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MICROPEPTIDES AND USE THEREOF FOR MODULATING GENE EXPRESSION

The present invention relates to micropeptides (peptides encoded by microRNAs or
5 "miPEPs") and use thereof for modulating gene expression.

The microRNAs (miRNAs) are small non-coding RNAs, about 21 nucleotides in length after maturation, which control expression of target genes at the post-transcriptional level, by degrading the target mRNA or by inhibiting its translation. The miRNAs occur in plants and
10 animals.

The target genes are often key genes in developmental processes. For example they encode transcription factors or proteins of the proteasome.

The regulation of expression of the miRNAs is very poorly understood, but it is known in particular that the latter involves, like most coding genes, an RNA polymerase II: this
15 enzyme produces a primary transcript, called "*pri-miRNA*", which is then matured by a protein complex in particular containing the Dicer type enzymes. This maturation leads firstly to the formation of a precursor of miRNA called "*pre-miRNA*", having a stem-loop secondary structure containing the *miRNA* and its complementary sequence *miRNA**. Then the precursor is matured, which leads to formation of a shorter double-stranded RNA
20 containing the miRNA and the miRNA*. The miRNA is then manipulated by the RISC complex, which cleaves the mRNA of the target gene or inhibits its translation.

Moreover, it has been shown that the presence of introns in the primary transcript of the microRNA increases the expression of the mature microRNA (Schwab et al., *EMBO Rep.*, 14(7): 615-21, 2013). However, owing to experimental difficulties, the primary transcripts
25 of microRNAs, or pri-miRNAs, have received very little study.

About 50% of eukaryotic genes have small open reading frames within their 5'UTR region (5' UnTranslated Region) upstream of the coding sequence. These small open reading frames (or "uORFs" for upstream ORFs) may perform a role of translation regulator, mainly in *cis*, by modulating the fixation and the rate of the ribosomes on the mRNA, but also in *trans* by
30 an as yet unknown mechanism, by means of peptides encoded by said uORFs (Combiér et al., *Gene Dev.*, 22: 1549-1559, 2008). By definition, the uORFS are present upstream of coding genes.

Recently, small ORFs have also been discovered in long intergenic non-coding RNAs (lincRNAs), the putative function of which, if it exists, is not known (Ingolia et al., *Cell*, 147(4): 789-802, 2011; Guttman & Rinn, *Nature*, 482(7385): 339-46, 2012).

However, no example has yet been reported concerning the existence of ORFs encoding
 5 peptides within non-coding microRNAs. Until now, the microRNAs, and by extension their primary transcript, have always been regarded, based on their particular mode of action, as non-coding regulatory RNAs that do not produce any peptide.

Brennincke (2010), Crappe *et al.* (2011) and Galindo *et al.* (2007) described the identification of micropeptides, which regulate the function of certain genes. These
 10 micropeptides are encoded by microORFs.

The invention is defined in the claims.

The invention thus relates to a process for detecting and identifying a micropeptide (miPEP)
 15 encoded by a nucleotide sequence contained in the sequence of the primary transcript of a microRNA,
 comprising:

- a) a step of detecting an open reading frame from 12 to 303 nucleotides contained in the sequence of the primary transcript of said microRNA, then
- 20 b) a step of comparison between:
 - the phenotype of a plant expressing said miPEP,
 in the presence of a peptide encoded by a nucleotide sequence that is identical or degenerate with respect to that of said open reading frame, said peptide being present in the plant independently of transcription of the
 25 primary transcript of said microRNA, and
 - the phenotype of the same plant le ph  notype expressing said miPEP in the absence of said peptide,

wherein, a change in the phenotype of the plant in the presence of said peptide compared to the phenotype of the plant in the absence of said peptide indicates the existence of a
 30 miPEP encoded by said open reading frame.

In a first step, the process for detecting and identifying a micropeptide therefore consists of detecting, on the primary transcript of a microRNA, the existence of an open reading frame potentially encoding a peptide.

For its part, the second step makes it possible to characterize said peptide, i.e. to determine whether said peptide corresponds to a peptide really produced in the cell, by searching for an effect of said peptide on the accumulation of said microRNA.

In order to demonstrate an effect of the peptide on the accumulation of the microRNA, a large quantity of peptide is introduced into a first cell expressing said microRNA. The accumulation of the microRNA in this first cell is then measured and compared with the accumulation of the microRNA in a second cell identical to the first, but not containing said peptide.

Observation of a variation of the quantities of microRNA between the cells in the presence and in the absence of the peptide thus indicates (i) that there is a peptide encoded on the primary transcript of said microRNA, (ii) that the sequence of this peptide is encoded by the open reading frame identified on the primary transcript of said microRNA, and (iii) that said peptide has an effect on the accumulation of said microRNA.

The invention is therefore based on the unexpected double observation made by the inventors that, on the one hand, there are open reading frames that are able to encode micropeptides present on the primary transcripts of microRNAs, and on the other hand that said micropeptides are capable of modulating the accumulation of said microRNAs.

In the invention, the terms "*microRNA*", "*non-coding microRNA*" and "*miRNA*" are equivalent and may be used interchangeably. They define small molecules of RNA of about 21 nucleotides, which are not translated and do not lead to a peptide or a protein.

However, in this mature form, the microRNAs perform a function of regulation of certain genes via post-transcriptional mechanisms, for example by means of the RISC complex.

The primary transcript of the microRNA or "*pri-miRNA*" corresponds to the RNA molecule obtained directly from transcription of the DNA molecule. Generally, this primary transcript undergoes one or more post-transcriptional modifications, involving for example a particular structure of the RNA or cleavage of certain portions of the RNA by splicing phenomena, and which lead to the precursor form of the microRNA or "*pre-miRNA*", then to the mature form of the microRNA or "*miRNA*".

The terms "*micropeptides*" and "*miPEPs*" (*microRNA encoded PEptides*) are equivalent and may be used interchangeably. They define a peptide that is encoded by an open reading frame present on the primary transcript of a microRNA, and which is capable of modulating the accumulation of said microRNA.

The micropeptides within the meaning of the present invention are not to be understood as necessarily being small peptides, as "micro" does not correspond to the size of the peptide.

According to the invention, a miPEP can also be considered as a transcription modulator, and in particular a transcription activator. Such a transcription modulator can operate at the transcription level to modulate the accumulation of pri-miR, pre-miR and miR.

Taking into account the degeneracy of the genetic code, one and the same micropeptide may be encoded by several nucleotide sequences. Nucleotide sequences of this kind, differing from one another by at least one nucleotide but encoding one and the same peptide, are called "*degenerate sequences*".

The terms "*open reading frame*" or "*ORF*" are equivalent and may be used interchangeably. They correspond to a nucleotide sequence in a DNA or RNA molecule that may potentially encode a peptide or a protein: said open reading frame begins with a start codon (the start codon generally encoding a methionine), followed by a series of codons (each codon encoding an amino acid), and ends with a stop codon (the stop codon not being translated).

In the invention, the ORFs may be called specifically "*miORFs*" when they are present on the primary transcripts of microRNA.

The miORFs as defined in the particular invention may have a size from 12 to 303 nucleotides and may encode peptides from 3 to 100 amino acids.

In particular, the miORFs as defined in the invention may have a size from 15 to 303 nucleotides. As an amino acid is encoded by a codon of 3 nucleotides, the miORFs from 15 to 303 nucleotides encode miPEPS from 4 to 100 amino acids.

In particular, the miORFs have a size of:

15, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45, 47, 51, 54, 57, 60, 63, 66, 69, 72, 75, 78, 81, 84, 87, 90, 93, 96, 99, 102, 105, 108, 111, 114, 117, 120, 123, 126, 129, 132, 135, 138, 141, 144, 147, 150, 153, 156, 159, 162, 165, 168, 171, 174, 177, 180, 183, 186, 189, 192, 195, 198, 201, 204, 207, 210, 213, 216, 219, 222, 225, 228, 231, 234, 237, 240, 243, 246, 249, 252, 255, 258, 261, 264, 267, 270, 273, 276, 279, 282, 285, 288, 291, 294, 297, 300 or 303 nucleotides, and encode respectively miPEPs having a size of:

4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100 amino acids.

In the invention, "*accumulation*" means the production of a molecule, such as a microRNA or a micropeptide, in the cell.

Thus, "*modulation*" of the accumulation of a molecule in a cell corresponds to a modification of the quantity of this molecule present in the cell.

- 5 Moreover, the effect of a miPEP can be observed through the modulation of the accumulation of the miR, but also through the modulation of the accumulation of the corresponding pri-miR or pre-miR.

In an embodiment, the invention relates to a process for detecting and identifying a miPEP as defined above, in which the modulation of the accumulation of said microRNA is a
10 decrease or an increase in the accumulation of said microRNA, in particular an increase.

A "*decrease in the accumulation*" corresponds to a decrease in the quantity of said molecule in the cell.

Conversely, an "*increase in the accumulation*" corresponds to an increase in the quantity of said molecule in the cell.

- 15 In an advantageous embodiment, the invention relates to a process for detecting and identifying a miPEP as defined above, in which the modulation of the accumulation of said microRNA is an increase in the accumulation of said microRNA.

In an embodiment, the invention relates to a process for detecting and identifying a miPEP as defined above, in which the presence of said peptide in the cell results from:

- 20 - the introduction of a nucleic acid encoding said peptide into the cell, or
 - the introduction of said peptide into the cell.

In order to characterize a miPEP, it is necessary to have a cellular model expressing a microRNA in which said peptide to be tested is present. For this, it is possible to introduce a peptide into the cell, either by bringing the cell into contact with said peptide, or by
25 introducing a nucleic acid encoding said peptide into the cell, and this nucleic acid will then be translated into peptide within the cell.

In an embodiment, the invention relates to a process for detecting and identifying a miPEP as defined above, in which said open reading frame in step a) is contained in the 5' or 3' portion of said primary transcript of the microRNA, preferably in the 5' portion.

- 30 The 5' or 3' portions of the primary transcript of the microRNA correspond to the terminal portions of the RNA molecule that are cleaved during maturation of the microRNA.

In an embodiment, the invention relates to a process for detecting and identifying a miPEP as defined above, in which said microRNA is present in a wild-type plant cell.

In the invention, a wild-type plant cell corresponds to a plant cell that has not been genetically modified by humans.

In an embodiment, the invention relates to a process for detecting and identifying a miPEP as defined above, in which said specified eukaryotic cell and said eukaryotic cell of the same
 5 type as the aforesaid specified eukaryotic cell, used in step b, are plant cells of a cruciferous plant such as *Arabidopsis thaliana*, of a leguminous plant such as *Glycine max* (soya), *Medicago truncatula* and *Medicago sativa* (alfalfa) or of a plant of the Solanaceae family such as *Nicotiana benthamiana* (tobacco), *Solanum tuberosum* (potato), *Solanum lycopersicum* (tomato) or *Solanum melongena* (aubergine).

10 In an embodiment, the invention relates to a process for detecting and identifying a miPEP as defined above, in which said specified eukaryotic cell and said eukaryotic cell of the same type as the aforesaid specified eukaryotic cell, used in step b, are plant cells, preferably cells of *Medicago truncatula*, *Nicotiana benthamiana* or *Arabidopsis thaliana*.

In an embodiment, the invention relates to a process for detecting and identifying a miPEP
 15 as defined above, in which said specified eukaryotic cell and said eukaryotic cell of the same type as the aforesaid specified eukaryotic cell, used in step b, are animal cells, preferably human cells or *Drosophila* cells.

In the process for detecting and identifying a micropeptide as defined above, after identifying an ORF that is able to encode a peptide on the primary transcript of a microRNA, it is
 20 necessary to have a cellular model having said microRNA and said peptide, so as to be able to demonstrate a possible effect of the peptide on said microRNA.

Two options are therefore conceivable:

- the cellular model in which the miORF has been identified and that in which the effect of the peptide on the miRNA has been demonstrated are identical, or
- 25 - the cellular model in which the miORF has been identified and that in which the effect of the peptide on the miRNA has been demonstrated are different.

In the first option, the cellular model used for observing an effect of the peptide is the same as that in which the primary transcript of said microRNA was isolated. In this cellular model, the specified eukaryotic cells contain said microRNA naturally and only the peptide to be
 30 tested has to be introduced into these cells. In this context, said microRNA is qualified as "of endogenous origin" as it exists naturally in the cells. Nevertheless, other copies of a microRNA of endogenous origin may be added to a cell, for example by introducing a vector encoding said microRNA of endogenous origin into the cell.

In the second option, the cellular model used for observing an effect of the peptide is different from that in which the primary transcript of said microRNA was isolated. In this cellular model, the specified eukaryotic cells contain neither the microRNA, nor the peptide to be tested. These two elements must therefore be introduced into these cells. In this context, 5 said microRNA is qualified as "of exogenous origin" as it does not exist naturally in the cells.

In an embodiment, the invention relates to a process for detecting and identifying a miPEP as defined above, in which said microRNA is of endogenous origin in said eukaryotic cell and in said eukaryotic cell of the same type as the aforesaid specified eukaryotic cell, used 10 in step b).

In an embodiment, the invention relates to a process for detecting and identifying a miPEP as defined above in which said microRNA is of exogenous origin in said eukaryotic cell and in said eukaryotic cell of the same type as the aforesaid specified eukaryotic cell, used in step b), said eukaryotic cells containing a vector allowing the expression of said microRNA.

15 In an embodiment, the invention relates to a process for detecting and identifying a miPEP as defined above, in which the accumulation of said microRNA is determined using quantitative RT-PCR or Northern blot.

In an embodiment, the invention relates to a process for detecting and identifying a miPEP as defined above, in which the accumulation of said microRNA is determined using a DNA 20 or RNA chip.

The accumulation of said microRNA may be determined using the techniques of molecular biology for assaying specific nucleic acid molecules.

In an embodiment, the invention relates to a process for detecting and identifying a 25 microRNA as defined above, in which the modulation of the accumulation of said microRNA is a decrease or an increase in the accumulation of said microRNA, in particular an increase.

In an embodiment, the invention relates to a process for detecting and identifying a microRNA as defined above, in which the presence of said peptide in the cell results from:

- 30
- the introduction of a nucleic acid encoding said peptide into the cell, or
 - the introduction of said peptide into the cell.

In an embodiment, the invention relates to a process for detecting and identifying a microRNA as defined above, in which said open reading frame in step a) is contained in the 5' or 3' portion of said primary transcript of the microRNA, preferably in the 5' portion.

In an embodiment, the invention relates to a process for detecting and identifying a
5 microRNA as defined above, in which said microRNA is present in a wild-type plant cell.

In an embodiment, the invention relates to a process for detecting and identifying a microRNA as defined above, in which said eukaryotic cell, and said eukaryotic cell of the same type as the aforesaid specified eukaryotic cell, used in step b) are plant cells, preferably cells of *Medicago truncatula*.

10 In an embodiment, the invention relates to a process for detecting and identifying a microRNA as defined above, in which said microRNA is of endogenous origin in said eukaryotic cell and in said eukaryotic cell of the same type as the aforesaid specified eukaryotic cell, used in step b).

In an embodiment, the invention relates to a process for detecting and identifying a
15 microRNA as defined above in which said microRNA is of exogenous origin in said eukaryotic cell and in said eukaryotic cell of the same type as the aforesaid specified eukaryotic cell, used in step b), said eukaryotic cells containing a vector allowing the expression of said microRNA.

In an embodiment, is described a process for detecting and identifying a microRNA as
20 defined above, in which the accumulation of said microRNA is determined using quantitative RT-PCR or Northern blot.

In an embodiment, is described a process for detecting and identifying a microRNA as defined above, in which the accumulation of said microRNA is determined using a DNA or RNA chip.

25 In another aspect, the invention relates to a vector comprising at least one nucleic acid molecule as defined above.

In another aspect, the invention also relates to the use of at least:

- a miPEP as defined above,
 - a nucleic acid encoding said miPEP, or
 - 30 - a vector containing said nucleic acid,
- as a phytopharmaceutical agent,

- for promoting the growth and/or development of plants, in particular for modulating the physiological parameters of a plant, in particular the biomass, foliar surface area, flowering, fruit size; or
- for preventing or treating plant diseases, in particular for promoting resistance to infectious diseases,

said miPEP having:

- a size from 3 to 100 amino acids, preferably 4 to 20 amino acids;
- a peptide sequence identical to that encoded by a nucleotide sequence contained in the primary transcript of a microRNA regulating the expression of said gene,
- and
- being capable of modulating the accumulation of said microRNA,

said composition being applied by foliar spraying.

The invention is based on the surprising observation made by the inventors that it is possible to modulate the expression of one or more target genes of one and the same microRNA by modulating the accumulation of said microRNA using a miPEP.

In an embodiment, the invention relates to the use as defined above in which said specified eukaryotic cell is a plant cell.

In an embodiment, the invention relates to the use as defined above in which said specified eukaryotic cell is a plant cell of a crucifer such as *Arabidopsis thaliana*, of a leguminous plant such as *Glycine max* (soya), *Medicago truncatula* and *Medicago sativa* (alfalfa) or of a plant of the Solanaceae family such as *Nicotiana benthamiana* (tobacco), *Solanum tuberosum* (potato), *Solanum lycopersicum* (tomato) or *Solanum melongena* (aubergine).

In an embodiment, the invention relates to the use as defined above in which said microRNA and said gene are of endogenous origin in said specified eukaryotic cell.

In an embodiment, the invention relates to the use as defined above in which said microRNA and said gene are of exogenous origin in said specified eukaryotic cell, said specified eukaryotic cell containing at least one vector allowing the expression of said microRNA and of said gene.

In the invention, the expressions "*of endogenous origin*" and "*of exogenous origin*" are used for distinguishing said microRNAs and/or the genes of different species, in view of the conservation of the sequences between species.

Thus, the term "*of endogenous origin*" indicates that the microRNA and/or gene may be present naturally in the cell in question. Other copies of the microRNA and/or of the gene of

endogenous origin may nevertheless be added artificially to the cell in question, for example by cloning.

Conversely, the term "*of exogenous origin*" indicates that the microRNA and/or the gene are never present naturally in the cell in question. It is a microRNA and/or a gene identified in
5 another cellular type or in an organism of another species; this microRNA and/or this gene are therefore necessarily introduced artificially into the cell in question.

In the invention, a genetically transformed cell may therefore contain 2 groups of microRNAs and/or of genes potentially similar in terms of sequence, one of endogenous origin and the other of exogenous origin.

10 In an embodiment, the invention relates to the use as defined above in which the primary transcript of the miRNA and said gene are of exogenous origin in said specified eukaryotic cell, said specified eukaryotic cell containing at least one vector allowing the expression of the primary transcript of the microRNA.

In an embodiment, the invention relates to the use as defined above in which the primary
15 transcript of the miRNA is encoded by a vector introduced into the cell artificially.

In the invention, by the term "*modified eukaryotic cell*" is meant that said eukaryotic cell contains a miPEP introduced into the cell artificially, whether as a peptide, or via a vector encoding said miPEP.

In addition to a miPEP introduced artificially in the cell, a modified eukaryotic cell according
20 to the invention also contains at least one nucleic acid corresponding to the miORF encoding said miPEP.

In addition to a miPEP introduced artificially in the cell and of the miORF, a modified eukaryotic cell according to the invention also contains at least one miR, the primary transcript of which contains said miORF.

25 The inventors have surprisingly found that the use of peptides the sequence of which comprises or consists of a sequence identical to that of miPEPs encoded on the primary transcripts of miRNAs makes it possible to promote the growth of the plants.

In the invention, the term "plant" refers generally to the whole or part of a plant irrespective of its stage of development (including the plant in the form of a seed or a young shoot), to
30 one or more organs of the plant (for example the leaves, roots, stem, flowers), to one or more cells of the plant, or to a cluster of cells of the plant.

In the invention, the term "*growth*" refers to the development of the whole or part of a plant over time. The growth of the plant may thus be determined and quantified by monitoring

developmental parameters observable for certain parts, cells or organs of the plant, such as the leaves, roots, stems or flowers.

Non-limitatively, the parameters for determining and quantifying the growth of a plant may in particular be:

- 5 - the size, surface area, volume, mass and the number of leaves,
- the size and number of flowers,
- the size of the stem (or spike),
- the length and number of roots,
- the earliness of germination,
- 10 - the earliness of budding,
- the earliness of floral induction (or floral transition),
- or also the number of cells.

In the case of leguminous plants, plant growth may also be linked to the rate of nodulation, or also to the size and number of nodules on the roots.

15 Moreover, in the invention, the expression "*promote plant growth*", or "*improve plant growth*", indicates:

- either an acceleration of development (such as for example a larger leaf size for a plant at a given point in time relative to a reference plant),
- or an increase in development (such as for example a larger leaf size for a plant that cannot
- 20 be attained by a reference plant),
- or an acceleration and an increase in the development of the plant.

It is important to note that the use according to the invention has the advantage of being ecological, in comparison with the chemical methods used conventionally in horticulture or in agriculture, as the miPEP is a peptide that is present naturally in the plant.

25 In the invention, the expression "*miPEP introduced*" refers to a miPEP introduced into the plant artificially as opposed to the "*miPEP present naturally in the plant*". The introduction of a miPEP into the plant therefore involves a technological step, which is not a natural phenomenon and corresponds neither to crossing, nor to selection.

The miPEP introduced may be either a peptide produced outside of the plant (for example

30 an isolated and/or purified peptide, a synthetic peptide or a recombinant peptide), or a peptide produced in the plant following the non-natural introduction of a nucleic acid encoding said miPEP into said plant.

The plant into which the miPEP has not been introduced has a basal quantity of said miPEP, which corresponds to the quantity of said miPEP naturally present. The use of a miPEP comprising, or consisting of, a sequence identical to that of said miPEP leads to an increase in the total quantity of miPEP, which modulates the accumulation of the miRNA the primary
5 transcript of which contains the sequence encoding said miPEP.

Moreover, the miPEP introduced is present in the plant and its introduction has no impact on its stability.

In an embodiment, the invention relates to the use as defined above, in which said gene, involved in the development of the vegetative or reproductive parts of the plant, is selected
10 from the group consisting of: *NAC1* (Accession No. AT1G56010.1), *NAC4* (Accession No. AT5G07680.1), *NAC5* (Accession No. AT5G61430.1), *CUC1* (Accession No. AT3G15170.1), *CUC2* (Accession No. AT5G53950.1), *TCP3* (Accession No. AT1G53230.1) and *TCP4* (Accession No. AT3G15030.1) (accession numbers according to the database *The Arabidopsis Information Resource "TAIR"*).

15 In particular, the invention relates to the use as defined above, in which said gene involved in the development of the vegetative or reproductive parts of the plant is selected from the group consisting of: *NAC1*, *NAC4*, *NAC5*, *CUC1* and *CUC2*.

In an embodiment, the invention relates to the use as defined above, in which said gene involved in the development of the vegetative or reproductive parts of the plant is selected
20 from the group consisting of: *TCP3* and *TCP4*.

In an embodiment, the invention relates to the use as defined above, in which said miRNA is selected from miR164a and mir319a.

In an embodiment, the invention relates to the use as defined above, in which said miR is selected from miR164a, miR319a, miR171b, miR165a, miR160b, miR169d and miR171e.

25 In an embodiment, the invention relates to the use as defined above, in which said miPEP is selected from AtmiPEP164a1, AtmiPEP319a1, AtmiPEP319a2, MtmPEP171b1, AtmiPEP165a1, AtmiPEP160b1, MtmPEP169d, MtmPEP171e.

In particular, the invention relates to the use as defined above, in which said miR164a has a nucleotide sequence consisting of SEQ ID NO: 297.

30 In particular, the invention relates to the use as defined above, in which said miR164a has a nucleotide sequence having at least 80% identity, preferably at least 90% identity, with the nucleotide sequence SEQ ID NO: 297.

In an embodiment, the invention relates to the use as defined above, in which said miPEP is AtmiPEP164a1, in particular in which said AtmiPEP164a1 has an amino acid sequence consisting of SEQ ID NO: 24.

In particular, the invention relates to the use as defined above, in which said miR319a has a
5 nucleotide sequence consisting of SEQ ID NO: 331.

In particular, the invention relates to the use as defined above, in which said miR319a has a nucleotide sequence having at least 80% identity, preferably at least 90% identity, with the nucleotide sequence SEQ ID NO: 331.

In an embodiment, the invention relates to the use as defined above, in which said miPEP is
10 AtmiPEP319a1, in particular in which said AtmiPEP319a1 has an amino acid sequence consisting of SEQ ID NO: 76.

In an embodiment, the invention relates to the use as defined above, in which said plant is a crucifer such as *Arabidopsis thaliana*, a leguminous plant such as *Glycine max* (soya), *Medicago truncatula* and *Medicago sativa* (alfalfa) or a plant of the Solanaceae family such
15 as *Nicotiana benthamiana* (tobacco), *Solanum tuberosum* (potato), *Solanum lycopersicum* (tomato) or *Solanum melongena* (aubergine).

In an embodiment, the invention relates to the use as defined above, in which said plant is a crucifer.

In an embodiment, the invention relates to the use as defined above, in which said plant is
20 *Arabidopsis thaliana*.

In an embodiment, the invention relates to the use as defined above, for promoting the growth of an *Arabidopsis thaliana* plant, in which AtmiPEP164a1 is introduced into said *Arabidopsis thaliana* plant, said AtmiPEP164a1 also being naturally present in said *Arabidopsis thaliana* plant,

25 said AtmiPEP164a1 introduced being a peptide the sequence of which comprises or consists of a sequence identical to that of said AtmiPEP164a1 naturally present, said sequence of AtmiPEP164a1 naturally present being encoded by an open reading frame located at 5' on the primary transcript of the miR164a, which miR164a controls the expression of at least one gene involved in the development of the vegetative or reproductive parts of *Arabidopsis*
30 *thaliana*,

the sum total of the quantity of said AtmiPEP164a1 introduced and that of said AtmiPEP164a1 naturally present being strictly greater than the quantity of said AtmiPEP164a1 naturally present in said *Arabidopsis thaliana* plant.

In an embodiment, the invention relates to the use as defined above, for promoting the growth of an *Arabidopsis thaliana* plant, in which the AtmiPEP319a1 is introduced into said *Arabidopsis thaliana* plant, said AtmiPEP319a1 also being naturally present in said *Arabidopsis thaliana* plant,

- 5 said AtmiPEP319a1 introduced being a peptide the sequence of which comprises or consists of a sequence identical to that of said AtmiPEP319a1 naturally present, said sequence of the AtmiPEP319a1 naturally present being encoded by an open reading frame located at 5' on the primary transcript of the miR319a, which miR319a controls the expression of at least one gene involved in the development of the vegetative or reproductive parts of *Arabidopsis*
10 *thaliana*,

the sum total of the quantity of said AtmiPEP319a1 introduced and that of said AtmiPEP319a1 naturally present being strictly greater than the quantity of said AtmiPEP319a1 naturally present in said *Arabidopsis thaliana* plant.

- In an embodiment, the invention relates to the use as defined above, in which said miPEP is
15 introduced into the plant externally, preferably by watering, by spraying or by adding a fertilizer, a compost, a culture substrate or an inert support.

In an embodiment, the invention relates to the use as defined above, in which said miPEP is introduced by watering and by spraying.

- In an embodiment, the invention relates to the use as defined above, in which said miPEP is
20 introduced by watering and by adding a fertilizer.

In an embodiment, the invention relates to the use as defined above, in which said miPEP is introduced by spraying and by adding a fertilizer.

In an embodiment, the invention relates to the use as defined above, in which said miPEP is introduced, by watering, by spraying and by adding a fertilizer.

- 25 The inventors have in fact unexpectedly found that it is possible to apply a composition comprising a miPEP directly to the plant in order to modulate the accumulation of the corresponding miRNA in the plant, which indicates that the miPEP is captured by the plant.

- In an embodiment, the invention relates to the use as defined above, in which the plant is treated with a composition comprising 10^{-9} M to 10^{-4} M of said miPEP, in particular 10^{-9} M,
30 10^{-8} M, 10^{-7} M, 10^{-6} M, 10^{-5} M or 10^{-4} M of said miPEP.

Preferably, the compositions have a concentration from 10^{-8} M to 10^{-5} M for application by watering or by spraying on the plant.

In addition, compositions of higher or lower concentration may be envisaged for treating the plant with the miPEP. As a non-limitative example, compositions of higher concentration comprising 10^{-1} M to 10^{-3} M, in particular 10^{-2} M of miPEP, may be used in the case where the miPEP introduced exogenously is administered to the plant by spreading.

- 5 In an embodiment, the invention relates to the use as defined above, in which said miPEP is introduced into the plant by means of a nucleic acid encoding said miPEP, said nucleic acid being introduced into the plant.

In an embodiment, the invention relates to the use as defined above, in which the size of the stem is increased in the plant into which said miPEP has been introduced relative to the size
10 of the stem of an identical plant of the same age into which no miPEP has been introduced, or relative to the size of the stem of an identical plant of the same age into which said miPEP has not been introduced.

In an embodiment, the invention relates to the use as defined above, in which the number of leaves is increased in the plant into which said miPEP has been introduced relative to the
15 number of leaves of an identical plant of the same age into which no miPEP has been introduced, or relative to the number of leaves of an identical plant of the same age into which said miPEP has not been introduced.

In an embodiment, the invention relates to the use as defined above, in which the size of the leaves is increased in the plant into which said miPEP has been introduced relative to the
20 size of the leaves of an identical plant of the same age into which no miPEP has been introduced, or relative to the size of the leaves of an identical plant of the same age into which said miPEP has not been introduced.

In an embodiment, the invention relates to the use as defined above, in which the number of roots is increased in the plant into which said miPEP has been introduced relative to the
25 number of roots of an identical plant of the same age into which no miPEP has been introduced, or relative to the number of roots of an identical plant of the same age into which said miPEP has not been introduced.

In an embodiment, the invention relates to the use as defined above, in which the length of the roots is increased in the plant into which said miPEP has been introduced relative to the
30 length of the roots of an identical plant of the same age into which no miPEP has been introduced, or relative to the length of the roots of an identical plant of the same age into which said miPEP has not been introduced.

In an embodiment, the invention relates to the use as defined above, in which the rate of nodulation is increased in the plant into which said miPEP has been introduced relative to the rate of nodulation of an identical plant of the same age into which no miPEP has been introduced, or relative to the rate of nodulation of an identical plant of the same age into
5 which said miPEP has not been introduced.

In an embodiment, the invention relates to the use as defined above, in which the number of nodules is increased in the plant into which said miPEP has been introduced relative to the number of nodules of an identical plant of the same age into which no miPEP has been introduced, or relative to the number of nodules of an identical plant of the same age into
10 which said miPEP has not been introduced.

The increase in the parameters for determining and quantifying growth in the plant into which the miPEP has been introduced (such as the size of the stem, the number and size of the leaves, the number and length of the roots, the rate of nodulation or also the number of nodules on the roots) is preferably demonstrated by comparison with an identical plant (i.e.
15 a plant of the same species and/or variety), of the same age and grown under the same conditions but into which no miPEP has been introduced.

All the sequences of the miPEPs, miORFs, miRNAs and primary transcripts of miRNAs are presented in Tables 1, 2, 3, 4, 5 and 6.

20

Table 7 presents an analysis of the polymorphism of the DNA sequence of the different regions of pri-miR171b (a haplotype is defined when it differs by at least one amino acid from the other haplotypes).

miPEP (pI / size MW)	miRNA	Organism	Target genes of the miRNA	Sequence of the miPEP	SEQ ID
AtmiPEP156a1 (10.57 / 3824)	miR156a	<i>Arabidopsis thaliana</i>	<i>SPL</i> gene family, involved in development of the stem and flowering	MFCSIQCVARHLFPLHVREIKKATRAI KKGKTL	SEQ ID NO:1
AtmiPEP156a2	miR156a	<i>Arabidopsis thaliana</i>		MRRQTSVPFACKRDKESDKSHKER	SEQ ID NO:2
AtmiPEP156a3	miR156a	<i>Arabidopsis thaliana</i>		MVMFFLDLDKNPRFDLLKGLKWNLF SSHISPSLPPSL	SEQ ID NO:3
AtmiPEP156c1 (8.5 / 1359)	miR156c	<i>Arabidopsis thaliana</i>		MKDNFPLLLRL	SEQ ID NO:4
AtmiPEP156c2	miR156c	<i>Arabidopsis thaliana</i>		MSDD	SEQ ID NO:5
AtmiPEP156e1 (4.03 / 1818)	miR156e	<i>Arabidopsis thaliana</i>		MIYINKYGSISAVEDD	SEQ ID NO:6
AtmiPEP156f1 (9.5 / 520)	miR156f	<i>Arabidopsis thaliana</i>		MSQR	SEQ ID NO:7
AlmiPEP159a	miR159a	<i>Arabidopsis lyrata</i>	<i>MYB</i> gene family, involved in germination and flowering	MTCPLLSLSFLLSKYI	SEQ ID NO:8
AtmiPEP159a1 (8.34 / 1898)	miR159a	<i>Arabidopsis thaliana</i>		MTWPLLSLSFLLSKYV	SEQ ID NO:9
CmiPEP159a	miR159a	<i>Capsella rubella</i>		MTCTLSALSLSLNMFRVN	SEQ ID NO:10
AtmiPEP159b1 (5.27 / 659)	miR159b	<i>Arabidopsis thaliana</i>		MFYLS	SEQ ID NO:11
AtmiPEP159b2	miR159b	<i>Arabidopsis thaliana</i>		MVNTSSFFISSFILPLVLSESNCLLFRTI YKFSMVLY	SEQ ID NO:12
AtmiPEP160a1 (8.02 / 2936)	miR160a	<i>Arabidopsis thaliana</i>	<i>ARF</i> gene family, involved in germination, development and flowering	MFCLLIPIFSFVFSPNRHLRLQEQ	SEQ ID NO:13
AtmiPEP160b1 (5.28 / 608)	miR160b	<i>Arabidopsis thaliana</i>		MFSPQ	SEQ ID NO:14
AtmiPEP160b2	miR160b	<i>Arabidopsis thaliana</i>		MKYIHILILFKSRSTYKLSTNHI	SEQ ID NO:15
AtmiPEP161 (10 / 1199)	miR161	<i>Arabidopsis thaliana</i>	<i>PPR</i> gene family	MKIPLFLPKL	SEQ ID NO:16

AtmiPEP162a1 (4.03 / 3045)	miR162a	<i>Arabidopsis thaliana</i>	DCL1 gene, involved in development	MVSGQEDSWLKLSSL CFLFLSLLD SLI	SEQ ID NO:17
AtmiPEP162b1 (5.71 / 4114)	miR162b	<i>Arabidopsis thaliana</i>		MFLLI FLRLIMICVCSSTDFLR SVNYFC LFIYDL	SEQ ID NO:18
AtmiPEP163-1 (6.5 / 1076)	miR163	<i>Arabidopsis thaliana</i>	SAMT gene family, involved in the production of secondary metabolites	MSTTQEHS	SEQ ID NO:19
AtmiPEP163-2	miR163	<i>Arabidopsis thaliana</i>		MILKCWSSRFLRVSPYQNAHSLSLG	SEQ ID NO:20
AlmiPEP164a1	miR164a	<i>Arabidopsis lyrata</i>	NAC gene family, involved in root, foliar and floral development	MPLAVIRQGIVWP	SEQ ID NO:21
AlmiPEP164a2	miR164a	<i>Arabidopsis lyrata</i>		MPSWHD MVLLPYVKHTHANTRHIT	SEQ ID NO:22
AlmiPEP164a3	miR164a	<i>Arabidopsis lyrata</i>		MTWFFCLT	SEQ ID NO:23
AtmiPEP164a1 (7.05 / 4256)	miR164a	<i>Arabidopsis thaliana</i>		MPSWHGMVLLPYVKHTHASTHTHTH NIYGCACELVFH	SEQ ID NO:24
AtmiPEP164a2	miR164a	<i>Arabidopsis thaliana</i>		MAWYG SFALRKTHSRQHTHTHT	SEQ ID NO:25
AtmiPEP164a3	miR164a	<i>Arabidopsis thaliana</i>		MVWFFCLT	SEQ ID NO:26
BrmiPEP164a1	miR164a	<i>Brassica rapa</i>		MMILWK	SEQ ID NO:27
BrmiPEP164a2	miR164a	<i>Brassica rapa</i>		MLWAKLV SFSTLHSLVFL LSPSFA	SEQ ID NO:28
BrmiPEP164a3	miR164a	<i>Brassica rapa</i>		MPSWHGIVILPFVKHTHANIHYSSC VCI	SEQ ID NO:29
CpmiPEP164a1	miR164a	<i>Carica papaya</i>		MIACHPYLPFPLFSLTFYSIFFSPSPPS PSLPL	SEQ ID NO:30
CpmiPEP164a2	miR164a	<i>Carica papaya</i>		MPSLLAFSPFPFSNILLNLLLPLPPFPLS AIIHKPLSLSLPLSLSLSGFSV	SEQ ID NO:31
CrmiPEP164a1	miR164a	<i>Capsella rubella</i>		MELKGLRTWQLLDKV	SEQ ID NO:32
CrmiPEP164a2	miR164a	<i>Capsella rubella</i>		MPSWHG MACFYCLT	SEQ ID NO:33
CrmiPEP164a3	miR164a	<i>Capsella rubella</i>		MAWHGMFLLPYVKHTHANTYSLYM	SEQ ID NO:34
GrmPEP164a1	miR164a	<i>Gossypium raimondii</i>		MMRSRLKFQYRFGMGIGGRKQLKN QLCQIQGRIS	SEQ ID NO:35

GrmiPEP164a2	miR164a	<i>Gossypium raimondii</i>		MSNSRSYQLK	SEQ ID NO:36
GrmiPEP164a3	miR164a	<i>Gossypium raimondii</i>		MNEDLEISTRKRTPQLC	SEQ ID NO:37
MtmiPEP164a1	miR164a	<i>Medicago truncatula</i>		MPKFDIFFYIFV	SEQ ID NO:38
MtmiPEP164a2	miR164a	<i>Medicago truncatula</i>		MSYISLSPKLLPINTKPPFWLVQFNFY FSSNTKCNKLHFLGEKLLVGEAGHVQ ILFLIHSLIMHINIFCTCSPSPTRLPHPSL	SEQ ID NO:39
OsmiPEP164a1	miR164a	<i>Oryza sativa</i>		MQTHSNTQPSTYSLSLSLSE	SEQ ID NO:40
OsmiPEP164a2	miR164a	<i>Oryza sativa</i>		MCVCDINMHSMLMLL	SEQ ID NO:41
AlmiPEP165a	miR165a	<i>Arabidopsis lyrata</i>	HD-ZIPIII gene family, involved in vascular, root, foliar and floral development, and nodulation	MRIKLFQLRGMLSGSRILYIYTCVC	SEQ ID NO:42
AtmiPEP165a (12.3 / 2105)	miR165a	<i>Arabidopsis thaliana</i>		MRVKLFQLRGMLSGSRIL	SEQ ID NO:43
BcmiPEP165a	miR165a	<i>Brassica carinata</i>		MRMKLFQLRGMLSGSRILYIHKYVY MLIQVFDHICI	SEQ ID NO:44
BjmiPEP165a	miR165a	<i>Brassica juncea</i>		MRMKLFQLRGMLSGSRILYIHKYVYI C	SEQ ID NO:45
BnmiPEP165a	miR165a	<i>Brassica napus</i>		MRMKLFQLRGMLSGSRILYIHKYVY MIIQVFDHICI	SEQ ID NO:46
BomiPEP165a	miR165a	<i>Brassica oleracea</i>		MRMKLFQLRGMLSGSRILYIHKYVY MLIQVFDHICI	SEQ ID NO:47
BrmPEP165a	miR165a	<i>Brassica rapa</i>		MRMKLFQLRGMLSGSRILYIHKYVYI C	SEQ ID NO:48
AtmiPEP166a (4.68 / 2372)	miR166a	<i>Arabidopsis thaliana</i>		MLDLFRSNNRIEPSDFRFD	SEQ ID NO:49
AtmiPEP166b (9.35 / 576)	miR166b	<i>Arabidopsis thaliana</i>		MRDR	SEQ ID NO:50
AtmiPEP167a (11 / 1148)	miR167a	<i>Arabidopsis thaliana</i>	ARF gene family, involved in root and floral development	MNRKISLSLS	SEQ ID NO:51
AtmiPEP167b1 (5.27 / 891)	miR167b	<i>Arabidopsis thaliana</i>		MMGCFVGF	SEQ ID NO:52
AtmiPEP167b2	miR167b	<i>Arabidopsis thaliana</i>		MQEETYEG	SEQ ID NO:53

