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## SOYBEAN FGAM SYNTHASE PROMOTERS USEFUL IN NEMATODE CONTROL: U.S. Patent No. US 7,223,901 B2

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**MacKenzie et al.**

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(54) **SOYBEAN FGAM SYNTHASE PROMOTERS  
USEFUL IN NEMATODE CONTROL**

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26, 2004.

(51) **Int. Cl.**

**C12N 15/09** (2006.01)

**C12N 15/82** (2006.01)

**A01H 5/00** (2006.01)

(52) **U.S. Cl.** ..... **800/279**; 800/287; 800/278;  
800/298; 800/312; 536/24.1; 435/468; 435/320.1;  
435/419

(58) **Field of Classification Search** ..... 800/278,  
800/279, 312; 536/24.1; 435/468, 69.1

See application file for complete search history.

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(57) **ABSTRACT**

The subject invention relates to nematode responsive domains obtained from soybean promoters for phosphoribosylformylglycinamide ribonucleotide (FGAM) synthase paralogs. The nematode responsive domains can be used in promoters that are linked to heterologous DNA. Such constructs can be expressed in transfected or transformed soybean and used in the control of nematode infection of soybean.

**10 Claims, 16 Drawing Sheets**

ttgtttttta ttttttaaaa aagttttgac atgtacctgt aatataatat ccatgtagga 60  
ggctttttta acaactgtat cccatataac atatcatgtg agaactctata gtccacttta 120  
taagaatgtg tgaggtcagg tggattaaca ttttaacaatt ttcctatfff cccatgcata 180  
aaaaaaaaac atttatcaat ttttccacgt agtccatfff ttttaaaaaa agtaatgcga 240  
catgtgaaat tgccatataa tgattttgat aggatgtctt aaaacagtct cattttaata 300  
aaatatffta aaataatatac atttaattat tattttctaaf tttgcctcaa ttttatcaaf 360  
cagttaaaga agtcacgaga ttttcatata tctatffttat ttcaatattt aaattgaaac 420  
tttcaattga tttttttatt gtcattcatt ctgtaaccaa taaaattctt tgaattfftt 480  
gagattgatt tctogtatgt taaattataa tatgacaaca ttatatttaa tttttcttaa 540  
ttacaaagtt ttcaataaca aaattggatc garagaraaf gtcatcatat agtaactfff 600  
tttaaagatg acacataata acttgcactt taaaaaaaga cttgcactff gcagatcaag 660  
grcataaaf aatfftttagc atatgtctga atacgcgta tcaaaaaata aatcaaacgt 720  
ctaagtcaaa agtcactctc acaactcaca agtttctgtg tctffttggga agttgatgff 780  
aaaatgagag aatgaaccga tatatatata tatatatata tatatatcaa ttgcgatgff 840  
aagattatta ttgaagtaga cacatgacaa gatagaaaaa atttacttat aaaagaaaf 900  
aataacatgc aatgaatta tctcagtcaa gtaaaaaatt taatttatta tttffttgaa 960  
aggcaaaaf ttaaatttat tatataagaa tgaatcttat actfftatata actatagaag 1020  
ataaagttat attgagatat tttactcat tagttatcaa tttaacgatt tcaactfftt 1080  
ataaaccaca ggcaatttga tagaaacgff aaaactffaa aaagaaaatc caaactgtac 1140  
ttacagttcc cacagggcca attctaccta gagttfftagt gaagagccaa ttctaattff 1200  
ttttctctct ataaaaatcaa atacacacaf ttttaataaa agttffttff taaatctaga 1260  
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atacaattgg ctgtaaaaaa aaacagtcaf acaattatta cattgcacca aatatacatc 1380  
ttattattat ctgatatgaa ttaaattatta tacatgatta aagtctattt tgctcttatac 1440  
ttatttatca tatattatta tttgatttat tatctffctt taaaaaaatc tcattcttat 1500  
ttattfftat catgttctta tttgttgc gactctctc ttattffaac agttffttca 1560  
tagataataa tttffttcat aaataaaagt taacgatact tgaaaatact tctcaaaacta 1620  
acactagfff ttactffttt ttttatffaa aaatatctta gtaatttaca gcttcgagff 1680  
tcacaaagaa acaagtgtgt ttatatatag gcttctffta tgaactffgg attacgcatac 1740  
cgattcggct aaaaaaggta agcatoggca gacaaagaaa tctctgataa aacagagaaa 1800

Figure 1A- FGAM1

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atataaaaat agcgccaacg caaccaatag ttaaattgaa aggggtgaaaa cttttaatat 1860
ttttactcgt ttgatttgaa gggagagaaa gagagtacta agtggctagt aggggtttat 1920
tgtgtgccac accaaaaccc tctcttcggt ttacgtcact tccacactca ctctgttttg 1980
ttctgtact ctctgattct acttcttcta cttgattccc acatttctta ttttgcgtag 2040
tgaatatttt tttcttcttc tttttttaga gctttccac acttgatcga ggatatggcg 2100
actgcgacgg aatttgggggt atcgcaattc ttgaagggtt gattttaatt cctctcttgg 2160
aattaacctc atatgctgca ccccttttgt taatttatta attgttgttc ttgttggggg 2220
aaaaaggcca tgctttgatg ctgcagtgac atgtttcgat gcactcttgc ttattggggt 2280
ttgtgatttt ggtttcaggg gacctccagg caaactctgt tttttagaaa gaagcctcag 2340
aggcagaaaa gtccgatgct ttggggtgca ctctggaatc ggaattgggg tctgggatca 2400
actcgcagag ctttgccttt aagggtgcag actcaggaaa atcccagagc tgtggtttct 2460
gggtggcgtaa gcagttctgt agaggagcaa cctgccttgt ttgagaagcc cgcttccgaa 2520
gttgttcatt tgtaccgtgt cccgttt atg caa gaa agt gca gct gct gag ctt 2574
                Met Gln Glu Ser Ala Ala Ala Glu Leu
                1                    5

ttg aag gag gct caa gtg aaa atc tcc agt cag atc gtg gaa ata cta 2622
Leu Lys Glu Ala Gln Val Lys Ile Ser Ser Gln Ile Val Glu Ile Leu
10                    15                    20                    25

acg gag cag tgc tat aat gtt ggc ctt agt tgc caa ctt tcc ggt gga 2670
Thr Glu Gln Cys Tyr Asn Val Gly Leu Ser Ser Gln Leu Ser Gly Gly
30                    35                    40

aaa ttt tca gtt ctt gga tgg ctt ctt caa gaa aca ttc gag cct gag 2718
Lys Phe Ser Val Leu Gly Trp Leu Leu Gln Glu Thr Phe Glu Pro Glu
45                    50                    55

aat ctg gga act gag agc ttt ctt gag aag aag agg aag gag ggt ctg 2766
Asn Leu Gly Thr Glu Ser Phe Leu Glu Lys Lys Arg Lys Glu Gly Leu
60                    65                    70

att cca gtt att gtt gaa gtt ggc ccc agg ttg tca ttc acc aca gca 2814
Ile Pro Val Ile Val Glu Val Gly Pro Arg Leu Ser Phe Thr Thr Ala
75                    80                    85

tgg tct act aat gct gtt gca att tgc cag gcc tgt ggt ttg aca gaa 2862
Trp Ser Thr Asn Ala Val Ala Ile Cys Gln Ala Cys Gly Leu Thr Glu
90                    95                    100                    105

gtt aac cgt ttg gaa cgg tcc agg agg tac ttg ttg ttc acc acc act 2910
Val Asn Arg Leu Glu Arg Ser Arg Arg Tyr Leu Leu Phe Thr Thr Thr
110                    115                    120

gaa ctg caa gat tat caa atc aat gat ttt gca tct atg gtg cat gat 2958
Glu Leu Gln Asp Tyr Gln Ile Asn Asp Phe Ala Ser Met Val His Asp
125                    130                    135

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Figure 1A Cont.- FGAM1

agg atg act gaa tgt gtt tat att cag aaa cta aca tcc ttt gag acc	3006
Arg Met Thr Glu Cys Val Tyr Ile Gln Lys Leu Thr Ser Phe Glu Thr	
140 145 150	
agt gtt gtt ccg gag gag att cat tat ata cct gtc atg gag agg gga	3054
Ser Val Val Pro Glu Glu Ile His Tyr Ile Pro Val Met Glu Arg Gly	
155 160 165	
cga aag gca tta gaa gag att aat ttg gag atg ggt ttt gcc ttt gat	3102
Arg Lys Ala Leu Glu Glu Ile Asn Leu Glu Met Gly Phe Ala Phe Asp	
170 175 180 185	
gac cag gat tta gaa tac tac acc aaa ctt ttc aga gaa gac att aag	3150
Asp Gln Asp Leu Glu Tyr Tyr Thr Lys Leu Phe Arg Glu Asp Ile Lys	
190 195 200	
cgc aac ccg aca aat gtg gaa ttg ttt gat ata gca cag tcc aac agt	3198
Arg Asn Pro Thr Asn Val Glu Leu Phe Asp Ile Ala Gln Ser Asn Ser	
205 210 215	
gag cac agc aga cac tgg ttt ttt act gga aag att ttc att gat gga	3246
Glu His Ser Arg His Trp Phe Phe Thr Gly Lys Ile Phe Ile Asp Gly	
220 225 230	
cag ccc gtg aat aga act ctc atg cag att gtg aaa agt act ctg cag	3294
Gln Pro Val Asn Arg Thr Leu Met Gln Ile Val Lys Ser Thr Leu Gln	
235 240 245	
gca aac cca aat aac tca gtt att ggc ttc aag gat aac tct agt gca	3342
Ala Asn Pro Asn Asn Ser Val Ile Gly Phe Lys Asp Asn Ser Ser Ala	
250 255 260 265	
atc agg ggt tth cca gtg aag cag ctc cga cca gtt cag cct ggt tca	3390
Ile Arg Gly Xaa Pro Val Lys Gln Leu Arg Pro Val Gln Pro Gly Ser	
270 275 280	
gca tgt cca tta gaa gtt gca gtc cat gag tta gat atc ttg ttt aca	3438
Ala Cys Pro Leu Glu Val Ala Val His Glu Leu Asp Ile Leu Phe Thr	
285 290 295	
gct gaa aca cat aat ttt cca tgc gca gtg gca cct tat cct ggt gca	3486
Ala Glu Thr His Asn Phe Pro Cys Ala Val Ala Pro Tyr Pro Gly Ala	
300 305 310	
gag acg ggt gca gga ggt cgc att agg gat aca cac gct acc gga agg	3534
Glu Thr Gly Ala Gly Gly Arg Ile Arg Asp Thr His Ala Thr Gly Arg	
315 320 325	
ggg tcc ttt gtc cag gca gct aca gct ggt tat tgc gtt ggg aat ctc	3582
Gly Ser Phe Val Gln Ala Ala Thr Ala Gly Tyr Cys Val Gly Asn Leu	
330 335 340 345	
aac aca ccg ggc ttt tat gct cca tgg gaa gat ccc tcc ttt act tat	3630
Asn Thr Pro Gly Phe Tyr Ala Pro Trp Glu Asp Pro Ser Phe Thr Tyr	
350 355 360	
cca tca aat ttg gca cca cct tta cag att ctg ata gat tct agt aat	3678
Pro Ser Asn Leu Ala Pro Pro Leu Gln Ile Leu Ile Asp Ser Ser Asn	
365 370 375	

Figure 1A Cont.- FGAM1

ggt gca tct gac tat ggg aac aaa ttt gga gag cca ttg atc cag ggt	3726
Gly Ala Ser Asp Tyr Gly Asn Lys Phe Gly Glu Pro Leu Ile Gln Gly	
380 385 390	
ttc tgt aga act ttc gga atg aga ctt cct ggt ggg gag agg cga gaa	3774
Phe Cys Arg Thr Phe Gly Met Arg Leu Pro Gly Gly Glu Arg Arg Glu	
395 400 405	
tgg ttg aag cca atc atg ttc agc gca ggc ata gga cag att gac cac	3822
Trp Leu Lys Pro Ile Met Phe Ser Ala Gly Ile Gly Gln Ile Asp His	
410 415 420 425	
ctt cat ata tca aag gga gag cct gac att ggg atg ctg gtt gtt aag	3870
Leu His Ile Ser Lys Gly Glu Pro Asp Ile Gly Met Leu Val Val Lys	
430 435 440	
att gga ggc ccg gct tat cgt att ggt atg gga ggt ggg gca gcc tca	3918
Ile Gly Gly Pro Ala Tyr Arg Ile Gly Met Gly Gly Gly Ala Ala Ser	
445 450 455	
agc atg gtc gat ggg cag aat gat gca gag ctt gat ttc aat gct gtg	3966
Ser Met Val Asp Gly Gln Asn Asp Ala Glu Leu Asp Phe Asn Ala Val	
460 465 470	
caa cgt ggg gat gct gag atg gct caa aaa cta tat cgt ctt gtg cgt	4014
Gln Arg Gly Asp Ala Glu Met Ala Gln Lys Leu Tyr Arg Leu Val Arg	
475 480 485	
gct tgt att gag atg ggg gat aaa aac cca att atc agc att cat gat	4062
Ala Cys Ile Glu Met Gly Asp Lys Asn Pro Ile Ile Ser Ile His Asp	
490 495 500 505	
cag gga gct ggt ggg aac tgc aat gtt gta aag gaa att ata tat ccg	4110
Gln Gly Ala Gly Gly Asn Cys Asn Val Val Lys Glu Ile Ile Tyr Pro	
510 515 520	
aag ggt gct gag ata gat gtc cga gca att gtg gtt ggt gat cat aca	4158
Lys Gly Ala Glu Ile Asp Val Arg Ala Ile Val Val Gly Asp His Thr	
525 530 535	
atg tct gtt cta gaa att tgg ggt gca gag tat cag gag cag gat gca	4206
Met Ser Val Leu Glu Ile Trp Gly Ala Glu Tyr Gln Glu Gln Asp Ala	
540 545 550	
atc tta gtg aag cct gaa agc cgt gat ctc cta gaa tca atc tgt aac	4254
Ile Leu Val Lys Pro Glu Ser Arg Asp Leu Leu Glu Ser Ile Cys Asn	
555 560 565	
agg gaa aaa gtt tca atg gct gtt att gga act atc agt gga gat gga	4302
Arg Glu Lys Val Ser Met Ala Val Ile Gly Thr Ile Ser Gly Asp Gly	
570 575 580 585	
cgt gtt gtt tta gtt gac agt gta gca gct cag aag tct att tca aat	4350
Arg Val Val Leu Val Asp Ser Val Ala Ala Gln Lys Ser Ile Ser Asn	
590 595 600	
gga ctc cct cca cct ccc cct gct gtg gat ctt gaa ctg gag aaa gtc	4398
Gly Leu Pro Pro Pro Pro Pro Ala Val Asp Leu Glu Leu Glu Lys Val	
605 610 615	

Figure 1A Cont.- FGAM1

ctt ggt gac atg cct aag aaa act ttt aag ttt aat cgg gtt gtt tat	4446
Leu Gly Asp Met Pro Lys Lys Thr Phe Lys Phe Asn Arg Val Val Tyr	
620 625 630	
gag cgg gag cca ctt gat att gtc cct ggg att gaa gtg ata gat tct	4494
Glu Arg Glu Pro Leu Asp Ile Val Pro Gly Ile Glu Val Ile Asp Ser	
635 640 645	
ctg aag agg gta ttg agt tta ccg tct gtt tgt tca aag cgc ttc ttg	4542
Leu Lys Arg Val Leu Ser Leu Pro Ser Val Cys Ser Lys Arg Phe Leu	
650 655 660 665	
aca aca aaa gtt gac agg tgt gtt act ggt cta gtg gca caa cag caa	4590
Thr Thr Lys Val Asp Arg Cys Val Thr Gly Leu Val Ala Gln Gln Gln	
670 675 680	
act gtt ggc cct ttg cag att ccc att gct gat gtt gct gtt aca gct	4638
Thr Val Gly Pro Leu Gln Ile Pro Ile Ala Asp Val Ala Val Thr Ala	
685 690 695	
caa act ttt gct gat gtg act gga ggt gct tgt gcc att gga gaa caa	4686
Gln Thr Phe Ala Asp Val Thr Gly Ala Cys Ala Ile Gly Glu Gln	
700 705 710	
cca atc aaa ggt ttg tta gac ccc aaa gca atg gct cgg ttg gct gtt	4734
Pro Ile Lys Gly Leu Leu Asp Pro Lys Ala Met Ala Arg Leu Ala Val	
715 720 725	
gga gaa gca cta aca aat ctt gta tgg gcg aag gtc act tcc ctt tct	4782
Gly Glu Ala Leu Thr Asn Leu Val Trp Ala Lys Val Thr Ser Leu Ser	
730 735 740 745	
gat gtc aag gct agt ggt aac tgg atg tat gct gcc aag ctt gat ggg	4830
Asp Val Lys Ala Ser Gly Asn Trp Met Tyr Ala Ala Lys Leu Asp Gly	
750 755 760	
gaa gga gct gac atg tat gat gct gct ata tct cta tct gaa gca atg	4878
Glu Gly Ala Asp Met Tyr Asp Ala Ala Ile Ser Leu Ser Glu Ala Met	
765 770 775	
att gaa ctt ggc att gct att gat gga ggg aaa gac agt ctt tct atg	4926
Ile Glu Leu Gly Ile Ala Ile Asp Gly Gly Lys Asp Ser Leu Ser Met	
780 785 790	
gca gcc cac gcc gag agt gaa gtt gtc aag gct ccg gga aat ctt gtc	4974
Ala Ala His Ala Glu Ser Glu Val Val Lys Ala Pro Gly Asn Leu Val	
795 800 805	
atc agt gtt tat gtt act tgt cct gat ata aca aaa aca gtg acg cca	5022
Ile Ser Val Tyr Val Thr Cys Pro Asp Ile Thr Lys Thr Val Thr Pro	
810 815 820 825	
gat tta aaa ctc aag gat gat ggt att ttg ctt cat att gat ttg tca	5070
Asp Leu Lys Leu Lys Asp Asp Gly Ile Leu Leu His Ile Asp Leu Ser	
830 835 840	
aaa ggt aag agg cgg tta ggt gga tct gct ctt gcc cag gca ttt gac	5118
Lys Gly Lys Arg Arg Leu Gly Gly Ser Ala Leu Ala Gln Ala Phe Asp	
845 850 855	

