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He et al.(10) **Patent No.:** US 12,385,058 B2
(45) **Date of Patent:** Aug. 12, 2025(54) **HERBICIDE TOLERANCE PROTEIN,
ENCODING GENE THEREOF AND USE
THEREOF**2019/0029257 A1 1/2019 Xie et al.
2019/0106705 A1 4/2019 Xie et al.
2019/0249187 A1 8/2019 He et al.(71) Applicants: **Beijing Dabeinong Biotechnology Co., Ltd.**, Beijing (CN); **Nanjing Agricultural University**, Nanjing (CN)

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(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 472 days.

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(22) PCT Filed: **Dec. 28, 2018**

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(57) **ABSTRACT**(30) **Foreign Application Priority Data**

The present invention relates to an herbicide tolerance protein, an encoding gene thereof and use thereof, the herbicide tolerance protein comprising: a protein (a) having an amino acid sequence as shown in SEQ ID NO: 1, and having an alanine substitution at least at position 176 and/or having a valine substitution at position 178 of SEQ ID NO: 1; or (b) having an amino acid sequence as shown in SEQ ID NO: 3; or (c) having an amino acid sequence as shown in SEQ ID NO: 5; or (d) having an amino acid sequence as shown in SEQ ID NO: 7; or (e) being derived from (a) by means of the amino acid sequence of (a) undergoing substitution and/or deletion and/or by added one or several amino acids, and having the activity of thifensulfuron hydro-lase. The herbicide tolerance protein of the present invention has a broad application prospects in plants.

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(51) **Int. Cl.***C12N 15/82* (2006.01)*A01N 47/36* (2006.01)*C12N 9/14* (2006.01)(52) **U.S. Cl.**CPC *C12N 15/8278* (2013.01); *A01N 47/36* (2013.01); *C12N 9/14* (2013.01); *C12N 15/8202* (2013.01); *C12N 15/8275* (2013.01)(58) **Field of Classification Search**

None

See application file for complete search history.

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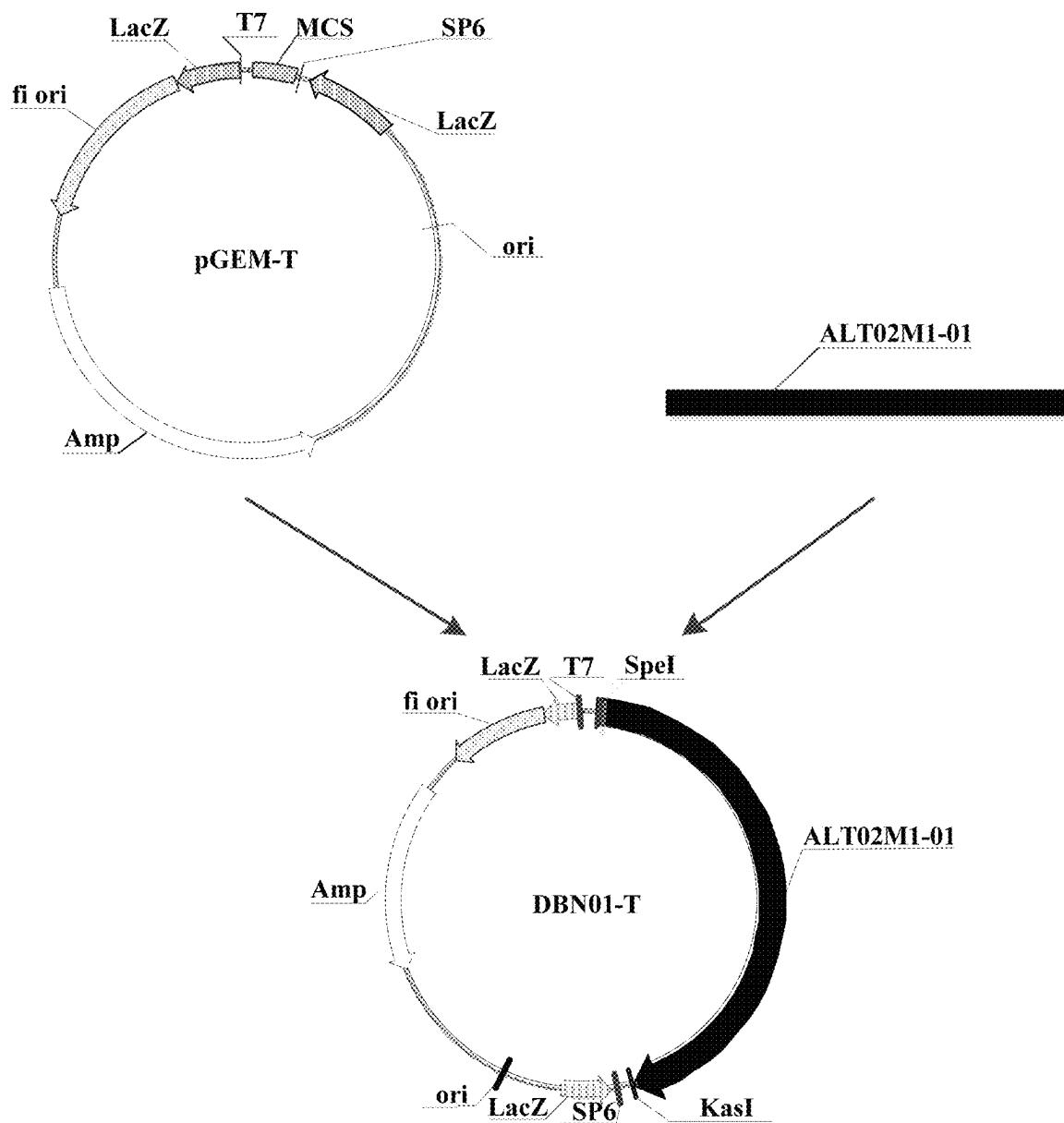


Figure 1

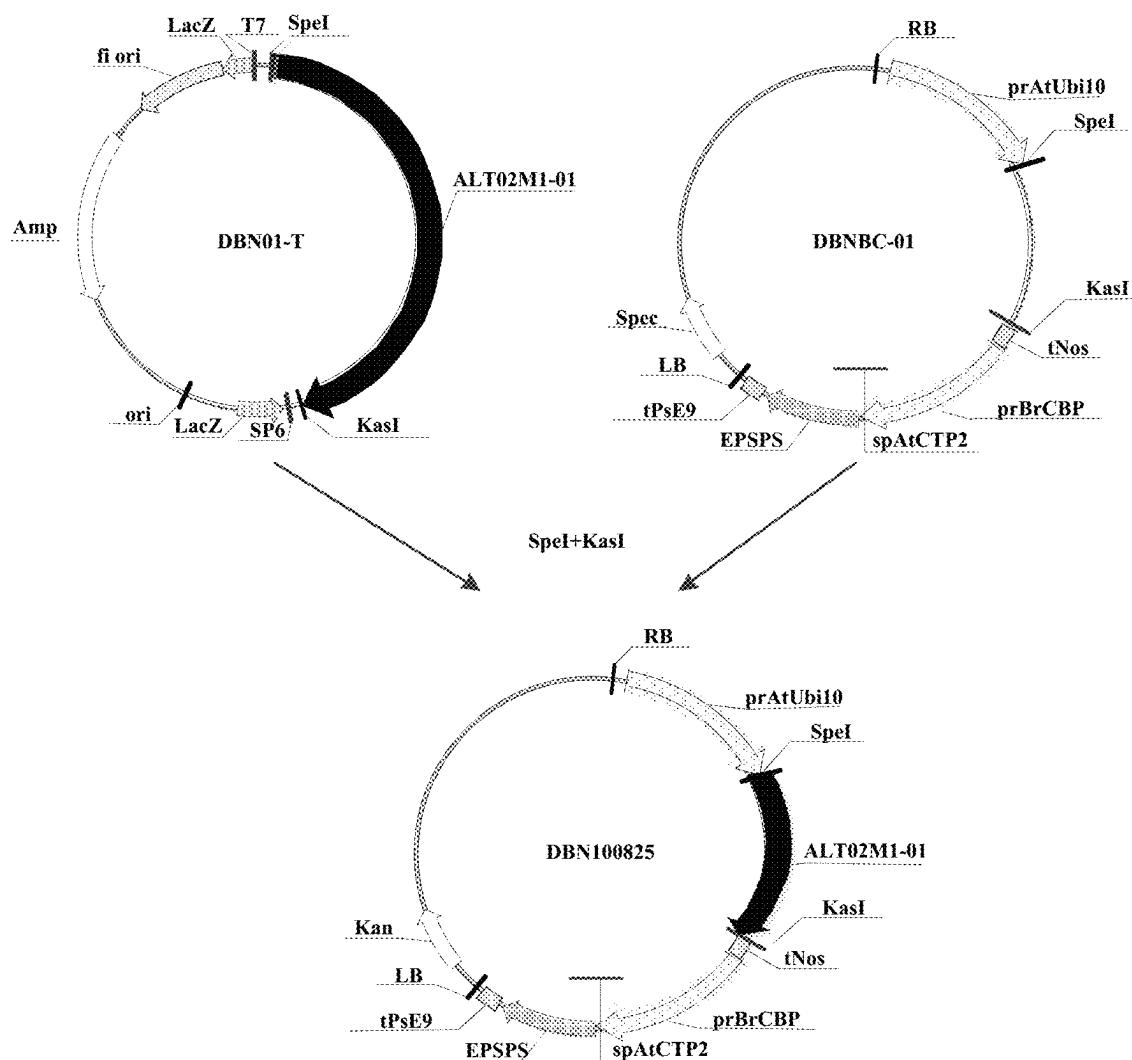


Figure 2

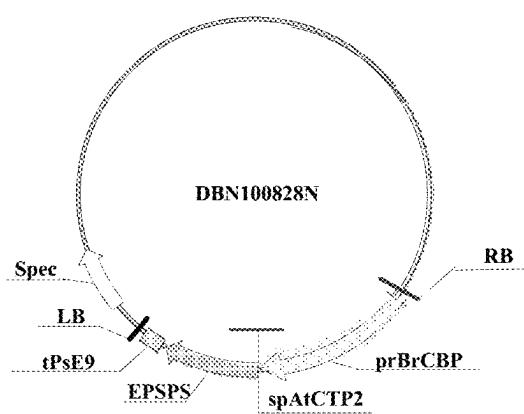


Figure 3

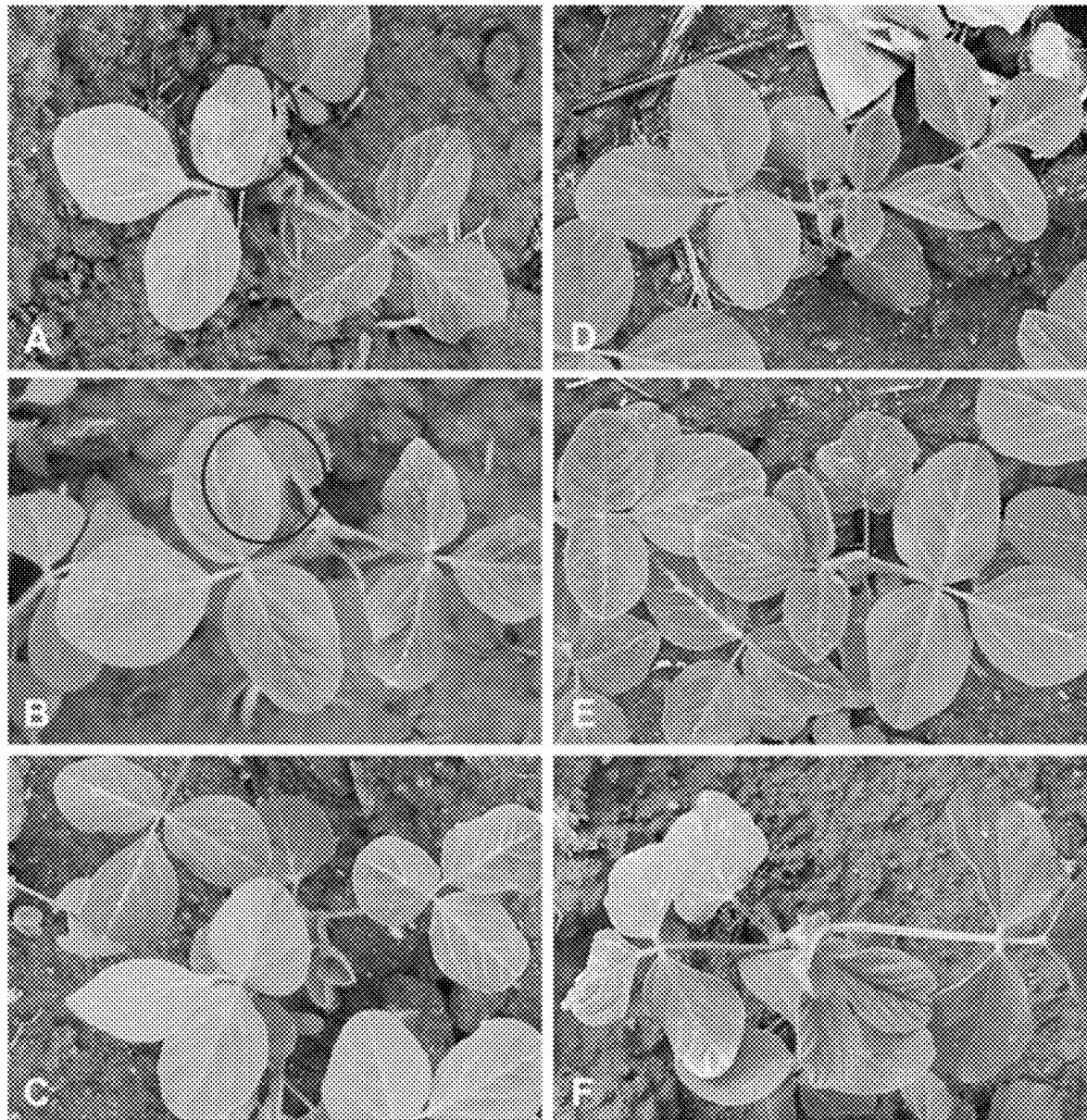


Figure 4

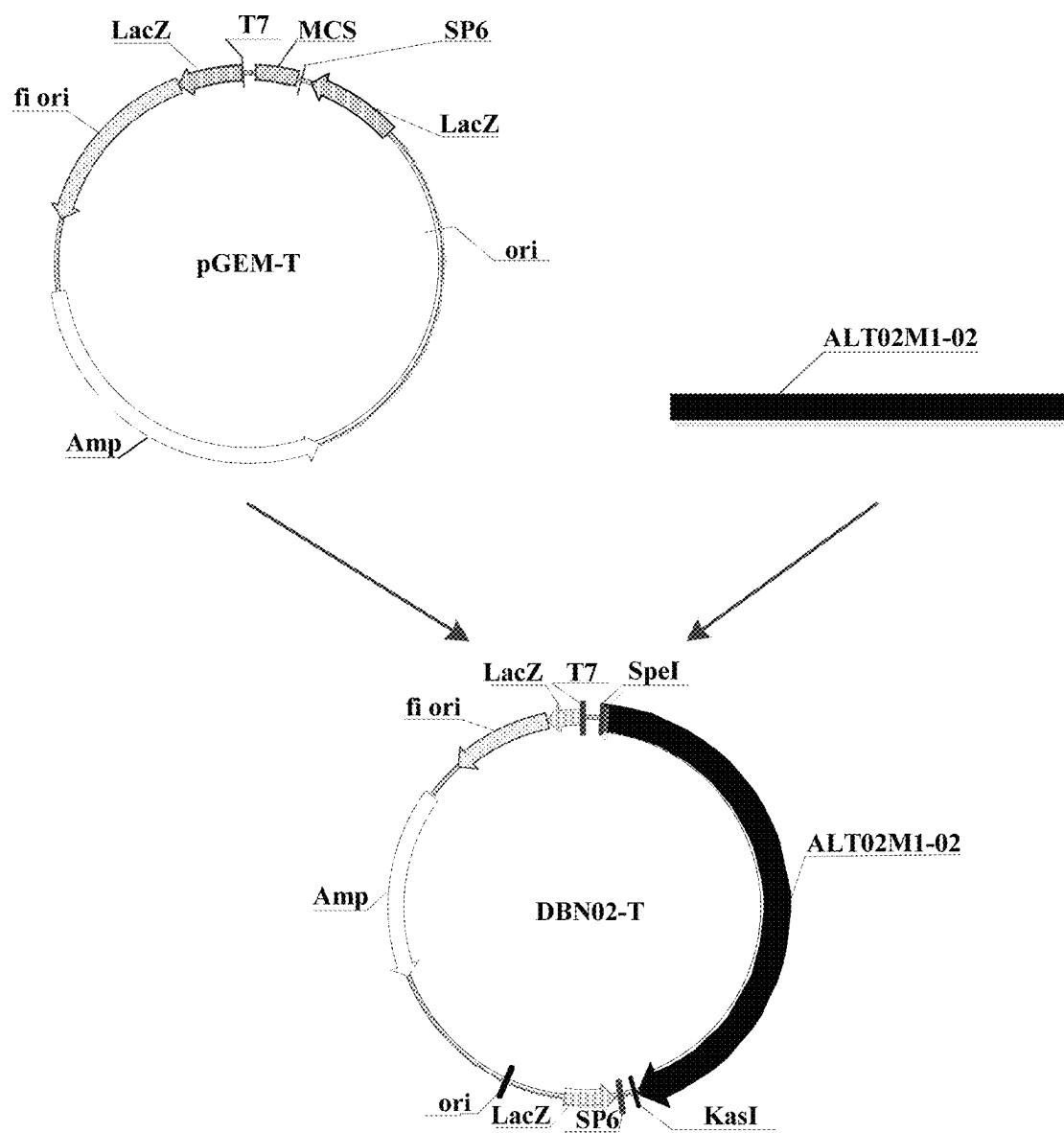


Figure 5

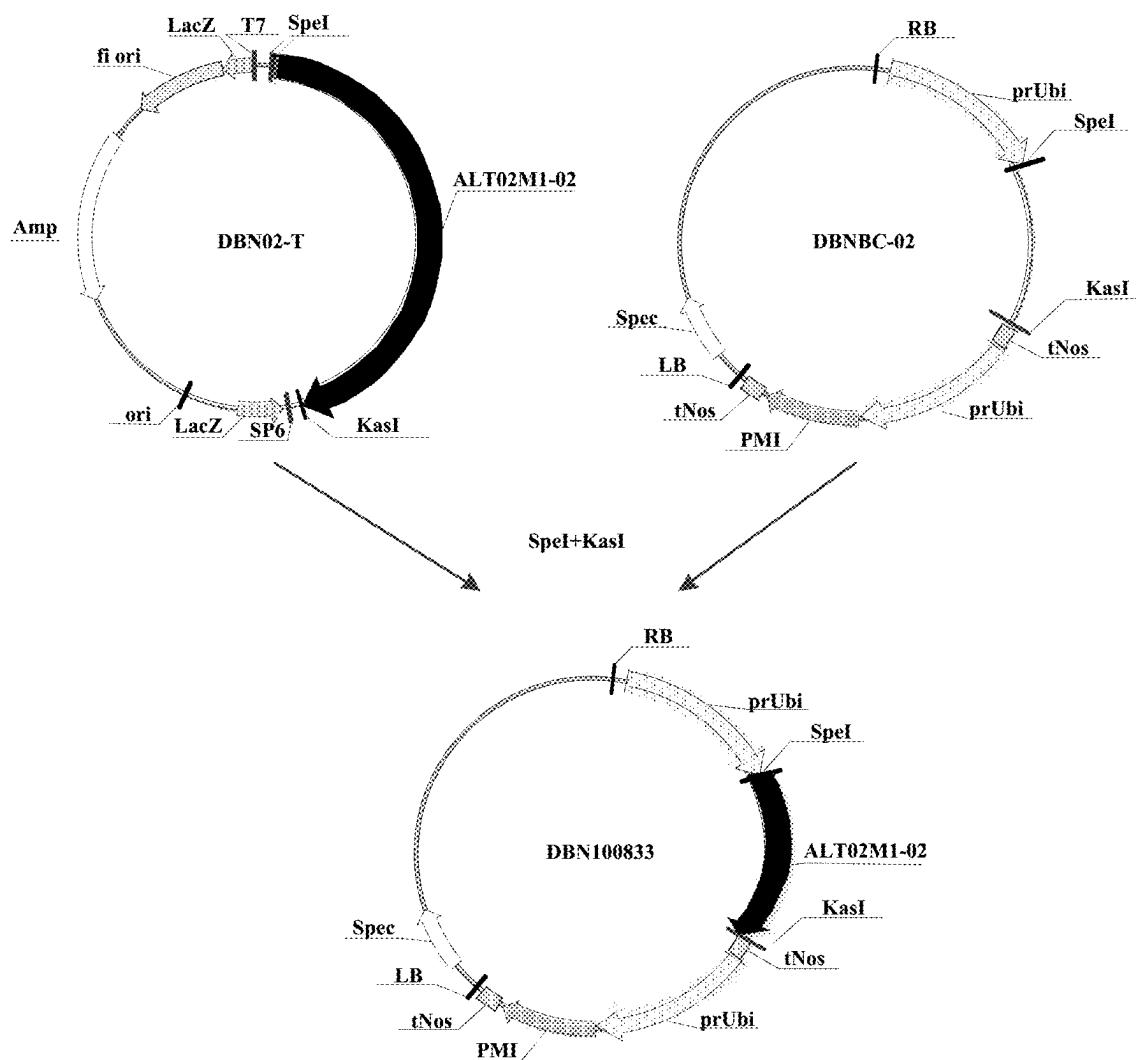


Figure 6

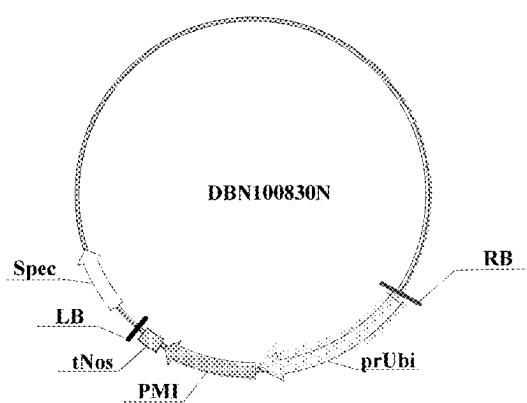


Figure 7

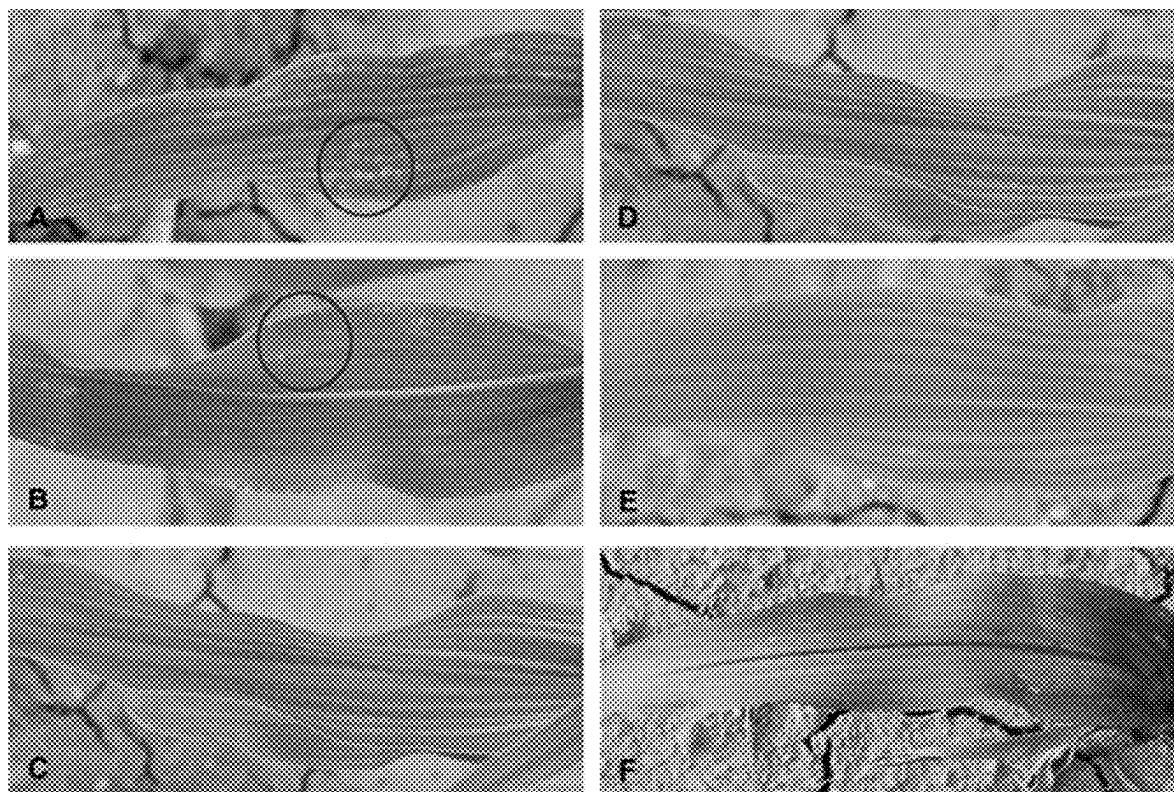


Figure 8

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**HERBICIDE TOLERANCE PROTEIN,
ENCODING GENE THEREOF AND USE
THEREOF**

REFERENCE TO RELATED APPLICATIONS

This application is a U.S. national stage of PCT/CN2018/124916, filed Dec. 28, 2018, which claims priority to Chinese application No. 201810124124.9, filed Feb. 7, 2018, the entire content of both of which is incorporated herein by reference.

