


Novel chimeric plant promoter sequences are provided, together with plant gene expression cassettes comprising such sequences. In certain preferred embodiments, the chimeric plant promoters comprise the BoxII cis element and/or derivatives thereof. In addition, novel transcription factors are provided, together with nucleic acid sequences encoding such transcription factors and plant gene expression cassettes comprising such nucleic acid sequences. In certain preferred embodiments, the novel transcription factors comprise the acidic domain, or fragments thereof, of the RF2a transcription factor. Methods for using the chimeric plant promoter sequences and novel transcription factors in regulating the expression of at least one gene of interest are provided, together with transgenic plants comprising such chimeric plant promoter sequences and novel transcription factors.

14 Claims, 29 Drawing Sheets
Figure 1
Figure 2
Figure 4
Figure 5
Box II  5' CCAGTGTGCCCCCTGG 3'
Box IIIm1  5' CCAGTGTGCGGCTGG 3'
Box IIIm2  5' GGAGTGTGCCCCTTC 3'

Figure 6
Figure 7
<table>
<thead>
<tr>
<th></th>
<th>RF2a</th>
<th></th>
<th>RF2b</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Ka (1/M)</td>
<td>Kd(M)</td>
<td>Ka (1/M)</td>
<td>Kd(M)</td>
</tr>
<tr>
<td>Box II</td>
<td>8.67 x 10^6</td>
<td>1.15 x 10^-7</td>
<td>2.19 x 10^6</td>
<td>4.57 x 10^-7</td>
</tr>
<tr>
<td>Box II m1</td>
<td>1.08 x 10^-7</td>
<td>9.26 x 10^-8</td>
<td>4.17 x 10^6</td>
<td>2.40 x 10^-7</td>
</tr>
<tr>
<td>Box II m2</td>
<td>8.13 x 10^-6</td>
<td>1.23 x 10^-7</td>
<td>1.85 x 10^6</td>
<td>5.40 x 10^-7</td>
</tr>
</tbody>
</table>

Figure 8
Figure 9
Figure 10
Figure 11
-1.0hBoxII-48CaMV:
tgatcaaaagt CCAGTGTGCCCCTGGtcgcaagaccttcctc

-1.5hBoxII-53CaMV:
tgatcaaaagt CCAGTGTGCCCCTGGatccttcgcaagacct

-1.5hBoxII-53CaMV-c:
tgatcaaaagt tatccttcgcaagacct

-3.0hBoxII-69CaMV:
tgatcaaaagt CCAGTGTGCCCCTGGgaacgcacaatccacta

-3.5hBoxII-74CaMV:
tgatcaaaagt CCAGTGTGCCCCTGGggatgacgcacaatcc

-3.5hBoxII-74CaMV-c:
tgatcaaaagt tgggatgacgcacaatcc

-5.0hBoxII-90CaMV:
tgatcaaaagt CCAGTGTGCCCCTGGatctcactgacgtaag

-5.5hBoxII-95CaMV:
tgatcaaaagt CCAGTGTGCCCCTGGgtgatctcactgac

-5.5hBoxII-95CaMV-c:
tgatcaaaagt gtgatctcactgac

Figure 12
Figure 13

Relative GUS activity

- p1nbox1-8CaMV
- p4CaMV
- p5CaMV
- p5box1-74CaMV
- p7CaMV
- p8CaMV
- p9CaMV
- p10CaMV
- p11CaMV
- p12CaMV

Values: 6.9, 1, 1.6, 9, 11.8, 13.6, 9.6, 123.8, 182.5
Figure 14
A

-32::GUS

-68::GUS

-100::GUS

E(IIm1)::GUS

E(IIm2)::GUS

E::GUS

B

Figure 15
Figure 16
Figure 17

A

<table>
<thead>
<tr>
<th>Reporter</th>
<th>35S-P</th>
<th>GUS</th>
<th>Nos</th>
</tr>
</thead>
<tbody>
<tr>
<td>pBH-48Ca:GUS</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Effector</th>
<th>35S-P</th>
<th>b-Zip</th>
<th>Q</th>
<th>Nos</th>
</tr>
</thead>
<tbody>
<tr>
<td>pMON999</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>p35S:RF2a</td>
<td>35S-P</td>
<td>b-Zip</td>
<td>Q</td>
<td>Nos</td>
</tr>
<tr>
<td>p35S:RF2a-ΔP</td>
<td>35S-P</td>
<td>b-Zip</td>
<td>Q</td>
<td>Nos</td>
</tr>
<tr>
<td>p35S:RF2a-ΔQ</td>
<td>35S-P</td>
<td>b-Zip</td>
<td>Q</td>
<td>Nos</td>
</tr>
<tr>
<td>p35S:RF2a-ΔPΔA</td>
<td>35S-P</td>
<td>b-Zip</td>
<td>Q</td>
<td>Nos</td>
</tr>
<tr>
<td>p35S:RF2a-3Δ</td>
<td>35S-P</td>
<td>b-Zip</td>
<td>Q</td>
<td>Nos</td>
</tr>
</tbody>
</table>

B

Relative GUS Activity

![Graph showing relative GUS activity for different combinations of Reporter and Effector]
A

Reporter
pC7er2:GUS

Effector
p35S:2C7
p35S:2C7-A
p35S:2C7-P
p35S:2C7-Q
p35S:A-2C7
p35S:P-2C7
p35S:Q-2C7

B

Figure 18
<table>
<thead>
<tr>
<th>Plant Lines</th>
<th>Wt</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
</tr>
</thead>
<tbody>
<tr>
<td>Abnormal Phenotype</td>
<td>-</td>
<td>+++</td>
<td>++++</td>
<td>++++</td>
<td>+++</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+++</td>
</tr>
</tbody>
</table>

Figure 20
Figure 22
Figure 23
Figure 25
Figure 26
Figure 27
Figure 28
Figure 29
METHODS AND COMPOSITIONS FOR REGULATING GENE EXPRESSION IN PLANT CELLS

BACKGROUND OF THE INVENTION

Gene expression may be regulated in several ways, which include the activation or suppression of transcription, the differential processing and stabilization of messenger RNA ("mRNA") and the extent of translation of the mRNA. The control of transcription plays a particularly critical role in the regulation of gene expression in eukaryotic cells. There are several structural elements that are involved in the regulation of transcription.

Promoters represent a class of nucleic acid structures that are involved in the regulation of transcription. In general, promoters are located next to the transcription start site and interact with RNA polymerase, either directly or indirectly. Promoters often comprise several discrete "cis elements," each of which may be recognized by one or more trans-acting regulatory proteins known as transcription factors. Among the various cis elements well-known in the art is the "TATA box," which is known to interact with certain regulatory proteins, e.g., transcription factors, and is generally located about 20-30 base pairs upstream from the transcription initiation site.

The binding of such transcription factors to promoters or other regulatory sequences is often responsible for the initiation, maintenance and/or down-regulation of transcription. A typical gene-specific eukaryotic transcription factor includes a DNA-binding domain and one or more additional domains that influence the activation or repression of transcription, e.g., "trans-acting domains." Transcription factors bind in the general proximity (although occasionally at great distances) of the point of transcription initiation of a gene. Such transcription factors often act to influence the efficiency of formation or function of a transcription initiation complex at the promoter. Transcription factors can act in a positive fashion (transactivation) or in a negative fashion (transrepression). Furthermore, the effect that transcription factors may have on gene expression can be constitutive (always "on") or conditional.

Over the years, several classes of DNA-binding domains of various transcription factors have been characterized and the nucleic acid sequences to which such domains interact identified. Non-limiting examples of such domains include motifs known as the leucine zipper, the bZIP domain, the zinc-finger, the homeobox, the basic helix-loop-helix and others. The trans-acting domains of transcription factors are often characterized as having a high content of specific amino acids, which include domains rich in acidic amino acids, proline or glutamine (Ginger et al., 1985; Meshi and Iwabuchi, 1995; Mitchell and Tjian, 1989). Acidic domains have been reported to possess activation functions that include interactions with TATA-binding proteins ("TBP") (Truant et al., 1993), TBP-associated factors ("TAFs") (Usugui et al., 1997), TFIIA (Pugh, 2000), TFIIB (Klemm et al., 1995) and other general transcription complexes (Stargell and Struhl, 1995).

Yin and Beachy, in "The regulatory regions of the rice tungro bacilliform virus promoter and interacting nuclear factors in rice (Oryza sativa L.), The Plant Journal, 7(6): 969-980 (1995)," described the E fragment (−164 to +45 in relation to the transcription start site) within the RTBV promoter, which was shown to be sufficient to cause tissue-specific gene expression. The article also disclosed a critical cis element, Box II (−53 to −39), within the E fragment that was shown to be essential for promoter activity. The same authors identified other cis elements of the RTBV promoter in "Promoter elements required for phloem-specific gene expression from the RTBV promoter in rice, The Plant Journal: 12(5): 1179-1188 (1997)," including the ASL Box (−98 to −79) and a GATA motif (−143 to −135). Together, these cis elements were shown to confer phloem-specific reporter gene expression.

Yin et al., in "RF2a, a bZIP transcriptional activator of phloem-specific rice tungro bacilliform virus promoter, function in vascular development, The EMBO Journal, 16(17): 5247-5259 (1997)," identified a 1.8 Kb transcription factor consisting of 368 amino acids—designated as RF2a. The RF2a transcription factor is currently known to represent a bZIP transcription activator found in rice plants that contains acidic, proline-rich and glutamine-rich putative functional domains. RF2a has been shown to bind the Box II element of the RTBV promoter and stimulate Box II-dependent transcription in vitro. Another bZIP protein, RF2b, has been isolated through interaction with RF2a, which also has been shown to interact with the Box II element.

The inventors have discovered that the Box II cis-element of the RTBV promoter is portable and that it can be used to modulate gene expression in unrelated promoters in connection with RF2a and/or RF2b. That is, until now, it was not known that the Box II element, and similar sequences, could be used in chimeric promoters to regulate gene expression in connection with RF2a and/or RF2b. What’s more, the inventors have discovered that the acidic domain of RF2a is particularly critical to the activation function of this transcription factor and, moreover, that it can be transferred to unrelated DNA-binding proteins to modulate gene expression. Accordingly, the inventors have discovered a new system for modulating gene expression, as described further below.
SUMMARY OF THE INVENTION

Until now, it was not known that the Box II element of the RTBV promoter is portable and that it can be used in connection with unrelated promoters to activate and/or enhance gene expression in the presence of RF2a and/or RF2b. Similarly, the inventors have discovered that operational derivatives of the Box II element can be used to regulate gene expression in a like fashion. Still further, the inventors have discovered that the acidic domain of RF2a is also portable and that it can be transferred to unrelated DNA-binding proteins to activate and/or enhance gene expression.

Accordingly, the present invention exploits the portability of the Box II sequence, its operational derivatives and its interaction with RF2a and/or RF2b to provide novel compositions and methods that can be used to control the expression of one or more genes of interest. Further, the present invention provides novel transcription factors, which contain at least one domain that comprises an amino acid sequence that is at least substantially similar to the acidic domain of RF2a, which can be used in connection with unrelated DNA-binding domains to regulate gene expression.

In one preferred embodiment, the invention provides novel chimeric promoters, which comprise (a) nucleic acid sequences derived from any promoter (other than the RTBV promoter), or promoter fragment, that are capable of driving gene expression in plant cells and (b) at least one nucleic acid sequence to which the one or more chimeric promoters are operatively linked. Still further, the invention provides methods of regulating the expression level of at least one gene of interest comprising transforming a plant cell with at least one plant gene expression cassette of the present invention. Still further, the invention provides methods of regulating the expression level of at least one gene of interest comprising transforming a plant cell with at least one plant gene expression cassette of the present invention. Still further, the invention provides methods of regulating the expression level of at least one gene of interest comprising transforming a plant cell with at least one plant gene expression cassette of the present invention.

In other embodiments, the invention provides methods of regulating the expression level of at least one gene of interest comprising transforming a plant cell with at least one plant gene expression cassette of the present invention. Still further, the invention provides methods of regulating the expression level of at least one gene of interest comprising transforming a plant cell with at least one plant gene expression cassette of the present invention.
enous and/or exogenous genes of interest. The foregoing combination, for example, can be used to activate or enhance the expression of particular sequences that encode molecules that selectively hybridize to specific target nucleic acid sequences. The hybridization of an oligomeric compound, for example, with its target nucleic acid sequence can have the effect of interfering with the normal function of the target sequence (this effect is generally referred to as “antisense”). The functions of DNA that can be affected in this embodiment, for example, include replication and transcription. The functions of RNA that can be affected include translocation of the RNA to the site of protein translation, translation of protein from the RNA, splicing of the RNA to yield one or more mRNA species, and catalytic activity that may be imparted or facilitated by the RNA. The effect of such interference with target nucleic acid function may provide the ability to modulate the expression of particular gene products.

In yet a further embodiment, the invention provides plant cells, plant embryos, plant tissues, whole plants and seeds that have been transformed with at least one plant gene expression cassette of the present invention.

The above-mentioned and additional features of the present invention are further illustrated in the Detailed Description contained herein. All references disclosed herein, including U.S. patents, are hereby incorporated by reference in their entirety as if each was incorporated individually.

DESCRIPTION OF THE FIGURES

FIG. 1: Comparison of RTBV promoter activity with different constitutive promoters in BY-2 protoplasts. “RTBV” represents the promoter of RTBV; “E” represents the E fragment of the RTBV promoter; “35S” refers to the enhanced 35S promoter of CaMV; “35S(-46)” refers to the deletion mutation of the CaMV 35S promoter, which ends at position −46 as described herein; “CsVMV” represents the promoter of CsVMV. The results presented are the mean value of three independent experiments with standard variations. Each experiment included three repeats and all data were normalized against GFP as internal control.

FIG. 2: Relative GUS activity of each plasmid driven by truncated mutants of the RTBV promoter. The results presented are the mean value of three independent experiments. Each experiment includes three repeats and all data were normalized against GFP as internal control.

FIG. 3: Diagram of constructs that were prepared with the Box II element inserted into different locations in the context of the E fragment of the RTBV promoter. The modified promoters were then inserted into a vector, wherein the modified promoters were operatively linked to the uidA coding sequence followed by a Nos terminator. The names of the derived plasmids are shown to the right side of the diagram.

FIG. 4: Activities of the modified promoters shown in FIG. 3. The results presented are the mean value of three independent experiments with standard variation. Each experiment included three repeats and all data were normalized against GFP as internal control.

FIG. 5: E fragment of the RTBV promoter was activated in tobacco BY-2 protoplasts by co-transfection of E::GUS with CsVMV::RF2b; CaMV 35S::RF2a and CaMV 35S::RF2a/CsVMV::RF2b.

FIG. 6: Sequences of wild type Box II (labeled Box II) and two non-limiting examples of its operational derivatives (labeled as Box IIm1 and Box IIm2). The mutated nucleotides in each operational derivative are identified in bold underline.

FIG. 7: Relative GUS activity of constructs pE(IIml)::GUS, pE(IIm2)::GUS and pE::GUS in BY-2 protoplasts as described herein. pE(IIml) comprised the E fragment, wherein the wild type Box II was replaced with the Box IIm1 element; pE(IIm2) comprised the E fragment, wherein the wild type Box II was replaced with the Box IIm2 element; pE comprised the E fragment and the wild type Box II element; and the bar labeled “BY-2” represents non-transgenic protoplasts.

FIG. 8: Comparative analysis of DNA binding affinities of RF2a and RF2b.

FIG. 9: The pE(IIml)::GUS construct was co-transfected into tobacco BY-2 protoplasts with CsVMV::RF2b, CaMV 35S::RF2a and 35S::RF2a/CsVMV::RF2b. All samples were normalized with GFP internal control.

FIG. 10: The pE(IIm2)::GUS construct was co-transfected into tobacco BY-2 protoplasts with CsVMV::RF2b, CaMV 35S::RF2a and CaMV 35S::RF2a/CsVMV::RF2b. All samples were normalized with GFP internal control.

FIG. 11: Diagram of Box II and CaMV 35S chimeric promoters (and control). The chimeric promoters were ligated with a plasmid cassette that contained the uidA coding sequence followed by a Nos terminator. The names of the derived plasmids are shown to the right side of the diagram.

FIG. 12: Primers used in generating the chimeric promoters containing the Box II element and portions of the CaMV 35S promoter, which are illustrated in FIG. 11. To facilitate the cloning process, a HindIII restriction site was added to the 5’ end of the primers (underlined). Box II elements are shown in bold and upper case letters. The sequences from the CaMV 35S promoter are shown in lower case italic letters.

FIG. 13: Relative GUS activities in non-transgenic BY-2 protoplasts of constructs in which uidA was driven by promoters that comprised Box II and portions of the CaMV 35S promoter, which are illustrated in FIG. 11. The GUS activity of each sample was normalized against the GFP internal control.

FIG. 14: A: Relative GUS activities of constructs in which the uidA gene was driven by Box II and CaMV 35S fusion promoters (which are illustrated in FIG. 11), wherein the constructs were inserted into BY-2 protoplasts that produce RF2a. B: Relative GUS activities of the constructs referenced in (A) above, wherein the constructs were inserted into BY-2 protoplasts that produce RF2a and RF2b. The GUS activity of each sample was normalized against the GFP internal control.

FIG. 15: A: Diagram of the T-DNA regions of binary plasmids used for Agrobacterium-mediated transformation of Arabidopsis thaliana. B: GUS activity of transgenic Arabidopsis plants. The results present the mean value of at least 15 independent transgenic plants. The relative GUS activity was calculated by comparison with E::GUS (=1).

FIG. 16: Electrophoretic mobility shift assay of protein-DNA complexes formed between mutants of RF2a and the Box II element. A: Schematic diagram of mutants of RF2a. “A” represents the acidic domain; “P” represents the proline-rich domain; and “Q” represents the glutamine-rich domain. B: SDS-PAGE analysis of the purified RF2a mutant proteins. C: Gel mobility shift assay using purified mutant proteins of RF2a as labeled. A control lane without protein (labeled “Free”) was included in the assay. Box IIml DNA was labeled with 35S, and radioactivity was detected by autoradiography.

FIG. 17: Effects of RF2a and mutants of RF2a on gene expression in BY-2 protoplasts. A: Reporter and effector gene constructs. The GUS reporter gene (uidA sequence) was driven by a promoter that comprised the Box II element operatively linked to nucleotides −48 to +8 of the CaMV 35S
Arabidopsis thaliana was marked with "+++" for stunting and "++++" for by the 35S promoter were grown under greenhouse condi-
tions. The results represent the averages of detected GUS activities (with S.D.) of three independent experiments, three samples per experiment, after normalization with GFP.

FIG. 18: The effects of RF2a domains on gene expression when in fusion with the 2C7 DNA-binding domain. A: Diagram of reporter and effector constructs used for transient assays involving fusion proteins of RF2a functional domains with the 2C7 synthetic zinc finger DNA-binding domain. B: Relative GUS activities in BY-2 protoplasts that were co-transfected with the reporter and effector gene constructs as indicated herein. The results represent the averages (with S.D.) of three independent experiments, three samples per experiment, after normalization with GFP.

FIG. 19: Impact of RF2a and RF2a mutants on development of transgenic tobacco plants. A: Two-month old transgenic tobacco plants with RF2a and mutants of RF2a driven by the 35S promoter were grown under greenhouse conditions. Only transgenic plants with mutants lacking the acidic domain (RF2a-ΔPAA and RF2a-3A) showed severe stunting phenotype. B: Transgenic plants at 105 days. Leaves of plants with RF2a-ΔPAA and RF2a-3A were curved downward, and flowering time was significantly delayed. C: Panel 1: Transverse section of the stem of transgenic plants with RF2a-ΔPAA in low magnification; Panel 2-4: Transverse sections of the lower part of stems of two-month old tobacco plants stained with toluidine blue O. Panel 2, transgenic plant with RF2a-ΔPAA. Panel 3, transgenic plant with RF2a-3A. Panel 4, Non-transgenic plant.

FIG. 20: Correlation between severity of abnormal phenotypes shown in FIG. 19 and accumulation of RF2a-ΔPAA. Severity of the abnormal phenotype of transgenic tobacco plants was marked with "+++" for stunting and "++++" for severe stunted phenotype, whereas "-" indicates that no abnormal phenotype was observed. Upper panel, 40-µg protein samples were separated by 10% SDS-PAGE and detected with antibody against full-length RF2a after being probed with nitrocellulose membrane. The band that contains RF2a-ΔPAA is marked on the right. Lower panel, the membrane used in the immunoblot was stained with Ponceau S (Sigma Chemical Company, St. Louis, Mo.) prior to the antibody reaction.

FIG. 21: Activation of GUS expression in non-vascular tissues by induction of RF2a. Leaf tissues from transgenic Arabidopsis plants were stained in buffer containing X-Gluc to detect GUS expression. The transgenic Arabidopsis plants (shown at the top of FIG. 21) included the E:GUS, 5G35Sm:RF2a, and Cs:VGE cassettes described herein. "Treated" leaf tissue was subjected to applications of Intrepid® 2F as described herein, whereas "Untreated" leaf tissue was not subjected to Intrepid® 2F. The shaded leaf tissue in the "Treated" leaf correlates with the GUS expression pattern observed. Leaf tissue transformed with only E:GUS is shown at the bottom of FIG. 21.