Figure 1A Cont.- FGAM1

caa gtt ggg aat gag tgt cct gat ctt gat gat gtt cct tac ctt aaa Gln Val Gly Asn Glu Cys Pro Asp Leu Asp Asp Val Pro Tyr Leu Lys 860 865 870	5166
aag gtc ttt gaa ggt gtt caa gac ctt ctt tct gat gaa ctg ata tct Lys Val Phe Glu Gly Val Gln Asp Leu Leu Ser Asp Glu Leu Ile Ser 875 880 885	5214
gct ggt cat gac atc agt gat ggt ggg ctg cta gtt tgt gcc tta gag Ala Gly His Asp Ile Ser Asp Gly Gly Leu Leu Val Cys Ala Leu Glu 890 895 900 905	5262
atg gca ttt gct ggt aat tgt gga ctt agt ttg gac ttt gca tcg caa Met Ala Phe Ala Gly Asn Cys Gly Leu Ser Leu Asp Phe Ala Ser Gln 910 915 920	5310
ggt aac agc ctt ttc caa aca ctc tat gct gaa gag ctt ggg tta gtt Gly Asn Ser Leu Phe Gln Thr Leu Tyr Ala Glu Glu Leu Gly Leu Val 925 930 935	5358
ctt gag gta agc aag aaa aat ctg gct ttg gta gtg aat aaa ttg agc Leu Glu Val Ser Lys Lys Asn Leu Ala Leu Val Val Asn Lys Leu Ser 940 945 950	5406
aat gtg gga gtt tct gct gaa atc ata ggt caa gta aca gcc aat cca Asn Val Gly Val Ser Ala Glu Ile Ile Gly Gln Val Thr Ala Asn Pro 955 960 965	5454
tca ata gaa gtt aag gtt gat ggg gag act tat tta act gaa aaa act Ser Ile Glu Val Lys Val Asp Gly Glu Thr Tyr Leu Thr Glu Lys Thr 970 975 980 985	5502
agt atc ctt agg gac atg tgg gaa gag acc agt ttt cag ctg gaa aag Ser Ile Leu Arg Asp Met Trp Glu Glu Thr Ser Phe Gln Leu Glu Lys 990 995 1000	5550
ttc caa agg ttg gca tct tgt gtg gat atg gag aaa gaa gga cta Phe Gln Arg Leu Ala Ser Cys Val Asp Met Glu Lys Glu Gly Leu 1005 1010 1015	5595
aaa cat cgt tat gaa ccc tca tgg gaa ctg cct ttt act cct tcc Lys His Arg Tyr Glu Pro Ser Trp Glu Leu Pro Phe Thr Pro Ser 1020 1025 1030	5640
ttc act gat gaa aag ctt tat gtc tgc aac tat aaa acc taa ag Phe Thr Asp Glu Lys Leu Tyr Val Cys Asn Tyr Lys Thr 1035 1040	5684

Figure 1A Cont.- FGAM1



ctcgagtgca ctttataaga atgtgtcagg tggattaaca attttgatag gatgtgataa 60  
aaacagtctc attttaataa aacattttaa ataatatcat ttttaataatt atttctaatt 120  
ttggctcaaa tttatcaacc agttcaagaa gatcgtgaga ttttcatata tctatTTTTat 180  
ttcaatattt aaattgaaac tttcagttga tttttttttt gtcattcatt ttgtaatcaa 240  
taaaattcctt tgaatttgtt gagattgatt tctcttataa tatgatgaca ttatatttaa 300  
tttttcttaa ttacaggttt ttcaataaca aaattggatt gttccttaaa aaattgaatt 360  
gaaaaaaaa tgttgtcaca tagtaacttt ttttttgaaa atgtcgtata gtaacttgca 420  
ctttacaaat caaggacata aattaatttt agcataagtt tggctatgca tttttaaaaa 480  
atagatcaac gtctaataca aaagccactc ccgcaactca caagtttctg aatcttttgg 540  
gaatttaatg tgaaaatgag agaatacaacc gataagaatt ttttatatat atttcaatta 600  
agatgtgaag attattattg aagtagacac atgataagat agaaaatata cttataaaag 660  
aaaataaata atatgcagat gaattatctc actcaagtaa aaatctaaac ttattatata 720  
agaatgaatt ttatatttta tgtagctata gaagataatt tatcttgaga tattttaatt 780  
cattaattat taatttaacg atttcaactt ttataaaacc acaggcaatt tgatagagac 840  
gttaaaactt taaaaagaaa atccaaattg tacttacggt tcccacagge ccaattctac 900  
ctagagttta ttgaagagcc aattctattt tgttttcttc ccataaaatc aaatacacct 960  
tttttgataa aagttttttt ttttatctag attacataag agataatctc ttttgatttt 1020  
tttatagaga aatatctttc gaattaaata tctaaaagtc actttttact gcatttaaaa 1080  
gtcatataat gcactaaata ttatatataa ttaaaggata tcttgctttt atcttatttt 1140  
atcatattct ttgtcaaatt ctctcttatt aaacaaaatt ttaataataa tttgggaata 1200  
aataataata taatttttaa cacaagacta attttatgat cttatattaa tacaagttaa 1260  
ctatagttga aaatgctttt ttttttttta cggataactt gaaaataactt cttaaaataa 1320  
taagtaggaa tatatcgtgt aaatttgttt aaatttattc tataaaaaat acttatttta 1380  
ataaaataaa caattttttt ttctttttta gtgtttgttt aaatcgtttt tacctatttt 1440  
atttttcttg ttttaaaaaa aatcttatct atttatgtaa aaagcattta aaaaacactt 1500  
actttaaat aaaaaatatt aatactagct tttagttttt ttttttataa gatatcttac 1560  
caatttacag cttcgagttt cacaaagaaa ctagtgtgtt tatactgaca aagctcttat 1620  
cggcgtctgt tatgaacttt ggataacgca tccgattcgg attcggctaa aagtaagcat 1680  
cagcagacaa agaaattgtc gataaaacag aggaaggaga attaaaatat ataaagtagc 1740  
gccaacgcaa ccaatagttg aattgaaagg ttgaaaactt tttatatttt attggtttga 1800  
ttggaacttg gaagggaaag aaagagagta ccaagtggct agtagggttt tattttgtgc 1860

Figure 1B- FGAM2

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cacacaaaa ccctctcttc gttttacgcc actgccacac tctgttttgt tctggttatc 1920
tctgattcta cttcttcttc ttgattctca ctatactcat tgtgccacag ttctgattgt 1980
gcttagtgat tctttctcaa gctttttttt tttttttttt aatttattta gagctttccc 2040
tacacttggt cgaggacatg gcggtcgca cggaaatttg ggtgtcgcaa ttcttgcaag 2100
tttgatttta atccctctct ttgaattaac atcatatgct gctgcacccc ttttattaat 2160
ttattaattg ctgctcttgt tgggggaaaa agtttcatgc tttgatgctg tttggttttg 2220
tgatttttgt ttcaggtacc tccaggcaaa ctctgttttt gaagaagaag ccacagagac 2280
agagaagaag catgttttgg ggtgcgctct ggaataggaa ttgggctctg ggatcaactc 2340
acagagcttt gcctttaagg tgccaggctc aggaaaatcc cagagctgta gtttctggtg 2400
gcggtgagcag ttctgtagag gagcaacctg ccttggttga gaagcccgct tccgaagttg 2460
ttcatttgta tctgtctccg ttt atg caa gca agt gca gct gct gag ctt ttg 2513
                Met Gln Ala Ser Ala Ala Ala Glu Leu Leu
                1             5             10

aag gaa gct caa gtg aaa atc tcc ggt cag atc gtg gaa ata cag act 2561
Lys Glu Ala Gln Val Lys Ile Ser Gly Gln Ile Val Glu Ile Gln Thr
                15             20             25

gag cag tgt tat aat gtt ggc ctt agt tca caa ctt tct ggt gga aaa 2609
Glu Gln Cys Tyr Asn Val Gly Leu Ser Ser Gln Leu Ser Gly Gly Lys
                30             35             40

ttt tcg gtc ctt aga tgg ctt ctt caa gaa aca ttt gag cct gag aat 2657
Phe Ser Val Leu Arg Trp Leu Leu Gln Glu Thr Phe Glu Pro Glu Asn
                45             50             55

ctg gga act gag agc ttt ctt gag aag aag aag aaa gag ggt ctg agt 2705
Leu Gly Thr Glu Ser Phe Leu Glu Lys Lys Lys Lys Glu Gly Leu Ser
                60             65             70

cca gtt att gtt gaa gtt ggc ccc agg ctg tca ttt acc acg gca tgg 2753
Pro Val Ile Val Glu Val Gly Pro Arg Leu Ser Phe Thr Thr Ala Trp
                75             80             85             90

tct acc aat gct gtt gca att tgc caa gcc tgt ggt ttg aca gaa gtg 2801
Ser Thr Asn Ala Val Ala Ile Cys Gln Ala Cys Gly Leu Thr Glu Val
                95             100             105

aac cgt ttg gaa cgg tcc agg agg tac ttg ttg ttc acc acc act gaa 2849
Asn Arg Leu Glu Arg Ser Arg Arg Tyr Leu Leu Phe Thr Thr Thr Glu
                110             115             120

ctg caa gat tat caa atc aat gat ttt acg tct atg gtg cat gat agg 2897
Leu Gln Asp Tyr Gln Ile Asn Asp Phe Thr Ser Met Val His Asp Arg
                125             130             135