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted electronically as a file in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII format file, created on Dec. 1, 2020, is named 2020-12-1_Sequence_listing_BDBC0001PA.txt and is 144, 15 324 bytes in size.

TECHNICAL FIELD

The present invention relates to a herbicide tolerant protein, a coding gene thereof and use thereof, and in particular to a sulfonylurea herbicide tolerant protein, a 25 coding gene thereof and use thereof.

BACKGROUND

Weeds may exhaust valuable nutrients required by crops and other plants of interest in the soil rapidly. Currently, there are many types of herbicides used to control weeds, among which a particularly popular herbicide is glyphosate. Crops resistant to glyphosate have been developed, such as maize, soybean, cotton, sugar beet, wheat and rice. Therefore, glyphosate can be sprayed onto the field where glyphosate resistant crops are planted, so as to control weeds without significant damage to the crops.

Glyphosate has been widely used in the world for more than 20 years, resulting in an over-reliance on glyphosate and glyphosate tolerant crop technologies, as well as applying a high selection pressure to plants that are naturally more tolerant to glyphosate or have developed a glyphosate-resistant activity in wild weed species. It has been reported that a few weeds have developed resistance to glyphosate, including broad-leaved weeds and gramineous weeds, such as *Lolium rigidum*, *Lolium multiflorum*, *Eleusine indica* Gaertn., *Ambrosia artemisiifolia*, *Conyza canadensis*, *Conyza bonariensis* and *Plantago lanceolata*. Moreover, weeds that were not agricultural problems before the wide use of glyphosate tolerant crops have become prevalent gradually, and are difficult to control with glyphosate tolerant crops, wherein these weeds mainly appear together with (but not only with) difficult-to-control broad-leaved weeds, such as the *Amaranthus*, *Chenopodium*, *Taraxacum* and *Commelinaceae* species.

In areas where glyphosate resistant weeds or difficult-to-control weed species are present, growers can compensate for the weakness of glyphosate by tank mixing or alternating with other herbicides that can control the missed weeds, such as sulfonylurea herbicides. Sulfonylurea herbicides have become the third most popular herbicides after organophosphorus and acetamide herbicides, with global annual sales of more than \$3 billion. The annual application area of sulfonylurea herbicides in our country has been more than 2 million hectares and still shows an expanding trend.

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With the emergence of glyphosate resistant weeds and the expanding application of sulfonylurea herbicides, there is a need for more genes capable of degrading sulfonylurea herbicides and for introducing the genes into plants of interest that are sensitive to sulfonylurea herbicides so as to increase the tolerance of the plants to sulfonylurea herbicides.

SUMMARY OF THE INVENTION

The objective of the present invention is to provide a herbicide tolerant protein, a coding gene thereof and use thereof, wherein the herbicide tolerant protein is capable of better degrading sulfonylurea herbicides and making the plants into which the herbicide tolerant protein-coding gene is introduced have higher tolerance to sulfonylurea herbicides.

In order to achieve the above objective, the present invention provides a herbicide tolerant protein, comprising:

- (a) a protein consisting of an amino acid sequence as shown in SEQ ID NO: 1, and at least having an alanine substitution at position 176 and/or a valine substitution at position 178 of SEQ ID NO: 1; or
- (b) a protein consisting of an amino acid sequence as shown in SEQ ID NO: 19, and at least having an alanine substitution at position 140 and/or a valine substitution at position 142 of SEQ ID NO: 19; or
- (c) a protein consisting of an amino acid sequence as shown in SEQ ID NO: 35, and at least having an alanine substitution at position 140 and/or a valine substitution at position 142 of SEQ ID NO: 35; or
- (d) a protein consisting of an amino acid sequence as shown in SEQ ID NO: 51, and at least having an alanine substitution at position 131 and/or a valine substitution at position 133 of SEQ ID NO: 51; or
- (e) a protein which is derived from (a) to (d) by substituting and/or deleting and/or adding one or more amino acids in the amino acid sequences of (a) to (d), and has thifensulfuron hydrolase activity.

Furthermore, said herbicide tolerant protein comprises:

- (f) an amino acid sequence of (a), wherein the amino acid sequence of (a) also has an arginine substitution at position 80 and/or an alanine substitution at position 81 and/or an arginine substitution at position 182 of SEQ ID NO: 1; or
- (g) an amino acid sequence of (b), wherein the amino acid sequence of (b) also has an arginine substitution at position 44 and/or an alanine substitution at position 45 and/or an arginine substitution at position 146 of SEQ ID NO: 19; or
- (h) an amino acid sequence of (c), wherein the amino acid sequence of (c) also has an arginine substitution at position 44 and/or an alanine substitution at position 45 and/or an arginine substitution at position 146 of SEQ ID NO: 35; or
- (i) an amino acid sequence of (d), wherein the amino acid sequence of (d) also has an arginine substitution at position 35 and/or an alanine substitution at position 36 and/or an arginine substitution at position 137 of SEQ ID NO: 51; or
- (j) a protein which is derived from (a) to (d) by substituting and/or deleting and/or adding one or more amino acids in the amino acid sequences of (f) to (i), and has thifensulfuron hydrolase activity.

Furthermore, the herbicide tolerant protein comprises:

- (k) a protein consisting of an amino acid sequence as shown in SEQ ID NO: 7, SEQ ID NO: 11 or SEQ ID NO: 15; or
- (l) a protein consisting of an amino acid sequence as shown in SEQ ID NO: 23, SEQ ID NO: 27 or SEQ ID NO: 31; or
- (m) a protein consisting of an amino acid sequence as shown in SEQ ID NO: 39, SEQ ID NO: 43 or SEQ ID NO: 47; or
- (n) a protein consisting of an amino acid sequence as shown in SEQ ID NO: 55, SEQ ID NO: 59 or SEQ ID NO: 63.

In order to achieve the above objective, the present invention further provides a herbicide tolerant gene, comprising:

- (o) a nucleotide sequence encoding the herbicide tolerant protein according to (a)-(n); or
- (p) a nucleotide sequence as shown in SEQ ID NO: 8, 9, 10, 12, 13, 14, 16, 17 or 18; or
- (q) a nucleotide sequence as shown in SEQ ID NO: 24, 25, 26, 28, 29, 30, 32, 33 or 34; or
- (r) a nucleotide sequence as shown in SEQ ID NO: 40, 41, 42, 44, 45, 46, 48, 49 or 50.

In order to achieve the above objective, the present invention further provides an expression cassette, wherein the expression cassette comprises the herbicide tolerant gene under the regulation of an effectively linked regulatory sequence.

In order to achieve the above objective, the present invention further provides a recombinant vector containing the herbicide tolerant gene or the expression cassette.

In order to achieve the above objective, the present invention also provides a method for producing a herbicide tolerant protein, comprising:

- obtaining a cell of a transgenic host organism containing the herbicide tolerant gene or the expression cassette;
- cultivating the cell of the transgenic host organism under conditions allowing production of a herbicide tolerant protein; and
- recovering the herbicide tolerant protein.

Further, the transgenic host organism comprises plants, animals, bacteria, yeasts, baculoviruses, nematodes, or algae.

In order to achieve the above objective, the present invention further provides a method for increasing herbicide tolerance ranges, comprising co-expressing the herbicide tolerant protein or the herbicide tolerant protein encoded by the expression cassette together with at least one second protein which is different from the herbicide tolerant protein or the herbicide tolerant protein encoded by the expression cassette in a plant.

Furthermore, the second protein is 5-enolpyruvylshikimate-3-phosphate synthase, glyphosate oxidoreductase, glyphosate-N-acetyltransferase, glyphosate decarboxylase, glufosinate acetyltransferase, α -ketoglutarate-dependent dioxygenase, dicamba monooxygenase, 4-hydroxyphenylpyruvate dioxygenase, acetolactate synthase, cytochrome-like proteins and/or protoporphyrinogen oxidase.

The expression of the herbicide tolerant protein of the present invention in a transgenic plant can be accompanied by the expression of one or more other herbicide (glyphosate or glufosinate) tolerant proteins. This co-expression of more than one herbicide tolerant protein in the same transgenic plant can be achieved by allowing the plant to comprise and express a desired gene through genetic engineering. In

addition, a plant (the first parent) can express the herbicide tolerant protein of the present invention through genetic engineering manipulation, and a second plant (the second parent) can express other herbicide (glyphosate or glufosinate) tolerant proteins through genetic engineering manipulation. Progeny plants expressing all the genes introduced into the first parent and the second parent are obtained by hybridizing the first parent with the second parent.

In order to achieve the above objective, the present invention also provides a method for selecting transformed plant cells, comprising: transforming a plurality of plant cells with the herbicide tolerant gene or the expression cassette, and cultivating the cells under a concentration of herbicide allowing the growth of the transformed cells expressing the herbicide tolerant gene or the expression cassette, while killing the untransformed cells or inhibiting the growth of the untransformed cells, wherein the herbicide is a sulfonylurea herbicide.

In order to achieve the above objective, the present invention also provides a method for controlling weeds, comprising applying an effective dose of a sulfonylurea herbicide to a field for planting a target plant, the plant containing the herbicide tolerant gene or the expression cassette.

In order to achieve the above objective, the present invention also provides a method for protecting a plant from damages caused by sulfonylurea herbicides, comprising introducing the herbicide tolerant gene, the expression cassette or the recombinant vector into a plant to make the resultant plant produce a sufficient amount of herbicide tolerant proteins for protecting the plant from damages caused by sulfonylurea herbicides.

In order to achieve the above objective, the present invention also provides a method for controlling glyphosate resistant weeds in a field for a glyphosate tolerant plant, comprising applying an effective dose of a sulfonylurea herbicide to a field for planting a glyphosate tolerant plant, the glyphosate tolerant plant containing the herbicide tolerant gene or the expression cassette.

In order to achieve the above objective, the present invention also provides a method for imparting sulfonylurea herbicide tolerance to a plant, comprising introducing the herbicide tolerant gene, the expression cassette or the recombinant vector into the plant.

In order to achieve the above objective, the present invention also provides a method for producing a sulfonylurea herbicide tolerant plant, comprising introducing the herbicide tolerant gene, the expression cassette or the recombinant vector into the genome of the plant.

In order to achieve the above objective, the present invention also provides a method for cultivating a sulfonylurea herbicide tolerant plant, comprising:

- planting at least one plant propagule, whose genome contains the herbicide tolerant gene or the expression cassette;
- allowing the plant propagule to grow into a plant;
- applying an effective dose of a sulfonylurea herbicide to a plant growth environment comprising at least the plant, and harvesting the plant which has reduced plant damage and/or an increased plant yield compared to other plants which do not contain the herbicide tolerant gene or the expression cassette.

Further, the plant is a monocotyledonous plant or a dicotyledonous plant.

Preferably, the plant is maize, soybean, *Arabidopsis thaliana*, cotton, rape, rice, sorghum, wheat, barley, millet, sugar cane or oat.

On the basis of the above-mentioned technical solution, the sulfonylurea herbicide is tribenuron-methyl, sulfometuron-methyl, halosulfuron-methyl, pyrazosulfuron-ethyl, thifensulfuron methyl, bensulfuron-methyl, metsulfuron-methyl, ethametsulfuron-methyl or chlorimuron-ethyl.

In order to achieve the above objective, the present invention also provides a planting system for controlling weed growth, comprising a sulfonylurea herbicide and a plant growth environment in which at least one target plant exists, wherein the plant contains the herbicide tolerant gene or the expression cassette.

In order to achieve the above objective, the present invention also provides a planting system for controlling glyphosate resistant weeds in a field of a glyphosate tolerant plant, comprising a sulfonylurea herbicide, a glyphosate herbicide and a field for planting at least one glyphosate tolerant plant, wherein the glyphosate tolerant plant contains the herbicide tolerant gene or the expression cassette.

Further, the plant is a monocotyledonous plant or a 20 dicotyledonous plant.

Preferably, the plant is maize, soybean, *Arabidopsis thaliana*, cotton, rape, rice, sorghum, wheat, barley, millet, sugar cane or oat.

On the basis of the above-mentioned technical solution, the sulfonylurea herbicide is tribenuron-methyl, sulfometuron-methyl, halosulfuron-methyl, pyrazosulfuron-ethyl, thifensulfuron methyl, bensulfuron-methyl, metsulfuron-methyl, ethametsulfuron-methyl or chlorimuron-ethyl.

In order to achieve the above objective, the present invention also provides use of a herbicide tolerant protein for degrading sulfonylurea herbicides, wherein the herbicide tolerant protein comprises:

- (1) a protein consisting of an amino acid sequence as shown in SEQ ID NO: 1, and at least having an alanine substitution at position 176 and/or a valine substitution at position 178 of SEQ ID NO: 1; or
- (2) a protein consisting of an amino acid sequence as shown in SEQ ID NO: 19, and at least having an alanine substitution at position 140 and/or a valine substitution at position 142 of SEQ ID NO: 19; or
- (3) a protein consisting of an amino acid sequence as shown in SEQ ID NO: 35, and at least having an alanine substitution at position 140 and/or a valine substitution at position 142 of SEQ ID NO: 35; or
- (4) a protein consisting of an amino acid sequence as shown in SEQ ID NO: 51, and at least having an alanine substitution at position 131 and/or a valine substitution at position 133 of SEQ ID NO: 51; or
- (5) a protein which is derived from (1) to (4) by substituting and/or deleting and/or adding one or more amino acids in the amino acid sequences of (1) to (4), and has thifensulfuron hydrolase activity.

Furthermore, said herbicide tolerant protein comprises:

- (6) an amino acid sequence of (1), wherein the amino acid sequence of (1) has an arginine substitution at position 80 and/or an alanine substitution at position 81 and/or an arginine substitution at position 182 of SEQ ID NO: 1; or
- (7) an amino acid sequence of (2), wherein the amino acid sequence of (2) has an arginine substitution at position 44 and/or an alanine substitution at position 45 and/or an arginine substitution at position 146 of SEQ ID NO: 19; or
- (8) an amino acid sequence of (3), wherein the amino acid sequence of (3) has an arginine substitution at position

44 and/or an alanine substitution at position 45 and/or an arginine substitution at position 146 of SEQ ID NO: 35; or

- (9) an amino acid sequence of (4), wherein the amino acid sequence of (4) has an arginine substitution at position 35 and/or an alanine substitution at position 131 and/or a valine substitution at position 133 of SEQ ID NO: 51; or
- (10) a protein which is derived from (6) to (9) by substituting and/or deleting and/or adding one or more amino acids in the amino acid sequences of (6) to (9), and has thifensulfuron hydrolase activity.

Furthermore, the herbicide tolerant protein comprises:

- (11) a protein consisting of an amino acid sequence as shown in SEQ ID NO: 7, SEQ ID NO: 11 or SEQ ID NO: 15; or
- (12) a protein consisting of an amino acid sequence as shown in SEQ ID NO: 23, SEQ ID NO: 27 or SEQ ID NO: 31; or
- (13) a protein consisting of an amino acid sequence as shown in SEQ ID NO: 39, SEQ ID NO: 43 or SEQ ID NO: 47; or
- (14) a protein consisting of an amino acid sequence as shown in SEQ ID NO: 55, SEQ ID NO: 59 or SEQ ID NO: 63.

Preferably, the sulfonylurea herbicide is tribenuron-methyl, sulfometuron methyl, halosulfuron-methyl, pyrazosulfuron-ethyl, thifensulfuron-methyl, bensulfuron-methyl, metsulfuron-methyl, ethametsulfuron-methyl or chlorimuron ethyl.

The sulfometuron-methyl in the present invention refers to methyl 2-(4,6-dimethylpyrimidin-2-ylcarbamoylamino-sulfonyl)benzoate as a white solid. Commonly used dosage forms are 10% sulfometuron-methyl wettable powder and 35% sulfometuron-methyl suspension (also known as dry suspension). Commercial formulations of sulfometuron-methyl include, but are not limited to, Oust and Sencaojing.

The effective dose of sulfometuron-methyl according to the present invention is 9 to 120 g ai/ha, including 10-100 g ai/ha, 15-90 g ai/ha, 20-80 g ai/ha, 25-70 g ai/ha, 30-60 g ai/ha or 40-50 g ai/ha.

The tribenuron-methyl in the present invention refers to methyl 2-[N-(4-methoxy-6-methyl-1,3,5-triazin-2-yl)-N-methylcarbamoylamino]sulfonyl]benzoate as a white solid. 45 Commonly used dosage forms are 10% tribenuron-methyl wettable powder, and 75% tribenuron-methyl suspension (also known as dry suspension). Commercial formulations of tribenuron-methyl include, but are not limited to, GRAN-STAR and kuoyejing.

The effective dose of tribenuron-methyl according to the present invention is 9 to 144 g ai/ha, including 15-120 g ai/ha, 30-110 g ai/ha, 40-100 g ai/ha, 50-90 g ai/ha, 60-80 g ai/ha or 65-75 g ai/ha.

The herbicide tolerant gene, the expression cassette or the 55 recombinant vector according to the present invention is introduced into a plant. In order to introduce the exogenous DNA into plant cells in the present invention, the conventional transformation methods include, but are not limited to, the *Agrobacterium*-mediated transformation, microprojectile bombardment, the direct DNA uptake into the protoplast, electroporation or silicon whisker-mediated DNA introduction.

The herbicide tolerant gene and the subsequent herbicide 60 resistant crop according to the present invention provide an excellent choice for controlling glyphosate-resistant (or highly tolerant and successive) broad-leaved weed species in the crop. The sulfonylurea herbicides have a broad spectrum

and are potent herbicides for broad-leaved weeds, and would provide excellent utility for planters if the stronger crop tolerance could be provided in both dicotyledons and monocotyledons alike. A transgenic dicotyledonous plant with a tolerance to sulfonylurea herbicide also has higher flexibilities in the timing and amount of application. Another use of the sulfonylurea herbicide resistant trait is that it can be used for preventing normally sensitive crops from damage caused by the drifting, volatilization, conversion (or other movement over a long distance), misuse, destruction, etc., of the sulfonylurea herbicides. The use of the herbicide tolerant gene according to the present invention in a plant can provide protection against a broader spectrum of sulfonylurea herbicides, thereby improving the flexibility and spectra of weeds that can be controlled, and can provide protection against damage caused by the drifting of a full range of commercially available sulfonylurea herbicides or caused by other sulfonylurea herbicides over a long distance.

It has now been identified that the herbicide tolerant gene according to the present invention has the characteristic of allowing the use of sulfonylurea herbicides in plants after being genetically modified for the expression in the plants, wherein the absence or lack of inherent tolerance in the plants does not allow the use of these herbicides. In addition, the herbicide tolerant gene of the present invention can provide protection against the sulfonylurea herbicides in plants where the natural tolerance is insufficient for selectivity. At present, the plants containing only the herbicide tolerant gene of the present invention can be treated sequentially or tank-mixed with one, two or a combination of several sulfonylurea herbicides. The application amount of each sulfonylurea herbicide for controlling a broad spectrum of dicotyledonous weeds ranges from 7.5 to 150 g ai/ha, more generally from 20 to 50 g ai/ha. Use of the herbicides of different chemical categories and having different modes and ranges of actions in the same field in combination (sequentially or tank-mixed) can provide control for most potential weeds that need to be controlled by the herbicides.

Glyphosate is widely used, as it controls a very broad spectrum of broad-leaved and gramineous weed species. However, reusing glyphosate in glyphosate tolerant crops and non-crop applications has selected (and still will select) to make weeds evolve into naturally more tolerant species or glyphosate tolerant biotypes. Most herbicide tolerance management strategies suggest using an effective amount of tank-mixed herbicide partners as a means of delaying the emergence of tolerant weeds, wherein the herbicide partners provide control of the same species, but have different modes of action. Stacking the herbicide tolerant gene according to the present invention gene with a glyphosate tolerance trait (and/or another herbicide tolerance trait) can achieve control of glyphosate tolerant weed species (broad-leaved weed species controlled by one or more sulfonylurea herbicides) in glyphosate tolerant crops by allowing selective use of glyphosate and sulfonylurea herbicides in the same crop. The application of these herbicides can be performed by using simultaneously in a tank mixture containing two or more herbicides with different modes of action, or using a single herbicide composition alone in continuous use (e.g., before planting or before or after emergence) (with an interval time range used being from 2 hours to 3 months), or alternatively, can be performed by using a combination of any number of herbicides representative of each applicable compound category at any time (from any time within 7 months after planting a crop to the time when the crop is harvested (or the pre-harvest interval for a single herbicide, with the shortest being taken)).

The flexibility in controlling broad-leaved weeds is very important, i.e., application time, single application amount of herbicide, and abilities to control the stubborn or resistant weeds. The application range of glyphosate stacked with a glyphosate tolerant gene/the herbicide tolerant gene of the present invention in crops can be from 200 to 1600 g ai/ha; and that of (one or more) sulfonylurea herbicides can be from 7.5 to 150 g ai/ha. The optimal combination of time for these applications depends on the specific conditions, species and environments.