FIG. 22: Quantitative analysis of the activation of the E element by RF2a upon chemical induction. A: Relative GUS activity of T2 transgenic Arabidopsis plants, which comprise the E:GUS, 5G35Sm:RF2a, and Cs:VGE sequences described herein. Each set of bars represents 1 of 12 groups of transgenic plant lines, namely, EGaV-3, EGaV-5, EGaV-17, EGaV-31, EGaV-50, EGaV-51, EGaV-56, EGaV-59, EGaV-63, EGaV-70, EGaV-72, and E:GUS. Each bar represents the average of three repeats, three plants for each repeat (with standard deviation). Open bars represent control leaf tissue that was not subjected to Intrepid® 2F treatment. Solid bars represent leaf tissue treated with 1:8,000 dilution of Intrepid® 2F.

SEQ ID NO. 1: The nucleic acid sequence of the Box II element.
SEQ ID NO. 2: The nucleic acid sequence of the Box Ilm1 element—an operational derivative of the Box II element.
SEQ ID NO. 3: The nucleic acid sequence of the Box Ilm2 element—an operational derivative of the Box II element.
SEQ ID NO. 4: The amino acid sequence of the RF2a transcription factor.
SEQ ID NO. 5: The amino acid sequence of the RF2b transcription factor.
SEQ ID NO. 6: The amino acid sequence of the acidic domain of the RF2a transcription factor.
SEQ ID NO. 7: Non-limiting example of nucleic acid sequence that encodes the RF2a transcription factor.
SEQ ID NO. 8: Non-limiting example of nucleic acid sequence that encodes the RF2b transcription factor.
promoter.

(iii) the Box IIml element (SEQ ID NO:2); (iii) the Box IIml element (SEQ ID NO:1); (ii) the Box IIml element.

The first of the at least two components relates to (i) the Box II element (SEQ ID NO:1); (ii) the Box IIml element.

The promoters of the present invention comprise a first nucleic acid sequence derived from any promoter (other than the RTBV promoter (SEQ ID NO:62)), or promoter fragment, that is capable of driving gene expression in plant cells.

In one preferred embodiment, the invention provides novel chimeric promoters. The promoters of the present invention comprise a first nucleic acid sequence derived from any promoter (other than the RTBV promoter (SEQ ID NO:62)), or promoter fragment, that is capable of driving gene expression in plant cells.

The following will describe in detail several preferred embodiments of the invention. These embodiments are provided by way of explanation only, and thus, should not unduly restrict the scope of the invention. In fact, those of ordinary skill in the art will appreciate upon reading the present specification and viewing the present drawings that many variations and modifications of the invention may be employed, used and made without departing from the scope and spirit of the invention.

The present invention can be viewed as having at least two components. The first of the at least two components relates to the Box II element; operational derivatives of the Box II element, plant gene expression cassettes containing one or more of these elements; plant gene expression cassettes containing at least one chimeric promoter of the present invention; plant cells, embryos and tissues transformed with at least one expression cassette of the present invention and methods of using the foregoing compositions in connection with RF2a and/or RF2b to regulate the expression of at least one gene of interest.

The second of the at least two components relates to (i) novel transcription factors that comprise at least one DNA-binding domain and an amino acid sequence that is at least substantially similar to the acidic domain of RF2a and (ii) methods of using the novel transcription factors to regulate the expression of at least one gene of interest.

Novel Chimeric Promoters

In one preferred embodiment, the invention provides novel chimeric promoters. The promoters of the present invention comprise a first nucleic acid sequence derived from any promoter (other than the RTBV promoter (SEQ ID NO:62)), or promoter fragment, that is capable of driving gene expression in plant cells.

The promoters further comprise at least one nucleic acid sequence selected from the group consisting of: (i) the Box II element (SEQ ID NO:1); (ii) the Box IIml element (SEQ ID NO:2); (iii) the Box IIml element (SEQ ID NO:3); (iv) sequences that are substantially similar to either SEQ ID NO:1, 2 or 3, or (v) other operational derivatives of the Box II element. As used herein, the term “operational derivative” shall refer, generally, to the Box II element, the Box IIml element, sequences that are substantially similar to either the Box II element, the Box IIml element, sequences that are substantially similar to either SEQ ID NO:1, 2 or 3, or (v) other operational derivatives of the Box II element.
and most preferably at least about 90% or 95%) of the nucleotides match over the defined length of the nucleic acid sequence. Sequences that are substantially homologous can be identified by comparing the sequences using readily accessible computer software, or in a Southern hybridization experiment under, for example, stringent conditions as defined for that particular system. Defining appropriate hybridization conditions for a particular system is within the skill of the art. It will be further understood by those skilled in the art that the phrase “at least substantially similar” refers to sequences that are “substantially similar” as described above or, alternatively, identical to one another.

As used herein, “substantially similar” is further meant to include a nucleic acid sequence which, by virtue of the degeneracy of the genetic code, is not identical with that shown in any of the sequences shown in the Sequence Listing, but which still encodes the same amino acid sequence; or a modified nucleic acid sequence that encodes a different amino acid sequence that retains substantially the same activities of the original proteins, either because one amino acid is replaced with a similar amino acid, or because the change (whether it be substitution, deletion or insertion) does not affect the active site of the protein. Thus, it is contemplated by the inventors that various changes may be made in the nucleic acid sequences disclosed, and, of course, the encoded polypeptides, without appreciable loss of their biological activity or utility in the present invention.

The chimeric promoters of the present invention are preferably, constructed by combining the first nucleic acid sequence derived from any plant functional promoter, or promoter fragment, with at least one nucleic acid sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, and sequences substantially similar to SEQ ID NO: 1, 2 or 3. More preferably, however, the chimeric promoters of the present invention are constructed by combining the first nucleic acid sequence derived from any plant functional promoter, or promoter fragment, with at least one nucleic acid sequence selected from the group consisting of SEQ ID NO: 1, 2 and 3. The term “chimeric promoter,” as used herein, refers to any plant functional promoter sequence, or promoter fragment, that comprises SEQ ID NO: 1, 2, 3, or sequences substantially similar thereeto, wherein such plant functional promoter sequence is not derived from the RTBV promoter.

The nucleic acid sequences consisting of SEQ ID NO: 1, 2, 3, and sequences substantially similar thereto, may be positioned within the first nucleic acid sequence described above, which comprises any plant functional promoter (or promoter fragment). Alternatively, the nucleic acid sequences consisting of SEQ ID NO: 1, 2, 3, and sequences that are substantially similar to SEQ ID NO: 1, 2 or 3, may be fused to the 5’ or 3’ end of such plant functional promoter (or promoter fragment).

Although SEQ ID NO: 1, 2, 3, and sequences substantially similar thereto, may be positioned within, or fused to the end of, a chimeric promoter, such sequences are, preferably, positioned in specific locations of the DNA helix. In particular, such nucleic acid sequences are, preferably, operably linked to the 5’ end of the selected promoter, or promoter fragment, with a space of approximately 7 nucleotides from the TATA box plus one or more full “turns of DNA helix.” It is well-known in the art that one turn of DNA helix equals, approximately, 10.4 base pairs. Furthermore, the TATA box, which, generally, is the module within a promoter that functions to position the start site for RNA synthesis, and its location in a promoter can be easily identified by those skilled in the art. In many cases, the TATA box consensus sequence (TATAAT) is present near the start site (by convention —30 to —20 base pairs relative to the transcription start site).

The Box II element and its operational derivatives may be used in connection with a variety of promoters, or promoter fragments, to create novel chimeric promoters. Preferably, however, the Box II element and/or its operational derivatives are operably linked to a promoter, or promoter fragment, that comprises a transcription initiation domain. The term “transcription initiation domain” refers to a sequence having at least an RNA polymerase binding site and an mRNA initiation site.

Such basic guidelines for promoter, or promoter fragment, selection emphasize the notion that the Box II element and its operational derivatives are, indeed, “portable” and can be transferred to a plurality of promoter sequences. Of course, the promoter sequence with which the Box II element and/or its operational derivatives will be used, preferably, relates to the target cell-type in which gene expression is desired.

For example, some promoters are known to be active in particular cell-types, in certain tissues, under certain conditions and/or in the presence of certain inducible agents. Thus, the cell-type and/or conditions in which expression is desired will impact the identity of the promoter sequence with which Box II and/or its operational derivatives will be used. Although the endogenous promoter of the gene of interest may be utilized herein for transcriptional regulation, preferably, the promoter is a foreign regulatory sequence. For plant expression vectors, suitable viral promoters include, for example, the RTBV promoter; the 35S RNA and 19S RNA promoters of the cauliflower mosaic virus ("CaMV"); the full-length transcript promoter from fijgwort mosaic virus ("FMV"); and the cassava vein mosaic virus ("CsVMV") promoter.

The Box II element, of course, can be isolated from natural sources, e.g., the Box II element can be isolated from the E fragment of the RTBV promoter (SEQ ID NO: 62) using techniques well-known in the art. More preferably, however, the Box II element and its operational derivatives are synthesized using standard DNA synthesis techniques (see, for example, Current Protocols in Molecular Biology, Unit 2.11, eds. Ausubel, et al., John Wiley & Sons, 1995).

Expression Cassettes Comprising Novel Chimeric Promoters

The present invention further provides plant gene expression cassettes that comprise a first chimeric promoter of the present invention operatively linked to one or more genes of interest. The expression cassettes may further comprise a second promoter operatively linked to a nucleic acid sequence that encodes a polypeptide, which comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NO: 4; (b) SEQ ID NO: 5; (c) SEQ ID NO: 6 and (d) sequences that are substantially similar to either SEQ ID NO: 4, 5 or 6. Non-limiting examples of nucleic acid sequences that encode the amino acid sequences set forth in SEQ ID NO: 4, SEQ ID NO: 5 and SEQ ID NO: 6 are shown in SEQ ID NO: 7, SEQ ID NO: 8 and SEQ ID NO: 9, respectively.

The one or more genes of interest operatively linked to a first chimeric promoter of the present invention, when including an open reading frame ("ORF"), may encode a protein. Of course, the gene of interest can be an endogenous or exogenous sequence. In addition, the ORF may include certain 5’ and 3’ untranslated sequences. Still further, appropriate transcription termination and polyadenylation sequences may, preferably, be included.

Genes of interest, the expression of which may be regulated according to the present invention, may include, for
example, sequences that naturally exist in plants, animals, bacteria, viruses or fungi; synthetic DNA sequences that encode a specific RNA or protein product; cDNA sequences derived from mRNA; DNA sequences modified by mutagenesis, for example, through site specific mutagenesis; chimeras of any of the above (to produce fusion proteins); and DNA sequences encoding complementary RNA molecules (for "antisense" applications); and combinations and/or fragments of the above.

Examples of proteins that can be encoded by the gene of interest include, but are not limited to, nutritionally important proteins; growth promoting factors; proteins for early flowering in plants; proteins that impart protection to the plant under certain environmental conditions, e.g., proteins conferring resistance to metals or other toxic substances, such as herbicides or pesticides; stress related proteins that confer tolerance to temperature or hydration extremes; proteins conferring resistance to fungi, bacteria, viruses, insects and nematodes; and proteins of specific commercial value, e.g., enzymes involved in metabolic pathways, proteins having therapeutic activity in humans, and others.

The term "operably linked," as used herein, refers to the functional linkage between, for example, the Box II element and/or its operational derivatives and a plant functional promoter or promoter fragment; between a promoter sequence, including the novel chimeric promoters of the present invention, and any gene of interest; and between a promoter sequence and any sequence encoding the RF2a protein, RF2b protein, a protein comprising the acidic domain of RF2a and/or any protein that is substantially similar to the foregoing proteins.

The second promoter operatively linked to a nucleic acid sequence that encodes a polypeptide, which comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NO:4; (b) SEQ ID NO:5; (c) SEQ ID NO:6; and (d) sequences that are substantially similar to either SEQ ID NO:4, 5, or 6, may constitute any promoter that is capable of driving gene expression in the target plant cells. As described above, certain promoters are known to be active in particular cell-types, in certain tissues, under certain abiotic conditions and/or in the presence of certain inducible agents. Thus, the cell-type and/or conditions in which gene expression is desired will impact the identity of the promoter that is selected to drive expression of sequences encoding RF2a, RF2b, polypeptides comprising the acidic domain of RF2a or polypeptides that are substantially similar to any of the foregoing. Of course, such promoters may include both constitutive, e.g., the CaMV promoter, and inducible promoters.

By placing the nucleic acid sequence encoding RF2a, RF2b, polypeptides comprising the acidic domain of RF2a or polypeptides that are substantially similar to any of the foregoing under the control of a chemically-inducible promoter, the gene expression system can be activated at will. The use of inducible promoters in this capacity provides control over the effect that the encoded proteins may have on the expression of promoter sequences (and genes operatively linked to such sequences) comprising the Box II element and/or its operational derivatives. In short, expression of the nucleic acid sequence to which the second promoter is operatively linked is stimulated and/or enhanced by applying an effective amount of the chemical inducer to the plant cells, embryos or tissues that have been transformed with the appropriate expression cassette of the present invention. Application of the inducer, therefore, allows the expressed transcription factor to interact with, and stimulate (or enhance) the expression of, the chimeric promoter and the one or more genes of interest to which it is operatively linked.

To be most useful, an inducible promoter should 1) provide low expression in the absence of the inducer, 2) provide high expression in the presence of the inducer; 3) employ an induction scheme that does not interfere with the normal physiology of the plant; and 4) has no effect on the expression of other genes. Examples of inducible expression schemes useful in plants include those induced by chemical means, such as the ecdysone agonist-inducible gene expression systems (Christopherson et al., 1992; Martinez et al., 1999). The ecdysone agonist-inducible gene expression systems, preferably, employ commercially-available non-steroidal ecdysone agonists, such as tebufenozide and methoxyfenozide.

Additional examples of inducible promoters useful in plants include, but are not limited to, promoters that respond to tetracycline (Gatz et al., 1992; Weinmann et al., 1994); the yeast metallothionein promoter, which is activated by copper ions; the In2-1 and In2-2 regulator sequences, which are activated by substituted benzenesulfonamides, e.g., herbicide safeners; and GRE regulatory sequences, which are induced by glucocorticoids. In addition, plant promoters such as the lipo-inducible promoter from the small subunit of ribulose bis-phosphate carboxylase (suRUBISCO); mannopine synthase promoter; nopaline synthase ("NOS") and octopine synthase ("OCS") promoters (carried on tumor-inducing plasmids of Agrobacterium tumefaciens) or heat shock promoters, e.g., soybean hsp71.5-5 or hsp17.3-B, may be used. Other promoters, both constitutive and inducible, will be known to those of skill in the art.

It will be appreciated by those skilled in the art that the first chimeric promoter, which is operatively linked to at least one gene of interest, and the second promoter, which is operatively linked to a sequence encoding RF2a, RF2b, polypeptides comprising the acidic domain of RF2a or polypeptides that are substantially similar to any of the foregoing, may exist in a single gene expression cassette (or vector), or, alternatively, in separate cassettes (or vectors). Still further, those skilled in the art will appreciate that an expression cassette may comprise a single chimeric promoter, or, alternatively, a plurality of chimeric promoters, each operatively linked to at least one gene of interest. Moreover, the plurality of chimeric promoters may be substantially similar in sequence, or, alternatively, may comprise significantly different sequences.

Novel Transcription Factors

Over the years, several classes of DNA-binding proteins have been characterized and the nucleic acid sequences with which such proteins interact identified. For example, zinc finger proteins represent a class of motifs that are known to be involved in the sequence-specific recognition of DNA. As the name implies, this DNA-binding domain is folded around a zinc ion. To date, more than two hundred proteins, many of them transcription factors, have been shown to possess zinc finger domains. In general, zinc fingers connect transcription factors to their target locations by binding to specific DNA sequences.

The RF2a and RF2b transcription factors described herein represent yet another class of DNA-binding proteins. Specifically, RF2a and RF2b are representative examples of which are commonly referred to as bZIP transcription factors. The bZIP transcription factors are generally characterized by a bipartite DNA-binding domain consisting of a basic region involved in sequence-specific binding, and a leucine zipper region required for dimerization. The bZIP domain of RF2a shares high similarity with bZIP proteins that exist naturally in plants such as Arabidopsis, tobacco, tomato, and other plants (Fukazawa et al., 2000; Jakoby et al., 2002; Ringli and Keller, 1998). In particular, this group of proteins is known to have a
lysine residue at the −10 position relative to the first leucine residue of the leucine zipper region (Yin et al., 1997). The amino acid sequence signature of the DNA-binding regions of this class of proteins is NXXSXAXXXK (Fujii et al., 2000) (SEQ ID NO: 109).

The present invention provides novel transcription factors, and uses thereof, which provide the ability to regulate the expression of at least one gene of interest. In particular, the inventors have discovered that the acidic domain of RF2a (SEQ ID NO:6), and amino acid sequences substantially similar to SEQ ID NO:6, can be fused to unrelated transcription factors, or transcription factor-like complexes, to regulate gene expression. In certain embodiments, the invention provides that novel transcription factors, which comprise the acidic domain of RF2a and at least one DNA-binding domain, can be used to modulate the expression of one or more genes driven by promoters that comprise nucleic acid sequences recognized by such DNA-binding domain of the novel transcription factors.

In certain embodiments, the acidic domain of RF2a (SEQ ID NO:6), and/or amino acid sequences substantially similar to SEQ ID NO:6, can be fused to any class of DNA-binding domains (and/or unrelated transcription factors comprising such domains). The acidic domain of RF2a, and/or substantially similar sequences, can be fused, for example, to any polypeptide comprising a leucine zipper, bZIP domain, zinc-finger, homeobox, basic helix-loop-helix domain, or other DNA-binding domains currently known in the art (or discovered hereafter). It should be appreciated, however, that the DNA-binding domain selected (or the polypeptide comprising such domain) must be capable of interacting with the promoter operatively linked to the gene of interest for which control of expression is desired.

It will be appreciated by those skilled in the art that two amino acid sequences are “substantially similar” when approximately 70% or more (preferably at least about 80%, and more preferably at least about 90% or 95%) of the amino acids match over the defined length of the sequences. The term “substantially similar” is further meant to refer to amino acid sequences that have been modified from an original sequence, wherein the modified amino acid sequence retains substantially the same level of activity as the original amino acid sequence. This retention in activity, of course, may occur when one or more amino acids are replaced with similar amino acids, or because the change (whether it be substitution, deletion or insertion) does not affect the active site of the protein. Thus, it is contemplated by the inventors that various changes may be made to the acidic domain of RF2a, without appreciable loss of its biological activity and utility in the present invention. It will be further understood by those skilled in the art that the phrase “at least substantially similar” as it is used herein with respect to amino acid sequences refers to sequences that are “substantially similar” as described above or, alternatively, identical to one another.

In certain embodiments, for example, novel transcription factors are provided, which comprise a fragment of the acidic domain of RF2a (SEQ ID NO:6). More particularly, the present invention contemplates that internal regions and fragments of the acidic domain of RF2a (SEQ ID NO:6) may be used to form novel transcription factors, which are capable of regulating gene expression as described herein.

As used herein, “fragments of the acidic domain” and “fragment of the acidic domain” refer to amino acid sequences comprising less than all of the amino acid residues of SEQ ID NO:6, wherein such amino acid sequence is substantially similar to the corresponding region of the full-length SEQ ID NO:6. More particularly, for example, a “fragment of the acidic domain” includes an amino acid sequence encompassing at least 30%, 40%, 50%, 60%, 70%, 80%, or 90% of SEQ ID NO:6, wherein such amino acid sequence is substantially similar to the corresponding region of the full-length SEQ ID NO:6.

The acidic domain of RF2a (SEQ ID NO:6) (and/or amino acid sequences substantially similar to SEQ ID NO:6) and fragments of the acidic domain may be fused to any class of DNA-binding domains (and/or unrelated transcription factors comprising such domains) to create novel transcription factors as described herein, the invention provides that such sequences may act in the absence of DNA-binding domains to regulate gene expression. In such embodiment, the acidic domain of RF2a may be used alone or in combination with other regulatory proteins or domains to modulate gene expression. For example, the invention provides novel transcription factors that comprise the acidic domain of RF2a and any other amino acid sequence not derived from RF2a or RF2b, which are capable of regulating the expression of at least one gene of interest. The numerous mechanisms by which such transcription factors may regulate expression are well-known to those skilled in the art, which include, for example, affecting the formation of the transcription initiation complex and recruiting other regulatory proteins to the transcription initiation region.

Expression Cassette Encoding Novel Transcription Factors
The present invention further provides plant gene expression cassettes comprising (i) a first promoter, which comprises a nucleic acid sequence that is capable of interacting with at least one DNA-binding domain of at least one polypeptide, operatively linked to a gene of interest and (ii) a second promoter operatively linked to a nucleic acid sequence that encodes a polypeptide, which comprises an amino acid sequence that is at least substantially similar to SEQ ID NO:6 and a DNA-binding domain that is capable of interacting with the corresponding nucleic acid sequence of the first promoter.

Of course, in light of the foregoing, nucleic acid sequences encoding the acidic domain of RF2a, and/or substantially similar amino acid sequences, may be operatively linked to, for example, nucleic acid sequences that encode polypeptides comprising any motif known to interact with the first promoter (or, more specifically, elements contained within or near the first promoter), which is operatively linked to the one or more genes of interest. This interaction will, preferably, initiate and/or enhance the expression of the one or more genes of interest. An example of a nucleic acid sequence that encodes the acidic domain of RF2a (SEQ ID NO:6) includes, but is not limited to, the sequence shown in SEQ ID NO:9.