atg act gaa tgt gtt tat gtt cag aag cta aca tcc ttc gag act agt 2945
Met Thr Glu Cys Val Tyr Val Gln Lys Leu Thr Ser Phe Glu Thr Ser
                140             145             150

```

Figure 1B Cont.- FGAM2

ggt gtt cca gag gag att cgt tat ata cct gtc atg gag aag ggg cga	2993
Val Val Pro Glu Glu Ile Arg Tyr Ile Pro Val Met Glu Lys Gly Arg	
155 160 165 170	
aag gca tta gaa gag att aat ctg gag atg ggt ttt gcc ttt gat gac	3041
Lys Ala Leu Glu Glu Ile Asn Leu Glu Met Gly Phe Ala Phe Asp Asp	
175 180 185	
cag gat ttg gaa tac tac acc aaa ctc ttc agg gaa gac att aag cgt	3089
Gln Asp Leu Glu Tyr Tyr Thr Lys Leu Phe Arg Glu Asp Ile Lys Arg	
190 195 200	
aac cca aca aat gtg gaa ttg ttt gat att gcg cag tcc aac agt gag	3137
Asn Pro Thr Asn Val Glu Leu Phe Asp Ile Ala Gln Ser Asn Ser Glu	
205 210 215	
cac agc aga cac tgg ttt ttt act gga aat att ttc att gat gga cag	3185
His Ser Arg His Trp Phe Phe Thr Gly Asn Ile Phe Ile Asp Gly Gln	
220 225 230	
cct gtg aat aga act ctc atg cag att gtg aaa agt act ctg cag gca	3233
Pro Val Asn Arg Thr Leu Met Gln Ile Val Lys Ser Thr Leu Gln Ala	
235 240 245 250	
aac cca aat aac tca gtt att ggc ttc aag gat aac tcg agt gca atg	3281
Asn Pro Asn Asn Ser Val Ile Gly Phe Lys Asp Asn Ser Ser Ala Met	
255 260 265	
cag ggg ttt tcc agt gaa gca gct ccg acc agt tca acc tgg ttc aac	3329
Gln Gly Phe Ser Ser Glu Ala Ala Pro Thr Ser Ser Thr Trp Phe Asn	
270 275 280	
ttg tcc att aga agt tgc agt cat gag tta gat atc ttg ttt aca gcc	3377
Leu Ser Ile Arg Ser Cys Ser His Glu Leu Asp Ile Leu Phe Thr Ala	
285 290 295	
gaa aca cat aat ttt cca tgt gca gtg gca cct tat cct ggt gca gag	3425
Glu Thr His Asn Phe Pro Cys Ala Val Ala Pro Tyr Pro Gly Ala Glu	
300 305 310	
aca ggt gca gga ggt cgt att agg gat aca cat gct aca gga agg ggg	3473
Thr Gly Ala Gly Gly Arg Ile Arg Asp Thr His Ala Thr Gly Arg Gly	
315 320 325 330	
tcc ttt gtc caa gca gct aca gct ggt tat tgc gtt ggg aat ctc aac	3521
Ser Phe Val Gln Ala Ala Thr Ala Gly Tyr Cys Val Gly Asn Leu Asn	
335 340 345	
aca cca ggc ttt tat gct cca tgg gaa gat tcc tcc ttt act tat cca	3569
Thr Pro Gly Phe Tyr Ala Pro Trp Glu Asp Ser Ser Phe Thr Tyr Pro	
350 355 360	
tca aat ttg gca cca cct tta cag att ctg ata gat tct agt aat ggt	3617
Ser Asn Leu Ala Pro Pro Leu Gln Ile Leu Ile Asp Ser Ser Asn Gly	
365 370 375	
gca tct gac tat ggg aac aaa ttt gga gag cca ttg atc cag ggt ttc	3665
Ala Ser Asp Tyr Gly Asn Lys Phe Gly Glu Pro Leu Ile Gln Gly Phe	
380 385 390	

Figure 1B Cont.- FGAM2

tgt aga act ttt gga atg aga ctt ccc agt ggg gag agg cga gaa tgg	3713
Cys Arg Thr Phe Gly Met Arg Leu Pro Ser Gly Glu Arg Arg Glu Trp	
395 400 405 410	
ttg aag cct atc atg ttc agc gca ggc att gga cag att gac cac ctt	3761
Leu Lys Pro Ile Met Phe Ser Ala Gly Ile Gly Gln Ile Asp His Leu	
415 420 425	
cat ata tca aag gga gag cct gac att ggg atg ctg gtt gtt aag att	3809
His Ile Ser Lys Gly Glu Pro Asp Ile Gly Met Leu Val Val Lys Ile	
430 435 440	
gga ggc ccg gct tat cgt att ggt atg gga ggc ggg gca gcc tca agc	3857
Gly Gly Pro Ala Tyr Arg Ile Gly Met Gly Gly Gly Ala Ala Ser Ser	
445 450 455	
atg gtc agt ggg cag aat gat gca gag ctt gat ttc aat gct gtg caa	3905
Met Val Ser Gly Gln Asn Asp Ala Glu Leu Asp Phe Asn Ala Val Gln	
460 465 470	
cgt ggg gat gct gag atg gct caa aaa cta tat cgt ctt gtg cgt gct	3953
Arg Gly Asp Ala Glu Met Ala Gln Lys Leu Tyr Arg Leu Val Arg Ala	
475 480 485 490	
tgt att gag atg ggg gat aaa aac cca att atc agc att cat gat cag	4001
Cys Ile Glu Met Gly Asp Lys Asn Pro Ile Ile Ser Ile His Asp Gln	
495 500 505	
gga gct ggt ggg aat tgc aat gtt gta aag gaa att ata tat cca aag	4049
Gly Ala Gly Gly Asn Cys Asn Val Val Lys Glu Ile Ile Tyr Pro Lys	
510 515 520	
ggt gct gag ata gat gtt cga gca att gtg gtt ggc gat cat aca atg	4097
Gly Ala Glu Ile Asp Val Arg Ala Ile Val Val Gly Asp His Thr Met	
525 530 535	
tct gtt cta gaa att tgg ggt gca gag tat cag gag cag gat gca atc	4145
Ser Val Leu Glu Ile Trp Gly Ala Glu Tyr Gln Glu Gln Asp Ala Ile	
540 545 550	
ttg gtg aag cct gaa agt cgt gat ctt ctg gaa tca atc tgt aac agg	4193
Leu Val Lys Pro Glu Ser Arg Asp Leu Leu Glu Ser Ile Cys Asn Arg	
555 560 565 570	
gag aaa gtt tca atg gct gtt att gga act atc agt ggt gat gga cgt	4241
Glu Lys Val Ser Met Ala Val Ile Gly Thr Ile Ser Gly Asp Gly Arg	
575 580 585	
gtt gtt tta gtt gac agt gta gca gtc cag aag tct att tca aat gga	4289
Val Val Leu Val Asp Ser Val Ala Val Gln Lys Ser Ile Ser Asn Gly	
590 595 600	
ctc act tca cct ccc cct gcc gtg gat ctt gaa ttg gag aaa gtc ctt	4337
Leu Thr Ser Pro Pro Pro Ala Val Asp Leu Glu Leu Glu Lys Val Leu	
605 610 615	
ggt gac atg cct aag aaa act ttt aaa ttt aat cgg gtt gtt tat gag	4385
Gly Asp Met Pro Lys Lys Thr Phe Lys Phe Asn Arg Val Val Tyr Glu	
620 625 630	

Figure 1B Cont.- FGAM2

agg gag cca ctt gat att gcc cct ggg att gaa gtg ata gat tcc cta	4433
Arg Glu Pro Leu Asp Ile Ala Pro Gly Ile Glu Val Ile Asp Ser Leu	
635 640 645 650	
aag agg gta ttg agt tta ccg tct gtt tgt tca aag cgc ttc tta aca	4481
Lys Arg Val Leu Ser Leu Pro Ser Val Cys Ser Lys Arg Phe Leu Thr	
655 660 665	
aca aaa gtt gat agg tgt gtt act ggt cta gtg gca caa caa caa act	4529
Thr Lys Val Asp Arg Cys Val Thr Gly Leu Val Ala Gln Gln Gln Thr	
670 675 680	
gtt ggc cct ttg cag att ccc att gct gat gtt gct gtt aca gct caa	4577
Val Gly Pro Leu Gln Ile Pro Ile Ala Asp Val Ala Val Thr Ala Gln	
685 690 695	
act ttt gtt gat gtg act gga ggt gct tgt gcc att ggt gag caa ccc	4625
Thr Phe Val Asp Val Thr Gly Gly Ala Cys Ala Ile Gly Glu Gln Pro	
700 705 710	
atc aaa ggc ctg tta gac ccc aaa gca atg gct cgg ttg gct gtt gga	4673
Ile Lys Gly Leu Leu Asp Pro Lys Ala Met Ala Arg Leu Ala Val Gly	
715 720 725 730	
gaa gca cta aca aat ctt gta tgg gca aag gtc act tcc ctt tct gat	4721
Glu Ala Leu Thr Asn Leu Val Trp Ala Lys Val Thr Ser Leu Ser Asp	
735 740 745	
gtc aag gct agt ggt aac tgg atg tat gct gcc aag ctt gat ggg gaa	4769
Val Lys Ala Ser Gly Asn Trp Met Tyr Ala Ala Lys Leu Asp Gly Glu	
750 755 760	
gga gct gac atg tat gat gca gct ata tct cta tct gaa gca atg att	4817
Gly Ala Asp Met Tyr Asp Ala Ala Ile Ser Leu Ser Glu Ala Met Ile	
765 770 775	
gaa ctt ggc att gct att gat gga ggg aaa gac agc ctt tct atg gca	4865
Glu Leu Gly Ile Ala Ile Asp Gly Gly Lys Asp Ser Leu Ser Met Ala	
780 785 790	
gcc cac gct gaa agt gaa gtt gtc aag gca cca ggr aat ctt gtc atc	4913
Ala His Ala Glu Ser Glu Val Val Lys Ala Pro Xaa Asn Leu Val Ile	
795 800 805 810	
agt gtk tat gtt act tgt cct gat ata aca aaa aca gtg act cca gat	4961
Ser Xaa Tyr Val Thr Cys Pro Asp Ile Thr Lys Thr Val Thr Pro Asp	
815 820 825	
tta aaa ctc aag gat gat ggt att ttg ctt cat att gat ttg tca aaa	5009
Leu Lys Leu Lys Asp Asp Gly Ile Leu Leu His Ile Asp Leu Ser Lys	
830 835 840	
ggt aag agg cgg tta ggt gga tct gct ctt gcc cag gcg ttt gac caa	5057
Gly Lys Arg Arg Leu Gly Gly Ser Ala Leu Ala Gln Ala Phe Asp Gln	
845 850 855	
gtt gga gat gag tgt cct gat cct gat gat gtt cct tac ctt aaa aag	5105
Val Gly Asp Glu Cys Pro Asp Pro Asp Val Pro Tyr Leu Lys Lys	
860 865 870	

Figure 1B Cont.- FGAM2

gcc ttt gaa ggt gtt caa gac ctt ctt tct gat gaa ttg ata tct gct Ala Phe Glu Gly Val Gln Asp Leu Leu Ser Asp Glu Leu Ile Ser Ala 875 880 885 890	5153
ggt cat gac atc agt gat ggt ggg ctg cta gtt tgt gcc tta gag atg Gly His Asp Ile Ser Asp Gly Gly Leu Leu Val Cys Ala Leu Glu Met 895 900 905	5201
gca ttt gct ggt aac tgt ggt ctt agt ttg gac ttg gcg tcg caa ggt Ala Phe Ala Gly Asn Cys Gly Leu Ser Leu Asp Leu Ala Ser Gln Gly 910 915 920	5249
acc agc ctt ttc caa aca ctc tat gct gaa gag ctt ggg tta gtt ctt Thr Ser Leu Phe Gln Thr Leu Tyr Ala Glu Glu Leu Gly Leu Val Leu 925 930 935	5297
gag gta aac aag aaa aat ctg gct ttg gta atg gat aaa ttg agt aat Glu Val Asn Lys Lys Asn Leu Ala Leu Val Met Asp Lys Leu Ser Asn 940 945 950	5345
gtg gga gtt tca gct gaa atc att ggt caa gta aca gcc aat cca tca Val Gly Val Ser Ala Glu Ile Ile Gly Gln Val Thr Ala Asn Pro Ser 955 960 965 970	5393
ata gaa gtt aag gtt gat ggg gag act tat tta act gaa aaa act agt Ile Glu Val Lys Val Asp Gly Glu Thr Tyr Leu Thr Glu Lys Thr Ser 975 980 985	5441
atc ctt agg gac ttg tgg gaa gag acc agt ttt cag ctg gaa aag ttc Ile Leu Arg Asp Leu Trp Glu Glu Thr Ser Phe Gln Leu Glu Lys Phe 990 995 1000	5489
caa aga ttg gca tcc tgt gtg gat atg gag aaa gaa gga ctt aaa Gln Arg Leu Ala Ser Cys Val Asp Met Glu Lys Glu Gly Leu Lys 1005 1010 1015	5534
cat cga tat gag ccc tca tgg gaa ctg cct ttt act ccc acc ttc His Arg Tyr Glu Pro Ser Trp Glu Leu Pro Phe Thr Pro Thr Phe 1020 1025 1030	5579
act gat gga aag ctt ctg tct gca act ata aaa cct aaa gtg gct Thr Asp Gly Lys Leu Leu Ser Ala Thr Ile Lys Pro Lys Val Ala 1035 1040 1045	5624
gtg att aga gaa gaa ggc agt aat gga gac aga gaa atg gct gca Val Ile Arg Glu Glu Gly Ser Asn Gly Asp Arg Glu Met Ala Ala 1050 1055 1060	5669
gca ttt tat gct gct ggt ttt gaa cca tgg gat att act atg tca Ala Phe Tyr Ala Ala Gly Phe Glu Pro Trp Asp Ile Thr Met Ser 1065 1070 1075	5714
gac ctt ctt aat gga aag atc tct ttg caa gac ttc cgc gga att Asp Leu Leu Asn Gly Lys Ile Ser Leu Gln Asp Phe Arg Gly Ile 1080 1085 1090	5759
gtg ttt gtt ggt gga ttt agc tat gct gat gtg ctt gat tct gca Val Phe Val Gly Gly Phe Ser Tyr Ala Asp Val Leu Asp Ser Ala 1095 1100 1105	5804

Figure 1B Cont.- FGAM2

aaa ggt tgg tct gct agc ata aga ttc aat gag tcc gtt tta caa	5849
Lys Gly Trp Ser Ala Ser Ile Arg Phe Asn Glu Ser Val Leu Gln	
1110 1115 1120	
caa ttt cag gag ttt tac aag cgt cca gac act ttc agt ctc ggt	5894
Gln Phe Gln Glu Phe Tyr Lys Arg Pro Asp Thr Phe Ser Leu Gly	
1125 1130 1135	
gta tgc aat gga tgt cag cta atg gct ttg ttg gga tgg gta ccg	5939
Val Cys Asn Gly Cys Gln Leu Met Ala Leu Leu Gly Trp Val Pro	
1140 1145 1150	
ggt cca caa gtt ggg ggt gtg cat ggt gct ggt ggc gac cta tca	5984
Gly Pro Gln Val Gly Gly Val His Gly Ala Gly Gly Asp Leu Ser	
1155 1160 1165	
caa ccg agg ttc att cat aat gag tca ggg cgg ttt gag tgc cgc	6029
Gln Pro Arg Phe Ile His Asn Glu Ser Gly Arg Phe Glu Cys Arg	
1170 1175 1180	
ttt aca agt gtg acc ata aag gac tca ccg gct ata atg ttc aaa	6074
Phe Thr Ser Val Thr Ile Lys Asp Ser Pro Ala Ile Met Phe Lys	
1185 1190 1195	
gac atg gca ggt agc aca ttg ggt ata tgg gct gct cat ggt gag	6119
Asp Met Ala Gly Ser Thr Leu Gly Ile Trp Ala Ala His Gly Glu	
1200 1205 1210	
gga aga gct tat ttc cca gat gaa ggc gtg ttg gac cgt ata gtt	6164
Gly Arg Ala Tyr Phe Pro Asp Glu Gly Val Leu Asp Arg Ile Val	
1215 1220 1225	
cat tct gag ttg gct cct ata aga tac tgt gat gat gct ggg aat	6209
His Ser Glu Leu Ala Pro Ile Arg Tyr Cys Asp Asp Ala Gly Asn	
1230 1235 1240	
cca aca gag gcc tac cct ttc aat gtg aat ggc tct cct tta ggg	6254
Pro Thr Glu Ala Tyr Pro Phe Asn Val Asn Gly Ser Pro Leu Gly	
1245 1250 1255	
gtg gca gct att tgt tcc cca gat ggg agg cat ctt gcc atg atg	6299
Val Ala Ala Ile Cys Ser Pro Asp Gly Arg His Leu Ala Met Met	
1260 1265 1270	
cct cat cct gag cgt tgc ttc tta atg tgg cag ttc cca tgg tat	6344
Pro His Pro Glu Arg Cys Phe Leu Met Trp Gln Phe Pro Trp Tyr	
1275 1280 1285	
cca aag cag tgg gat gtg gag aag aag ggg cct agt cct tgg tta	6389
Pro Lys Gln Trp Asp Val Glu Lys Lys Gly Pro Ser Pro Trp Leu	
1290 1295 1300	
cgc atg ttc cag aat gca aga gag tgg tgt tcc tga aatgatcaaa	6435
Arg Met Phe Gln Asn Ala Arg Glu Trp Cys Ser	
1305 1310	

Figure 1B Cont.- FGAM2

Fig. 2A

			Seq ID Nos.
<b>ATP Binding</b>			
FGAM1	309	PYPGAETGAGGRIRDTHATGRGSFVQAATAGYCVGNLNTPGFYAPWEDPSFTYPSNLAPP	2
FGAM2	309	PYPGAETGAGGRIRDTHATGRGSFVQAATAGYCVGNLNTPGFYAPWEDSSFTYPSNLAPP	4
DM-FGAM		PFSGATTGTGGRLRDVQGVGRGGVPIAGTAGYCVGALHIPGYKQPYEPLDFKYPATFAPP	5
HUMAN-FGAM		PFSGATTGTGGRIIRDVQCTGRGAHVVAGTAGYCFGNLHIPGYNLPWEDLSFQYPGNFARP	6
ECOLI-FGAM		PWPGAATGSGGEIRDEGATGRGAKPKAGLVGFSVSNLRIPGFEQPWEE-DFGKPERIVTA	7
<b>Gln Binding</b>			
FGAM1	1051	EEGSNGDREMAAAFYAAGFE PWDITMSDLLNGKISLLDFRGIVFVGGFSYADVLD SAKGW	2
FGAM2	1051	EEGSNGDREMAAAFYAAGFE PWDITMSDLLNGKISLQDFRGIVFVGGFSYADVLD SAKGW	4
DM-FGAM		EEGVNSEREMMACLLRANFEVHDVTMSDLLQGTASVSQYRGLIFPGGFSYADTLGSAKW	8
HUMAN-FGAM		EEGSNGDREMADAPHLAGFEVVDVTMQDLCSGAIGLDTFRGVAFVGGFSYADVLD SAKGW	9
ECOLI-FGAM		EQGVNSHVEMAAAFHRAGFDAIDVHMSDLLTGRGTGLEDFHALVACGGFSYGDVLDGAGEGW	10
<b>Gln Binding</b>			
FGAM1	1111	SASIRFNESVLQQFQEFYKRPDTFSLGVCNGCQLMALLGWVPGPQVGGVHGAGG----DL	2
FGAM2	1111	SASIRFNESVLQQFQEFYKRPDTFSLGVCNGCQLMALLGWVPGPQVGGVHGAGG----DL	4
DM-FGAM		AANILHNPRLLPQFEAFKRRQDV FSLGICNGCQLMTLIGFVGSAKSEVGADP-----	11
HUMAN-FGAM		AAAVTFHPRAGAE LRFRKRPDTFSLGVCNGCQLLALLGWVGGDPNEDAAEMGPDSQPAR	12
ECOLI-FGAM		AKSILFNDRVRDEFATFFHRPQTLALGVCNGCQMSNLRRELI PGSE-----L--W	13
<b>Gln Binding</b>			
FGAM1	1227	VHSELAPIRYCDDAGNPTEAYPFNANGSPLGVAAICSPDGRHLAMMPHPERCFLMWQFPW	2
FGAM2	1227	VHSELAPIRYCDDAGNPTEAYPFNVNGSPLGVAAICSPDGRHLAMMPHPERCFLMWQFPW	4
DM-FGAM		QSEQLVTLQYVDDVGKPTELYPLNPNNGSPQGIAGLCSSDGRHLALMPHPERCSSMYQWPY	14
HUMAN-FGAM		EARGLAPLHWADDDGNPTEQYPLNPNNGSPGVAGICSCDGRHLAVMPHPERAVR PWQAW	15
ECOLI-FGAM		ESKGLVALRYVDNFGKVTETYPANPNNGSPNGITAVTTESGRVTIMMPHPERVFTVSNW	16



**Figure 2B**

*FGAM1* promoter alignment to *wun1* promoter

Percent Similarity: 94.595 Percent Identity: 94.595

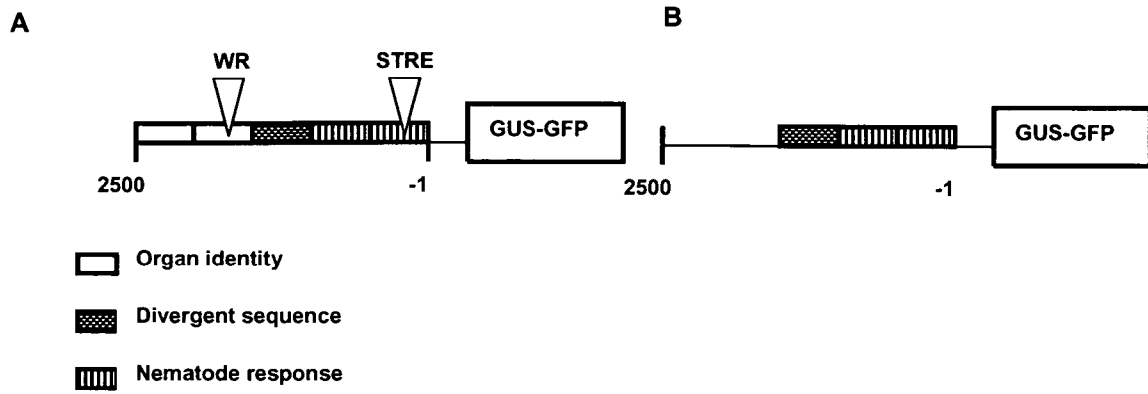
	Nt. no.		Seq ID
			Nos.
<i>FGAM1</i>	795	AACCGATATATATATATATATATATATATATATATATCAAT	831
<i>Wun1</i>		aaccgatatatatatatatatatatatatatatat	17

*FGAM2* promoter alignment to *wun1* promoter

Percent Similarity: 68.354 Percent Identity: 68.354

	Nt. no.		Seq ID
			Nos.
<i>FGAM2</i>	1332	ATATCGTGTA AATTTGTTAAATTTATTC TATAAAAAATACTTATTTTAA	1381
<i>Wun1</i>		at at cgt taaa at at t t t t a at at c t t g t t g a a t a t a a t t t t t t a t t t a g	18
	1382	TAAAATAA...ACAATTTTTTTTCTTTTAA	1410
		t a a a t a a t a t g a g a a t t a a t t t t t t t a t t a a	18

Fig. 3



## SOYBEAN FGAM SYNTHASE PROMOTERS USEFUL IN NEMATODE CONTROL

### GOVERNMENT INTEREST

The U.S. Government may have certain rights in this invention pursuant to United States Department of Agriculture Grant No. 96-35302-3385.

### RELATEDNESS OF THE APPLICATION

The subject application claims the benefit of priority from U.S. Ser. No. 60/556,745, filed Mar. 26, 2004, which is incorporated herein in its entirety.

### REFERENCE TO SEQUENCE LISTING

The present application incorporates by reference a file named:1231-221 Sequence Listing. ST25. txt including SEQ ID NO: 1 to SEQ ID NO: 20, provided in a computer readable form and paper copy. The sequence listing information recorded on the computer readable form is identical to the paper copy sequence listing.

### FIELD OF THE INVENTION

The subject invention relates to nematode responsive domains from the soybean FGAM synthase gene, which can be useful in reducing parasite infection or infestation.

### BACKGROUND OF THE INVENTION

The soybean cyst nematode (SCN) *Heterodera glycines* Ichinohe is considered the most economically debilitating disease-causing pathogen to affect soybean cultivation (Noel, G. R. (1992) in Riggs, R. D., Wrather, J. A. (eds) Biology and management of the soybean cyst nematode, APS Press, St. Paul, Minn., pp 8-10), causing losses of up to one billion dollars annually (Kim, D. G. et al. (1997) J. Nematol. 29:173-179). Several Hg types of SCN (Nieblack, T. L. et al. (2002) J. Nematol. 34:279-288) exist in the field (Riggs, R. D. et al. (1988) J. Nematol. 23:149-154) and several soybean genes that confer resistance have been identified. The most important of these genes have been mapped to linkage groups G and A2 of the soybean genetic map (Webb, D. M. et al (1995) Theor. Appl. Genet. 85:136-138; Concibido, V. C. et al. (1996) Theor. Appl. Genet. 93:234-241; and Meksem, K. et al. (2001) Theor. Appl. Genet. 103:710-718).

Several approaches have been undertaken to characterize nematode-responsive gene expression patterns within feeding sites of the soybean root. Changes in mRNA abundance were studied by in vitro translation to proteins (Hammond-Kossack, K. E. et al. (1989) Physiol. Mol. Plant Pathol. 37:339-354; Potenza, C. L. et al. (1996) J. Nematol. 28:475-484; and Oberschmidt, I. et al. (1996) Fourth annual meeting of the European union AIR-CAP on Mechanisms for resistance against plant parasitic nematodes, Toledo, Spain, p. 13). Subtractive hybridization of cDNA libraries prepared from nematode-infected and uninfected roots has yielded "infection-specific" clones. This approach has been utilized in tomato plants infected with root-knot nematodes (Van der Eycken, W. et al. (1996) Plant J. 9:45-54), and in potatoes infected with cyst nematodes (Niebel, A. et al. (1995) MPMI 8:371-378). Likewise, several PCR-based libraries have been constructed to permit the cloning of "giant cell-specific" transcripts (Wilson, M. A. et al. (1994)

Phytopathol. 84:299-303; and Bird, D. M. et al. (1994) MPMI 7:419-424). Use of the differential display technique has yielded several interesting candidate genes in the *Ara-bidopsis-Meloidogyne* interaction (Vercauteren, I. et al. (2001) MPMI 14:288-299) and the soybean-SCN interaction (Hermesmeier, D. et al. (1998) MPMI 11:1258-1263). Promoter-GUS fusion (Opperman, C. H. et al. (1994) Science 263:221-223) and promoter trap (Barthels, N. et al. (1997) The Plant Cell 9:2119-2134; and Puzio, P. S. et al. (1998) Physiol. Mol. Plant Pathol. 53:177-193) approaches have also been implemented to identify nematode-responsive loci.