A herbicide preparation (e.g., an ester, acid or salt formula or soluble concentrate, emulsifying concentrate or soluble liquid) and a tank mix additive (e.g., an adjuvant or compatilizer) can significantly affect weed control of a given herbicide or a combination of one or more herbicides. Any chemical combination of any of the foregoing herbicides is within the scope of the present invention.

It is well known for a person skilled in the art that the benefits of a combination of two or more modes of action in improving the controlled spectrum of weed and/or naturally more tolerant species or resistant weed species can also be extended to artificial (transgenic or non-transgenic) production of herbicide tolerant chemicals in addition to glyphosate tolerant crops in crops. In fact, the traits encoding the following resistances can be stacked alone or in multiple combinations to provide the ability to effectively control or prevent weeds from developing tolerance to any of the above categories of herbicides: 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS), glyphosate oxidoreductase (GOX), glyphosate-N-acetyltransferase (GAT), glyphosate decarboxylase, glufosinate acetyltransferase (PAT), α -ketoglutarate dependent dioxygenase (AAD), dicamba monooxygenase (DMO), 4-hydroxyphenylpyruvate dioxygenase (HPPD), acetolactate synthase (ALS), cytochrome-like proteins (P450) and/or protoporphyrinogen oxidase (Protox).

In addition, the herbicide tolerant gene of the present invention alone or the herbicide tolerant gene of the present invention stacked with other characteristics of herbicide tolerant crops can be stacked with one or more other input traits (for example, insect tolerance, fungal tolerance or stress tolerance) or output traits (for example, increased yield, improved oil amount or increased fiber quality). Therefore, the present invention can be used to provide the abilities to flexibly and economically control any number of agricultural pests and complete agricultural solutions for improving qualities of crops.

The herbicide tolerant gene of the present invention can degrade a sulfonylurea herbicide, and is an important basis of herbicide tolerant crops and the possibility for selecting marker features.

Transgenic expression can be performed in the present invention, and almost all combinations of herbicides for broad-leaved weeds can be controlled. The herbicide tolerant gene of the present invention as an excellent trait of herbicide tolerant crops can be stacked with, for example, other traits of herbicide tolerant crops (for example, glyphosate tolerance, glufosinate tolerance, tolerance to other ALS inhibitor (for example, imidazolinones and triazolopyrimidinyl sulfonamides), bromoxynil tolerance, HPPD inhibitor tolerance, PPO inhibitor tolerance, and the like) and traits of insect tolerance (Cry1Ab, Cry1F, Vip3, other *Bacillus thuringiensis* proteins or insect tolerant proteins derived from non-bacillus bacterial species, etc.). In addition, the herbicide tolerant gene of the present invention can be used as a

selective marker for the assistant selection of primary transformants of plants genetically modified with another gene or gene group.

The traits of herbicide tolerant crops of the present invention can be used in a new combination with other traits (including but not limited to glyphosate tolerance) of herbicide tolerant crops. A new method for controlling the weed species can be produced by the combination of these traits due to newly obtained tolerance or inherent tolerance to a herbicide (for example, glyphosate). Therefore, apart from the traits of herbicide tolerant crops, the scope of the present invention includes the new method for controlling weeds with herbicides, wherein the tolerance to the herbicides can be produced by the enzyme in the transgenic crops.

The present invention can be applied to various types of plants, and the dicotyledonous plant includes, but is not limited to, alfalfa, beans, cauliflowers, cabbages, carrots, celery, cotton, cucumbers, eggplants, lettuces, melon, peas, peppers, zucchinis, radishes, rape, spinach, soybeans, pumpkins, tomatoes, *Arabidopsis thaliana* or watermelons; preferably, the dicotyledonous plant refers to soybeans, *Arabidopsis thaliana*, tobacco, cotton or rape. The monocotyledonous plant includes, but is not limited to, maize, rice, sorghum, wheat, barley, rye, millet, sugar cane, oats or turfgrass; preferably, the monocotyledonous plant refers to maize, rice, sorghum, wheat, barley, millet, sugar cane or oats. The herbicide tolerant gene according to the present invention can be more positively used in gramineous crops with moderate tolerance, and thus the improved tolerance obtained by such traits can provide planters with the possibility of using these herbicides with a more effective application amount and a broader application time without crop damage risks.

The planting system in the present invention refers to a combination of a plant and any herbicide tolerance thereof and/or an available herbicide treatment in different plant developmental stages, thus producing plants with high yields and/or reduced damage.

In the present invention, the weeds refer to plants competing with the cultivated target plants in the plant growth environment.

The term "control" and/or "prevention" in the present invention refers to at least a direct application (e.g., by spraying) of an effective dose of a sulfonylurea herbicide to the plant growth environment, so as to minimize weed development and/or stop weeds from growing. At the same time, the cultivated target plants should be morphologically normal and can be cultivated under conventional methods for product consumption and/or production; and preferably, compared to non-transgenic wild-type plants, the cultivated plants have reduced plant damage and/or an increased plant yield. The specific performances of the reduced plant damage include, but are not limited to, an improved stem resistance and/or an increased grain weight. The "control" and/or "prevention" effect of the herbicide tolerant protein of the present invention on weeds can exist independently, and will not be diminished and/or lost due to the presence of other substances that can "control" and/or "prevent" the weeds. Specifically, if any tissue of a transgenic plant (containing the herbicide tolerant gene of the present invention) has and/or produces the herbicide tolerant protein of the present invention and/or another substance that can control weeds simultaneously and/or separately, then the presence of the other substance will neither affect the "control" and/or "prevention" effect of the herbicide tolerant protein of the present invention on the weeds, nor result in that the "control" and/or "prevention" effect is achieved

completely and/or partially by the other substance and has nothing to do with the herbicide tolerant protein of the present invention.

The genome of a plant, plant tissue or plant cell in the present invention refers to any genetic material within the plant, plant tissue or plant cell, and includes cell nuclear, plastid and mitochondrial genome.

The "plant propagule" in the present invention includes, but is not limited to, plant sexual propagules and plant vegetative propagules. The plant sexual propagules include, but are not limited to, plant seeds; and the plant vegetative propagules refer to vegetative organs or a specific tissue of a plant, which can generate a new plant under ex vivo conditions. The vegetative organs or the specific tissue include, but are not limited to, roots, stems and leaves; for example, plants with roots as the vegetative propagules include strawberries, sweet potatoes and the like; plants with stems as the vegetative propagules include sugar cane, potatoes (tubers) and the like; and plants with leaves as the vegetative propagules include aloe, begonias and the like.

The "resistance" in the present invention is heritable, and allows a plant to grow and propagate in the case where an effective treatment by a general herbicide is performed on a given plant. As recognized by a person skilled in the art, even if a certain damage degree of a plant treated with a herbicide is apparent, the plant can still be considered "resistant". The term "tolerance" in the present invention is more extensive than the term "resistance", and includes "resistance" and an improved ability of a particular plant to resist various degrees of damage induced by a herbicide, and generally, damages to a wild-type plant with the same genotype can be caused at the same herbicide dose.

The polynucleotide and/or nucleotide in the present invention form a complete "gene", which encodes a protein or a polypeptide in a desired host cell. A person skilled in the art will readily appreciate that the polynucleotide and/or nucleotide in the present invention can be placed under the control of a regulatory sequence in a host of interest.

As is well known to a person skilled in the art, DNA is typically present in a double-stranded form. In this arrangement, one strand is complementary to the other, and vice versa. Additional complementary strand of DNA is produced as DNA is replicated in a plant. As such, the present invention includes the use of the polynucleotides as exemplified in the sequence listing and complementary strands thereof. The "coding strand" commonly used in the art refers to a strand bound to an antisense strand. In order to express a protein in vivo, one strand of DNA is typically transcribed to one complementary strand of mRNA, which acts as a template for translating the protein. Actually, mRNA is transcribed from the "antisense" strand of DNA. The "sense" or "coding" strand has a series of codons (a codon is composed of three nucleotides, and a specific amino acid can be produced by reading three codons at a time), which can be read as an open reading frame (ORF) to form a protein or peptide of interest. The present invention also includes RNA having an equivalent function to the exemplary DNA.

The nucleic acid molecule or a fragment thereof in the present invention hybridizes with the herbicide tolerant gene of the present invention under stringent conditions. Any conventional nucleic acid hybridization or amplification method can be used to identify the presence of the herbicide tolerant gene of the present invention. A nucleic acid molecule or a fragment thereof is capable of specifically hybridizing with other nucleic acid molecules under certain circumstances. In the present invention, if two nucleic acid

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molecules can form an anti-parallel double stranded nucleic acid structure, then it can be considered that these two nucleic acid molecules can be specifically hybridized with each other. If two nucleic acid molecules exhibit a complete complementarity, then one nucleic acid molecule of the two is said to be the "complement" of the other nucleic acid molecule. In the present invention, when each nucleotide of a nucleic acid molecule is complementary to the corresponding nucleotide of another nucleic acid molecule, then these two nucleic acid molecules are said to exhibit a "complete complementarity". If two nucleic acid molecules can be hybridized with each other with a sufficient stability such that they are annealed and bound to each other at least under conventional "low stringency" conditions, then these two nucleic acid molecules are said to be "minimally complementary". Similarly, if two nucleic acid molecules can be hybridized with each other with a sufficient stability such that they are annealed and bound to each other under conventional "high stringency" conditions, then these two nucleic acid molecules are said to be "complementary". Deviation from a complete complementarity is permissible, as long as this deviation does not completely prevent two molecules from forming a double-stranded structure. In order to enable a nucleic acid molecule to act as a primer or probe, it is only necessary to ensure that the nucleic acid molecule has a sufficient complementarity in its sequence to allow a stable double-stranded structure to be formed in case of the particular solvent and salt concentration used.

In the present invention, a substantially homologous sequence is a nucleic acid molecule, wherein the nucleic acid molecule can be specifically hybridized with the complementary strand of a matched nucleic acid molecule under high stringency conditions. Suitable stringent conditions that promote DNA hybridization are well known to a person skilled in the art; for example, the suitable stringent conditions can be achieved by treating with 6.0 \times sodium chloride/sodium citrate (SSC) under conditions of approximately 45°, and then washing with 2.0 \times SSC under conditions of 50°. For example, the salt concentration in the washing step can be selected from the low stringency condition of about 2.0 \times SSC and 50° C. to the high stringency condition of about 0.2 \times SSC and 50° C. In addition, the temperature condition in the washing step can rise from the low stringency condition of room temperature (about 22° C.) to the high stringency condition of about 65° C. The temperature condition and the salt concentration can both vary, and it is also possible that one of the two remains unchanged, while the other variable varies. Preferably, the stringent conditions in the present invention can be achieved by specifically hybridizing a sequence with the herbicide tolerant gene in the present invention in a 6 \times SSC, 0.5% SDS solution at 65° C., and then washing the membrane once with 2 \times SSC, 0.1% SDS and once with 1 \times SSC, 0.1% SDS.

Consequently, sequences which have the herbicide tolerant activity and are hybridized with the herbicide tolerant gene of the present invention under stringent conditions are included in the present invention. These sequences are at least approximately 40%-50% homologous, or approximately 60%, 65% or 70% homologous, or even at least approximately 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more to the sequence of the present invention.

The present invention provides a functional protein. In the present invention, the "functional activity" (or "activity") means that the protein/enzyme used in the present invention (alone or in combination with other proteins) has the ability to degrade a sulfonylurea herbicide or diminish the activity

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of a sulfonylurea herbicide. A plant producing the herbicide tolerant protein of the present invention preferably produces an "effective amount" of the protein, so that when the plant is treated with a herbicide, the protein expression level is sufficient to impart to the plant a complete or partial resistance or tolerance to the sulfonylurea herbicide (unless otherwise specified, in a general amount). The herbicide can be used in an amount which would usually kill a target plant or in a normal field amount and concentration. Preferably, the plant cell and plant of the present invention are protected from growth inhibition or damage caused by treatment with the herbicide. The transformed plant and plant cell of the present invention preferably has tolerance or resistance to sulfonylurea herbicides; that is, the transformed plant and plant cell can grow in the presence of an effective amount of sulfonylurea herbicides.

The gene and protein in the present invention not only comprise a specific exemplary sequence, but also comprise a portion and/or a fragment (including an internal deletion and/or terminal deletion compared to the full-length protein), a variant, a mutant, a substitute (a protein having substituted amino acids), a chimera and a fusion protein, which retain the herbicide tolerance activity characteristic of the specific exemplary protein. The "variant" or "variation" refers to a nucleotide sequence that encodes the same protein or encodes an equivalent protein having a herbicide resistance activity. The "equivalent protein" refers to a protein having the same or substantially the same bioactivity of herbicide tolerance as the claimed protein.

The "fragment" or "truncation" of a DNA molecule or protein sequence in the present invention refers to a portion of the original DNA or protein sequence (nucleotides or amino acids) or an artificially modified form thereof (e.g., a sequence suitable for plant expression), wherein the length of the foregoing sequences may vary, but the length is sufficient to ensure that the (encoded) protein is a herbicide tolerant protein.

Because of the degeneracy of the genetic codon, a variety of different DNA sequences may encode the same amino acid sequence. It is within the skill of a person skilled in the art to produce these alternative DNA sequences encoding the same or substantially the same protein. These different DNA sequences are included in the scope of the present invention. The aforementioned "substantially the same" sequence refers to a sequence with an amino acid substitution, deletion, addition or insertion that does not substantively affect the herbicide tolerance activity, and includes a fragment retaining the herbicide tolerance activity.

The substitution, deletion or addition of an amino acid sequence in the present invention is a conventional technique in the art. Preferably, this amino acid change is a small characteristic change, that is, a conservative amino acid substitution that does not significantly affect the folding and/or activity of a protein; a small deletion, typically a deletion of about 1-30 amino acids; a small amino or carboxyl terminal extension, e.g., a methionine residue extending at the amino terminus; or a small linker peptide, e.g., about 20-25 residues in length.

Examples of conservative substitutions are substitutions occurring within the following amino acid groups: basic amino acids (e.g., arginine, lysine and histidine), acidic amino acids (e.g., glutamic acid and aspartic acid), polar amino acids (e.g., glutamine and asparagine), hydrophobic amino acids (e.g., leucine, isoleucine and valine), aromatic amino acids (e.g., phenylalanine, tryptophan and tyrosine) and small molecule amino acids (e.g., glycine, alanine, serine, threonine and methionine). Those amino acid sub-

stitutions that generally do not alter the specific activity are well known in the art, and have been described by, for example, N. Neurath and R. L. Hill in *Protein*, published by Academic Press in New York in 1979. The most common substitutions are Ala/Ser, Val/Ile, Asp/Glu, Thu/Ser, Ala/Thr, Ser/Asn, Ala/Val, Ser/Gly, Tyr/Phe, Ala/Pro, Lys/Arg, Asp/Asn, Leu/Ile, Leu/Val, Ala/Glu and Asp/Gly, as well as the reverse substitutions thereof.

As will be apparent to a person skilled in the art, this substitution can occur outside the region that is important for molecular functions, and still produces an active polypeptide. Amino acid residues that are essential for the activity of the polypeptide of the present invention and are thus chosen not to be substituted can be identified according to methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (see e.g., Cunningham and Wells, 1989, *Science* 244: 1081-1085). The latter technique is to introduce a mutation at each positively charged residue in a molecule and detect the herbicide resistance activity of the resulting mutant molecule to determine the amino acid residues that are important for the molecular activity. Substrate-enzyme interaction sites can also be determined by analyzing the three-dimensional structure thereof, wherein this three-dimensional structure can be determined by nuclear magnetic resonance analysis, crystallography, photoaffinity labeling and other techniques (see e.g., de Vos et al., 1992, *Science* 255: 306-312; Smith et al., 1992, *J. Mol. Biol.* 224: 899-904; and Wlodaver et al., 1992, *FEBS Letters* 309: 59-64).

The regulatory sequence in the present invention includes, but is not limited to, a promoter, a transit peptide, a terminator, an enhancer, a leader sequence, an intron and other regulatory sequences operably linked to the herbicide tolerant gene of the present invention.

The promoter is a plant expressible promoter. The "plant expressible promoter" refers to a promoter that ensures the expression of the coding sequence linked thereto in a plant cell. The plant expressible promoter can be a constitutive promoter. Examples of the promoters directing the constitutive expression in plants include, but are not limited to, a 35S promoter derived from a cauliflower mosaic virus, maize Ubi promoters, rice GOS2 gene promoters, and the like. Alternatively, the plant expressible promoter can be a tissue specific promoter; i.e. the promoter directs the expression of a coding sequence in several tissues, such as green tissues, at a level higher than in other tissues of the plant (which can be measured through conventional RNA trials), such as a PEP carboxylase promoter. Alternatively, the plant expressible promoter can be a wound-inducible promoter. The wound-inducible promoter or a promoter directing a wound-induced expression pattern means that when a plant suffers from a wound caused by a mechanical factor or the gnawing of insects, the expression of the coding sequence under the regulation of the promoter is significantly improved compared to normal growth conditions. Examples of the wound-inducible promoters include, but are not limited to, promoters of potato and tomato protease inhibitor genes (pin I and pin II) and a maize protease inhibitor gene (MPI).

The transit peptide (also known as secretion signal sequence or targeting sequence) directs a transgenic product to a specific organelle or cell compartment. For a receptor protein, the transit peptide may be heterologous, for example, targeting the chloroplast using a sequence encoding the chloroplast transit peptide, or targeting the endoplasmic reticulum using a 'KDEL' retention sequence, or targeting the vacuole using CTPP of a barley phytolectin gene.

The leader sequence includes, but is not limited to, a small RNA virus leader sequence, such as an EMCV leader sequence (a 5' non-coding region of encephalomyocarditis virus); a potato virus Y group leader sequence, such as a MDMV (Maize Dwarf Mosaic Virus) leader sequence; human immunoglobulin heavy chain binding protein (BiP); an untranslated leader sequence of the coat protein mRNA of alfalfa mosaic virus (AMV RNA4); and a tobacco mosaic virus (TMV) leader sequence.

10 The enhancer includes, but is not limited to, a cauliflower mosaic virus (CaMV) enhancer, figwort mosaic virus (FMV) enhancer, carnation etched ring virus (CERV) enhancer, cassava vein mosaic virus (CsVMV) enhancer, mirabilis mosaic virus (MMV) enhancer, cestrum yellow leaf curling virus (CmYLCV) enhancer, cotton leaf curl Multan virus (CLCuMV) enhancer, commelina yellow mottle virus (CoYMV) enhancer and peanut chlorotic streak virus (PCSV) enhancer.

15 For use in a monocotyledonous plant, the intron includes, but is not limited to, a maize hsp70 intron, maize ubiquitin intron, Adh intron 1, sucrose synthase intron or rice Act1 intron. For use in a dicotyledonous plant, the intron includes, but is not limited to, a CAT-1 intron, pKANNIBAL intron, PIV2 intron and "super ubiquitin" intron.

20 25 The terminator can be a suitable polyadenylation signal sequence that functions in a plant, including, but not limited to, a polyadenylation signal sequence derived from the *Agrobacterium tumefaciens* nopaline synthetase (NOS) gene, a polyadenylation signal sequence derived from the protease inhibitor II (pinII) gene, a polyadenylation signal sequence derived from the pea ssRUBISCO E9 gene and a polyadenylation signal sequence derived from the α -tubulin gene.

30 35 The "effective linking" in the present invention indicates the binding of nucleic acid sequences, wherein the binding enables a sequence to provide a function required for the sequence linked thereto. The "effective linking" in the present invention can be achieved by linking a promoter to a sequence of interest, so that the transcription of the 40 sequence of interest is controlled and regulated by the promoter. When a sequence of interest encodes a protein and the expression of the protein is desired, "effective linking" means that a promoter is linked to the sequence in such a manner that the resulting transcript is efficiently translated. 45 If the linking of a promoter to a coding sequence is a transcript fusion and expression of the encoded protein is intended to be achieved, such linking is created that the first translation initiation codon in the resulting transcript is the initiation codon in the coding sequence. Alternatively, if the 50 linking of a promoter to a coding sequence is a translation fusion and expression of the encoded protein is intended to be achieved, such a linking is created that the first translation initiation codon contained in the 5' untranslated sequence is linked to the promoter in such a manner that the relationship 55 of the resulting translation product with the translation open reading frame encoding the desired protein is in-frame. Nucleic acid sequences that can be "effectively linked" include, but are not limited to: sequences providing gene expression functions (i.e., gene expression elements, such as 60 promoters, 5' untranslated regions, introns, protein coding regions, 3' untranslated regions, polyadenylation sites and/or transcription terminators), sequences providing DNA transfer and/or integration functions (i.e., T-DNA boundary sequences, site-specific recombinase recognition sites and integrase recognition sites), sequences providing selective 65 functions (i.e., antibiotic resistance markers and biosynthesis genes), sequences providing marker scoring functions,

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sequences assisting in sequence manipulation in vitro or in vivo (i.e., polylinker sequences and site-specific recombination sequences) and sequences providing replication functions (i.e., bacterial origins of replication, autonomously replicating sequences and centromeric sequences).

The present invention may impart a new herbicide resistance trait to a plant, and no adverse effects on phenotypes (including yields) are observed. The plant in the present invention can tolerate, e.g., 2x, 3x, 4x or 8x the general application level of at least one herbicide tested. The improvement of these levels of tolerance is within the scope of the present invention. For example, foreseeable optimization and further development can be performed on various techniques known in the art, to increase the expression of a given gene.

The herbicide tolerant protein of the present invention can be a protein consisting of an amino acid sequence shown in SEQ ID NO: 1 and at least having an alanine substitution at position 176 and/or a valine substitution at position 178 of SEQ ID NO: 1, with an example shown in SEQ ID NO: 7, SEQ ID NO: 11 or SEQ ID NO: 15 in the sequence listing. The herbicide tolerant gene of the present invention can be a coding gene of the above-mentioned herbicide tolerant protein, with examples shown in SEQ ID NOS: 8-10, SEQ ID NOS: 12-14 and SEQ ID NOS: 16-18 in the sequence listing.

The herbicide tolerant protein of the present invention can be a protein consisting of an amino acid sequence shown in SEQ ID NO: 19 and at least having an alanine substitution at position 140 and/or a valine substitution at position 142 of SEQ ID NO: 19, with an example shown in SEQ ID NO: 23, SEQ ID NO: 27 or SEQ ID NO: 31 in the sequence listing. The herbicide tolerant gene of the present invention can be a coding gene of the above-mentioned herbicide tolerant protein, with examples shown in SEQ ID NOS: 24-26, SEQ ID NOS: 28-30 and SEQ ID NOS: 32-34 in the sequence listing.

The herbicide tolerant protein of the present invention can be a protein consisting of an amino acid sequence shown in SEQ ID NO: 35 and at least having an alanine substitution at position 140 and/or a valine substitution at position 142 of SEQ ID NO: 35, with an example shown in SEQ ID NO: 39, SEQ ID NO: 43 or SEQ ID NO: 47 in the sequence listing. The herbicide tolerant gene of the present invention can be a coding gene of the above-mentioned herbicide tolerant protein, with examples shown in SEQ ID NOS: 40-42, SEQ ID NOS: 44-46 and SEQ ID NOS: 48-50 in the sequence listing.