Examples of nucleic acid sequences encoding DNA-binding domains that can be used in this capacity include, but are not limited to, sequences encoding a leucine zipper, the bZIP domain, the zinc-finger, the homeobox, the basic helix-loop-helix domain or others. It will be appreciated by those skilled in the art that the selected DNA-binding domain must be capable of interacting with the promoter operatively linked to the one or more genes of interest for which control of expression is desired. Still further, it will be appreciated by those skilled in the art that sequences encoding the acidic domain of RF2a, for example, and at least one DNA-binding domain may be tethered directly to one another, or, alternatively, may be connected indirectly through intervening sequences, e.g., spacers, other polypeptide-encoding sequences, etc.

In certain alternative embodiments, the second promoter is operatively linked to a nucleic acid sequence that encodes a novel transcription factor, which comprises an amino acid
The present invention relates generally to the field of molecular biology, and more specifically to transgenic plant methods of expression regulation through the use of transcription factors.

Methods of Regulating Gene Expression

The invention further provides methods of regulating the expression level of at least one gene of interest, which comprise transforming a plant cell with at least one plant gene expression cassette of the present invention. Still further, the invention provides methods of regulating the expression level of at least one gene of interest, which comprise (a) constructing at least one plant gene expression cassette of the present invention; (b) transforming a plant cell with the plant gene expression cassette of the present invention; and (c) regenerating whole plants from the transformed plant cell. In a related embodiment, for plants, plant tissues or plant cells that have been transformed with a gene expression cassette comprising a chemically-inducible promoter operatively linked to a nucleic acid sequence that encodes a polypeptide comprising an amino acid sequence that is at least substantially similar to SEQ ID NO:4, 5 or 6, the method further comprises contacting the transformed plants, plant tissues or plant cells, directly or indirectly, with an activating amount of the expression-inducing chemical.

In other embodiments, plant gene expression cassettes comprising two or more chimeric promoters of the present invention, which are operatively linked to one or more genes of interest, can be transformed into a plant cell in connection with, for example, RF2a- and/or RF2b-encoding sequences to achieve a "cascade-type" system. In such embodiments, the expression of RF2a and/or RF2b activates and/or enhances the expression of the nucleic acid sequences to which the two or more chimeric promoters are operatively linked. Still further, the nucleic acid sequences encoding the RF2a and/or RF2b proteins, for example, may be operably linked to chemically-inducible promoters. In such case, upon contacting plants, plant tissues or plant cells, which have been transformed with such sequences, with the expression-inducing chemical, the RF2a and/or RF2b transcription factors are produced. The RF2a and/or RF2b transcription factors subsequently interact with the Box II elements (and/or operational derivatives of Box II) to regulate gene expression. This interaction, of course, results in the synchronized activation and/or enhancement of expression of all Box I-dependent genes (or all genes operatively linked to promoters containing operational derivatives of Box II).

In other embodiments, plant gene expression cassettes comprising at least one chimeric promoter of the present invention, which is operatively linked to one or more genes of interest, can be transformed into plant cells in connection with RF2a- and/or RF2b-encoding sequences to "turn-off" or modulate the expression of one or more unrelated endogenous and/or exogenous genes. The foregoing expression cassettes can be used, for example, to activate and/or enhance the expression of the one or more genes of interest that encode molecules that selectively hybridize to specific target nucleic acid sequences, e.g., endogenous and/or exogenous genes. The hybridization of an oligomeric compound, for example, with its target nucleic acid sequence can have the effect of interfering with the normal function of the target sequence (this effect is generally referred to as "antisense"). The functions of DNA that can be affected in this embodiment, for example, include replication and transcription. The functions of RNA that can be affected include all vital functions such as translational and posttranslational events, translation of protein from the RNA, splicing of the RNA to yield one or more mRNA species, and catalytic activity that may be imparted or facilitated by the RNA. The effect of such interference with target nucleic acid function provides the ability to modulate the expression of particular gene products.

The transformation of plant cells in accordance with the present invention may be carried out in essentially any of the various ways known to those skilled in the art of plant molecular biology. That is, the method employed for transformation of target plant cells is not relevant to the present invention and any method suitable for the target plant cell type may be utilized. As used herein, the term "transformation" refers to the alteration of the genotype of a host plant, including within plant cells, embryos and tissues, by the introduction of endogenous or exogenous nucleic acid sequences. Further, the terms "transfection" and "transformation," as used herein, may be used interchangeably, wherein the meaning accorded to both terms is, generally, as described above with respect to "transformation."
ous embodiments of the present invention may be applied to any plant, plant tissue, seed or plant cell for which transformation techniques are, or become, available.

In general, to commence a transformation process in accordance with the present invention, it is first necessary to construct a suitable vector and properly introduce the vector into a plant cell. The details of the construction of vectors utilized herein are known to those skilled in the art of plant molecular biology. As described above, one or more plant gene expression cassettes may be constructed to practice the methods, and to generate the plants, plant tissues and plant cells of, the present invention. In practice, the construct or constructs comprising the expression cassettes of the present invention will be inserted into a plant cell by transformation.

For example, constructs that include chimeric promoters of the present invention, which comprise the Box II element and/or its operational derivatives, can be introduced into plant cells using Ti plasmids, root-inducing (Ri) plasmids, and plant virus vectors. In the first instance, for example, the nucleic acid sequences of the present invention can be introduced into plant cells through Agrobacterium-mediated transformation. Methods involving the use of Agrobacterium-mediated transformation include, but are not limited to: 1) co-cultivation of Agrobacterium with cultured isolated protoplasts; 2) transforming (or infecting) plant cells or tissues with transformed Agrobacterium (as described herein); or 3) transformation of seeds, explants, apices or meristems with Agrobacterium. Under appropriate conditions known in the art, the transformed plant cells may be grown to form shoots, roots, and develop further into plants.

In some cases, it may be preferred to introduce the nucleic acid sequences of the present invention into plant cells utilizing Agrobacterium tumefaciens containing the Ti plasmid. When using an A. tumefaciens culture as a transformation vehicle, it is most advantageous to use a non-oncogenic strain of the Agrobacterium as the vector so that normal non-oncogenic differentiation of the transformed tissues is possible. It is also preferred that the Agrobacterium harbor a binary Ti plasmid system. Such a binary system comprises 1) a first Ti plasmid having a virulence region essential for the introduction of transfer DNA (T-DNA) into plants and 2) a chimeric plasmid. The chimeric plasmid contains at least one border region of the T-DNA region of a wild-type Ti plasmid flanking the nucleic acid sequence to be transferred. Binary Ti plasmid systems have been shown to be effective in transforming plant cells.

Alternatively, the nucleic acid sequences of the present invention can be introduced into plant cells using mechanical or chemical means. For example, nucleic acid sequences can be mechanically transferred by direct microinjection into plant cells utilizing micropipettes. Still further, the nucleic acid sequences may be transferred into plant cells using polyethylene glycol, which is capable of forming a precipitation complex with nucleic acid sequences that is taken up by target plant cells.

The nucleic acid sequences of the present invention can also be introduced into plant cells by electroporation. In this technique, plant protoplasts, for example, are electroporated in the presence of vectors or nucleic acid sequences to be transformed into the protoplasts. Electrical impulses of high field strength reversibly permeabilize plant membranes allowing the introduction of nucleic acids. Electroporated plant protoplasts reform the cell wall, divide and form a plant callus. Selection of the transformed plant cells with the transformed gene can be accomplished using, for example, phenotypic markers.

Another well-known method for introducing nucleic acid sequences of the present invention into plant cells is high velocity BIOLISTIC® penetration by small particles with the nucleic acid sequences to be introduced contained either within the matrix of small beads or particles, or on the surface thereof. See, for example, U.S. Pat. Nos. 5,932,479 and 5,693,507.

Additionally, DNA viruses may be used as vectors for introducing heterologous nucleic acid sequences into plant cells. See, for example, U.S. Pat. No. 4,407,956. Non-limiting examples of such DNA viruses include the Cauliflower mosaic virus ("CaMV") and the Gemini virus. The CaMV viral DNA genome, for example, may be inserted into a parent bacterial plasmid creating a recombinant DNA molecule which can be propagated in bacteria. After cloning, the recombinant plasmid may be re-cloned and further modified by introduction of the desired nucleic acid sequence of the present invention. The modified viral portion of the recombinant plasmid is then excised from the parent bacterial plasmid, and used to inoculate the target plant cells.

In any of the foregoing methods of transformation, a selectable marker may, optionally, be associated with constructs comprising nucleic acid sequences of the present invention. As used herein, "marker" refers to a gene that encodes a protein that confers a particular trait or a phenotype that permits the selection of, or the screening for, a plant or plant cell containing the marker. In some cases, the marker gene may encode a protein that confers antibiotic resistance to transformed plant cells, whereby the appropriate antibiotic can be used to select for transformed plant cells among cells that are not transformed. Examples of suitable selectable markers include adenine deaminase, dihydrofolate reductase, hygromycin-B-phosphotransferase, thymidine kinase, xanthine-guanine phosphoribosyltransferase and amino-glycoside 3'-O-phosphotransferase II (kanamycin, neomycin and G418 resistance). Other suitable markers will be known to those of skill in the art. For example, screenable markers, such as the uidA gene, which encodes β-glucuronidase ("GUS"), luciferase or the gene encoding the green fluorescent protein ("GFP"), may also be used.

Plants and Plant Parts

Still further, the invention provides plant cells, plant embryos, plant tissues, whole plants and seeds that have been transformed with at least one plant gene expression cassette of the present invention. Methods of regenerating whole plants from transformed plant cells, embryos and tissues are well-known to those skilled in the art.

The following Examples are included to demonstrate certain embodiments of the invention. It should be appreciated by those skilled in the art that the techniques disclosed in the Examples that follow represent techniques discovered by the inventors to function well in the practice of the invention, and thus, can be considered to constitute preferred modes for its practice. However, those of ordinary skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments that are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

EXAMPLES

Example 1

Analysis of the Box II Sequence in BY-2 Protoplasts

Until now, the behavior of the RBTV promoter in the tobacco BY-2 cell line and the contribution of its various cis elements to the promoter activity in BY-2 cells was unknown.
To compare the relative activity of the RTBV promoter with other constitutive promoters, tobacco BY-2 protoplasts were transfected with gene constructs in which the uidA open reading frame ("ORF") was driven by the enhanced cauliflower mosaic virus ("CaMV") 35S promoter, the enhanced CaMV promoter with a 5′ deletion (at position −46 in relation to the transcription start site), the cassava vein mosaic virus ("CVMMV") promoter, the RTBV promoter or the E fragment of the RTBV promoter. The results are shown in Fig. 1, which indicate that the RTBV promoter and, more particularly, the E fragment of the RTBV promoter exhibit strong activity in BY-2 cells. Specifically, the E fragment exhibited more than one third of the activity that was observed with the CaMV 35S promoter, which is generally considered a strong promoter in plant cells.

To evaluate the functional contribution of different cis elements to the activity of the RTBV promoter, deletion mutants were generated from the E fragment by removing the GATA motif, ASL box and the Box II element at positions −100, −68 and −32, respectively. In Fig. 2, "pE" represents the entire E fragment; "p-100" represents a truncated E fragment at position −100, which excludes the GATA motif; "p-68" represents a truncated E fragment at position −68, which excludes the GATA motif and ASL box; and "p-32" represents a truncated E fragment at position −32, which excludes the GATA motif, ASL box and Box II element. All of the foregoing fragments included the TATA box and Box I element of the RTBV promoter.

The mutated promoters were then fused with the uidA gene. The GUS expression levels of the derived plasmids were determined in BY-2 protoplasts. The data in Fig. 2 show that the Box II element is crucial for promoter function in BY-2 protoplasts. As long as the Box II element was retained, the minimal promoter exhibited an expression level similar to that of the full E fragment. Once the Box II element was removed, however, the promoter activity decreased to less than 20% of the E fragment. Examples of the PCR products generated in the first reaction were used as templates for the second PCR reaction using R/GUS3′ as primers (SEQ ID NO:73/13). The PCR products from the second reaction were purified and cloned into the pE:GUS vector to replace the E promoter through the restriction sites HindIII/NcoI. The resultant plasmids were named pE(ΔBoxII):GUS. The Box II element was re-introduced into pE(ΔBoxII):GUS using the same fusion PCR strategy as described above. To generate the E-Box II+11, E-Box II−9, E-Box II−17, E-Box II−58, E-Box II−63, E-Box II−74, E-Box II−79, E-Box II−100, E-Box II−116, E-Box II−147 and E-Box II−164 promoters, the first PCR reactions were carried out using the primer sets shown in the following Table 1:

<table>
<thead>
<tr>
<th>Promoters</th>
<th>Primer Sets</th>
<th>Respective SEQ ID Nos.</th>
</tr>
</thead>
<tbody>
<tr>
<td>E-Box II+11</td>
<td>R/mtEBoxII(−0.5 h)-3′</td>
<td>SEQ ID NO: 73/14</td>
</tr>
<tr>
<td>E-Box II−9</td>
<td>R/mtEBoxII(−0.5 h)-5′/GUS3′</td>
<td>SEQ ID NO: 73/15</td>
</tr>
<tr>
<td>E-Box II−17</td>
<td>R/mtEBoxII(−1.0 h)-5′/GUS3′</td>
<td>SEQ ID NO: 17/13</td>
</tr>
<tr>
<td>E-Box II−58</td>
<td>R/mtEBoxII(−2.5 h)-5′/GUS3′</td>
<td>SEQ ID NO: 19/13</td>
</tr>
<tr>
<td>E-Box II−63</td>
<td>R/mtEBoxII(−4.5 h)-5′/GUS3′</td>
<td>SEQ ID NO: 21/13</td>
</tr>
<tr>
<td>E-Box II−74</td>
<td>R/mtEBoxII(−6.0 h)-5′/GUS3′</td>
<td>SEQ ID NO: 23/13</td>
</tr>
<tr>
<td>E-Box II−79</td>
<td>R/mtEBoxII(−9.0 h)-5′</td>
<td>SEQ ID NO: 25/13</td>
</tr>
<tr>
<td>E-Box II−100</td>
<td>R/mtEBoxII(−111 nt)-3′</td>
<td>SEQ ID NO: 73/28</td>
</tr>
<tr>
<td>E-Box II−116</td>
<td>R/mtEBoxII(−111 nt)-5′/GUS3′</td>
<td>SEQ ID NO: 29/13</td>
</tr>
<tr>
<td>E-Box II−147</td>
<td>R/mtEBoxII(+29 nt)+3′</td>
<td>SEQ ID NO: 31/13</td>
</tr>
<tr>
<td>E-Box II−164</td>
<td>R/mtEBoxII(+60 nt)+3′</td>
<td>SEQ ID NO: 33/13</td>
</tr>
</tbody>
</table>

The PCR products generated in the first reaction were used as templates for the second PCR reaction using R/GUS3′ as primers (SEQ ID NO:73/13). The PCR products from the second reactions were purified and cloned into the pE:GUS vector to replace the E promoter with the same set of restriction sites. The resultant construct was named pE(ΔBoxII):GUS. The Box II element was re-introduced into pE(ΔBoxII):GUS using the same fusion PCR strategy as described above. To generate the E-Box II+11, E-Box II−9, E-Box II−17, E-Box II−58, E-Box II−63, E-Box II−74, E-Box II−79, E-Box II−100, E-Box II−116, E-Box II−147 and E-Box II−164 promoters, the first PCR reactions were carried out using the primer sets shown in the following Table 1:
BoxII, which indicates that the position of the Box II element in its native promoter is important.

Example 3
Effect of RF2a and RF2b on Expression of a Reporter Gene

As shown in FIG. 1, the E fragment of the RTBV promoter showed strong activity in tobacco BY-2 protoplasts, presumably because the BY-2 cell line contains RF2a- and RF2b-like transcription factors (Fukazawa et al., 2000). Nevertheless, the E fragment may be further stimulated by co-transfecting the BY-2 protoplasts with constructs that encode the RF2a and/or RF2b transcription factors. In this Example, the E fragment was activated in tobacco BY-2 protoplasts by co-transfection of E::GUS with CaMV::RF2b, CaMV 35S::RF2a and CaMV 35S::RF2a/CaMV::RF2b using methods well-known in the art. As shown in FIG. 5, the E fragment can be activated above a strong background expression by over-expression of RF2a and/or RF2b.

Example 4
Mutants of Box II

To investigate the possibility of reducing the background expression level in BY-2 protoplasts, the activities of certain Box II mutants (or “operational derivatives”), as shown in FIG. 6, were tested in BY-2 protoplasts. Specifically, the operational derivatives Box IIm1 (SEQ ID NO:2) and Box IIm2 (SEQ ID NO:3) were tested in the context of the E fragment (SEQ ID NO:63 and SEQ ID NO:64, respectively). The mutated promoters were ligated with the uidA coding sequence to create fusion genes, which are referred to herein as pE(Box IIm1)::GUS and pE(Box IIm2)::GUS. BY-2 protoplasts were then transfected with the pE(Box IIm1)::GUS and pE(Box IIm2)::GUS constructs. When the Box IIm1 and Box IIm2 elements were used, the GUS activity was decreased, and the GUS activity relative to the wild type Box II element (pE::GUS) dropped significantly (FIG. 7).

In the case of the chimeric sequence pE(Box IIm2)::GUS, there was little, if any, GUS activity above that of non-transfected BY-2 cells (FIG. 7). These data suggest that there are endogenous transcription factors in BY-2 cells that can interact with the wild type Box II element, which results in expression of pE::GUS in protoplasts (FIGS. 1, 2 and 7). When operational derivatives of the Box II element were used, e.g., Box IIm1 and Box IIm2, the promoter activity was significantly abolished.

Example 5
Binding Affinities of RF2a and RF2b

A previous report showed that RF2a binds to the Box II element and its mutants with different affinities (Yin et al., 1997). To compare the binding affinities of RF2a and RF2b with the Box II element and its mutants, real time Surface Plasmon Resonance (“SPR”) measurements were conducted using a BIAcore 2000 instrument. The binding affinities of RF2a and RF2b to these DNA targets were measured on chips on which biotin labeled-Box II, -Box IIm1 and -Box IIm2 elements were immobilized.

The association and dissociation constants were determined using BIAevaluation 3.1 software—using 1:1 binding with a mass transfer model. The results are presented in FIG. 8. In general, RF2a has relatively higher binding affinities to the Box II, Box IIm1 and Box IIm2 elements when compared to RF2b. Furthermore, the DNA binding behavior of RF2a and RF2b are quite different from each other. RF2a appears to bind rapidly to the DNA target and slowly dissociates from the target, while RF2b binds slowly to the DNA target and releases from the target relatively quickly. The differences in the affinity of RF2a to the Box II element and its mutants, however, are not as dramatic as the differences of RF2b, while the relative order of affinities to the different target elements is the same for both proteins (FIG. 8).

To illustrate the biological relevance of the differences in the binding affinities described above, the pE::GUS, pE(Box IIm1)::GUS and pE(Box IIm2)::GUS constructs were used as reporters in BY-2 protoplast transient assays. In these assays, CaMV 35S::RF2a, CaMV::RF2b and CaMV 35S::RF2a/ CaMV::RF2b were used as effectors. All results were normalized against the GFP internal control. The relative GUS activities of different sets of transfection assays are shown in FIG. 9 for the Box IIm1 element, and FIG. 10 for the Box IIm2 element.

When the foregoing constructs were co-transfected with CaMV 35S::RF2a, the promoter activity of E(Box IIm1) and E(Box IIm2) increased 5 to 7 fold (FIGS. 9 and 10). Furthermore, there was no apparent difference between the activation of promoters containing the Box IIm1 and Box IIm2 elements. Different results were observed when the foregoing constructs were co-transfected with CaMV::RF2b. The E(Box IIm2) promoter was activated about 5.8 fold by RF2b, while the E(Box IIm1) promoter was activated about 7 fold (FIGS. 9 and 10). Importantly, this Example shows that the activity of the E(Box IIm1) promoter with RF2b was as high as the expression of the E wild type promoter in BY-2 protoplasts.

The foregoing data related to the interactions between the RF2a and/or RF2b transcription factors and the target chimeric promoters suggest that such promoters may, optionally, be designed to comprise the Box IIm1 and/or Box IIm2 elements of the chimeric promoters, using compositions and methods described herein.

Example 6
Use of Box II and RF2a to Control Expression of Novel Chimeric Promoters

The following shows that the Box II element can be transferred to unrelated promoters, or promoter fragments, in a position dependent manner to control heterologous gene expression. To show that the Box II element is portable, Box II was fused with different lengths of the CaMV 35S promoter (FIG. 11). Specifically, the Box II element was fused to the 5' end of the chimeric promoters with a space of 7 nucleotides from the TATA box plus 1, 1.5, 3.0, 3.5, 5.0 and 5.5 “turns of DNA helix” (one turn = 10.4 base pairs). The chimeric promoters were then inserted into a cassette with the uidA coding sequencing and Nos terminator.

Construction of Plasmids Comprising the Box II Element and Different Lengths of the CaMV 35S Promoter—To construct Box II and CaMV 35S chimeric promoters, the Box II element was introduced into CaMV 35S promoter sequences of different lengths through PCR reactions using Pfu DNA polymerase (Stratagen Systems, Kirkland, Wis.). Forward
primes for the PCR reactions were designed to have a HindIII restriction site, followed by the Box II sequence, which was followed by part of the 5' CaMV promoter at desired positions (see FIG. 12 and Table 2 for specific primer sequences). The GUS 3' primer (SEQ ID NO:36) was used as reverse primer for all reactions.