In a previous report (Vaghchhipawala, Z. E. et al. (2001) MPMI 14:42-54), we showed that several genes were up-regulated within the syncytium during colonization of the root by SCN. We determined the map locations of some of the soybean genes responsive to nematode infection by locating them on the public soybean map (Shoemaker, R. C. et al. (1996) in D. P. S. Verma and R. C. Shoemaker (eds) Biotechnology in Agriculture, No. 14, Soybean: genetics, Molecular Biology and Biotechnology, CAB International, Wallingford, Oxon, UK, pp. 37-56). A particularly interesting candidate was phosphoribosylformylglycinamide ribonucleotide (FGAM) synthase. This gene mapped to the same 3.0-cM interval of Linkage Group G where the major soybean SCN resistance locus Rhg1 maps (Mudge, J. et al. (1997) Crop Sci. 37:1611-1615).

FGAM synthase was of interest because of its coincident location within the genomic interval containing Rhg1 and its up-regulated expression within the nematode feeding site. The enzyme FGAM synthase catalyzes the fifth step of the de novo purine biosynthetic pathway, effecting the ATP-dependent transfer of the glutamine amido group to the C-4 carbonyl of FGAR (5'-phosphoribosyl-N-formylglycinamide). To investigate this soybean gene further, we isolated and characterized two FGAM synthase loci. The two loci were highly similar in sequence. Analysis of the two copies revealed distinct functions and/or expression profiles during development and syncytium formation. As is described herein, the promoters of both FGAM synthase copies were found to contain novel nematode responsive domains that are active during syncytium formation.

### SUMMARY OF THE INVENTION

The subject invention concerns the identification of soybean gene promoter sequences that contain nematode responsive domains. The nematode responsive domain is active during nematode establishment of a feeding site on the soybean, resulting in altered expression of downstream coding sequences.

As discussed herein, the soybean cyst nematode (SCN) is an economically debilitating disease-causing pathogen in soybean cultivation. Several soybean genes that confer resistance have been identified. One of the most important nematode resistance genes, rhg1, has been mapped to a distal region of MLG-G in soybean. A simplified genetic system to identify soybean genes with modified expression in response to SCN led to the identification of several genes within the nematode feeding sites (Vaghchhipawala et al. (2001) supra). The genes were mapped to reveal their linkage relationship to known QTLs associated with soybean cyst nematode (SCN) resistance. One candidate, a phosphoribosylformylglycinamide (FGAM) synthase (EC# 6.3.5.3) gene, mapped to the same genomic interval as

the major SCN resistance gene *rhg1* within Linkage Group G. As is detailed herein, isolation of FGAM synthase from a soybean bacterial artificial chromosome (BAC) library revealed two highly homologous paralogs. The genes appeared to be well conserved from bacteria to humans. Promoter analysis of the two soybean homologs was carried out with the *Arabidopsis thaliana*-*Heterodera schachtii* system to investigate gene response to nematode feeding. As reported herein, the two promoters and their derived deletion constructions effected green fluorescent protein expression within nematode feeding sites. It was found that the 1.0-kbp promoter sequence immediately adjacent to the translation start site was sufficient to direct expression of GFP within syncytia at the feeding site. The observed expression of GFP within the feeding sites indicates that plant gene expression is redirected within feeding sites to benefit the parasitic nematode.

Thus, in one embodiment, the subject invention is a molecule that comprises a soybean promoter sequence that comprises a nematode responsive domain, i.e., a domain that is responsive to nematode establishment of a feeding site in the plant.

As is set forth in the Examples, the promoter sequence can comprise a sequence selected from the group consisting of soybean FGAM synthase Pr1-1.0 (nucleotides 1790–2483 of SEQ. ID NO. 2), Pr2-1.0 (nucleotides 1551–2547 of SEQ. ID NO. 1), Pr1-1.5 (nucleotides 1271–2483 of SEQ. ID NO. 2), Pr2-1.5 (nucleotides 991–2547 of SEQ. ID NO. 1), Pr1-2.5 (nucleotides 124–2483 of SEQ. ID NO. 2) and Pr2-2.5 (nucleotides 19–2547 of SEQ. ID NO. 1).

Further, the promoter sequence can be a sequence that has at least 50% homology with that of Pr1-1.0 or Pr2-1.0 of soybean FGAM synthase. With increasing preference, the promoter sequence has at least 60%, 70%, 80%, 90% or 95% homology to Pr1-1.0 or Pr2-1.0. To be encompassed within the scope of the subject invention, these variant promoter sequences must remain functional as nematode responsive domains.

It will be apparent that minor additions, deletions or substitutions can be made to Pr1-1.0 or Pr2-1.0, while retaining or perhaps enhancing the nematode responsive function. All of these variants are encompassed within the scope of the subject invention.

In another embodiment, the subject invention includes a molecule that is a promoter comprising the nematode responsive domain and a heterologous DNA operatively linked to the promoter. The heterologous DNA encodes a product that is disruptive of nematode attack. The disruptive product may be toxic to the plant cell or to the nematode.

The subject invention also includes a transfected plant (e.g., soybean) cell comprising the above-described molecule comprising the nematode responsive domain. It also includes transgenic plants comprising the transfected plant cells.

In another embodiment, the invention includes a method of reducing nematode infection of a plant (e.g., soybean) comprising transfecting plant cells of said plant with a vector comprising a promoter containing the nematode responsive domain and a heterologous DNA operatively linked to the promoter.

All references cited herein are incorporated in their entirety by reference.

#### BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1A is the nucleotide sequence and amino acid sequence for FGAM1 (SEQ. ID NOS. 1 and 2).

FIG. 1B is the nucleotide sequence and amino acid sequence for FGAM2 (SEQ. ID NOS. 3 and 4).

FIG. 2A is the sequence alignments of the soybean FGAM synthase gene with other known FGAM sequences. Multiple alignment of amino acid sequences (Higgins, D.G. et al. (1988) Gene 73:237–244) for genes FGAM1 (SEQ ID NO: 2), FGAM2 (SEQ ID NO: 4), *Drosophila melanogaster* (SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 11, and SEQ ID NO: 14), *Homo sapiens* (SEQ ID NO: 6, SEQ ID NO: 9, SEQ ID NO: 12, and SEQ ID NO: 15) and *E.coli* (SEQ ID NO: 7, SEQ ID NO: 10, SEQ ID NO: 13 and SEQ ID NO: 16) using the ClustalW program are shown. Only conserved domains are shown. Identical amino acids are in bold. The ATP-binding domain and the three glutamine-binding domains are overlined.

FIG. 2B is the Bestfit analysis of the sequence homology of promoter regions of FGAM1 (SEQ ID NO: 1) and FGAM2 (SEQ ID NO: 3) genes with the *wun1* promoter (SEQ ID NO: 17 and SEQ ID NO: 18) from potato (Hansen, E. et al. (1996) Physiol. Mol. Plant Pathol. 48:161–170).

FIG. 3 is a diagrammatic representation of promoter organization for genes FGAM1 (A) and FGAM2 (B). Promoter deletions were generated from the approximately 2500 bp end using PCR. Domains identified in these promoters via functional or sequence analysis are indicated. WR indicates a wound response element identified by sequence homology and shown functionally in Pr1-2.5 plants. STRE designates a stress response element.

#### DETAILED DESCRIPTION

The subject invention concerns the identification of soybean gene promoter sequences that contain a nematode responsive domain, and the use of said domain in the control of nematode infection of soybeans.

A “nematode responsive domain” is a region of the plant (e.g., soybean) promoter that is active in a nematode established feeding site on the plant. Without wishing to be bound by a particular theory, it is believed that a nematode protein or other molecule may bind to the nematode responsive domain of the promoter to control expression of downstream coding sequences during establishment of a feeding site. A nematode responsive domain is “functional” if the mRNA expression of the downstream coding sequence is up-regulated in the feeding site syncytium by at least 10% as compared to plant cells of the same tissue type that are not nematode feeding sites. “Functional” nematode responsive domain can also mean, with increasing preference, increased expression of 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100% or more. Methods for determining increase in amount of mRNA expression are known to persons skilled in the art.

A “promoter” is a control sequence that is a region of a nucleic acid sequence at which initiation and rate of transcription are controlled. It may contain genetic elements at which regulatory proteins and molecules may bind such as RNA polymerase and other transcription factors. The phrases “operatively positioned,” “operatively linked,” “under control,” and “under transcriptional control” mean that a promoter is in a correct functional location and/or orientation in relation to a nucleic acid sequence to control transcriptional initiation and/or expression of that sequence. A promoter may or may not be used in conjunction with an “enhancer,” which refers to a cis-acting regulatory sequence involved in the transcriptional activation of a nucleic acid sequence.

Plant transformation involves the construction of an expression vector which will function in plant cells. Such a

vector comprises a heterologous DNA under control of or operatively linked to a regulatory element (for example, a promoter). The expression vector may contain one or more such operatively linked gene/regulatory element combinations. The vector(s) may be in the form of a plasmid, and can be used alone or in combination with other plasmids, to provide transformed plants, using transformation methods as described below to incorporate heterologous sequences into the genetic material of the plant.

The heterologous DNA may encode any product that is disruptive of nematode attack when that DNA is transcribed (and if necessary, translated) in a plant cell. The product can include proteins, peptides, and non-protein products such as antisense RNAs, aptamers and the like. Atkinson, H. J. et al. (2003) *Ann. Rev. Phytopathol.* 41:615, review information on direct effectors that act against the nematode and effectors that disrupt the nematode feeding site.

The heterologous DNAs may encode a product that is toxic to the plant cells, as described in U.S. Pat. No. 5,750,386 to Conkling et al. A wide variety of protein or peptide products which are toxic to plant cells can be used, including (but not limited to) enzymes capable of degrading nucleic acids (DNA, RNA) such as nucleases, restriction endonucleases, micrococcal nuclease, Rnase A, and Barnase (*Bacillus amyloliquefaciens* RNase); enzymes which attack proteins such as trypsin, pronase A, carboxypeptidase, endoproteinase Asp-N, endoproteinase Glu-C, and endoproteinase Lys-C; ribonucleases such as RNase CL-3 and RNase T<sub>1</sub>, toxins from plant pathogenic bacteria such as phaseolotoxin, tabtoxin, and syringotoxin; lipases such as produced from porcine pancrease and *Candida cylindracea*, membrane channel proteins such as glp F and connexins (gap junction proteins), and antibodies which bind proteins in the cell so that the cell is thereby killed or debilitated. Genes which produce antibodies to plant cell proteins can be produced as described in Huse, W. et al. (1989) *Science* 246:1275-1281. Proteins to which such antibodies can be directed include, but are not limited to, RNA polymerase, respiratory enzymes, cytochrome oxidase, Krebs cycle enzymes, protein kinases, aminocyclopropane-1-carboxylic acid synthase, and enzymes involved in the shikimic acid pathway such as enolpyruvyl shikimic acid-5-phosphate synthase. In preferred embodiments, the heterologous DNA is an anti-apoptosis gene (Dickman, M. B. et al. (2001) *Proc. Natl. Acad. Sci.* 98:6957), a gene involved in the hypersensitive response, a gene involved in MAPK signal transduction, or a gene encoding an RNA interference construct that down-regulates a gene needed for feeding site establishment (Campbell, M. A. et al. (2002) *Transgenic Res.* 11 (6):599).

Note that the toxic product may either kill the plant cell in which it is expressed or simply disable the cell so that it is less capable of supporting the pathogen. It is preferred that the plant-toxic product be non-toxic to animals, and particularly be non-toxic to humans.

The heterologous DNA may encode any other product disruptive of nematode attack, including but not limited to those described in U.S. Pat. No. 5,589,622 to Gurr et al. (e.g., products toxic to the nematode). Thus the heterologous DNA may encode a *Bacillus thuringiensis* crystal protein toxic to insects. Strains of *B. thuringiensis* which produce polypeptide toxins active against nematodes are disclosed in U.S. Pat. Nos. 4,948,734 and 5,093,120 (Edwards et al.). Additionally, the heterologous DNA may encode other natural pesticides such as that found in *cyanobacterium Nostoc* strain ATCC 53789 (Biondi et al. (2004) *Appl. Environ. Microbiol.* 70(6):3313).

Again note that the toxic product may either kill the nematode attempting to feed on the plant cell in which it is expressed or simply disable the nematode so that it is less capable of feeding on the plant cell or establishing a feeding site. For example, the heterologous DNA may encode a peptide, antibody or the like that disrupts feeding by interacting with the ingestion or digestion of food such as one of the antibodies described for soybean cyst nematode including that against the dorsal pharyngeal gland (Atkinson et al., 1988 *Annals of Applied Biology* 112:459-469), using the procedures for transgenic expression of antibodies in plants described by Hiatt, A. et al. (1989) *Nature* 342:76-78).

Again it is preferred that the nematode-toxic product be non-toxic to other animals, and particularly be non-toxic to birds, reptiles, amphibians, mammals and humans.

Plant transformation is achieved via known methods of using expression vectors. Expression vectors generally include at least one genetic marker, operatively linked to a regulatory element (a promoter) that allows transformed cells containing the marker to be either recovered by negative selection, i.e., inhibiting growth of cells that do not contain the selectable marker gene, or by positive selection, i.e., screening for the product encoded by the genetic marker. Many commonly used selectable marker genes for plant transformation are well known in the transformation arts, and include, for example, genes that code for enzymes that metabolically detoxify a selective chemical agent which may be an antibiotic or an herbicide, or genes that encode an altered target which is insensitive to the inhibitor. A few positive selection methods are also known in the art.

One class of marker genes for plant transformation require screening of presumptively transformed plant cells rather than direct genetic selection of transformed cells for resistance to a toxic substance such as an antibiotic. These genes are particularly useful to quantify or visualize the spatial pattern of expression of a coding sequence in specific tissues and are frequently referred to as reporter genes because they can be fused to a gene or gene regulatory sequence for the investigation of gene expression. Commonly used genes for screening presumptively transformed cells include  $\beta$ -glucuronidase (GUS),  $\beta$ -galactosidase, luciferase, chloramphenicol and acetyltransferase (Jefferson, R. A. (1987) *Plant Mol. Biol. Rep.* 5:387; Teeri et al. (1989) *EMBO J.* 8:343; Koncz et al. (1987) *Proc. Natl. Acad. Sci. USA* 84:131; and DeBlock et al. (1984) *EMBO J.* 3:1681).

Also available are in vivo methods for visualizing GUS activity that do not require destruction of plant tissue (Molecular Probes publication 2908, *Imagene Green™* p. 1-4 (1993); and Naleway et al. (1991) *J. Cell Biol.* 115:151a). Additionally, a gene encoding Green Fluorescent Protein (GFP) has been utilized as a marker for gene expression in prokaryotic and eukaryotic cells (Chalfie et al. (1994) *Science* 263:802). GFP and mutants of GFP may be used as screenable markers.

Numerous methods for plant transformation have been developed, including biological and physical plant transformation protocols. See, for example, Miki et al., "Procedures for Introducing Foreign DNA into Plants" in *Methods in Plant Molecular Biology and Biotechnology*, Glick, B. R. and Thompson, J. E. Eds. (CRC Press, Inc. Boca Raton, 1993) pages 67-88.

One method for introducing an expression vector into plants is based on the natural transformation system of *Agrobacterium*. See, for example, Horsch et al. (1985) *Science* 227:122. *A. tumefaciens* and *A. rhizogenes* are plant pathogenic soil bacteria which genetically transform plant cells. The Ti and Ri plasmids of *A. tumefaciens* and *A.*