The herbicide tolerant protein of the present invention can be a protein consisting of an amino acid sequence shown in SEQ ID NO: 51 and at least having an alanine substitution at position 131 and/or a valine substitution at position 133 of SEQ ID NO: 51, with an example shown in SEQ ID NO: 55, SEQ ID NO: 59 or SEQ ID NO: 63 in the sequence listing. The herbicide tolerant gene of the present invention can be a coding gene of the above-mentioned herbicide tolerant protein, with examples shown in SEQ ID NOS: 56-58, SEQ ID NOS: 60-62 and SEQ ID NOS: 64-66 in the sequence listing.

The herbicide tolerant gene of the present invention can be used in plants; and can contain, apart from a coding region of the herbicide tolerant gene of the present invention, other elements such as a coding region encoding a transit peptide, and a coding region encoding a selective marker protein or a protein imparting insect resistance.

The herbicide tolerant protein of the present invention has tolerance to most of the sulfonylurea herbicides. The plant in

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the present invention contains an exogenous DNA in its genome, wherein the exogenous DNA comprises the herbicide tolerant gene of the present invention, and the plant is protected from the threat of a sulfonylurea herbicide by expressing an effective amount of the protein. The effective amount refers to a dose causing no or minor damage. At the same time, the plant should be morphologically normal and can be cultivated under conventional methods for product consumption and/or production.

The expression level of the herbicide tolerant protein in a plant material can be detected by a variety of methods described in the art, for example, by quantifying the mRNA encoding the herbicide tolerant protein produced in a tissue by employing specific primers, or specifically detecting the amount of the produced herbicide tolerant protein directly.

The present invention provides a herbicide tolerant protein, a coding gene thereof and a use thereof, having the following advantages:

1. The herbicide tolerant protein of the present invention has a strong tolerance to sulfonylurea herbicides and can tolerate eight-fold field concentration of tribenuron-methyl.
2. The herbicide tolerant protein of the present invention has a broad prospect of application in plants.

The technical solution of the present invention is further described in details through the figures and examples below.

DESCRIPTION OF THE FIGURES

FIG. 1 is a construction flow chart of a recombinant cloning vector DBN01-T containing an ALT02M1-01 nucleotide sequence for the herbicide tolerant protein, the coding gene thereof and a use thereof in the present invention;

FIG. 2 is a construction flow chart of a recombinant expression vector DBN100825 containing an ALT02M1-01 nucleotide sequence for the herbicide tolerant protein, the coding gene thereof and a use thereof in the present invention;

FIG. 3 is a schematic structural diagram of a control recombinant expression vector DBN100828N for the herbicide tolerant protein, the coding gene thereof and a use thereof in the present invention;

FIG. 4 is a diagram showing the tolerance of a transgenic soybean T₁ plant to benzenesulfonic acid for the herbicide tolerant protein, the coding gene thereof and a use thereof in the present invention; A: ALT02-01 transgenic soybean plant; B: ALT02M1-01 transgenic soybean plant; C: ALT02M2-01 transgenic soybean plant; D: ALT02M3-01 transgenic soybean plant; E: control soybean plant; F: wild-type soybean plant;

FIG. 5 is a construction flow chart of a recombinant cloning vector DBN02-T containing an ALT02M1-02 nucleotide sequence for the herbicide tolerant protein, the coding gene thereof and a use thereof in the present invention;

FIG. 6 is a construction flow chart of a recombinant expression vector DBN100833 containing an ALT02M1-02 nucleotide sequence for the herbicide tolerant protein, the coding gene thereof and a use thereof in the present invention;

FIG. 7 is a schematic structural diagram of a control recombinant expression vector DBN100830N for the herbicide tolerant protein, the coding gene thereof and a use thereof in the present invention; and

FIG. 8 is a diagram showing the tolerance of a transgenic maize T₁ plant to benzenesulfonic acid for the herbicide

tolerant protein, the coding gene thereof and a use thereof in the present invention; A: ALT02-02 transgenic maize plant; B: ALT02M1-02 transgenic maize plant; C: ALT02M2-02 transgenic maize plant; D: ALT02M3-02 transgenic maize plant; E: control maize plant; F: wild-type maize plant.

PARTICULAR EMBODIMENTS

The technical solutions of the herbicide tolerant protein, the coding gene thereof and use thereof in the present invention are further described through specific examples below.

Example 1. Mutation and Screening of ALT Gene

1. Synthesis of ALT Gene

The nucleotide sequence (1197 nucleotides) of the ALT01 gene as shown in SEQ ID NO: 2 in the sequence listing was synthesized, which encodes the ALT01 protein (398 amino acids) as shown in SEQ ID NO: 1 in the sequence listing. The nucleotide sequence (SEQ ID NO: 2) of the synthetic ALT01 gene was ligated with a SpeI restriction enzyme site at the 5' end and a KasiI restriction enzyme site at the 3' end. The ALT01-01 nucleotide sequence as shown in SEQ ID NO: 3 in the sequence listing encoding the amino acid sequence corresponding to ALT01 was obtained based on soybean codon usage bias, and the ALT01-02 nucleotide sequence as shown in SEQ ID NO: 4 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT01 was obtained based on the maize codon usage bias.

2. Construction of a Mutant Library of ALT01 Gene

The above synthetic ALT01 gene was amplified by PCR, and then was cloned into the vector pGEM-T according to the operational procedure in the instructions of product pGEM-T vector (Promega, Madison, USA, CAT: A3600) of Promega Corporation. Then, the above ligated product was introduced into *Escherichia coli* DH5 α as a template to carry out error-prone PCR using primer 1 and primer 2, so that the ALT01 gene was mutated due to random base mismatch. The primers and error-prone PCR reaction system were as follows:

primer 1:
ATGGAAACCGATAAAAAAACCG,
as shown in SEQ ID NO: 5 in the sequence listing;

primer 2:
TCAGCTTCGTTCTGATCTAAG,
as shown in SEQ ID NO: 6 in the sequence listing;

Error-Prone PCR Reaction System (Total Volume: 50 μ L):

2 x StarMut Random System	25 μ L
Plasmid DNA template	1 μ L
Primer 1	1 μ L
Primer 2	1 μ L
StarMut Enhancer	0.20 μ L
Water (ddH ₂ O)	added to 50 μ L

The plasmid DNA template having a concentration of 1-10 ng/ μ L, the primer 1 having a concentration of 10 μ M, and the primer 2 having a concentration of 10 μ M, were stored at 4° C. in an amber tube.

Error-Prone PCR Reaction Conditions:

Step	temperature	time
11	95° C.	2 min
12	94° C.	30 s
13	55° C.	1 min
14	72° C.	1.5 min
15	back to step 12,	30 cycles
16	72° C.	10 min

The above error-prone PCR product was transformed into tribenuron-methyl-sensitive *Escherichia coli* DH10B ilvG⁺ by heat shock at 42° C. to construct a random mutant library of ALT01 gene.

3. Screening of a Mutant Library of ALT01 Gene

The transformed product in the above mutant library was inoculated onto a screening medium (glucose 5 g/L, ampicillin 100 mg/L, valine 200 mg/L, leucine 200 mg/L, (NH₄)₂SO₄ 2 g/L, MgSO₄·7H₂O 200 mg/L, CaCl₂·2H₂O 10 mg/L, FeSO₄·7H₂O 1 mg/L, Na₂HPO₄·12H₂O 1.5 g/L and KH₂PO₄ 1.5 g/L) containing tribenuron-methyl at a concentration of 200 mg/L, and was cultured at a temperature of 37° C. for 24 h.

In view of the ability of a resistance gene to transform tribenuron-methyl to benzenesulfonic acid which is non-toxic to bacteria, the above mutant library was subjected to high-throughput screening using the principle, and *Escherichia coli* DH10B ilvG⁺, which is still able to grow on the screening medium containing tribenuron-methyl at a concentration of 200 mg/L, was isolated to obtain a resistance gene.

4. Acquisition of Mutant Resistance Genes

The sequencing results showed acquisition of three mutant resistance genes of ALT01, which were named ALT01M1, ALT01M2 and ALT01M3 genes respectively. The nucleotide sequence of ALT01M1 was mutated at position 527 from G to C, resulting in mutation from glycine to alanine at position 176 of the amino acid sequence of ALT01M1; the nucleotide sequence of ALT01M2 was mutated at positions 532 and 533 from TC to GT, resulting in mutation from serine to valine at position 178 of the amino acid sequence of ALT01M2; the nucleotide sequence of ALT01M3 was mutated at positions 239 to 242 from CATA to GAGC, and at positions 527 to 544 from GAAACTCCAGTAAAGAAG to CAAACGTCAGTAAAGAAA, resulting in mutation from proline and tyrosine to arginine and alanine at positions 80 to 81 and mutation from glycine, serine and glycine to alanine, valine and arginine at positions 176, 178 and 182 of the amino acid sequence of ALT01M3.

The amino acid sequence of the herbicide tolerant protein ALT01M1 is shown in SEQ ID NO: 7 in the sequence listing, and the ALT01M1 nucleotide sequence which encodes the amino acid sequence of the herbicide tolerant protein ALT01M1 is shown in SEQ ID NO: 8 in the sequence listing; the ALT01M1-01 nucleotide sequence as shown in SEQ ID NO: 9 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT01M1 was obtained based on the soybean codon usage bias; the ALT01M1-02 nucleotide sequence as shown in SEQ ID NO: 10 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT01M1 was obtained based on the maize codon usage bias.

The amino acid sequence of the herbicide tolerant protein ALT01M2 is shown in SEQ ID NO: 11 in the sequence listing, and the ALT01M2 nucleotide sequence which encodes the amino acid sequence of the herbicide tolerant

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protein ALT01M2 is shown in SEQ ID NO: 12 in the sequence listing; the ALT01M2-01 nucleotide sequence as shown in SEQ ID NO: 13 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT01M2 was obtained based on the soybean codon usage bias; the ALT01M2-02 nucleotide sequence as shown in SEQ ID NO: 14 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT01M2 was obtained based on the maize codon usage bias.

The amino acid sequence of the herbicide tolerant protein ALT01M3 is shown in SEQ ID NO: 15 in the sequence listing, and the ALT01M3 nucleotide sequence which encodes the amino acid sequence of the herbicide tolerant protein ALT01M3 is shown in SEQ ID NO: 16 in the sequence listing; the ALT01M3-01 nucleotide sequence as shown in SEQ ID NO: 17 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT01M3 was obtained based on the soybean codon usage bias; the ALT01M3-02 nucleotide sequence as shown in SEQ ID NO: 18 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT01M3 was obtained based on the maize codon usage bias.

Synthesis of the Following Nucleotide Sequences:

The amino acid sequence (369 amino acids) of ALT02 is shown in SEQ ID NO: 19 in the sequence listing, and the ALT02 nucleotide sequence (1110 nucleotides) which encodes the amino acid sequence of ALT02 is shown in SEQ ID NO: 20 in the sequence listing; the ALT02-01 nucleotide sequence as shown in SEQ ID NO: 21 in the sequence listing encoding the amino acid sequence corresponding to the ALT02 was obtained based on the soybean codon usage bias; the ALT02-02 nucleotide sequence as shown in SEQ ID NO: 22 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT02 was obtained based on the maize codon usage bias.

The herbicide tolerant protein ALT02M1 includes a mutation from glycine to alanine at position 140 of the amino acid sequence of the ALT02. The amino acid sequence of ALT02M1 is shown in SEQ ID NO: 23 in the sequence listing, and the ALT02M1 nucleotide sequence which encodes the amino acid sequence of the herbicide tolerant protein ALT02M1 is shown in SEQ ID NO: 24 in the sequence listing; the ALT02M1-01 nucleotide sequence as shown in SEQ ID NO: 25 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT02M1 was obtained based on the soybean codon usage bias; the ALT02M1-02 nucleotide sequence as shown in SEQ ID NO: 26 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT02M1 was obtained based on the maize codon usage bias.

The herbicide tolerant protein ALT02M2 includes a mutation from serine to valine at position 142 of the amino acid sequence of the ALT02. The amino acid sequence of the ALT02M2 is shown in SEQ ID NO: 27 in the sequence listing, and the ALT02M2 nucleotide sequence which encodes the amino acid sequence of the herbicide tolerant protein ALT02M2 is shown in SEQ ID NO: 28; the ALT02M2-01 nucleotide sequence as shown in SEQ ID NO: 29 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT02M2 was obtained based on the soybean codon usage bias; the ALT02M2-02 nucleotide sequence as shown in SEQ ID NO: 30 in the sequence listing encoding the amino acid sequence

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corresponding to the herbicide tolerant protein ALT02M2 was obtained based on the maize codon usage bias.

The herbicide tolerant protein ALT02M3 includes mutations from proline and tyrosine to arginine and alanine at positions 44 to 45 and mutations from glycine, serine and glycine to alanine, valine and arginine at positions 140, 142 and 146 of the amino acid sequence of the ALT02. The amino acid sequence of the ALT02M3 is shown in SEQ ID NO: 31 in the sequence listing, and the ALT02M3 nucleotide sequence which encodes the amino acid sequence of the herbicide tolerant protein ALT02M3 is shown in SEQ ID NO: 32 in the sequence listing; the ALT02M3-01 nucleotide sequence as shown in SEQ ID NO: 33 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT02M3 was obtained based on the soybean codon usage bias; the ALT02M3-02 nucleotide sequence as shown in SEQ ID NO: 34 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT02M3 was obtained based on the maize codon usage bias.

The amino acid sequence (362 amino acids) of ALT03 is shown in SEQ ID NO: 35 in the sequence listing, and the ALT03 nucleotide sequence (1089 nucleotides) which encodes the amino acid sequence of the ALT03 is shown in SEQ ID NO: 36 in the sequence listing; the ALT03-01 nucleotide sequence as shown in SEQ ID NO: 37 in the sequence listing encoding the amino acid sequence corresponding to the ALT03 was obtained based on the soybean codon usage bias; the ALT03-02 nucleotide sequence as shown in SEQ ID NO: 38 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT03 was obtained based on the maize codon usage bias.

The herbicide tolerant protein ALT03M1 includes a mutation from glycine to alanine at position 140 of the amino acid sequence of the ALT03. The amino acid sequence of the ALT03M1 is shown in SEQ ID NO: 39 in the sequence listing, and the ALT03M1 nucleotide sequence which encodes the amino acid sequence of the herbicide tolerant protein ALT03M1 is shown in SEQ ID NO: 40 in the sequence listing; the ALT03M1-01 nucleotide sequence as shown in SEQ ID NO: 41 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT03M1 was obtained based on the soybean codon usage bias; the ALT03M1-02 nucleotide sequence as shown in SEQ ID NO: 42 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT03M1 was obtained based on the maize codon usage bias.

The herbicide tolerant protein ALT03M2 includes a mutation from serine to valine at position 142 of the amino acid sequence of the ALT03. The amino acid sequence of the ALT03M2 is shown in SEQ ID NO: 43 in the sequence listing, and the ALT03M2 nucleotide sequence which encodes the amino acid sequence of the herbicide tolerant protein ALT03M2 is shown in SEQ ID NO: 44 in the sequence listing; the ALT03M2-01 nucleotide sequence as shown in SEQ ID NO: 45 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT03M2 was obtained based on the soybean codon usage bias; the ALT03M2-02 nucleotide sequence as shown in SEQ ID NO: 46 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT03M2 was obtained based on the maize codon usage bias.

The herbicide tolerant protein ALT03M3 includes mutations from proline and tyrosine to arginine and alanine at

positions 44 to 45 and mutations from glycine, serine and glycine to alanine, valine and arginine at positions 140, 142 and 146 of the amino acid sequence of the ALT03. The amino acid sequence of the ALT03M3 is shown in SEQ ID NO: 47 in the sequence listing, and the ALT03M3 nucleotide sequence which encodes the amino acid sequence of the herbicide tolerant protein ALT03M3 is shown in SEQ ID NO: 48 in the sequence listing; the ALT03M3-01 nucleotide sequence as shown in SEQ ID NO: 49 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT03M3 was obtained based on the soybean codon usage bias; the ALT03M3-02 nucleotide sequence as shown in SEQ ID NO: 50 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT03M3 was obtained based on the maize codon usage bias.

The amino acid sequence (350 amino acids) of ALT04 is shown in SEQ ID NO: 51 in the sequence listing, and the ALT04 nucleotide sequence (1053 nucleotides) which encodes the amino acid sequence of the ALT04 is shown in SEQ ID NO: 52 in the sequence listing; the ALT04-01 nucleotide sequence as shown in SEQ ID NO: 53 in the sequence listing encoding the amino acid sequence corresponding to the ALT04 was obtained based on the soybean codon usage bias; the ALT04-02 nucleotide sequence as shown in SEQ ID NO: 54 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT04 was obtained based on the maize codon usage bias.

The herbicide tolerant protein ALT04M1 includes a mutation from glycine to alanine at position 131 of the amino acid sequence of the ALT04. The amino acid sequence of the ALT04M1 is shown in SEQ ID NO: 55 in the sequence listing, and the ALT04M1 nucleotide sequence which encodes the amino acid sequence of the herbicide tolerant protein ALT04M1 is shown in SEQ ID NO: 56 in the sequence listing; the ALT04M1-01 nucleotide sequence as shown in SEQ ID NO: 57 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT04M1 was obtained based on the soybean codon usage bias; the ALT04M1-02 nucleotide sequence as shown in SEQ ID NO: 58 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT04M1 was obtained based on the maize codon usage bias.

The herbicide tolerant protein ALT04M2 includes a mutation from serine to valine at position 133 of the amino acid sequence of the ALT04. The amino acid sequence of the ALT04M2 is shown in SEQ ID NO: 59 in the sequence listing, and the ALT04M2 nucleotide sequence which encodes the amino acid sequence of the herbicide tolerant protein ALT04M2 is shown in SEQ ID NO: 60 in the sequence listing; the ALT04M2-01 nucleotide sequence as shown in SEQ ID NO: 61 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT04M2 was obtained based on the soybean codon usage bias; the ALT04M2-02 nucleotide sequence as shown in SEQ ID NO: 62 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT04M2 was obtained based on the maize codon usage bias.

The herbicide tolerant protein ALT04M3 includes mutations from proline and tyrosine to arginine and alanine at positions 35 to 36 and mutations from glycine, serine and glycine to alanine, valine and arginine at positions 131, 133 and 137 of the amino acid sequence of the ALT04. The amino acid sequence of the ALT04M3 is shown in SEQ ID

NO: 63 in the sequence listing, and the ALT04M3 nucleotide sequence which encodes the amino acid sequence of the herbicide tolerant protein ALT04M3 is shown in SEQ ID NO: 64 in the sequence listing; the ALT04M3-01 nucleotide sequence as shown in SEQ ID NO: 65 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT04M3 was obtained based on the soybean codon usage bias; the ALT04M3-02 nucleotide sequence as shown in SEQ ID NO: 66 in the sequence listing encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT04M3 was obtained based on the maize codon usage bias.

Example 2. Expression and Purification of Protein

1. PCR Amplification of Genes

A pair of primers were designed:

primer 3:
TGCAGACATATGGAAACCGATAAAAAAAC
 (the portion underlined being Nde I restriction enzyme site), as shown in SEQ ID NO: 67 in the sequence listing;

primer 4:
CCCAAGCTTCTAGCTTCTGATCTAAGCCGTGC
 (the portion underlined being Hind III restriction enzyme site), as shown in SEQ ID NO: 68 in the sequence listing;

The ALT01M1 gene (terminal containing Nde I and Hind III restriction enzyme sites) was amplified using the following PCR amplification system:

Taq DNA polymerase (5 U/ μ L)	0.5 μ L
5 \times PrimeSTARBuffer (Mg^{2+} Plus)	25 μ L
dNTP mixture (each 2.5 mM)	5 μ L
Template DNA (M1 gene)	10 ng
Primer 3 (25 μ M)	1 μ L
Primer 4 (25 μ M)	1 μ L
Water (ddH ₂ O)	added to 50 μ L

PCR reaction conditions: denaturation at 98° C. for 1 min; then entering the following cycle: denaturation at 98° C. for 15 s, annealing at 55° C. for 15 s, extension at 72° C. for 1 min, totally including 29 cycles; finally extension at 72° C. for 10 min, and cooling to room temperature.

According to the above PCR amplification method, the ALT01M2 nucleotide sequence, the ALT01M3 nucleotide sequence, the ALT01 nucleotide sequence, the ALT03M1 nucleotide sequence, the ALT03M2 nucleotide sequence, the ALT03M3 nucleotide sequence, ALT04M1 nucleotide sequence, ALT04M2 nucleotide sequence, ALT04M3 nucleotide sequence and ALT04 nucleotide sequence, which contain the Nde I and Hind III restriction enzyme sites at terminals, were amplified. ALT02M1 nucleotide sequence, ALT02M2 nucleotide sequence, ALT02M3 nucleotide sequence, and ALT02 nucleotide sequence (terminals of which contain Nde I and Hind III restriction enzyme sites, respectively) were synthesized.

2. Construction of a Bacterial Expression Vector and Acquisition of Recombinant Microorganisms

The above PCR amplification product (the ALT01M1 nucleotide sequence, the ALT01M2 nucleotide sequence, the ALT01M3 nucleotide sequence, the ALT01 nucleotide sequence, the ALT02M1 nucleotide sequence, the ALT02M2 nucleotide sequence, the ALT02M3 nucleotide

sequence, the ALT02 nucleotide sequence, the ALT03M1 nucleotide sequence, the ALT03M2 nucleotide sequence, the ALT03M3 nucleotide sequence, the ALT03 nucleotide sequence, the ALT04M1 nucleotide sequence, the ALT04M2 nucleotide sequence, the ALT04M3 nucleotide sequence and the ALT04 nucleotide sequence, which contain the Nde I and Hind III restriction enzyme sites at terminals) and a bacterial expression vector pET-30a (+) were digested respectively with restriction enzymes Nde I and Hind III, the excised gene fragments mentioned above were enzymatically linked respectively with the bacterial expression vector pET-30a (+) after enzyme digestion, and the enzymatically linked products were transformed respectively to the expression host strain BL21 (DE3) to obtain the recombinant microorganisms BL21 (ALT01M1), BL21 (ALT01M2), BL21 (ALT01M3), BL21 (ALT01), BL21 (ALT02M1), BL21 (ALT02M2), BL21 (ALT02M3), BL21 (ALT02), BL21 (ALT03M1), BL21 (ALT03M2), BL21 (ALT03M3), BL21 (ALT03), BL21 (ALT04M1), BL21 (ALT04M2), BL21 (ALT04M3), and BL21 (ALT04).