The p35S-GUS plasmid was used as template in the foregoing reactions. In the p35S-GUS plasmid, a Ncol restriction site was located between the CaMV 35S promoter and the GUS coding sequence. Thus, a Ncol site was present in all PCR products. The PCR products were restricted with HindIII/NcoI to replace the E promoter through the same set of restriction sites. The constructed plasmids containing the chimeric promoters labeled 1 through 6 in Table 2 were named p-1.0hBoxII-48CaMV:GUS, p-1.5hBoxII-53CaMV:GUS, p-3.0hBoxII-69CaMV:GUS, p-3.5hBoxII-74CaMV:GUS, p-5.0hBoxII-90CaMV:GUS, and p-5.5hBoxII-95CaMV:GUS, respectively. The controls for this set of plasmids were generated using primer sets 1.5h-35CaMV-c (SEQ ID NO:37)/GUS3', -3.5h-74CaMV-c (SEQ ID NO:41)/GUS3', and -5.5h-95CaMV-c (SEQ ID NO:42)/GUS3', which products were cloned into pE:GUS with HindIII/NcoI to replace the E promoter. The derived plasmids/constructs were named p-5.3h-53CaMV:GUS, p-7.4h-74CaMV:GUS, and p-9.5h-95CaMV:GUS, respectively.

The foregoing constructs were then transfected into non-transgenic BY-2 protoplasts, and the resulting GUS activity determined. The data in FIG. 13 show that when the Box II element is fused with the CaMV 35S promoter with a space of 7 nucleotides from the TATA box plus one or more full turns of DNA helix (p.1.0hBoxII-48CaMV and p.5.0hBoxII-90CaMV), gene expression was dramatically stimulated, compared to reporter genes that lack Box II (p-48CaMV and p-90CaMV, respectively). The p.1.0hBoxII-48CaMV and p.5.0hBoxII-90CaMV constructs yielded 6.9 and 4.7 fold increases in expression level above p-48CaMV and p-90CaMV, respectively, which did not contain the Box II element.

In contrast, when the Box II element was fused to fragments of the CaMV 35S promoter at positions of 7 nucleotides from the TATA box plus multiples of 0.5 turns of DNA helix (p.1.5hBoxII-53CaMV versus p-53CaMV; p-3.5hBoxII-74CaMV versus p-74CaMV; and p-5.5hBoxII-95CaMV versus p-95CaMV), there was much less or no stimulation of gene expression. Of course, these results indicate that the Box II element, and its operational derivatives, can be used to control and/or enhance gene expression in unrelated promoters, preferably, when it is located approximately 7 nucleotides from the TATA box plus one or more full turns of DNA helix.

TABLE 2

<table>
<thead>
<tr>
<th>Promoter</th>
<th>Primer Set</th>
<th>5' Primer</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>-1.0hBoxII-48CaMV</td>
<td>1.0hBoxII-48CaMV/GUS 3' SEQ ID NO:37</td>
</tr>
<tr>
<td>2</td>
<td>-1.5hBoxII-53CaMV</td>
<td>1.5hBoxII-53CaMV/GUS 3' SEQ ID NO:38</td>
</tr>
<tr>
<td>3</td>
<td>-3.0hBoxII-69CaMV</td>
<td>3.0hBoxII-69CaMV/GUS 3' SEQ ID NO:39</td>
</tr>
<tr>
<td>4</td>
<td>-3.5hBoxII-74CaMV</td>
<td>3.5hBoxII-74CaMV/GUS 3' SEQ ID NO:40</td>
</tr>
<tr>
<td>5</td>
<td>-5.0hBoxII-90CaMV</td>
<td>5.0hBoxII-90CaMV/GUS 3' SEQ ID NO:41</td>
</tr>
<tr>
<td>6</td>
<td>-5.5hBoxII-95CaMV</td>
<td>5.5hBoxII-95CaMV/GUS 3' SEQ ID NO:42</td>
</tr>
</tbody>
</table>

To illustrate the regulatory effect of transcription factors RF2a and RF2b on the activity of the Box II element and novel chimeric promoters containing the Box II element, each plasmid/construct illustrated in FIG. 11 was tested in transgenic BY-2 protoplasts that produce RF2a, or RF2a plus RF2b. In these experiments, as shown in FIG. 14, the trend of promoter stimulation was consistent with that shown in non-transgenic BY-2 cells, i.e., activation of promoters that contain the Box II element at 7 nucleotides plus 1.0 and 5.0 helices distance from the TATA box was higher than that of the promoters in which the Box II element was placed 1.5, 3.5, and 5.5 helices distance from the TATA box. The total amount of GUS expression exhibited by the chimeric promoter constructs, however, was much greater in transgenic cell lines that produce elevated levels of RF2a (FIG. 14(A)), or RF2a plus RF2b (FIG. 14(B)), than in non-transgenic protoplasts that did not contain elevated levels of such proteins (compare the relative GUS expression levels in FIG. 14 to FIG. 13).

The foregoing data from BY-2 wild type and transgenic cell lines indicate that the Box II element, and its operational derivatives, is, preferably, imparted in a position and/or orientation dependent manner—as described above.

Example 7 Validation of Transient Assay Data From Tobacco BY-2 Protoplasts in Transgenic Arabidopsis

To evaluate the data presented above from the transient assays, binary vectors were built and transformed into Arabidopsis plants through Agrobacterium-mediated transformation. The set of binary vectors that were transformed into plants were constructs with different deletions of the RTBV promoter, which comprised the various portions of the E fragment described in Example 1; the E fragment containing either the Box IIa or Box IIb element; or the wild type E fragment (See FIG. 15A). In the transformed Arabidopsis plants, the activity of the chimeric promoters, which comprised the Box IIa or Box IIb element, was near the basal level of expression, which was observed for the construct p-E(32)::GUS, in which all the cis elements of RTBV promoter, which comprised the various portions of the E fragment described in Example 1; the E fragment containing either the Box IIa or Box IIb element; or the wild type E fragment (See FIG. 15A). In the transformed Arabidopsis plants, the activity of the chimeric promoters, which comprised the Box IIa or Box IIb element, was near the basal level of expression, which was observed for the construct p-E(32)::GUS, in which all the cis elements of RTBV promoter up-stream of the TATA box were removed (FIG. 15B).

Thus, the foregoing data agree with the data generated in the transient protoplasts analysis described in Example 5, wherein the chimeric promoters of the present invention may, for example, be designed to comprise the operational derivatives Box IIa and/or Box IIb to create a near "zero" background expression level in the absence of RF2a and/or RF2b.

Example 8 RF2a Mutants with Deletions of Functional Domains

It has been shown that the bZIP protein RF2a enhances transcription in vivo and in vitro. It is further known that the RF2a transcription factor comprises a proline-, acidic- and glutamine-rich domain. To analyze the function of each domain, mutants of RF2a were created by removing one or more of the foregoing putative domains as shown in FIG. 16(A). More particularly, mutants of RF2a were created in which the proline-rich domain was removed (RF2a-A).
glutamine-rich domain was removed (RF2a-ΔQ); the proline-rich and acidic domains were removed (RF2a-ΔPΔA); the proline- and glutamine-rich domains were removed (RF2a-ΔPΔQ); and the glutamine-rich, proline-rich and acidic domains were removed (RF2a-3A).

The coding sequence for each mutant was cloned into the bacterial expression vector pET28a, in which a His tag was placed at the N-terminus of the fusion protein. The derived plasmids were named pET-RF2a (encoding full-length RF2a), pET-RF2a-ΔP, pET-RF2a-ΔQ, pET-RF2a-ΔPΔA, pET-RF2a-ΔPΔQ, and pET-RF2a-3A.

Plasmid Construction for Protein Purification—The sequences encoding the foregoing mutants of RF2a were created through PCR amplification. A NdeI restriction site was added to the 5' end of all primers, and the ATG in the transcription start codon was in frame with the His tag in vector pET28a (Invitrogen Corp., Carlsbad, Calif.) and served as the restriction site. All of the mutations were verified by DNA sequence analysis. The derived plasmids were designated pET-RF2a, pET-RF2a-AP, pET-RF2a-AQ, pET-RF2a-APAA, pET-RF2a-APAQ, and pET-RF2a-3A.

From a complete RF2a-encoding sequence (SEQ ID NO:7), the ΔP fragment was amplified using primers RF2a-ΔP 5' and RF2a-ΔP 3'; ΔPΔA was amplified using primers RF2a-ΔPΔA 5' and RF2a-ΔPΔA 3'; and ΔPΔQ was amplified using primers RF2a-ΔP 5' and RF2a-ΔPΔQ 3'. The construction of pET-RF2a-3A and pET-RF2a were described by Petruccelli et al. (2001). All of the fragments were restricted with NdeI and BamHI and were cloned into pET28a through the same set of restriction sites. All of the mutations were verified by DNA sequence analysis. The derived plasmids were designated pET-RF2a-ΔP, pET-RF2a-AP, pET-RF2a-AQ, pET-RF2a-APAA, pET-RF2a-APAQ, and pET-RF2a-3A (encoding full-length RF2a) and pET-RF2a-3A.

Protein Purification—The pET28a-derived plasmids were transformed into *Escherichia coli* strain BL21 (DE3)pLysS for protein expression. Protein expression was induced with 0.5 mM isopropyl-β-D-thiogalactopyranoside at room temperature for 3 hours after the cell density reached A600 of ~0.6. The His-tagged proteins were purified according to procedures provided by Novagen, Inc. (Madison, Wis.) under non-denaturing conditions. The purified recombinant proteins were dialyzed in 1x phosphate-buffered saline with 20% glycerol to remove imidazole and stored at ~70° C.

The purified mutant proteins were then analyzed by SDS-PAGE to confirm that each protein was its expected size (FIG. 16(B)). To confirm that each of the mutant proteins bind to the DNA target, i.e., the Box II element and/or its operational derivatives, gel mobility shift assays were carried out with the purified recombinant proteins (FIG. 16(C)). The electrophoretic mobility shift assays were carried out essentially as described in Yin and Beachy (1995). 100 ng of proteins purified from the transformed E. coli were incubated with 32P-labeled Box IIml DNA probe followed by electrophoresis in a 5% acrylamide gel (Yin et al., 1997) (FIG. 16(C)). The data presented in FIG. 16(C) demonstrate that proteins ΔP (SEQ ID NO:68), ΔQ (SEQ ID NO:69), ΔPΔA (SEQ ID NO:70), ΔPΔQ (SEQ ID NO:71), and ΔA (SEQ ID NO:72) of RF2a bind to the Box IIml element.

**Example 9**

Contribution of RF2a Domains to Activity

The relative activity of RF2a and the RF2a mutants (described in Example 8) was then measured. First, a chimeric promoter was developed with a single copy of the Box II element fused to the 5' end of a minimal CaMV 35S promoter comprising nucleotides ~48 to +8 (SEQ ID NO:66). The chimeric promoter was ligated to the uidA coding sequence to create the reporter pBI1-48Ca::GUS.

To analyze the function of the several domains of RF2a, effectors were created by inserting coding sequences of RF2a or the mutants of RF2a (described in Example 8) downstream of the enhanced CaMV 35S promoter in the pMON9999 vector (a gift from Monsanto Company, St. Louis, Mo.). The resultant constructs, p35S::RF2a, p35S::RF2a-AP, p35S::RF2a-ΔP, p35S::RF2a-ΔQ, p35S::RF2a-ΔPΔA, p35S::RF2a-ΔPΔQ, and p35S::RF2a-3A, were co-transfected into BY-2 protoplasts with pBI1-48Ca::GUS (FIG. 17(A)). Plasmid pCat-GFP, in which the GFP gene was driven by CaMV 35S promoter, was co-introduced to serve as an internal control. The following describes, in greater detail, the construction of these vectors and the methods employed in transfecting the same into BY-2 protoplasts.

Plasmids for protoplast transfection—The coding sequences for mutants of RF2a were released from pET28a-derived plasmids and cloned into the plant expression vector pMON9999 (a gift from Monsanto Company, St. Louis, Mo.) to place each gene downstream of an enhanced CaMV 35S promoter, followed by a nopaline synthase terminator sequence. The resulting effector constructs were named p35S::RF2a, p35S::RF2a-AP, p35S::RF2a-ΔP, p35S::RF2a-ΔQ, p35S::RF2a-ΔPΔA, p35S::RF2a-ΔPΔQ, and p35S::RF2a-3A. The reporter gene construct, pBI1-48Ca::GUS, was built using PCR to introduce the Box II element into a minimal CaMV 35S promoter comprising nucleotides ~48 to +8 with primers BII-48Ca 5' (SEQ ID NO:53) (which contained the Box II element) and GUS 3' (SEQ ID NO:36) using a p35S::GUS plasmid as template. The PCR product was restricted with HindIII and NcoI, and the resulting fragment was inserted into p35S::GUS to replace the original 35S promoter.

Transfection of tobacco BY-2 protoplasts—The protoplasts were isolated from tobacco cell line BY-2 as described by Watanabe et al. (1987). Approximately one million protoplasts were transfected by electroporation with 20 µg of effector construct DNA, 15 µg of herring sperm DNA, 2.5 µg of reporter gene construct DNA, and 15 µg of pCai-GFP DNA. In samples with reporter gene alone, the total amount of DNA was adjusted by adding 20 µg of herring sperm carrier DNA. The electroporation parameters used were 300 V and 250 microfarads with the Bio-Rad electroporation system (Bio-Rad Laboratories, Hercules, Calif.). Protoplast samples were cultured in Murashige and Skoog medium with 0.4 M mannitol, pH 5.8, at 28° C. The protoplasts were collected 24 hours after electroporation.

As shown in FIG. 17(B), the transactivation function of RF2a was not decreased by removing either the proline-rich (35S::RF2a-AP) or glutamine-rich (35S::RF2a-ΔQ) domains or both of the domains (35S::RF2a-ΔPΔQ). In fact, the activation function of each of these mutants was greater than that of full-length RF2a. RF2a-AP was significantly different from RF2a at the P<0.05 level, whereas RF2a-ΔQ and RF2a-
Functions of RF2a Domains in Fusion Proteins

To determine whether domains of RF2a can serve as independent modules to regulate transcription, the various putative functional domains were fused with the synthetic 2C7 protein (SEQ ID NO: 75), a synthetic zinc finger DNA-binding domain that specifically binds to the 2C7 DNA-binding site (SEQ ID NO: 74), to create various "effector" constructs (FIG. 18(A)). The various RF2a domains were placed either at the N-terminus or the C-terminus of the 2C7 DNA-binding domain ("DBD"). The "reporter" construct pC7er2:GUS carried the uidA coding sequence located downstream of a chloramphenicol promoter comprising 6x2C7-binding sites ligated with the minimal promoter of erbB-2 ("er2"). p35S:2C7 encoded the 2C7 protein without an activation domain and served as a control (FIG. 18(A)).

To create effectors with RF2a domains fused to the N-terminus of 2C7 DBD, coding sequences for the acidic (A) (SEQ ID NO: 9), proline-rich (P) (SEQ ID NO: 54) and glutamine-rich (Q) (SEQ ID NO: 55) domains were amplified using primer pairs A-2C7 5'/A-2C7 3', P-2C7 5'/P-2C7 3', and Q-2C7 5'/Q-2C7 3', respectively, with pET-RF2a as template. BglII and BamHI restriction sites were introduced into the 5' and 3' primers, respectively. The particular sequences of the following primers are referenced in Table 4 below:

<table>
<thead>
<tr>
<th>Domain</th>
<th>Forward Primer 5'</th>
<th>Reverse Primer 3'</th>
</tr>
</thead>
<tbody>
<tr>
<td>A-2C7 5'</td>
<td>SEQ ID NO: 56</td>
<td></td>
</tr>
<tr>
<td>P-2C7 5'</td>
<td>SEQ ID NO: 58</td>
<td></td>
</tr>
<tr>
<td>Q-2C7 5'</td>
<td>SEQ ID NO: 60</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>5' Primer</th>
<th>3' Primer</th>
<th>Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>2C7</td>
<td>A-2C7</td>
</tr>
<tr>
<td>P</td>
<td>2C7</td>
<td>P-2C7</td>
</tr>
<tr>
<td>Q</td>
<td>2C7</td>
<td>Q-2C7</td>
</tr>
</tbody>
</table>

The products created by the foregoing PCR reactions were restricted with the BglII and BamHI and cloned into pMON9999 through BglII and EcoRI sites along with the DNA fragment that encoded the 2C7 DNA-binding domain (SEQ ID NO: 76). The 2C7 DNA-binding domain coding sequence was previously released from p35S::2C7 using BamHI and EcoRI. The resulting plasmids were designated p35S::2C7-A, p35S::2C7-P, and p35S::2C7-Q.

For effectors with RF2a domains at the C-terminus of the 2C7 DBD, coding sequences for the A, P, Q, and P plus A (PA) domains were released from pET-RF2a-A, pET-RF2a-P, pET-RF2a-Q, and pET-RF2a-PA using the enzymes XbaI and EcoRI and cloned into p35S:2C7-VP16 to replace the VP16 domain with the same restriction sites. The resultant plasmids were named p35S::2C7-A, p35S::2C7-P, p35S::2C7-Q, and p35S::2C7-PA.

Each of the foregoing effector constructs, as illustrated in FIG. 18(A), were co-transfected into BY-2 protoplasts along with the reporter construct. The relative GUS activities of the transfected protoplasts were subsequently determined. As shown in FIG. 18(B), when domains of RF2a were placed at the C-terminus of the 2C7 protein, 2C7-A and 2C7-PA showed significant activation function. When the domains were fused individually at the N-terminus of 2C7, the acidic domain (A-2C7) conferred stronger activation than the PP-2C7 or Q-Q-2C7 domains. The function of the acidic domain in the fusion proteins is consistent with its function in RF2a, although the position of this domain in the fusion proteins appears to affect its activity. The proline- and glutamine-rich domains had no effect on gene expression when they were placed at the C-terminus of the 2C7 DBD; however, these domains showed mild activation function when they were fused at the N-terminus of the 2C7 DBD.

Example 11

Impact of Mutants of RF2a on Plant Development

Previous studies have shown that transgenic rice and tobacco plants that overexpressed RF2a were normal in appearance and reproduction. (Yin et al., 1997; Petruccelli et al., 2001). To determine whether mutants of RF2a in which one or more domains were removed had a positive or negative effect on plant development, transgenic plants that overexpress mutants of RF2a were produced. Fifteen or more independent transgenic tobacco lines were developed with the constructs described below through Agrobacterium-mediated transformation.

Plasmids for Agrobacterium-mediated transformation—The fusion genes described above relating to the plant expression cassettes comprising RF2a deletion mutants were released from pMON9999-derived plasmids using NotI (blunted) and cloned into the binary vector pGA-E::GUS (Petruccelli et al., 2001) using the blunt HindIII site (downstream of a CaMV 35S promoter sequence). The final plasmids were named pGA-E::GUS/P-35S::AP, pGA-E::GUS/P-35S::AQA, and pGA-E::GUS/P-35S::APQA. A plasmid encoding full-length RF2a, p35S::RF2a, was also constructed using the methods described herein.

Tobacco transformation—the plasmids described above were introduced into Agrobacterium tumefaciens strain LBA4404 and used for tobacco transformation. Leaf discs from Nicotiana tabacum cv. Xanthi NN were transformed with the various plasmids following the protocol of Horsch et al. (1988). At least 15 independent transgenic lines were produced with each gene construct. Transgenic plants were self-fertilized, and T1 seeds were collected. The T1 seeds were germinated on Murashige and Skoog medium (Murashige and Skoog, 1962) with kanamycin (100 mg/L) selection, and Kan' seedlings were grown in a greenhouse for observation.

Following PCR analysis, transgenic lines expressing each mutant were observed for phenotypic changes. T1 generation plants with 35S::RF2a, 35S::RF2a-AP, 35S::RF2a-A, and 35S::RF2a-APQA did not exhibit abnormal phenotypes (FIG. 19(A)). However, 11 of 15 independent transgenic lines with 35S::RF2a-APQA exhibited mild to severe stunting with curved leaves and substantial delay in flowering times (FIGS. 19(A) & (B)). Furthermore, the intermodal elongation of transgenic plants was strongly repressed by RF2a-APQA (FIG. 19(C), Panel 1). The phenotype caused by 35S::RF2a-APQA was similar to, but less severe than, the phenotype caused by 35S::RF2a-3A. Cross-sections of the stem of transgenic plants with either 35S::RF2a-APQA or RF2a-3A showed that...
the xylem of stunted plants was not uniformly lignified and that phloem development was altered. (FIG. 19(C)).

To confirm that the phenotype was related to transgene expression, protein extracts of the transgenic plants were analyzed via a Western blot assay using an antibody against RF2a. Protein samples from the transgenic leaf tissues were extracted in buffer (50 mM Na$_2$PO$_4$, pH 7.0, 10 mM EDTA, 0.1% Triton X-100, 0.1% sodium lauryl sarcosine) and quantified using the DC protein assay kit (Bio-Rad Laboratories, Hercules, Calif.). 40 µg of such protein sample was separated via SDS-PAGE and blotted onto nitrocellulose membrane. The membrane was stained with Ponceau S (Sigma Chemical Company, St. Louis, Mo.) to monitor protein loading prior to immuno-detection. The primary antibody used in the immuno-detection was raised in rabbits against full-length RF2a; the secondary antibody was horseradish peroxidase-conjugated to goat anti-rabbit antibody (Southern Biotechnology Associates, Inc., Birmingham, Ala.). FIG. 20 shows that there is a direct correlation between the abnormal phenotype and the accumulation of RF2a-APAA.