*rhizogenes*, respectively, carry genes responsible for genetic transformation of the plant. See, for example, Kado, C. I. (1991) Crit. Rev. Plant Sci. 10:1. Descriptions of *Agrobacterium* vector systems and methods for *Agrobacterium*-mediated gene transfer are provided by Gruber Miki et al., supra. and Moloney et al. (1989) Plant Cell Reports 8:238. See also, U.S. Pat. No. 5,563,055, issued Oct. 8, 1996.

Several methods of plant transformation collectively referred to as direct gene transfer, have been developed as an alternative to *Agrobacterium*-mediated transformation. A generally applicable method of plant transformation is microprojectile-mediated transformation wherein DNA is carried on the surface of microprojectiles measuring 1 to 4  $\mu\text{m}$ . The expression vector is introduced into plant tissues with a ballistic device that accelerates the microprojectiles to speeds of 300 to 600 m/s which is sufficient to penetrate plant cell walls and membranes (Sanford, J. C. (1990) Physiol. Plant 7:206; Klein et al. (1992) Biotechnology 10:268; U.S. Pat. No. 5,015,580, issued May 14, 1991; and U.S. Pat. No. 5,322,783, issued Jun. 21, 1994).

Another method for physical delivery of DNA to plants is sonication of target cells (Zhang et al. (1991) Bio/Technology 9:996). Alternatively, liposome or spheroplast fusions have been used to introduce expression vectors into plants (Deshayes et al. (1985) EMBO J. 4:2731; Christou et al. (1987) Proc. Natl. Acad. Sci. USA 84:3962). Direct uptake of DNA into protoplasts using  $\text{CaCl}_2$  precipitation, polyvinyl alcohol or poly-L-ornithine has also been reported (Hain et al. (1985) Mol. Gen. Genet. 199:161; and Draper et al. (1982) Plant Cell Physiol. 23:451). Electroporation of protoplasts and whole cells and tissues have also been described (Donn et al., in Abstracts of VIIth International Congress on Plant Cell and Tissue Culture IAPTC, A2-38, p 53 (1990); D'Halluin et al. (1992) Plant Cell 4:1495-1505; and Spencer et al. (1994) Plant Mol. Biol. 24:51-61).

A transformed soybean cell is one which has been transformed or transfected with DNA constructs as described herein. The transformed or transfected cell is then clonally propagated using known methods to generate a soybean plant. Tissue culture of various tissues of soybeans and regeneration of plants therefrom is well known and widely published. For example, reference may be had to Komatsuda, T. et al., Crop Sci. 31:333-337 (1991); Stephens, P. A., et al., Theor. Appl. Genet. (1991) 82:633-635; Komatsuda, T. et al., Plant Cell, Tissue and Organ Culture, 28:103-113 (1992); Dhir, S. et al., Plant Cell Reports (1992) 11:285-289; Pandey, P. et al., Japan J. Breed. 42:1-5 (1992); and Shetty, K., et al., Plant Science 81:245-251 (1992); as well as U.S. Pat. No. 5,024,944 issued Jun. 18, 1991 to Collins et al., and U.S. Pat. No. 5,008,200 issued Apr. 16, 1991 to Ranch et al.

As used herein, the term "tissue culture" indicates a composition comprising isolated cells of the same or a different type or a collection of such cells organized into parts of a plant. Exemplary types of tissue cultures are protoplasts, calli, plant clumps, and plant cells that can generate tissue culture that are intact in plants or parts of plants, such as embryos, pollen, flowers, seeds, pods, leaves, stems, roots, root tips, anthers, and the like. Means for preparing and maintaining plant tissue culture are well known in the art. By way of example, a tissue culture comprising organs has been used to produce regenerated plants. U.S. Pat. Nos. 5,959,185; 5,973,234 and 5,977,445 describe certain techniques, the disclosures of which are incorporated herein by reference.

The Examples set forth herein describe in detail the isolation and characterization of duplicate copies of the

FGAM synthase gene from soybean. This gene was identified by differential display analysis and confirmed by RT-PCR to be upregulated within the feeding sites of *Heterodera glycines* in soybean roots (Vaghchhipawala et al. (2001), supra). Isolation and characterization of the gene from the Williams 82 cultivar of soybean revealed the presence of three copies of the gene, two with high sequence homology and one distantly related. The presence of multiple gene copies was anticipated given the duplicated nature of the soybean genome (Shoemaker, R. C. et al. (1996) Genetics 144:329-338).

As is discussed in the Examples, the FGAM1 gene was encompassed within BAC 53M17, while FGAM2 resides within the BAC 42013/52C8 contig. The high sequence similarity between the genes suggests that the two loci have likely arisen by gene duplication. The degree of sequence identity between the two open reading frames (95.5%) and promoter regions (85%) implies that the duplication occurred fairly recently in evolutionary terms. Although the two gene copies show high protein sequence identity, an estimation of the coalescence time following the procedure of Lynch et al. (Science 290:1151-1155 (2000)) yields a date of approximately 11 Mya. The two loci apparently continue to carry out duplicate functions in differing spatial and temporal patterns or in response to varying stimuli.

Evidence for multi-gene copies in soybean is extensive. A recent study (Jin et al., 1999) reported at least 12 classes of  $\beta$ -1,3-glucanase genes displaying divergent gene expression patterns. Members of a BURP domain-containing protein family, from soybean were also shown to possess diverse expression patterns (Granger, C. et al. (2002) Genome 45:693-701). Mahalingam, R. et al. (1999) MPMI 12:490-498, identified two copies of a polygalacturonase gene, also from soybean, with expression up-regulated during syncytium establishment. Yamamoto, E. (2001) Mol. Biol. Evol. 18:1522-1531, identified three soybean orthologs of *A. thaliana* receptor-like protein kinases showing high sequence homology and predicted to have arisen from recent duplication events. The advantage of gene redundancy in soybean and other plant genomes is not known, but it has been suggested that members of a gene family generally retain a set of standard functions but acquire unique expression patterns and responses to environmental stimuli. It has been proposed that tissue specificity is an early step in functional divergence of a gene family, while divergence at the amino acid level occurs later (Pickett, F. B et al. (1995) Plant Cell 7:1347-1356). The differential expression of FGAM1 and FGAM2 and the observed divergence between their promoters are consistent with this hypothesis.

The essential function provided by FGAM synthase would predict its activity in areas of rapid cell proliferation. These tissues should include reproductive organs and apical and lateral meristems. This anticipated pattern of expression was evident in the GUS expression assays for FGAM1 full-length promoter (Pr1-2.5). A surprising exception was the pollen sacs, in which no FGAM1 expression was detected. Possibly, sequences for anther expression were present further upstream to the region tested and were omitted from the tested constructions, or a different FGAM synthase copy might be expressing within anther tissues. Lack of detectable GUS expression in the FGAM1 promoter deletions (Pr1-1.5 and Pr1-1.0) suggests that enhanced expression levels or tissue specificity of expression may reside within the interval 1.5 kbp upstream to the translation start site.

To investigate the divergent expression that has arisen between the two loci, we focused on promoter sequence differences. Alignment of promoter sequences revealed a FGAM1 stress response element close to the translation start site. Moreover, FGAM2 promoter constructions showed no GUS expression, suggesting that expression of this locus is much lower or responsive to particular stimuli.

Sequences responsible for feeding site GFP expression were located within an upstream 1.0-kbp interval present in both promoters. Observation of enhanced GFP expression in feeding sites from all constructions, and the considerable sequence homology within the upstream 1.0-kbp interval that confers nematode-responsive expression, suggest that nematode-inducible activity was acquired prior to the gene duplication event.

It is conceivable that nematode responsiveness in the expression of FGAM synthase has facilitated co-evolution of the host-nematode interaction. Purine biosynthesis gene expression in the root has already been shown to be inducible by *Rhizobium* (Schnorr, K. M. et al. (1996) *Plant Molec. Biol.* 32:751–757). In fact, several examples of reprogrammed plant gene expression have been found in response to nematode infection (Gheysen, G. et al. (2002) *Ann. Rev. Phytopathol.* 40:191–219). Juergensen, K. et al. (2003) *Plant Physiol* 131:61–69, demonstrated activated expression of AtSuc2, which mediates the transmembrane transfer of sucrose into syncytia that acts as nutrient sinks for the nematode. Down regulation of a novel Glycine max ethylene-responsive element-binding protein 1 (GmEREBP1) has also been reported. This protein binds to GCC motifs located within PR gene promoters in *H. glycines*-infected soybean roots during a susceptible interaction (Mazarei, M. et al. (2002) *MPMI* 15:577–586) to undermine host defenses. Vercauteren, I. et al. (2002) *MPMI* 15:404–407, report the up-regulation of a pectin acetyltransferase gene in feeding sites of root and cyst-knot nematodes. This gene encodes a pectin-degrading enzyme that may be involved in softening and loosening the primary cell wall in nematode-infected plant roots, leading to expansion of the syncytium. These reports reflect the very broad spectrum of genes thought to be redirected in expression by the nematode for feeding site establishment. The feasibility of disrupting gene expression patterns essential to feeding site establishment as a method of plant protection has not been fully assessed.

Sijmons, P. C. et al. (1991) *Plant J.* 1: 245–254, were first to document in detail the requirements for successful infection of *Arabidopsis* by economically important nematodes. In Golinowski, W. et al. (1996) *Protoplasma* 194:103–116; and Golinowski, W. et al. (1997) in *Cellular and molecular aspects of plant-nematode interactions* (C. Fenoll et al. (eds.), pp. 80–97, ultrastructural studies were undertaken on root cellular architecture to follow the course of development of *H. schachtii* in *Arabidopsis* roots. The nematode developmental life-cycle (~6 weeks) of *H. schachtii* is similar to that of *Heterodera glycines*. Likewise, the sequence of changes in *Arabidopsis* root cell morphology appears to follow a similar course to that in soybean roots. For these reasons, it appears that the observations made in *Arabidopsis* are likely to parallel events in the infected soybean root.

Interestingly, the expression profiles observed in the full length and deletion constructions for the FGAM1 promoter were similar to the pattern reported for the promoter of gene *pyk20*, isolated from *Arabidopsis thaliana* by a promoter tagging strategy (Puzio, P. S. et al. (2000) *Plant Sci.* 157: 245–255). This approach was used to identify genes that were active in nematode feeding sites. The investigators

detected expression within the feeding sites as well as floral organs, and a wound response within leaves. Likewise, they reported a region of 963 bp upstream to the first ATG of *pyk20* that was sufficient to direct expression within the nematode feeding site in *Arabidopsis* roots. The lack of expression within feeding sites by vector control constructions (35S::GFP) in our study agrees with previous published data (Urwin et al., 1997, *Plant J.* 12(2):455–61 and van Poucke et al., 2001, *Meded Rijksuniv Gent Fak Landbouwk Toegep Biol Wet.* 66(2b):591–8).

Opperman, C. H. et al. (1994) *Science* 263:221–223, reported a requirement of 300 bp of upstream sequence to the TobRB7 gene of tobacco for localized expression in *Meloidogyne*-induced giant cells. Moreover, Escobar, C. et al. (1999) *MPMI* 12:440–449, identified a sequence 111 bp upstream of the TATA box where nuclear proteins from nematode-induced galls formed DNA protein complexes. These reports indicate that putative nematode responsive domains are generally present in regions of the promoter very close to the transcription initiation sites. It is conceivable that an array of common nematode responsive promoter domains serve as the primary means of coordinating plant gene expression during syncytium establishment.

Based on observations described herein, it appears that the FGAM1 locus likely serves housekeeping functions, while FGAM2 may respond to specific environmental stimuli. Yamamoto, E. et al. (2000) *MPMI* 12: 440–449, reported the cloning of two identical CLAVATA 1-like genes from soybean which show differential expression patterns and suggest that the function of the two genes is slightly different in different organs. In contrast, both FGAM full-length promoters (and deletion fragments thereof) were found to be nematode inducible, indicating that the nematode inducible domain is located in the 1.0 kbp domain immediately 5' to the translation start site.

The present invention is explained in greater detail in the following non-limiting Examples.

## EXAMPLES

### Example 1—Materials and Methods

#### Vectors and Strains

The genomic copies of FGAM synthase were isolated from a bacterial artificial chromosome (BAC) library prepared from the partial Hind III digestion of genomic DNA of the soybean line 'Williams 82' (Marek, L. F. (1997) *Genome* 40:420–427). Gene promoter constructions utilized the vector pCAMBIA 1303. Transgene constructions were introduced into ELECTROMAX DH10B cells (Life Technologies, USA) of *Escherichia coli* via electroporation.

#### DNA Gel Blot Analysis, PCR and DNA Sequencing Procedures

DNA gel blot analysis was carried out using standard procedures (Sambrook, J. et al. (1989) *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.). DNA sequencing was accomplished using the fluorescently-labeled primer cycle sequencing kit with 7-deaza-dGTP (Amersham Intl., Buckinghamshire, England) in an ALFexpress automated sequencer (Pharmacia, Biotech AB, Umeå, Sweden). The polymerase chain reaction (PCR) was carried out using genomic DNA from transgenic *Arabidopsis* leaves prepared according to published protocol (Li, J. et al. (1998) in *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.) as

template. Primers were designed from the uidA sequence to amplify a product of approximately 1189 bp.

#### Genomic, Plasmid and BAC DNA Preparations and Sequence Homology Searches

Genomic DNA was prepared by the method of Vallejos, C. E. et al. (1992) *Genetics* 131:733–740. Plasmid DNA preparations were carried out using the CONCERT™ plasmid miniprep kit (Life Technologies, USA), while BAC DNA was prepared using a modified alkaline lysis protocol (Felicielo, I. et al. (1993) *Anal. Biochem.* 212:394–401). GCG package software “SEQWEB” function “Bestfit” was used to identify sequence homologies, and the “motifs” function was used to locate protein motifs of interest.

#### Preparation of Promoter Constructions

The subcloning of the promoter region was carried out in the vector pCAMBIA1303, which incorporates the reporter genes β-glucuronidase (GUS) and enhanced green fluorescent protein (GFP) under the control of the CaMV 35S promoter. Cloning was accomplished by excising the 35S promoter from the vector by digestion with enzymes BamHI and NcoI, and introducing putative promoter fragments from the two identified FGAM synthase genes, FGAM1 and FGAM2. Promoter inserts (2.48 kbp) and their derived truncations were generated by PCR amplification with primers designed to contain BamHI and NcoI restriction sites.

#### Generation of *Arabidopsis* Transformants

The transformation of *Arabidopsis thaliana*, grown in a 16-hr day, 8-hr night light regime, was carried out using the floral dip method (Clough, S. J. (1998) *Plant J.* 16:735–743). The *Agrobacterium tumefaciens* strain C58C1 (provided by Dr. Thomas Clemente, University of Nebraska-Lincoln) was used to transform *Arabidopsis* ecotype Columbia. Transgene constructions were mobilized into the *Agrobacterium* strain via electroporation. Upon transformation, selection of transgenic plants was carried out by plating surface-sterilized seeds on 0.5×MS-B medium with 2% (w/v) sucrose, vitamins and 20 mg/L Hygromycin. Selected plants were subjected to GUS staining (Jefferson, R. A. et al. (1987) *EMBO J.* 6:3901–3907), PCR analysis, and DNA gel blot analysis before inclusion in the nematode assay.