AtmiPEP169c1 (9.3 / 7110)	miR169c	<i>Arabidopsis thaliana</i>	gene family of CCAAT-binding factor, involved in nodulation, drought resistance, resistance to nitrogen deficiency	MPHTNLKDLFIFSPNVFFSFAIYLNHNS WNKNYIHKRENFHNTSFALIFFFSSIM SINYG	SEQ ID NO:54
AtmiPEP169c2	miR169c	<i>Arabidopsis thaliana</i>		MFFFRLLFISTILGKTTFNTERIFTTPL LLSFFFFRPL	SEQ ID NO:55
AtmiPEP169l (8.52 / 786)	miR169l	<i>Arabidopsis thaliana</i>		MRHKES	SEQ ID NO:56
AtmiPEP171a1 (11.05 / 4057)	miR171a	<i>Arabidopsis thaliana</i>	GRAS gene family, involved in floral, foliar, and root development, mycorrhization, nodulation	MNLLKKERQRRRQRSIGSHCIASLVL KDGVMKKI	SEQ ID NO:57
AtmiPEP171b (8.5 / 995)	miR171b	<i>Arabidopsis thaliana</i>		MVLSGKLTF	SEQ ID NO:58
MtmiPEP171b1	miR171b	<i>Medicago truncatula</i>		MLLHRLSKFCKIERDIVYIS	SEQ ID NO:59
MtmiPEP171b2	miR171b	<i>Medicago truncatula</i>		MKIEE	SEQ ID NO:60
ZmmiPEP171b	miR171b	<i>Zea mays</i>		MHLPSTPSRPPQHTSLSFLGKEMTKG TTTACFG	SEQ ID NO:61
AtmiPEP171c1 (6.68 / 1187)	miR171c	<i>Arabidopsis thaliana</i>		MLSLSHFHIC	SEQ ID NO:62
MtmiPEP171e	miR171e	<i>Medicago truncatula</i>		MMVFGKPKKAMLVRFPKTDLHV	SEQ ID NO:63
MtmiPEP171h	miR171h	<i>Medicago truncatula</i>		MASAAKVYMA	SEQ ID NO:64
AtmiPEP172a1 (8.5 / 734)	miR172a	<i>Arabidopsis thaliana</i>	AP2 gene family, involved in floral development	MASKIW	SEQ ID NO:65
AtmiPEP172a3	miR172a	<i>Arabidopsis thaliana</i>		MVRFQLSIRD	SEQ ID NO:66
AtmiPEP172b1 (7.9 / 1621)	miR172b	<i>Arabidopsis thaliana</i>		MCTYYYLINKYF	SEQ ID NO:67
AtmiPEP172c1 (7.98 / 1367)	miR172c	<i>Arabidopsis thaliana</i>		MFPAKWCRLES	SEQ ID NO:68
AtmiPEP172e1 (8.35 / 2452)	miR172e	<i>Arabidopsis thaliana</i>		MGSLSLFKSQLEILMLLSLSK	SEQ ID NO:69
AtmiPEP172e2	miR172e	<i>Arabidopsis thaliana</i>		MSVYIHVPISLNCFSKSSC	SEQ ID NO:70
AtmiPEP172e3	miR172e	<i>Arabidopsis thaliana</i>		MGVPNFRPRNR	SEQ ID NO:71

AcmiPEP319a1	miR319a	<i>Arabidopsis cebennensis</i>	TCP gene family, involved in floral and foliar development	MRSRVSFFFFKIMLFRL LGYRSM	SEQ ID NO:72
AcmiPEP319a2	miR319a	<i>Arabidopsis cebennensis</i>		MHTYIHTISNISSIFFCSKRSFSPFTYIRI IVVIDPFRIALTFR	SEQ ID NO:73
AhmiPEP319a	miR319a	<i>Arabidopsis halleri</i>		MRSRVSLFLSFSSNFAAYS PRS	SEQ ID NO:74
AlmiPEP319a	miR319a	<i>Arabidopsis lyrata</i>		MHTYIPSSSFPISSNISSVFFCYKRSFSPY TYIRIIVVIDPFRIALTFR	SEQ ID NO:75
AtmiPEP319a1 (6.56 / 5917)	miR319a	<i>Arabidopsis thaliana</i>		MNIHTYHHLLFPSLVFHQSSDVPNALSL LHIHTYEYIIVVIDPFRIALTFR	SEQ ID NO:76
AtmiPEP319a2	miR319a	<i>Arabidopsis thaliana</i>		MFQTLYLFIYIHTNILLS	SEQ ID NO:77
BrmiPEP319a	miR319a	<i>Brassica rapa</i>		MFKLYFSAILSTQYMHTYHHRIALIFL SILYPSTNYLMSPILNPT	SEQ ID NO:78
CpmiPEP319a	miR319a	<i>Carica papaya</i>		MKIKLGFSLIKIIILLDKNS	SEQ ID NO:79
CrmiPEP319a	miR319a	<i>Capsella rubella</i>		MHPHTYIHIPSSSFLISSFCL	SEQ ID NO:80
EgmiPEP319a	miR319a	<i>Eucalyptus grandis</i>		MKHIQRWRYGETSGRQGDWKRLEIK VHSNPSLKVKKNTNNFSSSL	SEQ ID NO:81
GrmiPEP319a	miR319a	<i>Gossypium raimondii</i>		MIHFNLSQWRAICMANFHLTYSFLFG VL	SEQ ID NO:82
MtmiPEP319a	miR319a	<i>Medicago truncatula</i>		MHVYLELFMVIKGLGFLLLVK	SEQ ID NO:83
OsmiPEP319a	miR319a	<i>Oryza sativa</i>		MEMIQRPCILKFFFKLSTLYIP	SEQ ID NO:84
PpmiPEP319a	miR319a	<i>Physcomitrella patens</i>		MFHRRRSSVLLPPFGQTQPNPRCLPDL RFPSCFTPCTA	SEQ ID NO:85
ThmiPEP319a1	miR319a	<i>Thellungiella halophila</i>		MTICKVSKACFYAGKIENSRLIKKIGIP KREGAPFSPIRENQ	SEQ ID NO:86
ThmiPEP319a2	miR319a	<i>Thellungiella halophila</i>		MEIQIKKKNLYIMNTQKLPNLYIYIYK YVFIKLMVVE	SEQ ID NO:87
AtmiPEP319b1 (8.04 / 5120)	miR319b	<i>Arabidopsis thaliana</i>		MVPQINLWSSRVILKIRIDSSTHREED HCIQNHKHGLSFISF	SEQ ID NO:88
AtmiPEP394a1 (9.7 / 1977)	miR394a	<i>Arabidopsis thaliana</i>	F-box gene family, involved in foliar	MSLQFYERVVSFKNTVK	SEQ ID NO:89

			development and drought resistance		
AtmiPEP395c1 (3.58 / 1429)	miR395c	<i>Arabidopsis thaliana</i>	Family of the <i>APS</i> and <i>AST</i> genes, involved in germination and sulphur metabolism	MTEQEEESQMST	SEQ ID NO:90
AtmiPEP395e1 (9.98 / 4700)	miR395e	<i>Arabidopsis thaliana</i>		MYLQYIDNVISIYSNNRRVGRMFSRV PLSTSLEIQFFIK	SEQ ID NO:91
AtmiPEP397b1 (4.53 / 1418)	miR397b	<i>Arabidopsis thaliana</i>	Family of the genes of laccases, involved in copper metabolism, their overexpression improves growth	MSKEIFFSPGFE	SEQ ID NO:92
AtmiPEP398c1	miR398c	<i>Arabidopsis thaliana</i>	<i>CSD</i> gene family, involved in copper metabolism, its overexpression improves growth	MRTHEQSTAITTLRHCYSSRFMC SQV TPAELFLYRPCFINA VAR	SEQ ID NO:93
AtmiPEP399b (11 / 678)	miR399b	<i>Arabidopsis thaliana</i>	<i>PHO2</i> gene family, involved in phosphorus metabolism	MKRNM	SEQ ID NO:94
AtmiPEP399d1 (4 / 622)	miR399d	<i>Arabidopsis thaliana</i>		MQCEI	SEQ ID NO:95
AtmiPEP403 (5.27470)	miR403	<i>Arabidopsis thaliana</i>	<i>AGO</i> gene family	MFCA	SEQ ID NO:96
AtmiPEP447a1 (6.69 / 724)	miR447a	<i>Arabidopsis thaliana</i>	Family of the genes of phosphoglycerate kinase	MVMAHH	SEQ ID NO:97
AtmiPEP447a2	miR447a	<i>Arabidopsis thaliana</i>		MMKPRWNC SLYGITEWTNNQNQKSK RKGRRTQIWRIGDRLDTVECITLML SAY	SEQ ID NO:98
AtmiPEP447b1 (4 / 1155)	miR447b	<i>Arabidopsis thaliana</i>		MLLIIVELVL	SEQ ID NO:99
AtmiPEP447b2	miR447b	<i>Arabidopsis thaliana</i>		MLCFNFR CVRRFAE	SEQ ID NO:100
AtmiPEP447c	miR447c	<i>Arabidopsis thaliana</i>		MYTYQLDNSFSWFLCTRFCLYRYFLF NFRCFRRFSE	SEQ ID NO:101

DmmiPEP1a	miR1	<i>Drosophila melanogaster</i>	<i>Muscular differentiation</i>	MWREVCAQKSQTKRRNFITGNQRRN KTKANRKAETKQKQVYEFFVQARER CKTRKKHEKKTLLKTKKIQNRYRAV SENEWGKGFP SHI	SEQ ID NO:102
DmmiPEP1b	miR1	<i>Drosophila melanogaster</i>	<i>Muscular differentiation</i>	MRTKKSNNKKAQFYYGQPTTKQNKSQ PKSRNKA AKSL	SEQ ID NO:103
DmmiPEP8	miR8	<i>Drosophila melanogaster</i>	Growth	MEPGFVFVLFPTHLSTQHTQREKSILV MGLNLQSAKQSDKQNSKERKKNTQI NSQRIPYRQGGQC SKVLSP	SEQ ID NO:104
HsmiPEP155	miR155	<i>Homo sapiens</i>	inflammation	MEMALMVAQTRKGKSVV	SEQ ID NO:355
AtmiPEP157c (5.95 / 1776)	miR157c	<i>Arabidopsis thaliana</i>	SPL gene family, involved in development of the stem and flowering	MMLHITHRFESDVGC	SEQ ID NO:375
AtmiPEP157d (5.27 / 524)	miR157d	<i>Arabidopsis thaliana</i>		MLYV	SEQ ID NO:376
AtmiPEP160c (9.98 / 1790)	miR160c	<i>Arabidopsis thaliana</i>	ARF gene family, involved in germination, development and flowering	MFMRRLVYNNIYI	SEQ ID NO:377
AtmiPEP164b (4.72 / 1949)	miR164b	<i>Arabidopsis thaliana</i>	NAC gene family, involved in root, foliar and floral development	MMKVCDEQDGEAGHVHY	SEQ ID NO:378

AtmiPEP166c (10.42 / 3407)	miR166c	<i>Arabidopsis thaliana</i>	HD-ZIPIII gene family, involved in vascular, root, foliar and floral development and nodulation	MKKRITRINLEEQIKKTLDDSRTRLHSP	SEQ ID NO:379
AtmiPEP166d (8.35 / 1125)	miR166d	<i>Arabidopsis thaliana</i>		MKKIGSIDSF	SEQ ID NO:380
AtmiPEP169a (9.5 / 784)	miR169a	<i>Arabidopsis thaliana</i>	Gene family of CCAAT-binding factor, involved in nodulation, drought resistance, resistance to nitrogen deficiency	MTCRFK	SEQ ID NO:381
AtmiPEP169h1 (5.28 / 349)	miR169h	<i>Arabidopsis thaliana</i>		MVT	
AtmiPEP169h2	miR169h	<i>Arabidopsis thaliana</i>		MKNENLCGSQG	SEQ ID NO:382
AtmiPEP169n (8.96 / 5315)	miR169n	<i>Arabidopsis thaliana</i>		MKCMMKKRGLTWRKASCLVAKDDL PDLFRLHDSISNSCILDYYTF	SEQ ID NO:383
AtmiPEP170 (5.75 / 879)	miR170	<i>Arabidopsis thaliana</i>	GRAS gene family, involved in floral, foliar, and root development, mycorrhization, nodulation	MFPRESL	SEQ ID NO:384

AtmiPEP396a (5.3 / 3636)	miR396a	<i>Arabidopsis thaliana</i>	Family of the GRF genes involved in root development and cellular proliferation, mycorrhization	MTLSVFFHSFLELQNFFRFFFSFDISY A	SEQ ID NO:385
AtmiPEP399c (8.66/2703)	miR399c	<i>Arabidopsis thaliana</i>	PHO2 gene family, involved in phosphorus metabolism	MSLAKGELPCHCFRLNTVYNRFC	SEQ ID NO:386
MtmiPEP169d	miR169d	<i>Medicago tuncatula</i>	Family NF-YA genes (or HAP2 genes)	MVKESFMERLKVR	SEQ ID NO: 424

Table 1. List of potential miPEPs (miPEPs)

miPEP	Organism	Sequence of the miORF	SEQ ID
AtmiPEP156a1	<i>Arabidopsis thaliana</i>	ATGTTCTGTTCAATTCAATGCGTCGCCAGACATCTGTTCCCTTTGC ATGTAAGAGAGATAAAGAAAGCGACAAGAGCCATAAAGAAAGG TAA	SEQ ID NO:105
AtmiPEP156a2	<i>Arabidopsis thaliana</i>	ATGCGTCGCCAGACATCTGTTCCCTTTGCATGTAAGAGAGATAAA GAAAGCGACAAGAGCCATAAAGAAAGGTAA	SEQ ID NO:106
AtmiPEP156a3	<i>Arabidopsis thaliana</i>	ATGGTTATGTTTTTCTCGATTTAGACAAAAACCCTAGATTTGATC TTCTAAAGGGTCTCAAATGGAATCTCTTCTCTTCTCATATCTCTCC CTCTCTCCCTCCCTCTCTTTGA	SEQ ID NO:107
AtmiPEP156c1	<i>Arabidopsis thaliana</i>	ATGAAGGACAACCTTCCTCTTCTCCTTCGGTTATAA	SEQ ID NO:108
AtmiPEP156c2	<i>Arabidopsis thaliana</i>	ATGAGTGATGACTGA	SEQ ID NO:109
AtmiPEP156e1	<i>Arabidopsis thaliana</i>	ATGATATATATAAATAAATATGGGTCGATATCGGCTGTGGAGGAC GACTAG	SEQ ID NO:110
AtmiPEP156f1	<i>Arabidopsis thaliana</i>	ATGAGCCAAAGATAA	SEQ ID NO:111
AlmiPEP159a	<i>Arabidopsis lyrata</i>	ATGACGTGTCCTCTTCTCTCTCTCTTTCCTTCTCTCTAAGTATAT TTAG	SEQ ID NO:112
AtmiPEP159a1	<i>Arabidopsis thaliana</i>	ATGACGTGGCCTCTTCTCTCTCTCTTTCCTTCTCTCTAAGTATGT TTAG	SEQ ID NO:113
CrmiPEP159a	<i>Capsella rubella</i>	ATGACGTGTACTCTCTCTGCTCTATCTCTCTCTCTCTAAATATGTTA GGGTAA	SEQ ID NO:114
AtmiPEP159b1	<i>Arabidopsis thaliana</i>	ATGTTTTATCTTTCATAA	SEQ ID NO:115
AtmiPEP159b2	<i>Arabidopsis thaliana</i>	ATGGTTAATACTAGTAGCTTTTTTCATTTCAAGTTTTATCCTTCCAT TGGTTCTTTCTGAGTCAAATTGTCTCCTGTTTCGAACCATATATAA GTTTTCAATGGTTTTGTATTAA	SEQ ID NO:116
AtmiPEP160a1	<i>Arabidopsis thaliana</i>	ATGTTTTGTTTGTTGATTCCCATCTTCTCTTTTGTCTTTTCACCAA TCGTCATTTAAGGCTTCAAGAACAGTAA	SEQ ID NO:117
AtmiPEP160b1	<i>Arabidopsis thaliana</i>	ATGTTTTCCCCTCAATGA	SEQ ID NO:118
AtmiPEP160b2	<i>Arabidopsis thaliana</i>	ATGAAATACATACACATTTTGATTTTATTTAAATCAAGATCGACG TATAAGCTATCCACCAATCATATTTAA	SEQ ID NO:119
AtmiPEP161	<i>Arabidopsis thaliana</i>	ATGAAAATTCCATTGTTTCTGCCGAAGCTTTGA	SEQ ID NO:120

AtmiPEP162a1	<i>Arabidopsis thaliana</i>	ATGGTATCTGGTCAAGAAGATTCCTGGTTAAAACCTTTCATCTCTCTGTTTCCTTTTTCTTTCTTTGTGGATTCAATTAATTGA	SEQ ID NO:121
AtmiPEP162b1	<i>Arabidopsis thaliana</i>	ATGTTTCTTTTAATCTTTTGAGATTAATAATGATTTGTGTTTGTTCATCAACCGATTTTCTCAGATCTGTCAATTATTTTGTTTATTTATTTATGATTTATGA	SEQ ID NO:122
AtmiPEP163-1	<i>Arabidopsis thaliana</i>	ATGTCCACTACTCAAGAGCATAGGTCTTGA	SEQ ID NO:123
AtmiPEP163-2	<i>Arabidopsis thaliana</i>	ATGATACTAAAGTGCTGGAGTTCCTGGTTCCTGAGAGTGAGTCCATATCAAAATGCGCATTTCGTTATCACTTGGTTGA	SEQ ID NO:124
AlmiPEP164a1	<i>Arabidopsis lyrata</i>	ATGCCCTTAGCAGTTATTAGACAAGGGATTGTTTGGCCCTAG	SEQ ID NO:125
AlmiPEP164a2	<i>Arabidopsis lyrata</i>	ATGCCATCATGGCATGACATGGTTCTTTTGCCTTACGTAAAACACACTCACGCCAACACACGCCACATAACATAA	SEQ ID NO:126
AlmiPEP164a3	<i>Arabidopsis lyrata</i>	ATGACATGGTTCTTTTGCCTTACGTAA	SEQ ID NO:127
AtmiPEP164a1	<i>Arabidopsis thaliana</i>	ATGCCATCATGGCATGGTATGGTTCTTTTGCCTTACGTAAAACACACTCACGCCAGCACACACACACACATAACATATACGGATGTGCGTGTGAGCTAGTCTTCCATTAA	SEQ ID NO:128
AtmiPEP164a2	<i>Arabidopsis thaliana</i>	ATGGCATGGTATGGTTCTTTTGCCTTACGTAAAACACACTCACGCCAGCACACACACACACACATAA	SEQ ID NO:129
AtmiPEP164a3	<i>Arabidopsis thaliana</i>	ATGGTATGGTTCTTTTGCCTTACGTAA	SEQ ID NO:130
BrmiPEP164a1	<i>Brassica rapa</i>	ATGATGATAATTTTGTGGAAATAA	SEQ ID NO:131
BrmiPEP164a2	<i>Brassica rapa</i>	ATGCTTTGGGCCAAGCTAGTTTCTTTTAGCACTCTTCACTCACTAGTTTTTCTTCTCAGCCCTTCTTTTGCCTGA	SEQ ID NO:132
BrmiPEP164a3	<i>Brassica rapa</i>	ATGCCATCATGGCATGGCATTGTCATTTTGCCTTTCGTAAAACACACTCACGCCAACATACATTATTCATATTCATGTGTATGTATATGATGCCATCATGGCATATGCCATCATGGCAT	SEQ ID NO:133
CpmiPEP164a1	<i>Carica papaya</i>	ATGATTGCATGCCATCCCTACTTGCCTTTTCCCCTTTTCCCTTTCTCTAACATTTTACTCAATCTTCTTCTCCCCCTCCCCCTTCCCCCTCTCTGCCATTATAA	SEQ ID NO:134
CpmiPEP164a2	<i>Carica papaya</i>	ATGCCATCCCTACTTGCCTTTTCCCCTTTTCCCTTTCTCTAACATTTTACTCAATCTTCTTCTCCCCCTCCCCCTTCCCCCTCTCTGCCATTATAACCATAATTAAACCTCTCTCCCTCTCTCTCCCTCTCTCTCTCTCTCTCTCTGGGTTCTCAGTATAA	SEQ ID NO:135
CrmiPEP164a1	<i>Capsella rubella</i>	ATGGAATTAAAAGTTTGAGAACTTGGCAGTTATTAGACAAGGTATAG	SEQ ID NO:136

CrmiPEP164a2	<i>Capsella rubella</i>	ATGCCATCATGGCATGGCATGGCATGTTTCTATTGCCTTACGTAA	SEQ ID NO:137
CrmiPEP164a3	<i>Capsella rubella</i>	ATGGCATGGCATGTTTCTATTGCCTTACGTAAAACACACTCACGC CAACACATACTCACTATACATGTAAATAAGTATGTGCGCGTGTGA	SEQ ID NO:138
GrmiPEP164a1	<i>Gossypium raimondii</i>	ATGATGAGATCAAGAATTTTAAAGTTTCAATATAGATTTGGCATG GGTATTGGCGGCAGAAAGCAATTAAAAAACCAGTTATGTCAAAT TCAAGGTCGTATCAGTTAA	SEQ ID NO:139
GrmiPEP164a2	<i>Gossypium raimondii</i>	ATGTCAAATTCAAGGTCGTATCAGTTAAAATGA	SEQ ID NO:140
GrmiPEP164a3	<i>Gossypium raimondii</i>	ATGAATGAAGATTTAGAAATTTCAACAAGGAAGAGGACCCCA GCTTTGTAA	SEQ ID NO:141
MtmiPEP164a1	<i>Medicago truncatula</i>	ATGCCCCAAATTTGATATTTTTTTTTTATATATTTGTATAG	SEQ ID NO:142
MtmiPEP164a2	<i>Medicago truncatula</i>	ATGTCATATATCTCTCTCTCTCCTAAGTTGCTACCTATAAATACTA AGCCTTTCCCTTGTTGGTTCAATTCAACTTCTACTTCTCATCAA CACAAAGTGCAATAAGCTTCATTTCTGGGTGAGAAGCTCCTTGT TGGAGAAGCAGGGCACGTGCAAATCCTCTTTCTGATTCATTCTCT CATAATGCATATCAATATCTTTTGCACGTGCTCCCTTCTCCA AGG	SEQ ID NO:143
OsmiPEP164a1	<i>Oryza sativa</i>	ATGCAAACCCACTCCAACACTCCACAATCCACATACTCTCTCTCT CTCTCTCTCTCTGAGTAG	SEQ ID NO:144
OsmiPEP164a2	<i>Oryza sativa</i>	ATGTGTGTGTGTGATATCAATATGCATTTCGATGTTGATGCTACTGT AG	SEQ ID NO:145
AlmiPEP165a	<i>Arabidopsis lyrata</i>	ATGAGAATTAAGCTATTTTCAGTTGAGGGGAATGTTGTCTGGATCG AGGATATTATACATATATACATGTGTATGTTGA	SEQ ID NO:146
AtmiPEP165a	<i>Arabidopsis thaliana</i>	ATGAGGGTTAAGCTATTTTCAGTTGAGGGGAATGTTGTCTGGATCG AGGATATTATAG	SEQ ID NO:147
BcmiPEP165a	<i>Brassica carinata</i>	ATGAGAATGAAGCTATTTTCAGTTGAGGGGAATGTTGTCTGGATCG AGGATATTATATATACACAAATACGTATATATGTTAATACAAGTG TTTGATCATATATGTATATAG	SEQ ID NO:148
BjmiPEP165a	<i>Brassica juncea</i>	ATGAGAATGAAGCTATTTTCAGTTGAGGGGAATGTTGTCTGGATCG AGGATATTATATATACACAAATATGTATATATATGTTAA	SEQ ID NO:149
BnmiPEP165a	<i>Brassica napus</i>	ATGAGAATGAAGCTATTTTCAGTTGAGGGGAATGTTGTCTGGATCG AGGATATTATATATACACAAATACGTATATATGATAATACAAGTG TTTGATCATATATGTATATAG	SEQ ID NO:150

BomiPEP165a	<i>Brassica oleracea</i>	ATGAGAATGAAGCTATTTTCAGTTGAGGGGAATGTTGTCTGGATCG AGGATATTATATATACACAAGTACGTATATATGTTAATACAAGTG TTTGATCATATATGTATATAG	SEQ ID NO:151
BrmiPEP165a	<i>Brassica rapa</i>	ATGAGAATGAAGCTATTTTCAGTTGAGGGGAATGTTGTCTGGATCG AGGATATTATATATACACAATATGTATATATATGTAA	SEQ ID NO:152
AtmiPEP166a	<i>Arabidopsis thaliana</i>	ATGTTGGATCTCTTTTCGATCTAACAATCGAATTGAACCTTCAGATT TCAGATTTGATTAG	SEQ ID NO:153
AtmiPEP166b	<i>Arabidopsis thaliana</i>	ATGAGAGATAGATAA	SEQ ID NO:154
AtmiPEP167a	<i>Arabidopsis thaliana</i>	ATGAACAGAAAAATCTCTCTTTCTCTTTCTTGA	SEQ ID NO:155
AtmiPEP167b1	<i>Arabidopsis thaliana</i>	ATGATGGGTTGTTTTGTGGGATTTTAA	SEQ ID NO:156
AtmiPEP167b2	<i>Arabidopsis thaliana</i>	ATGCAGGAGGAAACATATGAGGGGTGA	SEQ ID NO:157
AtmiPEP169c1	<i>Arabidopsis thaliana</i>	ATGCCACATACAACTTGAAAGATCTCTTCATCTTTTCTCCAAATG TTTTTTTTTCGTTTGCTATTTATCTCCACAATTCTTGGAACAAAA CTACATTCACAAACGAGAGAATTTTCACAACACCTCTTTTGCTCTC ATTTTTTTTTTTTCGTCCATTATGAGTATTAATTATGGTTAG	SEQ ID NO:158
AtmiPEP169c2	<i>Arabidopsis thaliana</i>	ATGTTTTTTTTTCGTTTGCTATTTATCTCCACAATTCTTGGAACAA AACTACATTCACAAACGAGAGAATTTTCACAACACCTCTTTTGC TCTCATTTTTTTTTTTTCGTCCATTATGA	SEQ ID NO:159
AtmiPEP169l1	<i>Arabidopsis thaliana</i>	ATGAGACATAAAGAGAGTTAA	SEQ ID NO:160
AtmiPEP171a1	<i>Arabidopsis thaliana</i>	ATGAACCTCCTCAAGAAGGAAAGACAGAGGAGGAGACAAAGAA GTATAGGTTACATTGCATAGCCAGTTTAGTTTTGAAGGATGGAT ATATGAAAAAATATGA	SEQ ID NO:161
AtmiPEP171b	<i>Arabidopsis thaliana</i>	ATGGTTCTCTCCGGTAAATTAACATTTTAG	SEQ ID NO:162
MtmiPEP171b1	<i>Medicago truncatula</i>	ATGCTTCTTCATAGGCTCTCCAAATTTTGCAAAATTGAAAGAGAC ATAGTATATATATCTTAG	SEQ ID NO:163
MtmiPEP171b2	<i>Medicago truncatula</i>	ATGAAGATTGAAGAGTAA	SEQ ID NO:164
ZmmiPEP171b	<i>Zea mays</i>	ATGCATCTGCCTTCAACTCCCTCTCGCCCCCACCACACACAT CTCTCTCTTTTCTAGGGAAGGAAATGACGAAGGGGACGACGACG GCATGCTTCGGCTAG	SEQ ID NO:165
AtmiPEP171c1	<i>Arabidopsis thaliana</i>	ATGTTGTCTCTTTCTCATTTTCATATCTGCTAA	SEQ ID NO:166
MtmiPEP171e	<i>Medicago truncatula</i>	ATGATGGTGTGTTGGGAAGCCGAAAAAAGCGATGTTGGTGAGGTT CAATCCGAAGACGGATTACATGTATAG	SEQ ID NO:167

MtmiPEP171h	<i>Medicago truncatula</i>	ATGGCTTCAGCTGCAAAAGTATACATGGCGTGA	SEQ ID NO:168
AtmiPEP172a1	<i>Arabidopsis thaliana</i>	ATGGCTTCCAAGATCTGGTAA	SEQ ID NO:169
AtmiPEP172a3	<i>Arabidopsis thaliana</i>	ATGGTTAGGTTCCTCACTAAGTATACGAGATTAA	SEQ ID NO:170
AtmiPEP172b1	<i>Arabidopsis thaliana</i>	ATGTGTACGTACTATTATCTCATAAATAAATATTTTTAA	SEQ ID NO:171
AtmiPEP172c1	<i>Arabidopsis thaliana</i>	ATGTTTCCAGCAAAATGGTGCCGTCTTGAGTCTTGA	SEQ ID NO:172
AtmiPEP172e1	<i>Arabidopsis thaliana</i>	ATGGGATCTCTCTCTTTATTTAAAAGTCAATTAGAGATCTTGATGC TACTTCTGTCCCTTTCCAAGTGA	SEQ ID NO:173
AtmiPEP172e2	<i>Arabidopsis thaliana</i>	ATGAGTGTATATATTCATGTACCTATCTCTCTCAATTGCTTCTCAC CAAAATCATCTTGCTGA	SEQ ID NO:174
AtmiPEP172e3	<i>Arabidopsis thaliana</i>	ATGGGAGTTCCCAACTTTAGACCTCGAAACCGATAA	SEQ ID NO:175
AcmiPEP319a1	<i>Arabidopsis cebennensis</i>	ATGAGATCTAGGGTTTCTTTCTTTTTCTTCAAAATCATGCTTTTTTC GCTTGCTAGGTTATAGATCCATGTAA	SEQ ID NO:176
AcmiPEP319a2	<i>Arabidopsis cebennensis</i>	ATGCATACATACATACATACCATCTCTAATATTTTCATCAATCTTCT TTTGTTCCAAACGCCTTTCTCTCCATTTACATACATACGAATCATT GTTGTCATAGATCCGTTTAGAATTGCTTTAACTTTTAGATGA	SEQ ID NO:177
AhmiPEP319a	<i>Arabidopsis halleri</i>	ATGAGATCTAGGGTTTCTTTGTTTCTTTTCGTTTTCTTCAAATTTTGC TGCATATTCTCCAAGATCATGA	SEQ ID NO:178
AlmiPEP319a	<i>Arabidopsis lyrata</i>	ATGCATACATACATACCATCATCATCTTTTCCCATCTCTAATATTT CATCAGTCTTCTTTTGTTACAAACGCTCTTTCTCGCCATATACATA CATAAGAATCATTGTTGTCATAGATCCGTTTAGAATTGCTTTAACT TTTAGATGA	SEQ ID NO:179
AtmiPEP319a1	<i>Arabidopsis thaliana</i>	ATGAATATACATACATACCATCATCTTCTTTTCCCATCTCTAGTTT TTCATCAATCTTCTGATGTTCCAAACGCTCTATCTTTCATATACA TACATACGAATATATTATTGTTGTCATAGATCCATTTAGAATCACT TTAGCTTTTAGATGA	SEQ ID NO:180
AtmiPEP319a2	<i>Arabidopsis thaliana</i>	ATGTTCCAAACGCTCTATCTCTTCATATACATACATACGAATATAT TATTGTTGTCATAG	SEQ ID NO:181
BrmiPEP319a	<i>Brassica rapa</i>	ATGTTTAAAGCTCTACTTCTCAGCAATTCTCTCCACCCAATACATGC ATACATACCATCATCGTATCGCTCTAATTTTTCTATCAATCTTGTA TCCTTCCACAAATTATCTTATGTCTCCCATTTTAAATCCTACATAG	SEQ ID NO:182
CpmiPEP319a	<i>Carica papaya</i>	ATGAAGATTAAATTAGGTTTTAGTCTTATTAAGATTATTATATTAC TAGACAAAAACAGTTAA	SEQ ID NO:183

CrmiPEP319a	<i>Capsella rubella</i>	ATGCATCCACATACATACATATACCATCATCTTCTTTTCTCA TCTCTAGTTTTTTGTTTATAA	SEQ ID NO:184
EgmiPEP319a	<i>Eucalyptus grandis</i>	ATGAAGCATATTCAAAGGTGGAGATATGGGGAGACTTCCGGAAG GCAAGGGGATTGGAAGGCTCGAGATCAAAGTGCATAGCAACC CTTCGCTAAAGGTGAAAAAGAATACGAATAACTTCAGTAGCTCAC TTTAA	SEQ ID NO:185
GrmiPEP319a	<i>Gossypium raimondii</i>	ATGATCCATTTCAACCTGTCACAGTGGAGAGCAATTTGTATGGCT AATTTCCATCTCACCTATTCTTTTCTGTTTGGGGTTCTCTAG	SEQ ID NO:186
MtmiPEP319a	<i>Medicago truncatula</i>	ATGCATGTATATCTTGAATTGTTTATGGTAATAAAGGGGTAGGA TTTCTCCTTTTGGTGAAGTGA	SEQ ID NO:187
OsmiPEP319a	<i>Oryza sativa</i>	ATGGAAATGATACAAAGGCCGTGTTTAATTTTAAAATTTTTTTTCA AACTTTCAACACTTTACATCCCATAA	SEQ ID NO:188
PpmiPEP319a	<i>Physcomitrella patens</i>	ATGTTCCACCGTCGGAGATCCTCGGTGCTGCTACCCCCGTTCCGGC CAAACCCAACCAACCCTAGGTGTCTGCCGGACCTCCGCTTCCCC TCCTGCTTACCCCCCTGCACCGCTTAA	SEQ ID NO:189
ThmiPEP319a1	<i>Theellungiella halophila</i>	ATGACGATATGTAAAGTAAGCAAGGCATGTTTTTATGCAGGGAA GATTGAAAATTCAAGATTAATCAAGAAAATTGGAATACCAAAAA GAGAGGGAGCTCCCTTCAGTCCAATCAGAGAGAATCAATGA	SEQ ID NO:190
ThmiPEP319a2	<i>Theellungiella halophila</i>	ATGGAGATTCAAATTAAGAAAGAAACTTATATATAATGAATAC ACAAAAGCTACCTAATCTGTATATATATATATAAATATGTCTT CATTAAATTAATGGTCGTGGAATAG	SEQ ID NO:191
AtmiPEP319b1	<i>Arabidopsis thaliana</i>	ATGGTACCTCAAATTAATCTATGGTCATCTAGGGTTATCTTGAAG ATTAGAATTGATTCTAGCACGCACAGAGAGGAAGATCATTGCATC CAGAATCACAAACATG ³ GCCTATCTTTTATCTTTTCTTTTGA	SEQ ID NO:192
AtmiPEP394a1	<i>Arabidopsis thaliana</i>	ATGTCTCTCCAATTTTATGAGAGGGTTTCCTTCAAGAACACAGTA AAATAG	SEQ ID NO:193
AtmiPEP395c1	<i>Arabidopsis thaliana</i>	ATGACAGAGCAAGAAGAAGAAAGTCAAATGTCCACATGA	SEQ ID NO:194
AtmiPEP395e1	<i>Arabidopsis thaliana</i>	ATGTATCTACAATATATTGATAATGTAATATCTATATATTCAAAC AATCGTCGTGTTGGTCGGATGTTTTCTAGAGTTCCTCTGAGCACTT CATTGGAGATACAATTTTTTATAAAATAG	SEQ ID NO:195
AtmiPEP397b1	<i>Arabidopsis thaliana</i>	ATGAGCAAGGAGATATTTTTTCCCTGGGTTTGAATGA	SEQ ID NO:196

AtmiPEP398c1	<i>Arabidopsis thaliana</i>	ATGAGAACACACGAGCAATCAACGGCTATAACGACGCTACGTCA TTGTTACAGCTCTCGTTTCATGTGTTCTCAGGTCACCCCTGCTGAG CTCTTTCTCTACCGTCCATGTTTTATCAACGCCGTGGCCCGTG	SEQ ID NO:197
AtmiPEP399b	<i>Arabidopsis thaliana</i>	ATGAAGAGAAACATGTAA	SEQ ID NO:198
AtmiPEP399d1	<i>Arabidopsis thaliana</i>	ATGCAATGTGAAATATGA	SEQ ID NO:199
AtmiPEP403	<i>Arabidopsis thaliana</i>	ATGTTTTGTGCTTGA	SEQ ID NO:200
AtmiPEP447a1	<i>Arabidopsis thaliana</i>	ATGGTCATGGCTCATCATTAG	SEQ ID NO:201
AtmiPEP447a2	<i>Arabidopsis thaliana</i>	ATGATGAAACCTCGATGGAACCTGCTCTCTTTATGGAATCACGGAA TGGACAAATAATCAAAATCAGAAATCGAAGCGAAAAGGGAGGA GAAAAACGCAGATTTGGAGGATTGGGGACAGATTAGATACTGTT GAATGCATCACTCTAATGCTATCAGCCTATTAA	SEQ ID NO:202
AtmiPEP447b1	<i>Arabidopsis thaliana</i>	ATGCTGCTTATCATCGTGGAGTTGGTTCTGTAA	SEQ ID NO:203
AtmiPEP447b2	<i>Arabidopsis thaliana</i>	ATGCTTTGTTTCAATTTTCAGGTGCGTTAGAAGGTTTGCAGAGTAG	SEQ ID NO:204
AtmiPEP447c	<i>Arabidopsis thaliana</i>	ATGTACACCTACCAGCTTGATAACTCTTTTTTCGTGGTTTCTGTGTA CTCGTTTCTGTTTGTACAGATACTTCTTGTTCAATTTTCAGATGCTTT AGAAGGTTTTTCGGAG	SEQ ID NO:205
dmimiPEP1a	<i>Drosophila melanogaster</i>	ATGTGGCGCGAAGTATGCGCACAAAAAGTCAAACAAAAAGGCG CAATTTTATTACGGGCAACCAACGACGAAACAAAAACAAAAGCCA ACCGAAAAGCAGAAACAAAGCAGCAAAAAAGTTTATGAATTTTTT GTGCAGGCGCGTGAAAGATGCAAAACGAGAAAAAACATGAAA AAAAAACATTAAAAAAAACAAAAAAATCCAAAACAGATACCG AGCTGTATCCGAAAACGAGTGGGGAAAGGGGTTTCCCAGTCACA TATAA	SEQ ID NO:206
DmimiPEP1b	<i>Drosophila melanogaster</i>	ATGCGCACAAAAAGTCAAACAAAAAGGCGCAATTTTATTACGG GCAACCAACGACGAAACAAAAACAAAAGCCAACCGAAAAGCAGA AACAAAGCAGCAAAAAAGTTTATGA	SEQ ID NO:207
DmimiPEP8	<i>Drosophila melanogaster</i>	ATGGAGCCTGGCTTTGTTTTTGTGTTTTATTTCCAACCCACTTGAGCA CACAGCACACAGAGAGAAAAATCAATACTCGTTATGGGATTA AATTTACAAAGCGCAAAGCAAAGCGACAAACAAAATTCAAAGA AAGAAAAAAAACACTCAAATAAACTCACAAAGAATTCCTTATC GCCAAGGGGGCCAAATGTTCTAAGGTTCTTTTCGCCTTGA	SEQ ID NO:208
HsmiPEP155	<i>Homo sapiens</i>	TGGAGATGGCTCTAATGGTGGCACAACACAGGAAGGGGAAATCT GTGGTTTAA	SEQ ID NO:356

AtmiPEP157c	<i>Arabidopsis thaliana</i>	ATGATGTTGCATATCACACATAGGTTTGAGAGTGATGTTGGTTGT TGA	SEQ ID NO : 387
AtmiPEP157d	<i>Arabidopsis thaliana</i>	ATGCTGTATGTATAG	SEQ ID NO : 388
AtmiPEP160c	<i>Arabidopsis thaliana</i>	ATGTTTCATGCGTAGAGGTTTGGTATACAACAATATATACATATAA	SEQ ID NO : 389
AtmiPEP164b	<i>Arabidopsis thaliana</i>	ATGATGAAGGTGTGTGATGAGCAAGATGGAGAAGCAGGGCACGT GCATTACTAG	SEQ ID NO : 390
AtmiPEP166c	<i>Arabidopsis thaliana</i>	ATGAAGAAGAGAATCACTCGAATTAATTTGGAAGAACAATTAA GAAAACCCTAGATGATTCTCGGACCAGGCTTCATTCCCCCTAA	SEQ ID NO : 391
AtmiPEP166d	<i>Arabidopsis thaliana</i>	ATGAAGAAGATCGGTAGtATTGATTTCATTTTAA	SEQ ID NO : 392
AtmiPEP169a	<i>Arabidopsis thaliana</i>	ATGACTTGCCGATTTAAATGA	SEQ ID NO : 393
AtmiPEP169h1	<i>Arabidopsis thaliana</i>	ATGGTGACATGA	SEQ ID NO : 394
AtmiPEP169h2	<i>Arabidopsis thaliana</i>	ATGAAGAATGAGAACTTGTGTGGTAGCCAAGGATGA	SEQ ID NO : 395
AtmiPEP169n	<i>Arabidopsis thaliana</i>	ATGAAGTGTATGATGAAGAAGAGAGGTCTAACATGGCGGAAAGC GTCATGTTTAGTAGCCAAGGATGACTTGCCCTGATCTTTTTTCGCCTC CACGATTCAATTTCAAATTCATGCATTTTGGATTATTATACCTTTT AA	SEQ ID NO : 396
AtmiPEP170	<i>Arabidopsis thaliana</i>	ATGTTTCCGAGAGAGTCCCTCTGA	SEQ ID NO : 397
AtmiPEP396a	<i>Arabidopsis thaliana</i>	ATGACCCTCTCTGTATTCTTCCACAGCTTTCTTGAACTGCAAACT TCTTCAGATTTTTTTTTTTTTCTTTTGATATCTCTTACGCATAA	SEQ ID NO : 398
AtmiPEP399c	<i>Arabidopsis thaliana</i>	ATGTCACTTGCCAAAGGAGAGTTGCCCTGTCACTGCTTCCGCTTA AACACAGTCTATAACCGGTTCTGCTAA	SEQ ID NO : 399
MtmiPEP169d	<i>Medicago truncatula</i>	ATGGTCAAAGAGTCTTTCATGGAGAGGTTGAAAGTGAGATGA	SEQ ID NO : 425