Example 12

Versatility of the Gene Regulation System

As shown herein, the acidic domain of RF2a may be linked to any DNA binding domain to regulate the expression of corresponding promoters. More specifically, the novel transcription factors of the present invention that comprise the acidic domain of RF2a (or substantially similar sequences) and at least one DNA binding domain ("DBD"), may be used to regulate the expression of plant functional promoters that comprise one or more cis elements wherein such elements are capable of interacting with such DNA binding domain. The interaction between such novel transcription factors through such DNA binding domains with corresponding cis elements, preferably, results in the initiation, or enhancement of, transcription.

Similarly, the chimeric promoters of the present invention have been shown to regulate transcription in the presence of RF2a and/or RF2b. More particularly, the inventors have demonstrated that the Box II element and/or its operational derivatives (or substantially similar sequences) may be used in connection with any plant functional promoter to regulate gene expression. The interaction of RF2a, RF2b, and/or any novel transcription factor contemplated herein which comprises an amino acid sequence at least substantially similar to the acidic domain of RF2a. Accordingly, it is contemplated that a plurality of different combinations of novel transcription factors and/or novel chimeric promoters of the present invention may be employed to regulate gene expression.

For example, in addition to the Box II element and its operational derivatives described herein, the RF2a and RF2b transcription factors and related bZIP proteins) have been found to interact with certain additional cis elements to impart regulation of transcription. Non-limiting examples of such additional cis elements are summarized in Table 5 below:

<table>
<thead>
<tr>
<th>Common Name of cis Element</th>
<th>DNA Sequence</th>
<th>SEQ ID NO.</th>
</tr>
</thead>
<tbody>
<tr>
<td>rbe</td>
<td>CCCCAGCTGGAGGAT</td>
<td>SEQ ID NO:77</td>
</tr>
<tr>
<td>G3</td>
<td>TAAATCCGACTTGAGAAATG</td>
<td>SEQ ID NO:78</td>
</tr>
</tbody>
</table>

TABLE 6

| Class of DBD | Representative DBD | Sequence of DBD | cis Element |
|--------------|---------------------|----------------|
| bHLH         | "bHLH/Z domain of USF" - from H. Sapiens   | SEQ ID NO:84 | SEQ ID NO:85 |
| bZIP         | "Jun" - from H. Sapiens | SEQ ID NO:86 | SEQ ID NO:87 |
| Zinc-Finger  | "C2H2"               | SEQ ID NO:88 | SEQ ID NO:89 |
| E2F/DP       | "E2F4"               | SEQ ID NO:90 | SEQ ID NO:91 |

The present invention contemplates that such additional cis elements, including, without limitation, the elements referenced in Table 6, may be used to construct novel chimeric promoters in accordance with the present invention. Of course, such novel chimeric promoters may be used, for example, to regulate gene expression in connection with RF2a and/or RF2b transcription factors—similar to the chimeric promoters shown and described in previous Examples. It will be appreciated by those skilled in the art that chimeric promoters of the present invention, which comprise, for example, one or more of the additional cis elements listed in Table 5 (or substantially similar sequences), may be constructed and used in a manner similar to that described above with respect to chimeric promoters comprising Box II and/or its operational derivatives.

Still further, the present invention contemplates that the acidic domain of RF2a (SEQ ID NO:6); or substantially similar sequences, may be used with other DNA binding domains in the art. More particularly, the present invention contemplates that the acidic domain of RF2a, or substantially similar sequences, may be linked to any DNA binding domain from a plurality of classes of such domains to create novel transcription factors capable of regulating gene expression (which was demonstrated in Example 10). The invention provides, for example, that the following classes of DNA binding domains may be used in such capacity: (i) basic helix-loop-helix domains ("bHLH"); (ii) DNA binding domains of bZIP proteins; (iii) native or synthetic zinc finger DNA binding domains; and (iv) DNA binding domains of the E2F/DP family of transcription factors. Non-limiting examples of such DNA binding domains for each class are listed in Table 6 below. Additionally, Table 6 references the specific cis element with which such DNA binding domains are known to interact (and affect gene expression).

Many of the DNA binding domains and cognate cis elements referenced in Table 6 are described in the literature (among others). See, for example, Ferre-D’Amare, R. et al. (1994); Toledo-Ortiz, G. et al. (2003); Jakoby, M. et al.
domains referenced in Table 6 may be used to regulate the
transcription factors. The methods employed to produce such novel trans-
scription factors may parallel those described above with respect to the transcription factors comprising, for example, the 2C7 domain. Those of skill in the art, however, will appreciate that any number of methods may be used to express such novel transcription factors based on the amino acid sequences described herein.

The novel transcription factors of the present invention, which comprise, for example, one or more DNA binding domains referenced in Table 6 may be used to regulate the expression of appropriately designed chimeric promoters. More particularly, such transcription factors may be used to regulate the expression of chimeric promoters that comprise, for example, the corresponding cis element referenced in Table 6 (or substantially similar sequences). In light of the foregoing, it should be appreciated that the acidic domain of RF2a (or substantially similar sequences) may be linked to any DNA binding domain known in the art (including, without limitation, the domains listed in Table 6) to regulate the expression of corresponding promoters (which contain one or more cis elements that may interact with such DNA binding domain to regulate transcription).

Example 13

Use of Inducible Promoters with the Gene Expression System

The gene expression system of the present invention (including the chimeric promoters, gene expression cassettes, and novel transcription factors described above) may, optionally, be used in connection with a plurality of inducible promoters. In certain preferred embodiments, the present invention is used in connection with chemically-inducible promoters. The following provides a non-limiting example of such embodiments of the present invention.

Plasmid construction—The coding sequence of RF2a was released from a cassette comprising the CaMV 35S minimal promoter operably linked to a RF2a-encoding sequence, p35S::RF2a, through EcoRI/BamHI restriction. The excised DNA fragment was made blunt by Klenow treatment in the presence of dNTPs. The resulting fragment was then cloned into plasmid RH3 (Rohm & Haas, Philadelphia, Pa.) to replace a luciferase coding sequence. The RH3 plasmid originally comprised a luciferase coding sequence downstream of a chimeric promoter comprising Ga14 DNA binding sites operably linked to the uidA sequence.

RF2a sequence in pSL-5G35Sm:RF2a through Ndel (blunted)/BamHI restriction sites (pSL::GUS/5G35Sm: RF2a). The sequences encoding E:GUS, together with 5G35Sm:RF2a, were released from pSL-::GUS/5G35Sm: RF2a through HindIII restriction. The excised fragment was then blunt using Klenow treatment in the presence of dNTPs.

The excised GUS- and RF2a-encoding fragment was subsequently cloned into the binary vector pCa-5GRbm:DsRed-

Agrobacterium-mediated transformation—Arabidopsis transformation was conducted using the well-known dipping method described in Clough and Bent, 1998. More specifically, Agrobacterium GV3101 and pCa-EG2aV were cultured in LB medium and monitored by spectrophotometry. Once the optical density, OD, reached 0.6, the culture was collected via centrifugation. The bacterial cell pellet was re-suspended in 5% sucrose, 0.2% Silwet 77 solution and used for inoculating the flowering Arabidopsis plants. The transformed Arabidopsis seeds were collected at maturity and sterilized with 70% ethanol. The sterilized seeds were germinated on MS medium containing 50 mg/L of hygromycin B to select transgenic seedlings. The transgenic plants were grown to maturity and seeds were collected, which are referred to as T1种子. The T1 seeds were subsequently germinated and grown to maturity.

Induction of RF2a expression—RF2a expression was induced in the transgenic Arabidopsis plants described herein by application of a 1:8000 dilution of the pesticide Intrepid® 2F (Dow AgroSciences, Indianapolis, Ind.). The active ingredient in Intrepid® 2F pesticide is methoxyfenozide. The methoxyfenozide compound was found to enhance RF2a expression by interaction with the expressed VGE receptor and chimeric promoter comprising Ga14 DNA binding sites described above. Accordingly, the methoxyfenozide compound served as an expression-inducing ligand, which functioned to enhance expression of the RF2a-encoding sequence. Upon application of the methoxyfenozide compound, RF2a expression was induced, thereby allowing RF2a to interact with the Box II-containing E fragment, which was operably linked to the uidA sequence.

Analysis of GUS activity—The relative GUS activity in the transgenic Arabidopsis plants described herein was measured by histochemical analysis. In each of sixty-seven (67) T1 transgenic Arabidopsis plants carrying E::GUS, 5G35Sm: RF2a and Cs:VGE, the 1:8000 dilution of Intrepid® 2F described above was applied to one true leaf, while the other leaves in each plant remained untreated. Two days following the application of the expression-inducing ligand, the treated leaf together with one untreated leaf from the same plant were detached and subjected to GUS staining.

More particularly, the plant leaf tissues mentioned above were submerged in stain solution containing 1 mM oX-Gluc in 100 mM sodium phosphate buffer (pH 7.0), 2 mM KFe(CN)6, 2 mM KFe(CN)6, 0.1% Triton X-100 and 20% methanol (Petruccelli et al. 2001). In order to evaluate GUS activity, several substrates are available. The most commonly used are 5-bromo-4-chloro-3-indolyl glucuronide (X-Gluc) and 4-methylumbelliferyl-glucuronic acid (MUG). The reaction of GUS with X-Gluc generates a blue color that is useful in histochemical detection of uidA gene activity. uidA activity (GUS expression) is shown in the “Treated” leaf in FIG. 21.
by a grey, shaded color (compared to the predominately white, "Untreated" leaf). For quantification purposes, MUG is preferred, because the umbelliferyl radical emits fluorescence under UV stimulation, thus providing better sensitivity and easy measurement by fluorometry.

Following vacuum infiltration of the previously submerged leaf tissues, the tissues were incubated at 37° C. overnight before washing with 70% (v/v) ethanol. In approximately 70% of the sixty-seven (67) plants analyzed, a constitutive GUS expression pattern was observed in the methoxyfenozide-treated leaves. See FIG. 21 for a subjective comparison of GUS expression in "Treated" and "Untreated" leaf tissue.

Quantitative analysis of GUS activity in methoxyfenozide-treated plants was then conducted. T2 generation transgenic Arabidopsis plants from twelve T1 primary lines were selected on hygromycin selection medium. The lines are individually referred to herein as EGaV-3, EGaV-5, EGaV-17, EGaV-31, EGaV-50, EGaV-51, EGaV-56, EGaV-59, EGaV-63, EGaV-70, EGaV-72, and E:GUS. For each primary line, eighteen 14-day-old T2 plants were used. Nine plants, in three groups, were cultured in MS hydroponic solution containing various fragments of the acidic domain of RF2a were selected on hygromycin selection medium. The lines are individually referred to herein as EGaV-3, EGaV-5, EGaV-17, EGaV-31, EGaV-50, EGaV-51, EGaV-56, EGaV-59, EGaV-63, EGaV-70, EGaV-72, and E:GUS. For each primary line, eighteen 14-day-old T2 plants were used. Nine plants, in three groups, were cultured in MS hydroponic solution containing various fragments of the acidic domain of RF2a were selected on hygromycin selection medium. The lines are individually referred to herein as EGaV-3, EGaV-5, EGaV-17, EGaV-31, EGaV-50, EGaV-51, EGaV-56, EGaV-59, EGaV-63, EGaV-70, EGaV-72, and E:GUS. For each primary line, eighteen 14-day-old T2 plants were used. Nine plants, in three groups, were cultured in MS hydroponic solution containing various fragments of the acidic domain of RF2a were selected on hygromycin selection medium. The lines are individually referred to herein as EGaV-3, EGaV-5, EGaV-17, EGaV-31, EGaV-50, EGaV-51, EGaV-56, EGaV-59, EGaV-63, EGaV-70, EGaV-72, and E:GUS. For each primary line, eighteen 14-day-old T2 plants were used. Nine plants, in three groups, were cultured in MS hydroponic solution containing various fragments of the acidic domain of RF2a were selected on hygromycin selection medium. The lines are individually referred to herein as EGaV-3, EGaV-5, EGaV-17, EGaV-31, EGaV-50, EGaV-51, EGaV-56, EGaV-59, EGaV-63, EGaV-70, EGaV-72, and E:GUS. For each primary line, eighteen 14-day-old T2 plants were used. Nine plants, in three groups, were cultured in MS hydroponic solution containing various fragments of the acidic domain of RF2a were selected on hygromycin selection medium. The lines are individually referred to herein as EGaV-3, EGaV-5, EGaV-17, EGaV-31, EGaV-50, EGaV-51, EGaV-56, EGaV-59, EGaV-63, EGaV-70, EGaV-72, and E:GUS. For each primary line, eighteen 14-day-old T2 plants were used. Nine plants, in three groups, were cultured in MS hydroponic solution containing various fragments of the acidic domain of RF2a were selected on hygromycin selection medium. The lines are individually referred to herein as EGaV-3, EGaV-5, EGaV-17, EGaV-31, EGaV-50, EGaV-51, EGaV-56, EGaV-59, EGaV-63, EGaV-70, EGaV-72, and E:GUS. For each primary line, eighteen 14-day-old T2 plants were used. Nine plants, in three groups, were cultured in MS hydroponic solution containing various fragments of the acidic domain of RF2a were selected on hygromycin selection medium. The lines are individually referred to herein as EGaV-3, EGaV-5, EGaV-17, EGaV-31, EGaV-50, EGaV-51, EGaV-56, EGaV-59, EGaV-63, EGaV-70, EGaV-72, and E:GUS. For each primary line, eighteen 14-day-old T2 plants were used. Nine plants, in three groups, were cultured in MS hydroponic solution containing various fragments of the acidic domain of RF2a were selected on hygromycin selection medium. The lines are individually referred to herein as EGaV-3, EGaV-5, EGaV-17, EGaV-31, EGaV-50, EGaV-51, EGaV-56, EGaV-59, EGaV-63, EGaV-70, EGaV-72, and E:GUS. For each primary line, eighteen 14-day-old T2 plants were used. Nine plants, in three groups, were cultured in MS hydroponic solution containing various fragments of the acidic domain of RF2a were selected on hygromycin selection medium. The lines are individually referred to herein as EGaV-3, EGaV-5, EGaV-17, EGaV-31, EGaV-50, EGaV-51, EGaV-56, EGaV-59, EGaV-63, EGaV-70, EGaV-72, and E:GUS. For each primary line, eighteen 14-day-old T2 plants were used. Nine plants, in three groups, were cultured in MS hydroponic solution containing various fragments of the acidic domain of RF2a were selected on hygromycin selection medium. The lines are individually referred to herein as EGaV-3, EGaV-5, EGaV-17, EGaV-31, EGaV-50, EGaV-51, EGaV-56, EGaV-59, EGaV-63, EGaV-70, EGaV-72, and E:GUS. For each primary line, eighteen 14-day-old T2 plants were used. Nine plants, in three groups, were cultured in MS hydroponic solution containing various fragments of the acidic domain of RF2a were selected on hygromycin selection medium. The lines are individually referred to herein as EGaV-3, EGaV-5, EGaV-17, EGaV-31, EGaV-50, EGaV-51, EGaV-56, EGaV-59, EGaV-63, EGaV-70, EGaV-72, and E:GUS. For each primary line, eighteen 14-day-old T2 plants were used. Nine plants, in three groups, were cultured in MS hydroponic solution containing various fragments of the acidic domain of RF2a were selected on hygromycin selection media...
linked to a GFP-encoding sequence, and 10 µg of herring sperm DNA. The electroporation was conducted using a discharge of 500 µF and 250 V through disposable 0.4 cm cuvettes. Each transient assay was repeated three times per experiment and each experiment was conducted two times.

In addition, electroporation was carried out as described above without effector construct (negative control), without reporter construct (negative control); or, in place of effector construct, 35S-VP16 (a sequence encoding the activation domain of the herpes simplex virus) (positive control).

Quantification of GUS activity in the transfected protoplasts was carried out 24 hours after transfection. More specifically, transfected protoplasts were lysed by freezing and thawing in GUS extraction buffer (pH 7.7), centrifuged, and the supernatants used for GUS enzyme assays. GUS activity was determined by the method of Jefferson et al. (1987). GFP activity was determined by quantifying fluorescing using 490 nm excitation wavelength and 530 nm emission wavelength using a standard fluorometer (Molecular Devices, Sunnyvale, Calif.).

The relative GUS activity in the BY-2 protoplasts containing reporter and effector construct, as well as the controls described above, is shown in FIG. 23. The results shown in FIG. 23 include GUS enzyme activity compared with GFP activity and are expressed as relative fluorescent units per second. The results are the average of three independent transfections (with standard deviations). The results show that the acidic domain of RF2a is a strong activator of gene expression (35S-A-2C7) and, more specifically, fragments of the acidic domain comprising residues 49-96 of SEQ ID NO:4 (35S-A1-2C7) encompass the majority of such activity.

Example 15

Additional Fragments of the Acidic Domain of RF2a

The results of the previous Example 14 were confirmed in this Example 15 and, furthermore, the activity of two additional fragments of the RF2a acidic domain were measured. The 35S-A-2C7, 35S-A1-2C7, 35S-A2-2C7, and 35S-A3-2C7 effector constructs were prepared as described in Example 14 above. The two additional fragments tested in this Example comprised residues 49-84 (referred to herein as “35S-49/84-2C7”) and 56-84 (referred to herein as “35S-56/84-2C7”) of the full-length RF2a protein (SEQ ID NO:4). The 35S-56/84-2C7 construct was amplified from the plasmid template described in Example 14 using primer pairs containing the respective plasmid were used to transform Arabidopsis thaliana (Col-0) by the standard floral dip method (Clough and Bent, 1998). T1 seeds were germinated in Murashige and Skoog medium (Murashige and Skoog, 1962) containing glutamate ammonium (10 mg/L) and seedlings that survived

<table>
<thead>
<tr>
<th>Location within RF2a</th>
<th>FIG. 24(B) Reference</th>
<th>Example 14 Reference</th>
</tr>
</thead>
</table>

Additional Fragments of the Acidic Domain of RF2a

The effector constructs identified in Table 8 were electroporated into BY-2 protoplasts as described in Example 14 above (along with the “reporter constructs” described therein), with the exception that a discharge of 125 µF and 300V (through disposable 0.4 cm cuvettes) was used. Each transient assay was repeated three times per experiment and each experiment was conducted three times. Quantification of GUS activity was carried out as described in Example 14 above.

As shown in FIG. 24(B), the results confirm that the acidic domain of RF2a, and certain fragments thereof, represent strong activators of gene expression and, furthermore, that the fragment comprising residues 56-84 (relative to the full RF2a protein) produce an activation effect as strong as the full acidic domain.

Example 16

Expression Activation of the RF2a Acidic Domain in Plants

This Example further demonstrates that the acidic domain of RF2a may be transferred to unrelated proteins (e.g., DNA binding domains) and used to regulate gene expression in plants. In this example, effector constructs were prepared that comprised the CaMV 35S promoter operatively linked to a nucleic acid sequence (SEQ ID NO:9) encoding the acidic domain of RF2a (SEQ ID NO:6), which was operatively linked to a sequence encoding the synthetic 2C7 protein (SEQ ID NO:75). The reporter construct used in this Example included the minimal retinoblastoma promoter erbB, which comprised the 2C7 DNA-binding site (SEQ ID NO:74) (wherein the chimeric promoter is also referred to herein as “C7er”), operatively linked to the uidA gene (i.e., GUS-encoding sequence). The control construct used in this Example included the enhanced 35S promoter operably linked to the 2C7 zinc finger protein (without the acidic domain of RF2a or any fragment thereof).

The effector constructs are referred to in FIG. 26 as “C7erG/35S-A2C7” followed by the subject plant line, namely, 5-5, 9-8, 11-1, or 12-16. The control constructs are referred to in FIG. 26 as “C7erG/35S-2C7.” A second control, including only the reporter construct, is referred to as “C7er: G” (followed by the subject plant line) in FIG. 26.

The foregoing effector, reporter, and/or control constructs were transfected into Arabidopsis thaliana plants. More particularly, plasmids containing the effector, reporter, and/or control constructs were transferred by electroporation into A. tumefaciens strain GV3101. Agrobacterium isolates that contained the respective plasmid were used to transform A. thaliana Col-0 by the standard floral dip method (Clough and Bent, 1998). T1 seeds were germinated in Murashige and Skoog medium (Murashige and Skoog, 1962) containing glutamate ammonium (10 mg/L) and seedlings that survived

TABLE 8-continued

<table>
<thead>
<tr>
<th>Location within RF2a</th>
<th>FIG. 24(B) Reference</th>
<th>Example 14 Reference</th>
</tr>
</thead>
</table>

*Not shown in the previous Example 14.
the selection were grown in soil in a growth chamber. Leaves from six week old plants were collected for GUS expression analysis.

The leaves were homogenized, added to GUS extraction buffer, and subsequently centrifuged. The resulting supernatants were used to determine enzymatic activity by the method of Jefferson et al. (1987). The enzyme activity was determined by quantifying fluorescence using a spectrophuorometer (Spectramax Gemini, Molecular Devices Corp., Sunnyvale, Calif.), with a 365 nm excitation wavelength and 455 nm emission wavelength.

As shown in FIG. 26, the various effector constructs activated and/or enhanced GUS expression in the A. thaliana plants (relative to the C7erG/35S-2C7 controls). In addition, FIG. 26 shows that each plant line/effector construct combination produced variable results—albeit all well above the expression levels observed in the C7erG/35S-2C7 controls.