#### GUS Staining and Microscopy Procedures

Plant tissues were immersed in X-Gluc (0.8 mg/ml) solution and kept overnight at 37° C. for color development. After staining, 70% (v/v) ethanol was added for clearing of pigments, following the procedure of Jefferson et al. (1987), supra. The infection of transgenic *Arabidopsis* roots by *Heterodera schachtii* was examined for GFP fluorescence with a Confocal Laser Scanning Microscope (CLSM) (Bio-Rad, USA).

#### *Heterodera schachtii* Infection Assays of *Arabidopsis* Transformants

Seeds from confirmed transgenic *Arabidopsis* plants were germinated on selective media as described above, then transferred to individual wells of a 12-well petri plate containing 1.5 ml of a modified Knop’s medium (Sijmons et al. (1991), supra) minus antibiotics. Infection was carried out on 11 to 13-day-old seedlings whose roots had penetrated into the medium. Each 12-well plate contained 10 individual T<sub>1</sub> transgenic seedlings derived from one independent transformant; the last two plants in the plate served as uninoculated controls. This system, following the procedure of Baum, T. J. et al. (2000) *J. Nematol.* 32:166–173, provided ample experimental replications without undue contamination. The plants were inoculated near the roots

with 50–100 surface-sterilized J2 juveniles of *Heterodera schachtii* suspended in 1.5% (w/v) low melting agarose. After 6–8 days incubation in a growth chamber at 25° C. and 16 hr daylength, allowing for feeding site establishment on the roots, plants were examined for GFP expression at root feeding sites by confocal laser scanning microscopy. Subsequently, GUS expression was assayed by filling the entire well with X-Gluc staining solution and incubating at 37° C. overnight. Clearing of tissues involved adding 70% (v/v) ethanol, and cleared roots were observed under the dissecting microscope.

#### Surface Sterilization of *Heterodera schachtii* J2 Juveniles

Worms freshly hatched after a 2–3-day incubation in a hatch chamber in 3.14 mM ZnSO<sub>4</sub> were used for inoculation. Juveniles were counted in a haemocytometer and approximately 100,000 individuals were placed in a sterile 50-ml centrifuge tube. The samples were washed once in sterile distilled water by pelleting at 1500–2000 rpm for 3 minutes in a centrifuge using a swinging bucket rotor and no brake. The nematodes were resuspended in 50 ml of 0.001% Hibitane (Chlorhexidine, diacetate salt, Sigma #C6143) for 30 min mixing continuously. The sample was centrifuged at 1500 rpm for 3 minutes and resuspended in 50 ml of 0.01% (w/v) HgCl<sub>2</sub>. This suspension was incubated for 7 minutes, including the time to pellet the worms and remove supernatant. The sample was centrifuged to remove the HgCl<sub>2</sub>, followed by 3 washes with sterile distilled water. After the last wash, enough 1.5% (w/v) LMP agarose was added to achieve the desired final concentration of nematodes, and the sample was maintained at 37° C. The slurry was pipeted over roots in each well. J2 motility was observed after the LMP agarose had solidified.

#### Example 2—Assembly of Soybean FGAM Synthase Gene Contigs

The sequence of FGAM synthase cDNA (AF000377) was used to generate two primers for use in RT-PGR. Primer 113: 5'-GGT AU GAT GGA GGG AAA GAC AG-3' (SEQ ID NO: 19) and Primer 114: 5'-GCC ATC TCT AAG GCA GAA ACT AG-3' (SEQ ID NO: 20) were used to screen soybean genomic BAG library DNA pools by PCR. The search yielded four putative hits and the corresponding BAG clones 81J4, 42013, 53M17, and 52C8 were selected. The four BAG clones were digested with NotI enzyme and subjected to pulsed field gel electrophoresis to estimate insert sizes ranging from 110 kb to 160 kb. To assemble the BAG clones into contigs, multi-enzyme DNA digestions were separated by agarose gel electrophoresis. The BAG clones 42013 and 52C8 were found to share several bands in common, while the fingerprint of BAG 53M17 shared fewer bands. BAG 81J4 had a distinct banding pattern. Overlaps were confirmed by DNA gel blot hybridization. When probed with the FGAM synthase cDNA clone (890 bp), BACs 42013 and 52C8 produced identical hybridization patterns, while the pattern produced by BAG 53M17 differed. A very faint hybridization signal was detected in BAG 81J4, suggesting that the FGAM homology contained within this locus was weak. The two distinct forms of FGAM synthase represented in BACs 53M17 and 42013/52C8 were henceforth referred to as FGAM1 and FGAM2, respectively. Digestion of Williams 82 genomic DNA with HhaI also revealed 2 prominent and one faint band, consistent with presence in the genome of two homologous loci and one divergent sequence.

Genetic mapping of the original FGAM cDNA in the soybean genome indicated that at least one copy of the



FGAM loci is derived from Linkage Group G at the same map location as the major SCN resistance gene, Rhg1. Mapping data were derived from a mapping population of 57 F<sub>2</sub> individuals and a RIL mapping population of 100 individuals (Vaghchhipawala et al. (2001) supra). BAC analyses confirmed that the FGAM locus is duplicated. However, the location of the duplicate FGAM locus was not determined. Overlapping fragment analysis was used to determine full-length genomic sequence of genes FGAM1 and FGAM2 using the FGAM synthase cDNA clone to generate end probes. At the 5' end of each gene, approximately 2.5 kb of promoter sequence was also determined.

#### Example 3—Characterization of the Duplicate FGAM Synthase Loci

DNA sequence analysis of FGAM1 (Genbank AY178840) and FGAM2 (Genbank AY178839) revealed an open reading frame of 3132 bp and 3940 bp respectively (see FIGS. 1A and 1B). The two DNA sequences were 95.5% identical. Cluster analysis to assess amino acid sequence conservation among homologous FGAM synthase sequences available for soybean, *Drosophila*, Human and *E. coli* revealed highest sequence conservation among these genes within the ATP-binding domain and three glutamine binding domains as shown in FIG. 2A. Dendrogram analysis of 12 FGAM sequences from Genbank revealed a separate clustering of microbial and higher eukaryotic sequences. Among the higher eukaryotic genes identified, plant and animal sequences form distinct groups. Sequence analysis of the 2.5-kbp promoter region of the FGAM1 and FGAM2 genes revealed 85% identity. Scanning of the promoter sequences for various motifs revealed the presence of a stress response element (STRE) (Schuller, C. et al. (1994) EMBO J. 13:4382–4389) within the promoter of gene FGAM1 (nt 2361–2369 from 5' end) with 97% conservation of the consensus. This element is shown to activate transcription of a yeast gene in response to a variety of stress stimuli (Schuller et al. (1994), supra). Alignment of the two promoter sequences to the wun1 wound-inducible promoter from potato, inducible during cyst nematode infection (Hansen, E. et al. (1996) Physiol. Mol. Plant Pathol. 48:161–170), revealed a 39-bp interval with 95% sequence identity within the FGAM1 promoter but only 68% identity within the FGAM2 promoter (FIG. 2B).

#### Example 4—Promoter Analysis in the *Arabidopsis thaliana*-*Heterodera schachtii* System

To determine which FGAM synthase gene was responsive to nematode infection, we conducted transgenic promoter analysis in the established *A. thaliana*-*H. schachtii* system (Sijmons et al. (1991), supra). This system has been reported to parallel cellular events of the soybean-SCN infection process (Golinowski, W. et al. (1996) Protoplasma 194: 103–116). To determine which promoter intervals were serving to modify gene expression within syncytia, we developed two deletion constructions from each full-length promoter. The deletions were made at the 5' end of each original 2.48-kbp promoter, leaving 1.5-kbp and 1.0-kbp sequences immediately 5' to the translation start site in association with GUS (*uidA*) and *gfp* reporter genes as diagrammed in FIG. 3. The most divergent interval between the two promoters was located between nucleotides –1483 and –1983 (in relation to the +1 translation start site) in the FGAM2 promoter and nucleotides –1314 and –1014 (in relation to +1 start site) in the FGAM1 sequence. Within this

region exists a stretch of sequence of 70 nucleotides in the FGAM2 promoter that is absent from the FGAM1 promoter. To test whether the divergent sequences might account for nematode responsiveness, two deletion constructions containing this region, Pr1-1.5 (FGAM1) and Pr2-1.5 (FGAM2), were derived. The effect of deleting these divergent regions was assessed with constructions Pr1-1.0 and Pr2-1.0 (FIG. 3).

#### Example 5—FGAM1 and FGAM2 Promoter Expression

Transformants for the six promoter constructions of FGAM1 and FGAM2, as well as the vector control, were stained with X-Gluc solution. Two independent vector-transformed control lines, harboring the 35S promoter fused to GUS-GFP, produced GUS staining in leaves, inflorescence, stem and roots. Five independent transformants containing the full length (2.48-kbp) FGAM synthase promoter from gene FGAM2 (Pr2-2.5) were evaluated for GUS expression, and none produced detectable GUS staining in any part of the seedling including inflorescence. The same results were obtained for the four independent transformants of deletion construction Pr2-1.5 and for seven transformants of construction Pr2-1.0.

Experiments with the 2.48-kbp full-length FGAM1 promoter (Pr1-2.5) produced four independent transformants. With some minor plant variation, Pr1-2.5 transformants showed GUS staining in leaf margins and veins, the root tip and lateral root meristems and inflorescence with the exception of anthers. The FGAM1 deletion constructions, Pr1-1.5 (two events) and Pr1-1.0 (two events) showed no visible GUS staining anywhere in the seedling including flowers. Non-transformed seedlings produced no GUS staining. These results imply that the two promoters differ markedly in strength as a consequence of sequences located more than 1.5 kbp from the translation start site in FGAM1. They also indicate that sequences located more than 1.5 kbp from the translation start site are important in housekeeping growth functions unrelated to nematode responsive expression in established feeding sites.

#### Example 6—Promoter Expression Analysis in *H. schachtii*-inoculated *Arabidopsis* roots

Twelve individual T<sub>3</sub> progeny per gene construction were used in the *H. schachtii* infection assay carried out in twelve-well plates. Two plants served as uninoculated controls. Each plant was infected with 50–100 J2 juveniles, maintained in the growth chamber for 6 days, and then observed under a confocal laser-scanning microscope for GFP expression within feeding sites.

Roots of the vector control showed a uniform green fluorescence, and did not show significant elevation of GFP fluorescence at the sites of infection. Localized at the region of the root where a nematode had established a syncytium, a significant elevation of GFP expression above background was observed in all FGAM1 and FGAM2 promoter constructions. This observation was documented at least five times in each inoculated well (50 replicates for each independent transformant) for all promoter constructions. No localized elevation of GFP expression was seen in the uninoculated controls. Instances in which the nematode had penetrated the root tissue but had not yet established a feeding site showed no localized elevation of GFP. This observation suggests that the establishment of a feeding site was necessary for the enhancement of local GFP expression

levels, and indicates that the elevated expression was not simply a localized wound response.

#### Example 7—Wound Response

Sequence homology data indicated that the FGAM1 gene promoter contains a 39-bp sequence with 95% sequence identity to the *wun1* wound inducible promoter from potato. The FGAM2 gene promoter displayed only 68% sequence identity to the *wun1* promoter. A leaf from each transformant was excised from the seedling and assayed for GUS expression. Of all transformants tested, one containing the full-

length FGAM1 promoter construction (Pr1-2.5) showed what appeared to be a wound response. The excised leaf produced a visible staining pattern in the area around the wounded edge, while the remainder of the leaf remained unstained. This observation suggests that the FGAM1 promoter effects a weak wound response. None of the transformants containing the FGAM2 full length or deletion promoter constructions showed evidence of wound response. These results, again, imply that the nematode responsive expression observed in all transformants did not represent a general wound response.

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atc agt gtt tat gtt act tgt cct gat ata aca aaa aca gtg acg cca	5022
Ile Ser Val Tyr Val Thr Cys Pro Asp Ile Thr Lys Thr Val Thr Pro	825
810	815 820
gat tta aaa ctc aag gat gat ggt att ttg ctt cat att gat ttg tca	5070
Asp Leu Lys Leu Lys Asp Asp Gly Ile Leu Leu His Ile Asp Leu Ser	840
	830 835
aaa ggt aag agg cgg tta ggt gga tct gct ctt gcc cag gca ttt gac	5118
Lys Gly Lys Arg Arg Leu Gly Gly Ser Ala Leu Ala Gln Ala Phe Asp	855
	845 850
caa gtt ggg aat gag tgt cct gat ctt gat gat gtt cct tac ctt aaa	5166
Gln Val Gly Asn Glu Cys Pro Asp Leu Asp Asp Val Pro Tyr Leu Lys	870
	860 865
aag gtc ttt gaa ggt gtt caa gac ctt ctt tct gat gaa ctg ata tct	5214
Lys Val Phe Glu Gly Val Gln Asp Leu Leu Ser Asp Glu Leu Ile Ser	885
	875 880
gct ggt cat gac atc agt gat ggt ggg ctg cta gtt tgt gcc tta gag	5262
Ala Gly His Asp Ile Ser Asp Gly Gly Leu Leu Val Cys Ala Leu Glu	905
	890 895
atg gca ttt gct ggt aat tgt gga ctt agt ttg gac ttt gca tcg caa	5310
Met Ala Phe Ala Gly Asn Cys Gly Leu Ser Leu Asp Phe Ala Ser Gln	920
	910 915
ggt aac agc ctt ttc caa aca ctc tat gct gaa gag ctt ggg tta gtt	5358
Gly Asn Ser Leu Phe Gln Thr Leu Tyr Ala Glu Glu Leu Gly Leu Val	935
	925 930
ctt gag gta agc aag aaa aat ctg gct ttg gta gtg aat aaa ttg agc	5406
Leu Glu Val Ser Lys Lys Asn Leu Ala Leu Val Val Asn Lys Leu Ser	950
	940 945
aat gtg gga gtt tct gct gaa atc ata ggt caa gta aca gcc aat cca	5454
Asn Val Gly Val Ser Ala Glu Ile Ile Gly Gln Val Thr Ala Asn Pro	965
	955 960
tca ata gaa gtt aag gtt gat ggg gag act tat tta act gaa aaa act	5502
Ser Ile Glu Val Lys Val Asp Gly Glu Thr Tyr Leu Thr Glu Lys Thr	985
	970 975
agt atc ctt agg gac atg tgg gaa gag acc agt ttt cag ctg gaa aag	5550
Ser Ile Leu Arg Asp Met Trp Glu Glu Thr Ser Phe Gln Leu Glu Lys	1000
	990 995
ttc caa agg ttg gca tct tgt gtg gat atg gag aaa gaa gga cta	5595
Phe Gln Arg Leu Ala Ser Cys Val Asp Met Glu Lys Glu Gly Leu	1015
	1005 1010
aaa cat cgt tat gaa ccc tca tgg gaa ctg cct ttt act cct tcc	5640
Lys His Arg Tyr Glu Pro Ser Trp Glu Leu Pro Phe Thr Pro Ser	1030
	1020 1025
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Phe Thr Asp Glu Lys Leu Tyr Val Cys Asn Tyr Lys Thr	
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<210> SEQ ID NO 2  
 <211> LENGTH: 1044  
 <212> TYPE: PRT  
 <213> ORGANISM: Glycine max  
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 <221> NAME/KEY: misc\_feature  
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 <223> OTHER INFORMATION: The 'Xaa' at location 269 stands for Leu, or Phe.

<400> SEQUENCE: 2

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 Gly Leu Ser Ser Gln Leu Ser Gly Gly Lys Phe Ser Val Leu Gly Trp  
                   35                                  40                                  45  
 Leu Leu Gln Glu Thr Phe Glu Pro Glu Asn Leu Gly Thr Glu Ser Phe  
                   50                                  55                                  60  
 Leu Glu Lys Lys Arg Lys Glu Gly Leu Ile Pro Val Ile Val Glu Val  
                   65                                  70                                  75                                  80  
 Gly Pro Arg Leu Ser Phe Thr Thr Ala Trp Ser Thr Asn Ala Val Ala  
                                   85                                  90                                  95  
 Ile Cys Gln Ala Cys Gly Leu Thr Glu Val Asn Arg Leu Glu Arg Ser  
                   100                                  105                                  110  
 Arg Arg Tyr Leu Leu Phe Thr Thr Thr Glu Leu Gln Asp Tyr Gln Ile  
                   115                                  120                                  125  
 Asn Asp Phe Ala Ser Met Val His Asp Arg Met Thr Glu Cys Val Tyr  
                   130                                  135                                  140  
 Ile Gln Lys Leu Thr Ser Phe Glu Thr Ser Val Val Pro Glu Glu Ile  
                   145                                  150                                  155                                  160  
 His Tyr Ile Pro Val Met Glu Arg Gly Arg Lys Ala Leu Glu Glu Ile  
                                   165                                  170                                  175  
 Asn Leu Glu Met Gly Phe Ala Phe Asp Asp Gln Asp Leu Glu Tyr Tyr  
                   180                                  185                                  190  
 Thr Lys Leu Phe Arg Glu Asp Ile Lys Arg Asn Pro Thr Asn Val Glu  
                   195                                  200                                  205  