Table 2. List of the miORFs

miPEP	Organism	Sequence of the Pri-miRNA	SEQ ID
AtmiPEP156a1 AtmiPEP156a2 AtmiPEP156a3	<i>Arabidopsis thaliana</i>	ATTCATTGTTCACTCTCAAATCTCAAGTTCATTGCCATTTTTAGGTCTCTC TATAAATTCAAATGTTCTGTTCAATTCAATGCGTCGCCAGACATCTGTTC CCTTTGCATGTAAGAGAGATAAAGAAAAGCGACAAGAGCCATAAAGAAA GGTAAGACTCTTTGAAATAGAGAGAGATAAGGTTTTCTCTTATCTTCTTC TCATCAGATCTTTGTTTCTTTACCCTCTTTCTTTCTTTTTTTGCTTTTTATG GTTATGTTTTTTCTCGATTTAGACAAAAACCCTAGATTTGATCTTCTAAAG GGTCTCAAATGGAATCTTCTCTTCTCTCATATCTCTCCCTCTCTCCCTCCC TCTCTTTGATTCTTTGTCTTCTCCAGTTAAAACTCAGATCTAACACAAAGC TTAAAAGATTCTCATCGTTTCTTGTTTTCTTTGTTTCATCTTGTAGATCTCT GAAGTTGGACTAATTGTGAATGAAAGAGTTGGGACAAGAGAAACGCAA AGAAACTGACAGAAGAGAGTGAGCACACAAAGGCAATTTGCATATCATT GCACTTGCTTCTCTTGCGTGCTCACTGCTCTTCTGTCTAGATTCCGGTGCT GATCTCTTT	SEQ ID NO:209
AtmiPEP156c1 AtmiPEP156c2	<i>Arabidopsis thaliana</i>	CTCTGCCTTTAGTTCTTTCTTTTTTTGGTAATATATTTATTTTTTCGTTACGAT TTGGTCAAAACCCTAGATTTGTTTTCCAAAAGCATATCTGAAAATGAAGG ACAACTTTTCTCTTCTCCTTCGGTTATAAATATTCTCTCCGGTTTTGCTTGT TTAACCTAAAAGCCTCAGATCTAACTCCAACACCTTCAAAGTCTGCCTCC TTTCCAATCTTCTTTCTTCTGTTTCGATCTCTAATCTCAGAAATTTGTGTGGT AAGGTAAAGGTGATAATGAGTGATGACTGATGAGGGAGTTTTGGGACAA ATTTTAAGAGAAACGCATAGAACTGACAGAAGAGAGTGAGCACACAA AGGCACTTTGCATGTTTCGATGCATTTGCTTCTCTTGCGTGCTCACTGCTCT ATCTGTCAGATTCCGGCT	SEQ ID NO:210
AtmiPEP156e1	<i>Arabidopsis thaliana</i>	TCCCACATCCAAAGATAGAAAGATGTAAGGTCTAGAGTCTTGTTCTTAAT CCCCTAACAGAACAAATGATATATATAAATAAATATGGGTTCGATATCGGC TGTGGAGGACGACTAGCTACGGTTTCGAGCCTGGTCACATGCGTAGAGT GTGAAAGGTAATTAGGAGGTGACAGAAGAGAGTGAGCACACATGGTGG TTTCTTGATGCTTTTTTTGATTAGGGTTTCATGCTTGAAGCTATGTGTGCT TACTCTCTCTGTCAACCCCT	SEQ ID NO:211
AtmiPEP156f1	<i>Arabidopsis thaliana</i>	TCCCACAGCCAATGAGCCAAAGATAAAGAAACACCTATCCTATAATAAT TTAGAGCAATATACCTCCATAATGGAACATCTATATATATAAAGGTATCC	SEQ ID NO:212

		GTATATCTCTATATATTATATTCATTGAGTTTAAAGTGGCTAGGGTTTATA GATGTATGTGATATTAAGAGATATGAAACATATTTGTTCGACGGTTTGAGT GGTGAGGAATTGATGGTGACAGAAGAGAGTGAGCACACATGGTGGCTTT CTTGCATATTTGAAGGTTCCATGCTTGAAGCTATGTGTGCTCACTCTCTAT CCGTCACCCCCTTCTCTCCCTCTCCCTC	
AlmiPEP159a	<i>Arabidopsis lyrata</i>	AAAAAATGACGTGTCCTCTTCTCTCTCTCTCTTTTCCTTCTCTCTAAGTATA TTTAGGGTTAATTATTAGGGTTCTTTATCTCTTTCTTCAGTCTTTGAAGTTT CTTCAATAGCTTTAATTGAAGTGATTTACCTCTCTGGGTGTTTTTAGTATA TATATCATGTACATGATCGAATTTCTTTCTATCCAAGTTCTCATCAAACCT TCTCATGTTTTGAAGAGTTAAAGGCTTTATAGTTTGCTTAGGTCAGATCC ATAACATACTGTATTTGACAAGTTTCTTTGTCTCACGATAGATCTTGGTCT GACCAAAATGATTTTCTCGAGAAAAAAAAGATGGAAGTAGAGCTCCTT GAAGTTCAAACGAGAGTTGAGCAGGGTAAAGAAAAGCTGCTAAGCTATG GATCCCATAAGCCCTAATCCTTATAAAGAAAAAAAAGGATTTGGTTATAT GGCTTGCATATCTCAGGAGCTTTAACTTGCCCTTTAATGGCTTTTACTCTT CTTTGGATTGAAGGGAGCTCTACATCTTCTTTACCTTCTCTATTTTTCTTT CTTTATTTTCTCCTCTACAGTAATTTATTTGGATT	SEQ ID NO:213
AtmiPEP159a1	<i>Arabidopsis thaliana</i>	TTCCAAAACATGACGTGGCCTCTTCTCTCTCTCTCTTTTCCTTCTCTCTAAG TATGTTTAGGGTTAATAATTAGGGTTCCTCCTCTCTTTTGTTCTGTCTTTAT ATCTCCTTCATAGCTCTAATGTAAGAGATTTACCTCTTTTGTTGTTTTGT TAATCCACGTTCTCATCAAACTTTCTCATTGTTTTATGAAGAGTTAAAG GTCTTTACAGTTTGCTTATGTCAGATCCATAATATATTTGACAAGATACTT TGTTTTTCGATAGATCTTGATCTGACGATGGAAGTAGAGCTCCTTAAAGT TCAAACATGAGTTGAGCAGGGTAAAGAAAAGCTGCTAAGCTATGGATCC CATAAGCCCTAATCCTTGTAAGTAAAAAAGGATTTGGTTATATGGATTG CATATCTCAGGAGCTTTAACTTGCCCTTTAATGGCTTTTACTCTTCTTTGG ATTGAAGGGAGCTCTACATCTTCTTTACCTTCTCTATTTTTTATTTTTCTT TATTTCTACTCAACAATTATTTATTCGGATTTCATCTTTAATTTTCCGTTAT AATTTCTTTTTGGTAAGGATTATTCGCTATAATTTGAGAAT	SEQ ID NO:214
CrmiPEP159a	<i>Capsella rubella</i>	TTCCAACGAATGACGTGACTCTCTCTGCTCTATCTCTCTCTCTCTAAATATG TTTAGGGTTAATTAGGGTTCTTCATCTGTCTCTCTCTCTCTCTCTTCAG AGTCTTTATAGCTTCTTCCAAGATTTTTAATTGAAAGTAATTTACCTCTTT TGGAGTTCTGTACATATAGAATATCAGGAGTCGTGTTTCTTTTTTATCAA GGTTCTCATCTAACCTTTATAGTATTTTCATTAGTTGATAAAGGTCTTCAT	SEQ ID NO:215

		AGTTTGCTTAGATCAGATCTTGTCTTCGTCTTTTCGATAGATCTTGTCTG TCCAATATACAGTGATTTTATTTTCGAGAGCAAAAAGATGAGAGGTAGA GCTCCTTGAAGTTCAAACGAGAGTTTAGCAGGGTAGAGAAAAGCTGCTA AGCTATGGATCCCATAAGCCCTAATCCTTGTTAATGATAAAGGATTTGGT TATATGGCTTGCATATCTCAGGAGCTTTAACTTGCCCTTTAATTGCTTTTA CTCTTCTTTGGATTGAAGGGAGCTCTACATCTTCTTTGACTTCTCTCTA TTAAGTCTTTCTTTATTTTCTTCTCTACAATAGTTGTTTTGGATCGGAAGA TCTTTAAGTTTCCCTTA	
AtmiPEP159b1 AtmiPEP159b2	<i>Arabidopsis thaliana</i>	TTTCACTTTTGTCTCCTCCTCCCTTTTTTCTTTTCAGGATTCTTCTTTTCT ATGTTTTATCTTTCATAATAGATCTGATAATTTTGATTTTCACTATATAT ATTATGGTTAATACTAGTAGCTTTTTTCATTTCAAGTTTTATCCTTCCATTG GTTCTTTCTGAGTCAAATTGTCTCCTGTTTCGAACCATATATAAGTTTCA ATGGTTTTGTATTAACCTCAAGTATTCAACATTATGTCTCTCTTTTTCTTGC TTGGATCTCTAATGCTGTTCAATTTTAAAGCATAGGTTTAGGTTAGATG CATGTAAGTGCCAATTAAGAAGAGGTCAAGAGTTTTTTGATTGTATGAAT ATATGAGTTAGTCAAAGCAGATCCACACGATTATATAGAAAAACAAAGG AAGAAGAAGAGGAAGAGCTCCTTGAAGTTCAATGGAGGGTTTAGCAGGG TGAAGTAAAGCTGCTAAGCTATGGATCCCATAAGCCTTATCAAATTCAAT ATAATTGATGATAAGGTTTTTTTTTATGGATGCCATATCTCAGGAGCTTTC ACTTACCCCTTTAATGGCTTCACTCTTCTTTGGATTGAAGGGAGCTCTTCA TCTCTC	SEQ ID NO:216
AtmiPEP160a1	<i>Arabidopsis thaliana</i>	CATCCCACCCTTAATTGTTTTATATAAACCATTTCTCCTCCTCTCTCCATC ACCTTCAATCTCTCTCGATCTCTCTCTGGATCCCCAATCTCACCTCCATGT TTTGTTTGTTGATTCCCATCTTCTCTTTTGTCTTTTCACCAAATCGTCATTT AAGGCTTCAAGAACAGTAACCCCAATTCCTCCACAAGAGGGAGAGAAAA CAAAAGATCTTCCAATTCCATTCTCGTACATGCAAATCACAATCCATGCC ATAGATTGTTTCTATTCTCCTTATTTATTGCTTGTATCTGTTTCATGCATG GACCAGGTGGAGAGAGCATTACTTAAAAATAGAATTAGCTATCTGTTTTA GGCGAATTAGTTTCCTTACATAACCATGTATATGTCATGACGCATATACA TATGTAGATGTATATGTATTATATATGTATGCCTGGCTCCCTGTATGCCAT ATGCTGAGCCCATCGAGTATCGATGACCTCCGTGGATGGCGTATGAGGA GCCATGCATAT	SEQ ID NO:217
AtmiPEP160b1 AtmiPEP160b2	<i>Arabidopsis thaliana</i>	ACTCATAACTCTCCCCAAATTCTTGACCAAAAATATCCGCCACTTTCTCTC TGGTTCATGTTTTCCCCTCAATGAAATACATACACATTTTGATTTTATTTA	SEQ ID NO:218

		AATCAAGATCGACGTATAAGCTATCCACCAATCATATTTAAGGGTTCCCG TATACATATATACTATATATATATATGGAATAATAGTCGTGCCTGGCTCC CTGTATGCCACAAGAAAACATCGATTTAGTTTCAAATCGATCACTAGTG GCGTACAGAGTAGTCAAGCATGAC	
AtmiPEP161	<i>Arabidopsis thaliana</i>	CTCTAACTCATCCTTCTCTTCTATGAAAATTCCATTGTTTCTGCCGAAGCT TTGATCAGTACTTCTCTTTTGCTTGATCTCGGTTTTTGACCAGTTTATTGC GTCGATCAATGCATTGAAAGTGAATACATCGGGGTCCGATTTTTTTTGT TCTTCATATGATGAAGCGGAAACAGTAATCAACCCTGGTTTAGTCACTTT CACTGCATTAATCAATGCATTTGTAAAAAGAGGGGAAAAGCA	SEQ ID NO:219
AtmiPEP162a1	<i>Arabidopsis thaliana</i>	CTAGAAGAAAAAACAGATCTATAAAGTTTGTTATTAAGATAGAGAG AGAGGAGGGATGTAGTAGGCCAATAGGCCAATCAGAGAATCACAAATG GTATCTGGTCAAGAAGATTCTGGTTAAACTTTTCATCTCTCTGTTTCCTT TTTCTTTCTTTGTTGGATTCAATTTGACATATCTCTATCATCACACTG ATTCTCTTTCTCCCAGTTTGTCTGCAGATGCATGTGTGTAATCTAGGGTAT ATGTTTTTGTCCATTGTTTCATAAGGCAATAAAGATCCAGCTATTTACT ACTTGTGGTATAGATTTTGACTGTTGAATTTTCAGATCTGATGTGTTTCGT TTGATCCGATTCCGAAAATTTATGTTTCGTTGACATTTTGGAGTTTAGTTG GAAGAAGAGTGAGAGTCGCTGGAGGCAGCGGTTTCATCGATCTCTTCCTG TGAACACATTAAAAATGTAAAAGCATGAATAGATCGATAAACCTCTGCA TCCAGCGTTTGCCTCTTGTATCTTTCTTATTGACTT	SEQ ID NO:220
AtmiPEP162b1	<i>Arabidopsis thaliana</i>	CTGCATCTATCCACCTCTCTCTGTAAATTTATCTAAATGTTTCTTTTAATC TTTTTGAGATTAATAATGATTTGTGTTTGTTCATCAACCGATTTTCTCAGA TCTGTCAATTATTTTGTATTATTTATGATTTATGAATGAGGAAAGAG TGAAGTCGCTGGAGGCAGCGGTTTCATCGATCAATTCCTGTGAATATTTAT TTTTGTTTACAAAAGCAAGAATCGATCGATAAACCTCTGCATCCAGCGCT GCTTGCTC	SEQ ID NO:221
AtmiPEP163-1 AtmiPEP163-2	<i>Arabidopsis thaliana</i>	TATCACAGTTCTCATCAAATATTTGAAAGTATCAAACAAAAAAGGAGA GTGAGAAAAATAAAGAGAGAGATAGAGAGAGATCATGTCCACTACTCA AGAGCATAGGTCTTGATTGGTGGAAGACAAGTACCTTAGATAAACCGAC CAAAACCCGGTGGATAAAATCGAGTTCCAACCTCTTCAACGACAACGAT TTCAACACTCTCTTCCAGGAACAACCTCCTCCAGGCAGATGATACTAAAG TGCTGGAGTTCCCGGTTCTGAGAGTGAGTCCATATCAAATGCGCATTC GTTATCACTTGGTTGAACCCATTTGGGGATTTAAATTTGGAGGTGAAATG GAACGCGTAATTGATGACTCCTACGTGGAACCTCTTCTTAGGAAGAGCAC	SEQ ID NO:222

		GGTCGAAGAAGTAACTGCGCAGTGCTTAAATCGTAGATGCTAAAGTCGT TGAAGAGGACTTGGAACCTTCGATATTATCCCCCGTGT	
AlmiPEP164a1 AlmiPEP164a2 AlmiPEP164a3	<i>Arabidopsis lyrata</i>	AGTAGGGTTGGAAAATTTTTTACATTTTTACTCTAAAATAGAATAGAGT TGGAGATGCCCTTAGCAGTTATTAGACAAGGGATTGTTTGGCCCTAGCGA TCCTCTCTTCACTCTCTCACTTTTGTAGTTCAACCCCTCTTTTGCCTGAGAT GCCATCATGGCATGACATGGTTCTTTTGCCTTACGTAAAACACACTCACG CCAACACACGCCACATAACATAAAATAAATTATATATACATATACGTATGT GCGTGTGAGTCTTCCATTAATGCAATCTTTGGGCCTATATATATATACAA ACCTTCCATAACCAAAGTTATCATACTACAAAAGCTCTCTCGTACTTGGGA AATGCGGGTGAGAATCTCCATGTTGGAGAAGCAGGGCACGTGCAAACCA ACAAACACGAAATCCGTCTCATGTGTTTTGCACGTACTCCCCTTCTCCAA CATGAGCTCCTGACCCATTG	SEQ ID NO:223
AtmiPEP164a1 AtmiPEP164a2 AtmiPEP164a3	<i>Arabidopsis thaliana</i>	AGACAAGCCCCACACTAAAAAAACAGTAATATGGAATAAAAAAAGC TTTCAAACTTAGCAGTTATTAGACAAGGTATTGTTTGGCCCTAGCTAGC GATCGTTTAGCTCTCTTCACTCTCTCACTTTTTTAGTTCAACCCCTCTTTTG CGTGAGATGCCATCATGGCATGGTATGGTTCTTTTGCCTTACGTAAAACA CACTCACGCCAGCACACACACACACACATAACATATACGGATGTGCG TGTGAGCTAGTCTTCCATTAATGCAATCTTTGGGCCTATATATACAAACC TTTCCATAACCAAAGTTCTCATACTACAAACGCCCTCATGTGCTTGGAA ATGCGGGTGAGAATCTCCATGTTGGAGAAGCAGGGCACGTGCAAACCAA CAAACACGAAATCCGTCTCATTTGCTTATTTGCACGTACTTAACTTCTCCA ACATGAGCTCTTCACCC	SEQ ID NO:224
BrmiPEP164a1 BrmiPEP164a2 BrmiPEP164a3	<i>Brassica rapa</i>	AGACAACCCACGTTTTAAAATAAGAAATGATGATAATTTTGTGGAAAT AAAAGCTAGTATACTTTTGAATAATTAGACAAGGTATTGATGCTTTGGG CCAAGCTAGTTTCTTTTAGCACTCTTCACTCACTAGTTTTTCTTCTCAGCC CTTCTTTTGCCTGAAATGCCATCATGGCATGGCATTGTCATTTTGCCTTTC GTAAAACACACTCACGCCAACATACATTATTCATATTTCATGTGTATGTAT ATGAATGTTCCATTAATGCAATCTTTGGGGCCTATATATACGAAGCTTAC ATCACCAAAGCTCTCATATTACAAAAGCTCACATATATACTTGGAAATGT AGGTGAGAACCTCCATGTTGGAGAAGCAGGGCACGTGCAAACCAAAAA ACATGAAATCTGTTTCATATGCTTTGCACGTGCTCCCCTCCTCCAACATG A	SEQ ID NO:225
CpmiPEP164a1 CpmiPEP164a2	<i>Carica papaya</i>	AGACAACACTCCTCTTTGTTCCCTTCCTCACGTATCCACTTTTGAAATTTG TAATTTGTGTGCACCACCATGATTGCATGCCATCCCTACTTGCTTTTCCC	SEQ ID NO:226

		CTTTTCCTTTCTCTAACATTTTACTCAATCTTCTTCTCCCCCTCCCCCCTT CCCCCTCTCTGCCATTATAACCATAATTAACCTCTCTCCCTCTCTCTCCC TCTCTCTCTCTCTCTCTCTGGGTTCTCAGTATAAATGCAGCTCTGCTTATA CTTCCACACCTATATATATATATACCTGACCCTTCTTCACCTCCTTCATCCAC CTCCTCCTTCTTCCCCAAAACCTTTCTTAACTGTTCTCTGCATACATATATA TCCACATACATATATATATATATATAGAGAGAGAGTGAGACAGAGAGGTTA CCGAGGCAATTGGGTGAGTAGCTCCCTGTTGGAGAAGCAGGGCACGTGC AAATTCTCCATGGCTTTCCCCTCTTGCACGTGCTCCCCTTCTCCAACATG GGTTCC	
CrmiPEP164a1 CrmiPEP164a2 CrmiPEP164a3	<i>Capsella rubella</i>	CGGCCACCCCCACATTTAACAAGAAAAAACTGATGGAATTAAGGTT TGAGAACTTGGCAGTTATTAGACAAGGTATAGTTTGGCCCTAGCTTCTTT TAATTTAGCTCTCTCCACTCTCACACTTTTCAACTTTCACCCTTCTCTTGC GTGAGTCGCGAGATGCCATCATGGCATGGCATGGCATGTTTCTATTGCCT TACGTAAACACACTCACGCCAACACATACTCACTATACATGTAAATAA GTATGTGCGCGTGTGAGTCTTCCATCCATCAATGCAATCTTTGGGGCTAT ATATATACAAACCTTTTCCATAACCAAAGCTCTCATATAAACTACAAAAG GCTCACTTGGGAAATGCGGGTGAGAATCTCCACGTTGGAGAAGCAGGGC ACGTGCAAACCAACAAACACGAAACCCTCCTCATGTGCTTTCACGTACT CCCCTTCTCCAACATG	SEQ ID NO:227
GrmiPEP164a1 GrmiPEP164a2 GrmiPEP164a3	<i>Gossypium raimondii</i>	GAAAACCCAAGTTCAGGCTAACAAGTTATCTGATGATGAGATCAAGAAT TTTAAAGTTTCAATATAGATTTGGCATGGGTATTGGCGGCAGAAAGCAAT TAAAAAACCAGTTATGTCAAATTCAAGGTCGTATCAGTTAAAATGAATG AAGATTTAGAAATTTCAACAAGGAAGAGGACCCACAGCTTTGTAAAT TAAGTGTGTGGTTTTTATAATTATCATCTCGAAAGTTTCATAATATCAATT AGATTAACCATCTCTGAATTTTATAATTACAAACCAGATAGATAGATAC ATGAAACTTAGACCCAGAGATCTGTCTTTAAAGAATGCCCACTTCTAG ACTCAATCTCTATTACTCTCTTTTTTTCTCTCTCTCTCTTTCGGAAAACT TGTATATAAATAAATGACACTTTCTTTGCTTTCTGCACTCACTCATGAAC TTGAAAAGCTTTACTTGGATGGGTGGTTGGGGGTGAGTATCTCTTGTG GAGAAGCAGGGCACGTGCAAGTTCCTATGTTTAAGTGAACCTTGCACGT GCTCCCCTTCTCCACCGTGAG	SEQ ID NO:228
MtmiPEP164a1 MtmiPEP164a2	<i>Medicago truncatula</i>	GAAGAGAAAAACCTAGTGTAATAATTTGATATACTCTTTATGTATAGTAC GAATGTTTTTTTAAAAATTATGTAAAAAATGATAAAATAATACTAATA AATTAACAGTAAAATTAGAAAAGTAAAATACTATGCCCAAATTTGATAT	SEQ ID NO:229

		TTTTTTTTATATATTTGTATAGATTATTATTATTTGATATGTAAAGTCCAA TTAAAAATTTGTTTTAACTAAGATTTGAACTAGGTTTTCTTAAAAGACTC ATCTTTTACTTCAAATTTATTTATCATTGGAATTCACATCTTCTAATATT ATTATTATTATTTCCACCATACTCATTGCTTCTGCCACGTTACTTTAGTTA GATCTCTTATGTCATATATCTCTCTCTCTCCTAAGTTGCTACCTATAAATA CTAAGCCTTTCCCTTGGTTGGTTCAATTCAACTTCTACTTCTCATCAAACA CAAAGTGCAATAAGCTTCATTTCTGGGTGAGAAGCTCCTTGTGGAGAA GCAGGGCACGTGCAAATCCTCTTTCTGATTCAATCTCTCATAATGCATAT CAATATCTTTTGCACGTGCTCCCTTCTCCAAGTAGG	
OsmiPEP164a1 OsmiPEP164a2	<i>Oryza sativa</i>	ATGCAAACCCACTCCAACACTCCACAATCCACATACTCTCTCTCTCTCTCT CTCTCTGAGTAGGAGTACATGTGTGTGTGTGATATCAATATGCATTGAT GTTGATGCTACTGTAGCCATCTTGTGGCTATATAAACCCAGCAGGCAGCA GCACAGCTTAGCTAGAGAGCCATATTGCATGCACACTCGCTAATCTCTTT TCTCTACTCTACTTGCATTACACCACCTCTGCATTGCATTTCAGTTCATTC ATTCCACTGATGCATGGATCGATGTTGCTACCTTCTTCTCTCTCCTCATG CATCCATGCATCGATCTCACCTAGCTTCTTCTCATCCTCTCTCGATCGAT TACAAGAGAAAAGTGTTTGCTGTTCTTGCTATCGATCTACAGGTGAGTAG GTTCTTGTGGAGAAGCAGGGTACGTGCAAAATGCACACCGGTTGGTCG AGCTAATTAACAAGCTCTGACGACCATGGTGATCGAATGCACGTGCTCCC CTTCTCCACCATGGCCT	SEQ ID NO:230
AlmiPEP165a	<i>Arabidopsis lyrata</i>	CTAGGGTTTAGGAATGACGACTTGTTTCTGTTGTGTCTTATTAAGGCC ATCTTCGTCTCCGCCACTCATCATTCCCTCATCATAACACCATCATCACCA TTCACCAACCTCTCTCTCTTTCTCTCTCTCCTCTCGATCTACAACAAAATG TGAATCTGCTAAGATCGATTATCATGAGAATTAAGCTATTTTCAGTTGAGG GGAATGTTGTCTGGATCGAGGATATTATACATATATACATGTGTATGTTG ATACATGTGATCATAGAGAGTATCCTCGGACCAGGCTTCATCCCCCACA CATGTTATTGCCTCTGATCACCATATATATGTCGTTACATTTTCATGGTTAA TTACTTGCAAAATCACAAAAGCTTGGTTTGTAACTTTCTATGACCTTTTT TAATGACTTTGAATCTTTCATGCATGACTTCTTAAGAGTAGATTTACACA TTTGCGGATCCGTTTATGCTTTTTGCTTTTGTTCGTTTATATATAT	SEQ ID NO:231
AtmiPEP165a	<i>Arabidopsis thaliana</i>	CTAGGGTTTAGGAATGACGACCTGTTTCTGTTGTGTCTTATTAAGGCC ATCTTCGTCTCCGCCACTCATCATTCCCTCATCATAACACCATCATCACCA TTCACCAACCTCTCTCTCTCTCTCCTCTATCACTCTCTACAACAAAATTT GTGAATCTGCTAAGATCGATTATCATGAGGGTTAAGCTATTTTCAGTTGAG	SEQ ID NO:232

[illegible]

[illegible]

		TTCAGATTTTCAGATTTGATTAGGGTTTTAGCGTCTTCGGACCAGGCTTCAT TCCCCCAATTGTTGCTCCCTGTTTACTCCATATTTCTTCCTTCTTTTCAA TTAGGGTTTCAGATCCAGTGAATGAACCCCTTGTTAAAGGTTTGATCTCTT ACCTTACTTT	
AtmiPEP166b	<i>Arabidopsis thaliana</i>	TCTCATCATTCTCTTCATCATCACCACATTCATCTCTCTCTCTCTCTCTC TCTCTCTCTTTCTCTTCCTTGATCTTAGCCGGATCTGTTGGGGGACGAACA CATGAGAGATAGATAAAATATAAGAAATTTCTCGAAAAACCTAATAGA AAAAGGTCTGTTTCTTAAAGAAGAAGAAGAAGAGGATTTAAAGAGGGAT TTTTCTTTTGAGGGGACTGTTGTCTGGCTCGAGGACTCTTATTCTAATACA ATCTCATTTGAATACATTCAGATCTGATGATTGATTAGGGTTTTAGTGTC GTCGGACCAGGCTTCATTCCCCCAA	SEQ ID NO:239
AtmiPEP167a	<i>Arabidopsis thaliana</i>	TGATGAACAGAAAAATCTCTCTTTCTCTTTCTTGATCTGCTACGGTGAAG TCTATGGTGCACCGGCATCTGATGAAGCTGCCAGCATGATCTAATTAGCT TTCTTTATCCTTTGTTGTGTTTCATGACGATGGTTAAGAGATCAGTCTCGA TTAGATCATGTTTCGCAGTTTCACCCGTTGACTGTTCGCACCC	SEQ ID NO:240
AtmiPEP167b1 AtmiPEP167b2	<i>Arabidopsis thaliana</i>	AACCACAAAGTACCGCTGCTATTTTCTTTTTACGTCTTTGTATTTGCATCG TCTAAGAGAATGATGGGTTGTTTTGTGGGATTTTAATGCAGGAGGAAAC ATATGAGGGGTGATTAAGGCAAAAACCTTAAGATGTGGTCATTTAGATA CATGGAGTCAAACATAAGAATGGACCTTGGCGAAAGCTTCTTCACGGTCA AGATTTAAAATCAGGTACGACACTGTGTACGTGAGAGAGAGAGAGAGAG AGAGAAAGAGATTATAGAAAGAAAGAGATGTATCACAATAAAGGAGTA TATTTAGGGTCACAGGTGGTGGAGATATAGGTATGCAGGGCCAAGGCTC TAATCTCTTCATAGCCCTATTGATTTTGTCCCTCTCTCTCTCTCTTTCTTCC TCTCTTAGCTGTATGCATTATGATGCGTCTTTTAATTCAGTGTTCAGGCT TCTTTAATTCGTGGTGTCTCTCTCCTTTTTACCCAACCATCTCTTAAATTT TTAACATCTGTTCTCAAATCCTCTCTCATCTCTTTCTATAAGTATCTATA GCGCCTCTTAAACCACAAAGCATCACCTCTGTCTTCTCTCATCTCCTTTCT GTATTCTCTTTCATTGCCTTCACGTCTGTTGCAATTTCTCCACTTCTTGAG CTTCCGTTTTTTACAATTATTGATCCGTCAAATATGTGAGATTTGCACAAC TTGTTGCTCAGGTATTTTGAAGACAAGTCCACAAGGGAACAAGTGAAGC TGCCAGCATGATCTATCTTTGGTTAAGAGATGAATGTGGAACATATTGC TTAAACCCAAGCTAGGTATGCTCTGACAGCCTCACTCCTTCT	SEQ ID NO:241
AtmiPEP169c1 AtmiPEP169c2	<i>Arabidopsis thaliana</i>	GAGCAAGACAATGCCACATACAACTTGAAAGATCTCTTCATCTTTTCTC CAATGTTTTTTTTTCGTTTGCTATTTATCTCCACAATTCTTGGAACAAAA	SEQ ID NO:242

		ACTACATTCACAAACGAGAGAATTTTTCACAACACCTCTTTTGCTCTCATT TTTTTTTTTTCGTCCATTATGAGTATTAATTATGGTTAGGGAATCTTACAG AATGAAAATGAAGGTGTGAATGGATTGTCTCATCTAAAGCCTTGAATGT GGGAAAAAGGCCATTGTTGTTTCAGCCAAGGATGACTTGCCGGTAGCTTG TATTATGATTACTCTATATTCGATTTATATTATGGAGATGATGGTTTATAT ATATTTACTTATCTACATAGTTTTAGTTGATTTTTTTTTTCGTACGTAATATA ATACGAAAAAGTATTTACTTATTTATATATGTGTGTTGGGGCAAGAAGTG TAACCAAGCTAGCCCGGCAAGTCATCTATGGCTATGCAACTGTCTCTTCC TCTCATTCTAGGCTTACGATGACACGTAAAAAATCCCAAATATCACTAAT ATGATATGAATATGGATGA	
AtmiPEP169l1	<i>Arabidopsis thaliana</i>	AGGCATGAGACATAAAGAGAGTTAAATATAATGAAGAAGAGAGGTCTA ATATGGCGAAAAGAGTCATGTTTAATAGCCAAGGATGACTTGCCTGATCT TTTTCACCTCCATGATTCAATTTTAAGTTCGTGGATTTTGGATTATTATGC GTTTAAAAGGTATAATAATTTGAGATCATGTTGAATCTTGCGGGTTAGGT TTCAGGCAGTCTCTTTGGCTATCTTGACATGCTTTCTTCATC	SEQ ID NO:243
AtmiPEP171a1	<i>Arabidopsis thaliana</i>	GAATTTTGATTTATGAACCTCCTCAAGAAGGAAAGACAGAGGAGGAGAC AAAGAAGTATAGGTTACATTGCATAGCCAGTTTAGTTTTGAAGGATGG ATATATGAAAAAATATGAAGAGAGAGAAGAGAGAAGAAGAGGAGGAT TAAAGAGGGTGAGGCCAGCTTTTGTGCTTTGGTAGTAGATGAGGTTTAAA TGCTCCATACCTTCCATTTCTCTCTTACCCTAATTTAATTCTTCCTCT CCTTTATAACTCCCCACAGACATTCTCACTTCTCCTCCTCACACTTCACAT CAACACTTCTTTCTTGTTTTTTCATTTTACAATGTTTCCTTTGATATCCGCA CTTTAAGCATGAGAGAGTCCCTTTGATATTGGCCTGGTTCACTCAGATCT TACCTGACCACACACGTAGATATACATTATTCTCTCTAGATTATCTGATT GAGCCGCGCCAATATCTCAGTACTCTCTCGTCTCTATTTTGGACTTTGTGG TCTTGATAGATCGATTTGTATGTGTGTGTTGAAATGGAGACAAGTACTTGT AACTTCTTTGTTGTTATATTGTTTACCTATAGGCTGATGTCATAAACTCTT TTGATCTTGTTTCTAACTTCCAGATTCTTGAAAAATCAAGTCGTGTGTGTG TCTCCATGGAAGCCTTTTCCATTTCTTCCTTTCCA	SEQ ID NO:244
AtmiPEP171b	<i>Arabidopsis thaliana</i>	ACTCATAAACTTTGCTACTGGCCGCATTTCTATTTTCTCCTTCGATTCTTC TAATTCGTAATTTGGTTTCTGACGTCCTTAAATTTTATAGACAGTAAGAG TTTCTCCAGGATCCGATGGTTCTCTCCGGTAAATTAACATTTTAGTGTCAA TAGTCATTTATACATATTTTATTTCACTTTTGTGTTTATTGGTTTTCTC TGGAGCTAAGTGGAGATTATAGTCGAACAAGAGTGGTTTTATGCAAGGT	SEQ ID NO:245

		AACGCGAGATATTAGTGCGGTTCAATCAAATAGTCGTCCTCTTAACTCAT GGAGAACGGTGTGTTTCGATTGAGCCGTGCCAATATCACGCGGTAAACC AAAAATGGCAAAGATAGTTATTATAACCTTAAAGGTATGTATCATTATCG TTTTATTGTTTCAATTTTGATTAATGGCTTGATATTTTCATTTTTTTTTT	
MtmiPEP171b1 MtmiPEP171b2	<i>Medicago truncatula</i>	ATTGGTCAAACATACATACAGTAGCACTAGCTGGTTTCATTATTCCACTA TGCTTCTTCATAGGCTCTCCAAATTTTGCAAAATTGAAAGAGACATAGTA TATATATCTTAGCAAGGAGAAATTCAGGATATTGAGGATGAAGATTGAA GAGTAATCAGTGATGAAGAAAGCAAGCAAGGTATTGGCGCGCCTCAATT TGAATACATGGCTATAAAAAATGCATCATATCAGCCATGTAGTTTGATTGA GCCGCGTCAATATCTTGTTTCCATCTCCAAATTTACCAATCTCATCAAATC AAATTAACACCACAATCAAGGCTTTCATTTAATGCAGTCAAAATAGGTTG ACCTTATCATCGAAGAAATTGTTTTCTCATTCTATCGAAGTTGGACTTGC CGAAAATGCTCGAAAGCATGTGTTTTAGTTTCGACAGGCGAAAAAGTTAC CGAAGGACAATTTGGTTGTGGTTTCGGATAAGATCAAGCAACGGATATTTT CAAGACACGTTTCGAAATTCAAATCAAATGGATAAGTATCGTTAGTTTACT GCAGTTATAGTTTTAAATTCAAATCTAGGCAGTTGTTTCTATTTGTATAAA TAGTAGTTTTTCCCTAGGGAAAAGGGGTCGCAATTCAATCATACAAAAA ACTTACAATCAAATTATCCGCATGGAAGAGAGAAACGAGTCACAAGTTG CAATGTATGAACATGTGTACCAATTTACATTCAATCAGTACAATTTAAGT TCATTTCCATAAAAAAAAAA	SEQ ID NO:246
ZmmiPEP171b	<i>Zea mays</i>	ACCAGGGTTAGGTATCCATCCACACAGCAATGCATCTGCCTTCAACTCCC TCTCGCCCCCACCACAACACACATCTCTCTTTTTCTAGGGAAGGAAAT GACGAAGGGGACGACGACGGCATGCTTCGGCTAGCTCGTTGGTGCTAGG ACAAGGGCGGAGGTATTGGCGCGCCTCAATCCGAAGGCGTGGCTGATAG ATTGGCGCGGCAGCCATGTTCTTGATTGAGCCGCGTCAATATCTCCCCT TGCCTGTCCCGTACCTAGCTAGCTTGCTTGCTCACTGATCGATGTCGTCC CTATTTTCATGGAGAAGCTGATGATTGATTATTCTCACAAGCAAGAAGTGT CTGATCTGTTGCCTGCATCGATCAGGATCTATATGCTGGAGAGTTCACAA GAACATGGACAGAACTCGCTTCAACAACCGATCAATCGATTGATTAGGT ATGTACCTACCTCATATGCCTCAGCTCTTCGTTATGGATTTCTTCAACCGA AGGGTCAGTAAGCTCTTGGTTCCATGCCACTGCGTGAAGTAAAGCGTTTAC AAAATCCGTTCCMCGGCATGAACCAAGCACTCAAAATCGCATGCAGCAT CTTTCGTTTCAAAAAAAAAAATTGACTTYTGAAAAAATAGATGAATCAGTT TCAAACATATATGATTATCCATTTTCTCAACCGGGAATTTATATCTCGTTG GGATGCAAAACCGTTCAGTAGTAAACTACTCCACGAGTATAAACTGTTT	SEQ ID NO:247

		CAGTTATTTTACTATTAATTAGTTACCCGTATGCTGTTATGGTTTCTATAT ATCTATAAGTAAACCTTACTTAAATAAGATAGTTATACAAAAAAAAAAAA AAAAA	
AtmiPEP171c1	<i>Arabidopsis thaliana</i>	CAAGAAAAAACATTGAAATAGCTCATGTTGTCTCTTTCTCATTTTCATAT CTGCTAAAAAAGAACCGTGTTTTCTAAACTGGTTTAACGGTAAGTACCT GTCTCTAGTAACTTACCTATCAATTTGTTCCAATCATTTACTTGCTTTGAC TTATTTGGTTTTCCTTTTGTTTTGTTTTCTTTAATATGTGGATGGAGTTTGG TGTAATAAGCAACTGAAGAGTCGATGAGCGCACTATCGGACATCAAATA CGAGATATTGGTGCGGTTCAATCAGAAAACCGTACTCTTTTGTTTTAAAG ATCGGTTTATTTGATTGAGCCGTGCCAATATCACGCGTTTAAATAGTTTA AAGATTCTATGTTAGTTGATGTGATCAATCAAGGTATGAATCTATATCAA TTCTCTTATGCATAGTTTTATTTACAGAGATGAGGTATTATCAATGTCT ATCGTCGAGGATCACGCTCTTACTTATGTTATATTTCTATATAATTTTATT AATTAGTTTTCTAAAAGAGAAGGACAATTTAAAATTATTTTAAAGAGTTT TTTTTAAGTAGTTTTGTTTTCATGTTTATCTTCTGCAGGCTCTGAAGTTAG GATAGTAACAAGAAAAAAGACAGAAAAAAGAAGAAAATTCATATACA TTCGTGA	SEQ ID NO:248
MtmiPEP171e	<i>Medicago truncatula</i>	GAATAAGTGAATATTATCGATATTTATATCATATATCAACTTTTCTTCTGT GCTTGCTTGCAAATTTGCAATTAAGCTTTTTTGATCTTATGTAAGAGAAT ATTATTGATGATGGTGTTTGGGAAGCCGAAAAAAGCGATGTTGGTGAGG TTCAATCCGAAGACGGATTTACATGTATAGAGTTGTAAAATACGATCTCA GATTGAGCCGCGCCAATATCACTTT	SEQ ID NO:249
MtmiPEP171h	<i>Medicago truncatula</i>	CCACAAAACCTATAACTAGCTAGAAGCTTTAATCGCCTTATTTATTATAAT AATAATAATAAATATGGCTTCAGCTGCAAAAGTATACATGGCGTGATATT GATCCGGCTCATCTATATCTTCAAGTTCAATCATCCATATTCATATCAATT TCAGACGAGCCGAATCAATATCACTCTTGTTTGCTTCATTGCATATTAATT ATATACTTCATTTATAAGTTATAGTTTGCCATATATATATTAGATTGATTC TGCAGAAGTAGACAGGAGTGGTGTTGTTTCTGCTCATCTTATTAAATAAT GAATGAATGAATGACATTTGCTTACTTATAAGACGAGCCGAATCAATATC ACTCCAGTACACCT	SEQ ID NO:250
AtmiPEP172a1 AtmiPEP172a3	<i>Arabidopsis thaliana</i>	CTCTCTCTCTCTCTCTCTCATCTGTGTTCTAGATCTCACCAGGTCTTTCT CTGGTTAATATATGGCTTCCAAGATCTGGTAATATGTTATAAATACGTCA TACTTAAGCTTTTTTCAAATCAAAAATAGAAATTTGTGGGTTTGTCTCGTT TTACTATTTTAGCAGTATATATTAAGAAGTTCAGATGTTATTTCGATCATCT	SEQ ID NO:251