### Example 17

**RF2a Acidic Domain Fragments/Ecdysone Receptor Fusion Proteins**

In this Example, fragments of the RF2a acidic domain and the chimeric VGE receptor (SEQ ID NO:100) were used to create novel transcription factors. More particularly, the chimeric VGE receptor was mutated to replace the "V" domain with (i) the full acidic domain of RF2a, (ii) a minimal acidic domain of RF2a ("A5") (amino acids 56-84 relative to the full RF2a protein) (SEQ ID NO:101), or (iii) a dimer, trimer, or tetramer of the A5 minimal acidic domain (at the N- and C-termini, e.g., to create A5GE and GEA proteins). As used herein, the "V" domain of the VGE chimeric receptor refers to the VP16 acidic activation domain of the SV40 animal virus, "E" refers to the DNA binding domain of the Gal4 protein (from Bakers yeast), and "EcR" refers to the DNA binding domain of the Gal4 protein from Cloristoneura fumiferana. The GE domain is represented herein by SEQ ID NO:103 (and encoded by SEQ ID NO:105), while the E domain is represented by SEQ ID NO:104 (and encoded by SEQ ID NO:106).

FIG. 27(A) further shows a diagram of the reporter construct, namely, 5XG-35S:GUS, which was transformed into BY-2 protoplasts along with the effector constructs. As used herein, "5XG" is represented by SEQ ID NO:108 and refers to a pentamer tandem repeat of the nucleic acid sequence that is recognized by, and binds with, the Gal4 protein/domain (from Bakers yeast) (SEQ ID NO:107). "35S" refers to the minimal CaMV 35S promoter (−455 to +101). Of course, the GUS-encoding uidA sequence was operably linked to the CaMV 35S promoter.

Protoplasts were co-transfected, by electroporation as described in Example 14 above, with 5 µg of reporter construct DNA, 20 µg of a single effector construct, 5 µg of a 3SS- GFP plasmid, and 10 µg of herring sperm DNA. Methoxyfenozide ("MOF") was provided to the transformed protoplasts at a final dilution of 1:25,000 (providing a 2.452 µM final concentration of MOF). Quantification of GUS activity from protoplast extracts 24 hours after transfection was performed.

The results of such quantification are shown in FIG. 27(B), which are expressed as the amount of GUS enzyme activity compared with GFP activity—expressed as relative fluorescent units per second. The results are the average of three independent transfections+/−standard deviation. The presence of MOF is represented in FIG. 27(B) by "+I" (wherein "I" means Inducer), whereas the absence of MOF is represented by "–I". For example, "AGE+I" represents protoplasts transfected with the AGE effector construct and cultured in the presence of MOF, whereas "AGE–I" represents protoplasts transfected with the AGE effector construct and cultured in the absence of MOF.

As shown in FIG. 27(B), the fusion of the acidic domain of RF2a at the amino-terminal position of GE activates GUS expression in the presence of the MOF inducer. Although the activation provided by the RF2a acidic domain (and frag-
41

ments thereof) was not as strong as that of VP16, those skilled in the art will appreciate that the RF2a acidic domain (and fragments thereof) produced a level of activation that is, at least, comparable to that of VP16 (and induced less background).

In addition, as shown in FIG. 27(B), the presence of two tandem repeats of A5 had an activation effect as strong as the full acidic domain. Furthermore, as shown in FIG. 27(B), proteins having the RF2a acidic domain (or fragment thereof) at the N-terminus (e.g., AGE proteins) were shown to be more active than proteins having the RF2a acidic domain (or fragment thereof) at the C-terminus (e.g., GEA proteins).

Example 18

RF2a Acidic Domain/Ecdysone Receptor Fusion Proteins in Plants

In this Example, Arabidopsis thaliana Col-0 plants were transformed with Agrobacterium tumefaciens (strain GV3101) containing effector constructs comprising the CsVMV promoter operably linked to a nucleic acid sequence (SEQ ID NO:104) encoding the GE protein, plus (i) a nucleic acid sequence encoding the VP16 acidic activation domain of the herpes simplex virus, (ii) a sequence (SEQ ID NO:9) encoding the full RF2a acidic domain, or (iii) a sequence (2xSEQ ID NO:102) encoding a dimer of the A5 minimal acidic domain of RF2a (“A5A5”). The foregoing VP16 acidic domain-, RF2a acidic domain-, and A5A5 domain-encoding sequences were oriented to express such domains at the N-terminal of the GE protein. FIG. 28 refers to these constructs as VGE, AGE, and A5A5GE, respectively.

The foregoing effector constructs were prepared using standard DNA cloning and PCR procedures, and plasmids containing nucleic acid sequences encoding the VP16 acidic domain, the full length RF2a acidic domain (SEQ ID NO:6), the A5A5 domain (2xSEQ ID NO:101), and the GE domain (SEQ ID NO:103). Those of ordinary skill in the art will appreciate, however, that such effector sequences (and derivatives thereof) may also be constructed synthetically using standard procedures. The reporter construct described in Example 17 above, 5XG-35S:GUS, was used in this Example.

Table 10 below provides a summary of the various effector constructs, and the amino acid sequences thereof (from the N- to C-terminals), analyzed in this Example.

<table>
<thead>
<tr>
<th>Construct (FIG. 27)</th>
<th>Promoter</th>
<th>Novel Transcription Factor Sequence</th>
<th>Termination Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>VGE</td>
<td>CsVMV</td>
<td>SEQ ID NO:100</td>
<td>Nos</td>
</tr>
<tr>
<td>AGE</td>
<td>CsVMV</td>
<td>SEQ ID NO:6 (A) +</td>
<td>Nos</td>
</tr>
<tr>
<td>A5A5GE</td>
<td>CsVMV</td>
<td>(2 x SEQ ID NO:101 (A5)) +</td>
<td>Nos</td>
</tr>
</tbody>
</table>

Next, plasmids containing the effector and reporter constructs described above were transferred by electroporation into A. tumefaciens strain GV3101. Agrobacterium isolates that contained the respective plasmids were used to transform A. thaliana Col-0 using a standard floral dip method (Clough and Bent, 1998). Seeds from the T1 generation were collected and germinated in Murashige and Skoog medium, which contained hygromycin B (30 μg/mL). The seedlings that survived the selection were grown in soil in a growth chamber and allowed to self-fertilize. Next, T2 generation seeds were collected and germinated in Murashige and Skoog medium, which contained hygromycin B (30 μg/mL). The seedlings that survived the selection in a 3:1 segregation pattern were grown in soil in a growth chamber (under 12 hours of light/12 hours of dark per day, at 22° C., 50% humidity). The leaves were homogenized and added to GUS extraction buffer. The supernatants were analyzed for GUS enzymatic activity as described in Example 16 above.

FIG. 28 shows the relative GUS activity of each plant grown in the presence of MOF compared to the relative GUS activity of each plant grown in the absence of MOF. As shown in FIG. 28, the fusion of the acidic domain of RF2a to the amino-terminal position of the GE protein (“AGE”; middle graph), or the presence of two tandem repeats of A5 (“A5A5GE”; bottom graph), activated GUS expression in the presence of the MOF inducer as strong as VP16 (“VGE”; top graph).

Analysis of T1 Generation Plants—In this Example, 22 T1 plants were analyzed for methoxylenoxide (MOF) induced gene expression. More particularly, leaf samples from each of the 22 plants were taken before and after induction with MOF (MOF was applied by drenching the soil with a 1:10,000 dilution of MOF (61.3 μM of MOF) for 60 hours). The leaves were homogenized and added to GUS extraction buffer. The supernatants were analyzed for GUS enzymatic activity as described in Example 16 above.

The seedslings that survived the selection were grown in soil in a growth chamber and allowed to self-fertilize. Next, T2 generation seeds were collected and germinated in Murashige and Skoog medium, which contained hygromycin B (30 μg/mL). The seedlings that survived the selection in a 3:1 segregation pattern were grown in soil in a growth chamber (under 12 hours of light/12 hours of dark per day, at 22° C., 50% humidity).

Analysis of T1 Generation Plants—In this Example, 22 T1 plants were analyzed for methoxylenoxide (MOF) induced gene expression. More particularly, leaf samples from each of the 22 plants were taken before and after induction with MOF (MOF was applied by drenching the soil with a 1:10,000 dilution of MOF (61.3 μM of MOF) for 60 hours). The leaves were homogenized and added to GUS extraction buffer. The supernatants were analyzed for GUS enzymatic activity as described in Example 16 above.

The seedslings that survived the selection were grown in soil in a growth chamber and allowed to self-fertilize. Next, T2 generation seeds were collected and germinated in Murashige and Skoog medium, which contained hygromycin B (30 μg/mL). The seedlings that survived the selection in a 3:1 segregation pattern were grown in soil in a growth chamber (under 12 hours of light/12 hours of dark per day, at 22° C., 50% humidity).

The seedslings that survived the selection were grown in soil in a growth chamber and allowed to self-fertilize. Next, T2 generation seeds were collected and germinated in Murashige and Skoog medium, which contained hygromycin B (30 μg/mL). The seedlings that survived the selection in a 3:1 segregation pattern were grown in soil in a growth chamber (under 12 hours of light/12 hours of dark per day, at 22° C., 50% humidity). The leaves were homogenized and added to GUS extraction buffer. The supernatants were analyzed for GUS enzymatic activity as described in Example 16 above.


<table>
<thead>
<tr>
<th>SEQ ID NO</th>
<th>LENGTH</th>
<th>TYPE</th>
<th>ORGANISM</th>
<th>OTHER INFORMATION</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>15</td>
<td>DNA</td>
<td>Artificial</td>
<td>This sequence was artificially derived and/or created by the inventors.</td>
</tr>
<tr>
<td>3</td>
<td>15</td>
<td>DNA</td>
<td>Artificial</td>
<td>This sequence was artificially derived and/or created by the inventors.</td>
</tr>
<tr>
<td>4</td>
<td>368</td>
<td>PRT</td>
<td>Artificial</td>
<td>This sequence was artificially derived and/or created by the inventors.</td>
</tr>
</tbody>
</table>

**Sequence 1:**
```
ccagtgtgcc cctgg
```

**Sequence 2:**
```
ccagtgtgcc gctgg
```

**Sequence 3:**
```
ggagtgtgcc ccttc
```

**Sequence 4:**
```
Met Asn Arg Glu Lys Ser Pro Ile Pro Gly Asp Gly Gly Asp Gly Leu 1
  5 10 15
Pro Pro Gln Ala Thr Arg Arg Ala Gly Pro Pro Ala Ala Ala Ala 20
  25 30
Ala Glu Tyr Asp Ile Ser Arg Met Pro Asp Phe Pro Thr Arg Aen Pro 35
  40 45
Gly His Arg Arg Ala His Ser Glu Ile Leu Ser Leu Pro Glu Asp Leu 50
  55 60
Asp Leu Cys Ala Gly Gly Gly Gly Pro Ser Leu Ser Asp Glu 65
  70 75 80
Asp Glu Glu Leu Phe Ser Met Phe Leu Asp Val Glu Lye Leu Aen 85
  90 95
Ser Thr Cys Gly Ala Ser Ser Glu Ala Glu Ala Glu Ser Ser Ser Ala 100
  105 110
Ala Ala His Gly Ala Arg Pro Lye His Gin His Ser Leu Ser Met Asp 115
  120 125
Glu Ser Met Ser Ile Lys Ala Glu Leu Val Gly Ala Ser Pro Gly 130
  135 140
Thr Gly Met Ser Ser Ala Glu Ala Lye Lys Ala Val Ser Ala Val 145
  150 155 160
Lye Leu Ala Glu Leu Ala Leu Val Aep Pro Lye Arg Ala Lye Arg Ile 165
  170 175
Trp Ala Aen Arg Gin Ser Ala Ala Arg Ser Lye Glu Arg Lye Met Arg 180
  185 190
Tyr Ile Ala Glu Leu Glu Arg Lye Val Gin Thr Leu Gin Thr Glu Ala 195
  200 205
```
Thr Thr Leu Ser Ala Gln Leu Ala Leu Leu Gln Arg Asp Thr Ser Gly
Leu Thr Thr Glu Asn Ser Glu Leu Lys Leu Arg Leu Gln Thr Met Gln
Gln Gln Val His Leu Gln Asp Ala Leu Asp Thr Leu Lys Ser Gln
Val Gln Arg Leu Lys Val Ala Thr Gly Gln Met Ala Asn Gly Gly Gly
Met Met Met Asn Phe Gly Gly Met Pro His Gln Phe Gly Gly Asn Gln
Gln Met Phe Gln Asn Asn Gln Met Gln Ser Met Leu Ala Ala His
Gln Leu Gln Gln Leu Gln Leu His Pro Gln Ala Gln Gln Gln Val
Leu His Pro Gln His Gln Gln Gln Pro Leu His Pro Leu Gln Ala
Gln Gln Leu Gln Ala Ala Arg Asp Leu Lys Met Lys Ser Pro Met
Gly Gly Gln Ser Gln Trp Gly Asp Gly Ser Gly Ser Ser Gly Asn

<210> SEQ ID NO 5
<211> LENGTH: 329
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.
<400> SEQUENCE: 5
Ala Glu Leu Lys Ile Arg Leu Gln Ala Met Glu Gln Gin Ala Gin Leu
195 200 205
Arg Asp Ala Leu Asn Asp Ala Leu Lys Gin Leu Leu Arg Leu Lys
210 215 220
Leu Ala Thr Gly Glu Met Thr Asn Asn Glu Thr Tyr Ser Met Gly
225 230 235 240
Leu Gin His Val Pro Tyr Asn Thr Pro Phe Phe Pro Leu Ala Gin His
245 250 255
Asn Ala Ala Arg Gin Asn Gly Gly Thr Gin Leu Pro Pro Gin Phe Gin
260 265 270
Pro Pro Arg Pro Asn Val Pro Asn His Met Leu Ser His Pro Asn Gly
275 280 285
Leu Gin Asp Ile Met Gin Gin Asp Pro Leu Gly Arg Leu Gin Leu Leu
290 295 300
Asp Ile Ser Lys Gly Pro Leu Val Val Lys Ser Gin Ser Ser Ser Ser
305 310 315 320
Ser Ala Ser Gin Ser Ser Ser Thr Phe 325

<210> SEQ ID NO 6
<211> LENGTH: 67
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.
<400> SEQUENCE: 6
Met Gly His Arg Arg Ala His Ser Gin Ile Leu Ser Leu Pro Gin Gin
1 5 10 15
Leu Asp Leu Cys Ala Ala Gly Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
20 25 30
Glu Gin Asp Leu Leu Leu Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
35 40 45
Ser Ser Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
50 55 60
Ala Ala Ala
65

<210> SEQ ID NO 7
<211> LENGTH: 1107
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.
<400> SEQUENCE: 7
atgaacaggg agaaatcccc gatcccggga gacggcggcg acgggttgcc gccgcaggcc 60
acccgccggg cgggccctcc ggcggcggcg gcggcggcgg agtacgacat cagccgcatg 120
cggatttcc cgacgaggaa cccccggccac aggccgcgccc actccgagat cctgagcctc 180
cctgacctgtg cgcggccggc ggcggcgacg ggccgtcgct gtcggacgag 240
aacgacgagg agctcttctc catgttcctc gacgtggaga agctgaacag cacgtgcggg 300
gcgtcgtcgg aggcggaggc ggagtcgtcg tccgccgccg cccatggagc gaggccgaag 360
caccagcaca gcctgtccat ggatgagtcg atgtcgatca aggctgagga gctcgtcggg 420
gcgtcgcccg ggacggaggg gatgtcgtcg gcggaggcga agaaggcgct gtcgcgccgtc 480
atgggccaca ggcgcgccca ctccgagatc ctgagcctcc ccgaggacct cgacctgtgc
60
gcggccggcg gcggcgacgg gccgtcgctg tcggacgaga acgacgagga gctcttctcc
120
atgttcctcg acgtggagaa gctgaacagc acgtgcgggg cgtcgtcgga ggcggaggcg
180
gtgctgctg cgcgcgcgc c
201
<210> SEQ ID NO 10
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 10
ctctttatat actggagttc attatacact cttac
35
<210> SEQ ID NO 11
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 11
gtaagagtgt ataatgaact ccagtatata aggag
35
<210> SEQ ID NO 12
<211> LENGTH: 209
<212> TYPE: DNA
<213> ORGANISM: Rice tungro bacilliform virus
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 12
acgaatcaat aaagaaggac cagaagatat aaagctggaa catcttcaca tgctaccaca
60
tggctagcat ctttacttta gcatctctat tattgtaaga gtgtataatg accagtgtgc
120
cctgtgac tcgattataa ggagcaccag agtagtgtaa tagatcatcg atcaagcaag
180
cgagagctca aacctcttaag agagcaaga
209
<210> SEQ ID NO 13
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 13
gatctcaggg gttggggttt cta
23
<210> SEQ ID NO 14
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 14
tcattccaggg gcacactcgg atacactctt acaataa
37
<210> SEQ ID NO 15
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 15

tgatccagt gtgcccctgg aatgaactcc agtatat

<210> SEQ ID NO 16
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 16

atacaccagg ggcacactgg ctcttacaat aatagag

<210> SEQ ID NO 17
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 17

aagagccagt gtgcccctgg tgtataatga actccag

<210> SEQ ID NO 18
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 18

caataccagg ggcacactgg atagagatgc taaagta

<210> SEQ ID NO 19
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 19

tctatccagt gtgcccctgg tattgtaaga gtgtata

<210> SEQ ID NO 20
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 20

atagaccagy ggcacactgg gatgctaaag taaagat

<210> SEQ ID NO 21
<211> LENGTH: 37
<212> TYPE: DNA
ORGANISM: Artificial
FEATURE: OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQUENCE: 21
gcatccagt gtgcccctgg tctattattg taagagt

SEQ ID NO: 22
LENGTH: 37
TYPE: DNA
ORGANISM: Artificial
FEATURE: OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQUENCE: 22
tgctaccagg ggcacactgg gccatgtggt agcatgt

SEQ ID NO: 23
LENGTH: 37
TYPE: DNA
ORGANISM: Artificial
FEATURE: OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQUENCE: 23
atggcccagt gtgcccctgg tagcatcttt actttag

SEQ ID NO: 24
LENGTH: 37
TYPE: DNA
ORGANISM: Artificial
FEATURE: OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQUENCE: 24
gcatgccagg ggcacactgg tgaagatgtt ccagctt

SEQ ID NO: 25
LENGTH: 37
TYPE: DNA
ORGANISM: Artificial
FEATURE: OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQUENCE: 25
cttcacccagt gtgccccctgg cttctttatt gattcgt

SEQ ID NO: 26
LENGTH: 37
TYPE: DNA
ORGANISM: Artificial
FEATURE: OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQUENCE: 26
tggtocccagt ggcacactgg cttotttatt gattgt

SEQ ID NO: 27
LENGTH: 37
TYPE: DNA
ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 27
agaagccagt gtgcccctgg gaccagaaga tataaag

<210> SEQ ID NO 28
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 28
tgatcaaagc ttccagtgtg cccctggacg aatcaataaa gaag

<210> SEQ ID NO 29
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 29
tgatcaaagc ttccagtgtg cccctggacg aatcaataaa gaag

<210> SEQ ID NO 30
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 30
cctgcaggg gccacactgg gtgcctctta tatac

<210> SEQ ID NO 31
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 31
tagcagggag gccacactgg cagagtagtg taataga

<210> SEQ ID NO 32
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 32
ttcacctagg gcacactgg ctactctggt gcctcttt

<210> SEQ ID NO 33
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQ ID NO 1: agtacagt gtgccccctgg tgtaatatag catcgat
LENGTH: 37
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQ ID NO 2: ttgctccagg ggcacactgg tgatcgatga tctatta
LENGTH: 37
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQ ID NO 3: gatlaccagt gtgccccctgg agcaagcgag agctcaa
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQ ID NO 4: tgaatccagg ggcttgggttt cta
LENGTH: 44
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQ ID NO 5: tgaatccagg ggcttgggttt cta
LENGTH: 44
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQ ID NO 6: tgaatccagg ggcttgggttt cta
created by the inventors.