3. Expression and Purification of Herbicide Tolerant Protein in *Escherichia coli*

The recombinant microorganisms BL21 (ALT01M1), BL21 (ALT01M2), BL21 (ALT01M3), BL21 (ALT01), BL21 (ALT02M1), BL21 (ALT02M2), BL21 (ALT02M3), BL21 (ALT02), BL21 (ALT03M1), BL21 (ALT03M2), BL21 (ALT03M3), BL21 (ALT03), BL21 (ALT04M1), BL21 (ALT04M2), BL21 (ALT04M3), and BL21 (ALT04) were cultured in 100 mL of LB medium (10 g/L of tryptone, 5 g/L of yeast extract, 10 g/L of NaCl and 100 mg/L of ampicillin, adjusted to pH 7.5 with NaOH) to a concentration of OD_{600nm}=0.6-0.8, and induced with isopropyl thio-galactoside (IPTG) added at a concentration of 0.4 mM at a temperature of 16° C. for 20 hours. Bacterial cells were collected by centrifugation and resuspended in 20 ml of Tris-HCl buffer (100 mM, pH 8.0), followed by performing ultrasonication (X0-900D ultrasonic processor ultrasonic processor, 30% intensity) for 10 min, then centrifuging, collecting the supernatant, purifying the acquired herbicide tolerant proteins mentioned above with nickel ion affinity chromatography column, and detecting the purification result using SDS-PAGE protein electrophoresis with the band size being consistent with theoretically predicted band size.

Example 3. Determination of Enzymatic Activity of Herbicide Tolerant Protein

Enzymatic reaction system (1 mL) contains 0.2 µg of reactive enzyme (the herbicide tolerant proteins ALT01M1,

ALT01M2, ALT01M3, ALT01, ALT02M1, ALT02M2, ALT02M3, ALT02, ALT03M1, ALT03M2, ALT03M3, ALT03, ALT04M1, ALT04M2, ALT04M3 and ALT04 obtained from the above purification), 0.2 mM of thifensulfuron-methyl (metsulfuron-methyl, chlorimuron-ethyl, benzulfuron-methyl, sulfometuron-methyl or tribenuron-methyl), and a buffer system of phosphate buffer at a concentration of 50 mM (pH 7.0), which were reacted in a water bath at a temperature of 30° C. for 20 min. Each 10 reaction was timed beginning with the addition of reactive enzyme, and was terminated with 1 mL of dichloromethane. The organic phase after delamination was dehydrated with anhydrous sodium sulfate.

The above dehydrated reaction solution was blown dry 15 with nitrogen and filtered by adding 1 mL of methanol, and 20 µL of the filtrate was subjected to liquid chromatography-mass spectrometry (LC-MS). High performance liquid chromatography (HPLC) conditions were as follows: mobile phase being methanol:water (80:20, V/V), Zorbax XDB-20 C18 chromatographic column (3.5 µm, 2.1×50 mm, Agilent, USA), column temperature being room temperature, UV detector, with a detection wavelength of 255 nm, a sample injection volume of 20 µL, and a flow rate of 0.25 mL/min. The primary ion mass spectrometry conditions were as follows: ion detection mode being multi-reactive ion detection; ion polarity being negative ion; ionization mode being electrospray ionization; a capillary voltage of 4000 volts; a dry gas temperature of 330° C., a flow rate of 10 L/min, an atomizing gas pressure of 35 psi, a collision voltage of 135 volts; and a mass scan range of 300-500 m/z. The secondary ion mass spectrometry conditions were as follows: a collision voltage of 90 volts; a mass scanning range of 30-400 m/z, and other conditions being the same as those of the primary ion mass spectrometry. It was identified by LC-MS that the metabolite of thifensulfuron-methyl was thiophene sulfonic acid, and the metabolite of metsulfuron-methyl, chlorimuron-ethyl, benzulfuron-methyl, sulfometuron-methyl or tribenuron-methyl was its corresponding sulfonic acid. The amount of the generated thiophene sulfonic acid (metabolite) was detected using high performance liquid chromatography (HPLC). An enzyme activity unit was defined as the amount of enzyme required for catalyzing the degradation of thifensulfuron-methyl (metsulfuron-methyl, chlorimuron-ethyl, benzulfuron-methyl, sulfometuron-methyl or tribenuron-methyl) at pH 7.0, at a temperature of 40 30° C. within 1 min to decrease 1 µmol of thifensulfuron-methyl (metsulfuron-methyl, chlorimuron-ethyl, benzulfuron-methyl, sulfometuron-methyl or tribenuron-methyl), which is expressed as U. Experimental results were shown in Table 1.

TABLE 1

Experimental results of degradation of sulfonylurea herbicides by herbicide tolerant proteins						
specific enzyme activity (µmol/min/mg)	tribenuron-methyl	benzulfuron-methyl	thifensulfuron-methyl	metsulfuron-methyl	chlorimuron-ethyl	sulfometuron-methyl
ALT01	1.8	1.7	27.4	2.0	2.7	1.9
ALT01M1	3.1	3.9	89.9	2.2	10.4	5.4
ALT01M2	10.8	2.4	106.0	1.2	9.0	3.5
ALT01M3	3.3	0.68	17.8	4.2	38.4	1.1
ALT02	1.9	1.8	28.8	2.1	2.8	2.0
ALT02M1	3.3	4.1	94.4	2.3	10.9	5.7
ALT02M2	11.3	2.5	111.3	1.3	9.5	3.7
ALT02M3	3.5	0.7	18.7	4.4	40.3	1.2
ALT03	1.7	1.6	26.0	1.9	2.6	1.8
ALT03M1	2.9	3.7	85.4	2.1	9.9	5.1
ALT03M2	10.3	2.3	100.7	1.1	8.6	3.3

TABLE 1-continued

specific enzyme activity ($\mu\text{mol}/\text{min}/\text{mg}$)	tribenuron-methyl	bensulfuron-methyl	thifensulfuron-methyl	metsulfuron-methyl	chlorimuron-ethyl	sulfometuron-methyl
ALT03M3	3.1	0.6	16.9	4.0	36.5	1.0
ALT04	1.6	1.5	24.7	1.8	2.4	1.7
ALT04M1	2.8	3.5	80.9	2.0	9.4	4.9
ALT04M2	9.7	2.2	95.4	1.1	8.1	3.2
ALT04M3	3.0	0.6	16.0	3.8	34.6	1.0

The above experimental results indicate that compared with the herbicide tolerant protein ALT01, the purified herbicide tolerant protein ALT01M1 degrades tribenuron-methyl, bensulfuron-methyl and thifensulfuron-methyl at efficiencies that are 1.7, 2.3 and 3.3-fold of those of ALT01 respectively; the purified herbicide tolerant protein ALT01M2 degrades tribenuron-methyl, bensulfuron-methyl and thifensulfuron-methyl at efficiencies that are 6.0, 1.4 and 3.9-fold of those of ALT01 respectively; the purified herbicide tolerant protein ALT01M3 degrades tribenuron-methyl, metsulfuron-methyl and chlorimuron-ethyl at efficiencies that are 1.9, 2.1 and 14.2-fold of those of ALT01 respectively.

Compared with the herbicide tolerant protein ALT02, the purified herbicide tolerant protein ALT02M1 degrades tribenuron-methyl, bensulfuron-methyl and thifensulfuron-methyl at efficiencies that are 1.7, 2.3 and 3.3-fold of those of ALT02 respectively; the purified herbicide tolerant protein ALT02M2 degrades tribenuron-methyl, bensulfuron-methyl and thifensulfuron-methyl at efficiencies that are 5.9, 1.4 and 3.9-fold of those of ALT02 respectively; the purified herbicide tolerant protein ALT02M3 degrades tribenuron-methyl, metsulfuron-methyl and chlorimuron-ethyl at efficiencies that are 1.8, 2.1 and 14.2-fold of those of ALT02 respectively.

Compared with the herbicide tolerant protein ALT03, the purified herbicide tolerant protein ALT03M1 degrades tribenuron-methyl, bensulfuron-methyl and thifensulfuron-methyl at efficiencies that are 1.5, 2.1 and 3.0-fold of those of ALT03 respectively; the purified herbicide tolerant protein ALT03M2 degrades tribenuron-methyl, bensulfuron-methyl and thifensulfuron-methyl at efficiencies that are 5.4, 1.3 and 3.5-fold of those of ALT03 respectively; the purified herbicide tolerant protein ALT03M3 degrades tribenuron-methyl, metsulfuron-methyl and chlorimuron-ethyl at efficiencies that are 1.6, 1.9 and 13.0-fold of those of ALT03 respectively.

Compared with the herbicide tolerant protein ALT04, the purified herbicide tolerant protein ALT04M1 degrades tribenuron-methyl, bensulfuron-methyl and thifensulfuron-methyl at efficiencies that are 1.5, 1.9 and 2.8-fold of those of ALT04 respectively; the purified herbicide tolerant protein ALT04M2 degrades tribenuron-methyl, bensulfuron-methyl and thifensulfuron-methyl at efficiencies that are 5.1, 1.2 and 3.3-fold of those of ALT04 respectively; the purified herbicide tolerant protein ALT04M3 degrades tribenuron-methyl, metsulfuron-methyl and chlorimuron-ethyl at efficiencies that are 1.6, 1.8 and 12.4-fold of those of ALT04 respectively.

It thus can be seen that, in the amino acid sequence of the herbicide tolerant protein ALT01, mutation at position 176 from glycine to alanine and/or mutation at position 178 position from serine to valine both can enhance the ability of mutant genes (such as the ALT01M1, ALT01M2 or

ALT01M3 gene) to degrade sulfonylurea herbicides, especially tribenuron-methyl. In the amino acid sequence of the herbicide tolerant protein ALT02 (or ALT03), mutation at position 140 from glycine to alanine and/or mutation at position 142 from serine to valine both can enhance the ability of mutant genes (such as the ALT02M1, ALT02M2, ALT02M3, ALT03M1, ALT03M2 or ALT03M3 gene) to degrade sulfonylurea herbicides, especially tribenuron-methyl. In the amino acid sequence of the herbicide tolerant protein ALT04, mutation at position 131 from glycine to alanine and/or mutation at position 133 from serine to valine both can enhance the ability of mutant genes (such as the ALT04M1, ALT04M2 or ALT04M3 gene) to degrade sulfonylurea herbicides, especially tribenuron-methyl.

Example 4. Construction of Recombinant Expression Vectors for Soybean

1. Construction of Recombinant Cloning Vectors Containing ALT02M1-01 Nucleotide Sequence for Soybean

The ALT02M1-01 nucleotide sequence was ligated into cloning vector pGEM-T (Promega, Madison, USA, CAT: A3600) according to the operational procedure in the instructions of product pGEM-T vector of Promega Corporation, thereby obtaining a recombinant cloning vector DBN01-T, the construction process of which was as shown in FIG. 1 (wherein, Amp represents the ampicillin resistance gene; fl represents the origin of replication of phage fl; LacZ is LacZ initiation codon; SP6 is SP6 RNA polymerase promoter; T7 is T7 RNA polymerase promoter; ALT02M1-01 is the ALT02M1-01 nucleotide sequence (SEQ ID NO: 25); and MCS is a multiple cloning site).

Then, *Escherichia coli* T1 competent cells (Transgen, Beijing, China, CAT: CD501) were transformed with the recombinant cloning vector DBN01-T using the heat shock method under the following heat shock conditions: maintaining 50 μL of *Escherichia coli* T1 competent cells and 10 μL of plasmid DNA (recombinant cloning vector DBN01-T) in water bath at 42°C. for 30 seconds; shake culturing at 37°C. for 1 hour (using a shaker at a rotation speed of 100 rpm for shaking); and growing on an LB plate (10 g/L of tryptone, 5 g/L of yeast extract, 10 g/L of NaCl, and 15 g/L of agar, with a pH adjusted to 7.5 with NaOH) of ampicillin (100 mg/L) having its surface coated with IPTG (isopropylthio- β -D-galactoside) and X-gal (5-bromo-4-chloro-3-indole- β -D-galactoside) overnight. White colonies were picked out and cultured in an LB liquid culture medium (10 g/L of tryptone, 5 g/L of yeast extract, 10 g/L of NaCl, and 100 mg/L of ampicillin, with a pH adjusted to 7.5 with NaOH) at a temperature of 37°C. overnight. The plasmids in the cells were extracted through an alkaline method: centrifuging the bacteria solution at a rotation speed of 12000 rpm for 1 min, removing the supernatant, and suspending the precipitated thalli with 100 μL of ice pre-cooled

solution I (25 mM Tris-HCl, 10 mM EDTA (ethylenediaminetetraacetic acid), and 50 mM glucose, with a pH of 8.0); adding 200 μ L of newly formulated solution II (0.2M NaOH, 1% SDS (sodium dodecyl sulfate)), inverting the tube 4 times, and mixing and placing on ice for 3-5 min; adding 150 μ L of ice-cold solution III (3 M potassium acetate, 5 M acetic acid), mixing uniformly immediately and placing on ice for 5-10 min; centrifuging under the conditions of a temperature of 4° C. and a rotation speed of 12000 rpm for 5 min, adding 2-fold volumes of anhydrous ethanol to the supernatant and placing at room temperature for 5 min after mixing uniformly; centrifuging under the conditions of a temperature of 4° C. and a rotation speed of 12000 rpm for 5 min, discarding the supernatant, and air drying the precipitate after washing with ethanol at a concentration of 70% (V/V); adding 30 μ L of TE (10 mM Tris-HCl, and 1 mM EDTA, with a pH of 8.0) containing RNase (20 μ g/mL) to dissolve the precipitate; water bathing at a temperature of 37° C. for 30 min to digest the RNA; and storing at a temperature of -20° C. for use.

After identifying the extracted plasmid by SpeI and KasI digestion, positive clones were verified by sequencing. The results showed that the inserted ALT02M1-01 nucleotide sequence in the recombinant cloning vector DBN01-T was the nucleotide sequence as shown in SEQ ID NO: 25 in the sequence listing, that is, the ALT02M1-01 nucleotide sequence was inserted correctly.

2. Construction of Recombinant Expression Vectors Containing ALT02M1-01 Nucleotide Sequence for Soybean

The recombinant cloning vector DBN01-T and an expression vector DBNBC-01 (vector backbone: pCAMBIA2301 (which can be provided by the CAMBIA institution)) were both digested with restriction enzymes SpeI and KasI respectively; the excised ALT02M1-01 nucleotide sequence fragment was inserted between the SpeI and KasI sites in the expression vector DBNBC-01; and it is well known to a person skilled in the art to construct a vector using conventional enzyme digestion methods, wherein a recombinant expression vector DBN100825 was constructed, the construction process of which was as shown in FIG. 2 (Spec: the spectinomycin gene; RB: the right boundary; prAtUbi10: the *Arabidopsis thaliana* Ubiquitin 10 gene promoter (SEQ ID NO: 69); ALT02M1-01: the ALT02M1-01 nucleotide sequence (SEQ ID NO: 25); tNos: the terminator of a nopaline synthase gene (SEQ ID NO: 70); prBrCBP: the rape eukaryotic elongation factor gene 1a (Tsfl) promoter (SEQ ID NO: 71); spAtCTP2: the *Arabidopsis thaliana* chloroplast transit peptide (SEQ ID NO: 72); EPSPS: the 5-enolpyruvylshikimate 3-phosphate synthase gene (SEQ ID NO: 73); tPsE9: the pea RbcS gene terminator (SEQ ID NO: 74); LB: the left boundary).

Escherichia coli T1 competent cells were transformed with the recombinant expression vector DBN100825 by a heat shock method under the following heat shock conditions: maintaining 50 μ L of *Escherichia coli* T1 competent cells and 10 μ L of plasmid DNA (recombinant expression vector DBN100825) in water bath at 42° C. for 30 seconds; shake culturing at 37° C. for 1 hour (using a shaker at a rotation speed of 100 rpm for shaking); then culturing under the condition of a temperature of 37° C. on an LB solid plate containing 50 mg/L of spectinomycin (10 g/L of tryptone, 5 g/L of yeast extract, 10 g/L of NaCl, and 15 g/L of agar, with a pH adjusted to 7.5 with NaOH) for 12 hours, picking white colonies, and culturing under the condition of a temperature of 37° C. overnight in an LB liquid culture medium (10 g/L of tryptone, 5 g/L of yeast extract, 10 g/L of NaCl, and 50 mg/L of spectinomycin, with a pH adjusted to 7.5 with

NaOH). The plasmids in the cells were extracted through the alkaline method. The extracted plasmid was identified after digesting with restriction enzymes SpeI and KasI, and positive clones were identified by sequencing. The results showed that the nucleotide sequence between the SpeI and KasI sites in the recombinant expression vector DBN100825 was the nucleotide sequence as shown in SEQ ID NO: 25 in the sequence listing, i.e., the ALT02M1-01 nucleotide sequence.

The recombinant expression vector DBN100826 containing ALT02M2-01 nucleotide sequence, the recombinant expression vector DBN100827 containing ALT02M3-01 nucleotide sequence, and the recombinant expression vector DBN100828 containing ALT02-01 nucleotide sequence were constructed according to the method for constructing the recombinant expression vector DBN100825 containing ALT02M1-01 nucleotide sequence as described above. Positive clones were verified by sequencing, with the results showing that ALT02M2-01 nucleotide sequence, ALT02M3-01 nucleotide sequence and ALT02-01 nucleotide sequence inserted into the recombinant expression vectors DBN100825, DBN100826, DBN100827 and DBN100828 were the nucleotide sequences as shown in SEQ ID NO: 29, SEQ ID NO: 33 and SEQ ID NO: 21 in the sequence listing respectively, namely ALT02M2-01 nucleotide sequence, ALT02M3-01 nucleotide sequence and ALT02-01 nucleotide sequence were inserted correctly.

According to the method for constructing the recombinant expression vector DBN100825 containing ALT02M1-01 nucleotide sequence as described above, a control recombinant expression vector DBN100828N was constructed, the structure of which is as shown in FIG. 3 (vector backbone: pCAMBIA2301 (which can be provided by the CAMBIA institution); Spec: the spectinomycin gene; RB: the right boundary; prBrCBP: the rape eukaryotic elongation factor gene 1a (Tsfl) promoter (SEQ ID NO: 71); spAtCTP2: the *Arabidopsis thaliana* chloroplast transit peptide (SEQ ID NO: 72); EPSPS: the 5-enolpyruvylshikimate 3-phosphate synthase gene (SEQ ID NO: 73); tPsE9: the pea RbcS gene terminator (SEQ ID NO: 74); LB: the left boundary). Positive clones were verified by sequencing, with the results showing that the control recombinant expression vector DBN100828N was correctly constructed.

3. Transformation of *Agrobacterium* with the Recombinant Expression Vectors

Agrobacterium LBA4404 (Invitrogen, Chicago, USA, CAT: 18313-015) was transformed with the recombinant expression vectors DBN100825, DBN100826, DBN100827, DBN100828, and DBN100828N which had been constructed correctly using a liquid nitrogen method, under the following transformation conditions: placing 100 μ L of *Agrobacterium* LBA4404 and 3 μ L of plasmid DNA (recombinant expression vector) in liquid nitrogen for 10 minutes, and warm water bathing at 37° C. for 10 minutes; inoculating the transformed *Agrobacterium* LBA4404 into an LB tube, culturing under the conditions of a temperature of 28° C. and a rotation speed of 200 rpm for 2 hours, spreading on an LB plate containing 50 mg/L of rifampicin and 50 mg/L of spectinomycin until positive single clones were grown, picking out single clones for culturing and extracting the plasmids thereof, and performing enzyme digestion verification using restriction enzymes. The results showed that the structures of the recombinant expression vectors DBN100825, DBN100826, DBN100827, DBN100828, and DBN100828N were completely correct.

Example 5. Acquisition and Verification of
Transgenic Soybean Plants

1. Acquisition of Transgenic Soybean Plants

According to the *Agrobacterium* infection method conventionally used, the cotyledonary node tissue of steriley cultured soybean variety Zhonghuang13 was co-cultured with the *Agrobacterium* in part 3 of Example 4, so as to introduce the T-DNA (including the *Arabidopsis thaliana* Ubiquitin10 gene promoter sequence, the ALT02M1-01 nucleotide sequence, the ALT02M2-01 nucleotide sequence, the ALT02M3-01 nucleotide sequence, the ALT02-01 nucleotide sequence, the tNos terminator, the rape eukaryotic elongation factor gene 1 α promoter, the *Arabidopsis thaliana* chloroplast transit peptide, a 5-enolpyruvylshikimate-3 phosphate synthase gene, and the pea RbcS gene terminator) in the recombinant expression vectors DBN100825, DBN100826, DBN100827, DBN100828, and DBN100828N constructed in Part 2 of Example 4 into the soybean chromosome sets, thereby obtaining soybean plants into which the ALT02M1-01 nucleotide sequence was introduced, soybean plants into which the ALT02M2-01 nucleotide sequence was introduced, soybean plants into which the ALT02M3-01 nucleotide sequence was introduced, and soybean plants into which the ALT02-01 nucleotide sequence was introduced; meanwhile, control soybean plants into which T-DNA in a control recombinant expression vector DBN100828N was introduced and wild-type soybean plants were used as the control.

As regards the *Agrobacterium*-mediated soybean transformation, briefly, mature soybean seeds were germinated in a soybean germination culture medium (3.1 g/L of B5 salt, B5 vitamin, 20 g/L of sucrose, and 8 g/L of agar, with a pH of 5.6), and the seeds were inoculated on a germination culture medium and cultured under the conditions of a temperature of 25±1°C.; and a photoperiod (light/dark) of 16 h/8 h. After 4-6 days of germination, soybean sterile seedlings swelling at bright green cotyledonary nodes were taken, hypocotyledonary axes were cut off 3-4 mm below the cotyledonary nodes, the cotyledons were cut longitudinally, and apical buds, lateral buds and seminal roots were removed. A wound was made at a cotyledonary node using the knife back of a scalpel, and the wounded cotyledonary node tissues were contacted with an *Agrobacterium* suspension, wherein the *Agrobacterium* can transfer the ALT02M1-01 nucleotide sequence (ALT02M2-01 nucleotide sequence, ALT02M3-01 nucleotide sequence or ALT02-01 nucleotide sequence) to the wounded cotyledonary node tissues (step 1: the infection step). In this step, the cotyledonary node tissues were preferably immersed in the *Agrobacterium* suspension ($OD_{660}=0.5\text{--}0.8$, an infection culture medium (2.15 g/L of MS salt, B5 vitamin, 20 g/L of sucrose, 10 g/L of glucose, 40 mg/L of acetosyringone (AS), 4 g/L of 2-morpholine ethanesulfonic acid (MES), and 2 mg/L of zeatin (ZT), with a pH of 5.3)) to initiate the inoculation. The cotyledonary node tissues were co-cultured with *Agrobacterium* for a period of time (3 days) (step 2: the co-culturing step). Preferably, the cotyledonary node tissues were cultured in a solid culture medium (4.3 g/L of MS salt, B5 vitamin, 20 g/L of sucrose, 10 g/L of glucose, 4 g/L of MES, 2 mg/L of ZT, and 8 g/L of agar, with a pH of 5.6) after the infection step. After this co-culturing stage, there can be an optional “recovery” step. In the “recovery” step, there may be at least one antibiotic (cephalosporin) known to inhibit the growth of *Agrobacterium* in a recovery culture medium (3.1 g/L of B5 salt, B5 vitamin, 1 g/L of MES, 30 g/L of sucrose, 2 mg/L of ZT, 8 g/L of agar, 150 mg/L of cephalosporin, 100 mg/L of

of glutamic acid, and 100 mg/L of aspartic acid, with a pH of 5.6), without the addition of a selective agent for a plant transformant (step 3: the recovery step). Preferably, tissue blocks regenerated from the cotyledonary nodes were cultured in a solid culture medium with an antibiotic, but without a selective agent, to eliminate *Agrobacterium* and provide a recovery stage for the infected cells. Subsequently, the tissue blocks regenerated from the cotyledonary nodes were cultured in a culture medium containing a selective agent (glyphosate), and growing transformed calli were selected (step 4: the selection step). Preferably, the tissue blocks regenerated from the cotyledonary nodes were cultured in a screening solid culture medium (3.1 g/L of B5 salt, B5 vitamin, 1 g/L of MES, 30 g/L of sucrose, 1 mg/L of 6-benzyladenine (6-BAP), 8 g/L of agar, 150 mg/L of cephalosporin, 100 mg/L of glutamic acid, 100 mg/L of aspartic acid, and 0.25 mol/L of N-(phosphonomethyl)glycine, with a pH of 5.6) containing a selective agent, thus resulting in selective growth of the transformed cells. Then, plants were regenerated from the transformed cells (step 5: the regeneration step). Preferably, the tissue blocks regenerated from the cotyledonary nodes grown in a culture medium containing a selective agent were cultured in solid culture media (a B5 differentiation culture medium and B5 rooting culture medium) to regenerate plants.