		GTTTTTGCTTCCCCTCTGCCATCTTTATCTTTTAGGGTTTCAATTCTTTTC ACTTTTTTCTTCTGGTTTGGAGATGGTTAGGTTCCAACATAAGTATACGAG ATTAAATTTGACATCTTAGTTACTTCAAAATTCCTTCAATCAAAACAAGT CATCTCGACTATTCCGCCATGTTTGTATATACATATTTATATATTATATAT ATGAAGGTACGAGTTTCTAGTGTCTATAAAATTAAGAAGGTTAAGTACCAT ATAGATGATATTTGTTAAGTAGTAAGTCACTCAAAGTTTGAGTTTGGGTT TGAGTTTGAGTTTGAGTTTGAGTTTGAGAGACAAAAGATTACTACAAGA AGATTGTTAAACAAAAATGGAAGACTAATTTCCGGAGCCACGGTCGTTG TTGGCTGCTGTGGCATCATCAAGATTCACATCTGTTGATGGACGGTGCTG ATCACTCTCCACAAAGTTCTCTATGAAAATGAGAATCTTGATGATGCTG CATCGGC	
AtmiPEP172b1	<i>Arabidopsis thaliana</i>	ACTTGCACCTCTCACTCCCTTTCTCTAACTAGTCTTGTGTGCACCCATTTA TGTGTACGTACTATTATCTCATAAATAAATATTTTTAAAATTAGATGCATT TATTGATATGAAAAAGTTACAAGATTAGTTTGTGTGTGTGAGACTTTGG ATCGACAGATCGAAAAATTAATAACCGGTCAGTATTGAATATCAACTA TTATATGCTCCATGCATTTCGCTTATAGTTTCACACAATTTGTTTTCTTCAC GGTCTAAAATCAGAAGATTCCATATATTTTCTTATGACGTAAAAGGACCA CTTATAAGTTGACACGTCAGCCCTTGGATTTCGTGAGGTTTTTCTCTCTACT TCACCTATCTACTTTTCCTCATATCCCCTGCTTTTCTCCTTCTTGTCTTG TTTTTCTCGTTTTTTTCTTCTTCTTCTCCAAGAAAATAGAGATCGAAAAGA TTAGATCTATTTTGTGTAGCAAGAAATTATCATTTTCGTTTCTTCATTCAT ATATTGTTCTATTATGTTGTACAATAATAGATACTCGATCTCTTGTGCGTG CGTAAATTTTATACAAGTTGTCGGCGGATCCATGGAAGAAAGCTCATCTG TCGTTGTTTGTAGGCGCAGCACCATTAAGATTACATGGAAATTGATAAA TACCCTAAATTAGGGTTTTGATATGTATATGAGAATCTTGATGATGCTGC ATCAAC	SEQ ID NO:252
AtmiPEP172c1	<i>Arabidopsis thaliana</i>	TCACCAAATAGGCTCTTCTTTATCGCTTCATATATATAAAAGTCTACATCT ATCTCTTTCTAGGTCAGTACTAGTCTAGATTAAGGATTGAAATTAGG GTTTCATGTTTCCAGCAAAATGGTGCCGTCTTGAGTCTTGAAAAGATCCA AGACAAAACCAAATCACTACATACATCCCTATCATCAACCAGCTACTGTT CGCTGTTGGAGCATCATCAAGATTCACAAATCATCAAGTATTCGTGTAAA TAAACCCATTTATGATTAGATTTTTGATGTATGTATGAGAATCTTGATGA TGCTGCAGCTGCAATCAGTGGCT	SEQ ID NO:253

AtmiPEP172e1 AtmiPEP172e2 AtmiPEP172e3	<i>Arabidopsis thaliana</i>	TGTCATATTGAGAACTCTTTAGCCTTTGGCTTCTGTTCTGACACTTGTAT AGTGAAGTGGGCTTGTGTTATATAGATGGGATCTCTCTCTTTATTTAAAA GTCAATTAGAGATCTTGATGCTACTTCTGTCCCTTTCCAAGTGATTTTACG TCGACCAACTAGCTTTTTTTCATATGAGTGTATATATTCATGTACCTATCTC TCTCAATTGCTTCTCACCAAAATCATCTTGCTGATTCATTTGCTGTCTGAA TCCTCTTGCTTTTCTCTTTGCTTTTTTCATTTGTTGATTTAAACCATGGGAGT TCCCAACTTTAGACCTCGAAACCGATAAGGATCTTTCTCTGCGGTTGAAA TAGCTAGGTTCTCGATGAATAGGCTAGCCTTTGGTGGATGTTATCAGCCA GTAGTCGCAGATGCAGCACCATTAAGATTCACAAGAGATGTGGTTCCCTT TGCTTTTCGCTCTCGATCCGCAGAAAAGGGTTCCCTTATCGAGTGGGAATC TTGATGATGCTGCATCAGCAAATAC	SEQ ID NO:254
AcmiPEP319a1 AcmiPEP319a2	<i>Arabidopsis cebenensis</i>	TTGTATCCATAGTGTATTTCTCGCATCTACCATCCATTTTCTACGCCTCT CTCTCTCTCTTTCTCCATCAAATCTTGTTTTGTTCAAACCTCTCTCTCTCATC AATTCTCTCCATACAATACATGCATACATACATACATACCATCTCTAATA TTTCATCAATCTTCTTTTGTTCCAAACGCTCTTTCTCTCCATTTACATACAT ACGAATCATTGTTGTCATAGATCCGTTTAGAATTGCTTTAACTTTTAGATG AGATCTAGGGTTTCTTTCTTTTCTTCAAATCATGCTTTTTTCGCTTGCTA GGTTATAGATCCATGTAAGTTTAGAGTAGATGTACACACACACGCTCGG ACACTTATTAATAACATGTTGATACACTTAATACTCGCTGTTTTGAATTG ATGTTGTAGGAATATATAAATGTAGAGAGAGCTTCCTTGAGTCCATTACAC AGGTCGGATATGATCCAATTAGCTTCCGACTCATTATCCAAATACCGAG TCGCCAAAATTCAAATTAGACTCGTTAAATGAATGAATGATGCGGTAGA CAAATTGGATCATTGATTCTCTTTGATTGGACTGAAGGGAGCTCCCTCTC TCTTCTGTATTCC	SEQ ID NO:255
AhmiPEP319a	<i>Arabidopsis halleri</i>	TTGTATCCATAGTGTATTTCTCGCATCTACCATCCATTTTCTACGCCTCA CTCTCTCTTTCTCCATCAAATCTTGTTTTGATCAAACCTCTCTCTCTCTCT CTCATCAATTGTCTCCATACAATACATACATACCATCATCTTTCCCATCTC TAATATTTTCATCAATCTTCTTTTGTTCAAACGCTCTTCCTCTCCATATACA TATACATACATACGAATCACATTGGTGTATAGATCCGTTTAGAATTGCT TTAACTTTTAGATGAGATCTAGGGTTTCTTTGTTTCTTTTCGTTTTCTTCAA ATTTTGCTGCATATTCTCCAAGATCATGATTTTTTCGCTTGCTAGGTTATAG ATCCATGCAAATATAGAGTAGATTTACACACACACACGCTCGGACACTT ATTACATACATGTTGATACACTTAATACTCGCTGTTTTTAATTGATGTTGT AGGAATATATATATGTAGAGAGAGCTTCCTTGAGTCCATTACAGGTCGT GATATGATCCAATTAGCTTCCGACTCATTATCCAAATACCGAGTCGCCA	SEQ ID NO:256

		AAATTCGAACTAGACTCGTTAAATGAATGAATGATGCGGTAGACAAATT GGATCATTGATTCTCTTTGATTGGACTGAAGGGAGCTCCCTCTCTCTTCTG TAT	
AlmiPEP319a	<i>Arabidopsis lyrata</i>	TTGTATCCATAGTGTATTTCTCGCATCTACCATCCATTTTCTACGCCTCT CTCTTTCTCCATCAAATCTTGTTTTGTTCCAACCTCTCTCTCATCAATTCA TTCCATACAATACATGCATACATACATACCATCATCATCTTTTCCCATCTC TAATATTTTCATCAGTCTTCTTTTGTACAAACGCTCTTCTCGCCATATAC ATACATAAGAATCATTGTTGTCATAGATCCGTTTAGAATTGCTTTAACTTT TAGATGAGATCTAGGGTTTCTTTCTTTTCTTCAATTTTGTGCTGCATATTCT TCAAAATCATGATTTTTCGCTTGCTAGGTTATAGATCCATGCAAATATAG AGTAGATGTACACACATTCACGCTCGGACACTTATTACATACATGTTGAT ACACTTAATACTCGCTGTTTTGAATGGATGTTGTAGGAATATATATGTAG AGAGAGCTTCCTTGAGTCCATTACAGGTCGTGATATGATCCAATTAGCT TCCGACTCATTATCCAAATACCGAGTCGCCAAAATTTCGAACTAGACTCG TTAAATGAATGAATGATGCGGTAGACAAATTGGATCATTGATTCTCTTTG ATTGGACTGAAGGGAGCTCCCTCT	SEQ ID NO:257
AtmiPEP319a1 AtmiPEP319a2	<i>Arabidopsis thaliana</i>	TTGTATCCGCAGTGTATTTCTCGCATCTACCATCCCTTTTCTACGCCTCT CTCCCTCTCTCTCTTTCTCCATCAAATCTTGTTTTGTTCAAACCTCTCTCTCT CTCATCTATTCTCTCCATACAATACATGAATATACATACATACCATCATCT TCTTTTCCCATCTCTAGTTTTTCATCAATCTTCTGATGTTCCAAACGCTCT ATCTCTTCATATACATACATACGAATATATTATTGTTGTCATAGATCCATT TAGAATCACTTTAGCTTTTAGATGAGATCTAGGGTTTCTTTGTTTTCTTTC AAATTTTGTGTCATATTCTTCTAAATCATGGTTTTTTCGCTTGCTAGGTTAT AGATCCATGCAAATATGGAGTAGATGTACAAACACACGCTCGGACGCAT ATTACACATGTTTACATACACTTAATACTCGCTGTTTTGAATTGATGTTTTAG GAATATATATGTAGAGAGAGCTTCCTTGAGTCCATTACAGGTCGTGATA TGATTCAATTAGCTTCCGACTCATTATCCAAATACCGAGTCGCCAAAAT TCAAACCTAGACTCGTTAAATGAATGAATGATGCGGTAGACAAATTGGAT CATTGATTCTCTTTGATTGGACTGAAGGGAGCTCCCTCT	SEQ ID NO:258
BrmiPEP319a	<i>Brassica rapa</i>	TTGTATCCATTGTGTATTTCTTGCATCCATCAATAAATTTTATGTTACGC CTCTCTATTATTTCTCTCTACATCACACTGTCTTATGTTAAGCTCTACTTC TCAGCAATTCTCTCCACCCAATACATGCATACATACCATCATCGTATCGC TCTAATTTTTCTATCAATCTTGATCCTTCCACAAATTATCTTATGTCTCCC ATTTTAAATCCTACATAGATCCACACATACGAATTATTCTTGTCTGAAGA	SEQ ID NO:259

		TCCATCCATTTACGATTGCTTTAACTTTTACATGAGATCTAGGGCTTCTTT ATTTTCTTCAAATCTTGCTGCATATATTTCAAGATCATGCTTTTCGGCTT GCTAGGGTTCTAGATCCATGGATGTATAGCGTACATACATACACGCACTA ATTCATACCTGTAGTTTGTACGGAGAACATCATAAAATATCACTGTTTGG AATTAATCGTGTAGGAAATATAGATAGGTAGGGAGCTTCCTTTAGTCCAT TCACAGATCATGATATGATCCAATTAGCTTCCGACTCATTTCATCCAAATA CCGAGTCACGAAAATTTCAACTTAGACTCGTTAAATGAATGAATGATGC GGTAAACAAATTGGATCATTGATTCTCTCTGATTGGACTGAAGGGAGCTC CCTC	
CpmiPEP319a	<i>Carica papaya</i>	CTATATCCCTGTCAAATAGTACTTGGTTTTGTTTTAGCCACAAATCTTCTG GTCTTGCAAAGTTCCTTCTGATCTCTCCCCCTTCTCATTTTTCTCCTCT TATATATGGATCATCAATTTGCTGTACACACACACATTTACTGTAGTG ATAATTAGCTAGCTAATTTGTTAGTATGTAAATTAGATCCCAAGTACCCT GTTATATTTTTTAGGCTTATCCTATGCATACCTGATAGTACAAGAACTTA GTTTGTAATTAGGTACTTGGTAGTAGGGTTAGATTAATTACTGTCTTGAA AGAGAACTTATCCAACAAATAGAGCTATGAAGATTAATAATTAGGTTTTAG TCTTATTAAGATTATTATATTACTAGACAAAAACAGTTAAATTTTTTAAAT TGGGTAATTAGGTACTTAGCAATAGGGTTAGATTAATTACTGTTTTGAAA GAGAACCTACCTACAAATAGAGTTGAAATGATTATGTTTTAGTCTTACTA AGATTGTCATATTTCTGGAAAAAAACAAATCTTGAAACAGATAATTCAG ATAGTCATGATCAATGGAAAAAACATCATGGGTGTGTGCTTAATTAAGCT AATATATATATATATGAAGATATAATGTTATGCACACTAGCTATGAATTT GTAAGAATAATGAAGGATAAAGATGATATATTTAGATGTTATAAGTGTA AGTAAGGTGGAATGGGTTGATGGGTAGTAGTAGTAGTAGAGATGAT TGGTGGAGAGAGCTTCCTTCAGCCCACTCATGGATGGGTATGAAGGGGT AGAAGTAGCTGCCGACTCATTTCATTTCAGCCCACTCAGTATGTAACTCGTC CCACTGTTGACTGTATGAATGATGCGGGAGATATTTTACATCCATCTTT CTCTGTGCTTGGACTGAAGGGAGCTCCTTCTT	SEQ ID NO:260
CrmiPEP319a	<i>Capsella rubella</i>	TTGTATCCATAGTGTATTTCTCGCATCTACCATCTACTATTTTCTACGCC TCTCTCTTTTATCCCTCTATCTTTTCTTCATCAAATCTTCTTTTGTTC AGTCTCTCTCATCATTTTTCTCTATACACATACATGCATCCACATACATAC ATACATATACCATCATCTTCTTTTCTCATCTCTAGTTTTTGTATAAATTT TGTTCCAAGGATCTGTATCTCTCCAATAAAGATACATACAAATTATTGTT GTCATAGATCTATTAGAATTGCTTTAACTTTTATATGAGATCTAGGATTC TTCCTTTTCTTTCAAATTTGCTGCATATTTTCAAATCATGATTTATCG	SEQ ID NO:261

		CTTGCTAGGTTCTAGATCCATGCAAATTTAGAGTATTTTTACACACACAC ACGCTTGGACACAAGTACATACATGTAGTTTTCTTTATGTGGTGAAAAG TACATAACATGTAGTTTATAGTTACTAGTCGCTATATAATTTAAAATTGA TGTTATAGGAATATATGTACGGAGAGAGCTTCCTTGAGTCCATTACACAG TCGTGATATGATCCAATTAGCTTCCGACTCATTATCCAAATACCGAGTC TCACCAAATTGGAACAAGACTTGTTAAATGAATGAATGATGCGGTAGA CAAATTGGATCATTGATTCTCTTTGATTGGACTGAAGGGAGCTCC	
EgmiPEP319a	<i>Eucalyptus grandis</i>	TCGTTTCCCATCCCCATTTTCATAGAATAATGCCACCAAACAAAGAAGCAT TAGCTCAAAGACTAATTACCATCTGTTTTATTGATAGATACGTGCGAAAC GGTGATTGTTTTTTCCCAAATAAGAAACCAAATGAAGCATATTCAAAG GTGGAGATATGGGGAGACTTCCGGAAGGCAAGGGGATTGGAAAAGGCT CGAGATCAAAGTGCATAGCAACCCTTCGCTAAAGGTGAAAAAGAATACG AATAACTTCAGTAGCTCACTTTAAATTCCGAAACATTAAACAAATCAAAT CTCCCTCGCCCTCCTTGCCCTCCTCTCTTTACCTATATAAAGCCACCGCCCC TTCAATGAAATCCACGAGTGGAAGGTCACAGTATAGTAGGGTCCTGCAA AGGGAGAGCGAGAGCGGCTCCACTGTCTACCTATAAGCAGTTCCTTTCTT TTGTTTACATGTCTGTTGCACCTCACCGAGTTTTTCTATTCTCTTTCCTCTG GTTGGTTAGCAGATTTCTCAGGGGACTTCCCTCCTCCCTTGAGGATCCTTC TCTTGAAGCGATATGTCTCGAATGGGTAAGAGAGAGAGAGGAAGGGAGC TTTCTTCAGTCCACCCATGGGACGTGTTGGGTTTTAATTAGCTGCCGACTC ATTCATCCAAATACCGAGCGAGAGCAAGTAACAGAGCTCCGTAAATGAA TGGATGATGCGGGAGTCTTGTTGATTCCCAAGCTTTCCTGTATTGGACTG AAGGGAGCTCCCTCTATCT	SEQ ID NO:262
GrmiPEP319a	<i>Gossypium raimondii</i>	GCGTATCCTTCCACTTACGGATTACCCATAGCTGCTATAGCCCGAGTTTG CTTGTCATAATAGAAATAAACTAAGGGAGAAAAAAGCTCTCCACTCTCG CCTTTTTCTTCTTCGAGTCTCTCTCTTTGACTGGCCTTTGTGCAAAGATCTT CCTTTTTTAAACAGTCGCTTTCTTTACTCTCCCTTTCCTTCTTTCTCTTAA TTGCTAAAGCAGCTTCCACTTCCACTCACTTTAACCCATGATCCATTTCAA CCTGTCACAGTGGAGAGCAATTTGTATGGCTAATTTCCATCTCACCTATT CTTTTCTGTTTGGGGTTCTCTAGTCTAGGGTTGCATGACATGAGAGACAT GGCTCTTTTTTTTTTTTTTTCAGTTCACAGGTGTTTATATATGTTGTTGTGT ATTTTGTCTTAAAGCTTTGTGATTGATGATCTGATAGGTAAGAGAGAGCT TTCTTCAGTCCACTCATGGGATGGGGATGGGGTTTAATTAGCTGCCGACT CATTATCCAAATACTGTGTTACAAAACCCAGTAAATGAGTGAATGATGC	SEQ ID NO:263

		GGGAGACAAATTGAATCCTAATCTTCCTGTGCTTGGACTGAAGGGAGCTC CCTCCC	
MtmiPEP319a	<i>Medicago truncatula</i>	ATTTATCCAATCATGTTGCTCTCACTTCTTTTCAGCAGTTCTGTTGATATC ACCCTTTTAGTTGAAGCTTTGGATTTCATGACTTTATGAGATGGTAAATCTT TAAATTAAGTTTAAGTATGCACTTGATTTGTTTATATAATTTGTTTATTTA GATTTTAAACCCTAAGTTGACTTTTTTAATTTGATTTAAATTATGATATGA TTGTTATTTGGCTTACCATGGTCATAATTTAGGGTTTAGAAGATGCATGT ATATCTTGAATTGTTTATGGTAATAAAGGGGTTAGGATTTCTCCTTTTGGT GAAGTGAGAAAATCTCATAATTTTGTTCTGAAGGTAGTTTTTAAGATTTA GGGTTATGGGTTCTTTGTTTGAATGCTTTTTCAAGTCTTTTTCAATGATAT TTGCCTAGATCTGTTTTAATTTGAATTAATAATTCTGGGTTTGGATTAATA TTATTGAAGATTATTATTAATTAATTTATTAGAAATAGATGAAGAGAGCT TCCTTCAGTCCACTCATGGAAGGGTAAGGGGTTTGAATTTACCTGCTGAC TCATTGATTCAAACACAATAGACAATTATGGGGTTATGCTATTGTGAATT GTGTGAATGATGCAGGAGGTGAATTTCTTCCTTTTCTTCTTTGCTTGGACT GAAGGGAGTCTCCCTTT	SEQ ID NO:264
OsmiPEP319a	<i>Oryza sativa</i>	TTATATCTGACGCGTTGTAATCCTGTTTAATTAGGGCTTTGCCCATTCTT TTGACCCCTTCCGGACATTCGCTAGTTGGAACCTTGTTTTACTCCTAGCAG TGTACTGTGTAGTACTTATTACGAGCAAACGTAAAAATAAATAAATGGA AATGATACAAAGGCCGTGTTTAATTTTAAAATTTTTTTTCAAACCTTCAAC ACTTTACATCCCATAAAAAGCTTACTATACATACAAACCTTCCAACCTTTT CGTCACATCGTATCTAATTTCAACTAAACTTTTAATTTTAGCGTGAACATA AACACAGCCGAAGCCCGGCCACATTCTCACTATTTTTATTCAATTTTATCAT GCCTGTGATGTACGCTTGGCCCTATTTAATAGGCCTTCTCCATTTCTCT CCATATGATGTCTTCTCTTCTCTATCCCTCTTGCCATCTTCTATCTTCCCTC TTGCACCCATCTTTGTGATAACTTCTACTAGCTCCTCTCCTACTACCAGTC ATACCACTCTCACAAATCCTCCAAGATCCGCATGGGGAGAAGCTCCAAA AGTTTCGTGGTTAGTTTAATTTTCATGCTTGTTTGCTGCCGTTTTTCATGTT GATCTGATCTTAATATATGTAGACTGCTGTAAACATATTCTTTTAATTTGA TGGAAGAAGCGATCGATGGATGGAAGAGAGCGATCCTTCAGTCCACTCA TGGGCGGTGCTAGGGTCGAATTAGCTGCCGACTCATTACCCACAATGCC AAGCAAGAAACGCTTGAGATAGCGAAGCTTAGCAGATGAGTGAATGAA GCGGGAGAGTAACGTTCCGATCTCGCGCCGTCTTTGCTTGGACTGAAGGG TGCTCCCTCCT	SEQ ID NO:265

PpmiPEP319a	<i>Physcomitrella patens</i>	TGGGATCCACACGAGTAATTATTCCTCTCTCATGCATCACAACTTGGAC TTGCCCAGCTTTTACCTCTCTCCATGTTCCACCGTCGGAGATCCTCGGTGC TGCTACCCCCGTTTCGGCCAAACCCAACCCAACCCCTAGGTGTCTGCCGGAC CTCCGCTTCCCCTCCTGCTTCACCCCCTGCACCGCTTAAATTTGCACCTCG TAGTATTTATCTATGCCCCATTTTCAGATGACTTGCATGACACCCATCTGG ATTCGTCTCCAGGCGCCTTGTCTGATCTATTTCGCTATCAGTCTTTCTTTCA GTCTGTCTTTCTGCCAAGCACACCGTGCTGGTGGTGGTGTCTATCAGTCGA AGCAGTCGCCGAAGGGTCCTTGTATCCAGCCCTCACCGGAGACAGTTTCG CTTCGGGGTGGGGAGAACTGTTGAGACCGTCGATGTTGCATGCAGCAGC ACTGGCGAAGGTGCTTCTGATACTGGGTATTCCAGCCTCGCCGCTCGGTG CACTGCAGGTACGTGGTTACATGACACTACTGTGTGGGTAGTCTGGGCAC AAGTAGATCGACATGCCAGATTTGGCCCGTATGCGTGTATGTGCGGTTAT GTTCCCGTTTCGATTGCGGATACCTTGATTGTGGAGCTCCGTTTCGGTCCA ATAGTGGCTGCGACGGAAGGTGGTCCCGCTGCCGAATCACACGTCCGGG TTGCTTATCGGGGCAGGGCCCCGATACGGTATCCGAACGTTTGTCCCGGG AACTGGTCGACCTTCCGCCCGGCGTCTCTTGGACTGAAGGGAGCTCCACT	SEQ ID NO:266
ThmiPEP319a1 ThmiPEP319a2	<i>Theellungiella halophila</i>	TTTTATACAAATAATGTTTCGATAACACTAAACCCTAGCCATCCAACTAAT AGACAAAACCCTACTTGTAAATTTACAACCGCAAATTCCCAGAGAACAGA GTAACACGAGAGAGAGATGGAGATTCAAATTAAAAAGAAAACTTATA TATAATGAATACACAAAAGCTACCTAATCTGTATATATATATATAAAT ATGTCTTCATTAATAATGGTCGTGGAATAGAAAAAGGAAAACCTAAT TTGATCGCTAGGGCTTATCAGAGTAAAGATGGTTAACCTTCAAAGATG ACTAATTAACCGGGGAGATAATTAAGATTAAATACGCCAACAGAGAG TTAAGAGATACCAGATTTAAATTCCACAATTTGGTCATGTTCTTCTTCAC GTATTCATGACGATGTCTGAATTATAGAGAAACCCAAAATATAAAATGTT AATTTTACCAGACATTTACATACCAATAACTCTATGACGATATGTAAAGT AAGCAAGGCATGTTTTTATGCAGGGAAGATTGAAAATTCAAGATTAATC AAGAAAATTGGAATACCAAAAAGAGAGGGAGCTCCCTTCAGTCCAATCA GAGAGAATCAATGACCCAATTTGTCTACCGCATCATTCAATTTAACA AGTCTAGCTCGAATTCTTGGTGACTCGGTATTTGGATGAATGAGTCGGAA GCTAATTGGATCATATCACGACCTATGAATGGACTCAAGGAAGCTCTCTA CAATGTATTCTACCATCAACCCAAATATAGTGATTACAGATGCTGT TCTCACTGTAGACTACATTTACGTTT	SEQ ID NO:267
AtmiPEP319b1	<i>Arabidopsis thaliana</i>	AGACATCTCTTCTCTCTCATCTCTCTTTTCTTCTCTCTTTTCTCTCACATAA ACTCTCTTTTTTTACTATTAAATCCATATGGTACCTCAAATTAATCTATGG	SEQ ID NO:268

		TCATCTAGGGTTATCTTGAAGATTAGAATTGATTCTAGCACGCACAGAGA GGAAGATCATTGCATCCAGAATCACAAACATGGCCTATCTTTTATCTTTT CTTTTGTATCTAAGTCACTGTTTTATGCTATATATAGTATAATCAAATTCT TTACATGTGCTTGTATGTATGCGTATATATAGTAACGGAATTGTTAATAT GCTTATAGATGTTGAGTTGGTGGAGGAAGAGAGCTTTCTTCGGTCCACTC ATGGAGTAATATGTGAGATTTAATTGACTCTCGACTCATTATCCAAATA CCAAATGAAAGAATTTGTTCTCATATGGTAAATGAATGAATGATGCGAG AGACAAATTGAGTCTTCACTTCTCTATGCTTGGACTGAAGGGAGCTCCCT	
AtmiPEP394a1	<i>Arabidopsis thaliana</i>	TCTTATTCATCACAAATCATCTAGGGTTTTAAGCCAAGCTTATATAGCCC GTCATAAAGAGAACTCATCTGCCTCTCTCTCAATACCAATAAATATCACC ACCGTCCTTCTCTCCTATCACTATTCAATCTATCGCAAACCTCTTTATGTC TCTCCAATTTTATGAGAGGGTTTCCTTCAAGAACACAGTAAATAGATTG GATCTTTAACTTTTGTTCCTTTTCATGAGGGTTTGACAAAGATTTTCTTA CAGTCATCTTTGGCATTCTGTCCACCTCCTTCTATACATATATGCATGTGT ATATATATATGCGTTTCGTGTGAAAGAAGGAGGTGGGTATACTGCCAAT AGAGATCTGTTAG	SEQ ID NO:269
AtmiPEP395c1	<i>Arabidopsis thaliana</i>	TTGTATCATGACAGAGCAAGAAGAAGAAAGTCAAATGTCCACATGAGTT CCCTTTAACGCTTCATTGTTGAATACTCAAAGCCACATTGGTTTGTATATA ACACTGAAGTGTTTGGGGGGACTCTTGGTGTCAT	SEQ ID NO:270
AtmiPEP395e1	<i>Arabidopsis thaliana</i>	TTTCAAACCCTAACACTCTTATAAACCGATTGCGCCAAAATGTATCTACAA TATATTGATAATGTAATATCTATATATTCAAACAATCGTCGTGTTGGTCG GATGTTTTCTAGAGTTCCTCTGAGCACTTCATTGGAGATACAATTTTTTAT <u>AAAATAGTTTTCTACTGAAGTGTTTGGGGGAACCTCCCGGGCTGATTCCGGT</u> <u>ATTTTAAATTCAGTAGACTAGCTAGCTG</u>	SEQ ID NO:271
AtmiPEP397b1	<i>Arabidopsis thaliana</i>	TGGTAATAGAAATGAGCAAGGAGATATTTTTTCCCTGGGTTTGAATGA <u>ACATCATTGAGTGCATCGTTGATGTAATTTTACTTATTTTATTCATTGTT</u> <u>GAATTAATTAAGAAGTATATATCAGCGTTGCATTCAATTATGTTTTTCT</u> <u>AATTTTCAGGAAATACAAAAAAAATGAAAAAAAATCACTTAAAAG</u> <u>ACCTTGAGAGTTCTTTTGACT</u>	SEQ ID NO:272
AtmiPEP398c1	<i>Arabidopsis thaliana</i>	GGATATCGAAACTCAAACGTGTAACAGTCCTTTTATTACTGGTTTAGAAGA TAGATAAATATTGTTAAGGTAGTGGATCTCGACAGGGTTGATATGAGAA CACACGAGCAATCAACGGCTATAACGACGCTACGTCATTGTTACAGCTCT CGTTTCATGTGTTCTCAGGTCACCCCTGCTGAGCTCTTCTCTACCGTCCA TGTTTTATCAACGCCGTGGCCCGTG	SEQ ID NO:273

AtmiPEP399b	<i>Arabidopsis thaliana</i>	TCTTATAGAGATGAAGAGAAACATGTAAACTCACTAGTTTTAGGGCGCCT CTCCATTGGCAGGTCTTTTACTTCCAAATATACACATACATATATGAATA TCGAAAATTTCCGATGATCGATTTATAAATGACCTGCCAAAGGAGAGTTG CCCTGAAACTGGTTC	SEQ ID NO:274
AtmiPEP399d1	<i>Arabidopsis thaliana</i>	CAATAACTCAAAATGCAATGTGAAATATGAAGAATATATTAAATAGTAG TGAAGATGCATGTTTATGAAGACAGAGAGATAATGTATGGTTGGATTAC TGGGCGAATACTCCTATGGCAGATCGCATTGGCTAGATATGCAAGTAAA ATGCTTCTCTGCCAAAGGAGATTTGCCCCGCAATTCATCC	SEQ ID NO:275
AtmiPEP403	<i>Arabidopsis thaliana</i>	ATTTAGGTCTCTCTTCTTCTTCTTCTTTTCTTCTTGAGCGCCGGCGAAAA AAGTCTCTGTGAGAAAAAGATACGACGATTGTCATTAGAAGAGTCGTAT TACATGTTTTGTGCTTGAATCTAATTCAACAGGCTTTATGTAAGAGATTCT TTAACAATTCCTATAATCTTTGTTGTTGGATTAGATTCACGCACAACTC GTAATCTGTCTTTTCGATTTTACCAGATCTGTC	SEQ ID NO:276
AtmiPEP447a1 AtmiPEP447a2	<i>Arabidopsis thaliana</i>	AATTATATCCATGGTCATGGCTCATCTAGTCGCACTGCTCTCCTTTTCT CAAAGTTTAAATTCGACATTTGGTAAAATGATGAAACCTCGATGGAACT GCTCTCTTTATGGAATCACGGAATGGACAAATAATCAAAATCAGAAATC GAAGCGAAAAGGGAGGAGAAAAACGCAGATTTGGAGGATTGGGGACAG ATTAGATACTGTTGAATGCATCACTCTAATGCTATCAGCCTATTAATAGC GTCCTATATTTTCGAAGACTTTTAATGTTTAGGGTTATGGATTTTTCGAGC GAAGCATGGAGAGATGTTGAATTGGATACTATAGGATTTGGTACAACAC ATACATATGTTCTGCTTCTGCAAACTAACATATCAAGTTCAGAGAAACC AGTAAGTCGTTGAATATTTTATTATCCATTCAACGCTTTCTTCTTTTGGAT CATGTCTTGTTTGCTTGACCACTTCTTCTTGCTTAAGAGGATGGACAATAT ATAAAACTGGAGCCTTCTTTTCTATGAATGCTTATCATCGCGGAGTTG ATCTGTTCAATTCACCTGCCATTGGATGCTTTTTTTATATATACTTCACTG TTCAATTTAGATGCTTTAGAAGGTTTGCAGGAGTAGCTAGAGAATCTGGT ATCTTCAGTTCTTCAATTTAGCTACTTGGTATCAGCTTCGTCATTGTATA TCAACACATTCTTAATATATAATACTACTTTTTCATCCATTAAACCCCTTA CAATGTCGAGTAAACGAAGCATCTGTCCCCTGGTATTGTCTTCGAGCTTG GTGTTTTTTTCTAGCCAACTCCAAGTTCTCGAGTTGATCATTGTTTGTATT CTTGAGACATTATTTGGGGACGAGATGTTTTGTTGACTCGATATAAGAAG GGGCTTTATGGAAGAAATTGTAGTATTATATATCGAGAGTG	SEQ ID NO:277
AtmiPEP447b1 AtmiPEP447b2	<i>Arabidopsis thaliana</i>	CTATAAATGCTGCTTATCATCGTGGAGTTGGTTCTGTAAACATTTGAAAA TTCTGAACAGTTTCACCTGCCATTGGATGCTTTGTTTCAATTCAGGTGCG	SEQ ID NO:278

		TTAGAAGGTTTGCAGAGTAGCTAGAGAATCTCGTATCTTCACTTTCTGCT ACTTGGTATCAGCTTCGTCACCTTTATATCAACACATTCTTAATATACAATA CTACTTTTTTCATCCATTAATCCCCCTTACAATGTCGAGTAAACGAAGCATC TGTCCCCTGGTATTGTCTTCGAGCTTGGTGTGTTTTTCTAGCCAGCCCCAA GTTCTCGAGTTGATCATTGTTTGTATTCTGACACATTATTTGGGGACGAG ATGTTTTGTTGACTCGATATAAGAAGGGGCTTTATGGAAGAAATTGTAGT ATTATATATTGAGAATG	
AtmiPEP447c	<i>Arabidopsis thaliana</i>	TAGTATAACCGCTGATGTACACCTACCAGCTTGATAACTCTTTTTCTGTGG TTTCTGTGTACTCGTTTCTGTTTGTACAGATACTTCTTGTTC AATTTTCAGA TGCTTTAGAAGGTTTTTCGGAGTGGCTAGAGATCTGTTATCTGTATGAACA GCTACTTGGTATCAGCTTCGTCATTTTATCAACACATTCTTAATATACAAT ACTTCTTTTTTCATGCATTAAGCCCCCTTACAATGTCGAGTAAACAAAGCAT GTGTCCGCTAATATTGTCTTCGAGCTTGGTATTTTTGTATTCTGATACGGT ATTTGGGGACGACATCTTTTGTGACTCGATATAAGAAGGGGGTTTGTGG AAGAAATTGTAGTATTATATATCAAGAATG	SEQ ID NO:279
DmmiPEP1a DmmiPEP1b	<i>Drosophila melanogaster</i>	TTTGTGGAACACATTCGACCCACTGAAAAATTGATATAATTTAATGAAAG TGCATAAAAATGGTGGACAGTGCATTAACTGAGCATTGAACACAAAGG CCGCTCAGCAAATTGCTAATTAATAATTCACGATTGCCATTTACCTGACA CGTTGACGATTTTCATTACAATTCGATTATGTTTCGTTGCAGGGAATTTTA AATGTTAATTGCCAAGAATGTTTCAACAAATTCATTTCTCATTAAATGTGT CTTTTCATTTAATTTTATGTTGTATGAGCTGCACGAGAAATGAGTTGTACT TTTAGTTCGACGGCAGAGTCATGAATGTTTCGGCAAAGAATGTAATAATA ACTATCCTCTTTAGACAAATATAGATACAAATCTATCAGATTCTAAAAGT AGAATAATCAATTAATCAGAAAGCTAAAAATAAATAGGCATATTTATAT TTTAATGCGGATTTTTGAAGTTCAACGGGAGAAATGAATCCTTTTTTACCA GCCACAGGCGCAATTTGCAACAGAAAGTGTAGCAGAAGTACTCCTCGAA TATTTCCCTGCTCCAGGAGTCATCCATGTGGTTTCGAGGCACACATTTGA CAAATCATGCCCCGCTATTTGTTGTAAAAACACAATCGCACACATGGCC GCATTTTCGGCGACTTCCAGAGAGCGGTACACTTAAGGCGGCCTGGGAAA CGCCTGCAATCTGCTGGTCGCGAACTGCAGATTGCATCCATGTGCCAGGC GACCATGCGACCATGTGACCATGTGCCCCGCCGACGCCTCGCAGCCCAC ATCCTGCCCATCGAGGGCACAATCAGCGTGGGTATTGCCGCTCCGGCTG CTTCAAGTAGGTAAAAACCGAGAAGATTGAGGATGAATGTATGAGTATG AGAAAATACTCGGCGGAACATATGCTGCCGGGCTTGACCTGACCCTGCC TCATGTGTGGGTCTCCGATTTAATTTTAGGCACCTATATAAACGCGTGTTT	SEQ ID NO:280

		ACACTGCAGCCAGAACACAGTCGCCGTCTTCAGTTCGCGCCGTCAACTCC TCGATCGATCGATCGATCGTCTCGGATCGAATAGAGCTGGGCTTCTGCT CCGGAGCTACATCGCCGTACTTGTGCGGACGAGTGTGGTGATGAAAAGTC GCTTAGTCCGGGATTCTTGCCAGATCTCTAAGGGATGAGCTGGCATCCCCA GGCTGGCCATGTGGCGCGAAGTATGCGCACAAAAAAGTCAAACAAAAA GGCGCAATTTTATTACGGGCAACCAACGACGAAACAAAAACAAAAGCCAA CCGAAAAGCAGAAACAAAGCAGCAAAAAAGTTTATGAATTTTTTGTGCAG GCGCGTGAAAGATGCAAAACGAGAAAAAAACATGAAAAAAAACATTA AAAAAAACAAAAAAATCCAAAACAGATACCGAGCTGTATCCGAAAAC GAGTGGGGAAAGGGGTTTCCCAGTCACATATAAACACACTTCAGTGCGC TTAAAAATTGCTTTATTGTCAGTTGGACTATAAAAACGCACGGCAGCGAA CACCGCACACAAAAAGGACGAGCAGAAGTGGGCAAATAAACGAAAG CTCTTAAACGAAAAACAGGAAAATTTGCATGCCACAAAAATAAGCATAA GGATTTGCCGCGCACAAAGTAGAAGCAAAAAGGAATTGCCCAAATGCAG CCACAAAAGACTGTGGCAAATGTTTTGCAGCTTGCCCCTTTTCCCTGCA ATTACCGTCAGTCGTTGTCATTATTCAGCAGATTATATGGTTTTGCTTATT CCGGACCACCATCATCATCATTATCATCATCTTCGGTAAGTTAGACA ATCCCATAAAAAACTGTCCAAGTGAGTAGTGCCACCAAAGTTAGCCGC GTTGTGGAAAATCCAAAACAAAGACCATCCCATATTCAGCCTTTGAGAG TTCCATGCTTCCTTGCATTCAATAGTTATATTCAAGCATATGGAATGTAA AGAAGTATGGAGCGAAATCTGGCGAGACATCGGAGTTGAACTAAAACT GAAATTTGATTGAAACAGAAGTAGAACCGTAATGAAATGAATGAAATAT TAACCCGTTTCTACAATCCCTGAATAAAATTATTAATTAATTATAGAGCG GGCTAATTTTACAATATATATTGATTTTTTTTTTTGAAG	
DmmiPEP8	<i>Drosophila melanogaster</i>	ATTCTTTTTTGGTGCTCGATCGTGACGGTTTGCTCGCGCTCTCCGCTGCGC CGCTCTTTCCGTTGCATATGTGTGCGGGCGTTATTGTGCATGTTTCCGGTG GCCGAAAAAAATAGTAAAATAAAATATAGAAAACAGAAACCAAGAAT AATAACAGCCATACGATAAACAGTGTGCCAATGTGTGTGTCTGTGTGTGT GTGCATCTCGCGTAACAACAATAATTGCATTTATCGGATGGCGCCAGCTT CAATTTAATTATAAATAACATGTTCAACTTTTTATACTATTTTCCCTGCGT CAAAGTGGGCGTTGCAACTGCCCCCGGAAAAATCACGCGCCCCGGTTCAA AGTTAAAGTTTGCTGGGTAACGCACACACACACACACAATCACTCAC ACGCGGTCACACGCACATTTCAATAAACTAATG ¹ GAGCCTGGCTTTGTTTT TGTTTTATTTCCAACCCACTTGAGCACACAGCACACACAGAGAGAAAAA TCAATACTCGTTATGGGATTAAATTTACAAAGCGCAAAGCAAAGCGACA	SEQ ID NO:281