<400> SEQUENCE: 39
tgatcaaacg ttccaggtgct cccctgggac gcacaatccc acta

<210> SEQ ID NO 40
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 40
tgatcaaacg ttccaggtgc cccctggggg atgacgcaca atcc

<210> SEQ ID NO 41
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 41
tgatcaaacg ttccaggtgc cccctggagc ttccagtga caga

<210> SEQ ID NO 42
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 42
tgatcaaacg ttccaggtgc cccctggcct ttccagcgg taag

<210> SEQ ID NO 43
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 43
tgatcaaacg ttatccttcg caagaccct

<210> SEQ ID NO 44
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 44
tgatcaaacg ttgggatgac gcacaatcc
tgatcaagc tgtgtatct tccactgac

gccgcccata tggagaagat gaacagggag aaatcc

cgcggatcct cagttgccgc tgcttcctga

cgcggatcct cagtgtggca tgccaccgaa
<400> SEQUENCE: 51

tgatcaagc ttccagtgtg cccctggtcg caagaccctt cctc

<210> SEQ ID NO 52
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 52

gatttcacgg gttggggttt cta

<210> SEQ ID NO 53
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 53

tgatcaagc ttccagtgtg cccctggtcg caagaccctt cctc

<210> SEQ ID NO 54
<211> LENGTH: 48
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 54

Met Asn Arg Glu Lys Ser Pro Ile Pro Gly Asp Gly Asp Gly Leu 1 5 10 15
Pro Pro Gin Ala Thr Arg Arg Ala Gly Pro Pro Ala Ala Ala Ala 20 25 30
Ala Glu Tyr Asp Ile Ser Arg Met Pro Phe Pro Thr Arg Asn Pro 35 40 45

<210> SEQ ID NO 55
<211> LENGTH: 87
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 55

Met Gln Phe Gly Gly Asn Gln Gln Met Phe Gln Asn Asn Gln Ala Met 1 5 10 15
Gln Ser Met Leu Ala Ala His Gln Leu Gln Leu Gln Leu His Pro 20 25 30
Gln Ala Gln Gln Gln Gln Val Leu His Pro Gln His Gln Gln Gln Gln 35 40 45
Pro Leu His Pro Leu Gln Ala Gln Leu Gln Ala Ala Arg Asp 50 55 60
Leu Lys Met Lys Ser Pro Met Gly Gly Gln Ser Gln Trp Gly Asp Gly 65 70 75 80
Lys Ser Gly Ser Ser Gly Asn 85
<210> SEQ ID NO 56
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 56
gccagatcta tggccacag gcgcgccc

<210> SEQ ID NO 57
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 57
cgcggatcct ccatgggcgg cggcg

<210> SEQ ID NO 58
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 58
gccagatcta tgaacaggga gaaatcccc

<210> SEQ ID NO 59
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 59
cgcggatcctg gcggactctg agggag

<210> SEQ ID NO 60
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 60
gccagatcta tgaatctcgg agggaaccag c

<210> SEQ ID NO 61
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 61
cgcggatcctgc tcctgcgctgc tccctg
SEQ ID NO 62
LENGTH: 775
TYPE: DNA
ORGANISM: Rice tungro bacilliform virus
SEQUENCE:
agatcttctta caaagggag tagtaatat taatgagctt gaaggagat atcaaccttc 60
tccaggtttt atgagcacc ttatgtcct tgttttat aaaaasataaa acttcaaca 120
caggttccct gagggcctac gcgaatcctg tggaaaaaa cctcaagact ataatgcc 180
tgatcactc acctcttta ttaagggaga gattccctgc tggacacatc atgaataatg 240
aagagacaca cagagggga ccaacctata tattttcaag aatattcagt gttttctatg 300
cattacaca ttaagccacat acaacctgtaa gaattgggt gtaagctaaca 360
cagtgggaa aataggggrrt atgaagagca agggagaagt ttatactct caagatatac 420
taagattacc aagagcatgc atgggtcagag ccaacacat agtgagagca 480
aagttcttc acacatcata aagagagagc agttcctcgc atggaaaatg aatattcataa 540
aagtttcctc aaacaccacta ttaagtaagc acatcaataa agagacacag agatatataa 600
cgtgaacac tocctctggt accacatgac tagcctcttt acttttctt aatatatatt 660
gtaagagttt taagagctca tgtgcctcgc gactccagat atataagag caccagata 720
gtgaataagct catctgacat caaagggag agctcaactt ttaagagag caaga 775

SEQ ID NO 63
LENGTH: 209
TYPE: DNA
ORGANISM: Rice tungro bacilliform virus
SEQUENCE:
acgaatcaat aaagaaggac cagaagatat aaagctggaa catcttcaca tgctaccaca 60
tggctagcat ctttacttta gcatctctat tattgtaaga gtgtaataatg accggtgtgg 120
cggtggact cagatataa ggagacccag aagttctgtta tagatcctag tgtcaagcag 180
cgagagctcta aacccttcaag aaggaaga 209

SEQ ID NO 64
LENGTH: 209
TYPE: DNA
ORGANISM: Rice tungro bacilliform virus
SEQUENCE:
acgaatcaat aaagaaggac cagaagatat aaagctggaa catcttcaca tgctaccaca 60
tggctagcat ctttacttta gcatctctat tattgtaaga gtgtaataatg aggagtgtgc 120
ccttccact cagatataa ggagacccag aagttctgtta tagatcctag tgtcaagcag 180
cgagagctcta aacccttcaag aaggaaga 209

SEQ ID NO 65
LENGTH: 194
TYPE: DNA
ORGANISM: Artificial
FEATURE: OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.
SEQUENCE:
acgaatcaat aaagaaggac cagaagatat aaagctggaa catcttcaca tgctaccaca 60
tggctagcat ctttacttta gcatctctat tattgtaaga gtgtaataatg accggtgtgc 120
tataaggagc accagagtag tgtaatagat catcgatcaa gcaagcgaga gctcaaactt
180
taaggagc aaga
194

<210> SEQ ID NO 66
<211> LENGTH: 108
<212> TYPE: DNA
<213> ORGANISM: Cauliflower mosaic virus

<400> SEQUENCE: 66
ttgatgtgat aotccactg aogtaaggga tgacgcacaa tcccactatc cttcgcaaga 60
ccctcctct atataaggaa gttcatttca tttggagagg acacgctg
108

<210> SEQ ID NO 67
<211> LENGTH: 552
<212> TYPE: DNA
<213> ORGANISM: Cassava vein mosaic virus

<400> SEQUENCE: 67
ccagatgtga gcatcaagaa tccaatgttt acgggaaaaa ctatggaagt attatgtgag 60
tcagcaaga agcgacacga atatgcaac ttagtccaa aatgagaat 120
gtacagatgc aatcctcat atcgccagaa taacgaagag ataatctgaga aatggaaaaa 180
gaaagacacg gogaagaaaa aatgtggaa gaacttagga ctgcagcagaa caatggaaaaa 240
aagaagataa gctcgtgtat tgcagaagag atagagaga acacagtaag gttgaaatg 300
taagggcag aagacaccct atccacaaaa aatctccttt cccactactt atctttttat 360
atctttctt gcctttggtt ttcctttata aagatccacg ttcggcattt 420
gtgaaaaaca aaaaaaaaat ggtgtaagct attttctttg aagtactgag gatacaac 480
cagagaaact tgaaggagtt taatgttttt atgtttttata ataatagttgt tagtttgtt 540
tataaggagc gt 552

<210> SEQ ID NO 68
<211> LENGTH: 320
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 68
Met Gly His Arg Arg Ala His Ser Glu Ile Leu Ser Leu Pro Glu Asp
1 5 10 15
Leu Asp Leu Cys Ala Ala Gly Gly Gly Gly Pro Ser Leu Ser Asp
20 25 30
Glu Asn Asp Glu Leu Phe Ser Met Phe Leu Asp Val Glu Lys Leu
35 40 45
Asn Ser Thr Cys Gly Ala Ser Glu Ala Glu Ala Ser Ser Ser
50 55 60
Ala Ala Ala Gly Ala Gly Ala Arg Pro Lys His Glu His Ser Leu Ser Met
65 70 75 80
Asp Glu Ser Met Ser Ile Ala Glu Leu Val Gly Ala Ser Pro Gly
90 95
Thr Glu Gly Met Ser Ser Ala Glu Lys Lys Ala Val Ser Ala Val
100 105 110
Lys Leu Ala Glu Leu Ala Val Asp Pro Lys Arg Ala Lys Arg Ile
115 120 125
Trp Ala Asn Arg Gln Ser Ala Ala Arg Ser Lys Glu Arg Lys Met Arg
Trp Ala Asn Arg Gln Ser Ala Ala Arg Ser Lys Glu Arg Lys Met Arg
Tyr Ile Ala Glu Leu Glu Arg Lys Val Gin Thr Leu Gin Thr Glu Ala
Tyr Ile Ala Glu Leu Glu Arg Lys Val Gin Thr Leu Gin Thr Glu Ala
Thr Thr Leu Ser Ala Gin Leu Ala Leu Leu Gin Arg Asp Thr Ser Gly
Thr Thr Leu Ser Ala Gin Leu Ala Leu Leu Gin Arg Asp Thr Ser Gly
Leu Thr Thr Gln Asn Ser Gln Leu Lys Leu Arg Leu Gin Thr Met Glu
Leu Thr Thr Gln Asn Ser Gln Leu Lys Leu Arg Leu Gin Thr Met Glu
Gln Gln Val His Leu Gln Asp Ala Leu Asp Thr Leu Lys Ser Glu
Gln Gln Val His Leu Gln Asp Ala Leu Asp Thr Leu Lys Ser Glu
Val Gln Arg Leu Lys Val Ala Thr Gly Gin Met Ala Asn Gly Gly Gly
Val Gln Arg Leu Lys Val Ala Thr Gly Gin Met Ala Asn Gly Gly Gly
Met Met Met Asn Phe Gly Gly Met Pro His Gin Phe Gly Gly Asn Gin
Met Met Met Asn Phe Gly Gly Met Pro His Gin Phe Gly Gly Asn Gin
Gln Met Phe Gin Asn Gin Ala Met Gin Ser Met Leu Ala Ala His
Gln Met Phe Gin Asn Gin Ala Met Gin Ser Met Leu Ala Ala His
Gln Leu Gln Leu Gln Leu His Pro Gin Ala Gin Gin Gin Gin Val
Gln Leu Gln Leu Gln Leu His Pro Gin Ala Gin Gin Gin Gin Val
Leu His Pro Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Leu His Pro Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Gln Gin Leu Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Gln Gin Leu Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Gln Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Gly Gly Gin Ser Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Gly Gly Gin Ser Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
<210> SEQ ID NO 69
<211> LENGTH: 283
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or
<223> OTHER INFORMATION: This sequence was artificially derived and/or
created by the inventors.
<400> SEQUENCE: 69
Met Asn Arg Glu Lys Ser Pro Ile Pro Gly Asp Gly Asp Gly Leu
Met Asn Arg Glu Lys Ser Pro Ile Pro Gly Asp Gly Asp Gly Leu
Pro Pro Gin Ala Thr Arg Arg Arg Ala Gly Pro Pro Ala Ala Ala Ala
Pro Pro Gin Ala Thr Arg Arg Arg Ala Gly Pro Pro Ala Ala Ala Ala
Ala Glu Tyr Asp Ile Ser Arg Met Pro Asp Phe Pro Thr Arg Asn Pro
Ala Glu Tyr Asp Ile Ser Arg Met Pro Asp Phe Pro Thr Arg Asn Pro
Gly His Arg Arg Ala His Ser Glu Ile Leu Ser Leu Pro Glu Asp Leu
Gly His Arg Arg Ala His Ser Glu Ile Leu Ser Leu Pro Glu Asp Leu
Asp Leu Cys Ala Ala Gly Gly Gly Asp Gly Pro Ser Ser Leu Ser Asp Glu
Asp Leu Cys Ala Ala Gly Gly Gly Asp Gly Pro Ser Ser Leu Ser Asp Glu
Asp Asp Glu Gin Leu Gin Ser Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Asp Asp Glu Gin Leu Gin Phe Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Ser Thr Cys Gin Ala Ser Gin Gin Ala Gin Gin Gin Gin Gin Gin Gin Gin
Ser Thr Cys Gin Ala Ser Gin Gin Ala Gin Gin Gin Gin Gin Gin Gin Gin
Glu Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Glu Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Glu Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Glu Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Thr Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Thr Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Lys Leu Ala Gln Leu Leu Leu Leu Asp Gin Asp Gin Gin Gin Gin Gin Gin
Lys Leu Ala Gln Leu Leu Leu Leu Asp Gin Asp Gin Gin Gin Gin Gin Gin
Trp Ala Asn Arg Gin Ser Ala Ala Arg Ser Lys Glu Arg Lys Met Arg
Tyr Ile Ala Glu Leu Glu Arg Lys Val Gin Thr Leu Gin Thr Glu Ala
Thr Thr Leu Ser Ala Gin Leu Ala Leu Gin Arg Asp Thr Ser Gly
Leu Thr Thr Glu Asn Ser Glu Leu Lys Leu Arg Leu Gin Thr Met Glu
Gln Gin Val His Leu Gin Asp Ala Leu Asn Asp Thr Leu Lys Ser Glu
Val Gin Arg Leu Lys Val Ala Thr Gly Gin Met Ala Asn Gly Gly Gly
Met Met Met Asn Phe Gly Gly Met Pro His Gin

<210> SEQ ID NO 70
<211> LENGTH: 261
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 70
Met Ser Ser Ser Ala Ala His Gly Ala Arg Pro Lys His Gin His
Ser Leu Ser Met Asp Glu Ser Met Ser Ile Lys Ala Glu Glu Leu Val
Gly Ala Ser Pro Gly Thr Glu Gly Met Ser Ser Ala Glu Ala Lys Lys
Ala Val Ser Ala Val Lys Leu Ala Glu Leu Ala Val Asp Pro Lys
Arg Ala Lys Arg Ile Trp Ala Asn Arg Gin Ser Ala Arg Ser Lys
Glu Arg Lys Met Arg Tyr Ile Ala Glu Leu Glu Arg Lys Val Gin Thr
Leu Gin Thr Glu Ala Thr Thr Leu Ser Ala Gin Leu Leu Leu Gin
Arg Asp Thr Ser Gly Leu Thr Gin Gin Ser Gin Leu Lys Leu Arg
Leu Gin Thr Met Glu Gin Gin Val His Leu Gin Asp Ala Leu Gin Gin
Thr Leu Lys Ser Gin Val Gin Arg Leu Lys Val Ala Thr Gin Met
Ala Gin Gly Gin Met Met Gin Gin Ser Gin Gin Gin Gin Gin Gin Gin
Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin

-continued

Met Lys Ser Pro Met Gly Gly Gln Ser Gln Trp Gly Asp Gly Lys Ser
245 250 255
Gly Ser Ser Gly Asn
260

SEQ ID NO 71
LENGTH: 236
TYPE: PRT
ORGANISM: Artificial
OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQUENCE: 71
Met Gly His Arg Arg Ala His Ser Glu Ile Leu Ser Leu Pro Glu Asp
1 5 10 15
Leu Asp Leu Cys Ala Ala Gly Gly Asp Gly Pro Ser Leu Ser Asp
20 25 30
Glu Asn Asp Glu Glu Leu Phe Ser Met Phe Leu Asp Val Glu Lys Leu
35 40 45
Asn Ser Thr Cys Gly Ala Ser Ser Glu Ala Glu Ala Glu Ser Ser Ser
50 55 60
Ala Ala Ala His Gly Ala Arg Pro Lys His Gin His Ser Leu Met
65 70 75 80
Asp Glu Ser Met Ser Ile Lys Ala Glu Glu Leu Val Gly Ala Ser Pro
85 90 95
Gly Thr Glu Gly Met Ser Ser Ala Glu Lys Lys Ala Val Ser Ala
100 105 110
Val Lys Leu Ala Glu Leu Ala Leu Val Asp Pro Lys Arg Ala Lys Arg
115 120 125
Ile Trp Ala Asn Arg Gin Ser Ala Arg Ser Lys Glu Arg Lys Met
130 135 140
Arg Tyr Ile Ala Glu Leu Glu Arg Lys Val Gin Thr Leu Gin Thr Glu
145 150 155 160
Ala Thr Thr Leu Ser Ala Gin Leu Ala Leu Gin Arg Asp Thr Ser
165 170 175
Gly Leu Thr Thr Gin Gin Ser Leu Lys Leu Arg Leu Gin Thr Met
180 185 190
Glu Gin Gin Val His Leu Gin Gln Asp Leu Asn Asp Thr Leu Lys Ser
195 200 205
Glu Val Gin Arg Leu Lys Val Ala Thr Gin Met Ala Asn Gly Gly
210 215 220
Gly Met Met Met Asn Phe Gly Gly Met Pro His Gin
225 230 235

SEQ ID NO 72
LENGTH: 176
TYPE: PRT
ORGANISM: Artificial
OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQUENCE: 72
Met Ser Ser Ser Ala Ala Ala His Gly Ala Arg Pro Lys His Gin His
1 5 10 15
Ser Leu Ser Met Asp Glu Ser Met Ser Ile Lys Ala Glu Glu Leu Val
20 25 30
Gly Ala Ser Pro Gly Thr Glu Gly Met Ser Ser Ala Glu Ala Lys
35  40  45
Ala Val Ser Ala Val Lys Leu Ala Glu Leu Ala Leu Val Asp Pro Lys
50  55  60
Arg Ala Lys Arg Ile Trp Ala Asn Arg Gln Ser Ala Ala Arg Ser Lys
65  70  75  80
Glu Arg Lys Met Arg Tyr Ile Ala Glu Leu Glu Arg Lys Val Gin Thr
85  90  95
Leu Gln Thr Glu Ala Thr Thr Leu Ser Ala Gln Leu Ala Leu Leu Gln
100 105 110
Arg Asp Thr Ser Gly Leu Thr Thr Glu Ass Ser Glu Leu Lys Leu Arg
115 120 125
Leu Gln Thr Met Glu Gln Gln Val His Leu Gln Asp Ala Leu Ass Asp
130 135 140
Thr Leu Lys Ser Glu Val Gin Arg Leu Lys Val Ala Thr Gln Leu Met
145 150 155 160
Ala Asn Gly Gly Gly Met Met Met Asn Phe Gly Gly Met Pro His Gln
165 170 175

<210> SEQ ID NO 73
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.
<400> SEQUENCE: 73
ttcacacagg aaacagctat gac

<210> SEQ ID NO 74
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.
<400> SEQUENCE: 74
gcgtgggcgg cgtgggcg

<210> SEQ ID NO 75
<211> LENGTH: 172
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.
<400> SEQUENCE: 75
Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg
1  5  10  15
Phe Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr Gly
20  25  30
Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asp Phe Ser Arg Ser
35  40  46
Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Lys Pro Phe
50  55  60
Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys
65  70  75  80
Arg His Thr lys Ile His Thr Gly Glu Lys Pro Tyr Ala Cys Pro Val
Arg Ser Cys Asp Arg Arg Phe Ser Lys Ser Ala Asp Leu Lys Arg His
Ile Arg Ile His Thr Gly Gin Lys Pro Phe Gin Cys Arg Ile Cys Met
Arg Asn Phe Ser Arg Ser Asp His Leu Thr Thr His Ile Arg Thr His
Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala
Arg Ser Asp Glu Arg Lys Arg His Thr lys Ile His

<210> SEQ ID NO 76
<211> LENGTH: 516
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.
<400> SEQUENCE: 76
atgcctgagc tcccctatgc ttgccctgtc gagtcctgcg atcgccgctt ttctaagtcg
60
gctgatctga agcgccatat ccgcatccac acaggccaga agcctttcca gtgtcgaata
120
tgcgtctgta tagtgcaccac cttacccac acacccgac ccacacagcc
180
gagaagcctt ttgcctgtga catttgtggg aggaagtttg ccaggagtga tgaacgcaag
240
aggcatacca aatctatcct ccctatgctt gccctgtcga gtcctgcgat
300
cgccgctttt ctaagtcggc tgatctgaag cgccatatcc gcatccacac aggccagaag
360
cccttccagt gtcgaatatg catgcgtaac ttcagtcgta gtgaccacct taccacccac
420
atccgcaccc acacaggcga gaagcctttt gcctgtgaca ttttgtgggag gaagtttgcc
480
aggagtgatg aacgcaagag gcataccaaa atccat
516

<210> SEQ ID NO 77
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.
<400> SEQUENCE: 77
ccccaaagtc cagcttgaaa t
21

<210> SEQ ID NO 78
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.
<400> SEQUENCE: 78
ttaatccaac ttggaaaatg
20

<210> SEQ ID NO 79
<211> LENGTH: 11
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQUENCE: 79
ccacaccacc

SEQ ID NO: 80
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQUENCE: 80
ttcaccacc cact

SEQ ID NO: 81
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQUENCE: 81	tggacctac ca

SEQ ID NO: 82
LENGTH: 13
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQUENCE: 82	aggtacccc att

SEQ ID NO: 83
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQUENCE: 83	tggatatgga agacagca

SEQ ID NO: 84
LENGTH: 65
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQUENCE: 84
Met Asp Glu Lys Arg Arg Ala Gln His Asn Glu Val Glu Arg Arg Arg Arg Asp Lys Ile Asn Asn Trp Ile Val Gln Leu Ser Lys Ile Ile Pro

Arg Ser Ser Met Glu Ser Thr Lys Ser Gly Gln Ser Lys Gly Gly Ile

35 40 45
Leu Ser Lys Ala Ser Asp Tyr Ile Glu Leu Arg Gln Ser Asn His
50 55  60
Arg
65

<210> SEQ ID NO 85
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQ ID NO 85
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 85

CACCGTCA CGTGGCCTAC

21

<210> SEQ ID NO 86
<211> LENGTH: 62
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQ ID NO 86
<211> LENGTH: 62
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 86

LYS ALA GLU ARG LYS ARG MET ARG ASN ARG ILE ALA ALA SER LYS SER 1 5 10 15
ARG LYS ARG LYS LEU GLU ARG ILE ALA ARG LEU GLU GLU LYS VAL LYS 20 25 30
THR LEU LYS ALA GLN ASN SER GLU LEU ALA SER THR ALA ASN MET LEU 35 40 45
ARG GLU GLN VAL ALA GLN LEU LYS GLN LYS VAL ASN HIS 50 55  60

<210> SEQ ID NO 87
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQ ID NO 87
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 87

CGTGATGAC GTCATCGACG

20

<210> SEQ ID NO 88
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQ ID NO 88
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 88

MET GLU ARG PRO TYR ALA CYS PRO VAL GLU SER CYM ASP ARG ARG PHE 1 5 10 15
SER GLN LYS THR ASN LEU ASP THR HIS ILE ARG ILE HIS THR GLY GLN 20 25 30
LYS PRO PHE GLN CYM ARG ILE CYM MET ARG ASN PHE SER GLN HIS THR 35 40 45
GLY LEU ASN GLN HIS ILE ARG THR HIS THR GLY GLU LYS PRO PHE ALA 50 55  60
CYS ASP ILE CYM GLY ARG LYS PHE ALA THR LEU HIS THR ARG ASP ARG

CYS ASP ILE CYM GLY ARG LYS PHE ALA THR LEU HIS THR ARG ASP ARG
His Thr Lys Ile His Leu Arg Gln Lys Asp
85
90

<210> SEQ ID NO 89
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 89
gacgctataa aaggag

<210> SEQ ID NO 90
<211> LENGTH: 76
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 90
Pro Pro Gly Thr Pro Ser Arg His Glu Lys Ser Leu Gly Leu Leu Thr 1 5 10 15
Thr Lys Phe Val Ser Leu Leu Gln Glu Ala Lys Asp Gly Val Leu Asp 20 25 30
Leu Lys Leu Ala Ala Asp Thr Leu Ala Val Arg Gln Lys Arg Arg Ile 35 40 45
Tyr Asp Ile Thr Asn Val Leu Glu Gly Ile Gly Leu Ile Glu Lys Lys 50 55 60
Ser Lys Asn Ser Ile Gln Trp Lys Gly Val Gly Pro 65 70 75

<210> SEQ ID NO 91
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 91
atttccgagc ggtttt

<210> SEQ ID NO 92
<211> LENGTH: 163
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

<400> SEQUENCE: 92
gctcgaggaga cagctactcg ctcgaggac agtactcgcg tgcgggaca gtactcgcg
cggagacagt acctcgcctcg gagagcagta ctcgatcgcg tagatctgca agacccctcc
tctatataag gaagttcatt tcatttggag aggacacgct gaa

<210> SEQ ID NO 93
<211> LENGTH: 2595
<212> TYPE: DNA
<213> ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: This sequence was artificially derived and/or created by the inventors.