 Leu Phe Asp Ile Ala Gln Ser Asn Ser Glu His Ser Arg His Trp Phe  
                   210                                  215                                  220  
 Phe Thr Gly Lys Ile Phe Ile Asp Gly Gln Pro Val Asn Arg Thr Leu  
                   225                                  230                                  235                                  240  
 Met Gln Ile Val Lys Ser Thr Leu Gln Ala Asn Pro Asn Asn Ser Val  
                                   245                                  250                                  255  
 Ile Gly Phe Lys Asp Asn Ser Ser Ala Ile Arg Gly Xaa Pro Val Lys  
                   260                                  265                                  270  
 Gln Leu Arg Pro Val Gln Pro Gly Ser Ala Cys Pro Leu Glu Val Ala  
                   275                                  280                                  285  
 Val His Glu Leu Asp Ile Leu Phe Thr Ala Glu Thr His Asn Phe Pro  
                   290                                  295                                  300  
 Cys Ala Val Ala Pro Tyr Pro Gly Ala Glu Thr Gly Ala Gly Gly Arg  
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 Ile Arg Asp Thr His Ala Thr Gly Arg Gly Ser Phe Val Gln Ala Ala  
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 Thr Ala Gly Tyr Cys Val Gly Asn Leu Asn Thr Pro Gly Phe Tyr Ala  
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 Pro Trp Glu Asp Pro Ser Phe Thr Tyr Pro Ser Asn Leu Ala Pro Pro  
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 Leu Gln Ile Leu Ile Asp Ser Ser Asn Gly Ala Ser Asp Tyr Gly Asn  
                   370                                  375                                  380  
 Lys Phe Gly Glu Pro Leu Ile Gln Gly Phe Cys Arg Thr Phe Gly Met  
                   385                                  390                                  395                                  400  
 Arg Leu Pro Gly Gly Glu Arg Arg Glu Trp Leu Lys Pro Ile Met Phe  
                                   405                                  410                                  415  
 Ser Ala Gly Ile Gly Gln Ile Asp His Leu His Ile Ser Lys Gly Glu  
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 Pro Asp Ile Gly Met Leu Val Val Lys Ile Gly Gly Pro Ala Tyr Arg

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Asp	Ala	Glu	Leu	Asp	Phe	Asn	Ala	Val	Gln	Arg	Gly	Asp	Ala	Glu	Met
465					470					475					480
Ala	Gln	Lys	Leu	Tyr	Arg	Leu	Val	Arg	Ala	Cys	Ile	Glu	Met	Gly	Asp
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Lys	Asn	Pro	Ile	Ile	Ser	Ile	His	Asp	Gln	Gly	Ala	Gly	Gly	Asn	Cys
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Asn	Val	Val	Lys	Glu	Ile	Ile	Tyr	Pro	Lys	Gly	Ala	Glu	Ile	Asp	Val
			515				520							525	
Arg	Ala	Ile	Val	Val	Gly	Asp	His	Thr	Met	Ser	Val	Leu	Glu	Ile	Trp
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Gly	Ala	Glu	Tyr	Gln	Glu	Gln	Asp	Ala	Ile	Leu	Val	Lys	Pro	Glu	Ser
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Arg	Asp	Leu	Leu	Glu	Ser	Ile	Cys	Asn	Arg	Glu	Lys	Val	Ser	Met	Ala
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Val	Ile	Gly	Thr	Ile	Ser	Gly	Asp	Gly	Arg	Val	Val	Leu	Val	Asp	Ser
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Val	Ala	Ala	Gln	Lys	Ser	Ile	Ser	Asn	Gly	Leu	Pro	Pro	Pro	Pro	Pro
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Ala	Val	Asp	Leu	Glu	Leu	Glu	Lys	Val	Leu	Gly	Asp	Met	Pro	Lys	Lys
							615							620	
Thr	Phe	Lys	Phe	Asn	Arg	Val	Val	Tyr	Glu	Arg	Glu	Pro	Leu	Asp	Ile
625					630					635					640
Val	Pro	Gly	Ile	Glu	Val	Ile	Asp	Ser	Leu	Lys	Arg	Val	Leu	Ser	Leu
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Pro	Ser	Val	Cys	Ser	Lys	Arg	Phe	Leu	Thr	Thr	Lys	Val	Asp	Arg	Cys
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Val	Thr	Gly	Leu	Val	Ala	Gln	Gln	Gln	Thr	Val	Gly	Pro	Leu	Gln	Ile
			675					680						685	
Pro	Ile	Ala	Asp	Val	Ala	Val	Thr	Ala	Gln	Thr	Phe	Ala	Asp	Val	Thr
							695							700	
Gly	Gly	Ala	Cys	Ala	Ile	Gly	Glu	Gln	Pro	Ile	Lys	Gly	Leu	Leu	Asp
705					710					715					720
Pro	Lys	Ala	Met	Ala	Arg	Leu	Ala	Val	Gly	Glu	Ala	Leu	Thr	Asn	Leu
				725					730					735	
Val	Trp	Ala	Lys	Val	Thr	Ser	Leu	Ser	Asp	Val	Lys	Ala	Ser	Gly	Asn
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Trp	Met	Tyr	Ala	Ala	Lys	Leu	Asp	Gly	Glu	Gly	Ala	Asp	Met	Tyr	Asp
				755				760						765	
Ala	Ala	Ile	Ser	Leu	Ser	Glu	Ala	Met	Ile	Glu	Leu	Gly	Ile	Ala	Ile
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Asp	Gly	Gly	Lys	Asp	Ser	Leu	Ser	Met	Ala	Ala	His	Ala	Glu	Ser	Glu
785					790					795					800
Val	Val	Lys	Ala	Pro	Gly	Asn	Leu	Val	Ile	Ser	Val	Tyr	Val	Thr	Cys
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Pro	Asp	Ile	Thr	Lys	Thr	Val	Thr	Pro	Asp	Leu	Lys	Leu	Lys	Asp	Asp
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Gly	Ile	Leu	Leu	His	Ile	Asp	Leu	Ser	Lys	Gly	Lys	Arg	Arg	Leu	Gly
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Gly	Ser	Ala	Leu	Ala	Gln	Ala	Phe	Asp	Gln	Val	Gly	Asn	Glu	Cys	Pro
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Asp Leu Asp Asp Val Pro Tyr Leu Lys Lys Val Phe Glu Gly Val Gln  
 865 870 875 880

Asp Leu Leu Ser Asp Glu Leu Ile Ser Ala Gly His Asp Ile Ser Asp  
 885 890 895

Gly Gly Leu Leu Val Cys Ala Leu Glu Met Ala Phe Ala Gly Asn Cys  
 900 905 910

Gly Leu Ser Leu Asp Phe Ala Ser Gln Gly Asn Ser Leu Phe Gln Thr  
 915 920 925

Leu Tyr Ala Glu Glu Leu Gly Leu Val Leu Glu Val Ser Lys Lys Asn  
 930 935 940

Leu Ala Leu Val Val Asn Lys Leu Ser Asn Val Gly Val Ser Ala Glu  
 945 950 955 960

Ile Ile Gly Gln Val Thr Ala Asn Pro Ser Ile Glu Val Lys Val Asp  
 965 970 975

Gly Glu Thr Tyr Leu Thr Glu Lys Thr Ser Ile Leu Arg Asp Met Trp  
 980 985 990

Glu Glu Thr Ser Phe Gln Leu Glu Lys Phe Gln Arg Leu Ala Ser Cys  
 995 1000 1005

Val Asp Met Glu Lys Glu Gly Leu Lys His Arg Tyr Glu Pro Ser  
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Trp Glu Leu Pro Phe Thr Pro Ser Phe Thr Asp Glu Lys Leu Tyr  
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Val Cys Asn Tyr Lys Thr  
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<210> SEQ ID NO 3  
 <211> LENGTH: 6450  
 <212> TYPE: DNA  
 <213> ORGANISM: Glycine max  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
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<400> SEQUENCE: 3

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ttggctcaaa tttatcaacc agttcaagaa gatcgtgaga ttttcatata tctatthtat 180

ttcaatattt aaattgaaac tttcagttga tttttttttt gtcattcatt ttgtaatcaa 240

taaaattcct tgaatttggt gagattgatt tctcttataa tatgatgaca ttatatttaa 300

tttttcttaa ttacaggttt ttcaataaca aaattggatt gttccctaaa aaattgaatt 360

gaaaaaaaa tgttgtcaca tagtaacttt ttttttgaaa atgtcgtata gtaacttgca 420

ctttacaat caagacata aattaattht agcataagtt tggctatgca tttttaaaaa 480

atagatcaac gtctaagca aaagccactc ccgcaactca caagtttctg aatccttttg 540

gaatttaagt tgaaaatgag agaatcaacc gataagaatt ttttatatat atttcaatta 600

agatgtgaag attattattg aagtagacac atgataagat agaaaatata cttataaaaag 660

aaaaaaata atatgcgat gaattatctc actcaagtaa aaatctaaac ttattatata 720

agaatgaatt ttatatttta tgtagctata gaagataatt tatcttgaga tatttttaatt 780

cattaattat taatttaacg atttcaactt tttataaacc acaggcaatt tgatagagac 840

gttaaaactt taaaagaaa atccaaattg tacttacggt tcccacaggc ccaattctac 900

ctagagttha ttgaagacc aattctattht tgttttcctc ccataaaatc aaatacacct 960

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atcatattct ttgtcaaatt ctctcttatt aaacaaaatt ttaataataa tttgggaata	1200
aataataata taatttttaa cacaaagacta attttatgat cttatattaa tacaagttaa	1260
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ttcatttgta tcgtgtcccg ttt atg caa gca agt gca gct gct gag ctt ttg	2513
Met Gln Ala Ser Ala Ala Ala Glu Leu Leu	
1 5 10	
aag gaa gct caa gtg aaa atc tcc ggt cag atc gtg gaa ata cag act	2561
Lys Glu Ala Gln Val Lys Ile Ser Gly Gln Ile Val Glu Ile Gln Thr	
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gag cag tgt tat aat gtt ggc ctt agt tca caa ctt tct ggt gga aaa	2609
Glu Gln Cys Tyr Asn Val Gly Leu Ser Ser Gln Leu Ser Gly Gly Lys	
30 35 40	
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Phe Ser Val Leu Arg Trp Leu Leu Gln Glu Thr Phe Glu Pro Glu Asn	
45 50 55	
ctg gga act gag agc ttt ctt gag aag aag aag aaa gag ggt ctg agt	2705
Leu Gly Thr Glu Ser Phe Leu Glu Lys Lys Lys Lys Glu Gly Leu Ser	
60 65 70	
cca gtt att gtt gaa gtt ggc ccc agg ctg tca ttt acc acg gca tgg	2753
Pro Val Ile Val Glu Val Gly Pro Arg Leu Ser Phe Thr Thr Ala Trp	
75 80 85 90	
tct acc aat gct gtt gca att tgc caa gcc tgt ggt ttg aca gaa gtg	2801
Ser Thr Asn Ala Val Ala Ile Cys Gln Ala Cys Gly Leu Thr Glu Val	
95 100 105	

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Leu Gln Asp Tyr Gln Ile Asn Asp Phe Thr Ser Met Val His Asp Arg	
125 130 135	
atg act gaa tgt gtt tat gtt cag aag cta aca tcc ttc gag act agt	2945
Met Thr Glu Cys Val Tyr Val Gln Lys Leu Thr Ser Phe Glu Thr Ser	
140 145 150	
gtt gtt cca gag gag att cgt tat ata cct gtc atg gag aag ggg cga	2993
Val Val Pro Glu Glu Ile Arg Tyr Ile Pro Val Met Glu Lys Gly Arg	
155 160 165 170	
aag gca tta gaa gag att aat ctg gag atg ggt ttt gcc ttt gat gac	3041
Lys Ala Leu Glu Ile Asn Leu Glu Met Gly Phe Ala Phe Asp Asp	
175 180 185	
cag gat ttg gaa tac tac acc aaa ctc ttc agg gaa gac att aag cgt	3089
Gln Asp Leu Glu Tyr Tyr Thr Lys Leu Phe Arg Glu Asp Ile Lys Arg	
190 195 200	
aac cca aca aat gtg gaa ttg ttt gat att gcg cag tcc aac agt gag	3137
Asn Pro Thr Asn Val Glu Leu Phe Asp Ile Ala Gln Ser Asn Ser Glu	
205 210 215	
cac agc aga cac tgg ttt ttt act gga aat att ttc att gat gga cag	3185
His Ser Arg His Trp Phe Phe Thr Gly Asn Ile Phe Ile Asp Gly Gln	
220 225 230	
cct gtg aat aga act ctc atg cag att gtg aaa agt act ctg cag gca	3233
Pro Val Asn Arg Thr Leu Met Gln Ile Val Lys Ser Thr Leu Gln Ala	
235 240 245 250	
aac cca aat aac tca gtt att ggc ttc aag gat aac tcg agt gca atg	3281
Asn Pro Asn Asn Ser Val Ile Gly Phe Lys Asp Asn Ser Ser Ala Met	
255 260 265	
cag ggg ttt tcc agt gaa gca gct ccg acc agt tca acc tgg ttc aac	3329
Gln Gly Phe Ser Ser Glu Ala Ala Pro Thr Ser Ser Thr Trp Phe Asn	
270 275 280	
ttg tcc att aga agt tgc agt cat gag tta gat atc ttg ttt aca gcc	3377
Leu Ser Ile Arg Ser Cys Ser His Glu Leu Asp Ile Leu Phe Thr Ala	
285 290 295	
gaa aca cat aat ttt cca tgt gca gtg gca cct tat cct ggt gca gag	3425
Glu Thr His Asn Phe Pro Cys Ala Val Ala Pro Tyr Pro Gly Ala Glu	
300 305 310	
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Thr Gly Ala Gly Gly Arg Ile Arg Asp Thr His Ala Thr Gly Arg Gly	
315 320 325 330	
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Ser Phe Val Gln Ala Ala Thr Ala Gly Tyr Cys Val Gly Asn Leu Asn	
335 340 345	
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Thr Pro Gly Phe Tyr Ala Pro Trp Glu Asp Ser Ser Phe Thr Tyr Pro	
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365 370 375	
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Ala Ser Asp Tyr Gly Asn Lys Phe Gly Glu Pro Leu Ile Gln Gly Phe	
380 385 390	
tgt aga act ttt gga atg aga ctt ccc agt ggg gag agg cga gaa tgg	3713
Cys Arg Thr Phe Gly Met Arg Leu Pro Ser Gly Glu Arg Arg Glu Trp	
395 400 405 410	
ttg aag cct atc atg ttc agc gca ggc att gga cag att gac cac ctt	3761
Leu Lys Pro Ile Met Phe Ser Ala Gly Ile Gly Gln Ile Asp His Leu	
415 420 425	

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atg gtc agt ggg cag aat gat gca gag ctt gat ttc aat gct gtg caa Met Val Ser Gly Gln Asn Asp Ala Glu Leu Asp Phe Asn Ala Val Gln 460 465 470	3905
cgt ggg gat gct gag atg gct caa aaa cta tat cgt ctt gtg cgt gct Arg Gly Asp Ala Glu Met Ala Gln Lys Leu Tyr Arg Leu Val Arg Ala 475 480 485 490	3953
tgt att gag atg ggg gat aaa aac cca att atc agc att cat gat cag Cys Ile Glu Met Gly Asp Lys Asn Pro Ile Ile Ser Ile His Asp Gln 495 500 505	4001
gga gct ggt ggg aat tgc aat gtt gta aag gaa att ata tat cca aag Gly Ala Gly Gly Asn Cys Asn Val Val Lys Glu Ile Ile Tyr Pro Lys 510 515 520	4049
ggt gct gag ata gat gtt cga gca att gtg gtt ggc gat cat aca atg Gly Ala Glu Ile Asp Val Arg Ala Ile Val Val Gly Asp His Thr Met 525 530 535	4097
tct gtt cta gaa att tgg ggt gca gag tat cag gag cag gat gca atc Ser Val Leu Glu Ile Trp Gly Ala Glu Tyr Gln Glu Gln Asp Ala Ile 540 545 550	4145
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gag aaa gtt tca atg gct gtt att gga act atc agt ggt gat gga cgt Glu Lys Val Ser Met Ala Val Ile Gly Thr Ile Ser Gly Asp Gly Arg 575 580 585	4241
gtt gtt tta gtt gac agt gta gca gtc cag aag tct att tca aat gga Val Val Leu Val Asp Ser Val Ala Val Gln Lys Ser Ile Ser Asn Gly 590 595 600	4289
ctc act tca cct ccc cct gcc gtg gat ctt gaa ttg gag aaa gtc ctt Leu Thr Ser Pro Pro Pro Ala Val Asp Leu Glu Leu Glu Lys Val Leu 605 610 615	4337
ggt gac atg cct aag aaa act ttt aaa ttt aat cgg gtt gtt tat gag Gly Asp Met Pro Lys Lys Thr Phe Lys Phe Asn Arg Val Val Tyr Glu 620 625 630	4385
agg gag cca ctt gat att gcc cct ggg att gaa gtg ata gat tcc cta Arg Glu Pro Leu Asp Ile Ala Pro Gly Ile Glu Val Ile Asp Ser Leu 635 640 645 650	4433
aag agg gta ttg agt tta ccg tct gtt tgt tca aag cgc ttc tta aca Lys Arg Val Leu Ser Leu Pro Ser Val Cys Ser Lys Arg Phe Leu Thr 655 660 665	4481
aca aaa gtt gat agg tgt gtt act ggt cta gtg gca caa caa caa act Thr Lys Val Asp Arg Cys Val Thr Gly Leu Val Ala Gln Gln Thr 670 675 680	4529
gtt ggc cct ttg cag att ccc att gct gat gtt gct gtt aca gct caa Val Gly Pro Leu Gln Ile Pro Ile Ala Asp Val Ala Val Thr Ala Gln 685 690 695	4577
act ttt gtt gat gtg act gga ggt gct tgt gcc att ggt gag caa ccc Thr Phe Val Asp Val Thr Gly Gly Ala Cys Ala Ile Gly Glu Gln Pro 700 705 710	4625
atc aaa ggc ctg tta gac ccc aaa gca atg gct cgg ttg gct gtt gga Ile Lys Gly Leu Leu Asp Pro Lys Ala Met Ala Arg Leu Ala Val Gly 715 720 725 730	4673
gaa gca cta aca aat ctt gta tgg gca aag gtc act tcc ctt tct gat Glu Ala Leu Thr Asn Leu Val Trp Ala Lys Val Thr Ser Leu Ser Asp 735 740 745 750	4721

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735					740					745					
gtc aag gct agt ggt aac tgg atg tat gct gcc aag ctt gat ggg gaa	Val Lys Ala Ser Gly Asn Trp Met Tyr Ala Ala Lys Leu Asp Gly Glu	750	755	760	4769										
gga gct gac atg tat gat gca gct ata tct cta tct gaa gca atg att	Gly Ala Asp Met Tyr Asp Ala Ala Ile Ser Leu Ser Glu Ala Met Ile	765	770	775	4817										
gaa ctt ggc att gct att gat gga ggg aaa gac agc ctt tct atg gca	Glu Leu Gly Ile Ala Ile Asp Gly Gly Lys Asp Ser Leu Ser Met Ala	780	785	790	4865										
gcc cac gct gaa agt gaa gtt gtc aag gca cca ggr aat ctt gtc atc	Ala His Ala Glu Ser Glu Val Val Lys Ala Pro Xaa Asn Leu Val Ile	795	800	805	4913										
agt gtk tat gtt act tgt cct gat ata aca aaa aca gtg act cca gat	Ser Xaa Tyr Val Thr Cys Pro Asp Ile Thr Lys Thr Val Thr Pro Asp	815	820	825	4961										
tta aaa ctc aag gat gat ggt att ttg ctt cat att gat ttg tca aaa	Leu Lys Leu Lys Asp Asp Gly Ile Leu Leu His Ile Asp Leu Ser Lys	830	835	840	5009										
ggt aag agg cgg tta ggt gga tct gct ctt gcc cag gcg ttt gac caa	Gly Lys Arg Arg Leu Gly Gly Ser Ala Leu Ala Gln Ala Phe Asp Gln	845	850	855	5057										
ggt gga gat gag tgt cct gat cct gat gat gtt cct tac ctt aaa aag	Val Gly Asp Glu Cys Pro Asp Pro Asp Asp Val Pro Tyr Leu Lys Lys	860	865	870	5105										
gcc ttt gaa ggt gtt caa gac ctt ctt tct gat gaa ttg ata tct gct	Ala Phe Glu Gly Val Gln Asp Leu Leu Ser Asp Glu Leu Ile Ser Ala	875	880	885	5153										
ggt cat gac atc agt gat ggt ggg ctg cta gtt tgt gcc tta gag atg	Gly His Asp Ile Ser Asp Gly Gly Leu Leu Val Cys Ala Leu Glu Met	895	900	905	5201										
gca ttt gct ggt aac tgt ggt ctt agt ttg gac ttg gcg tcg caa ggt	Ala Phe Ala Gly Asn Cys Gly Leu Ser Leu Asp Leu Ala Ser Gln Gly	910	915	920	5249										
acc agc ctt ttc caa aca ctc tat gct gaa gag ctt ggg tta gtt ctt	Thr Ser Leu Phe Gln Thr Leu Tyr Ala Glu Glu Leu Gly Leu Val Leu	925	930	935	5297										
gag gta aac aag aaa aat ctg gct ttg gta atg gat aaa ttg agt aat	Glu Val Asn Lys Lys Asn Leu Ala Leu Val Met Asp Lys Leu Ser Asn	940	945	950	5345										
gtg gga gtt tca gct gaa atc att ggt caa gta aca gcc aat cca tca	Val Gly Val Ser Ala Glu Ile Ile Gly Gln Val Thr Ala Asn Pro Ser	955	960	965	5393										
ata gaa gtt aag gtt gat ggg gag act tat tta act gaa aaa act agt	Ile Glu Val Lys Val Asp Gly Glu Thr Tyr Leu Thr Glu Lys Thr Ser	975	980	985	5441										
atc ctt agg gac ttg tgg gaa gag acc agt ttt cag ctg gaa aag ttc	Ile Leu Arg Asp Leu Trp Glu Glu Thr Ser Phe Gln Leu Glu Lys Phe	990	995	1000	5489										
caa aga ttg gca tcc tgt gtg gat atg gag aaa gaa gga ctt aaa	Gln Arg Leu Ala Ser Cys Val Asp Met Glu Lys Glu Gly Leu Lys	1005	1010	1015	5534										
cat cga tat gag ccc tca tgg gaa ctg cct ttt act ccc acc ttc	His Arg Tyr Glu Pro Ser Trp Glu Leu Pro Phe Thr Pro Thr Phe	1020	1025	1030	5579										
act gat gga aag ctt ctg tct gca act ata aaa cct aaa gtg gct	Thr Asp Gly Lys Leu Leu Ser Ala Thr Ile Lys Pro Lys Val Ala	1035	1040	1045	5624										
gtg att aga gaa gaa ggc agt aat gga gac aga gaa atg gct gca					5669										

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Val Ile Arg	Glu Glu Gly Ser	Asn	Gly Asp Arg	Glu Met	Ala Ala	
1050		1055		1060		
gca ttt tat	gct gct ggt ttt	gaa	cca tgg gat	att act	atg tca	5714
