactct cctgggcact ttcgacgagt gctaccctac ctacttgtac	2160
cagaagatcg atgagtccaa gctcaaggct tacactcgct accagctccg cggctacatc	2220
gaagacagcc aagacctcga gatttacctg atccgctaca acgccaagca cgagaccgtc	2280
aacgtgcccc gtactgggtc cctctggccg ctgagcgccc ccagcccgat cggcaagtgt	2340
gcccaccaca gccaccactt ctcttggac atcgatgtgg gctgcaccga cctgaacgag	2400
gacctcggag tctgggtcat cttcaagatc aagaccagg acggccacgc gcgcctgggc	2460
aacctggagt tcctcgagga gaagcccctg gtcggtgagg ctctggccag ggtcaagagg	2520
gctgagaaga agtggaggga caagcgcgag aagctcgagt gggagaccaa catcgtttac	2580
aaggaggcca aggagagcgt cgacgccctg ttcgtgaact cccagtacga ccgcctgcag	2640
gccgacacca acatcgccat gatccacgct gccgacaaga ggggtgcacag cattcgcgag	2700
gcctacctgc ctgagctgtc cgtgatccct ggtgtgaacg ctgccatctt tgaggagctg	2760
gagggccgca tctttaccgc attctccctg tacgacgccc gcaacgtgat caagaacggt	2820
gacttcaaca atggcctcag ctgctggaac gtcaagggcc acgtggacgt cgaggaacag	2880
aacaaccacc gtcctgcctt ggtcgtccca gagtgggagg ctgaggtctc ccaagaggtc	2940

P34223W000_SEQ_PCT

```

cgcgctctgcc caggccgcgg ctacattctc agggtcaccg cttacaagga gggctacggt      3000
gagggctgtg tgaccatcca cgagatcgag aacaacaccg acgagcttaa gttctccaac      3060
tgcgtggagg aggaggtgta cccaaacaac accgttactt gcaacgacta caccgccacc      3120
caggaggagt acgagggcac ctacacttcc aggaacaggg gctacgatgg tgcctacgag      3180
agcaacagca gcgttcctgc tgactacgct tccgcctacg aggagaaggc ctacacggat      3240
ggccgcaggg acaacccttg cgagagcaac cgcggctacg gcgactacac tcccctgccc      3300
gccggctacg ttaccaagga gctggagtac ttcccggaga ctgacaaggt gtggatcgag      3360
atcggcgaga ccgagggcac cttcatcgtg gacagcgtgg agctgctcct gatggaggag      3420
tag                                                                    3423

```

<210> 42
 <211> 1140
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Amino acid sequence of the chimeric protein TIC844 encoded by a synthetic DNA sequence wherein an additional Alanine residue has been inserted at position 2.

<400> 42

```

Met Ala Glu Ile Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu
1           5           10          15

```

```

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

```

```

Asn Thr Val Ala Asp Ile Ser Leu Gly Leu Ile Asn Phe Leu Tyr Ser
35          40          45

```

```

Asn Phe Val Pro Gly Gly Gly Phe Ile Val Gly Leu Leu Glu Leu Ile
50          55          60

```

```

Trp Gly Phe Ile Gly Pro Ser Gln Trp Asp Ile Phe Leu Ala Gln Ile

```

P34223W000_SEQ_PCT

65		70		75		80									
Glu	Gln	Leu	Ile	Ser	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	Lys	Val	Tyr	Val	Arg
			100					105					110		
Ala	Phe	Ser	Asp	Trp	Glu	Lys	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	Ile	Thr	Ala
	130					135					140				
Ile	Pro	Leu	Phe	Arg	Val	Gln	Asn	Tyr	Glu	Val	Ala	Leu	Leu	Ser	Val
145					150					155					160
Tyr	Val	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Ile	Leu	Arg	Asp	Val	Ser
			165					170						175	
Val	Phe	Gly	Glu	Arg	Trp	Gly	Tyr	Asp	Thr	Ala	Thr	Ile	Asn	Asn	Arg
		180						185					190		
Tyr	Ser	Asp	Leu	Thr	Ser	Leu	Ile	His	Val	Tyr	Thr	Asn	His	Cys	Val
		195					200					205			
Asp	Thr	Tyr	Asn	Gln	Gly	Leu	Arg	Arg	Leu	Glu	Gly	Arg	Phe	Leu	Ser
	210					215					220				
Asp	Trp	Ile	Val	Tyr	Asn	Arg	Phe	Arg	Arg	Gln	Leu	Thr	Ile	Ser	Val
225					230					235					240
Leu	Asp	Ile	Val	Ala	Phe	Phe	Pro	Asn	Tyr	Asp	Ile	Arg	Thr	Tyr	Pro
			245						250					255	
Ile	Gln	Thr	Ala	Thr	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Leu	Asp	Leu	Pro