SEQUENCE: 93

atggcccccc cgaccgaagt gacgcctgggg gccgaacgctgg 60
ggcctgtgct gccgttggct ggacgaactgg gaccgaacgctgg 120
tccccagctt ccgcgcttgg gacgcctgggg gccgaacgctgg 180
gacgccgct ggacgcttcg gtggcctgggg gccgaacgctgg 240
cctccagctt cccggcctgg gacgcctgggg gccgaacgctgg 300
tctatcgcga aagcggacct tttctgccct ccacacacaagcggctgg 360
cgcgcgcgc cggcgcgcgc cggcgcgcgc cggcgcgcgc 420
tagctctctct cggcgcgcgc cggcgcgcgc cggcgcgcgc 480
ttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtg
gttctggtcg cgaacaacca agcgtacact cgcgacaact accgcaaggc tggcatggcc 2280
tacgtcatcg aggatctact gcacctctgc cgggtcatgt actctatggc gttggacaac 2340
atcattacg cgctgctcac ggctgtcgtc atcttttctg acocgcaccg gttgagcacg 2400
cgccactgg tgtgaagat ccagcggtac tacctgaata cgctgctaat etatatcttg 2460
acocgcactg tcgggtcggc gtctgtcgtc gtctcctac acacagatct ccagctcctc 2520
tctgagctac gcacgctcgg catgcaaaac tccaacatgt gcatctccct caagctcaag 2580
aaccacaaac tgtaa 2595

<210> SEQ ID NO 94
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer sequence that hybridizes to the coding sequence for the synthetic 2C7 zinc finger protein
<400> SEQUENCE: 94
gccagatcta tgggccacag gcgcgccc

<210> SEQ ID NO 95
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer sequence that hybridizes to the coding sequence for the synthetic 2C7 zinc finger protein
<400> SEQUENCE: 95
cgcggatcct ccatgggcgg cggcg

<210> SEQ ID NO 96
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer sequence that hybridizes to the coding sequence for the synthetic 2C7 zinc finger protein
<400> SEQUENCE: 96
cgcagatcta tggagatcct gagcctcccc

<210> SEQ ID NO 97
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer sequence that hybridizes to the coding sequence for the synthetic 2C7 zinc finger protein
<400> SEQUENCE: 97
cgcagatcta tggagatcct gagcctcccc

<210> SEQ ID NO 98
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer used to amplify sequence from rice (Oryza sp.)
<400> SEQUENCE: 98
cgcagatcta tggagatcct gagcctcccc
<210> SEQ ID NO 99
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer used to amplify sequence from Rice (Orzyza sp.)

<400> SEQUENCE: 99

cggcatgcc tcctcgtcgt tcctcgtc 27

<210> SEQ ID NO 100
<211> LENGTH: 584
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric VGE receptor, comprising the acidic domain of the SV40 virus (Simian virus 40), the Gal4 protein from Baker's yeast (Salmonella sp.), and the ecdysone receptor of Chloristoneura fumiferana

<400> SEQUENCE: 100

Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
  1   5   10   15
Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Phe Asp
  20 25 30
Leu Asp Met Leu Gly Asp Gly Ser Pro Gly Pro Gly Phe Thr Pro
  35 40 45
His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
  50 55 60
Glu Glu Met Phe Thr Asp Ala Leu Gly Ile Asp Gly Tyr Gly Gly Lys
  65 70 75 80
Leu Leu Gly Thr Ser Arg Arg Ile Ser Gly Gly Phe Gly Gly Met
  85 90 95
Lys Leu Leu Ser Ser Gly Ala Cys Asp Ile Cys Arg Leu Lys
 100 105 110
Lys Leu Lys Cys Ser Lys Gly Lys Pro Lys Cys Ala Lys Cys Leu Lys
 115 120 125
Asn Asn Trp Glu Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro Leu
 130 135 140
Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu Glu
 145 150 155 160
Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile Leu
 165 170 175
Lys Met Asp Ser Leu Glu Asp Ile Lys Ala Leu Thr Gly Leu Phe
 180 185 190
Val Gln Asp Glu Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala Ser
 195 200 205
Val Glu Thr Asp Met Pro Leu Thr Leu Arg Glu His Arg Ile Ser Ala
 210 215 220
Thr Ser Ser Ser Glu Ser Ser Asn Lys Gly Glu Arg Glu Leu Thr
 225 230 235 240
Val Ser Gly Glu Ser Arg Ile Ser Trp Pro Glu Cys Val Val Pro
 245 250 255
Glu Thr Gln Cys Ala Met Lys Arg Lys Glu Lys Lys Ala Glu Lys Glu
 260 265 270
Lys Asp Lys Leu Pro Val Ser Thr Thr Val Asp Asp His Met Pro
Pro Ile Met Gin Cys Glu Pro Pro Pro Pro Glu Ala Ala Arg Ile His
Glu Val Val Pro Arg Phe Leu Ser Asp Lys Leu Leu Glu Thr Asn Arg
Gln Lys Asn Ile Pro Gin Leu Thr Ala Asn Gin Gin Phe Leu Ile Ala
Arg Leu Ile Trp Tyr Gin Asp Gly Tyr Glu Gin Pro Ser Asp Glu Asp
Leu Lys Arg Ile Thr Gin Thr Trp Gin Gin Ala Asp Asp Glu Asn Glu
Glu Ser Asp Thr Pro Phe Arg Gin Ile Thr Glu Met Thr Ile Leu Thr
Val Gin Leu Ile Val Gin Ala Gly Leu Pro Gly Phe Ala Lys
Ile Ser Gin Pro Asp Gin Ile Thr Leu Lys Ala Phe Ser Ser Glu
Val Met Met Leu Arg Val Ala Arg Arg Tyr Asn Ala Ser Asp Ser
Val Leu Phe Ala Asn Gin Gin Ala Tyr Thr Arg Asp Asn Tyr Arg Lys
Ala Gly Met Ala Tyr Val Ile Gin Leu Asp Leu His Phe Cys Gin Gin
Met Tyr Ser Met Ala Leu Asp Asn Ile Thr Ala Leu Leu Thr Ala
Val Val Ile Phe Ser Gin Ser Phe Gin Leu Glu Gin Pro Gin Leu Val
Glu Gin Ile Gin Gin Tyr Tyr Leu Gin Thr Leu Arg Gin Gin Gin Gin
Asp Gin Leu Ser Gin Ser Ala Arg Ser Ser Gin Gin Gin Gin Gin Gin
Leu Ser Ile Leu Ser Gin Ser Gin Gin Gin Gin Gin Gin Gin Gin Gin
Met Cys Ile Ser Gin Leu Lys Leu Gin Gin Thr Gin Gin Gin Gin Gin
Glu Gin Ile Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Ile Leu Glu Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin

<210> SEQ ID NO 101
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Oryza sp.

Glu Ile Leu Ser Leu Pro Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
Gly Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin

<210> SEQ ID NO 102
<211> LENGTH: 87
<212> TYPE: DNA
<213> ORGANISM: Oryza sp.
<table>
<thead>
<tr>
<th>Residue</th>
<th>Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Lys Leu Leu Ser Ser Ile Glu Glu Ala Cys Asp Ile Cys Arg Leu Lys</td>
</tr>
<tr>
<td>5</td>
<td>Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys</td>
</tr>
<tr>
<td>10</td>
<td>Asn Asn Asn Asn Asn Trp Glu Cys Arg Tyr Ser Arg Ser Lys Thr Lys Thr Arg Ser Arg Ser Lys</td>
</tr>
<tr>
<td>15</td>
<td>Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu Glu</td>
</tr>
<tr>
<td>20</td>
<td>Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile Leu</td>
</tr>
<tr>
<td>25</td>
<td>Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu Phe</td>
</tr>
<tr>
<td>30</td>
<td>Val Gln Asp Thr Val Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala Ser</td>
</tr>
<tr>
<td>35</td>
<td>Val Glu Thr Asp Arg Met Pro Leu Thr Leu Arg Glu His Arg Ile Ser Ala</td>
</tr>
<tr>
<td>40</td>
<td>Thr Ser Ser Ser Glu Ser Ser Ser Tyr Ser Lys Gly Gin Arg Gin Leu Thr</td>
</tr>
<tr>
<td>45</td>
<td>Val Ser Gly Gin Ser Arg Ile Ser Trp Pro Glu Cys Val Val Pro</td>
</tr>
<tr>
<td>50</td>
<td>Glu Thr Gin Cys Ala Met Lys Arg Lys Ala Gln Lys Glu</td>
</tr>
<tr>
<td>55</td>
<td>Lys Asp Tyr Leu Pro Val Ser Thr Thr Thr Thr Val Asp Asp His Met Pro</td>
</tr>
<tr>
<td>60</td>
<td>Pro Ile Met Gin Cys Gin Pro Pro Pro Pro Glu Ala Ala Arg Ile His</td>
</tr>
<tr>
<td>65</td>
<td>Glu Val Val Pro Arg Phe Leu Ser Ser Lys Leu Leu Lys Glu Thr Asn Arg</td>
</tr>
<tr>
<td>70</td>
<td>Gln Lys Asn Ile Pro Gin Leu Thr Ala Asn Gin Gln Phe Leu Ile Ala</td>
</tr>
<tr>
<td>75</td>
<td>Arg Leu Ile Trp Tyr Gin Asp Gly Thr Glu Glu Pro Ser Asp Glu Asp</td>
</tr>
<tr>
<td>80</td>
<td>Leu Lys Arg Ile Thr Gin Thr Trp Gin Gin Ala Asp Gin Arg Glu</td>
</tr>
<tr>
<td>85</td>
<td>Glu Ser Asp Thr Pro Phe Arg Gin Ile Thr Glu Met Thr Ile Leu Thr</td>
</tr>
<tr>
<td>90</td>
<td>Glu Gin Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Gly Phe Ala Lys</td>
</tr>
<tr>
<td>95</td>
<td>Lys Ser Gin Pro Asp Gin Ile Thr Leu Leu Lys Ala Phe Ser Ser Glu</td>
</tr>
<tr>
<td>100</td>
<td>Val Met Met Leu Arg Val Ala Arg Arg Tyr Asp Ala Ala Ser Asp Ser</td>
</tr>
</tbody>
</table>

**SEQ ID NO**: 103
**LENGTH**: 488
**TYPE**: PRT
**ORGANISM**: Artificial
**FEATURE**: A combination of the Ga4 protein and Ecdysone receptor
Val Leu Phe Ala Asn Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys  
340  345  350
Ala Gly Met Ala Tyr Val Ile Glu Leu Leu His Phe Cys Arg Cys  
355  360  365
Met Tyr Ser Met Ala Leu Asp Asn Ile His Tyr Ala Leu Leu Thr Ala  
370  375  380
Val Val Ile Phe Ser Arg Pro Gly Leu Glu Gin Pro Gin Leu Val  
385  390  395  400
Glu Glu Ile Gin Arg Tyr Tyr Leu Arg Ile Tyr Ile Leu  
405  410  415
Asn Gin Leu Ser Gly Ser Ala Arg Ser Ser Val Ile Tyr Gly Lys Ile  
420  425  430
Leu Ser Ile Leu Ser Glu Arg Thr Leu Gin Met Gin Ann Ser Ann  
435  440  445
Met Cys Ile Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu  
450  455  460
Glu Glu Ile Trp Asp Val Ala Asp Met Ser His Thr Gin Pro Pro  
465  470  475  480
Ile Leu Gin Ser Pro Thr Ann Leu  
485

<210> SEQ ID NO 104
<211> LENGTH: 1464
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Nucleic acid sequence encoding SEQ ID NO:103 (a combination of the Gal4 protein and ecdysone receptor)
<400> SEQUENCE: 104

aagctactgc cttctatcga acaagcatgc gatatttgcc gacttaaaaa gctcaagtgc  
60
tccaaagaaa aaccgaagtg cgccaagtgt ctgaagaaca actgggagtg tcgctactct  
120
tccaaccgcc aaccgaagtg cgccaagtgt ctgaagaaca actgggagtg tcgctactct  
180
gaaagactgg aacagctatt tctactgatt tttcctcgag aagaccttga catgattttg  
240
aaaatggatt ctttacagga tataaaagca ttgttaacag gattatttgt acaagataat  
300
gtgaataaag atgccgtcac agatagatgt gttcagtttg agactgatat gctcttaca  
360
ttgagacago atagataaag tgcgaatcga tcataggaag aagagttgaa cagagttcag  
420
agacagttga ctgtatcggg cgggcttggg ctgagctttgcc aagaccttga catgattttg  
480
gagactcagt gcgccatgaa gcggaaagag aagaaagcac aagaggggtt ggcgagcggg  
540
gacatcgc cagcagctcct gcgcagcaggt gcgacagcag gcgacagcag gcgacagcag  
600
tccgcttggt cgaagctttgcc cagatcgcctgc gcgacagcag gcgacagcag gcgacagcag  
660
gacatcgc cagcagctcct gcgcagcaggt gcgagctttgcc aagaccttga catgattttg  
720
ggcgagcggc cagagttgaa cagagttgaa cagagttgaa cagagttgaa cagagttgaa  
780
tcccgccgct cagcagctcct gcgcagcaggt gcgagctttgcc aagaccttga catgattttg  
840
tccgcttggt cgaagctttgcc cagatcgcctgc gcgacagcag gcgacagcag gcgacagcag  
900
gacatcgc cagcagctcct gcgcagcaggt gcgagctttgcc aagaccttga catgattttg  
960
tccgcttggt cgaagctttgcc cagatcgcctgc gcgacagcag gcgacagcag gcgacagcag  
1020
gacatcgc cagcagctcct gcgcagcaggt gcgagctttgcc aagaccttga catgattttg  
1080
ctgctcaggg ctgctgcctat cttttctgac cggccagggt tggagcagcc gcaactggtg 1200
gagaagatcc agcggtacta cctgaatacg ctccgcatct atatcctgaa ccagctgagc 1260
gggttggcgg tctgctgctg cattacaaggg agatcctctc caatcctcctg tgaagctctg 1320
agctctggccc tgcacacagc acaacctgc acgacactcg ctgcaatctcg aggacatgg 1380
cggccttttc tgcacacagc acaacctgc acgacactcg ctgcaatctcg 1440
atctctggct cccccacaagc ttcctc 1464

<210> SEQ ID NO 105
<211> LENGTH: 334
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Ecdysone receptor domain from Cloristoneura fumiferana

<400> SEQUENCE: 105
Pro Glu Cys Val Val Pro Glu Thr Glu Cys Ala Met Lys Arg Lys Glu 1 5 10 15
Lys Lys Ala Glu Lys Glu Lys Asp Lys Leu Pro Val Ser Thr Thr Thr 20 25 30
Val Asp Aep His Met Pro Pro Ile Met Glu Cys Glu Pro Pro Pro Pro 35 40 45
Glu Ala Ala Arg Ile His Glu Val Val Pro Arg Phe Leu Ser Asp Lys 50 55 60
Leu Leu Glu Thr Asn Arg Glu Asn Ile Pro Glu Leu Thr Ala Asn 65 70 75 80
Gln Gln Phe Leu Ile Ala Arg Leu Ile Thr Tyr Gln Asp Gly Tyr Glu 85 90 95
Gln Gln Pro Ser Asp Glu Asp Leu Lys Arg Ile Thr Glu Thr Trp Glu Gln 100 105 110
Ala Asp Aep Glu Asn Glu Glu Ser Asp Thr Pro Phe Arg Glu Ile Thr 115 120 125
Glu Met Thr Ile Leu Thr Val Glu Ile Val Glu Phe Ala Lys Glu 130 135 140
Leu Pro Gly Phe Ala Lys Ile Ser Glu Pro Asp Glu Ile Thr Leu Leu 145 150 155 160
Lys Ala Phe Ser Ser Glu Val Met Met Leu Arg Val Ala Arg Arg Tyr 165 170 175
Asp Ala Ala Ser Asp Ser Val Leu Phe Ala Asn Asn Glu Ala Tyr Thr 180 185 190
Arg Asp Aep Tyr Arg Lys Ala Gly Met Ala Tyr Val Ile Glu Aep Leu 195 200 205
Leu His Phe Cys Arg Cys Met Tyr Ser Met Ala Leu Asp Asn Ile His 210 215 220
Tyr Ala Leu Leu Thr Ala Val Ile Phe Ser Asp Arg Pro Gly Leu 225 230 235 240
Glu Gln Pro Glu Leu Val Glu Glu Ile Glu Arg Tyr Leu Asn Thr 245 250 255
Leu Arg Ile Tyr Ile Leu Asn Glu Leu Ser Gly Ser Ala Arg Ser Ser 260 265 270
Val Ile Tyr Gly Lys Ile Leu Ser Ile Leu Ser Glu Leu Arg Thr Leu 275 280 285
Gly Met Glu Asn Ser Asn Met Cys Ile Ser Leu Lys Leu Lys Asn Arg
<210> SEQ ID NO 106
<211> LENGTH: 1002
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Nucleic acid sequence encoding the ecdysone receptor domain from Clistroneura fumiferana

<400> SEQUENCE: 106
cctgagtcgc tagtaccgcc gactcagtg gcccagaaac ggaagcacag aagtagtgga aacattgagc gcaagcagcg
cTGACGAGC GCGGTGGGC GCGAGCGTG ATCAGTGGT GCCCGGGGGA GCGCCCCGAC GCGAGCGGGC

<210> SEQ ID NO 107
<211> LENGTH: 154
<212> TYPE: PRT
<213> ORGANISM: Salmonella sp.

<400> SEQUENCE: 107
Lys Leu Leu Ser Ser Ile Glu Gin Ala Cys Asp Ile Cys Arg Leu Lys
Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys
Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Arg Ser Pro Leu
Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Gin Arg Gin
Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile Leu
Lys Asp Ser Leu Gin Leu Ile Leu Leu Thr Gly Leu Phe
What is claimed is:

1. A protein capable of regulating the expression level of at least one gene of interest, which comprises:
   (i) an amino acid sequence consisting of SEQ ID NO: 6; and
   (ii) a DNA binding domain selected from the group consisting of a 2C7 DNA binding domain and a GAL4 DNA binding domain, wherein the DNA binding domain is capable of recognizing and binding to a nucleic acid sequence, wherein the nucleic acid sequence is capable of regulating the expression level of at least one gene of interest.

2. The protein of claim 1, wherein the nucleic acid sequence is a promoter.

3. The protein of claim 1, which further comprises an ecdysone receptor domain.

4. The protein of claim 3, wherein the ecdysone receptor domain comprises an amino acid of SEQ ID NO: 105.

5. The protein of claim 4, wherein the nucleic acid sequence comprises a GaL4 binding domain, which comprises a nucleic acid sequence of SEQ ID NO: 108.

6. The protein of claim 1, wherein the nucleic acid sequence comprises a C7er domain, which comprises a sequence of SEQ ID NO: 74.

7. A protein capable of regulating the expression level of at least one gene of interest, which comprises:
   (i) an amino acid sequence that comprises SEQ ID NO: 101; and
   (ii) a DNA binding domain selected from the group consisting of a 2C7 DNA binding domain and a GaL4 DNA binding domain, wherein the DNA binding domain is capable of recognizing and binding to a nucleic acid sequence, wherein the nucleic acid sequence is capable of regulating the expression level of at least one gene of interest.

8. The protein of claim 7, wherein the nucleic acid sequence is a promoter.

9. The protein of claim 8, which further comprises an ecdysone receptor domain.

10. The protein of claim 9, wherein the ecdysone receptor domain comprises an amino acid sequence of SEQ ID NO: 105.

11. The protein of claim 8, which further comprises a 2C7 zinc finger domain.

12. The protein of claim 11, wherein the promoter comprises a C7er domain, which comprises a nucleic acid sequence of SEQ ID NO: 74.
13. The protein of claim 7, which comprises two or more repetitions of SEQ ID NO:101.

14. A protein capable of regulating the expression level of at least one gene of interest, which comprises:
   (i) an amino acid sequence represented by SEQ ID NO:6 or a fragment thereof which consists of SEQ ID NO:101;
   (ii) an ecdysone receptor domain; and
   (iii) a Gal4 protein.

   * * * * *