		AACAAAATTCAAAAGAAAGAAAAAAAACACTCAAATAAACTCACAAA GAATTCCTTATCGCCAAGGGGGCCAATGTTCTAAGGTTCTTTCGCCTTGA ¹ GAACTTTGAGCTTCCTCTGGCAAAGGAGATTATAATGTACAAATAATGTT GCAATAACCAGTTGAAACCAATGGAATACCGAATCTTGCTAATTAGCAA GGACATCTGTTACATCTTACCGGGCAGCATTAGATCCTTTTTATAACTCT AATACTGTCAGGTAAAGATGTCGTCCTTAACCTTCAGTACCACC AACAGCAGCAGCAGCACCAAAAAAAAAAAAAAAAAAATGCGTAAAAAT CCAAACAAATCATAAAAGTCGAAGGA	
HsmiPEP155	<i>Homo sapiens</i>	GCCGAGCCCCGGGCCAGCGCCGCTGCAGCCTCGGGAAGGGAGCGGATA GCGGAGCCCCGAGCCGCCGCAGAGCAAGCGCGGGGAACCAAGGAGAC GCTCCTGGCACTGCAGATAACTTGTCTGCATTTCAAGAACAACCTACCAG AGACCTTACCTGTCACCTTGGCTCTCCACCCAATGGAGATGGCTCTAAT GGTGGCACAACCAAGGAAGGGGAAATCTGTGGTTTAAATTCTTTATGCCT CATCCTCTGAGTGCTGAAGGCTTGCTGTAGGCTGTATGCTGTTAATGCTA ATCGTGATAGGGGTTTTTGCCTCCAACCTGACTCCTACATATTAGCATTAA CAGTGTATGATGCCTGTTACTAGCATTACATGGAACAAATTGCTGCCGT GGGAGGATGACAAAGAAGCATGAGTCACCCTGCTGGATAAACTTAGACT TCAGGCTTTATCATTTTTCAATCTGTTAATCATAATCTGGTCACTGGGATG TTCAACCTTAACTAAGTTTTGAAAGTAAGGTTATTTAAAAGATTTATCA GTAGTATCCTAAATGCAAACATTTTCATTTAAATGTCAAGCCCATGTTTG TTTTTATCATTAAACAGAAAATATATTCATGTCATTCTTAATTGCAGGTTTT GGCTTGTTCAATTATAATGTTTATAAACACCTTTGATTCAACTGTTAGAAA TGTGGGCTAAACACAAATTTCTATAATATTTTTGTAGTTAAAAATTAGAA GGACTACTAACCTCCAGTTATATCATGGATTGTCTGGCAACGTTTTTTAA AAGATTTAGAACTGGTACTTTCCCCCAGGTAACGATTTTCTGTTTCAGGC AACTTCAGTTTAAAATTAATACTTTTATTTGACTCTTAAAGGGAACTGA AAGGCTATGAAGCTGAATTTTTTTAATGAAATATTTTAAACAGTTAGCAG GGTAAATAACATCTGACAGCTAATGAGATATTTTTCCATACAAGATAAA AAGATTTAATCAAAAAATTTTATTTGAAATGAAGTCCCAAATCTAGGT TCAAGTTCAATAGCTTAGCCACATAATACGGTTGTGCGAGCAGAGAATCT ACCTTTCCACTTCTAAGCCTGTTTCTTCTCCATATGGGGATAATACTTTA CAAGGTTGTTGTGAGGCTTAGATGAGATAGAGAATTATTCCATAAGATA ATCAAGTGCTACATTAATGTTATAGTTAGATTAATCCAAGAACTAGTCAC CCTACTTTATTAGAGAAGAGAAAAGCTAATGATTTGATTTGCAGAATATT TAAGGTTTGGATTTCTATGCAGTTTTTCTAAATAACCATCACTTACAAAT	SEQ ID NO:357

		ATGTAACCAAACGTAATTGTTAGTATATTTAATGTAAACTTGTTTTAACA ACTCTTCTCAACATTTTGTCCAGGTTATTCAGTGTAAACCAATAAATCTCA TGAGTCTTTAGTTGATTTAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAA AA	
AtmiPEP157c	<i>Arabidopsis thaliana</i>	CTTTGTCACTTCATACACTCCCTATTGTCTATATATATATATACTTACA CATATTCAAACATTATAATACTTAATTACACATACATACTTTATGATGTT GCATATCACACATAGGTTTGAGAGTGATGTTGGTTGTTGACAGAAGATA GAGAGCACTAAGGATGACATGCAAGTACATACATATATATCATCACACC GCATGTGGATGATAAAATATGTATAACAAATTCAAAGAAAGAGAGGGAG AGAAAGAGAGAGAACCTGCATCTCTACTCTTTTGTGCTCTCTATACTTCT GTCACCACCTTTATCTCTTCTCTCTCTAACCT	SEQ ID NO: 400
AtmiPEP157d	<i>Arabidopsis thaliana</i>	ATTTACTCTTCACCGCCCTCTCTCTATATATAGTCTCTATCCTCACATATT ATATATCAAACCGCAAGAATGCTGTATGTATAGTGGAGGGTGATAGTGT GGTTGCTGACAGAAGATAGAGAGCACTAAGGATGCTATGCAAAACAGAC ACAGATATGTGTTTCTAATTGTATTTTCATACTTTAACCTCAAAGTTGATAT AAAAAAGAAAGAAAGATAGAAGAGCTAGAAGACTATCTGCATCTCTAT TCCTATGTGCTCTCTATGCTTCTGTCATCACCTTTCTTTCTCTATTTCTCTC TAC	SEQ ID NO: 401
AtmiPEP160c	<i>Arabidopsis thaliana</i>	AACCAAACTCTTCAACATTTCTCTCTGACTACTTCATTTCTCTTCCCAA CAGTTAAAAAAGTTCTGATTTCGATTCAAGCCAAGATCCACGTATAAAG ATATGTTTCATGCGTAGAGGTTTGGTATACAACAATATATACATATAATAG TTTGTCGTTATGCCTGGCTCCCTGTATGCCACGAGTGGATACCGATTTTG GTTTTAAATCGGCTGCCGGTGGCGTACAAGGAGTCAAGCATGAC	SEQ ID NO: 402
AtmiPEP164b	<i>Arabidopsis thaliana</i>	ATACATTCTCTCTTTCTCTCTCTCTCTCTCTCTCATCCCGGCCAGTTATGT GGTCGGAGAGAATGATGAAGGTGTGTGATGAGCAAGATGGAGAAGCAG GGCACGTGCATTACTAGCTCATATATACTCTCACCACAAATGCGTGTA TATATGCGGAATTTTGTGATATAGATGTGTGTGTGTGTTGAGTGTGATGA TATGGATGAGTTAGTTCTTCATGTGCCCATCTTCACCATC	SEQ ID NO: 403
AtmiPEP166c	<i>Arabidopsis thaliana</i>	TCACACATACCTTTCTTTCTTTCTTTCTTTCTTACGAAAAGTTTCATCACAT TCACATTATCTTTAACTTTGGTCTCTTTTCTTTTGTCTCTTTTCTCTTCTT GATAACGTGGTTCTAGTCTTGATTAATTCATTGTTGTGCGATTTAGTGTG AGAGGATTGTTGTCTGGCTCGAGGTATGAAGAAGAGAATCACTCGAAT TAATTTGGAAGAACAATAAAGAAAACCTAGATGATTCTCGGACCAGG CTTCATTCCCCCTAACCTACTTATCGC	SEQ ID NO: 404

AtmiPEP166d	<i>Arabidopsis thaliana</i>	ATTTAGCTTCTTCTTCTTCTTCTTCTTCTGTCTACTTACATAAAAGTTATCCTt GCTTTGGTTTtagggTTGAGAGGAATATTGTCTGGCTCGAGGTCATGAAGA AGATCGGTAGtATTGATTCATTTTAAAGAGTGAAATCCCTAAATGATTCTC GGACCAGGCTTCATTCCCCCAACC	SEQ ID NO: 405
AtmiPEP169a	<i>Arabidopsis thaliana</i>	TAGTATTCATAAGCACCAAAACAAATATGTAGAGATCTCCTCTTCCATTC TCTATTGTTACTTTTCGAGAAGAAACATACAAAACACATACATTTTTCTTTT GTTTGTGGTTTTTCATATATACAAGTGGGTATAGCTAGTGAAACGCGAATG TGACGAAAGTAGTGTGCAGCCAAGGATGACTTGCCGATTTAAATGATCTT TCTTTATACTCTATTAAGACAATTTAGTTTCAAACCTTTTTTTTTTTTTTTTT TTTGAAGGATTCAGGAAGAAATTAGGATATATTATTCCGTATAAAATACA AGATATATAAAACCAAAAAGAAAAAGTAACATGATCGGCAAGTTGTCTT TGGCTACACGTTACTTTGTGTGCGC	SEQ ID NO: 406
AtmiPEP169h1 AtmiPEP169h2	<i>Arabidopsis thaliana</i>	ACTCATCAACAACCTCTTCATAAATACATAAATCATATAAGAGAAAATG GTGACATGAAGAATGAGAACTTGTGTGG	SEQ ID NO: 407
AtmiPEP169n	<i>Arabidopsis thaliana</i>	AGGCAAAAACATATAGAGAGTAATGAAGTGTATGATGAAGAAGAGAGG TCTAACATGGCGGAAAGCGTCATGTTTAGTAGCCAAGGATGACTTGCCTG ATCTTTTTCGCCTCCACGATTCAATTTCAAATTCATGCATTTTGGATTATT ATACCTTTTAAAGTATAATAGGTCAAATATCATGTTGAATCTTGCGGGTT AGGTTTCAGGCAGTCTCTTTGGCTATCTTGACATGCTTTTTCCATCCAT	SEQ ID NO: 408
AtmiPEP170	<i>Arabidopsis thaliana</i>	ATTCACTCCCTTCTTCTTCTTAATCTCCTTACAGTTACAGACATTCTCTCA CTTGCGTTCTTGTCTTTTACAAAACAGATACACTATGTTTCCGAGAGA GTCCCTCTGATATTGGCCTGGTTCACTCAGATTCTCTTTTACTAACTCATC TGATTGAGCCGTGTCAATATCTCAGTCCTCTCTCG	SEQ ID NO: 409
AtmiPEP396a	<i>Arabidopsis thaliana</i>	TCTCACAACCTTCAACTTCCCTCTTTCTCTATATTACGCTTTTGCCCCTCACT CCCTCTTTCCACAATTAGGGTTTCGTCTGCTCTACATGACCCTCTCTGTAT TCTTCCACAGCTTTCTTGAAC TGCAAACTTCTTCAGATTTTTTTTTTTTTC TTTTGATATCTCTTACGCATAAAATAGTGATTTTCTTCATATCTCTGCTCG ATTGATTTGCGGTTCAATAAAGCTGTGGGAAGATACAGAC	SEQ ID NO: 410
AtmiPEP399c	<i>Arabidopsis thaliana</i>	GAATAACCAACCAGCCTTCTCTCAAAGCAAACCAAAAAGAAAAACCAAC ATTGAAAGAGGAAGTTACGATAAGCGGAGCAGTAATAGGGCATCTTTCT ATTGGCAGGCGACTTGGCTATTTGTATCTTTTGTGTTCTTGACTATTGGCT ATGTCACTTGCCAAAGGAGAGTTGCCCTGTCACTGCTTCCGCTTAAACAC AGTCTATAACCGGTTCTGCTAATATCAATCCTTCTTTTGGACATGTCCAA AGCCGAGATTGATTGATAGAGAATTGGTCTCTCTGGCTACAAAACCTAGTG	SEQ ID NO: 411

		CGGTTCTCTCGATTTAAGTTTTAATAGCATTCACTTTGCACATTGCATCTT TCACATCAAATTTCCATTTTCATCAACCATCTAAACCTCTTTGTTAGCTTTG ATATAAGCAACGATCTAAAGTCTAAAAACCATTAATCCTCTGAAAAAAA AGACAATTTTCGATGGTTCTATTATGTTTCTCCAATGCAGAAATTGTATCG TCTGAATTATAGTAGATTTTTTCTAGACTAAAGTGTAACCAAGACGAAT CTGCACTAACAAGACACACCAATAGACTTTACAGAGAAAGGTTACGAGT TTTGAAAATATTAACGGACCATAGTCATCGCG	
MtmiPEP169d	<i>Medicago truncatula</i>	TGGATAAGTTAATTTATGGTCAAAGAGTCTTTCATGGAGAGGTTGAAAGT GAGATGAAGCCAAGGATGACTTGCCGGTATAATAGTAATTTGCCACAAA TCTAGATAGCTATTAGCTATGTTTGGATGGGCGGTGAGATTAACAAAATT ACAGCAGCATTGTGATTTTGTTGATGCTTTAAAGTGTAAGTTTTATCAAA ATTACAGTGGTTCAGTGAATTATGAGAATCTCACCGTCAATCTAAATAT GCATTTAGTTTCATTTCCGGCAGGTCATCCTTCGGCTATATT	SEQ ID NO: 426

Table 3. List of the primary transcripts (pri-miRNAs)

miPEP	Organism	Sequence of the miRNA	SEQ ID
AtmiPEP156a1 AtmiPEP156a2 AtmiPEP156a3	<i>Arabidopsis thaliana</i>	ugacagaagagagugagcac	SEQ ID NO:282
AtmiPEP156c1 AtmiPEP156c2	<i>Arabidopsis thaliana</i>	ugacagaagagagugagcac	SEQ ID NO:283
AtmiPEP156e1	<i>Arabidopsis thaliana</i>	ugacagaagagagugagcac	SEQ ID NO:284
AtmiPEP156f1	<i>Arabidopsis thaliana</i>	ugacagaagagagugagcac	SEQ ID NO:285
AlmiPEP159a	<i>Arabidopsis lyrata</i>	uuuggauugaaggagcucua	SEQ ID NO:286
AtmiPEP159a1	<i>Arabidopsis thaliana</i>	uuuggauugaaggagcucua	SEQ ID NO:287
CrmiPEP159a	<i>Capsella rubella</i>	uuuggauugaaggagcucua	SEQ ID NO:288
AtmiPEP159b1 AtmiPEP159b2	<i>Arabidopsis thaliana</i>	uuuggauugaaggagcucuu	SEQ ID NO:289
AtmiPEP160a1	<i>Arabidopsis thaliana</i>	ugccuggcucccuguaugcca	SEQ ID NO:290
AtmiPEP160b1 AtmiPEP160b2	<i>Arabidopsis thaliana</i>	ugccuggcucccuguaugcca	SEQ ID NO:291
AtmiPEP161	<i>Arabidopsis thaliana</i>	ucaaugcauugaaagugacua	SEQ ID NO:292
AtmiPEP162a1	<i>Arabidopsis thaliana</i>	ucgauaaaccucugcauccag	SEQ ID NO:293
AtmiPEP162b1	<i>Arabidopsis thaliana</i>	ucgauaaaccucugcauccag	SEQ ID NO:294
AtmiPEP163-1 AtmiPEP163-2	<i>Arabidopsis thaliana</i>	uugaagaggacuuggaacuucgau	SEQ ID NO:295
AlmiPEP164a1 AlmiPEP164a2 AlmiPEP164a3	<i>Arabidopsis lyrata</i>	uggagaagcagggcacgugca	SEQ ID NO:296
AtmiPEP164a1 AtmiPEP164a2 AtmiPEP164a3	<i>Arabidopsis thaliana</i>	uggagaagcagggcacgugca	SEQ ID NO:297

BrmiPEP164a1 BrmiPEP164a2 BrmiPEP164a3	<i>Brassica rapa</i>	uggagaagcagggcacgugca	SEQ ID NO:298
CpmiPEP164a1 CpmiPEP164a2	<i>Carica papaya</i>	uggagaagcagggcacgugca	SEQ ID NO:299
CrmiPEP164a1 CrmiPEP164a2 CrmiPEP164a3	<i>Capsella rubella</i>	uggagaagcagggcacgugca	SEQ ID NO:300
GrmiPEP164a1 GrmiPEP164a2 GrmiPEP164a3	<i>Gossypium raimondii</i>	uggagaagcagggcacgugca	SEQ ID NO:301
MtmiPEP164a1 MtmiPEP164a2	<i>Medicago truncatula</i>	uggagaagcagggcacgugca	SEQ ID NO:302
OsmiPEP164a1 OsmiPEP164a2	<i>Oryza sativa</i>	uggagaagcagggcuacgugca	SEQ ID NO:303
AlmiPEP165a	<i>Arabidopsis lyrata</i>	ucggaccagggcucauuccccc	SEQ ID NO:304
AtmiPEP165a	<i>Arabidopsis thaliana</i>	ucggaccagggcucauuccccc	SEQ ID NO:305
BemiPEP165a	<i>Brassica carinata</i>	ucggaccagggcucauuccccc	SEQ ID NO:306
BjmiPEP165a	<i>Brassica juncea</i>	ucggaccagggcucauuccccc	SEQ ID NO:307
BnmiPEP165a	<i>Brassica napus</i>	ucggaccagggcucauuccccc	SEQ ID NO:308
BomiPEP165a	<i>Brassica oleracea</i>	ucggaccagggcucauuccccc	SEQ ID NO:309
BrmiPEP165a	<i>Brassica rapa</i>	ucggaccagggcucauuccccc	SEQ ID NO:310
AtmiPEP166a	<i>Arabidopsis thaliana</i>	ucggaccagggcucauuccccc	SEQ ID NO:311
AtmiPEP166b	<i>Arabidopsis thaliana</i>	ucggaccagggcucauuccccc	SEQ ID NO:312
AtmiPEP167a	<i>Arabidopsis thaliana</i>	ugaagcugccagcaugaucua	SEQ ID NO:313
AtmiPEP167b1 AtmiPEP167b2	<i>Arabidopsis thaliana</i>	ugaagcugccagcaugaucua	SEQ ID NO:314

AtmiPEP169c1 AtmiPEP169c2	<i>Arabidopsis thaliana</i>	cagccaagggaugacuugccgg	SEQ ID NO:315
AtmiPEP169l1	<i>Arabidopsis thaliana</i>	uagccaagggaugacuugccug	SEQ ID NO:316
AtmiPEP171a1	<i>Arabidopsis thaliana</i>	ugauugagccgcgccaauauc	SEQ ID NO:317
AtmiPEP171b	<i>Arabidopsis thaliana</i>	uugagccgugccaauaucag	SEQ ID NO:318
MtmiPEP171b1 MtmiPEP171b2	<i>Medicago truncatula</i>	ugauugagccgcgucaauauc	SEQ ID NO:319
ZmmiPEP171b	<i>Zea mays</i>	ggauugagccgcgucaauauc	SEQ ID NO:320
AtmiPEP171c1	<i>Arabidopsis thaliana</i>	uugagccgugccaauaucag	SEQ ID NO:321
MtmiPEP171e	<i>Medicago truncatula</i>	agaauugagccgcgccaauauc	SEQ ID NO:322
MtmiPEP171h	<i>Medicago truncatula</i>	cgagccgaaucaauaucacuc	SEQ ID NO:323
AtmiPEP172a1 AtmiPEP172a3	<i>Arabidopsis thaliana</i>	agaaucuugaugaugcugcau	SEQ ID NO:324
AtmiPEP172b1	<i>Arabidopsis thaliana</i>	gcagcaccauuuagauucac	SEQ ID NO:325
AtmiPEP172c1	<i>Arabidopsis thaliana</i>	agaaucuugaugaugcugcag	SEQ ID NO:326
AtmiPEP172e1 AtmiPEP172e2 AtmiPEP172e3	<i>Arabidopsis thaliana</i>	ggaaucugaugaugcugcau	SEQ ID NO:327
AcmiPEP319a1 AcmiPEP319a2	<i>Arabidopsis cebennensis</i>	uuggacugaaggagcucccu	SEQ ID NO:328
AhmiPEP319a	<i>Arabidopsis halleri</i>	uuggacugaaggagcucccu	SEQ ID NO:329
AlmiPEP319a	<i>Arabidopsis lyrata</i>	uuggacugaaggagcucccu	SEQ ID NO:330
AtmiPEP319a1 AtmiPEP319a2	<i>Arabidopsis thaliana</i>	uuggacugaaggagcucccu	SEQ ID NO:331
BrmiPEP319a	<i>Brassica rapa</i>	uuggacugaaggagcucccu	SEQ ID NO:332
CpmiPEP319a	<i>Carica papaya</i>	uuggacugaaggagcuccuu	SEQ ID NO:333
CrmiPEP319a	<i>Capsella rubella</i>	uuggacugaaggagcucc	SEQ ID NO:334

EgmiPEP319a	<i>Eucalyptus grandis</i>	uuggacugaagggagcucccu	SEQ ID NO:335
GrmiPEP319a	<i>Gossypium raimondii</i>	uuggacugaagggagcucccu	SEQ ID NO:336
MtmiPEP319a	<i>Medicago truncatula</i>	uuggacugaagggagucucccu	SEQ ID NO:337
OsmiPEP319a	<i>Oryza sativa</i>	uuggacugaagggugcucccu	SEQ ID NO:338
PpmiPEP319a	<i>Physcomitrella patens</i>	cuuggacugaagggagcucc	SEQ ID NO:339
ThmiPEP319a1	<i>Thellungiella halophila</i>	uggacucaaggaagcucucu	SEQ ID NO:340
ThmiPEP319a2			
AtmiPEP319b1	<i>Arabidopsis thaliana</i>	uuggacugaagggagcucccu	SEQ ID NO:341
AtmiPEP394a1	<i>Arabidopsis thaliana</i>	uuggcauucuguccaccucc	SEQ ID NO:342
AtmiPEP395c1	<i>Arabidopsis thaliana</i>	cugaaguguuugggggacuc	SEQ ID NO:343
AtmiPEP395e1	<i>Arabidopsis thaliana</i>	cugaaguguuugggggaacuc	SEQ ID NO:344
AtmiPEP397b1	<i>Arabidopsis thaliana</i>	ucauugagugcaucguugaug	SEQ ID NO:345
AtmiPEP398c1	<i>Arabidopsis thaliana</i>	uguguucucaggucaccucug	SEQ ID NO:346
AtmiPEP399b	<i>Arabidopsis thaliana</i>	ugccaaaggagaguugccug	SEQ ID NO:347
AtmiPEP399d1	<i>Arabidopsis thaliana</i>	ugccaaaggagauuugccccg	SEQ ID NO:348
AtmiPEP403	<i>Arabidopsis thaliana</i>	uuagauucacgcacaaacucg	SEQ ID NO:349
AtmiPEP447a1	<i>Arabidopsis thaliana</i>	uuggggacgagaguuuuguug	SEQ ID NO:350
AtmiPEP447a2	<i>Arabidopsis thaliana</i>	uuggggacgagaguuuuguug	
AtmiPEP447b1	<i>Arabidopsis thaliana</i>	uuggggacgagaguuuuguug	SEQ ID NO:351
AtmiPEP447b2	<i>Arabidopsis thaliana</i>	uuggggacgagaguuuuguug	
AtmiPEP447c	<i>Arabidopsis thaliana</i>	ccccuacaauugcagaaaa	SEQ ID NO:352
DmmiPEP1a	<i>Drosophila melanogaster</i>	uggaauuaaagaaguaaggag	SEQ ID NO:353
DmmiPEP1b			
DmmiPEP8	<i>Drosophila melanogaster</i>	uaauacugucagguaaagauguc	SEQ ID NO:354
HsmiPEP155	<i>Homo sapiens</i>	uuaaugcuaaucgugauaggggu	SEQ ID NO:358
AtmiPEP157c	<i>Arabidopsis thaliana</i>	uugacagaagauagagagcac	SEQ ID NO : 412
AtmiPEP157d	<i>Arabidopsis thaliana</i>	ugacagaagauagagagcac	SEQ ID NO : 413

AtmiPEP160c	<i>Arabidopsis thaliana</i>	ugccugggcucccuguaugcca	SEQ ID NO : 414
AtmiPEP164b	<i>Arabidopsis thaliana</i>	uggagaagcagggcacgugca	SEQ ID NO : 415
AtmiPEP166c	<i>Arabidopsis thaliana</i>	ucggaccaggcuucauucucc	SEQ ID NO : 416
AtmiPEP166d	<i>Arabidopsis thaliana</i>	ucggaccaggcuucauucucc	SEQ ID NO : 417
AtmiPEP169a	<i>Arabidopsis thaliana</i>	cagccaagggaugacuugccga	SEQ ID NO : 418
AtmiPEP169h	<i>Arabidopsis thaliana</i>	uagccaagggaugacuugccug	SEQ ID NO : 419
AtmiPEP169n	<i>Arabidopsis thaliana</i>	uagccaagggaugacuugccug	SEQ ID NO : 420
AtmiPEP170	<i>Arabidopsis thaliana</i>	ugauugagccgugucaauauc	SEQ ID NO : 421
AtmiPEP396a	<i>Arabidopsis thaliana</i>	uuccacagcuuucuugaacug	SEQ ID NO : 422
AtmiPEP399c	<i>Arabidopsis thaliana</i>	ugccaaaggagaguugcccug	SEQ ID NO : 423
AtmiPEP169d	<i>Medicago truncatula</i>	aagccaagggaugacuugccgg	SEQ ID NO : 427

Table 4. List of the microRNAs (miRNAs)

Pre-miRNA	Organism	Sequence of the Pre-miRNA	SEQ ID
Pre-miR169	<i>Medicago truncatula</i>	TTAGGGTTTTTCAGCTCATGGTAATAAAAATGTCATCTAATGTCTTGTCATGT GGGAATGAGGTCATATATGCAGCCAAGGATGACTTGCCGGCGAGCCTCTT TCGATACTTTTATGACATAATTAATCATGTGGATAGCCAAGGTACTAAACT CACTTTGCACTAAAACAAATATTTTTGCTTTAGTGCAAACCTTAGTTTAGGC GCTTCGCAACGGCTAGTCAAATGTCCTAGTTCCAATGTGATTGGTTGTCCG GCAAGTCGTCTCTGGCTACGTAAAGGCCTCCTTTTTTCATGCTAGATTTTTG ATGATTTGATATAGCCACACATATTTTGGA	SEQ ID NO:359
Pre-miR169a	<i>Medicago truncatula</i>	AAGAGGCAGAGAGAGTAATGCAGCCAAGGATGACTTGCCGACAACATTG GCGAATGTTTCATGTGATTTCTGCCTCATTGTGCCGGCAAGTTGTCCTTGGCT ATGTTAGTCTCTCATCTTCT	SEQ ID NO:360
Pre-miR171a MI 0001753	<i>Medicago truncatula</i>	TGAATTCCCTCCGCTTTTTGATGTTGGCTTGTCTCAATCAAATCAAAGTTC TTGAAATTTGAGTTCTTTAGTCTGATTGAGTCGTGCCAATATCATATTAAG CGATAAAAGTC	SEQ ID NO:361
Pre-miR171h	<i>Medicago truncatula</i>	CCACAAAACCTATAACTAGCTAGAAGCTTTAATCGCCTTATTTATTATAATA ATAATAATAAATATGGCTTCAGCTGCAAAAGTATACATGGCGTGATATTG ATCCGGCTCATCTATATCTTCAAGTTCAATCATCCATATTCATATCAATTC AGACGAGCCGAATCAATATCACTCTTGTGTTGCTTCATTGCATATTAATTAT ATACTTCATTTATAAGTTATAGTTTGCCATATATATATTAGATTGATTCTGC AGAAGTAGACAGGAGTGGTGTGTTTCTGCTCATCTTATTAAATAATGAAT GAATGAATGACATTTGCTTACTTATAAGACGAGCCGAATCAATATCACTCC AGTACACCT	SEQ ID NO:362
Pre-miR393a	<i>Medicago truncatula</i>	AACTGCAACTTGAGGAGGCATCCAAAGGGATCGCATTGATCCTATAATAT TTCAACTTTAGTCACTTTAATTTTCTCTCATATAATACTTAATTGGGATCAT GCCATCCCTTTGGATTTCTCCTTTAGTAGCTAC	SEQ ID NO:363
Pre-miR393b	<i>Medicago truncatula</i>	AGGCATCCAAAGGGATCGCATTGATCCCAAATCTAATTAAGTCCCTAGCTA CTTAATTAACAACCTAATTTCTTAATATCTCATAATATTTGGGATCATGCT ATCCCTTTGGATTTCAT	SEQ ID NO:364
Pre-miR396a	<i>Medicago truncatula</i>	TGCTTTTCCACAGCTTTCTTGAACCTCTTTTCGTATCTTAAATCTGTTTTCAA GATTAAGAGTCCTAGAAGCTCAAGAAAGCTGTGGGAGAATA	SEQ ID NO:365
Pre-miR396b	<i>Medicago truncatula</i>	TATTCTTCCACAGCTTTCTTGAACCTGCATCCAAATTGAGTTCCTTTGCATTG CCATGGCCATTGTTTTGCGGTTCAATAAAGCTGTGGGAAGATA	SEQ ID NO:366

Table 5. List of the control Pre-miRNAs

miRNA	Organism	Sequence of the miRNA	SEQ ID
miR169	<i>Medicago truncatula</i>	CAGCCAAGGAUGACUUGCCGG	SEQ ID NO:367
miR169a	<i>Medicago truncatula</i>	CAGCCAAGGAUGACUUGCCGA	SEQ ID NO:368
miR171a	<i>Medicago truncatula</i>	UGAUUGAGUCGUGCCAAUAUC	SEQ ID NO:369
miR171h	<i>Medicago truncatula</i>	GAGCCGAAUCAUAUCACUC	SEQ ID NO:370
miR393a	<i>Medicago truncatula</i>	UCCAAAGGGAUCGCAUUGAUC	SEQ ID NO:371
miR393b	<i>Medicago truncatula</i>	UCCAAAGGGAUCGCAUUGAUC	SEQ ID NO:372
miR396a	<i>Medicago truncatula</i>	UUCCACAGCUUUCUUGAACUU	SEQ ID NO:373
miR396b	<i>Medicago truncatula</i>	UUCCACAGCUUUCUUGAACUG	SEQ ID NO:374

Table 6. List of the control miRNAs

	Size	# SNPs	# mutations	%SNP	# haplotypes
pri-mir171b	1127	91	100	8.07	161
5' pri-miR171b	129	4	4	3.1	5
miPEP171b	62	2	2	3.22	3
Pre-miR171b	118	1	1	0.85	2
miR171b+miR171b*	42	0	0	0	1
3' pri-miR171b	259	39	42	15.06	89

Table 7. Polymorphism of the DNA sequence of the different regions of pri-miR171b

The following figures and examples will illustrate the invention better, but without limiting its scope.

5 LEGENDS OF THE FIGURES

FIGURE 1. Effects of overexpression of Mtmir171b (miR171b identified in *Medicago truncatula*) on the expression of the *HAM1* and *HAM2* genes (A) or on the number of lateral roots (B) in *M. truncatula*.

10 (A) The y-axis indicates the relative expression of Mtmir171b (left-hand columns), of *HAM1* (middle columns) or of *HAM2* (right-hand columns) in a control plant (white columns) or in a plant in which Mtmir171b is overexpressed (black columns). The error bar corresponds to the standard error of the mean (number of individuals = 10). The overexpression of Mtmir171b induces a decrease in the expression of the *HAM1* and *HAM2*
15 genes.

(B) The y-axis indicates the mean number of lateral roots observed in a control plant (white column) or in a plant in which Mtmir171b is overexpressed (black column). The error bar corresponds to the standard error of the mean (number of individuals = 100). The overexpression of Mtmir171b leads to a reduction in the number of lateral roots.

20

FIGURE 2. Effects of overexpression of MtmirPEP171b1 on the expression of Mtmir171b and of the *HAM1* and *HAM2* genes (A) or on the number of lateral roots (B) in *M. truncatula*.

(A) The y-axis indicates the relative expression of MtmirPEP171b1 (graph on left), miR171b
25 (graph on right, left-hand columns), of *HAM1* (accession No. MtGI9- TC114268) (graph on right, middle columns) or of *HAM2* (accession No. MtGI9- TC120850) (graph on right, right-hand columns) in a control plant (white columns) or in a plant in which MtmirPEP171b1 is overexpressed (black columns). The error bar corresponds to the standard error of the mean (number of individuals = 10). The overexpression of MtmirPEP171b1 induces an
30 increase in the accumulation of Mtmir171b, as well as a decrease in the expression of the *HAM1* and *HAM2* genes.

(B) The y-axis indicates the mean number of lateral roots observed in a control plant (white column) or in a plant in which MtmirPEP171b1 is overexpressed (black column). The error

bar corresponds to the standard error of the mean (number of individuals = 100). The overexpression of MtmiPEP171b1 leads to a reduction in the number of lateral roots.

FIGURE 3. Effects of MtmiPEP171b1 on the expression of MtmiR171b and the *HAMI* and *HAM2* genes (A) and on the number of lateral roots (B) in *M. truncatula*.

(A) The y-axis indicates the relative expression of MtmiR171b (left-hand columns), of *HAMI* (middle columns) or of *HAM2* (right-hand columns) in a control plant (white columns) or in a plant treated by watering once daily for 5 days with MtmiPEP171b1 at 0.01 μ M (light grey columns), 0.1 μ M (dark grey columns) or 1 μ M (black columns). The error bar corresponds to the standard error of the mean (number of individuals = 10). Application of MtmiPEP171b1 at different concentrations induces an increase in the accumulation of MtmiR171b, as well as a decrease in the expression of the *HAMI* and *HAM2* genes.

(B) The y-axis indicates the mean number of lateral roots observed in a control plant (white column) or in a plant treated by watering with MtmiPEP171b1 at 0.1 μ M once daily for 5 days (black column). The error bar corresponds to the standard error of the mean (number of individuals = 100). Application of MtmiPEP171b1 at 0.1 μ M leads to a reduction in the number of lateral roots.

(C) The y-axis indicates the relative expression of MtmiR171b (left-hand columns), of *HAMI* (middle columns) or of *HAM2* (right-hand columns) in a control plant (white columns) or in a plant treated by watering once daily for 5 days with MtmiPEP171b1 at 0.01 μ M (grey columns), 0.1 μ M (dark grey columns) or 1 μ M (black columns) or with 0.01 μ M of a scramble peptide (LIVSHLYSEKFDCMRKILRI, SEQ ID NO : 428) (light grey columns) the amino acid composition of which is identical to miPEP171b but the sequence of which is different. The error bar corresponds to the standard error of the mean (number of individuals = 10).

FIGURE 4. Effects of MtmiPEP171b1 on the expression of pre-MtmiR171b (A) and of MtmiR171b (B) in *M. truncatula*.

The y-axis indicates the relative expression of the precursors of the different forms of the microRNA in control plants (left-hand column) or in plants treated by watering once daily for 5 days with MtmiPEP171b1 at 0.01 μ M, 0.1 μ M or 1 μ M (right-hand columns). The error bar corresponds to the standard error of the mean (number of individuals = 200). Application

of MtmiPEP171b1 at different concentrations leads to an increase in the accumulation of pre-MtmiR171b (A) and of MtmiR171b (B).

FIGURE 5. Effects of overexpression of MtmiPEP171b1 (A) and effects of
5 MtmiPEP171b1 (B) on the expression of different precursors of microRNAs in *M. truncatula*.

The y-axis indicates the ratio of the expression of the precursors of microRNAs in plants overexpressing MtmiPEP171b1 to the expression of these same precursors in control roots (A), or the ratio of the expression of the precursors of microRNAs in plants treated with
 10 MtmiPEP171b1 (0.1 μ M) to the expression of these same precursors in control roots (B). The different precursors of microRNAs tested are indicated from left to right on the x-axis, namely pre-MtmiR171b (SEQ ID NO: 246), pre-MtmiR169 (SEQ ID NO: 359), pre-MtmiR169a (SEQ ID NO: 360), pre-MtmiR171a (SEQ ID NO: 361), pre-MtmiR171h (SEQ ID NO: 362), pre-MtmiR393a (SEQ ID NO: 363), pre-MtmiR393b (SEQ ID NO: 364), pre-
 15 MtmiR396a (SEQ ID NO: 365) and pre-MtmiR396b (SEQ ID NO: 366). The error bar corresponds to the standard error of the mean (number of individuals = 10). It is noted that MtmiPEP171b1 only leads to an effect on the accumulation of MtmiR171b and not on the other miRNAs.

20 FIGURE 6. Effects of translation of MtmiPEP171b1 on the expression of MtmiR171b demonstrated in the model plant *Nicotiana benthamiana*. The y-axis indicates the relative expression of MtmiR171b in tobacco plants transformed in order to express pri-MtmiR171b (white column) or a mutated pri-MtmiR171b in which the codon ATG has been replaced with ATT (black column). The mutated pri-MtmiR171b is therefore incapable of producing
 25 MtmiPEP171b1. The error bar corresponds to the standard error of the mean (number of individuals = 30). It is noted that the absence of translation of MtmiPEP171b1 leads to a marked decrease in the accumulation of miR171b.

FIGURE 7. Effects of overexpression of MtmiPEP171b1 on the expression of pre-
30 MtmiR171b demonstrated in the model plant *Nicotiana benthamiana*.

The y-axis indicates the relative expression of pre-MtmiR171b in tobacco plants that have been transformed in order to express MtmiR171b (left-hand column), MtmiR171b and MtmiPEP171b1 (middle column), or MtmiR171b and a mutated version of MtmiORF171b

in which the start codon ATG has been replaced with ATT (right-hand column). The error bar corresponds to the standard error of the mean (number of individuals = 30). It is noted that the expression of MtmiPEP171b1 increases the expression of MtmiR171b, and this effect is dependent on the translation of MtmiORF171b to MtmiPEP171b1.

5

FIGURE 8. Effects of MtmiPEP171b1 on the expression of pre-MtmiR171b demonstrated in the model plant *Nicotiana benthamiana*.

The y-axis indicates the relative expression of MtmiR171b in tobacco plants transformed in order to express MtmiR171b onto which MtmiPEP171b1 has been sprayed (0.1 μ M) twice, 10 12h and then 30 min before sampling (right-hand column) or not (left-hand column). The error bar corresponds to the standard error of the mean (number of individuals = 6). The peptide MtmiPEP171b1 applied by spraying induces an increase in the accumulation of MtmiR171b.

15 FIGURE 9. Effects of MtmiPEP171b1 on the expression of pri-miR171b (A), pre-MtmiR171b (B) and MtmiR171b (C) demonstrated in the model plant *Nicotiana benthamiana*.

The y-axis indicates the relative expression of the precursors of the different forms of the microRNA in tobacco plants modified in order to express MtmiR171b (left-hand column) or 20 modified in order to express MtmiR171b and overexpress MtmiPEP171b1 (right-hand columns, Figure 9A) or treated with 0.1 μ M of miPEP171b1 (Figure 9B and C). The error bar corresponds to the standard error of the mean (number of individuals = 30). The overexpression of MtmiPEP171b1 or application of miPEP171b1 increases the accumulation of pri-MtmiR171b (A), pre-MtmiR171b (B) and MtmiR171b (C).

25

FIGURE 10. Localization of MtmiPEP171b1 in tobacco leaf cells that have been modified in order to express MtmiPEP171b1.

The photographs show tobacco leaf cells modified in order to express the protein GFP alone (left panel) or the protein GFP fused to MtmiPEP171b1 (right panel). These observations 30 indicate that MtmiPEP171b1 is localized in small nuclear bodies.

FIGURE 11. Effects of the expression of AtmiPEP165a (identified in *Arabidopsis thaliana*) on the expression of AtmiR165a (A), and of the expression of AtmiPEP319a2

(identified in *Arabidopsis thaliana*) on AtmiR319a (B), demonstrated in the model plant of tobacco.

(A) The y-axis indicates the relative expression of AtmiR165a in tobacco plants modified in order to express AtmiR165a (left-hand column) or to express AtmiR165a and AtmiPEP165a (right-hand column).

(B) The y-axis indicates the relative expression of AtmiR319a in tobacco plants modified in order to express AtmiR319a (left-hand column) or in order to express AtmiR319a and AtmiPEP319a (right-hand column).

The error bar corresponds to the standard error of the mean (number of individuals = 30).

In both cases, it is noted that the expression of miORF, and therefore the production of miPEP, leads to an increase in the accumulation of pre-miRNA.

FIGURE 12. Effects of treatment with AtmiPEP165a on root growth in *Arabidopsis thaliana*.

The photograph shows two plants of the same age: a control plant (plant on the left) and a plant treated with AtmiPEP165a (plant on the right). The treatment with AtmiPEP165a leads to a phenotype with greatly accelerated root growth in *Arabidopsis thaliana*. The graph shows the expression of pre-miR165 in response to treatment with increasing doses of AtmiPEP165a.

FIGURE 13. Conservation of the sequence of miPEP8 identified in *Drosophila*.

The sequences of miPEP8 (SEQ ID NO: 104) were deduced from the sequences of miORF8 (SEQ ID NO: 208) of 12 different *Drosophila* species and were aligned. A histogram shows the conservation of each amino acid between the sequences of miORF8 in the 12 species analysed.

FIGURE 14. Evolution of the mass (kDa) and isoelectric point (pI) of miPEP8 in the *Drosophila* species.

The y-axis on the left indicates the size of the miPEP8 (in kD). The y-axis on the right indicates the isoelectric point of the miPEP. The x-axis indicates the origin of the miPEP, i.e. the *Drosophila* species. It is noted that despite a significant change in their size (by more than a factor of 3), the charge of the miPEPs is still very basic (>9.8) in the 12 species studied.

FIGURE 15. Effect of the addition of sequences on the function of miPEP.

The tobacco leaves were transformed in order to overexpress miPEP171b. These graphs show that the addition of sequences (tag His, HA or GFP) does not alter the function of miPEP. The y-axis indicates the relative expression of pre-MtmiR171b in tobacco plants that have been transformed in order to express MtmiR171b (left-hand column), MtmiR171b and MtmiPEP171b1 with or without addition of protein tags (right-hand columns). The error bar corresponds to the standard error of the mean (number of individuals = 6). It is noted that the expression of MtmiPEP171b1 increases the expression of MtmiR171b, and this effect is independent of the presence of tags.

10

FIGURE 16. Expression of MtmiPEP171b1 in the root system of *Medicago truncatula*.

The roots of *Medicago truncatula* were transformed in order to express fusions between GUS protein (in blue) and the promoter of miR17b (A, E), the ATG of miPEP171b1 (B, F), whole miPEP171b1 (C, G) or ATG2 (second ATG located on the precursor, after miPEP) (D, H). It is clear that there is expression of miRNA in the root tips (A) as well as the lateral roots (E). The transcriptional (B, F) and translational (C, G) fusions show an expression of miPEP171b in the same tissues, whereas the next ATG is not active (D, H).

15

FIGURE 17. Expression of DmmiPEP8 in cells of *Drosophila melanogaster*

The cells of *Drosophila melanogaster* were transfected in order to overexpress DmmiPEP8 (OE miPEP8) or miPEP8 of which the translation start codons have been mutated (OE miPEP8 mut). The y-axis indicates the relative expression of Pre-miR8. The error bar corresponds to the standard error of the mean (number of independent experiments = 6). It is noted that the expression of DmmiPEP8 increases the expression of DmmiR8, and this effect is linked to the translation of the mRNA.

25

FIGURE 18. Impact of DmmiPEP8 on accumulation of DmmiR8 in cells of *D. melanogaster*

The cells of *Drosophila melanogaster* were transfected in order to overexpress wild-type DmmiR8 (OE miR8) or DmmiR8 the translation start codons of which have been mutated (OE miR8 miPEP8 mut). The y-axis indicates the relative expression of Pre-miR8. The error bar corresponds to the standard error of the mean (number of independent experiments = 2). It is noted that the presence of DmmiPEP8 increases the expression of DmmiR8.