The resistant tissue blocks obtained from screening were transferred onto the B5 differentiation culture medium (3.1 g/L of B5 salt, B5 vitamin, 1 g/L of MES, 30 g/L of sucrose, 1 mg/L of ZT, 8 g/L of agar, 150 mg/L of cephalosporin, 50 mg/L of glutamic acid, 50 mg/L of aspartic acid, 1 mg/L of gibberellin, 1 mg/L of auxin, and 0.25 mol/L of N-(phosphonomethyl)glycine, with a pH of 5.6), and cultured at 25°C. for differentiation. The differentiated seedlings were transferred onto the B5 rooting culture medium (3.1 g/L of B5 salt, B5 vitamin, 1 g/L of MES, 30 g/L of sucrose, 8 g/L of agar, 150 mg/L of cephalosporin, and 1 mg/L of indole-3-butyric acid (IBA)), cultured in the rooting culture medium until reaching a height of about 10 cm at 25°C., and transferred to a greenhouse for culturing until fruiting. In the greenhouse, the plants were cultured at 26°C. for 16 hours, and then cultured at 20°C. for 8 hours every day.

2. Verification of the Transgenic Soybean Plants Using TaqMan

About 100 mg of leaves from the soybean plants into which the ALT02M1-01 nucleotide sequence was introduced, the soybean plants into which the ALT02M2-01 nucleotide sequence was introduced, the soybean plants into which the ALT02M3-01 nucleotide sequence was introduced, the soybean plants into which the ALT02-01 nucleotide sequence was introduced and control soybean plants respectively were taken as samples, and the genomic DNA thereof was extracted with a DNeasy Plant Maxi Kit of Qiagen, and copy numbers of an EPSPS gene were detected by the Taqman probe fluorescence quantitative PCR method so as to determine the copy numbers of the genes of interest. At the same time, wild-type soybean plants were used as controls, and detected and analyzed according to the above-mentioned method. Triple repeats were set for the experiments, and were averaged.

The specific method for detecting the copy number of the EPSPS gene was as follows:

Step 21. 100 mg of leaves from the soybean plants into which the ALT02M1-01 nucleotide sequence was introduced, soybean plants into which the ALT02M2-01 nucleotide sequence was introduced, soybean plants into which the ALT02M3-01 nucleotide sequence was introduced and soybean plants into which the ALT02-

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01 nucleotide sequence was introduced, control soybean plants and wild-type soybean plants respectively were taken, and ground into a homogenate using liquid nitrogen in a mortar respectively, and triple repeats were taken for each sample;

Step 22. The genomic DNA of the above-mentioned samples was extracted using a DNeasy Plant Mini Kit of Qiagen (for the particular method, refer to the product instructions thereof);

Step 23. The concentrations of the genomic DNA of the above-mentioned samples were detected using Nano-Drop 2000 (Thermo Scientific);

Step 24. The concentrations of the genomic DNA of the above-mentioned samples were adjusted to a consistent concentration value which ranges from 80 to 100 ng/ μ L;

Step 25. The copy numbers of the samples were identified using the Taqman probe fluorescence quantitative PCR method, wherein samples for which the copy numbers had been identified and known were taken as standards, the samples of the wild-type soybean plants were taken as the control, and triple repeats were taken for each sample, and were averaged; the sequences of fluorescence quantitative PCR primers and a probe were as follows:

The following primers and probe were used to detect the EPSPS gene sequence:

primer 5:
CTGGAAGGCAGGGACGTCATCAATA
as shown in SEQ ID NO: 75 in the sequence listing;

primer 6:
TGGCGGCATTGCCGAAATCGAG
as shown in SEQ ID NO: 76 in the sequence listing;

probe 1:
ATGCAGGGCATGGCGCCCGCATCCGTA
as shown in SEQ ID NO: 77 in the sequence listing;

PCR Reaction System:

JumpStart™ Taq ReadyMix™ (Sigma)	10 μ L
50 \times primer/probe mixture	1 μ L
genomic DNA	3 μ L
water (ddH ₂ O)	6 μ L

The 50xprimer/probe mixture comprises 45 μ L of each primer at a concentration of 1 mM, 50 μ L of the probe at a concentration of 100 μ M, and 860 μ L of 1xTE buffer, and was stored at 4° C. in an amber tube.

PCR Reaction Conditions:

Step	temperature	time
31	95° C.	5 min
32	95° C.	30 s
33	60° C.	1 min
34	back to step 32, repeated	40 times

Data was analyzed using software SDS2.3 (Applied Bio-systems).

It was further demonstrated, by analyzing the experimental results of the copy number of the EPSPS gene, that the ALT02M1-01 nucleotide sequence, the ALT02M2-01 nucleotide sequence, the ALT02M3-01 nucleotide sequence and the ALT02-01 nucleotide sequence had all been integrated

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into the chromosome set of the detected soybean plants, and all of the soybean plants into which the ALT02M1-01 nucleotide sequence was introduced, soybean plants into which the ALT02M2-01 nucleotide sequence was introduced, soybean plants into which the ALT02M3-01 nucleotide sequence was introduced and soybean plants into which the ALT02-01 nucleotide sequence was introduced and control soybean plants resulted in single-copy transgenic soybean plants.

Example 6. Detection of Herbicide Tolerance Effects of the Transgenic Soybean Plants

The effect of herbicide tolerance to tribenuron-methyl was detected on the soybean plants into which the ALT02M1-01 nucleotide sequence was introduced, the soybean plants into which the ALT02M2-01 nucleotide sequence was introduced, the soybean plants into which the ALT02M3-01 nucleotide sequence was introduced, the soybean plants into which the ALT02-01 nucleotide sequence was introduced, control soybean plants and wild-type soybean plants (at seedling stage V3-V4), respectively.

The soybean plants into which the ALT02M1-01 nucleotide sequence was introduced, the soybean plants into which the ALT02M2-01 nucleotide sequence was introduced, the soybean plants into which the ALT02M3-01 nucleotide sequence was introduced, the soybean plants into which the ALT02-01 nucleotide sequence was introduced, control soybean plants and wild-type soybean plants were taken and sprayed with tribenuron-methyl (144 g ai/ha, eight-fold field concentration) or a blank solvent (water), respectively. The degree of damage caused by the herbicide was measured for each plant according to the leaf curl degree and the growth point damage degree 3 days after spraying (3 DAT), 7 days after spraying (7 DAT), 14 days after spraying (14 DAT) and 21 days after spraying (21 DAT): the case where the leaves are flat as untreated plants and the growth points are intact is defined as having a damage degree of 0%; the case where veins are locally browned, new leaves are malformed and plant growth is slow is defined as having a damage degree of 50%; and the case where veins are purple, until the whole plant is dead and the growth points are browned and dry is defined as having a damage degree of 100%. The soybean plants into which the ALT02M1-01 nucleotide sequence was introduced were of three strains in total (S1, S2 and S3), the soybean plants into which the ALT02M2-01 nucleotide sequence was introduced were of three strains in total (S4, S5 and S6), the soybean plants into which the ALT02M3-01 nucleotide sequence was introduced were of three strains in total (S7, S8 and S9), the soybean plants into which the ALT02-01 nucleotide sequence was introduced were of three strains in total (S10, S11 and S12), the control soybean plants were of two strains in total (S13 and S14), and the wild-type soybean plants were of one strain in total (CK1); and 10-15 plants were selected from each strain and tested. The results were as shown in Table 2 and FIG. 4.

TABLE 2

Treatment	Soybean genotypes	Experimental results of the herbicide tolerance of transgenic soybean T ₁ plants			
		Average damage % 3DAT	Average damage % 7DAT	Average damage % 14DAT	Average damage % 21DAT
Blank solvent	S1	0	0	0	0
	S2	0	0	0	0

TABLE 2-continued

Treatment	Soybean genotypes	Average	Average	Average	Average
		damage % 3DAT	damage % 7DAT	damage % 14DAT	damage % 21DAT
(water)	S3	0	0	0	0
	S4	0	0	0	0
	S5	0	0	0	0
	S6	0	0	0	0
	S7	0	0	0	0
	S8	0	0	0	0
	S9	0	0	0	0
	S10	0	0	0	0
	S11	0	0	0	0
	S12	0	0	0	0
	S13	0	0	0	0
	S14	0	0	0	0
	CK1	0	0	0	0
144 g ai/ha	S1	15	8	0	0
tribenuron-	S2	16	9	0	0
methyl	S3	10	3	0	0
(8x Tri.)	S4	0	0	0	0
	S5	0	0	0	0
	S6	0	0	0	0
	S7	12	3	0	0
	S8	11	2	0	0
	S9	10	1	0	0
	S10	25	15	5	0
	S11	24	14	3	0
	S12	30	17	4	0
	S13	63	91	100	100
	S14	58	95	100	100
	CK1	76	87	100	100

For soybeans, eight-fold field concentration of tribenuron-methyl is an effective dose for high pressure treatment. The results in Table 2 and FIG. 4 showed that the herbicide tolerant proteins ALT02M1-01, ALT02M2-01, ALT02M3-01 and ALT02-01 all can impart transgenic soybean plants with the tolerance to benzenesulfonic acid; compared with the soybean plants into which the ALT02-01 nucleotide sequence was introduced, all of the soybean plants into which the ALT02M1-01 nucleotide sequence was introduced, the soybean plants into which the ALT02M2-01 nucleotide sequence was introduced and the soybean plants into which the ALT02M3-01 nucleotide sequence was introduced had a significantly increased tolerance to benzenesulfonic acid; while the control soybean plants and the wild-type soybean plants had no tolerance to benzenesulfonic acid.

Example 7. Construction of Recombinant Expression Vectors for Maize

1. Construction of Recombinant Cloning Vectors Containing ALT02M1-02 Nucleotide Sequence for Maize

The ALT02M1-02 nucleotide sequence was ligated into cloning vector pGEM-T (Promega, Madison, USA, CAT: A3600) according to the operational procedure in the instructions of product pGEM-T vector of Promega Corporation, thereby obtaining a recombinant cloning vector DBN02-T, the construction process of which is as shown in FIG. 5 (wherein, Amp represents the ampicillin resistance gene; fl represents the origin of replication of phage fl; LacZ is LacZ initiation codon; SP6 is SP6 RNA polymerase promoter; T7 is T7 RNA polymerase promoter; ALT02M1-02 is the ALT02M1-02 nucleotide sequence (SEQ ID NO: 26); and MCS is a multiple cloning site).

According to the method in Part 1 of Example 4, *Escherichia coli* T₁ competent cells were transformed with the

recombinant cloning vector DBN01-T using the heat shock method, and the plasmids in the cells were extracted through the alkaline method. The extracted plasmid was identified after digesting with restriction enzymes SpeI and KasI, and positive clones were identified by sequencing. The results

showed that the nucleotide sequence between the SpeI and KasI sites in the recombinant cloning vector DBN02-T was the nucleotide sequence as shown in SEQ ID NO: 26 in the sequence listing, i.e., the ALT02M1-02 nucleotide sequence.

10 2. Construction of Recombinant Expression Vectors Containing ALT02M1-02 Nucleotide Sequence for Maize

The recombinant cloning vector DBN02-T and an expression vector DBN0C-02 (vector backbone: pCAMBIA2301 (which can be provided by the CAMBIA institution)) were both digested with restriction enzymes SpeI and KasI; the excised ALT02M1-02 nucleotide sequence fragment was inserted between the SpeI and KasI sites in the expression vector DBN0C-02; and it is well known to a person skilled in the art to construct a vector using conventional enzyme digestion methods, wherein a recombinant expression vector DBN100833 was constructed, the construction process of which was as shown in FIG. 6 (Spec: the spectinomycin gene; RB: the right boundary; prUbi: the maize Ubiquitin 1 gene promoter (SEQ ID NO: 78); ALT02M1-02: the ALT02M1-02 nucleotide sequence (SEQ ID NO:26); tNos: the terminator of a nopaline synthase gene (SEQ ID NO:70); PMI: the phosphomannose isomerase gene (SEQ ID NO: 79); LB: the left boundary).

According to the method in Part 2 of Example 4, *Escherichia coli* T₁ competent cells were transformed with the recombinant expression vector DBN100833 using the heat shock method, and the plasmids in the cells were extracted through the alkaline method. The extracted plasmid was identified after digesting with restriction enzymes SpeI and KasI, and positive clones were identified by sequencing. The results showed that the nucleotide sequence between the SpeI and KasI sites in the recombinant expression vector DBN100833 was the nucleotide sequence as shown in SEQ ID NO: 26 in the sequence listing, i.e., the ALT02M1-02 nucleotide sequence.

The recombinant expression vector DBN100832 containing ALT02M2-02 nucleotide sequence, the recombinant expression vector DBN100831 containing ALT02M3-02 nucleotide sequence, and the recombinant expression vector DBN100830 containing ALT02-02 nucleotide sequence were constructed according to the method for constructing the recombinant expression vector DBN100833 containing ALT02M1-02 nucleotide sequence as described above. Positive clones were verified by sequencing, with the results showing that ALT02M2-02 nucleotide sequence, ALT02M3-02 nucleotide sequence and ALT02-02 nucleotide sequence inserted into the DBN100832, DBN100831 and DBN100830 were the nucleotide sequences as shown in SEQ ID NO: 30, SEQ ID NO: 34 and SEQ ID NO: 22 in the sequence listing respectively, namely ALT02M2-02 nucleotide sequence, ALT02M3-02 nucleotide sequence and ALT02-02 nucleotide sequence were inserted correctly.

According to the method for constructing the recombinant expression vector DBN100833 containing ALT02M1-02 nucleotide sequence as described above, a control recombinant expression vector DBN100830N was constructed, the structure of which is as shown in FIG. 7 (vector backbone: pCAMBIA2301 (which can be provided by the CAMBIA institution); Spec: the spectinomycin gene; RB: the right boundary; prUbi: the maize Ubiquitin 1 gene promoter (SEQ ID NO: 78); PMI: the phosphomannose isomerase gene (SEQ ID NO: 79); tNos: the terminator of a nopaline

synthase gene (SEQ ID NO:70); LB: the left boundary). Positive clones were verified by sequencing, with the results showing that the control recombinant expression vector DBN100830N was correctly constructed.

3. Transformation of *Agrobacterium* with the Recombinant Expression Vectors for Maize

Agrobacterium LBA4404 (Invitrogen, Chicago, USA, CAT: 18313-015) was transformed with the recombinant expression vectors DBN100833, DBN100832, DBN100831, DBN100830, and DBN100830N which had been constructed correctly using a liquid nitrogen method, under the following transformation conditions: placing 100 µL of *Agrobacterium* LBA4404, and 3 µL of plasmid DNA (recombinant expression vector) in liquid nitrogen for 10 minutes, and warm water bathing at 37° C. for 10 minutes; inoculating the transformed *Agrobacterium* LBA4404 into an LB tube, culturing under the conditions of a temperature of 28° C. and a rotation speed of 200 rpm for 2 hours, spreading on an LB plate containing 50 mg/L of rifampicin and 50 mg/L of spectinomycin until positive single clones were grown, picking out single clones for culturing and extracting the plasmids thereof, and performing enzyme digestion verification using restriction enzymes. The results showed that the structures of the recombinant expression vectors DBN100833, DBN100832, DBN100831, DBN100830, and DBN100830N were completely correct.

Example 8. Acquisition and Verification of Transgenic Maize Plants

1. Acquisition of Transgenic Maize Plants

According to the conventionally used *Agrobacterium* infection method, young embryos of steriley cultured maize variety Zong31 (Z31) were co-cultured with the *Agrobacterium* in Part 3 of Example 7, so as to introduce T-DNA (including the maize Ubiquitin1 gene promoter sequence, ALT02M1-02 nucleotide sequence, ALT02M2-02 nucleotide sequence, ALT02M3-02 nucleotide sequence and ALT02-02 nucleotide sequence, the PMI gene and the tNos terminator sequence) in the recombinant expression vectors DBN100833, DBN100832, DBN100831, DBN100830, and DBN100830N constructed in Part 2 of Example 7 into the maize chromosome set, thereby obtaining maize plants into which ALT02M1-02 nucleotide sequence was introduced, maize plants into which ALT02M2-02 nucleotide sequence was introduced, maize plants into which ALT02M3-02 nucleotide sequence was introduced and maize plants into which ALT02-02 nucleotide sequence was introduced; meanwhile, the control maize plants into which T-DNA in the control recombinant expression vector DBN100830N was introduced and wild type maize plants were used as the control.

As regards the *Agrobacterium*-mediated maize transformation, briefly, immature young embryos were separated from maize, and contacted with an *Agrobacterium* suspension, wherein the *Agrobacterium* can transfer the ALT02M1-02 nucleotide sequence (ALT02M2-02 nucleotide sequence, ALT02M3-02 nucleotide sequence or ALT02-02 nucleotide sequence) to at least one cell of one of the young embryos (step 1: the infection step). In this step, the young embryos were preferably immersed in an *Agrobacterium* suspension ($OD_{660}=0.4\text{--}0.6$, an infection culture medium (4.3 g/L of MS salt, MS vitamin, 300 mg/L of casein, 68.5 g/L of sucrose, 36 g/L of glucose, 40 mg/L of acetosyringone (AS), and 1 mg/L of 2,4-dichlorphenoxyacetic acid (2,4-D), with a pH of

5.3)) to initiate the inoculation. The young embryos were co-cultured with *Agrobacterium* for a period of time (3 days) (step 2: the co-culturing step). Preferably, the young embryos were cultured in a solid culture medium (4.3 g/L of MS salt, MS vitamin, 300 mg/L of casein, 20 g/L of sucrose, 10 g/L of glucose, 100 mg/L of acetosyringone (AS), 1 mg/L of 2,4-dichlorphenoxyacetic acid (2,4-D), and 8 g/L of agar, with a pH of 5.8) after the infection step. After this co-culturing stage, there can be an optional “recovery” step. In the “recovery” step, there may be at least one antibiotic (cephalosporin) known to inhibit the growth of *Agrobacterium* in a recovery culture medium (4.3 g/L of MS salt, MS vitamin, 300 mg/L of casein, 30 g/L of sucrose, 1 mg/L of 2,4-D, and 3 g/L of phytigel, with a pH of 5.8), without the addition of a selective agent for a plant transformant (step 3: the recovery step). Preferably, the young embryos were cultured in a solid culture medium with an antibiotic, but without a selective agent, in order to eliminate *Agrobacterium* and provide a recovery stage for the infected cells. Subsequently, the inoculated young embryos were cultured in a culture medium containing a selective agent (mannose), and growing transformed calli were selected (step 4: the selection step). Preferably, the young embryos were cultured in a screening solid culture medium (4.3 g/L of MS salt, MS vitamin, 300 mg/L of casein, 30 g/L of sucrose, 12.5 g/L of mannose, 1 mg/L of 2,4-D, and 3 g/L of phytigel, with a pH of 5.8) with a selective agent, resulting in the selective growth of transformed cells. Then, plants were regenerated from the calli (step 5: the regeneration step). Preferably, the calli grown in a culture medium containing a selective agent were cultured in solid culture media (an MS differentiation culture medium and MS rooting culture medium) to regenerate plants.

Resistant calli obtained from screening were transferred onto the MS differentiation culture medium (4.3 g/L of MS salt, MS vitamin, 300 mg/L of casein, 30 g/L of sucrose, 2 mg/L of 6-benzyladenine, 5 g/L of mannose, and 3 g/L of phytigel, with a pH of 5.8), and cultured at 25° C. for differentiation. The differentiated seedlings were transferred onto the MS rooting culture medium (2.15 g/L of MS salt, MS vitamin, 300 mg/L of casein, 30 g/L of sucrose, 1 mg/L of indole-3-acetic acid, and 3 g/L of phytigel, with a pH of 5.8), cultured at 25° C. to a height of about 10 cm, and transferred to a greenhouse for culturing until fruiting. In the greenhouse, the plants were cultured at 28° C. for 16 hours, and then cultured at 20° C. for 8 hours every day.

2. Verification of the Transgenic Maize Plants Using TaqMan

The maize plant into which the ALT02M1-02 nucleotide sequence was introduced, the maize plant into which the ALT02M2-02 was introduced, the maize plant into which the ALT02M3-02 was introduced, the maize plant into which the ALT02-02 was introduced and the control maize plant were detected and analyzed according to the method for verifying transgenic soybean plants with TaqMan as described in part 2 of Example 5. The copy number of the PMI gene was detected by the Taqman probe fluorescence quantitative PCR method so as to determine the copy number of the target gene. Meanwhile, wild-type maize plants were used as the control, and detected and analyzed according to the above-mentioned method. Triple repeats were set for the experiments, and were averaged.

The following primers and probe were used to detect the PMI gene sequence:

primer 7:
GCTGTAAAGAGCTTACTGAAAAAATTAAACA
as shown in SEQ ID NO: 80 in the sequence listing;

primer 8:
CGATCTGCAGGTCGACGG
as shown in SEQ ID NO: 81 in the sequence listing;

probe 2:
TCTCTTGCTAACGCTGGGAGCTCGATCC
as shown as SEQ ID NO: 82

in the sequence listing.

It was further demonstrated, by analyzing the experimental results of the copy number of PMI gene, that the ALT02M1-02 nucleotide sequence, the ALT02M2-02 nucleotide sequence, the ALT02M3-02 nucleotide sequence and the ALT02-02 nucleotide sequence had all been integrated into the chromosome set of the detected maize plants, and all of the maize plants into which the ALT02M1-02 nucleotide sequence was introduced, the maize plants into which the ALT02M2-02 nucleotide sequence was introduced, the maize plants into which the ALT02M3-02 nucleotide sequence was introduced, the maize plants into which the ALT02-02 nucleotide sequence was introduced and control maize plants resulted in single-copy transgenic maize plants.