P34223W000_SEQ_PCT

260

265

270

Phe Ile Asn Glu Asn Leu Ser Pro Ala Ala Ser Tyr Pro Thr Phe Ser
 275 280 285

Ala Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu
 290 295 300

Asn Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Tyr Ala Tyr Trp
 305 310 315 320

Gly Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu
 325 330 335

Ile Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val
 340 345 350

Thr Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr
 355 360 365

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

Glu Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro
 385 390 395 400

Ile Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro
 405 410 415

Ala Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg
 420 425 430

Ile Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg
 435 440 445

Ser Ala Ser Pro Thr Asn Glu Val Ser Pro Ser Arg Ile Thr Gln Ile

P34223W000_SEQ_PCT

450

455

460

Pro Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys
465 470 475 480

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

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

Tyr Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr
515 520 525

Phe Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr
530 535 540

Met Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr
545 550 555 560

Leu Phe Thr Pro Ile Thr Phe Ser Arg Ala Gln Glu Glu Phe Asp Leu
565 570 575

Tyr Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val
580 585 590

Thr Ala Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala
595 600 605

Val Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp
610 615 620

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

Ser Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val

P34223W000_SEQ_PCT

645

650

655

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

Asn Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser
 675 680 685

Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr
 690 695 700

Val Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr
 705 710 715 720

Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu
 725 730 735

Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg
 740 745 750

Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu
 755 760 765

Trp Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Ala His His Ser
 770 775 780

His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu
 785 790 795 800

Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His
 805 810 815

Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly
 820 825 830

Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys

P34223W000_SEQ_PCT

835

840

845

Arg Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys
 850 855 860

Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln
 865 870 875 880

Ala Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His
 885 890 895

Ser Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val
 900 905 910

Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe
 915 920 925

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

Gly Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln
 945 950 955 960

Asn Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val
 965 970 975

Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val
 980 985 990

Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu
 995 1000 1005

Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
 1010 1015 1020

Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr

P34223W000_SEQ_PCT

1025 1030 1035

Ala Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg
1040 1045 1050

Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser Val Pro Ala Asp
1055 1060 1065

Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr Asp Gly Arg Arg
1070 1075 1080

Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro
1085 1090 1095

Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu
1100 1105 1110

Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe
1115 1120 1125

Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
1130 1135 1140

<210> 43
<211> 3423
<212> DNA
<213> Artificial

<220>
<223> Synthetic DNA sequence designed for plant expression encoding
TIC844_8 with an additional Alanine residue inserted at position
2.

<400> 43
atggctgaga tcaacaacca gaaccagtgc gtcccgtaga actgcctgag caaccctaag 60
gagatcatcc tgggtgagga acgcctggag accggcaaca ccgtagccga cattagcctg 120
ggcctcatca acttcctcta cagcaacttc gtgcccggcg gtggcttcat cgtgggcctc 180

P34223W000_SEQ_PCT

ctggagctta tctggggctt catcgggccg tcccagtggg acatcttcct cgcccagatc	240
gagcaactga tcagccagcg gatcgaggag ttcgctagga accaggccat ctcccgctg	300
gagggactct ccaacctcta caaggtgtac gtgcgcgcgt tcagcgactg ggagaaggac	360
ccgaccaacc cggccctccg cgaggaaatg cgtatccagt tcaacgatat gaactcggcc	420
ctcatcaccg ccatcccgtt cttccgcgtg cagaactacg aggtggccct cctgtccgtg	480
tacgttcaag ccgccaacct ccacctctcc atcctccgcg acgtgagcgt gttcggcgag	540
cgctggggct acgacaccgc caccatcaac aaccgctact ccgacctcac ctccctcatc	600
cacgtttaca ccaaccactg cgtggacacg tacaaccagg gcctccgccg cctggagggc	660
cgcttcctct ccgactggat cgtgtacaac cgcttccgcc gccagctcac catctccgtc	720
ctggacatcg tcgccttctt tcccaactac gacatccgca cctaccctat ccagaccgcc	780
accagctca cccgcgaggt ctacctgac ctcccgttca tcaacgagaa cctcagcccg	840
gccgccgtct acccgacctt ctccgccgt gagtccgcca tcattcgag cccgcacctc	900
gtggacttcc tcaactcctt caccatctac accgactccc tcgcccgcag cgcctactgg	960
ggcggtcacc tcgtgaactc cttccgcacc ggcaccacta ccaacctcat ccgcagcccg	1020
ctctacggcc gcgagggcaa caccgagcgc ccggtgacca tcaccgccag cccgagcgtg	1080
cccattctcc gcacctcag ctaccccacc ggcttggaac acagcaaccc tgtggcgggc	1140
atcgagggcg tggagttcca gaacaccatc tccaggagca tctaccgcaa gagcggccct	1200
atcgacagct tcagcgagct gcctcctcag gacgccagcg tgagccctgc catcggctac	1260
agccacaggc tgtgccacgc caccttcctg gagcgcacga gcggccctcg catcgcgggc	1320
accgtgttct cgtggaccca ccgcagcgcc tctcctacga acgaggtgtc tcctagtgcg	1380
atcaccaga tcccttgggt caaggccac accctggcta gtggcgctag tgtcatcaag	1440
ggccctggct tcaccggtgg tgacatcctg accaggaact ctatgggcga gctgggcact	1500
ctgagggctca ctttactgg ccgcctgcct cagtcttact acatccgctt ccgctacgct	1560
agtgtcgcta accgctctgg tactttccgc tactctcagc ctccgtctta cggatatctt	1620