30

FIGURE 19. Impact of HsmiPEP155 on accumulation of HsmiR155 in cells of *Homo sapiens*

HeLa cells of *Homo sapiens* had been transfected in order to overexpress HsmiPEP155 (OE miPEP155). The y-axis indicates the relative expression of Pre-miR155. The error bar corresponds to the standard error of the mean (number of independent experiments = 2). It is noted that the expression of HsmiPEP155 increases the expression of HsmiR155.

FIGURE 20. Effects of translation of MtmPEP171b1 on the expression of MtmR171b demonstrated in the model plant *Nicotiana benthamiana*.

The y-axis indicates the relative expression of MtmR171b in tobacco plants transformed in order to express pri-miR171b (left-hand column), a pri-miR171b in which the miORF171b has been deleted (middle column) or a mutated pri-miR171b in which the codon ATG has been replaced with ATT (right-hand column). The mutated pri-miR171b is therefore incapable of producing miPEP171b1. The error bar corresponds to the standard error of the mean (number of individuals = 30). It is noted that the absence of translation of miPEP171b1 leads to a marked decrease in the accumulation of miR171b.

FIGURE 21. Effects of overexpression of MtmPEP171b1 on the expression of MtmR171b demonstrated in the model plant *Nicotiana benthamiana*.

The y-axis indicates the relative expression of MtmR171b in tobacco plants that had been transformed with a vector allowing the expression of miPEP171b and either a second empty vector (white column), or a vector allowing the expression of mtmiPEP171b (left black column), or a vector in which the codon ATG of the ORF encoding mtmiPEP171b has been replaced with ATT (middle black column), or a vector in which the nucleotide sequence of the ORF has been mutated without modifying the amino acid sequence of the translated peptide (miPEP encoded by a degenerate ORF) (right black column). The error bar corresponds to the standard error of the mean (number of individuals = 30). It is noted that the expression of MtmPEP171b1 increases the expression of MtmR171b, and this effect is dependent on the translation of MtmORF171b to MtmPEP171b1.

FIGURE 22. Effects of AtmiPEP165a on accumulation of AtmiR165a and of its target genes (*PHAVOLUTA*: *PHV*, *PHABOLUSA*: *PHB* and *REVOLUTA*: *REV*).

The y-axis indicates the relative expression of AtmiR165a, PHV, PHB and REV in roots of *Arabidopsis thaliana* treated with water (control) or different concentrations of AtmiPEP165a (0.01 μ M, 0.1 μ M, 1 μ M or 10 μ M). The error bar corresponds to the standard error of the mean (number of individuals = 10).

- 5 The treatment of plants with higher and higher concentrations of AtmiPEP165a demonstrates a dose-dependent effect of the accumulation of AtmiR165a and the negative regulation of its target genes as a function of the quantity of AtmiPEP165a.

FIGURE 23. Effects of treatment with AtmiPEP164a on the expression of AtmiR164a

10 **in *A. thaliana*.**

The photographs show the results of a Northern blot analysis of the accumulation of AtmiR164a in roots treated with water (control, photograph on left) or with 0.1 μ M of a synthetic peptide, having a sequence identical to that of AtmiPEP164a, dissolved in water (0.1 μ M miPEP164a). The RNA U6 is used as loading control making it possible to quantify

15 the quantity of AtmiR164a.

This experiment was repeated 4 times independently and led to similar results.

Treatment of shoots of *A. thaliana* with 0.1 μ M of miPEP164a leads to an increase in the accumulation of miR164a.

20 **FIGURE 24. Effects of treatment with AtmiPEP164a on the growth of *Arabidopsis thaliana*.**

The photographs show two plants (top views and side views) after 3 weeks of growth: a control plant watered with water (A), and a plant watered with a composition of 0.1 μ M of synthetic peptide corresponding to AtmiPEP164a (B). Watering plants of *Arabidopsis*

25 *thaliana* with AtmiPEP164a increases plant growth significantly.

FIGURE 25. Effects of treatment with AtmiPEP165a on the expression of AtmiR165a in *A. thaliana*.

The photographs show the results of a Northern blot analysis of the accumulation of AtmiR165a in roots treated with water (control, photograph on left) or with 0.1 μ M of a synthetic peptide, having a sequence identical to that of AtmiPEP165a, dissolved in water (0.1 μ M miPEP165a). The RNA U6 is used as loading control making it possible to quantify the quantity of AtmiR165a.

This experiment was repeated 4 times independently and led to similar results.

Treatment of *A. thaliana* shoots with 0.1 μ M of miPEP165a leads to an increase in the accumulation of miR165a.

5 FIGURE 26. Effects of overexpression of AtmiPEP319a1 on the expression of AtmiR319a in *A. thaliana*.

The y-axis indicates the relative expression of AtmiR319a in a control plant (left-hand column) or in a plant in which AtmiPEP319a1 is overexpressed (right-hand column). The error bar corresponds to the standard error of the mean (number of individuals = 10). The

10 overexpression of AtmiPEP319a1 induces an increase in the accumulation of AtmiR319a.

FIGURE 27. Effects of treatment with AtmiPEP319a on the growth of *Arabidopsis thaliana*.

The photographs show two plants (top views and side views) after 3 weeks of growth: a
15 control plant watered with water (A), and a plant watered with a composition of 0.1 μ M of synthetic peptide corresponding to AtmiPEP319a1 (B). Watering of the plants of *Arabidopsis thaliana* with AtmiPEP319a1 increases plant growth significantly.

FIGURE 28. Immunolocalization.

20 The roots of *Medicago truncatula* were transformed in order to express fusions between the GUS protein (in blue) and the ATG of miPEP171b (Pro_{miR171b}-ATG1:GUS) or ATG2 (second ATG located on the precursor, after miPEP) (Pro_{miR171b}-ATG2:GUS). Labelling was also carried out with an anti-miPEP171b antibody (miPEP171b). Immunolocalization of miPEP171b in the roots of *M. truncatula* reveals the presence of miPEP171b in the lateral
25 root initiation sites, showing a co-localization between the microRNA and the corresponding miPEP.

FIGURE 29. Effects of the overexpression of AtmiPEP160b1 on the expression of AtmiR160b in *A. thaliana*.

30 The y-axis indicates the relative expression of AtmiR160b in a control plant (left-hand column) or in a plant in which AtmiPEP160b1 is overexpressed (right-hand column). The error bar corresponds to the standard error of the mean (number of individuals = 10).

The overexpression of AtmiPEP160b1 induces an increase in the relative expression of AtmiR160b.

FIGURE 30. Effects of AtmiPEP164a1 on the expression of AtmiR164a.

- 5 The y-axis indicates the relative expression of AtmiR164a in a control plant (left-hand column) or in a plant watered once a day with AtmiPEP164a1 at 0.1 μ M (right-hand column). The error bar corresponds to the standard error of the mean (number of individuals = 10).

The addition of AtmiPEP164a1 induces an increase in the relative expression of
10 AtmiR164a.

FIGURE 31. Effects of the overexpression of AtmiPEP319a1 on the expression of AtmiR319a in *A. thaliana*.

- The y-axis indicates the relative expression of AtmiR319a in a control plant (left-hand
15 column) or in a plant in which AtmiPEP319a1 is overexpressed (right-hand column). The error bar corresponds to the standard error of the mean (number of individuals = 10).

The overexpression of AtmiPEP319a1 induces an increase in the relative expression of AtmiR319a.

20 **FIGURE 32. Effects of MtmiPEP169d on the expression of MtmiR169d in *M. truncatula*.**

The y-axis indicates the relative expression of MtmiR169d in a control plant (left-hand column) or in a plant watered once a day with MtmiPEP169d at 0.1 μ M (right-hand column). The error bar corresponds to the standard error of the mean (number of individuals = 10).

- 25 The addition of MtmiPEP169d induces an increase in the relative expression of MtmiR169d.

FIGURE 33. Effects of the overexpression of MtmiPEP171e on the expression of MtmiR171e in *M. truncatula*.

- The y-axis indicates the relative expression of MtmiR171e in a control plant (left-hand
30 column) or in a plant in which MtmiPEP171e is overexpressed (right-hand column). The error bar corresponds to the standard error of the mean (number of individuals = 10).

The overexpression of MtmiPEP171e induces an increase in the relative expression of MtmiR171e.

FIGURE 34. Localization of the MtmPEP171b1 in a wildtype plant *M. truncatula*.

Various amounts of synthetic peptides MtmPEP171b1 (1, 0.5, or 0.1 nmol) and a total root extract from *M. truncatula* have been analysed by immunoblotting with an antibody specific
 5 for MtmPEP171b1.

MtmPEP171b1 is naturally produced in the roots of *M. truncatula*.

FIGURE 35. Presence of AtmiPEP165a in a wildtype plant *A. thaliana*.

The upper picture corresponds to the western blotting analysis of the amount of
 10 AtmiPEP165a in a wildtype seedling plant of *A. thaliana* Col-0 (left-hand) and a seedling plant of *A. thaliana* overexpressing AtmiPEP165a (right-hand). The lower picture corresponds to the western blotting analysis of the amount of a control protein (tubulin) in a wildtype seedling plant of *A. thaliana* Col-0 (left-hand) and a seedling plant of *A. thaliana* overexpressing AtmiPEP165a (right-hand). AtmiPEP165a is naturally produced in *A.*
 15 *thaliana* and is present in larger amounts in plants overexpressing AtmiPEP165a.

FIGURE 36. Action of AtmiPEP165a in *A. thaliana*.

(A) The y-axis indicates the relative expression of pri-miR165a in control roots (left-hand column) or watered once a day with AtmiPEP165a at 10 μ M (right-hand column). The error
 20 bar corresponds to the standard error of the mean (number of individuals = 10).

The addition of AtmiPEP165a induces an increase in the relative expression of AtmiR165a.

(B) The y-axis indicates the relative expression of pri-miR165a, in the presence of cordycepin (inhibitor of the RNA synthesis), in control roots (grey curve) or watered once a day with AtmiPEP165a at 10 μ M (black curve). The x-axis indicates the duration of the
 25 treatment with cordycepin.

The addition of AtmiPEP165a does not induce a better stability of pri-miR165a.

(C) The y-axis indicates the relative expression of pri-miR165a, in wildtype plants (Col-0) or in plants mutated with a low allele of the second large subunit of RNA polymerase II (*nrb2-3*). The x-axis indicates if the plants have been watered with water or with
 30 AtmiPEP165a at 10 μ M.

Mutated plants, unlike wildtype plants, are not capable of accumulating AtmiR165a in response to AtmiPEP165a.

FIGURE 37. Effects of the pri-miR171b on the number of lateral roots in *M. truncatula*.

The y-axis indicates the mean number of lateral roots observed in a control plant (white column) or in a plant in which the pri-miR171b is overexpressed (black column). The error bar corresponds to the standard error of the mean (number of individuals = 100).

- 5 The overexpression of pri-miR171b induces a decrease in the number of lateral roots.

FIGURE 38. Translatability of DmmiPEP8 in *Drosophila melanogaster* cells

Some *Drosophila melanogaster* cells have been transfected to overexpress DmmiPEP8 (miPEP8::GFP) or DmmiPEPmt (of which start codons have been mutated (miPEP8 mt::GFP)). As a transfection control, a plasmid producing moesin-RFP protein (lower picture) has been co-transfected with the plasmids encoding DmmiPEP8 (left-hand picture) and DmmiPEP8 mt (right-hand picture). It is observed that the start codons of the DmmiPEP8 sequence are functional because they allow the synthesis of GFP (top left picture) whereas the constructions with mutated ATGs do not produce hardly any GFP (top right picture).

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Thus, these results suggest that the ORF of the miPEP is functional.

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EXAMPLES**A: Analysis of the miPEPS in plants**30 **EXAMPLE 1 - Characterization in the model plant *Medicago truncatula***

a) Identification and characterization of MtmPEP171b1 (miPEP171b1 identified in *Medicago truncatula*)

The microRNA MtmiR171b is expressed in the meristematic region of the roots. The overexpression of this microRNA in particular leads to a reduction in the expression of the genes *HAMI* (Accession No. MtGI9- TC114268) and *HAM2* (Accession No. MtGI9- TC120850) (Figure 1A), as well as to a reduction in the number of lateral roots (Figure 1B).

- 5 The overexpression of the pri-miR171b also induces a decrease in the number of lateral roots (Figure 37).

The sequence of the primary transcript of MtmiR171b was determined using the RACE-PCR technique. Analysis of the sequence of the primary transcript made it possible to identify the presence of several completely unexpected small open reading frames (sORFs).

- 10 These sORFs were called miORFs for "*microRNA ORFs*". These miORFs potentially encode short peptides, from about 4 to 100 amino acids. No significant homology relating to these miORFS was found in the databases.

- The overexpression of the first miORF, called MtmiORF171b, leads to an increase in the accumulation of MtmiR171b and a reduction in the expression of the *HAMI* and *HAM2* genes (see Figure 2A), as well as to a reduction in the number of lateral roots (Figure 2B), as was already observed in the overexpression of MtmiR171b.

- In order to determine whether MtmiORF171b leads to the real production of a peptide and whether the regulatory function observed above is indeed carried by said peptide, a synthetic peptide, the sequence of which is identical to that potentially encoded by MtmiORF171b, was applied on the roots of *Medicago truncatula*. Application of this peptide leads to the phenotype already observed above in the overexpression of MtmiORF171b, i.e. it leads to an increase in the accumulation of MtmiR171b and a reduction in the expression of the *HAMI* and *HAM2* genes (see Figure 3A), as well as a reduction in the number of lateral roots (Figure 3B).

- 25 The results of these experiments demonstrate that MtmiORF171b encodes a peptide capable of modulating the accumulation of MtmiR171b, and the expression of the target genes of MtmiR171b: *HAMI* and *HAM2*. Said peptide has been called MtmiPEP171b1 ("*miPEP*" corresponding to *microRNA encoded PEptide*).

- Moreover, MtPEP171b1 leads to an increase in the accumulation of MtmiR171b (Figure 4A) and of pre-MtmiR171b (Figure 4B).

b) Specificity of miPEP171b1

The expression of different microRNA precursors of *Medicago truncatula* (MtmiR171b SEQ ID NO: 319, MtmiR169 SEQ ID NO: 367, MtmiR169a SEQ ID NO: 368, MtmiR171a SEQ ID NO: 369, MtmiR171h SEQ ID NO: 370, MtmiR393a SEQ ID NO: 371, MtmiR393b SEQ ID NO: 372, MtmiR396a SEQ ID NO: 373 and MtmiR396b SEQ ID NO: 374) was
 5 determined and compared between control plants and plants in which MtmiORF171b encoding MtmiPEP171b1 was overexpressed (Figure 5A), or between control plants and plants grown on culture medium containing MtmiPEP171b1 (Figure 5B).

The results obtained indicate that MtmiPEP171b1 only leads to an increase in the accumulation of MtmiR171b and not of the other miRNAs, which indicates that a miPEP
 10 only has an effect on the microRNA from which it is derived.

c) Localization of miPEP171b1

Moreover, the immunolocalization of miPEP171b1 in the roots of *M. truncatula* reveals the presence of miPEP171b1 in the lateral root initiation sites, showing a co-localization
 15 between the microRNA and the corresponding miPEP (Figures 28 and 34).

EXAMPLE 1B - MtmiPEP169d

Regarding MtmiPEP169d, it has been demonstrated *in vivo* in *M. truncatula* that the overexpression of this miPEP induces an accumulation of MtmiR169d (Figure 32).
 20

EXAMPLE 1C - MtmiPEP171e

Regarding MtmiPEP171e, it has been demonstrated *in vivo* in *M. truncatula* that the overexpression of this miPEP induces an accumulation of MtmiR171e (Figure 33).

25 EXAMPLE 2 - Characterization in the model plant of tobacco

a) Conservation of the mechanism in tobacco

In order to determine whether the mechanism of regulation of the microRNAs is conserved in other plant species, the regulation of MtmiR171b by MtmiPEP171b1 was tested in a
 30 different cellular model. For this, MtmiR171b and MtmiPEP171b1 were introduced into tobacco leaves.

The accumulation of MtmiR171b was measured in tobacco leaves transformed in order to express MtmiR171b of *Medicago truncatula* starting from wild-type pri-miRNA capable of

producing MtmiPEP171b1, or starting from a mutated version of pri-miRNA incapable of producing MtmiPEP171b1 (in which the start codon ATG of MtmiORF171b has been replaced with ATT) (Figure 6 and Figure 20). Absence of translation of MtmiPEP171b1 leads to a marked decrease in the accumulation of MtmiR171b.

- 5 The accumulation of pre-MtmiR171b was measured in tobacco leaves transformed in order to express MtmiR171b of *Medicago truncatula* alone (control), or additionally expressing the wild-type MtmiORF171b of *Medicago truncatula* (35SmiPEP171b1 ATG), or a mutated version of MtmiORF171b in which the start codon ATG has been replaced with ATT (35SmiPEP171b1 ATT) (Figure 7 and Figure 21). The expression of MtmiORF171b leads
10 to an increase in the accumulation of pre-miR171b, and this accumulation of pre-miR171b depends on the translation of MtmiORF171b to micropeptide.

Moreover, in the tobacco leaves transformed in order to express MtmiR171b of *Medicago truncatula*, untreated or treated by spraying with MtmiPEP171b1 (0.1 μ M) for the first time 12h before sampling and then a second time 30 minutes before sampling, it was observed
15 that MtmiPEP171b1 may be used directly in peptide form by foliar sprayings (Figure 8).

Moreover, it was observed in tobacco (as in *Medicago truncatula*) that the MtmiPEP171b1 leads to an increase in the accumulation of MtmiR171b (Figure 9A) and of pre-MtmiR171b (Figure 9B), but reduces the accumulation of pri-MtmiR171b (Figure 9C).

Taken together, these results indicate that the mechanism of regulation of the microRNAs
20 and of their target genes under the control of miPEPs is conserved between the species.

b) Intracellular localization of MtmiPEP171b1

Tobacco leaves were transformed in order to overexpress MtmiPEP171b1 of *Medicago truncatula* fused with a fluorescent protein (GFP) (Figure 10). The results obtained indicate
25 that the miPEP is localized in small nuclear bodies.

c) Identification of miPEPS from databases

Genomic databases of plants were searched for the presence of open reading frames within primary transcripts of 70 miRNAs, and 101 miORFs capable of encoding a miPEP were
30 identified.

At present, AtmiPEP165a and AtmiPEP319a2, identified in *Arabidopsis thaliana*, have already been characterized. The experiments conducted in the model plant of tobacco made it possible to demonstrate that the overexpression of AtmiORF165a or of AtmiORF319a

leads to an increase in the accumulation of AtmiR165a or of AtmiR319a respectively (Figure 11).

miR165a regulates transcription factors such as *Revoluta*, *Phavoluta* and *Phabulosa*. miR319 regulates genes of the TCP family.

5

EXAMPLE 3 - Characterization in the *Arabidopsis thaliana* model plant

Example 3A - AtmiPEP165a

Regarding AtmiPEP165a, it has been demonstrated *in vivo* in *Arabidopsis thaliana* that
10 treatment with AtmiPEP165a leads to a phenotype with greatly accelerated root growth (Figure 12).

Moreover, treatment of plants with higher and higher concentrations of miPEP165a shows a dose-dependent effect on the accumulation of miR165a and the negative regulation of its target genes (PHAVOLUTA: *PHV*, PHABOLUSA: *PHB* and REVOLUTA: *REV*) as a
15 function of the amount of miPEP165A (see Figure 22).

Example 3B - AtmiPEP164a

Regarding AtmiPEP164a, this was synthesized and was used for investigating an increase in the accumulation of miR164a in roots of *A. thaliana* treated with the synthetic peptide.
20 Northern blot analyses indicate that treatment of the plant with the peptide miPEP164a leads to an increase in the accumulation of miR164a (Figure 23).

The same type of results has been obtained by qRT-PCR (Figure 30).

It has also been demonstrated *in vivo* in *Arabidopsis thaliana* that treatment of the plant with AtmiPEP164a increases plant growth significantly (Figure 24).

25

Example 3C - AtmiPEP165a

Regarding AtmiPEP165a, this was synthesized and was used for investigating an increase in the accumulation of miR165a in roots of *A. thaliana* treated with the synthetic peptide.
Northern blot analyses indicate that treatment of the plant with the peptide miPEP165a leads
30 to an increase in the accumulation of miR165a (Figure 25).

Moreover, to determinate the mode of action of miPEPs regarding the accumulation of their own miRs, the expression of pri-miR165a has been analysed in wildtype plants and in plants that have been transformed to overexpress miPEP165a (Figure 35).

The overexpression of pri-miR165a is enhanced in the plants that overexpress miPEP165a (Figure 36A).

In the presence of cordycepin, an inhibitor of RNA synthesis, the amount of pri-miR165a is identical in wildtype plants and in transformed plants (Figure 36B), it indicates that
5 miPEP165a does not operate as a RNA stabilizer, but rather as a transcription activator of pri-miR165a.

Moreover, the expression of pri-miR165a has been analysed in wildtype plants (Col-0 plants) and in mutated plants having a low allele of the second large subunit of RNA polymerase II (*nprb2-3* plants). The results obtained indicate that mutated plants do not show an increase
10 in the accumulation of pri-miR165 in response to miPEP165a, unlike wildtype plants. It appears that the miPEP operates as a transcription regulator.

Example 3D - AtmiPEP319a1

Regarding AtmiPEP319a1, this was also synthesized and was used for investigating an
15 increase in the accumulation of miR319a in roots of *A. thaliana* treated with the synthetic peptide.

Analyses by qRT-PCR show that the overexpression of AtmiPEP319a1 leads to an increase in the accumulation of miR319a (Figures 26 and 31).

It was also demonstrated *in vivo* in *Arabidopsis thaliana* that treatment of the plant with
20 AtmiPEP319a1 increases plant growth significantly (Figure 27).

Example 3E - AtmiPEP160b1

Regarding AtmiPEP160b1, it has been demonstrated *in vivo* in *A. thaliana* that the overexpression of this miPEP induces an accumulation of AtmiR160b (Figure 29).

25

Material and Methods

Biological material

The surface of seeds of *M. truncatula* was sterilized and they were left to germinate on agar plates for 5 days at 4°C in the dark. The young shoots were then grown on 12-cm square
30 plates filled with Fahraeus medium without nitrogen and containing 7.5 µM phosphate (Lauressergues et al., *Plant J.*, 72(3): 512-22, 2012). The lateral roots were counted every day. In pots, the plants were watered every other day with modified Long Ashton medium

with low phosphorus content (Balzergue et al., *Journal of Experimental Botany*, (62)1049-1060, 2011).

The peptides were synthesized by Eurogentec or Smartox-Biotech. MtmPEP171b1 was resuspended in a solution of 40% water/50% acetonitrile/10% acetic acid (v/v/v), and the

5 other peptides were resuspended in water.

The leaves were watered by spraying with the peptides using peptide solutions at different concentrations (0.01, 0.1, 1 μ M), firstly 12h before sampling and then a second time 30 min before sampling.

Reverse transcription of the microRNAs

10 The RNA was extracted using the reagent Tri-Reagent (MRC) according to the manufacturer's instructions, except for precipitation of the RNA, which was carried out with 3 volumes of ethanol. The reverse transcription of the RNA was carried out using the specific stem-loop primer RTprimer171b in combination with hexamers for performing the reverse transcription of RNA of high molecular weight.

15 In brief, 1 μ g of RNA was added to the stem-loop primer MIR171b (0.2 μ M), the hexamer (500 ng), the buffer RT (1X), the enzyme SuperScript Reverse transcriptase (SSIII) (one unit), the dNTPs (0.2 mM each), DTT (0.8 mM) in a final reaction mixture of 25 μ l. In order to carry out the reverse transcription, a reaction of pulsed reverse transcription was performed (40 repetitions of the following cycle: 16°C for 2 minutes, 42°C for one minute
20 and 50°C for one second, followed by a final inactivation of the reverse transcription at 85°C for 5 minutes).

Analyses by quantitative RT-PCR (qRT-PCR)

The total RNA was extracted from roots of *M. truncatula* or from tobacco leaves using the extraction kit RNeasy Plant Mini Kit (Qiagen). The reverse transcription was performed
25 using the reverse transcriptase SuperScript II (Invitrogen) starting from 500 ng of total RNA. Three repetitions (n = 3) were carried out, each with two technical repetitions. Each experiment was repeated from two to three times. The amplifications by qPCR were carried out using a LightCycler 480 System thermocycler (Roche Diagnostics) by the method described in Lauressergues et al. (*Plant J.*, 72(3): 512-22, 2012).

30 Statistical analyses

The mean values of the relative expression of the genes or of the production of lateral roots were analysed using the Student test or the Kruskal-Wallis test. The error bars represent the SEM (Standard Error of the Mean). The asterisks indicate a significant difference ($p < 0.05$).

Plasmid constructs

The DNA fragments of interest were amplified with Pfu polymerase (Promega). The DNA fragments were cloned using the XhoI and NotI enzymes into a pPEX-DsRED plasmid for an overexpression under the control of the constitutive strong promoter 35S, and using the
 5 KpnI-NcoI enzymes into a pPEX GUS plasmid for the reporter genes, by the method described in Combier et al. (*Genes & Dev*, 22: 1549-1559, 2008).

For the miPEPs 165a and 319a, the corresponding miORFs were cloned into pBIN19 by the method described in Combier et al. (*Genes & Dev*, 22: 1549-1559, 2008).

Transformation of the plants

- 10 The composite plants having roots transformed with *Agrobacterium rhizogenes* were obtained by the method described in Boisson-Dernier et al. (*Mol Plant-Microbe Interact*, 18: 1269-1276, 2005). The transformed roots were verified and selected by observations of DsRED with a binocular fluorescence magnifier. The control roots correspond to roots transformed with *A. rhizogenes* not containing the pPEX-DsRED vector. Transformation of
 15 the tobacco leaves was carried out by the method described in Combier et al. (*Genes & Dev*, 22: 1549-1559, 2008).

Northern blot

Northern blot analysis was carried out according to the protocol described in Laressergues et al. *Plant J*, 72(3): 512-22, 2012.

- 20 The biological samples were homogenized in a buffer containing 0.1 M of NaCl, 2% of SDS, 50 mM of Tris-HCl (pH 9), 10 mM of EDTA (pH 8) and 20 mM of mercaptoethanol, and the RNA was extracted twice with a phenol/chloroform mixture and was precipitated with ethanol.

- The RNA was loaded on PAGE 15% gel and transferred to a nylon membrane (HybondNX, Amersham). RNA was hybridized with a radioactive oligonucleotide probe labelled at its
 25 end, in order to detect the RNA U6 or for miR164a.

The hybridizations were carried out at 55°C. The hybridization signals were quantified using a phosphorimager (Fuji) and normalized with the signal of the specific probe of RNA U6.

RNA stability

- 30 For each condition, two week old plants that have been cultivated vertically on solid MS medium have been transferred in 6-well plates containing 1 ml of liquid MS medium. After a 16 hour incubation with 1 mM of miPEP, the plants have been treated with 100 µg/ml of

cordycepin or with water (as control), and harvested à different times to extract and quantify RNA. Each individual experiment has been made 3 times.

Histochemical labelling

Labelling with GUS was carried out by the method described in Combier et al., (*Genes & Dev*, 22: 1549-1559, 2008). The samples were observed with a microscope (axiozoom).

Immunolocalization

Roots or plantlets of tissues of *Medicago* were fixed for 2 hours in 4% formol (v/v) with 50 mM of phosphate buffer (pH 7.2), and then embedded in agarose LMP 5% in water (with a low melting point). Thin sections (100 µm) were obtained and were placed in Pbi (phosphate buffer for immunology) on Teflon-coated slides, blocked in Pbi, 2% Tween and 1% of bovine serum albumin for 2 hours (PbiT-BSA), then labelled overnight (12 h) at 4°C with the primary antibody diluted in BSA-PbiT. The sections were washed with PbiT and incubated at ambient temperature for 2 h with a secondary antibody diluted in PbiT-BSA. The slides were then washed in Pbi for 30 min and mounted in Citifluor (mounting medium).

The primary antibodies and the dilutions were as follows: 1716a (1:500, v/v). The secondary antibody was a goat anti-rabbit IgG antibody coupled to the Alexa Fluor 633 fluorescent probe (Molecular Probes), and was used at a dilution of 1:1000 (v/v).

Western blotting

A total extract of proteins has been prepared using the method described in Combier *et al.*, (*Genes & Dev*, 22: 1549-1559, 2008) and separated by SDS-PAGE. The transfer has been made using a phosphate buffer overnight at 4°C, at 15V, then the membrane has been incubated for 45 min at room temperature in a solution of glutaraldehyde 0,2% (v/v). Primary antibodies have been used at a 1:1000 (v/v) dilution and HRP-conjugated goat anti-rabbit Ig antibodies have used as secondary antibodies at a 1:40 000 (v/v) dilution.

25

AtmiR160bq5 (SEQ ID NO : 429)	TCCCCAAATTCTTGACCAAA
AtmiR160bq3 (SEQ ID NO : 430)	TTGAGGGGAAAACATGAACC
AtmiR164aq5 (SEQ ID NO : 431)	ACGAAATCCGTCTCATTTCG
AtmiR164aq3 (SEQ ID NO : 432)	GGGTGAAGAGCTCATGTTGG
AtmiR165q5 (SEQ ID NO : 433)	TGAGGGGAATGTTGTCTGG
AtmiR165q3 (SEQ ID NO : 434)	GAAGCCTGGTCCGAGGATA
AtmiR319q5 (SEQ ID NO : 435)	CGAGTCGCCAAAATTCAAAC
AtmiR319q3 (SEQ ID NO : 436)	GCTCCCTTCAGTCCAATCAA
AtPHVq5 (SEQ ID NO : 437)	GCAACTGCAGTGGAATAGCA
AtPHVq3 (SEQ ID NO : 438)	GCGACCTTCATGGGTTCTAA
AtPHBq5 (SEQ ID NO : 439)	CTCAGCATCAGCAACGTGAT
AtPHBq3 (SEQ ID NO : 440)	AACTCTGCTAGGGCCTCCTC

AtREVq5 (SEQ ID NO : 441)	TCACAACTCCTCAGCATTCG
AtREVq3 (SEQ ID NO : 442)	ACCCAATCAACAGCAGTTCC
Atactine2F (SEQ ID NO : 443)	GGTAACATTGTGCTCAGTGG
Atactine2R (SEQ ID NO : 444)	CTCGGCCTTGGAGATCCACA
miORF319acla5 (SEQ ID NO : 445)	tcatcgATGAATATACATACATACCATCAT
miORF319abam3 (SEQ ID NO : 446)	tccggatccTCTAAAAGCTAAAGTGATTCTA AA
AtmiR319cla5 (SEQ ID NO : 447)	tcatcgAGAGAGAGCTTCCTTGAGTC
AtmiR319bam3 (SEQ ID NO : 448)	tccggatccAGAGGGAGCTCCCTTCAGT
AtmiR165cla5 (SEQ ID NO : 449)	tcatcgGTTGAGGGGAATGTTGTCTG
AtmiR165bam3 (SEQ ID NO : 450)	tccggatccGTTGGGGGGGATGAAGCC
AtmiR165muorf5cla (SEQ ID NO : 451)	tcatcgATGAGGGTTAAGCTATTTCAGT
AtmiR165muorf3bam (SEQ ID NO : 452)	tccggatccTAATATCCTCGATCCAGACAAC
miR171bq5 (SEQ ID NO : 453)	CGCCTCAATTTGAATACATGG
miR171bq3 (SEQ ID NO : 454)	ACGCGGCTCAATCAAACACTAC
pri-miR171bq5 (SEQ ID NO : 455)	GCACTAGCTGGTTTCATTATTCC
pri-miR171bq3 (SEQ ID NO : 456)	TTGCAAAATTTGGAGAGCCTA
miR171eq5 (SEQ ID NO : 457)	AAGCGATGTTGGTGAGGTTC
miR171eq3 (SEQ ID NO : 458)	CGGCTCAATCTGAGATCGTAT
miR169dq5 (SEQ ID NO : 459)	GGGCGGTGAGATTAACAAAA
miR169dq3 (SEQ ID NO : 460)	CCTGCCGGAATGAAACTAA
miORF171e2Cla5 (SEQ ID NO : 461)	tcatcgATGATGGTGTGTTGGGAAGCC
miORF171e2bam3 (SEQ ID NO : 462)	tccggatccTACATGTAAATCCGTCTTCGG
miORF171b5'AGG (SEQ ID NO : 463)	AGGCTTCTTCATAGGCTCTCC
miR171e5'Xho (SEQ ID NO : 464)	TCAGTCCGCTCGAGGAATAAGTGAATAT TATCGATATTT
miR171e3'Not (SEQ ID NO : 465)	AAGGAAAAAAGCGGCCGCAAAGTGATA TTGGCGCGGCT
171b scramble F bis (SEQ ID NO : 466)	<u>TAGCATGTTATTACACCGCTTAAGTAAG</u> TTCTGTAAGATAGAGCGCGATATTGTTT ACATTAGCTAG
171b scramble R bis (SEQ ID NO : 467)	<u>CGTACTAGCTAATGTAAACAATATCGCG</u> CTCTATCTTACAGAACTTACTTAAGCGG TGTAATAACAT
PromiORF171b1 ATG BsaIR (SEQ ID NO : 468)	aaaaGGTCTCgCCATAAGCATAGTGGAAT AATGAAACC
PromiORF171b2 ATG BsaIR (SEQ ID NO : 469)	aaaaGGTCTCgCCATTTCCATACCTGAATT TCTCCTT
PromiORF171b6 ATG BsaI R (SEQ ID NO : 470)	aaaaGGTCTCgCCATCTTCATCCTCAATAT CCTAATTC
171b fusion GFP sans ATG BsaI R (SEQ ID NO : 471)	aGGTCTCgACACAGATATATATACTATGT CTCTTTCAATTTTGC
Pro171b fusionTranscript GUSpPEX BsaI R (SEQ ID NO : 472)	aaaGGTCTCgCCATGACCATTTTCCCACG AATATG

Pro171b fusionATG1 GUSpPEXsansATG BsaI R (SEQ ID NO : 473)	aaGGTCTCgACACAAGCATAGTGGAATA ATGAAACC
Pro171b fusionTraduc GUSpPEX BsaI R (SEQ ID NO : 474)	aaGGTCTCgACACAGATATATATACTATG TCTCTTTCA
171b NcoI F (SEQ ID NO : 475)	Gaattcctgcccattggttttcg
171b NcoI R (SEQ ID NO : 476)	Cgaaaaccatgggcaggaattc
171b AflII F (SEQ ID NO : 477)	cagtcctcgacttaagctcaatac
171b AflII R (SEQ ID NO : 478)	gtattgagcttaagtcgggactg
171b génomiq BsaI F (SEQ ID NO : 479)	aaaGGTCTC C TAGC TTGGTCAAACATACATACAGTAGCACTA G
171b génomiq BsaI R (SEQ ID NO : 480)	aaaGGTCTCgCGTAAAATTGTACTGATTG AATGTAAATTGGTACAC
AthmiORF160b F (SEQ ID NO : 481)	TAGCATGTTTTCCCCTCAATGA
AthmiORF160b R (SEQ ID NO : 482)	cgtaTCATTGAGGGGAAAACAT
AthMIR160b BsaI F (SEQ ID NO : 483)	aaaGGTCTCcTAGCACTCATAACTCTCCCC AAATTC
AthMIR160b BsaI R (SEQ ID NO : 484)	aaaGGTCTCgCGTAGAAAGAATGTTTCGAA AAACAATG
pro 165a BsaI F (SEQ ID NO : 485)	aGGTCTCCAAATcatgaagcaggcagtaataacct
165a muORF tagHA BsaI R (SEQ ID NO : 486)	aGGTCTCgCGTActaAGCGTAATCTGGAAC ATCGTATGGGTAtaatatcctcgatccagacaac
165a fusion transcript BsaI R (SEQ ID NO : 487)	aGGTCTCgccatagtggcgagacgaagatg
165a fusion traduc BsaI R (SEQ ID NO : 488)	aGGTCTCgccattaatcctcgatccagacaac
pro 165a BsaI F (SEQ ID NO : 489)	aGGTCTCCAAATtaaactgtcagtgcattgatgt
165a fusion GTG BsaI R (SEQ ID NO : 490)	aGGTCTCgACACattcacaattttgttagagag
165a fusion GTGmutGTT BsaI R (SEQ ID NO : 491)	aGGTCTCgACACattaacaaattttgttagagag
165a fusion CTG BsaI R (SEQ ID NO : 492)	aGGTCTCgACACtagcagattcacaattttgttg
165a fusion ATG BsaI R (SEQ ID NO : 493)	aGGTCTCgACACcctcatgataatcgatcttagca

Table 8. List of primers

B: Analysis of the miPEPs in animals

5

EXAMPLE 4 - Identification of candidate miPEPs in Drosophila

a) Identification of miPEP candidates

A first study carried out by RACE-PCR in the model animal *Drosophila melanogaster* shows the existence of miRNAs that are expressed during embryogenesis, miR1 and miR8.

As in the plants, miORFs were identified in each of the two miRNAs studied. For example, 5 miR8, known for its role in the regulation of growth in insects, has a miORF potentially encoding miPEP8.

Regarding DmmiR1 (identified in *Drosophila melanogaster*), it has two DmmiORFs potentially encoding DmmiPEP1a and DmmiPEP1b.

10 A phylogenetic analysis shows evolutionary conservation of the presence of the miORFs among the dozen *Drosophila* species analysed, i.e. since their divergence more than 60 million years ago (Figure 13).

Moreover, the miPEPs identified in *Drosophila* have several similarities with the plant 15 miPEPs. If their primary sequence and therefore their size evolve rapidly between species, a reduced size (from 32 to 104 AA) is found, as well as strong conservation for a basic overall charge (pHi from 9.5 to 12) (Figure 14).

Taken together, these results therefore indicate the existence of regulatory miPEPs, encoded 20 by the primary transcript of the microRNAs, over a broad spectrum of eukaryotic species. These discovered peptides represent an as yet unexplored reservoir of natural molecules that may regulate a variety of fundamental biological functions, both in plants and in animals.

b) Expression of the miPEPs

25 *Drosophila melanogaster* cells have been transfected to overexpress the DmmiPEP8 (from the sequence SEQ ID NO: 494) or the DmmiPEP mt of which start codons have been mutated (from the sequence SEQ ID NO: 495). As a transfection control, one moesin-RFP-producing plasmid has been co-transfected with the plasmids encoding DmmiPEP8 and DmmiPEP8 mt. It is observed that start codons in the DmmiPEP8 sequence are functional because they 30 allow the synthesis of a miPEP::GFP fusion protein shown by the GFP whereas the constructions with mutated ATGs do not produce hardly any GFP.

These results suggest that the ORF of the miPEP is functional (Figure 38).

Material and Methods

Cells of *Drosophila melanogaster*

S2 cells are cultured in a T75 flask in 12 mL of Schneider's medium (GIBCO), containing 1% of penicillin 100 U/mL and streptavidin 100 mg/mL (Sigma) and 10% of 5 decompemented foetal calf serum (30 min at 56°C).

The transient transfections are carried out using the FuGENE® HD transfection kit (Roche), according to the recommendations. Conventionally, 1.5 million S2 cells, previously seeded in 6-well plates (3 ml of medium per well), are transfected with 250 ng of total plasmid DNA. The DNA is brought into contact with the Fugene (3 µl) in 100 µl of OPTIMEM 10 (GIBCO). After 20 minutes, the transfection reagent formed is brought into contact with the cells in the culture medium. The RNA of the cells is extracted 66h after transfection.

Cloning of DmmiPEP8- and mutated DmmiPEP8-fragments

The DNA fragments, corresponding to the sequences of DmmiPEP8 (SEQ ID NO: 494) and of DmmiPEP8 mutated in the start codons (SEQ ID NO: 495), have been amplified by PCR in 15 order to be cloned in accordance with the GFP in a pUAS plasmid. The SE insect cells have been co-transfected with a mix of plasmids (1/1/1 ratio, a total of 300 ng) encoding DmmiPEP8::GFP or its mutated form DmmiPEP8 mt::GFP, a pACT-GAL4 allowing their overexpression by means of a GAL4 transcription factor produced under the control of the actin promotor and a expression vector encoding the moesin-RFP protein used as a 20 transfection control, also under the control of the actin promotor. 48h after transfection, the cells are fixed by the addition of formaldehyde in the final medium culture 4% (W/V) for 10 min. Then, the cells are washed 2X with PBS1X and coated on slides in order to be observed under a microscope (Leica SPE).

CGCACACACACACACACAATCACTCACACGCGGTCACAC GCACATTTCAATAAACTAATGGAGCCTGGCTTTGTTTTGTT TTATTTCCAACCCACTTGAGCACACAGCACACACAGAGAGA AAAATCAATACTCGTTATGGGATTAAATTTACAAAGCGCAA AGCAAAGCGACAAACAAAATTCAAAAGAAAGAAAAAAAAAA CACTCAAATAAACTCACAAAGAATTCCTTATCGCCAAGGGG GCCAATGTTCTAAGGTTCTTTCGCCT	SEQ ID NO : 494
CGCACACACACACACACAATCACTCACACGCGGTCACAC GCACATTTCAATAAACTA AGT GAGCCTGGCTTTGTTTTGTT TTATTTCCAACCCACT TTA AGCACACAGCACACACAGAGAGA AAAATCAATACTCGTT AGT GGATTAAATTTACAAAGCGCAA AGCAAAGCGACAAACAAAATTCAAAAGAAAGAAAAAAAAAA CACTCAAATAAACTCACAAAGAATTCCTTATCGCCAAGGGG GCCAATGTTCTAAGGTTCTTTCGCCT	SEQ ID NO : 495

Table 9. Cloned sequences.