Example 9. Detection of Herbicide Tolerance Effects of the Transgenic Maize Plants

The effect of herbicide tolerance to tribenuron-methyl was detected on the maize plants into which the ALT02M1-02 nucleotide sequence was introduced, maize plants into which the ALT02M2-02 nucleotide sequence was introduced, maize plants into which the ALT02M3-02 nucleotide sequence was introduced, maize plants into which the ALT02-02 nucleotide sequence was introduced, control maize plants and wild-type maize plants (at V3-V4 stages) respectively.

The maize plants into which the ALT02M1-02 nucleotide sequence was introduced, the maize plants into which the ALT02M2-02 nucleotide sequence was introduced, the maize plants into which the ALT02M3-02 nucleotide sequence was introduced, the maize plants into which the ALT02-02 nucleotide sequence was introduced, control maize plants and wild-type maize plants were taken and sprayed with tribenuron-methyl (144 g ai/ha, eight-fold field concentration) or a blank solvent (water), respectively. The degree of damage caused by the herbicide was measured for each plant according to the plant growth status 3 days after spraying (3 DAT), 7 days after spraying (7 DAT), 14 days after spraying (14 DAT) and 21 days after spraying (21 DAT): a growth status equivalent to that of the untreated plants is defined as having a damage degree of 0%; the case where leaves are locally chlorotic and yellow but the normal plant growth is substantially not affected is defined as having a damage degree of 50%; and the case where the whole plant is purple and dying is defined as having a damage degree of 100%. The maize plants into which the ALT02M1-02 nucleotide sequence was introduced were of three strains in total (S15, S16 and S17), the maize plants into which the ALT02M2-02 nucleotide sequence was introduced were of three strains in total (S18, S19 and S20), the maize plants into which the ALT02M3-02 nucleotide sequence was intro-

duced were of three strains in total (S21, S22 and S23), the maize plants into which the ALT02-02 nucleotide sequence was introduced were of three strains in total (S24, S25 and S26), the control maize plants were of two strains in total (S27 and S28), and the wild-type maize plants were of one strain in total (CK2); and 10-15 plants were selected from each strain and tested. The results were as shown in Table 3 and FIG. 8.

10

TABLE 3

Treatment	Maize genotypes	Experimental results of the herbicide tolerance of transgenic maize T ₁ plants			
		Average damage % 3DAT	Average damage % 7DAT	Average damage % 14DAT	Average damage % 21DAT
Blank solvent (water)	S15	0	0	0	0
	S16	0	0	0	0
	S17	0	0	0	0
	S18	0	0	0	0
	S19	0	0	0	0
	S20	0	0	0	0
	S21	0	0	0	0
	S22	0	0	0	0
	S23	0	0	0	0
	S24	0	0	0	0
	S25	0	0	0	0
	S26	0	0	0	0
	S27	0	0	0	0
	S28	0	0	0	0
	CK2	0	0	0	0
144 g ai/ha tribenuron-methyl (8x Tri.)	S15	5	0	0	0
	S16	6	0	0	0
	S17	3	0	0	0
	S18	0	0	0	0
	S19	0	0	0	0
	S20	0	0	0	0
	S21	3	0	0	0
	S22	2	0	0	0
	S23	0	0	0	0
	S24	14	5	0	0
	S25	15	4	0	0
	S26	20	7	0	0
	S27	61	82	100	100
	S28	53	78	100	100
	CK2	46	86	100	100

For the maize, eight-fold field concentration of tribenuron-methyl is an effective dose for high pressure treatment. The results in Table 3 and FIG. 8 showed that the herbicide tolerant proteins ALT02M1-02, ALT02M2-02, ALT02M3-02 and ALT02-02 all can impart transgenic maize plants with the tolerance to benzenesulfonic acid; compared with the maize plants into which the ALT02-02 nucleotide sequence was introduced, all of the maize plants into which the ALT02M1-02 nucleotide sequence was introduced, the maize plants into which the ALT02M2-02 nucleotide sequence was introduced and the maize plants into which the ALT02M3-02 nucleotide sequence was introduced had a significantly increased tolerance to benzenesulfonic acid; while the control maize plants and the wild-type maize plants had no tolerance to benzenesulfonic acid.

In conclusion, the herbicide tolerant protein ALT01 of the present invention can exhibit a higher tolerance to sulfonylurea herbicides, particularly tribenuron-methyl when its amino acid sequence is mutated at position 176 from glycine to alanine and/or at position 178 from serine to valine (such as the herbicide tolerant proteins ALT01M1, ALT01M2 or ALT01M3); the herbicide tolerant protein ALT02 (or ALT03) can exhibit a higher tolerance to sulfonylurea herbicides, particularly tribenuron-methyl when its amino acid sequence is mutated at position 140 from glycine to alanine

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and/or at position 142 from serine to valine (such as the herbicide tolerant proteins ALT02M1, ALT02M2, ALT02M3, ALT03M1, ALT03M2 or ALT03M3); the herbicide tolerant protein ALT04 can exhibit a higher tolerance to sulfonylurea herbicides, particularly tribenuron-methyl when its amino acid sequence is mutated at position 131 from glycine to alanine and/or at position 133 from serine to valine (such as the herbicide tolerant proteins ALT04M1, ALT04M2 or ALT04M3). Moreover, the coding genes of the above-mentioned herbicide tolerant proteins are particularly suitable for expression in plants due to the use of the preferred codons of plants. The soybean and maize plants into which the above-mentioned herbicide tolerant proteins are introduced have a strong tolerance to sulfonylurea her-

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bicides, and can tolerate tribenuron-methyl of an eight-fold field concentration particularly. Therefore, the above-mentioned herbicide tolerant proteins have a broad application prospect in plants.

Finally, it should be stated that the above examples are merely used for illustrating, rather than limiting, the technical solution of the present invention; and although the present invention has been described in detail with reference to the preferred examples, a person skilled in the art should understand that modifications or equivalent substitutions may be made to the technical solution of the present invention without departing from the spirit and scope of the technical solution of the present invention.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 82

<210> SEQ ID NO 1
<211> LENGTH: 398
<212> TYPE: PRT
<213> ORGANISM: Methylophilus sp.

<400> SEQUENCE: 1

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Met Gly Thr Ala Leu Leu Thr Gly Thr Ser Ala Ala Ser Pro Val Leu
 1           5           10          15

Ala Ala Gly Thr Gly Ala Ile Gly Ile Ala Thr Leu Pro Leu Ser Thr
 20          25          30

Ala Thr Ala Pro Ala Gly Thr Ala Ala Val Gly Leu Ala Gly Ser Leu
 35          40          45

Ala Leu Val Val Leu Ala Gly Gly Ser Pro Thr Ile Gly Gly Ala
 50          55          60

Thr Val Thr Gly Pro Gly Leu Pro Ala Pro Ser Leu Pro Val Ile Pro
 65          70          75          80

Thr Ser Ala Gly Gly Ala Thr Pro Thr Ile Ala Gly Met Thr Val Ala
 85          90          95

Pro Gly Ala Pro Val Ala Pro Ala Gly Leu Pro Leu Val Pro Thr His
100         105         110

Gly Gly Gly Leu Thr Gly His Ile Thr Gly Ser Thr Pro Ala Gly Ala
115         120         125

Pro Gly Pro Gly Thr Leu Pro Val Gly Ala Ala His Thr Val Thr Thr
130         135         140

Ile Ala Gly Pro Gly Ala Gly Ala Gly Ile Pro Thr Pro Ala Gly
145         150         155         160

Pro Pro Gly Gly Leu Gly Gly Ser Ile Val Ala Thr Val Thr Gly
165         170         175

Ala Ser Ser Leu Gly Gly Ala Thr Val Ala Ala Ala Leu Gly Pro Ala
180         185         190

Pro Gly Gly Pro Pro Gly Ala Ser Gly Pro Pro Ala Gly Thr Gly Ala
195         200         205

Ala Thr Pro Leu Gly Met Gly Pro Ser Pro Ser Ile Ser Ser Ala Gly
210         215         220

Ile Val Ala Ala Val Val Leu Leu Val Thr His Ile Gly Pro Cys Val
225         230         235         240

Leu Val Thr His Ser Ala Ser Gly Val Leu Gly Met Ala Val Ala Thr
245         250         255

His Ala Leu Ala Val Ala Gly Ile Val Ala Thr Gly Pro Ala Thr Ser
260         265         270

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Ile	Pro	Pro	Leu	Gly	Leu	Val	Pro	Gly	Ile	Pro	Pro	Leu	Ala	Ala	Leu
275					280							285			
Leu	Ser	Gly	Ile	Pro	Pro	Pro	Gly	Ile	Gly	Gly	Ser	Thr	Pro	Leu	
290				295					300						
Leu	Leu	Ala	Leu	Ile	Pro	Ile	Gly	Pro	Val	Pro	Gly	Ala	Ala	Ile	Pro
305					310				315						320
Leu	Ala	Pro	Leu	Ser	Ala	Thr	Thr	Pro	Leu	Ala	Thr	Thr	Ala	Val	Thr
						325			330			335			
Ala	Thr	Ala	His	Ser	Leu	Ser	Leu	Gly	Ala	Ile	Ala	Leu	Leu	Gly	Gly
						340			345			350			
Gly	Ala	Ser	Leu	Leu	Ala	Leu	Pro	Thr	Ala	Gly	Leu	Ala	Gly	Ala	Thr
						355			360			365			
His	Pro	Pro	Pro	Thr	Ala	Ala	Ala	Ala	Val	Gly	Val	Ala	Ser	Leu	Leu
						370			375			380			
Ser	Ala	Pro	Leu	Gly	Leu	His	Gly	Leu	Ala	Gly	Ala	Gly	Ser		
						385			390			395			

<210> SEQ ID NO 2

<211> LENGTH: 1197

<212> TYPE: DNA

<213> ORGANISM: Methylophilus sp.

<400> SEQUENCE: 2

atggaaaccg	ataaaaaaac	cggAACgtcc	cgcagatcat	ttgtgaaggc	tgctggaacc	60
ggcgcaatag	gaatagcgac	gctgccgctt	tgcactgcaa	ctgcttcgc	ggaaactgac	120
aacgtggagc	ttgccaatc	gaagcggaaag	gttgtccctt	ctgaacaagg	cagttctac	180
atcgaaaaaaca	gaacagtaac	cggccttgg	aaattcgatc	cgtcaaagcc	ggtaattcca	240
tattccaacg	aagggtccac	gttttatata	aatcaaatgt	acgtaaacctt	tcaagctcct	300
gtgcgcctc	gtgggctgcc	tctagtcttt	tggcatgggg	gcggactaac	cggccatatc	360
tggaaatcta	ccccagacgg	ccggcccgga	tttcagaccc	tctttgtca	agatcgccat	420
acggtctaca	cgattgatca	gccaggggcg	ggaaggggca	atattctac	ctttaatggc	480
ccttttggc	agtttggaaa	agagtctgatt	gttaacactg	ttaccggaaa	ctccagtaaa	540
gaaggagcgt	gggttagaga	tcgacttaggg	cccgctccc	gccagttttt	tgagaacacg	600
caattccac	gtggatatga	agacaactac	ttcaaggaga	tggggttcag	tccgtcgatc	660
tcatcagatg	agatagtcga	cgctgttgg	aaactagtaa	ctcacatagg	tccttgcgtt	720
ctgggtgaccc	attcggtttc	cgaggactt	ggcatgcgag	tcgcgcacaca	cggcaagAAC	780
gtgaggggga	tcgttgctta	tgagctctgc	acaagtatct	ttcccaaagg	aaaagtgcct	840
gagataccgc	ctctcgccga	taaaaaatcg	caaattttcc	cggccgttgc	gatccaggag	900
tcttacttta	agaagctcgc	gaagatacc	attcagtttgc	tcttcggaga	taatatcccc	960
aaaaacccta	aatccgccta	ttgggtcttg	gactgggtgg	gagtcaactcg	ctacgctcac	1020
agcttgcac	tcgaggctat	caataagctc	ggtggtaag	cgtctttttt	ggatttggcc	1080
actgcgggac	ttcgcggcaa	cacgcatttt	ccattcaccc	accggataaa	cgtgcaggtc	1140
gcttctctgt	tatctgattt	cctcgaaag	cacggcttag	atcagaacga	aagctga	1197

<210> SEQ ID NO 3

<211> LENGTH: 1197

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: the ALT01-01 nucleotide sequence encoding the

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amino acid sequence corresponding to ALT01 and based on soybean codon usage bias

<400> SEQUENCE: 3

atggagactg	ataagaaaac	tggcacatct	agaaggcat	ttgttaaggc	tgca	aggaaaca	60		
ggtgcatttgc	aatcgctac	ccttcatttgc	tccaccgc	ctgc	tttcgc	agagactgat	120		
aacgtggAAC	tcgcccatac	taagagaaAG	gtgggtctGG	ctgaacaAGG	gtc	atTTAC	180		
atagggggttA	ggactgttac	tggccttgc	aaggTTGATC	catccaAA	tgt	gtatCC	240		
tacagtaacG	aaggagcaAC	attctatATT	aaccAAatGT	atgttaACTT	ccagg	ccccCA	300		
gtgagaccta	ggggacttcc	attgggtttc	tggcatgg	gtggcttg	ac	tggtcacatc	360		
tgggagtcta	cacctgacgg	cagacccggg	tttcaaacc	tttcg	ttca	ggataggcat	420		
accgtgtaca	ctattgacca	acctggaga	ggaaggggta	acatccaa	ac	ttttaacgg	480		
ccttcggac	agttggagga	agagagtatt	gttaacactg	tgacaggaa	aa	ttcttcaag	540		
gaaggtgcct	gggtgagaga	taggottggc	cctgctcccc	ggcaatTTT	cgaga	actct	600		
cagtttccta	gaggctatga	agacaattac	tttaaggaga	tgggattc	ag	cccatctata	660		
tccagtgtat	aaattgttga	cgctgttgc	aaactcgta	cccatattgg	tc	cttgcgtt	720		
ctgggtgactc	actcagcata	cggcg	ttt	ggatgagag	tgg	ctacaca	780		
gttaggggaa	ttgtggccta	tgaaccag	ac	ctcaatct	tccc	caagg	aaaagt	tcca	840
gagataccac	ctctcgctga	taagaaaAGC	caa	atctt	cccattcg	aatacagg	900		
tcttacttta	agaaaacttgc	caagattca	atccaatttgc	ttttcg	aga	taacatccc	960		
aagaatccaa	aatcagcata	ttggttcctg	gactgg	ttgg	gaga	atacgcacat	1020		
agtctcagcc	tggaggccat	aaacaaatttgc	gggg	gaca	tttt	ggatcttct	1080		
actgcaggat	tgagaggtaa	tacacacttgc	cc	ttcacc	atagga	acaa	tgtt	cagg	1140
gcttc	tgtcagactt	tctggtaaa	ca	cggtctgg	atcaaa	atga	gag	ctga	1197

<210> SEQ ID NO 4

<211> LENGTH: 1197

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: the ALT01-02 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT01 and based on the maize codon usage bias

<400> SEQUENCE: 4

atggagacag	acaagaagac	cggcacgtcc	cgcaggagct	tcgtgaaggc	tgctgg	cacc	60
ggggctatcg	ggattgctac	gctcccactg	tcgacagcta	ctgc	c	ttcgc	120
aacgtggagc	tggcg	cagag	caagagga	gtgg	ttctgg	ctgagcagg	180
attggggggc	ggactgtgac	cggcccccggc	aagt	tcgacc	catcg	aaaggcc	240
tactctaacg	agggcgctac	gttctacatc	aacc	agatgt	acgt	gaattt	300
gtccgc	ccaa	ggggcctccc	actgg	gtt	tgg	cacggcg	360
tgggagtcc	atcc	cgatgg	ccgc	cc	cc	agacaggc	420
acagtgtaca	ctattgatca	gccagg	ggc	agg	ggg	acatcc	480
ccattcgggc	agctggagga	ggagtccatc	gtg	acac	cc	tccag	540
gagggggctt	gggtcagg	ga	ccgg	c	cc	ggcag	600
cagttcccc	ggggctacga	ggataattac	ttcaagg	aga	tgg	ctc accatccatc	660

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tcgtctgacg agattgtcga tgccgtggc aagctcgta cccacatcg ggcccttgcgtt	720
ctgggtgacgc atagcgcttc gggcggtcctc gggatgagggg ttgctacaca tgcgaaagac	780
gttcgcggca tcgtggctta cgagccggcc acttccattt tccccaaaggg caaggtgcc	840
gagatcccac cactggccga caagaagtca cagatctcc caccttcga gattcaggag	900
tcttacttca agaagtcgc taagatcccc attcagttcg tggatcgccga caacattcc	960
aagaatccga agagcgcgta ctgggtccctg gatgggtggc gcgtcacgcg ctacgcgcac	1020
tctctctcac tggaggctat caacaagctc gggggccagg cctcgctctt ggacccctt	1080
accgctggcc tgagggggaa caccatttc ccgttacgg atcggaaaca tgccaggtt	1140
gcgtccctcc tgagcgattt cctcgccaaag cacgggctgg atcagaatga gtcttga	1197

<210> SEQ ID NO 5
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the primer 1 for error-prone PCR reaction of
the ALT01 gene

<400> SEQUENCE: 5

atggaaaaccg ataaaaaaaaac cg 22

<210> SEQ ID NO 6
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the primer 2 for error-prone PCR reaction of
the ALT01 gene

<400> SEQUENCE: 6

tcagcttcg ttctgatcta ag 22

<210> SEQ ID NO 7
<211> LENGTH: 398
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the amino acid sequence of the herbicide
tolerant protein ALT01M1

<400> SEQUENCE: 7

Met Glu Thr Asp Lys Lys Thr Gly Thr Ser Arg Arg Ser Phe Val Lys
1 5 10 15Ala Ala Gly Thr Gly Ala Ile Gly Ile Ala Thr Leu Pro Leu Ser Thr
20 25 30Ala Thr Ala Phe Ala Glu Thr Asp Asn Val Glu Leu Ala Gln Ser Lys
35 40 45Arg Lys Val Val Leu Ala Glu Gln Gly Ser Phe Tyr Ile Gly Gly Arg
50 55 60Thr Val Thr Gly Pro Gly Lys Phe Asp Pro Ser Lys Pro Val Ile Pro
65 70 75 80Tyr Ser Asn Glu Gly Ala Thr Phe Tyr Ile Asn Gln Met Tyr Val Asn
85 90 95Phe Gln Ala Pro Val Arg Pro Arg Gly Leu Pro Leu Val Phe Trp His
100 105 110Gly Gly Gly Leu Thr Gly His Ile Trp Glu Ser Thr Pro Asp Gly Arg
115 120 125

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Pro Gly Phe Gln Thr Leu Phe Val Gln Asp Arg His Thr Val Tyr Thr
130 135 140

Ile Asp Gln Pro Gly Arg Gly Arg Gly Asn Ile Pro Thr Phe Asn Gly
145 150 155 160

Pro Phe Gly Gln Leu Glu Glu Ser Ile Val Asn Thr Val Thr Ala
165 170 175

Asn Ser Ser Lys Glu Gly Ala Trp Val Arg Asp Arg Leu Gly Pro Ala
180 185 190

Pro Gly Gln Phe Phe Glu Asn Ser Gln Phe Pro Arg Gly Tyr Glu Asp
195 200 205

Asn Tyr Phe Lys Glu Met Gly Phe Ser Pro Ser Ile Ser Ser Asp Glu
210 215 220

Ile Val Asp Ala Val Val Lys Leu Val Thr His Ile Gly Pro Cys Val
225 230 235 240

Leu Val Thr His Ser Ala Ser Gly Val Leu Gly Met Arg Val Ala Thr
245 250 255

His Ala Lys Asn Val Arg Gly Ile Val Ala Tyr Glu Pro Ala Thr Ser
260 265 270

Ile Phe Pro Lys Gly Lys Val Pro Glu Ile Pro Pro Leu Ala Asp Lys
275 280 285

Lys Ser Gln Ile Phe Pro Pro Phe Glu Ile Gln Glu Ser Tyr Phe Lys
290 295 300

Lys Leu Ala Lys Ile Pro Ile Gln Phe Val Phe Gly Asp Asn Ile Pro
305 310 315 320

Lys Asn Pro Lys Ser Ala Tyr Trp Phe Leu Asp Trp Trp Arg Val Thr
325 330 335

Arg Tyr Ala His Ser Leu Ser Leu Glu Ala Ile Asn Lys Leu Gly Gly
340 345 350

Gln Ala Ser Leu Leu Asp Leu Pro Thr Ala Gly Leu Arg Gly Asn Thr
355 360 365

His Phe Pro Phe Thr Asp Arg Asn Asn Val Gln Val Ala Ser Leu Leu
370 375 380

Ser Asp Phe Leu Gly Lys His Gly Leu Asp Gln Asn Glu Ser
385 390 395

<210> SEQ ID NO 8
<211> LENGTH: 1197
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT01M1 nucleotide sequence encoding the
amino acid sequence of the herbicide tolerant protein ALT01M1

<400> SEQUENCE: 8

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atggaaacctg ataaaaaaaaac cggAACgtcc cgcagatcat ttgtgaaggc tgctggacc 60
ggcgcaatag gaatagcgac gctggcgctt tcgactgcaa ctgctttcgc ggaaaactgac 120
aacgtggagc ttgcccaatc gaagcggaaag gttgtccttg ctgaaacaagg cagtttctac 180
atcggggca gaacagtaac cgggcctgga aaattcgatc cgtcaaagcc ggtattcca 240
tattccaacg aagggtgccac gtttatatac aatcaaatgt acgtaaaactt tcaagctcct 300
gtgcgcctc gtgggctgcc tctagtcttt tggcatgggg gcggactaac cggccatatc 360
tggaaatcta cccccagacgg ccgcggggta tttcagaccc tctttgttca agatcgccat 420
acgggtctaca cgattgtatca gccaggcgcc ggaaggggca atattcctac cttaatggc 480
ccttttgggc agtttggaga agagtcgatt gttaacactg ttaccgcaaa ctccagtaaa 540
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gaaggagcgt gggtagaga tcgactaggg cccgctccc ggcagtttt tgagaacagc      600
caattccac gtggttatga agacaactac ttcaaggaga tggggttcag tccgtcgatc      660
tcatcagatg agatagtcga cgctgttgtt aaactagtaa ctcacatagg tccttgtt      720
ctggtgaccc attcggctc cgaggactg ggcacatgcgag tcgcacacaca cgccaagaac      780
gtgaggggga tcggtgttga tgagcctcg acaagtatct ttccaaagg aaaagtgcct      840
gagataccgc ctctcgccga taaaaagtgc caaatttcc cgccgttgc gatccaggag      900
tcttacttta agaagctcgc gaagataccc attcagtttgc ttctggaga taatatcccc      960
aagaacccta aatccgccta ttgggtcttg gactgggtgg aagtcaactcg ctacgctcac    1020
agcttgcac tcgaggctat caataagctc ggtggtaaag cgtctttt ggatttgcg      1080
actgcgggac ttgcggcaa cacgcattt ccattcaccg accggaataa cgtgcaggc      1140
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<210> SEQ ID NO 9
<211> LENGTH: 1197
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT01M1-01 nucleotide sequence encoding the
      amino acid sequence corresponding to the herbicide tolerant
      protein ALT01M1 and based on the soybean codon usage bias