P34223W000_SEQ_PCT

ttccctaaga ctatggacgc tggtagacct ctgaccagta ggagcttcgc tcacactact	1680
ctgttcactc ctatcacttt ctctagggct caggaggagt tcgacctgta catccagtct	1740
ggtgtgtaca tcgacaggat cgagttcatc cccgtgaccg ccacgttcga ggccgagtac	1800
gaccttgagc gcgcccagaa ggctgtcaat gagctcttca cgtccagcaa tcagatcggc	1860
ctgaagaccg acgtcactga ctaccacatc gaccaagtct ccaacctcgt ggagtgcctc	1920
tccgatgagt tctgcctcga cgagaagaag gagctgtccg agaagggtgaa gcatgccaaag	1980
cgtctcagcg acgagaggaa tctcctccag gaccccaatt tccgcggcat caacaggcag	2040
ctcgaccgcg gctggcgcgg cagcaccgac atcacgatcc agggcggcga cgatgtgttc	2100
aaggagaact acgtgactct cctgggcact ttcgacgagt gctaccctac ctacttgtac	2160
cagaagatcg atgagtccaa gctcaaggct tacactcgct accagctccg cggctacatc	2220
gaagacagcc aagacctcga gatttacctg atccgctaca acgccaagca cgagaccgtc	2280
aacgtgcccc gtactgggtc cctctggccg ctgagcgccc ccagcccgat cggcaagtgt	2340
gcccaccaca gccaccactt ctcttggac atcgatgtgg gctgcaccga cctgaacgag	2400
gacctcggag tctgggtcat cttcaagatc aagaccaggg acggccacgc gcgcctgggc	2460
aacctggagt tcctcgagga gaagcccctg gtcggtgagg ctctggccag ggtcaagagg	2520
gctgagaaga agtggaggga caagcgcgag aagctcgagt gggagaccaa catcgtttac	2580
aaggaggcca aggagagcgt cgacgccctg ttcgtgaact cccagtacga ccgcctgcag	2640
gccgacacca acatcgccat gatccacgct gccgacaaga gggtgcacag cattcgcgag	2700
gcctacctgc ctgagctgtc cgtgatccct ggtgtgaacg ctgccatctt tgaggagctg	2760
gagggccgca tctttaccgc attctccctg tacgacgccc gcaacgtgat caagaacggt	2820
gacttcaaca atggcctcag ctgctggaac gtcaagggcc acgtggacgt cgaggaacag	2880
aacaaccacc gtcctgcctt ggtcgtccca gagtgggagg ctgaggcttc ccaagaggtc	2940
cgcgctctgcc caggccgcgg ctacattctc agggtcaccg cttacaagga gggctacggt	3000
gagggctgtg tgaccatcca cgagatcgag aacaacaccg acgagcttaa gttctccaac	3060

P34223W000_SEQ_PCT

tgctggagg aggaggtgta cccaaacaac accgttactt gcaacgacta caccgccacc	3120
caggaggagt acgagggcac ctacacttcc aggaacaggg gctacgatgg tgcctacgag	3180
agcaacagca gcgttcctgc tgactacgct tccgcctacg aggagaaggc ctacacggat	3240
ggccgcaggg acaacccttg cgagagcaac cgcggctacg gcgactacac tcccctgccc	3300
gccggctacg ttaccaagga gctggagtac ttcccgagga ctgacaaggt gtggatcgag	3360
atcggcgaga ccgagggcac cttcatcgtg gacagcgtgg agctgctcct gatggaggag	3420
tag	3423

<210> 44
 <211> 1140
 <212> PRT
 <213> Artificial

<220>
 <223> Amino acid sequence of the engineered insecticidal chimeric protein TIC844_8 encoded by a synthetic DNA sequence wherein an additional Alanine residue has been inserted at position 2.