5 **C: Characterization of miPEPs in humans**

EXAMPLE 5 - Characterization of HsmiPEP155

The DNA fragments of interest (HsmiPEP155 and the mutated miPEP) were synthesized or amplified by PCR using specific primers, and then cloned using the enzymes XhoI and NotI
 10 into a pUAS plasmid permitting their overexpression by means of the GAL4 transcription factor, the expression of which is controlled by a constitutive strong promoter.

The different constructs were produced either by PCR amplification on genomic DNA of HeLa cells, or by RT-PCR on total RNAs of L428 human cells. The amplified PCR fragments are digested with the HindIII/EcoRI restriction enzymes and then cloned into the
 15 vector pcDNA3.1. The DH5 α strain of *Escherichia coli* is electroporated and then cultured on a solid medium (2YT+agar+ampicillin). The plasmid DNA from different clones is then prepared and sequenced for verification. The constructs are then prepared using the QIAfilter Plasmid Midi kit (QIAGEN) and stored at -20°C.

20 The HeLa cells (established tumour line, ATCC CCL-2.2) are cultured in a 6-well plate in complete medium [(DMEM (1x) + Glutamax + 4.5g/L glucose without pyruvate + 1x penicillin/streptomycin + 1 mM Na-pyruvate + 10% calf serum] and placed in an incubator at 37°C and 5% CO₂.

25 The cells are transfected when they are at 50% confluence. At the start of the experiment, the complete medium containing the antibiotics is replaced with complete medium without antibiotics.

For each well, a mix A [250 μ l of Optimem (+Glutamax) (Gibco) + 2 μ g of DNA] and a mix B [250 μ l of Optimem + 4 μ l of Lipofectamine 2000 (Invitrogen)] is prepared, and left for 5
 30 min at ambient temperature. Then mix B is mixed dropwise into mix A, and left to incubate for 25 min at ambient temperature. The mixture is then deposited dropwise into the well. 4-5 hours later, the medium is changed and replaced with complete medium with antibiotics. 48 hours after transfection, the cells are stopped. The medium is aspirated and discarded; the

cells are rinsed with PBS 1X. It is then possible to store the cells at -20°C or extract the total RNAs directly.

For each well, the RNAs are extracted by depositing 1 ml of Tri-Reagent (Euromedex) on the cells. The Tri-reagent is aspirated and returned several times so that the cells are lysed correctly, and then it is transferred into a 1.5-ml tube. 0.2 ml of water-saturated chloroform is added. It is mixed by vortexing, then left for 2 to 3 minutes at ambient temperature. It is centrifuged for 5 minutes at 15300rpm and at 4°C. The aqueous phase is precipitated from 0.5 ml of isopropanol after incubation for 10 minutes at ambient temperature and centrifugation for 15 minutes at 15300rpm and at 4°C. The supernatant is discarded and the pellet is rinsed with 1 ml of 70% ethanol, with centrifugation for 5 minutes at 15300rpm at 4°C. The supernatant is again discarded and the pellet is dried for a few minutes in the air. For best-possible removal of the genomic DNA potentially remaining, the RNAs are treated with DNase. For this, the pellet is resuspended in 170 µl of ultra-pure water, 20µl of DNase buffer 10x and 10 µl of RQ1 RNase-free DNase and held at 37°C for 30 minutes. Then 20 µl of SDS10% and 5 µl of proteinase K (20 mg/ml) are added over 20 minutes at 37°C. A last phenol extraction is carried out with 225 µl of a phenol/H₂O/chloroform mixture, and centrifuged for 5 minutes at 15300 rpm at 4°C.

The aqueous phase is then precipitated from 20 µl of 3M sodium acetate and 600 µl of 100% ethanol for 20 minutes at -80°C. Then it is centrifuged for 15 min at 4°C at 15300rpm. The supernatant is discarded. The pellet is rinsed in 1 ml of 70% ethanol, centrifuged for 5 min at 15300rpm at 4°C, the supernatant is discarded again and the pellet is left to dry for some minutes in the air.

The pellet is then taken up in 15-20 µl of ultra-pure water and the RNAs are assayed.

25

10-15 µg of total RNAs is then analysed by Northern blot on 15% acrylamide gel [solution of acrylamide/40% bis-acrylamide, ratio 19:1], 7M urea in TBE 1x. Migration is carried out at 400V, in TBE1x as migration buffer, after preheating the gel. The RNAs are then electro-transferred onto a Biodyne Plus 0.45 µm nylon membrane, for 2 hours, at 1V and 4°C in a transfer tank. At the end of transfer, the membrane is irradiated with UV at 0.124 J/cm². The membrane is then pre-hybridized in a buffer 5xSSPE, 1xDenhardt's, 1%SDS and 150µg/ml of yeast tRNA, for 1 hour at 50°C in a hybridization oven. Then the nucleotide probe is added, labelled at 5' with γ -³²P-ATP (0.5 to 1.10⁶ cpm/ml of hybridization buffer) and is

30

hybridized overnight at 50°C. The membrane is then washed twice in 0.1xSSPE/0.1%SDS at ambient temperature and exposed in an autoradiography cassette containing a BioMax HE screen (Kodak) and a BioMax MS film (Kodak), in order to detect a microRNA, for 24-48 hours, at -80°C.

Patentkrav

1. Fremgangsmåde til detektering og identifikation af et mikropeptid (miPEP), der er kodet af en nukleotidsekvens, som er indeholdt i sekvensen af det primære transkript af et mikroRNA (miR), omfattende:

a) et trin til detektering af en åben læseramme fra 12 til 303 nukleotider, der er indeholdt i sekvensen af det primære transkript af miR'et, derefter

b) et trin til sammenligning mellem:

- fænotypen af en plante, der udtrykker miR'et,

- i nærvær af et peptid, der er kodet af en nukleotidsekvens, der er identisk eller degenereret med hensyn til den af den åbne læseramme, hvilket peptid er til stede i planten uafhængigt af transkriptionen af det primære transkript af miR'et, og

- fænotypen af den samme plante, der udtrykker miR'et i fravær af peptidet,

hvor en ændring i plantens fænotype i nærvær af peptidet i forhold til plantens fænotype i fravær af peptidet indikerer eksistensen af et miPEP, der er kodet af den åbne læseramme.

2. Fremgangsmåde til detektering og identifikation af et miPEP ifølge krav 1, hvor ændringen i plantens fænotype i nærvær af peptidet er konsekvensen af en modulering af akkumuleringen af miR'et med peptidet.

3. Fremgangsmåde til detektering og identifikation af et miPEP ifølge krav 2, hvor moduleringen af akkumuleringen af mikroRNA'et er et fald eller en stigning i akkumuleringen af mikroRNA'et, især en stigning.

4. Fremgangsmåde til detektering og identifikation af et miPEP ifølge et hvilket som helst af kravene 1 til 3, hvor tilstedeværelsen af peptidet i planten er et resultat:

- af introduktionen i planten af en nukleinsyre, der koder for peptidet, eller

- af introduktionen i planten af peptidet.

5 **5.** Fremgangsmåde til detektering og identifikation af et miPEP ifølge et hvilket som helst af kravene 1 til 4, hvor den åbne læseramme i trin a) er indeholdt i 5'- eller 3'-delen af det primære transkript af mikroRNA'et, fortrinsvis i 5'-delen.

10 **6.** Fremgangsmåde til detektering og identifikation af et miPEP ifølge et hvilket som helst af kravene 1 til 5, hvor planten er valgt blandt: *Arabidopsis ceben-*
nensis, *Arabidopsis helleri*, *Arabidopsis lyrat*, *Arabidopsis thaliana*, *Brassica*
carinata, *Brassica juncea*, *Brassica napus*, *Brassica oleracea*, *Brassica rapa*,
Capsella rubella, *Carica papaya*, *Eucalyptus grandis*, *Glycine max*, *Gossypium*
raimondii, *Medicago sativa*, *Medicago truncatula*, *Nicotiana benthamiana*,
Oryza sativa, *Physcomitrella patens*, *Solanum lycopersicum*, *Solanum melon-*
gena, *Solanum tuberosum*, *Thermophilia halophila* og *Zea mays*.

15 **7.** Fremgangsmåde til detektering og identifikation af et miPEP ifølge et hvilket som helst af kravene 1 til 6, hvor miR'et i planten, der er anvendt i trin b), er af endogen oprindelse.

20 **8.** Fremgangsmåde til detektering og identifikation af et miPEP ifølge et hvilket som helst af kravene 1 til 6, hvor miR'et i planten, der er anvendt i trin b), er af exogen oprindelse, hvor planten indeholder en vektor, der muliggør ekspres-
sion af miR'et.

25 **9.** Fremgangsmåde til detektering og identifikation af et miPEP ifølge et hvilket som helst af kravene 1 til 8, hvor den observerede fænotype er valgt blandt:
- størrelse, overfladeareal, volumen, masse og antallet af blade;
- størrelsen og antallet af blomster;
- størrelsen af stilken eller spidsen;
30 - længden og antallet af rødder;
- tidlig spiring;

- tidlig knopskydning;
- tidlig blomsterinduktion eller blomsterovergang;
- antallet af celler;
- modstand mod vandstress; og
- resistens over for infektionssygdomme.

5

10. Anvendelse af en sammensætning, der mindst omfatter:

- et miPEP,
- en nukleinsyre, der koder for miPEP'et, eller
- en vektor, der indeholder nukleinsyren,

10

som et fytofarmaceutisk middel,

- til at fremme væksten og/eller udviklingen af planter, især til at modulere en plantes fysiologiske parametre, især biomasse, bladoverfladeareal, blomstring, frugtstørrelse; eller
- til at forebygge eller behandle plantesygdomme, især til at fremme resistens over for infektionssygdomme

15

hvor miPEP'et har:

- en størrelse fra 3 til 100 aminosyrer, fortrinsvis 4 til 20 aminosyrer;
- en peptidsekvens, der er identisk med den, der kodes af en nukleotidsekvens indeholdt i det primære transkript af et mikroRNA, der regulerer ekspressionen af genet, og
- at være i stand til at modulere akkumuleringen af mikroRNA'et,

20

hvor sammensætningen påføres ved bladsprøjtning.

25

11. Anvendelse af en sammensætning ifølge krav 10, hvor planterne er udvalgt blandt: *Arabidopsis ceibennensis*, *Arabidopsis helleri*, *Arabidopsis lyrata*, *Arabidopsis thaliana*, *Brassica carinata*, *Brassica juncea*, *Brassica napus*, *Brassica oleracea*, *Brassica rapa*, *Capsella rubella*, *Carica papaya*, *Eucalyptus grandis*, *Glycine max*, *Gossypium raimondii*, *Medicago sativa*, *Medicago truncatula*, *Nicotiana benthamiana*, *Oryza sativa*, *Physcomitrella patens*, *Solanum*

30

lycopersicum, *Solanum melongena*, *Solanum tuberosum*, *Thellungiella halophila* og *Zea mays*.

12. Anvendelse af en sammensætning ifølge krav 10 eller 11, hvor miR'et er valgt fra gruppen af miR bestående af: miR155, miR156a1, miR156a2, miR156a3, miR156c1, miR156c2, miR156e1, miR156f1, miR157c, miR157d, miR159a, miR159a1, miR159b1, miR159b2, miR160a1, miR160b1, miR160b2, miR160c, miR161, miR162a1, miR162b1, miR163-1, miR163-2, miR164a1, miR164a1, miR164a2, miR164a2, miR164a3, miR164b, miR165a, miR166a, miR166b, miR166c, miR166d, miR167a, miR167b1, miR167b2, miR169a, miR169c1, miR169c2, miR169d, miR169h, miR169l1, miR169n, miR170, miR171a1, miR171b, miR171b1, miR171b2, miR171c1, miR171e, miR171h, miR172a1, miR172a3, miR172b1, miR172c1, miR172e1, miR172e2, miR172e3, miR1a, miR1b, miR319a, miR319a, miR319a1, miR319a2, miR319b1, miR394a1, miR395c1, miR395e1, miR396a, miR397b1, miR398c1, miR399b, miR399c, miR399d1, miR403, miR447a1, miR447a2, miR447b1, miR447b2, miR447c og miR8.

13. Anvendelse af en sammensætning ifølge et hvilket som helst af kravene 10 til 13, hvor miR'et er valgt fra gruppen af miR bestående af:

- SEQ ID NO: 282 til SEQ ID NO: 352;
- SEQ ID NO: 412 til SEQ ID NO: 423; og
- SEQ ID NO: 427,

især er miR'et valgt fra gruppen af miR bestående af: SEQ ID NO: 295, SEQ ID NO: 305, SEQ ID NO: 324, SEQ ID NO: 340, SEQ ID NO: 344, SEQ ID NO: 357, SEQ ID NO: 358 og SEQ ID NO: 427.

14. Anvendelse af en sammensætning ifølge et hvilket som helst af kravene 10 til 14, hvor miPEP'et er valgt fra gruppen af peptider bestående af:

- SEQ ID NO: 1 til SEQ ID NO: 101;
- SEQ ID NO: 375 til SEQ ID NO: 386; og

- SEQ ID NO: 424,

især er miPEP'et valgt fra gruppen af peptider bestående af: SEQ ID NO: 14, SEQ ID NO: 24, SEQ ID NO: 43, SEQ ID NO: 59, SEQ ID NO: 63, SEQ ID NO: 76, SEQ ID NO: 77 og SEQ ID NO: 424.

5

15. Anvendelse af en sammensætning ifølge et hvilket som helst af kravene 10 til 14, hvor nukleinsyren, der koder for miPEP'et, er valgt fra gruppen af nukleinsyrer bestående af:

- SEQ ID NO: 105 til SEQ ID NO: 205;

10

- SEQ ID NO: 387 til SEQ ID NO: 399; og

- SEQ ID NO: 425,

Hvor nukleinsyren, der koder for miPEP'et, er valgt fra gruppen af nukleinsyrer bestående af: SEQ ID NO: 118, SEQ ID NO: 128, SEQ ID NO: 147, SEQ ID NO: 163, SEQ ID NO: 167, SEQ ID NO: 180, SEQ ID NO: 181 og SEQ ID NO:

15

425.

FIGURE 1

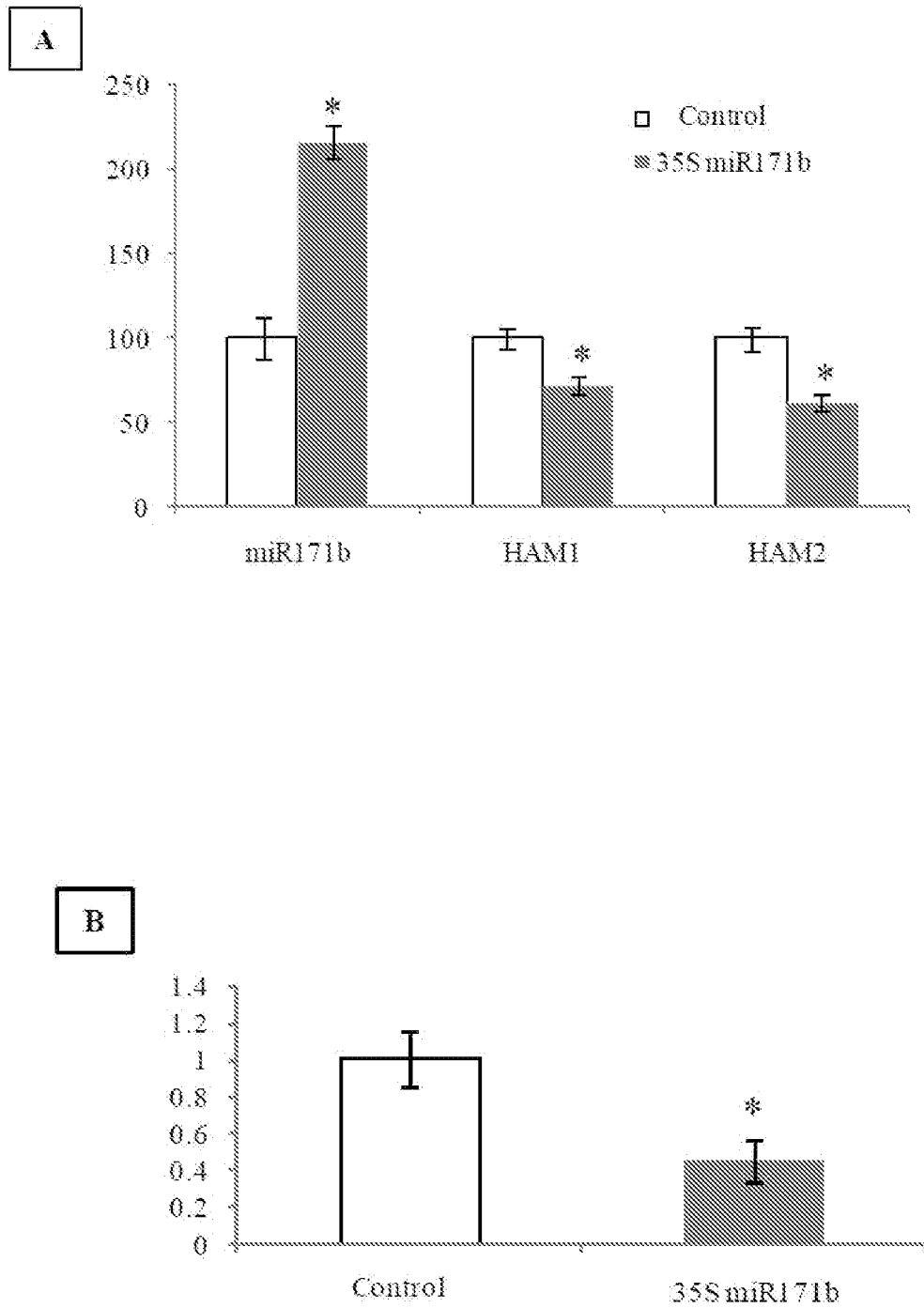


FIGURE 2

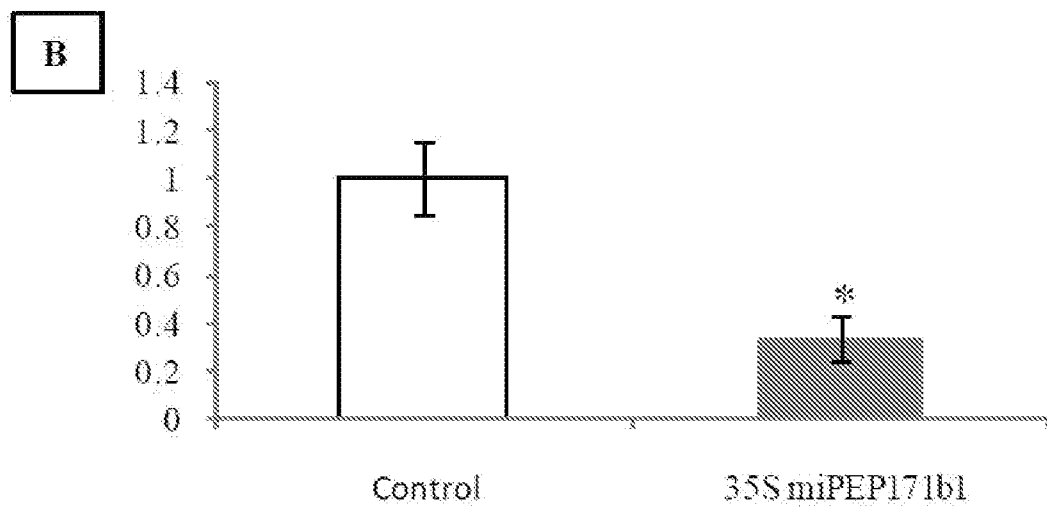
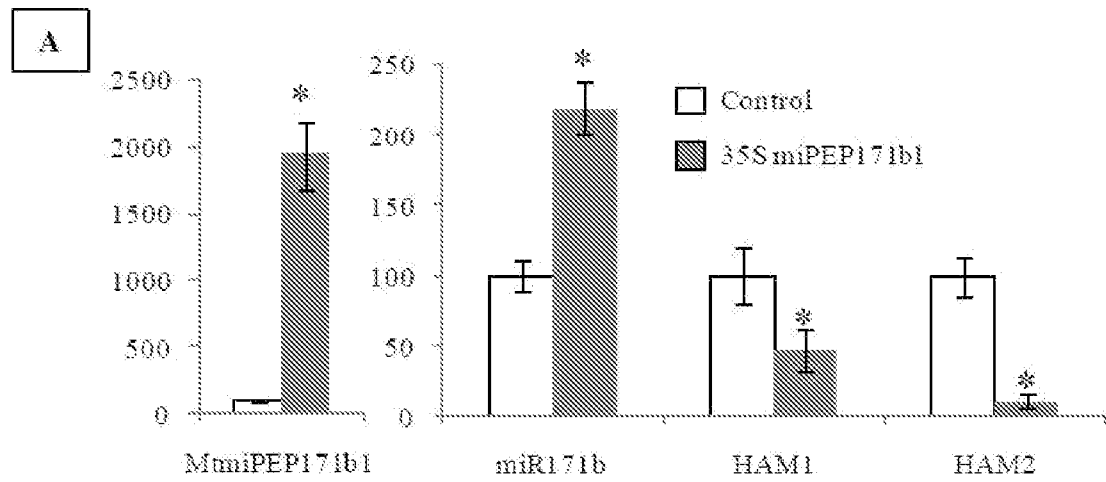


FIGURE 3

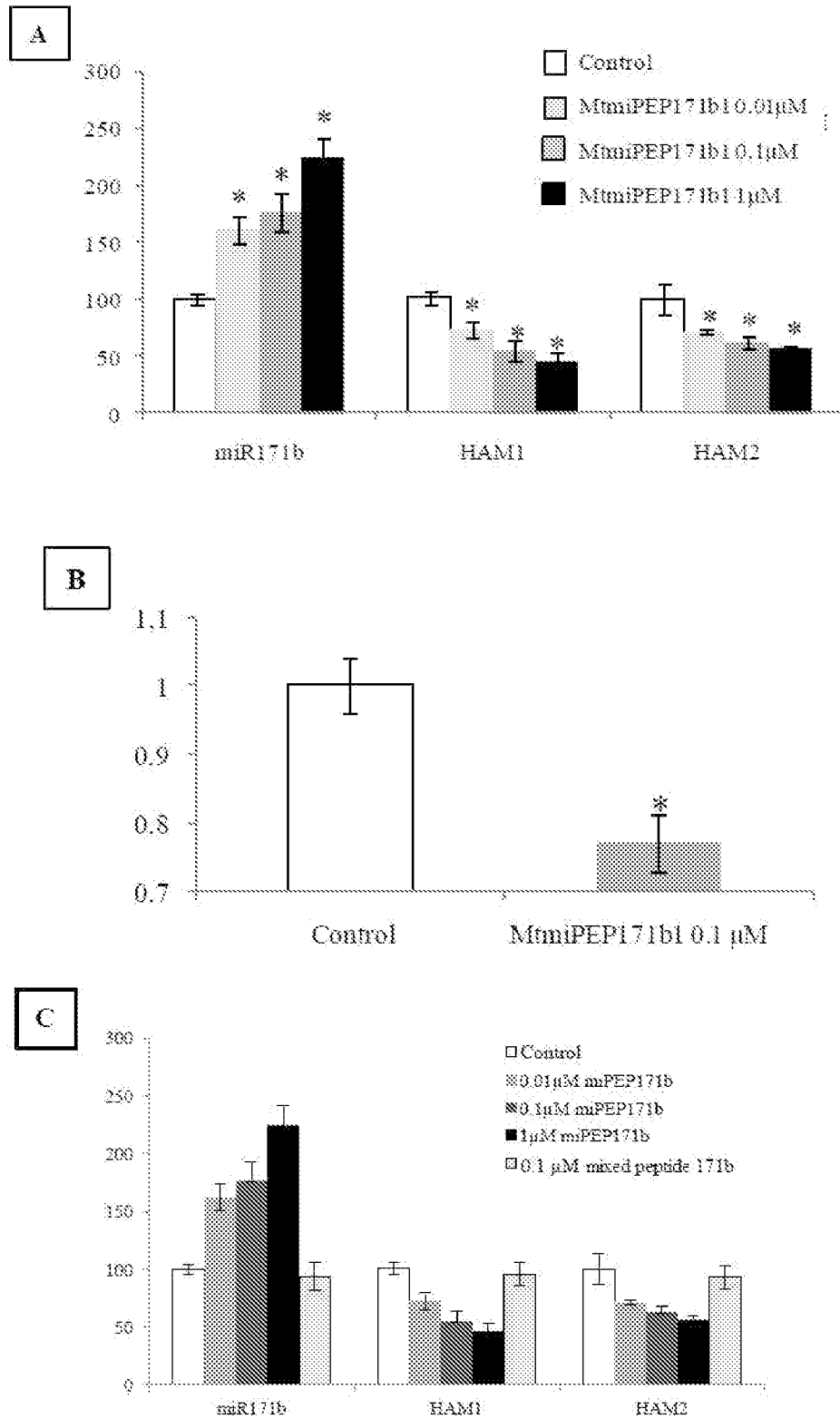
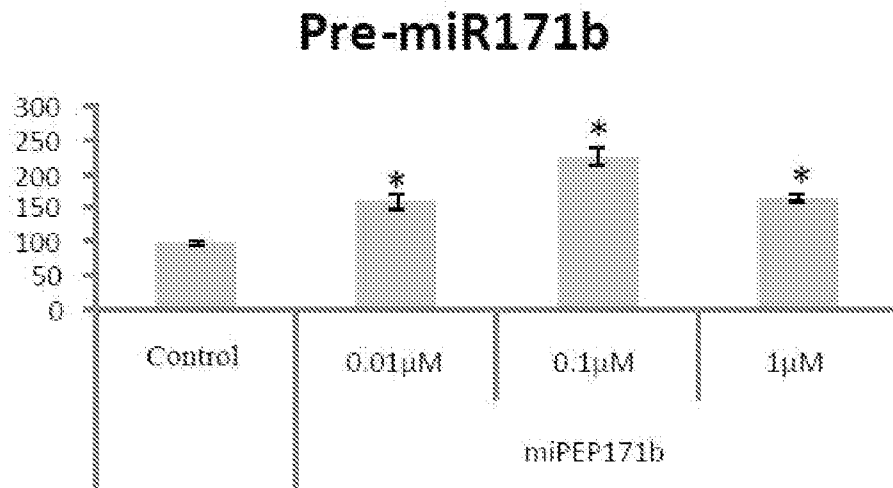