Ala Phe Tyr	Ala Ala Gly Phe	Glu	Pro Trp Asp	Ile Thr	Met Ser	
1065		1070		1075		
gac ctt ctt	aat gga aag atc	tct	ttg caa gac	ttc cgc	gga att	5759
Asp Leu Leu	Asn Gly Lys Ile	Ser	Leu Gln Asp	Phe Arg	Gly Ile	
1080		1085		1090		
gtg ttt gtt	ggg gga ttt agc	tat	gct gat gtg	ctt gat	tct gca	5804
Val Phe Val	Gly Gly Phe Ser	Tyr	Ala Asp Val	Leu Asp	Ser Ala	
1095		1100		1105		
aaa ggt tgg	tct gct agc ata	aga	ttc aat gag	tcc gtt	tta caa	5849
Lys Gly Trp	Ser Ala Ser Ile	Arg	Phe Asn Glu	Ser Val	Leu Gln	
1110		1115		1120		
caa ttt cag	gag ttt tac aag	cgt	cca gac act	ttc agt	ctc ggt	5894
Gln Phe Gln	Glu Phe Tyr Lys	Arg	Pro Asp Thr	Phe Ser	Leu Gly	
1125		1130		1135		
gta tgc aat	gga tgt cag cta	atg	gct ttg ttg	gga tgg	gta ccg	5939
Val Cys Asn	Gly Cys Gln Leu	Met	Ala Leu Leu	Gly Trp	Val Pro	
1140		1145		1150		
ggt cca caa	ggt ggg ggt gtg	cat	ggt gct ggt	ggc gac	cta tca	5984
Gly Pro Gln	Val Gly Gly Val	His	Gly Ala Gly	Gly Asp	Leu Ser	
1155		1160		1165		
caa ccg agg	ttc att cat aat	gag	tca ggg cgg	ttt gag	tgc cgc	6029
Gln Pro Arg	Phe Ile His Asn	Glu	Ser Gly Arg	Phe Glu	Cys Arg	
1170		1175		1180		
ttt aca agt	gtg acc ata aag	gac	tca ccg gct	ata atg	ttc aaa	6074
Phe Thr Ser	Val Thr Ile Lys	Asp	Ser Pro Ala	Ile Met	Phe Lys	
1185		1190		1195		
gac atg gca	ggg agc aca ttg	ggt	ata tgg gct	gct cat	ggt gag	6119
Asp Met Ala	Gly Ser Thr Leu	Gly	Ile Trp Ala	Ala His	Gly Glu	
1200		1205		1210		
gga aga gct	tat ttc cca gat	gaa	ggc gtg ttg	gac cgt	ata gtt	6164
Gly Arg Ala	Tyr Phe Pro Asp	Glu	Gly Val Leu	Asp Arg	Ile Val	
1215		1220		1225		
cat tct gag	ttg gct cct ata	aga	tac tgt gat	gat gct	ggg aat	6209
His Ser Glu	Leu Ala Pro Ile	Arg	Tyr Cys Asp	Asp Ala	Gly Asn	
1230		1235		1240		
cca aca gag	gcc tac cct ttc	aat	gtg aat ggc	tct cct	tta ggg	6254
Pro Thr Glu	Ala Tyr Pro Phe	Asn	Val Asn Gly	Ser Pro	Leu Gly	
1245		1250		1255		
gtg gca gct	att tgt tcc cca	gat	ggg agg cat	ctt gcc	atg atg	6299
Val Ala Ala	Ile Cys Ser Pro	Asp	Gly Arg His	Leu Ala	Met Met	
1260		1265		1270		
cct cat cct	gag cgt tgc ttc	tta	atg tgg cag	ttc cca	tgg tat	6344
Pro His Pro	Glu Arg Cys Phe	Leu	Met Trp Gln	Phe Pro	Trp Tyr	
1275		1280		1285		
cca aag cag	ttg gat gtg gag	aag	aag ggg cct	agt cct	tgg tta	6389
Pro Lys Gln	Trp Asp Val Glu	Lys	Lys Gly Pro	Ser Pro	Trp Leu	
1290		1295		1300		
cgc atg ttc	cag aat gca aga	gag	ttg tgt tcc	tga	aatgatcaaa	6435
Arg Met Phe	Gln Asn Ala Arg	Glu	Trp Cys Ser			
1305		1310				
tgtttttctc	atctt					6450

<210> SEQ ID NO 4  
 <211> LENGTH: 1313  
 <212> TYPE: PRP  
 <213> ORGANISM: Glycine max  
 <220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (806)..(806)
<223> OTHER INFORMATION: The 'Xaa' at location 806 stands for Gly.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (812)..(812)
<223> OTHER INFORMATION: The 'Xaa' at location 812 stands for Val.

<400> SEQUENCE: 4

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

Ile Ser Gly Gln Ile Val Glu Ile Gln Thr Glu Gln Cys Tyr Asn Val
20          25          30

Gly Leu Ser Ser Gln Leu Ser Gly Gly Lys Phe Ser Val Leu Arg Trp
35          40          45

Leu Leu Gln Glu Thr Phe Glu Pro Glu Asn Leu Gly Thr Glu Ser Phe
50          55          60

Leu Glu Lys Lys Lys Lys Glu Gly Leu Ser Pro Val Ile Val Glu Val
65          70          75          80

Gly Pro Arg Leu Ser Phe Thr Thr Ala Trp Ser Thr Asn Ala Val Ala
85          90          95

Ile Cys Gln Ala Cys Gly Leu Thr Glu Val Asn Arg Leu Glu Arg Ser
100         105         110

Arg Arg Tyr Leu Leu Phe Thr Thr Glu Leu Gln Asp Tyr Gln Ile
115         120         125

Asn Asp Phe Thr Ser Met Val His Asp Arg Met Thr Glu Cys Val Tyr
130         135         140

Val Gln Lys Leu Thr Ser Phe Glu Thr Ser Val Val Pro Glu Glu Ile
145         150         155         160

Arg Tyr Ile Pro Val Met Glu Lys Gly Arg Lys Ala Leu Glu Glu Ile
165         170         175

Asn Leu Glu Met Gly Phe Ala Phe Asp Asp Gln Asp Leu Glu Tyr Tyr
180         185         190

Thr Lys Leu Phe Arg Glu Asp Ile Lys Arg Asn Pro Thr Asn Val Glu
195         200         205

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

Phe Thr Gly Asn Ile Phe Ile Asp Gly Gln Pro Val Asn Arg Thr Leu
225         230         235         240

Met Gln Ile Val Lys Ser Thr Leu Gln Ala Asn Pro Asn Asn Ser Val
245         250         255

Ile Gly Phe Lys Asp Asn Ser Ser Ala Met Gln Gly Phe Ser Ser Glu
260         265         270

Ala Ala Pro Thr Ser Ser Thr Trp Phe Asn Leu Ser Ile Arg Ser Cys
275         280         285

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

Cys Ala Val Ala Pro Tyr Pro Gly Ala Glu Thr Gly Ala Gly Gly Arg
305         310         315         320

Ile Arg Asp Thr His Ala Thr Gly Arg Gly Ser Phe Val Gln Ala Ala
325         330         335

Thr Ala Gly Tyr Cys Val Gly Asn Leu Asn Thr Pro Gly Phe Tyr Ala
340         345         350

Pro Trp Glu Asp Ser Ser Phe Thr Tyr Pro Ser Asn Leu Ala Pro Pro
355         360         365

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Leu Gln Ile Leu Ile Asp Ser Ser Asn Gly Ala Ser Asp Tyr Gly Asn  
 370 375 380

Lys Phe Gly Glu Pro Leu Ile Gln Gly Phe Cys Arg Thr Phe Gly Met  
 385 390 395 400

Arg Leu Pro Ser Gly Glu Arg Arg Glu Trp Leu Lys Pro Ile Met Phe  
 405 410 415

Ser Ala Gly Ile Gly Gln Ile Asp His Leu His Ile Ser Lys Gly Glu  
 420 425 430

Pro Asp Ile Gly Met Leu Val Val Lys Ile Gly Gly Pro Ala Tyr Arg  
 435 440 445

Ile Gly Met Gly Gly Gly Ala Ala Ser Ser Met Val Ser Gly Gln Asn  
 450 455 460

Asp Ala Glu Leu Asp Phe Asn Ala Val Gln Arg Gly Asp Ala Glu Met  
 465 470 475 480

Ala Gln Lys Leu Tyr Arg Leu Val Arg Ala Cys Ile Glu Met Gly Asp  
 485 490 495

Lys Asn Pro Ile Ile Ser Ile His Asp Gln Gly Ala Gly Gly Asn Cys  
 500 505 510

Asn Val Val Lys Glu Ile Ile Tyr Pro Lys Gly Ala Glu Ile Asp Val  
 515 520 525

Arg Ala Ile Val Val Gly Asp His Thr Met Ser Val Leu Glu Ile Trp  
 530 535 540

Gly Ala Glu Tyr Gln Glu Gln Asp Ala Ile Leu Val Lys Pro Glu Ser  
 545 550 555 560

Arg Asp Leu Leu Glu Ser Ile Cys Asn Arg Glu Lys Val Ser Met Ala  
 565 570 575

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

Val Ala Val Gln Lys Ser Ile Ser Asn Gly Leu Thr Ser Pro Pro Pro  
 595 600 605

Ala Val Asp Leu Glu Leu Glu Lys Val Leu Gly Asp Met Pro Lys Lys  
 610 615 620

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

Ala Pro Gly Ile Glu Val Ile Asp Ser Leu Lys Arg Val Leu Ser Leu  
 645 650 655

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

Val Thr Gly Leu Val Ala Gln Gln Gln Thr Val Gly Pro Leu Gln Ile  
 675 680 685

Pro Ile Ala Asp Val Ala Val Thr Ala Gln Thr Phe Val Asp Val Thr  
 690 695 700

Gly Gly Ala Cys Ala Ile Gly Glu Gln Pro Ile Lys Gly Leu Leu Asp  
 705 710 715 720

Pro Lys Ala Met Ala Arg Leu Ala Val Gly Glu Ala Leu Thr Asn Leu  
 725 730 735

Val Trp Ala Lys Val Thr Ser Leu Ser Asp Val Lys Ala Ser Gly Asn  
 740 745 750

Trp Met Tyr Ala Ala Lys Leu Asp Gly Glu Gly Ala Asp Met Tyr Asp  
 755 760 765

Ala Ala Ile Ser Leu Ser Glu Ala Met Ile Glu Leu Gly Ile Ala Ile  
 770 775 780

Asp Gly Gly Lys Asp Ser Leu Ser Met Ala Ala His Ala Glu Ser Glu



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785	790	795	800
Val Val Lys Ala Pro Xaa Asn Leu Val Ile Ser Xaa Tyr Val Thr Cys	805	810	815
Pro Asp Ile Thr Lys Thr Val Thr Pro Asp Leu Lys Leu Lys Asp Asp	820	825	830
Gly Ile Leu Leu His Ile Asp Leu Ser Lys Gly Lys Arg Arg Leu Gly	835	840	845
Gly Ser Ala Leu Ala Gln Ala Phe Asp Gln Val Gly Asp Glu Cys Pro	850	855	860
Asp Pro Asp Asp Val Pro Tyr Leu Lys Lys Ala Phe Glu Gly Val Gln	865	870	875
Asp Leu Leu Ser Asp Glu Leu Ile Ser Ala Gly His Asp Ile Ser Asp	885	890	895
Gly Gly Leu Leu Val Cys Ala Leu Glu Met Ala Phe Ala Gly Asn Cys	900	905	910
Gly Leu Ser Leu Asp Leu Ala Ser Gln Gly Thr Ser Leu Phe Gln Thr	915	920	925
Leu Tyr Ala Glu Glu Leu Gly Leu Val Leu Glu Val Asn Lys Lys Asn	930	935	940
Leu Ala Leu Val Met Asp Lys Leu Ser Asn Val Gly Val Ser Ala Glu	945	950	955
Ile Ile Gly Gln Val Thr Ala Asn Pro Ser Ile Glu Val Lys Val Asp	965	970	975
Gly Glu Thr Tyr Leu Thr Glu Lys Thr Ser Ile Leu Arg Asp Leu Trp	980	985	990
Glu Glu Thr Ser Phe Gln Leu Glu Lys Phe Gln Arg Leu Ala Ser Cys	995	1000	1005
Val Asp Met Glu Lys Glu Gly Leu Lys His Arg Tyr Glu Pro Ser	1010	1015	1020
Trp Glu Leu Pro Phe Thr Pro Thr Phe Thr Asp Gly Lys Leu Leu	1025	1030	1035
Ser Ala Thr Ile Lys Pro Lys Val Ala Val Ile Arg Glu Glu Gly	1040	1045	1050
Ser Asn Gly Asp Arg Glu Met Ala Ala Ala Phe Tyr Ala Ala Gly	1055	1060	1065
Phe Glu Pro Trp Asp Ile Thr Met Ser Asp Leu Leu Asn Gly Lys	1070	1075	1080
Ile Ser Leu Gln Asp Phe Arg Gly Ile Val Phe Val Gly Gly Phe	1085	1090	1095
Ser Tyr Ala Asp Val Leu Asp Ser Ala Lys Gly Trp Ser Ala Ser	1100	1105	1110
Ile Arg Phe Asn Glu Ser Val Leu Gln Gln Phe Gln Glu Phe Tyr	1115	1120	1125
Lys Arg Pro Asp Thr Phe Ser Leu Gly Val Cys Asn Gly Cys Gln	1130	1135	1140
Leu Met Ala Leu Leu Gly Trp Val Pro Gly Pro Gln Val Gly Gly	1145	1150	1155
Val His Gly Ala Gly Gly Asp Leu Ser Gln Pro Arg Phe Ile His	1160	1165	1170
Asn Glu Ser Gly Arg Phe Glu Cys Arg Phe Thr Ser Val Thr Ile	1175	1180	1185
Lys Asp Ser Pro Ala Ile Met Phe Lys Asp Met Ala Gly Ser Thr	1190	1195	1200

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Leu Gly Ile Trp Ala Ala His Gly Glu Gly Arg Ala Tyr Phe Pro  
 1205 1210 1215

Asp Glu Gly Val Leu Asp Arg Ile Val His Ser Glu Leu Ala Pro  
 1220 1225 1230

Ile Arg Tyr Cys Asp Asp Ala Gly Asn Pro Thr Glu Ala Tyr Pro  
 1235 1240 1245

Phe Asn Val Asn Gly Ser Pro Leu Gly Val Ala Ala Ile Cys Ser  
 1250 1255 1260

Pro Asp Gly Arg His Leu Ala Met Met Pro His Pro Glu Arg Cys  
 1265 1270 1275

Phe Leu Met Trp Gln Phe Pro Trp Tyr Pro Lys Gln Trp Asp Val  
 1280 1285 1290

Glu Lys Lys Gly Pro Ser Pro Trp Leu Arg Met Phe Gln Asn Ala  
 1295 1300 1305

Arg Glu Trp Cys Ser  
 1310

<210> SEQ ID NO 5  
 <211> LENGTH: 60  
 <212> TYPE: PRT  
 <213> ORGANISM: Drosophila melanogaster

<400> SEQUENCE: 5

Pro Phe Ser Gly Ala Thr Thr Gly Thr Gly Gly Arg Leu Arg Asp Val  
 1 5 10 15

Gln Gly Val Gly Arg Gly Gly Val Pro Ile Ala Gly Thr Ala Gly Tyr  
 20 25 30

Cys Val Gly Ala Leu His Ile Pro Gly Tyr Lys Gln Pro Tyr Glu Pro  
 35 40 45

Leu Asp Phe Lys Tyr Pro Ala Thr Phe Ala Pro Pro  
 50 55 60

<210> SEQ ID NO 6  
 <211> LENGTH: 60  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 6

Pro Phe Ser Gly Ala Thr Thr Gly Thr Gly Gly Arg Ile Arg Asp Val  
 1 5 10 15

Gln Cys Thr Gly Arg Gly Ala His Val Val Ala Gly Thr Ala Gly Tyr  
 20 25 30

Cys Phe Gly Asn Leu His Ile Pro Gly Tyr Asn Leu Pro Trp Glu Asp  
 35 40 45

Leu Ser Phe Gln Tyr Pro Gly Asn Phe Ala Arg Pro  
 50 55 60

<210> SEQ ID NO 7  
 <211> LENGTH: 59  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 7

Pro Trp Pro Gly Ala Ala Thr Gly Ser Gly Gly Glu Ile Arg Asp Glu  
 1 5 10 15

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

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Ser Val Ser Asn Leu Arg Ile Pro Gly Phe Glu Gln Pro Trp Glu Glu  
 35 40 45

Asp Phe Gly Lys Pro Glu Arg Ile Val Thr Ala  
 50 55

<210> SEQ ID NO 8  
 <211> LENGTH: 60  
 <212> TYPE: PRT  
 <213> ORGANISM: *Drosophila melanogaster*

<400> SEQUENCE: 8

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

Ala Asn Phe Glu Val His Asp Val Thr Met Ser Asp Leu Leu Gln Gly  
 20 25 30

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

Ser Tyr Ala Asp Thr Leu Gly Ser Ala Lys Gly Trp  
 50 55 60

<210> SEQ ID NO 9  
 <211> LENGTH: 60  
 <212> TYPE: PRT  
 <213> ORGANISM: *Homo sapiens*

<400> SEQUENCE: 9

Glu Glu Gly Ser Asn Gly Asp Arg Glu Met Ala Asp Ala Phe His Leu  
 1 5 10 15

Ala Gly Phe Glu Val Trp Asp Val Thr Met Gln Asp Leu Cys Ser Gly  
 20 25 30

Ala Ile Gly Leu Asp Thr Phe Arg Gly Val Ala Phe Val Gly Gly Phe  
 35 40 45

Ser Tyr Ala Asp Val Leu Gly Ser Ala Lys Gly Trp  
 50 55 60

<210> SEQ ID NO 10  
 <211> LENGTH: 60  
 <212> TYPE: PRT  
 <213> ORGANISM: *Escherichia coli*

<400> SEQUENCE: 10

Glu Gln Gly Val Asn Ser His Val Glu Met Ala Ala Ala Phe His Arg  
 1 5 10 15

Ala Gly Phe Asp Ala Ile Asp Val His Met Ser Asp Leu Leu Thr Gly  
 20 25 30

Arg Thr Gly Leu Glu Asp Phe His Ala Leu Val Ala Cys Gly Gly Phe  
 35 40 45

Ser Tyr Gly Asp Val Leu Gly Ala Gly Glu Gly Trp  
 50 55 60

<210> SEQ ID NO 11  
 <211> LENGTH: 52  
 <212> TYPE: PRT  
 <213> ORGANISM: *Drosophila melanogaster*

<400> SEQUENCE: 11

Ala Ala Asn Ile Leu His Asn Pro Arg Leu Leu Pro Gln Phe Glu Ala  
 1 5 10 15

Phe Lys Arg Arg Gln Asp Val Phe Ser Leu Gly Ile Cys Asn Gly Cys  
 20 25 30

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Gln Leu Met Thr Leu Ile Gly Phe Val Gly Ser Ala Lys Ser Glu Val  
 35 40 45

Gly Ala Asp Pro  
 50

<210> SEQ ID NO 12  
 <211> LENGTH: 60  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 12

Ala Ala Ala Val Thr Phe His Pro Arg Ala Gly Ala Glu Leu Arg Arg  
 1 5 10 15

Phe Arg Lys Arg Pro Asp Thr Phe Ser Leu Gly Val Cys Asn Gly Cys  
 20 25 30

Gln Leu Leu Ala Leu Leu Gly Trp Val Gly Gly Asp Pro Asn Glu Asp  
 35 40 45

Ala Ala Glu Met Gly Pro Asp Ser Gln Pro Ala Arg  
 50 55 60

<210> SEQ ID NO 13  
 <211> LENGTH: 48  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 13

Ala Lys Ser Ile Leu Phe Asn Asp Arg Val Arg Asp Glu Phe Ala Thr  
 1 5 10 15

Phe Phe His Arg Pro Gln Thr Leu Ala Leu Gly Val Cys Asn Gly Cys  
 20 25 30

Gln Met Met Ser Asn Leu Arg Glu Leu Ile Pro Gly Ser Glu Leu Trp  
 35 40 45

<210> SEQ ID NO 14  
 <211> LENGTH: 60  
 <212> TYPE: PRT  
 <213> ORGANISM: Drosophila melanogaster

<400> SEQUENCE: 14

Gln Ser Glu Gln Leu Val Thr Leu Gln Tyr Val Asp Asp Val Gly Lys  
 1 5 10 15

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

Ala Gly Leu Cys Ser Ser Asp Gly Arg His Leu Ala Leu Met Pro His  
 35 40 45

Pro Glu Arg Cys Ser Ser Met Tyr Gln Trp Pro Tyr  
 50 55 60

<210> SEQ ID NO 15  
 <211> LENGTH: 60  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 15

Glu Ala Arg Gly Leu Ala Pro Leu His Trp Ala Asp Asp Asp Gly Asn  
 1 5 10 15

Pro Thr Glu Gln Tyr Pro Leu Asn Pro Asn Gly Ser Pro Gly Gly Val  
 20 25 30

Ala Gly Ile Cys Ser Cys Asp Gly Arg His Leu Ala Val Met Pro His

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35	40	45	
Pro Glu Arg Ala Val Arg Pro Trp Gln Trp Ala Trp			
50	55	60	
<p>&lt;210&gt; SEQ ID NO 16                  &lt;211&gt; LENGTH: 60                  &lt;212&gt; TYPE: PRT                  &lt;213&gt; ORGANISM: Escherichia coli</p>			
<p>&lt;400&gt; SEQUENCE: 16</p>			
Glu Ser Lys Gly Leu Val Ala Leu Arg Tyr Val Asp Asn Phe Gly Lys			
1	5	10	15
Val Thr Glu Thr Tyr Pro Ala Asn Pro Asn Gly Ser Pro Asn Gly Ile			
20	25	30	
Thr Ala Val Thr Thr Glu Ser Gly Arg Val Thr Ile Met Met Pro His			
35	40	45	
Pro Glu Arg Val Phe Arg Thr Val Ser Asn Ser Trp			
50	55	60	
<p>&lt;210&gt; SEQ ID NO 17                  &lt;211&gt; LENGTH: 37                  &lt;212&gt; TYPE: DNA                  &lt;213&gt; ORGANISM: Solanum tuberosum</p>			
<p>&lt;400&gt; SEQUENCE: 17</p>			
aaccgatata tatatatata tatatatata tatatat			37
<p>&lt;210&gt; SEQ ID NO 18                  &lt;211&gt; LENGTH: 83                  &lt;212&gt; TYPE: DNA                  &lt;213&gt; ORGANISM: Solanum tuberosum</p>			
<p>&lt;400&gt; SEQUENCE: 18</p>			
atatcgtaa aatatttttaa tatcttggtg aaatataatt tttatttag taaaataata			60
tgagaattaa tttttttat taa			83

The invention claimed is:

1. An isolated nucleic acid molecule comprising a soybean promoter sequence that comprises a nematode responsive domain, wherein the promoter sequence comprises a sequence selected from the group consisting of: Pr1-1.0 (the sequence from nucleotides 1790 to 2483 of SEQ ID NO: 2), Pr2-1.0 (the sequence from nucleotides 1551 to 2547 of SEQ ID NO: 1), Pr1-1.5 (the sequence from nucleotides 1271 to 2483 of SEQ ID NO: 2), Pr2-1.5 (the sequence from nucleotides 991 to 2547 of SEQ ID NO: 1), Pr1-2.5 (the sequence from nucleotides 124 to 2483 of SEQ ID NO: 2) and Pr2-2.5 (the sequence from nucleotides 19 to 2547 of SEQ ID NO: 1).
2. The nucleic acid molecule of claim 1, further comprising a heterologous DNA operatively linked to the promoter.
3. The nucleic acid molecule of claim 2, wherein the heterologous DNA encodes a product that is disruptive of nematode attack.
4. The nucleic acid molecule of claim 3, wherein the heterologous DNA encodes a product that is toxic to a plant cell.
5. The nucleic acid molecule of claim 4, wherein the heterologous DNA comprises a gene selected from the group consisting of anti-apoptosis genes, genes involved in the hypersensitive response, genes involved in MAPK signal transduction, and genes for RNA interference that down-regulate a gene needed for nematode feeding site establishment.
6. The nucleic acid molecule of claim 3, wherein the heterologous DNA encodes a product possessing anti-helminthic properties.
7. The nucleic acid molecule of claim 6, wherein the heterologous DNA encodes a *Bacillus thuringiensis* crystal protein toxic to nematodes.
8. A transfected soybean cell comprising the nucleic acid molecule of claim 1.
9. A transgenic soybean plant comprising the plant cell of claim 8.
10. A method of reducing nematode infection of a soybean plant comprising transfecting cells of the soybean plant with the nucleic acid molecule of claim 3.

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