<400> 44

Met	Ala	Glu	Ile	Asn	Asn	Gln	Asn	Gln	Cys	Val	Pro	Tyr	Asn	Cys	Leu
1				5				10						15	

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

Asn	Thr	Val	Ala	Asp	Ile	Ser	Leu	Gly	Leu	Ile	Asn	Phe	Leu	Tyr	Ser
		35					40					45			

Asn	Phe	Val	Pro	Gly	Gly	Gly	Phe	Ile	Val	Gly	Leu	Leu	Glu	Leu	Ile
	50					55					60				

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

Glu	Gln	Leu	Ile	Ser	Gln	Arg	Ile	Glu	Glu	Phe	Ala	Arg	Asn	Gln	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

P34223W000_SEQ_PCT

85

90

95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Lys Val Tyr Val Arg
 100 105 110

Ala Phe Ser Asp Trp Glu Lys 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 Ile Thr Ala
 130 135 140

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

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

Val Phe Gly Glu Arg Trp Gly Tyr Asp Thr Ala Thr Ile Asn Asn Arg
 180 185 190

Tyr Ser Asp Leu Thr Ser Leu Ile His Val Tyr Thr Asn His Cys Val
 195 200 205

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

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

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

Ile Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro
 260 265 270

Phe Ile Asn Glu Asn Leu Ser Pro Ala Ala Val Tyr Pro Thr Phe Ser

P34223W000_SEQ_PCT

275

280

285

Ala Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu
 290 295 300

Asn Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Ser Ala Tyr Trp
 305 310 315 320

Gly Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu
 325 330 335

Ile Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val
 340 345 350

Thr Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr
 355 360 365

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

Glu Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro
 385 390 395 400

Ile Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro
 405 410 415

Ala Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg
 420 425 430

Ile Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg
 435 440 445

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

Pro Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys

P34223W000_SEQ_PCT

465		470		475		480									
Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asp	Ile	Leu	Thr	Arg	Asn	Ser	Met	Gly
				485					490					495	
Glu	Leu	Gly	Thr	Leu	Arg	Val	Thr	Phe	Thr	Gly	Arg	Leu	Pro	Gln	Ser
			500					505					510		
Tyr	Tyr	Ile	Arg	Phe	Arg	Tyr	Ala	Ser	Val	Ala	Asn	Arg	Ser	Gly	Thr
		515					520					525			
Phe	Arg	Tyr	Ser	Gln	Pro	Pro	Ser	Tyr	Gly	Ile	Ser	Phe	Pro	Lys	Thr
	530						535				540				
Met	Asp	Ala	Gly	Glu	Pro	Leu	Thr	Ser	Arg	Ser	Phe	Ala	His	Thr	Thr
545					550					555					560
Leu	Phe	Thr	Pro	Ile	Thr	Phe	Ser	Arg	Ala	Gln	Glu	Glu	Phe	Asp	Leu
				565					570					575	
Tyr	Ile	Gln	Ser	Gly	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Ile	Pro	Val
			580					585					590		
Thr	Ala	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala
		595					600					605			
Val	Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp
	610					615					620				
Val	Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu
625					630					635					640
Ser	Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val
				645					650					655	
Lys	His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro

P34223W000_SEQ_PCT

660

665

670

Asn Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser
 675 680 685

Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr
 690 695 700

Val Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr
 705 710 715 720

Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu
 725 730 735

Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg
 740 745 750

Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu
 755 760 765

Trp Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Ala His His Ser
 770 775 780

His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu
 785 790 795 800

Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His
 805 810 815

Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly
 820 825 830

Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys
 835 840 845

Arg Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys

P34223W000_SEQ_PCT

850

855

860

Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln
865 870 875 880

Ala Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His
885 890 895

Ser Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val
900 905 910

Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe
915 920 925

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

Gly Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln
945 950 955 960

Asn Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val
965 970 975

Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val
980 985 990

Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu
995 1000 1005

Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
1010 1015 1020

Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr
1025 1030 1035

Ala Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg

P34223W000_SEQ_PCT

1040

1045

1050

Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser Ser Val Pro Ala Asp
1055 1060 1065

Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr Asp Gly Arg Arg
1070 1075 1080

Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro
1085 1090 1095

Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu
1100 1105 1110

Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe
1115 1120 1125

Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
1130 1135 1140