FIGURE 4

A



B

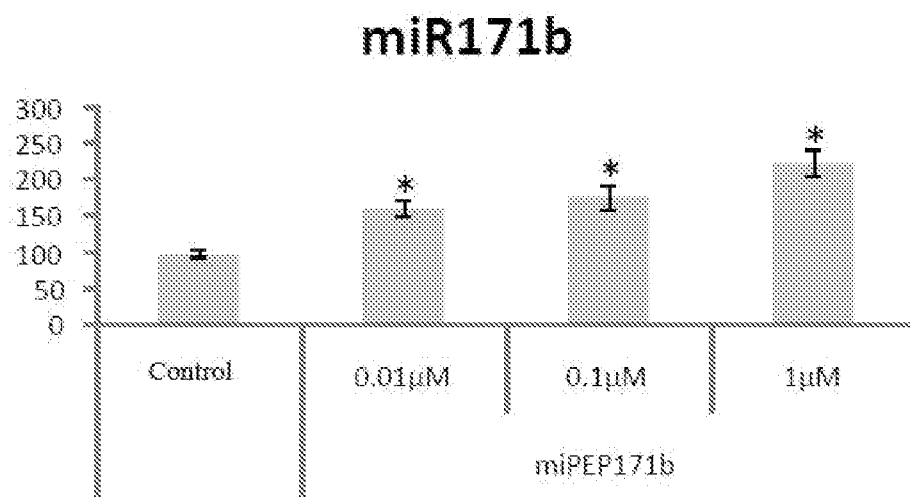


FIGURE 5

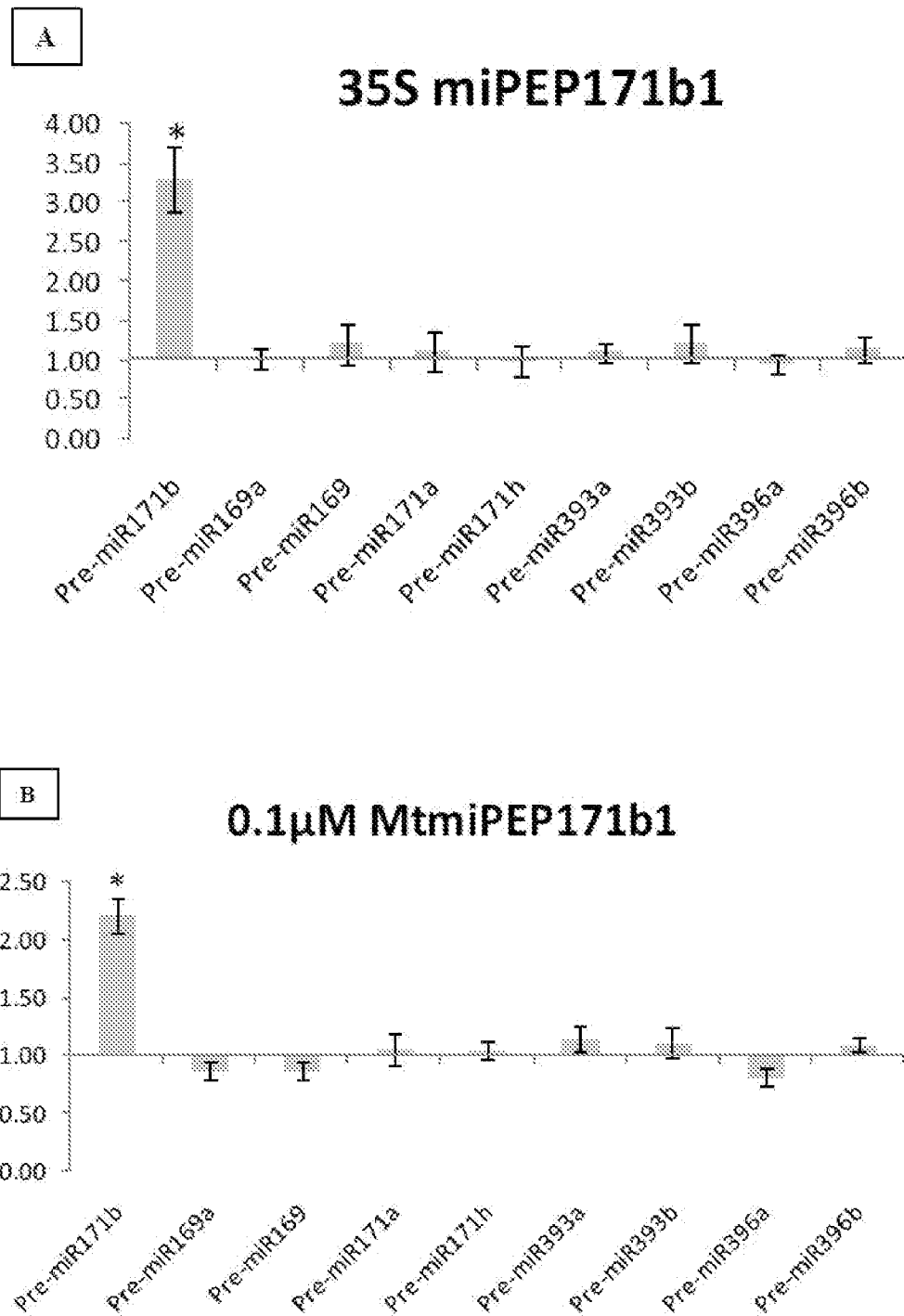


FIGURE 6

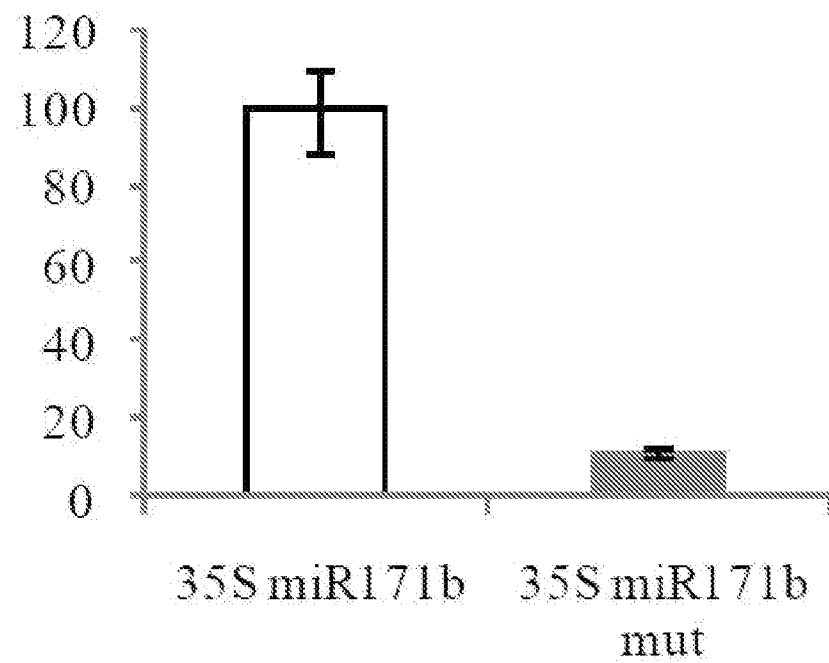


FIGURE 7

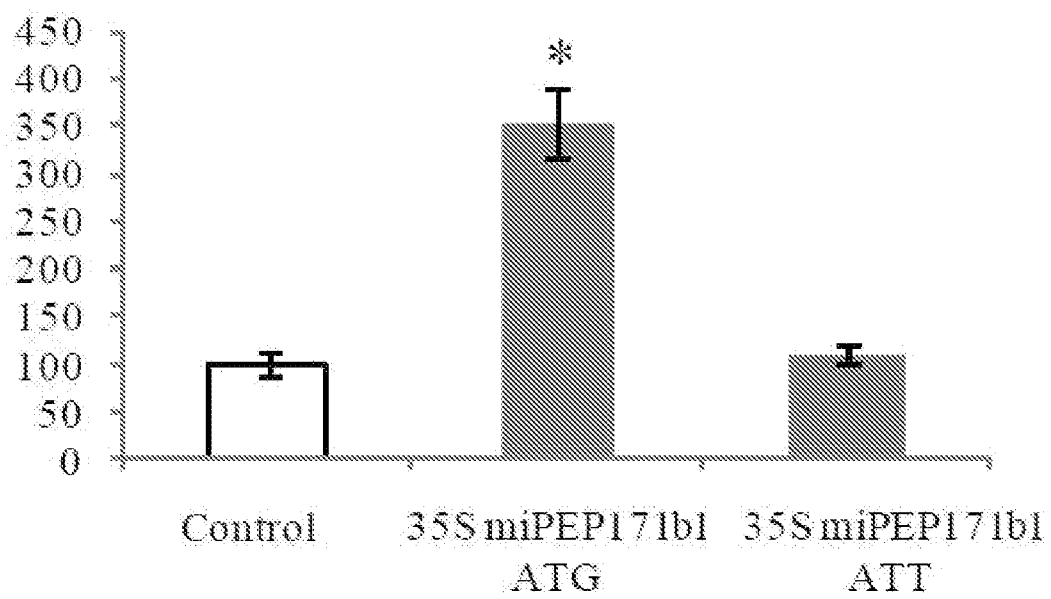


FIGURE 8

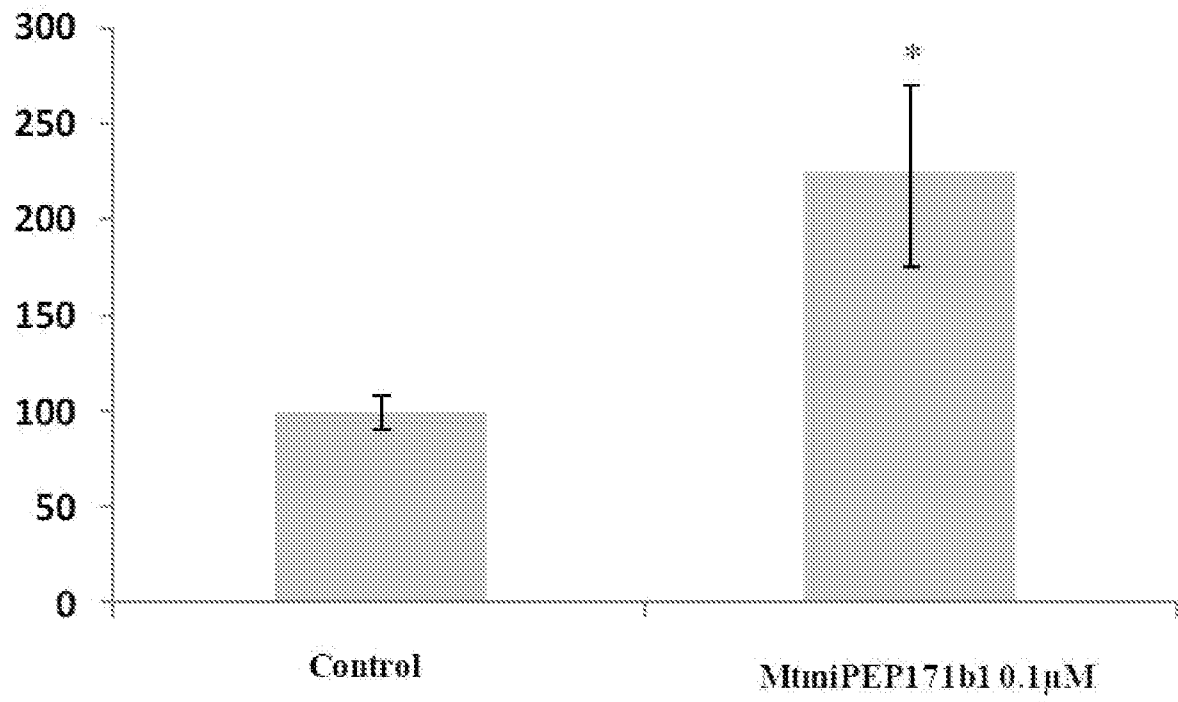


FIGURE 9

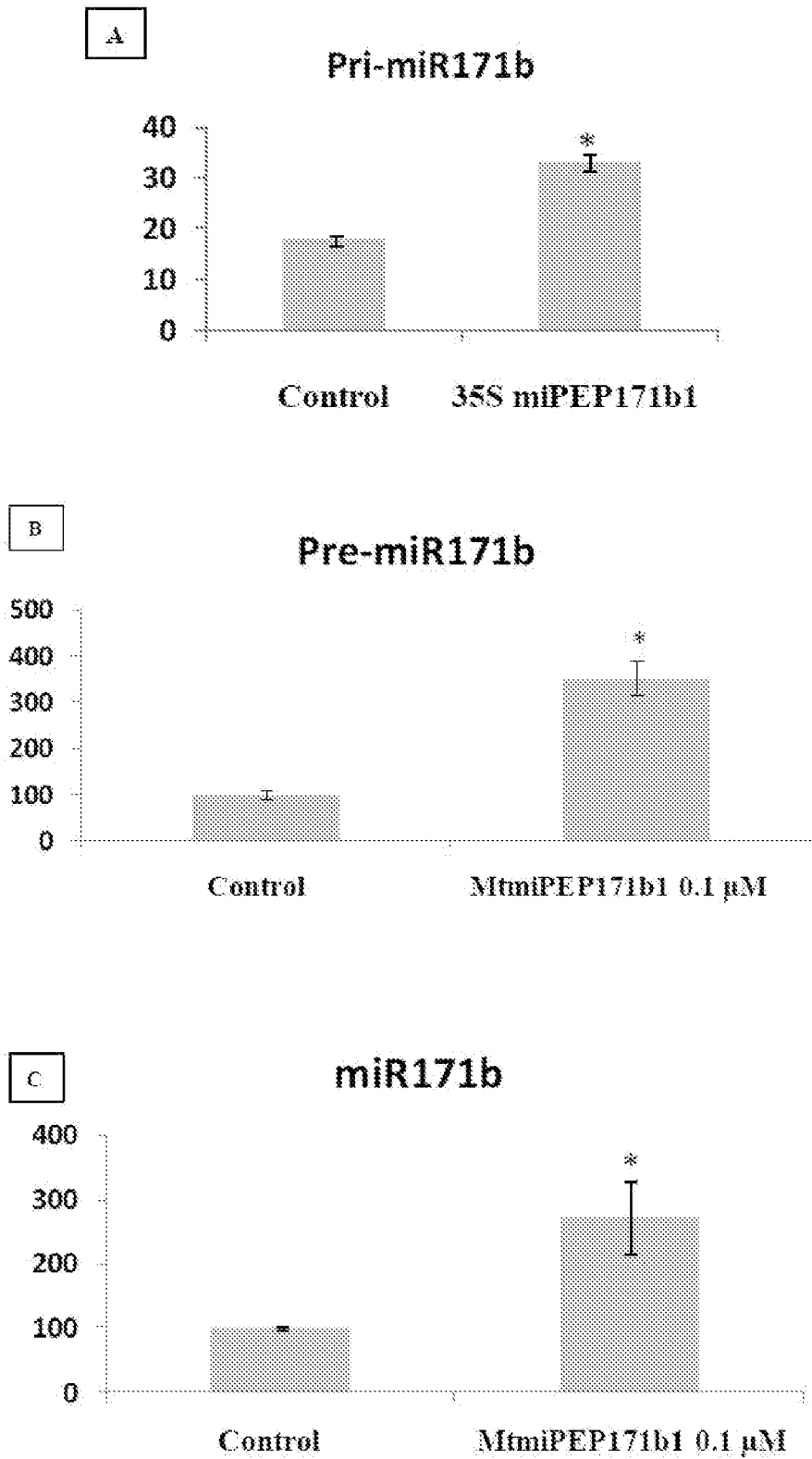


FIGURE 10

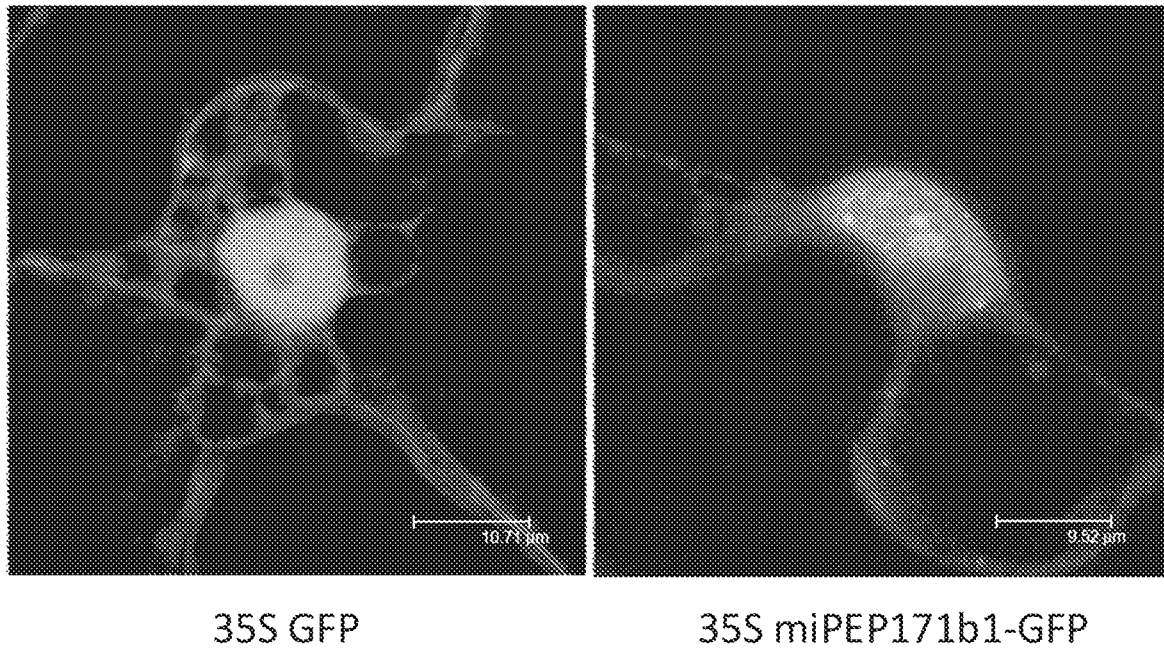


FIGURE 11

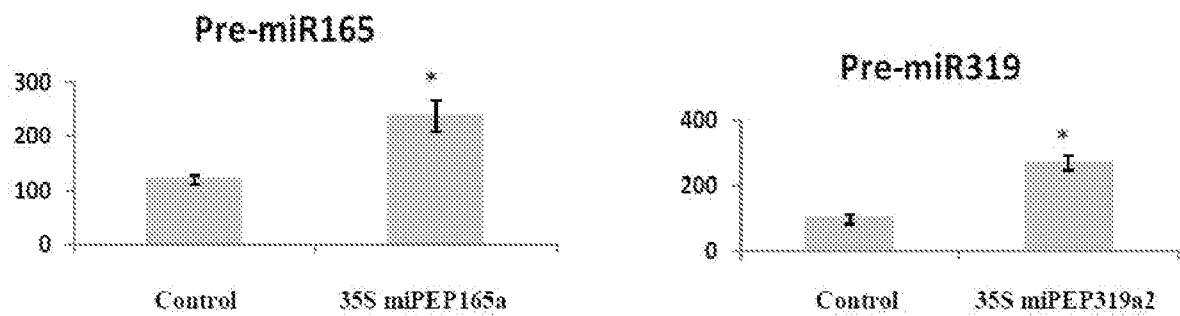


FIGURE 12

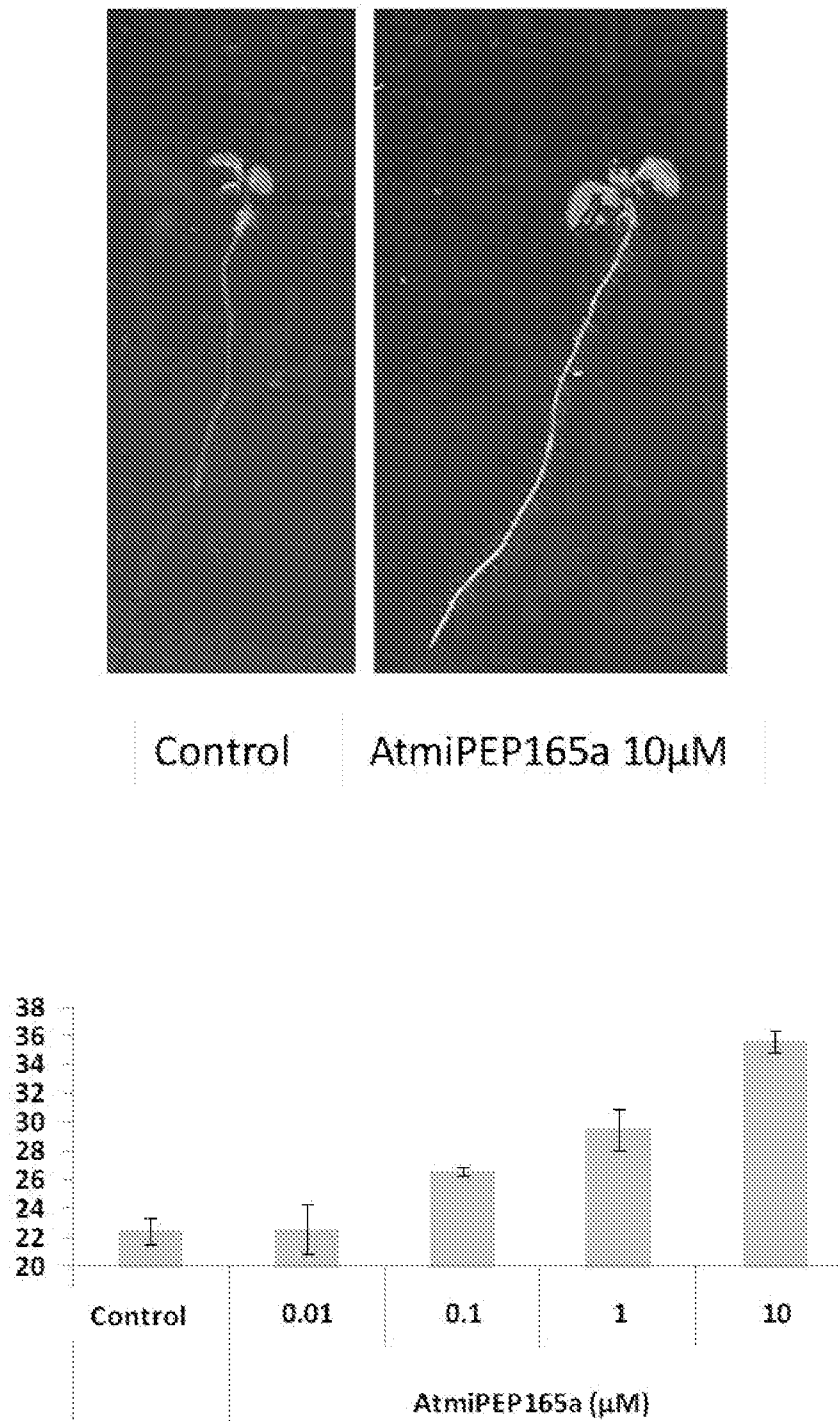


FIGURE 14

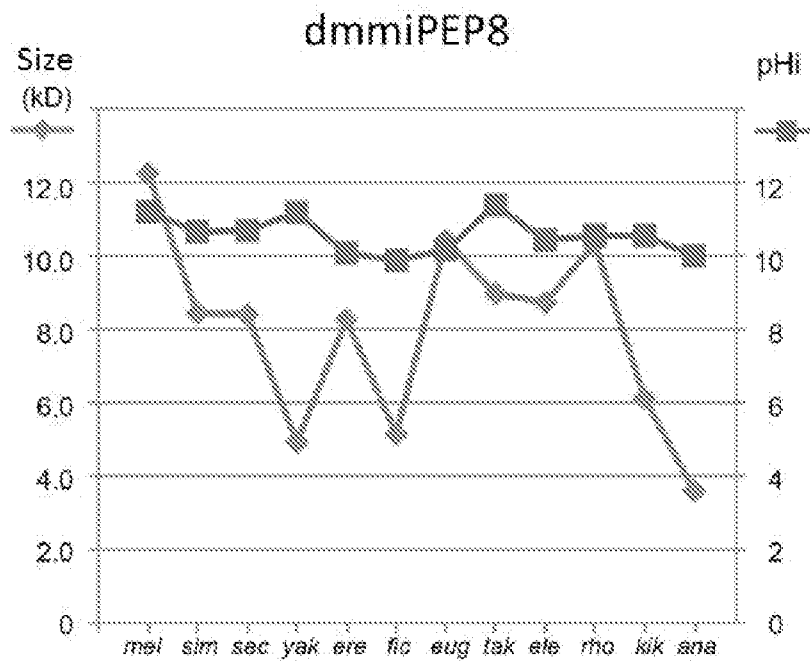


FIGURE 15

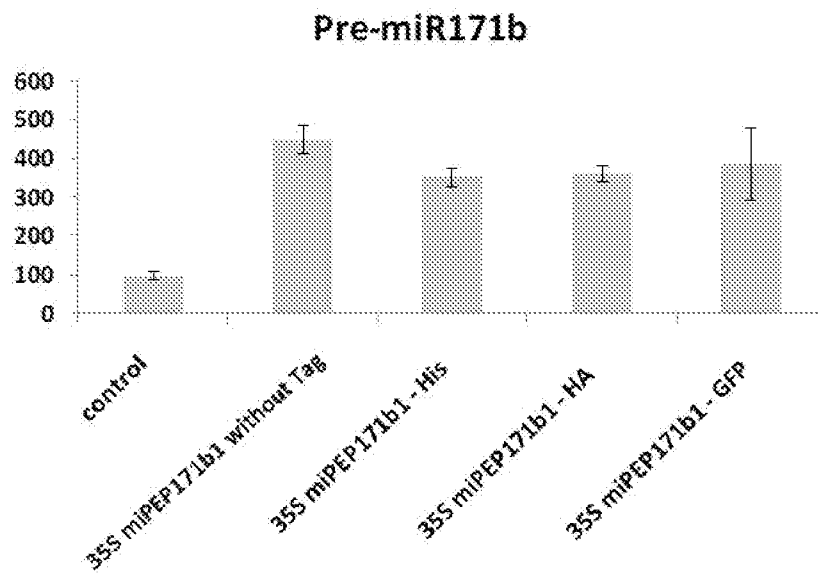


FIGURE 16

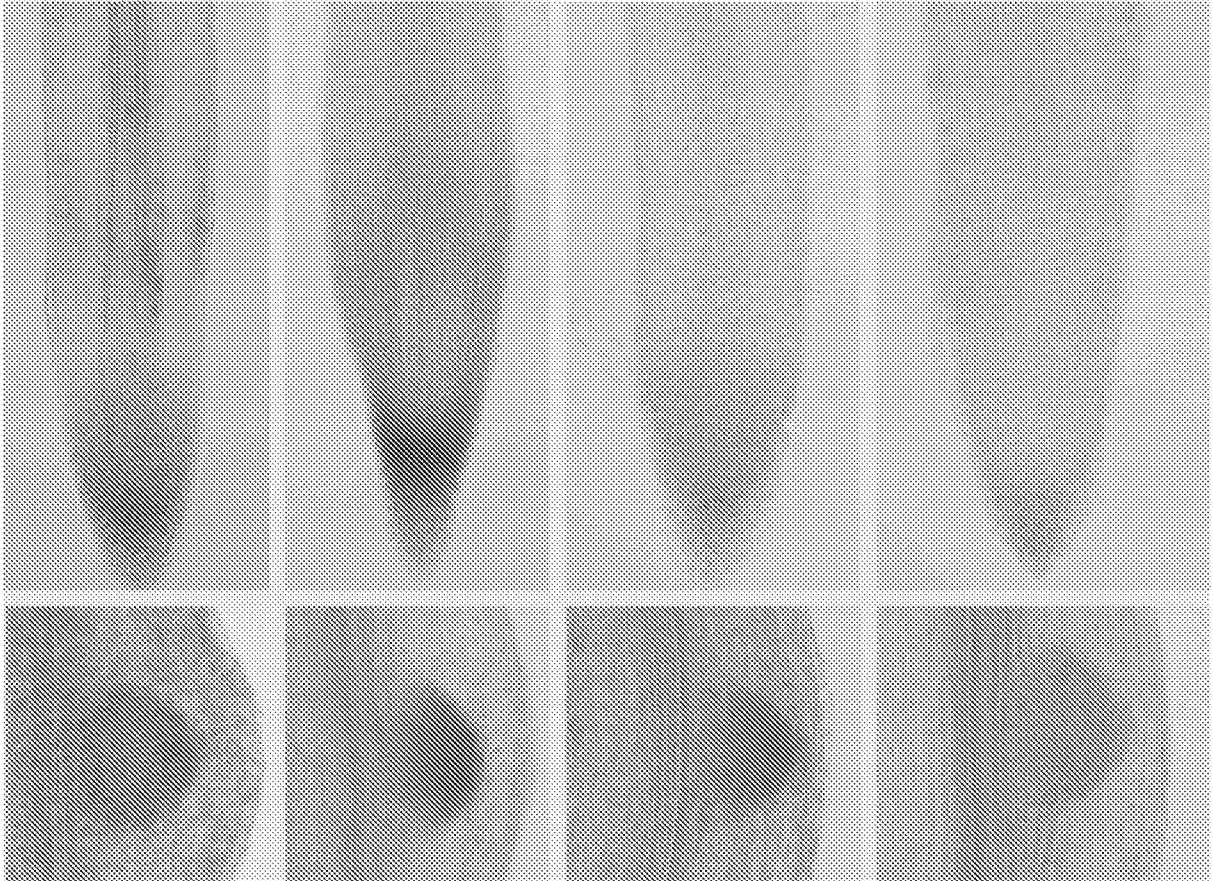


FIGURE 17

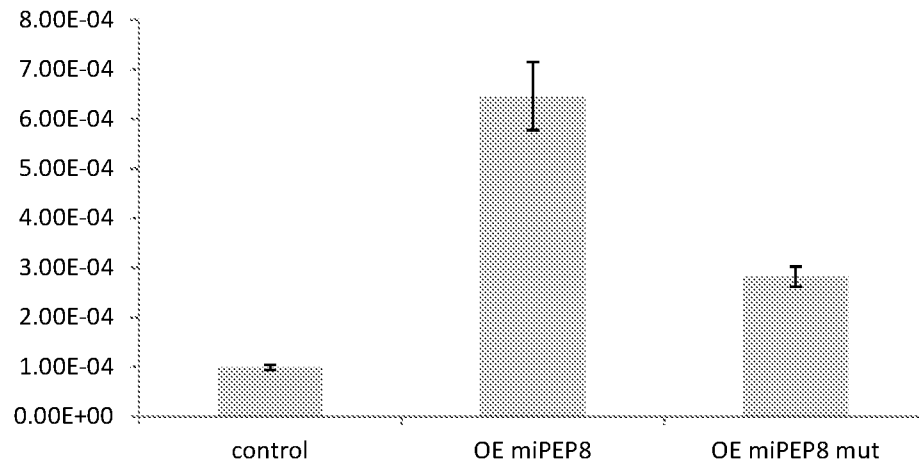
Pre-miR8

FIGURE 18

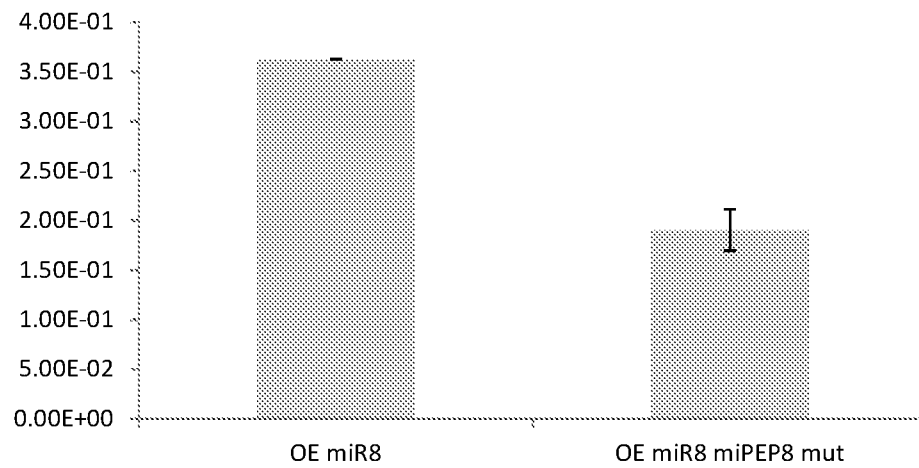
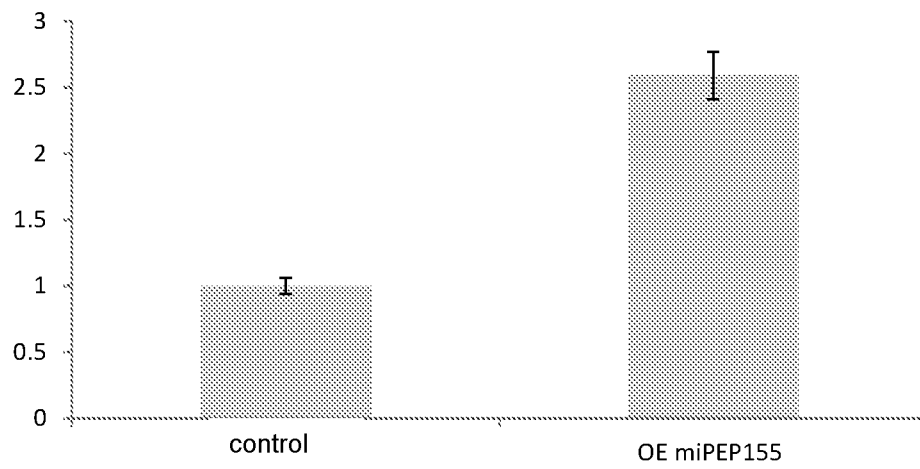
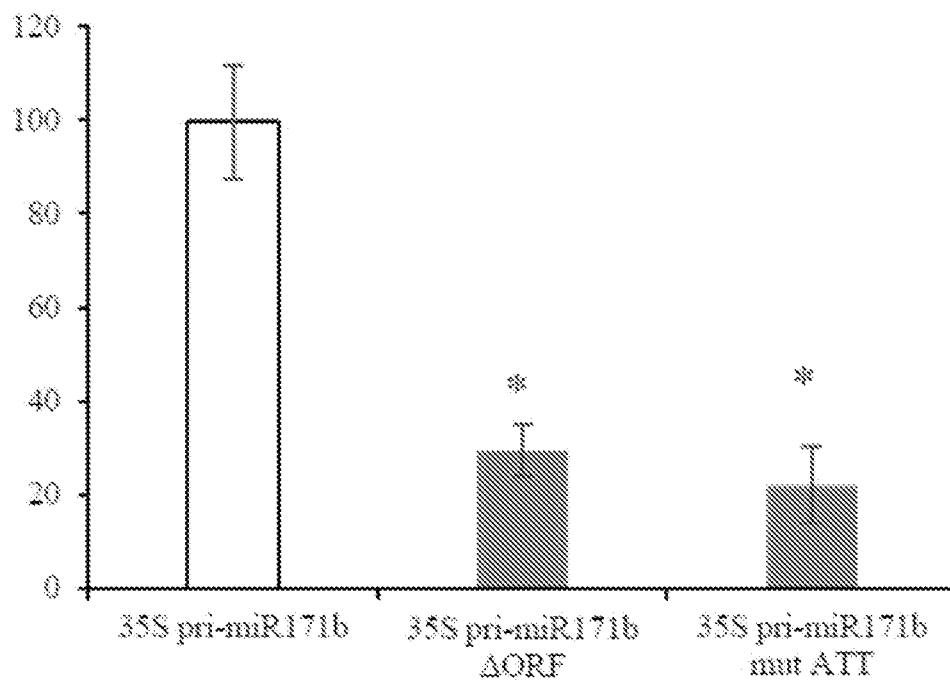
Pre-miR8

FIGURE 19

Pre-miR155**FIGURE 20****FIGURE 21**

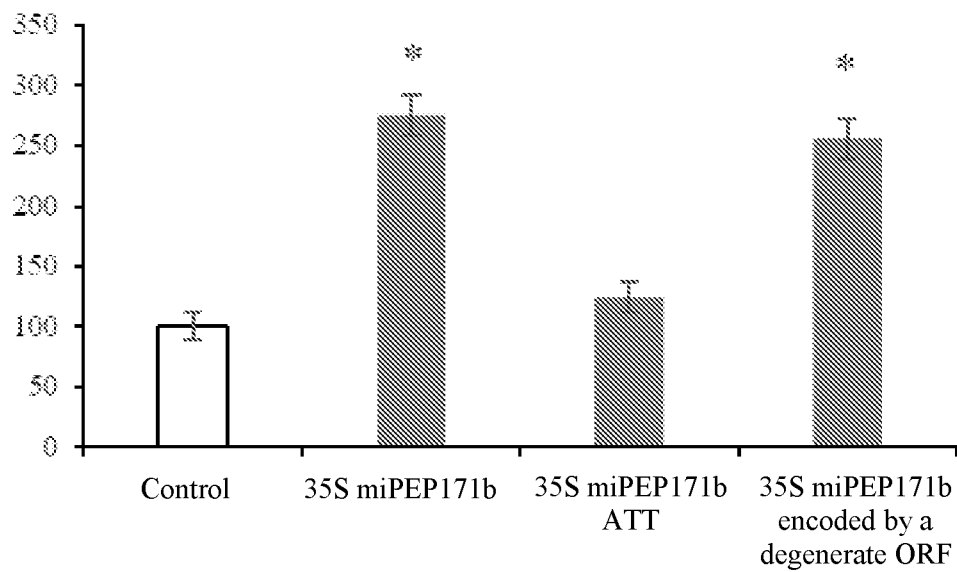


FIGURE 22

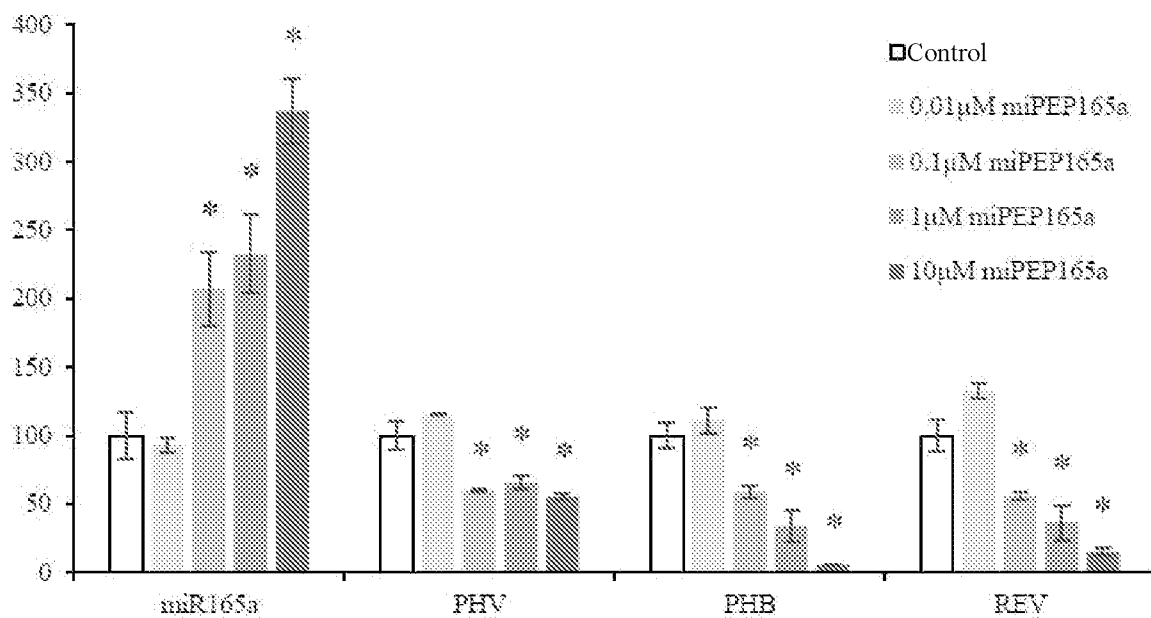
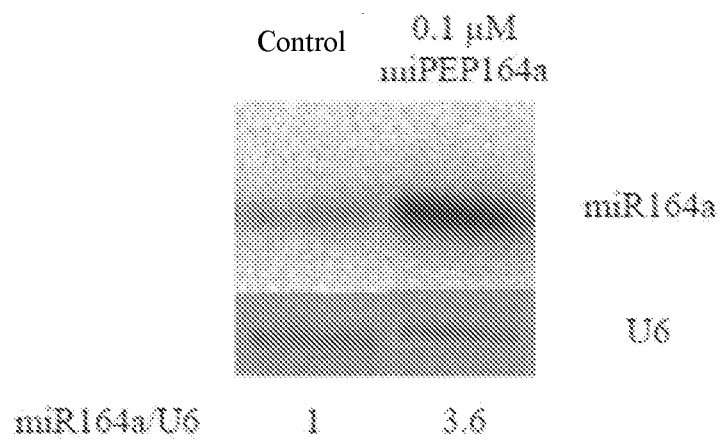
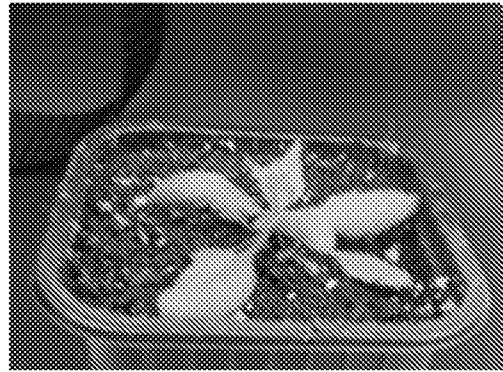
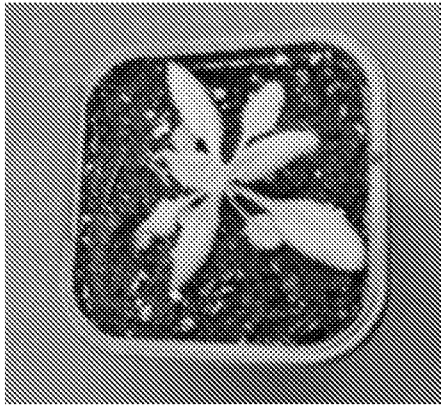


FIGURE 23**FIGURE 24**

A) Control plant



B) Plant treated with miPEP 164a

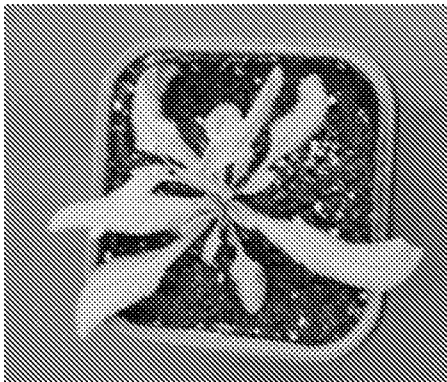
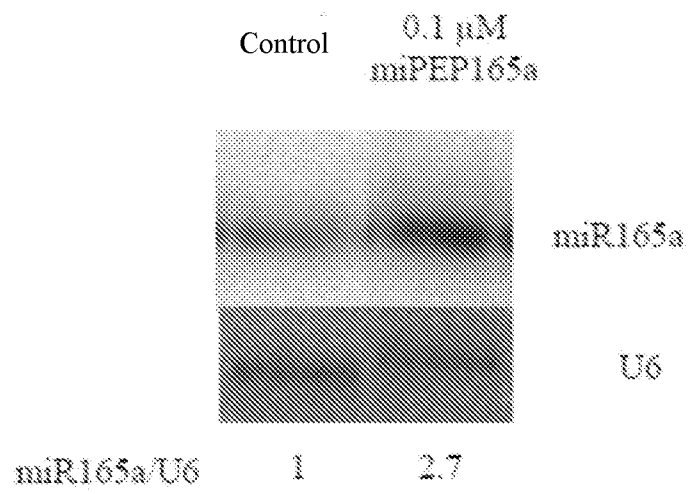
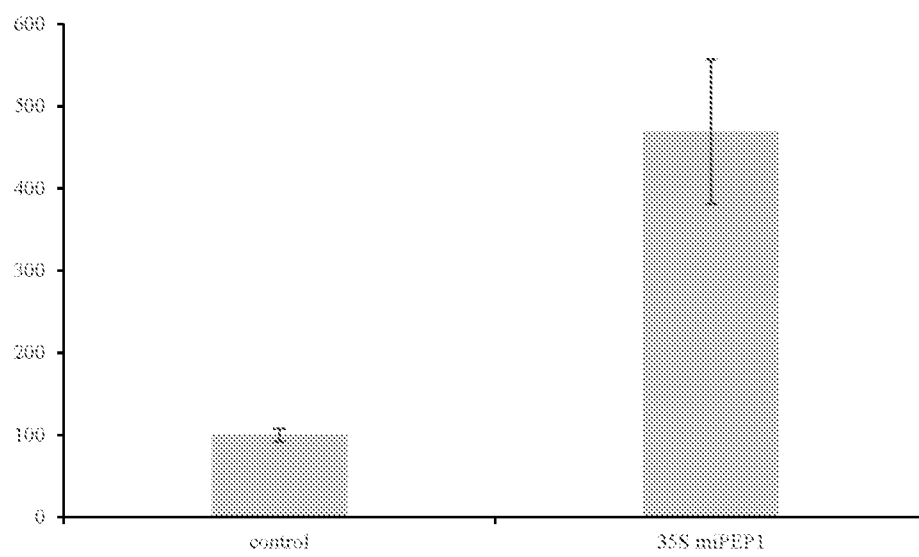
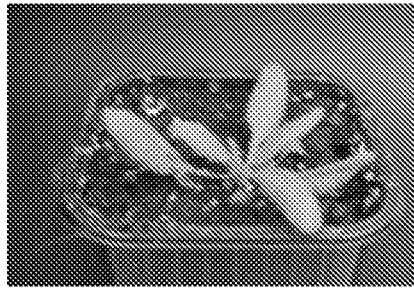
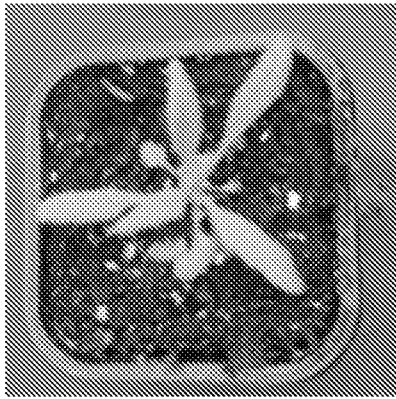


FIGURE 25

**FIGURE 26****FIGURE 27**

A) Control plant



B) Plant treated with miPEP319a

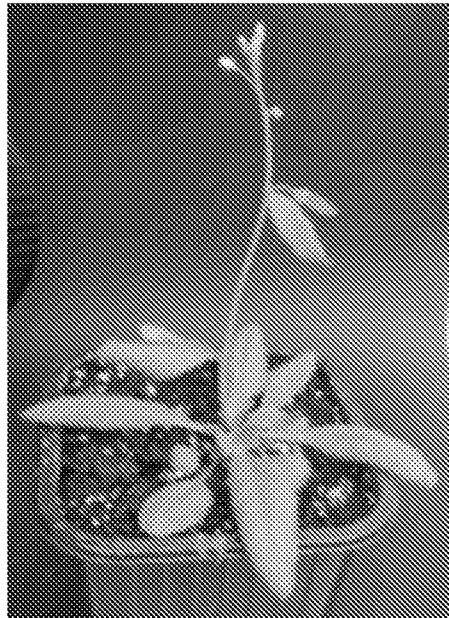
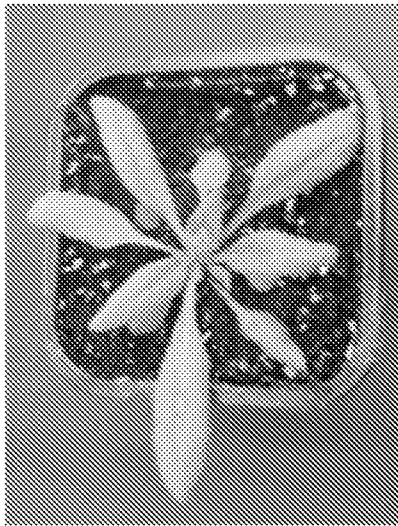


FIGURE 28

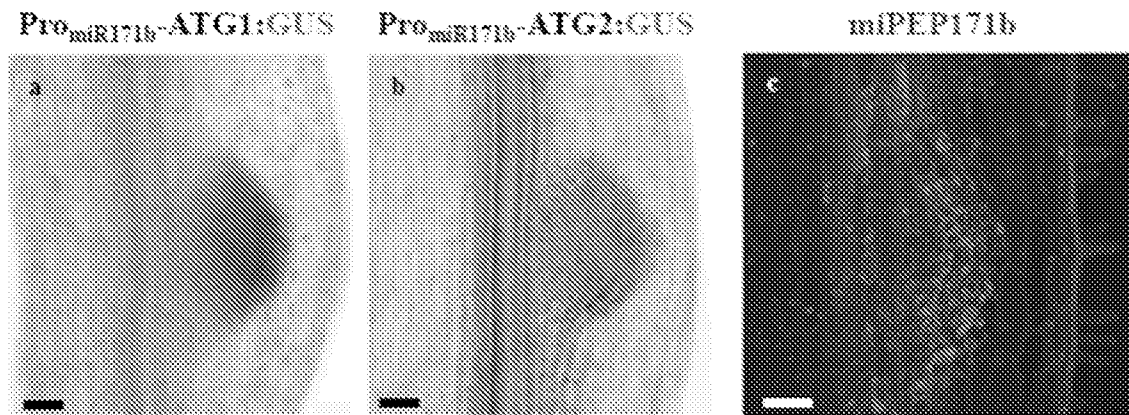


FIGURE 29

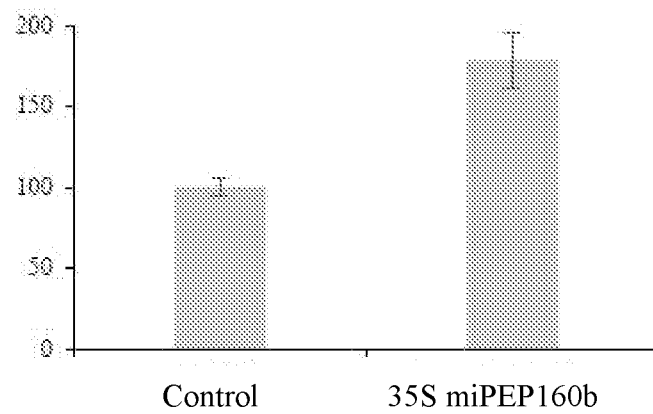


FIGURE 30

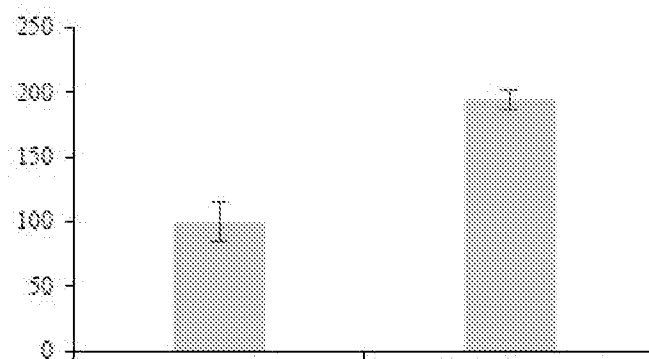


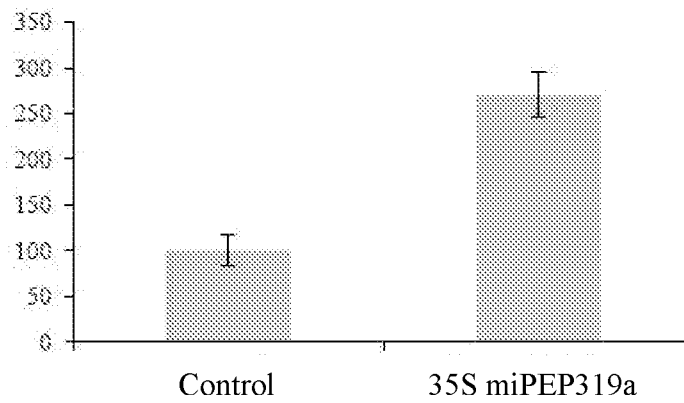
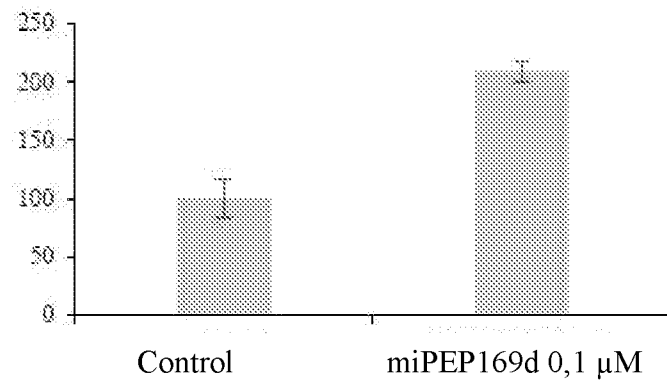
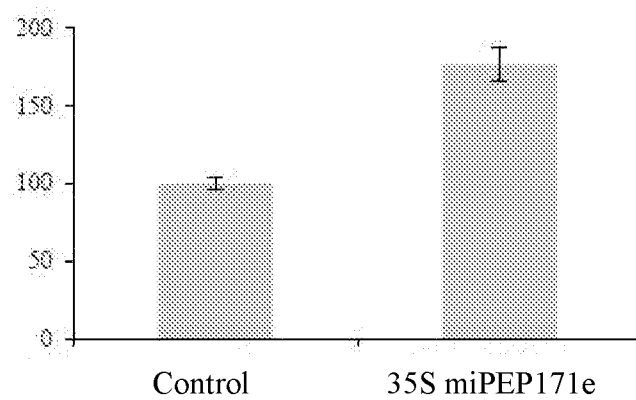
FIGURE 31**FIGURE 32****FIGURE 33**

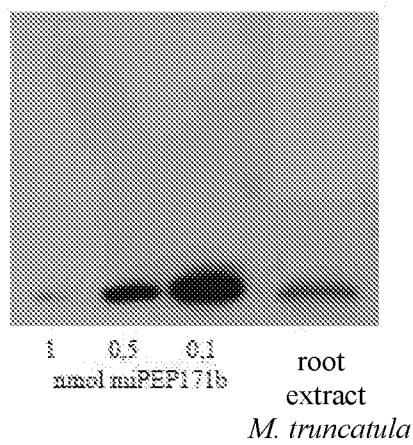
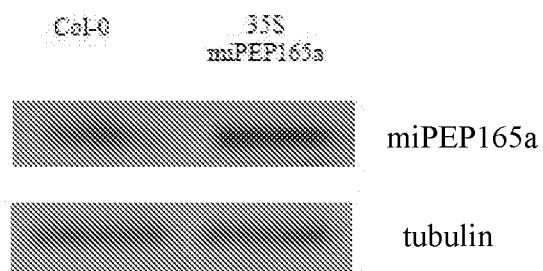
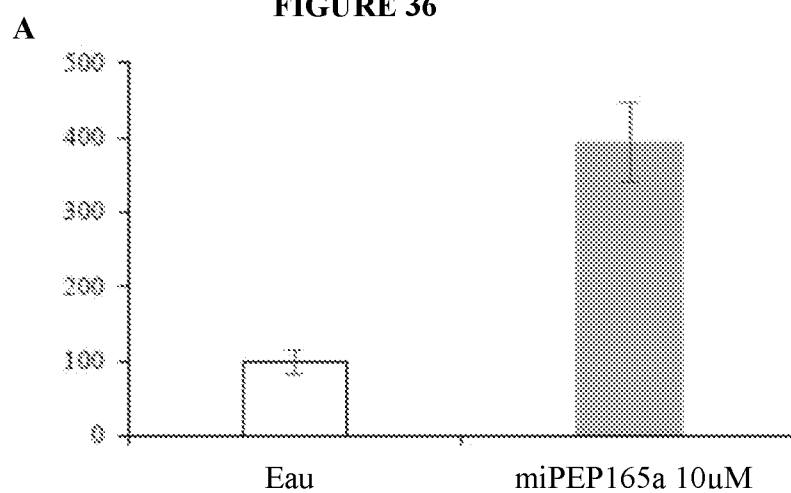
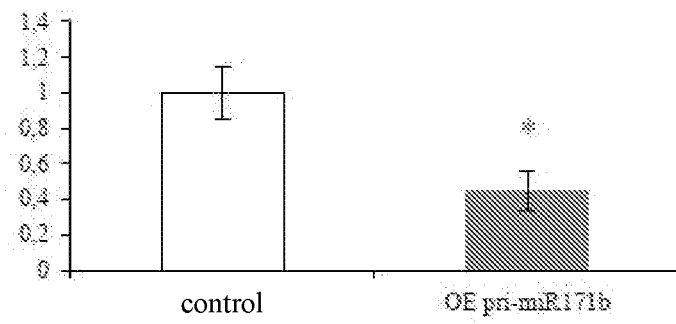
FIGURE 34**FIGURE 35****FIGURE 36**

FIGURE 33

B

C

FIGURE 37

**FIGURE 38**