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<400> SEQUENCE: 9
atggagactg ataagaaaac tggcacatct agaaggctat ttgttaaggc tgcaggaaca      60
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aacgtggaaac tcgccaatc taagaaaaag gtgggtgtgg ctgaacaagg gtcattttac      180
atagggggta ggactgttac tggcctggc aagtttgcat catccaaacc tgtgataccc      240
tacagtaacg aaggagcaac attctatatt aaccaaattgt atgttaactt ccaggccca      300
gtgagaccta ggggacttcc attggtttgc tggcatggag gtggcttgc tggcacatc      360
tgggagtcata cacctgacgg cagaccgggg tttcaaaacc ttttcgttca ggataggcat      420
accgtgtaca ctattgacca acctgggaga ggaaggggta acatccaaac ttttaacggg      480
ccttcggac agttggagga agagagtatt gttaacactg tgacagccaa ttcttcaag      540
gaaggtgcct gggtagaga taggcttgc cctgctcccg ggcaattttt cgagaactct      600
cagtttctta gaggctatga agacaattac tttaaggaga tgggattcag cccatctata      660
tccagtgtatg aaattgttgc cgctgttgtt aaactcgatc cccatattgg tccttgtt      720
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gttaggggaa ttgtggccta tgaaccagct acctcaatct tcccaaggaaaaggttcca      840
gagataccac ctctcgctga taagaaaagg caaatcttc cccattcga aatacaggag      900
tcttacttta agaaacttgc caagattcca atccaatttg ttttcggaga taacatcccc      960
aagaatccaa aatcagcata ttggttctcg gactgggtgg aagtgcacaa atacgcacat    1020
agtctcagcc tggaggccat aaacaatttg gggggacaag cttccctttt ggatcttcct    1080
actgcaggat tgagaggtaa tacacactt cccttcaccc ataggaacaa tggtcaggatg    1140
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<210> SEQ ID NO 10
<211> LENGTH: 1197
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT01M1-02 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT01M1 and based on the maize codon usage bias

<400> SEQUENCE: 10

atggagac	acaagaagac	cggcacgtcc	cgcaggagct	tcgtgaaggc	tgctggcacc	60
ggggctatcg	ggattgctac	gctcccactg	tcgacagcta	ctgccttcgc	ggagactgat	120
aacgtggagc	tggcgcagag	caagaggaag	gtggttctgg	ctgagcaggg	gtcgttctac	180
attggggggc	ggactgtgac	cgggccccgc	aagttcgacc	catcgaaagcc	tgtcattccg	240
tactctaacf	agggcgctac	gttctacatc	aaccagatgt	acgtgaattt	ccaggctccc	300
gtccgccccaa	ggggcctccc	actgggtgttc	tggcacggcg	ggggcctgac	aggccatata	360
tgggagtcca	ctccagatgg	ccgccccaggg	ttccagacac	tcttcgttca	ggacaggcac	420
acagtgtaca	ctattgtatc	gccaggggagg	ggcagggggga	acateccctac	cttcaatggc	480
ccatttcgggc	agctggagga	ggagtcacatc	gtgaacacccg	tcacggcgaa	ttccagcaag	540
gagggggcctt	gggtcaggga	ccggctcgcc	ccggccccag	ggcagtttctt	cgagaactct	600
cagttccccc	ggggctacga	ggataattac	ttcaaggaga	tgggcttctc	accatccatc	660
tcgtctgacg	agattgtcga	tgccgttgcc	aagctcgta	cccacatcg	cccttgcgtt	720
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gttcggggca	tcgtggctta	cgagccggcc	acttccattt	tccccaaggg	caaggtgcga	840
gagatccccac	caactggccga	caagaagtca	cagatcttcc	caccttcga	gattcaggag	900
tcctacttca	agaagctcgc	taagatcccc	attcagttcg	tgttggcga	caaacattct	960
aagaatccga	agagcgcgta	ctgggttcctg	gattggtggc	gcgtcacgcg	ctacgcgcac	1020
tctctctcac	tggaggctat	caacaagtc	gggggcctagg	cctcgctcct	ggacccctt	1080
accgtggcc	tgagggggaa	caccatttc	ccgttacccg	atcgaaacaa	tgtccagggt	1140
gcgtccctcc	tgaggcgatt	cctcgqcaaq	cacqgqctqq	atcagaatqa	qtcttqa	1197

<210> SEQ ID NO 11
<211> LENGTH: 398
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the amino acid sequence of the herbicide
tolerant protein ALT01M2

<400> SEQUENCE: 11

Met	Glu	Thr	Asp	Lys	Lys	Thr	Gly	Thr	Ser	Arg	Arg	Ser	Phe	Val	Lys
1				5					10						15

Ala Ala Gly Thr Gly Ala Ile Gly Ile Ala Thr Leu Pro Leu Ser Thr
 20 25 30

Ala Thr Ala Phe Ala Glu Thr Asp Asn Val Glu Leu Ala Gln Ser Lys
35 40 45

Arg Lys Val Val Leu Ile Ile Cys Cys Ser Thr Tyr Ile Cys Cys Arg
50 55 60

Thy-Ser-Ala-Glu-Gly-Gly-Ala-Thy-Phe-Thy-Ile-Ala-Glu-Met-Thy-His-Ala

Phe Gln Ala Pro Val Arg Pro Arg Gly Leu Pro Leu Val Phe Trp His

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Gly Gly Gly Leu Thr Gly His Ile Trp Glu Ser Thr Pro Asp Gly Arg
115 120 125

Pro Gly Phe Gln Thr Leu Phe Val Gln Asp Arg His Thr Val Tyr Thr
130 135 140

Ile Asp Gln Pro Gly Arg Gly Arg Asn Ile Pro Thr Phe Asn Gly
145 150 155 160

Pro Phe Gly Gln Leu Glu Glu Ser Ile Val Asn Thr Val Thr Gly
165 170 175

Asn Val Ser Lys Glu Gly Ala Trp Val Arg Asp Arg Leu Gly Pro Ala
180 185 190

Pro Gly Gln Phe Phe Glu Asn Ser Gln Phe Pro Arg Gly Tyr Glu Asp
195 200 205

Asn Tyr Phe Lys Glu Met Gly Phe Ser Pro Ser Ile Ser Ser Asp Glu
210 215 220

Ile Val Asp Ala Val Val Lys Leu Val Thr His Ile Gly Pro Cys Val
225 230 235 240

Leu Val Thr His Ser Ala Ser Gly Val Leu Gly Met Arg Val Ala Thr
245 250 255

His Ala Lys Asn Val Arg Gly Ile Val Ala Tyr Glu Pro Ala Thr Ser
260 265 270

Ile Phe Pro Lys Gly Lys Val Pro Glu Ile Pro Pro Leu Ala Asp Lys
275 280 285

Lys Ser Gln Ile Phe Pro Pro Phe Glu Ile Gln Glu Ser Tyr Phe Lys
290 295 300

Lys Leu Ala Lys Ile Pro Ile Gln Phe Val Phe Gly Asp Asn Ile Pro
305 310 315 320

Lys Asn Pro Lys Ser Ala Tyr Trp Phe Leu Asp Trp Trp Arg Val Thr
325 330 335

Arg Tyr Ala His Ser Leu Ser Leu Glu Ala Ile Asn Lys Leu Gly Gly
340 345 350

Gln Ala Ser Leu Leu Asp Leu Pro Thr Ala Gly Leu Arg Gly Asn Thr
355 360 365

His Phe Pro Phe Thr Asp Arg Asn Asn Val Gln Val Ala Ser Leu Leu
370 375 380

Ser Asp Phe Leu Gly Lys His Gly Leu Asp Gln Asn Glu Ser
385 390 395

<210> SEQ_ID NO 12
<211> LENGTH: 1197
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT01M2 nucleotide sequence encoding the
amino acid sequence of the herbicide tolerant protein ALT01M2

<400> SEQUENCE: 12

```

atggaaaaccg ataaaaaaac cggAACgtcc cgcagatcat ttgtgaaggc tgctggacc 60
ggcgcaatag gaatacgac gctgcgcctt tcgactgc aa ctgcttcgc ggaaactgac 120
aacgtggagc ttgccccatc gaagcggaa gttgtccctt ctgaacaagg cagttctac 180
atcggggca gaacagtaac cgggcctgaa aaattcgatc cgtcaaagcc ggtaattcca 240
tattccaacg aagggtccac gtttatatc aatcaaactg acgtaaactt tcaagctct 300
gtgcgcctc gtgggtcgcc tcttagtctt tggcatgggg gcggactaac cggccatatc 360
tggaaatcta ccccaagacgg ccggcccgga tttcagaccc tctttgttca agatcggcat 420

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acgggtctaca	cgattgatca	gccagggcgc	ggaaggggca	atattcctac	cttaatggc	480
ccttttggc	agtttgaaga	agagtgcatt	gttaacactg	ttaccggaaa	cgtcagtaaa	540
gaaggagcgt	gggttagaga	tcgacttaggg	cccgctccc	gccagtttt	tgagaacagc	600
caattccac	gtggttatga	agacaactac	ttaaggaga	tggggttcag	tccgtcgatc	660
tcatcagatg	agatagtcga	cgctgttgtt	aaactagtaa	ctcacatagg	tccttgttt	720
ctgggtgaccc	attcggcttc	cgggactctg	ggcatgcgag	tgcgcacaca	cggcaagaac	780
gtgaggggga	tcgttgctta	tgaggctcg	acaagtatct	ttcccaaagg	aaaagtgcct	840
gagataccgc	ctctcgccga	taaaaaagtgc	caaattttcc	cgcgcgttca	gatccaggag	900
tcttacttta	agaagctcgc	gaagataccc	attcagtttgc	tcttcggaga	taatatcccc	960
aagaacccta	aatccgccta	ttgggtcttg	gactgggtgg	gagtcaactcg	ctacgctcac	1020
agcttgtcac	tcgaggctat	caataagctc	ggtggtaag	cgtcttttt	ggatttgcgg	1080
actgcgggac	ttcgcggcaa	cacgcatttt	ccattcaccc	accggaaataa	cgtgcagggtc	1140
gcttctctgt	tatctgattt	cctcgaaag	cacggcttag	atcagaacga	aagctga	1197

<210> SEQ ID NO 13
<211> LENGTH: 1197
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT01M2-01 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT01M2 and based on the soybean codon usage bias

<400> SEQUENCE: 13						
atggagactg	ataagaaaac	tggcacatct	agaaggcat	ttgttaaggc	tgcaggaaca	60
ggtgccattg	gaatcgctac	ccttccattg	tccaccgc	ctgcttcgc	agagactgtat	120
aacgttggac	tcgccaatc	taagagaaag	gtgggtctgg	ctgaacaagg	gtcattttac	180
atagggggta	gactgttac	ttggccttgc	aagtttgc	atccaaacc	tgtgataccc	240
tcagtaacg	aaggagcaac	attctatatt	aaccaaatgt	atgttaactt	ccaggccca	300
gtgagaccta	ggggacttcc	attggtttcc	tggcatggag	gtggcttgc	tggtcacatc	360
tgggagtcta	cacctgacgg	cagaccgggg	tttcaaacc	tcttcgttca	ggataggcat	420
accgtgtaca	ctattgacca	acctgggaga	ggaagggtta	acatccaaac	tttaacggaa	480
ccttcggac	agttggagga	agagagtatt	gttaacactg	tgacaggaaa	tgtatcaaag	540
gaaggtgcct	gggtgagaga	taggcttgc	cctgctccc	ggcaattttt	cgagaactct	600
cagtttccata	gaggctatga	agacaattac	ttaaggaga	tggattcag	cccatctata	660
tccagtgatg	aaattgttga	cgctgttgtt	aaactcgta	cccatattgg	tccttgttt	720
ctgggtgactc	actcagcatc	cgcgcttctt	gggatgagag	tggctacaca	cgcaaagaat	780
gttaggggaa	ttgtggccta	tgaaccagct	acctcaatct	tcccaaggaa	aaaagtccca	840
gagataccac	ctctcgctga	taagaaaagc	caaattttc	ccccattcga	aatacaggag	900
tcttacttta	agaaacttgc	caagattca	atccaatttg	ttttcggaga	taatcatcccc	960
aagaatccaa	aatcagcata	ttggttcttg	gactgggtgg	gagtgacaag	atacgcacat	1020
agtctcagcc	tggaggccat	aaacaaatttgc	gggggacaag	cttccctttt	ggatcttcct	1080
actgcaggat	tgagaggtaa	tacacacttt	cccttcaccc	ataggaacaa	tgttcagggt	1140
gcttctctcc	tgtcagactt	tctgggtaaa	cacggcttgc	atcaaaatga	gagctga	1197

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<210> SEQ ID NO 14
<211> LENGTH: 1197
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT01M2-02 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT01M2 and based on the maize codon usage bias

<400> SEQUENCE: 14

atggagacag acaagaagac cggcacgtcc	cgcaggagct tcgtgaaggc tgctggcacc	60
ggggctatcg ggattgctac gctccactg	tcgcacagcta ctgccttcgc ggagactgat	120
aacgtggagc tggcgccagag caagaggaag	gtggttctgg ctgagcaggg gtcgttctac	180
attggggggc ggactgtgac cggccccgc	aagttcgacc catcgaagcc tgtcattccg	240
tactctaacf agggcgctac gttctacatc	aaccagatgt acgtgaattt ccaggctccc	300
gtccgccccaa ggggcctccc actgggttcc	tggcacggcg ggggcctgac aggccatatc	360
tgggagtcca ctccagatgg ccggcccgagg	ttccagacac tcttcgttca ggacaggcac	420
acagtgtaca ctattgtatca gccaggggagg	ggcagggggg acatccctac cttcaatggc	480
ccattcgggc agctggagga ggagtccatc	gtgaacaccg tcacgggcaa tgtgagcaag	540
gagggggcctt gggtcaggga ccggctcgcc	ccggcccccag ggcagtttt cgagaactct	600
cagttccccc ggggcctacga ggataattac	ttcaaggaga tgggcttctc accatccatc	660
tcgtctgacg agattgtcga tgccgtggcc	aagctcgta cccacatcg cccttgcgtt	720
ctgggtgacgc atagcgcttc gggcgctctc	ggatgaggg ttgctacaca tgcgaagaac	780
gttcgcggca tcgtggctta cgagccggcc	acttccattt tcccaaggg caaggtgcca	840
gagatccac cactggccga caagaagtca	cagatcttcc caccttcga gattcaggag	900
tcctacttca agaagctcgc taagatcccc	attcagttcg tggcggcga caacattcct	960
aagaatccga agagcgcgta ctgggtccctg	gattggtgcc gcgtcacgca ctacgcac	1020
tctctctcac tggaggctat caacaagctc	ggggccagg cctcgctctt ggacccct	1080
accgctggcc tgagggggaa caccatttc	cgttcacgg atcggaaaca tgtccaggtt	1140
gctccctcc tgagcgattt cctcggaag	cacggctgg atcagaatga gtcttga	1197

<210> SEQ ID NO 15
<211> LENGTH: 398
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the amino acid sequence of the herbicide tolerant protein ALT01M3

<400> SEQUENCE: 15

Met	Glu	Thr	Asp	Lys	Lys	Thr	Gly	Thr	Ser	Arg	Arg	Ser	Phe	Val	Lys		
1								5						10	15		
Ala	Ala	Gly	Thr	Gly	Ala	Ile	Gly	Ile	Ala	Thr	Leu	Pro	Leu	Ser	Thr		
														25	30		
Ala	Thr	Ala	Phe	Ala	Glu	Thr	Asp	Asn	Val	Glu	Leu	Ala	Gln	Ser	Lys		
														35	40	45	
Arg	Lys	Val	Val	Leu	Ala	Glu	Gln	Gly	Ser	Phe	Tyr	Ile	Gly	Gly	Arg		
														50	55	60	
Thr	Val	Thr	Gly	Pro	Gly	Lys	Phe	Asp	Pro	Ser	Lys	Pro	Val	Ile	Arg		
														65	70	75	80
Ala	Ser	Asn	Glu	Gly	Ala	Thr	Phe	Tyr	Ile	Asn	Gln	Met	Tyr	Val	Asn		

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85	90	95
Phe Gln Ala Pro Val Arg Pro Arg Gly Leu Pro Leu Val Phe Trp His		
100	105	110
Gly Gly Gly Leu Thr Gly His Ile Trp Glu Ser Thr Pro Asp Gly Arg		
115	120	125
Pro Gly Phe Gln Thr Leu Phe Val Gln Asp Arg His Thr Val Tyr Thr		
130	135	140
Ile Asp Gln Pro Gly Arg Gly Arg Gly Asn Ile Pro Thr Phe Asn Gly		
145	150	155
160		
Pro Phe Gly Gln Leu Glu Glu Ser Ile Val Asn Thr Val Thr Ala		
165	170	175
Asn Val Ser Lys Glu Arg Ala Trp Val Arg Asp Arg Leu Gly Pro Ala		
180	185	190
Pro Gly Gln Phe Phe Glu Asn Ser Gln Phe Pro Arg Gly Tyr Glu Asp		
195	200	205
Asn Tyr Phe Lys Glu Met Gly Phe Ser Pro Ser Ile Ser Ser Asp Glu		
210	215	220
Ile Val Asp Ala Val Val Lys Leu Val Thr His Ile Gly Pro Cys Val		
225	230	235
240		
Leu Val Thr His Ser Ala Ser Gly Val Leu Gly Met Arg Val Ala Thr		
245	250	255
His Ala Lys Asn Val Arg Gly Ile Val Ala Tyr Glu Pro Ala Thr Ser		
260	265	270
Ile Phe Pro Lys Gly Lys Val Pro Glu Ile Pro Pro Leu Ala Asp Lys		
275	280	285
Lys Ser Gln Ile Phe Pro Pro Phe Glu Ile Gln Glu Ser Tyr Phe Lys		
290	295	300
Lys Leu Ala Lys Ile Pro Ile Gln Phe Val Phe Gly Asp Asn Ile Pro		
305	310	315
320		
Lys Asn Pro Lys Ser Ala Tyr Trp Phe Leu Asp Trp Trp Arg Val Thr		
325	330	335
Arg Tyr Ala His Ser Leu Ser Leu Glu Ala Ile Asn Lys Leu Gly Gly		
340	345	350
Gln Ala Ser Leu Leu Asp Leu Pro Thr Ala Gly Leu Arg Gly Asn Thr		
355	360	365
His Phe Pro Phe Thr Asp Arg Asn Asn Val Gln Val Ala Ser Leu Leu		
370	375	380
Ser Asp Phe Leu Gly Lys His Gly Leu Asp Gln Asn Glu Ser		
385	390	395

<210> SEQ ID NO 16
 <211> LENGTH: 1197
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: the ALT01M3 nucleotide sequence encoding the
 amino acid sequence of the herbicide tolerant protein ALT01M3

<400> SEQUENCE: 16

atggaaaaccg ataaaaaaac cggAACgtcc cgcaGATCAT ttgtGAAGGC tgctggAACc	60
ggcgcaatag gaatAGCgac gctGCCGCTT tcgACTGCAA ctgcTTcgc ggAAactgac	120
aacGTggAGC ttGCCCAATC gaAGGGAAG gttGTCCTTG ctGAAACAGG cAGTTCTAC	180
atcGGGGGCA gaACAGTAAC cggGCTGGA aaATTcGATC cgtCAAAGCC ggTAATTcGA	240
gcttccaACG aaggTgCCAC gtttatATC aatcaaATG acgtAAACtt tcaAGCTCCT	300

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gtgcgcctc gtgggctgcc tctagtcttt tggcatgggg gcggactaac cggccatatc      360
tggaaatcta ccccagacgg ccgcggcgga ttccagacc tctttgttca agatccggcat      420
acgggtctaca cgattgtatca gccaggggcg ggaaggggca atattctac cttaatggc      480
ccttttgggc agtttggaga agagtcgatt gttaacactg ttaccgcaaa cgtcagtaaa      540
gaaagagcgt gggtagaga tcgactaggg cccgcctccg gccagtttt tgagaacagc      600
caattccac gtgggtatga agacaactac ttcaaggaga tggggttcag tccgtcgatc      660
tcatcagatg agatagtcga cgctgttgg aaacttagtaa ctcacatagg tccttgcgtt      720
ctgggtgaccc attcggcttc cgaggactg ggcatgcgag tccgcacaca cgccaagaac      780
gtgagggggga tcgttgctta tgagctcgg acaagtatct ttcccaaagg aaaagtgcct      840
gagataccgc ctctcgccga taaaaaagtgc caaatttcc cgccgttca gatccaggag      900
tcttacttta agaagctcgc gaagataccc attcagtttgc tcttcggaga taatatcccc      960
aagaacccta aatccgccta ttgggtcttg gactggtgaa gactcactcg ctacgctcac      1020
agcttgtcac tcgaggctat caataagctc ggtggtaag cgtctttt ggatttgcgg      1080
actgcgggac ttgcggcaa cacgcattt ccattcaccg accggaataa cgtgcaggc      1140
gtttctgttatctgattt cctcgaaaag cacggcttag atcagaacga aagctga      1197

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<210> SEQ ID NO 17
<211> LENGTH: 1197
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT01M3-01 nucleotide sequence encoding the
      amino acid sequence corresponding to the herbicide tolerant
      protein ALT01M3 and based on the soybean codon usage bias

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<400> SEQUENCE: 17

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atggagactg ataagaaaac tggcacatct agaaggcat ttgttaaggc tgcaggaaca      60
ggtgccattt gaatcgctac cttccattt tccaccgcga ctgcatttgc agagactgtat      120
aacgttggaa tcgcccatac taagagaaag gtgggtgttgc ctgaacaagg gtcattttac      180
atagggggta ggactgttac tggccttggc aagtttgcattt catccaaacc tgtgatacga      240
cccgactaacg aaggagcaac attctatatt aaccaaattgt atgttaactt ccaggccca      300
gtgagaccta ggggacttcc attgggttttgc tggcatggag gtggcttgc tggcacatc      360
tgggagtcata cacctgacgg cagaccggg tttccaaacc tcttcgttca ggataggcat      420
accgtgtaca ctattgacca acctgggaga ggaagggttgc acatccaaac ttttaacggg      480
ccttcggac agttggagga agagacttgc gttaacactg tgacagccaa tgtatcaaag      540
gaacgagccct ggggtggaga taggcttggc cctgcctccg ggcaattttt cgagaactct      600
cagtttccata gaggctatga agacaatttgc tttaaggaga tggatttgc cccatctata      660
tccagtgatg aaattgttgc cgctgttgc aaactcgatc cccatatttttgc tcccttgcgtt      720
ctgggtgactc actcagcatc cggcggttctt gggatggag tggctacaca cgccaaagaat      780
gttagggggaa ttgtggccata tgaaccatgc acctcaatct tccccaaggaaaaggttcca      840
gagataccac ctctcgctga taagaaaagc caaatcttc ccccatcgaa aatacaggag      900
tcttacttta agaaacttgc caagtttca atccaatttttgc ttttgcgttgc taacatcccc      960
aagaatccaa aatcagcata ttgggttccgttgc gactggtgaa gactgacaag atacgcacat      1020
agtctcagcc tggaggccat aaacaaatttgc gggggacaag cttccctttt ggatcttcc      1080

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actgcaggat tgagaggtaa tacacacttt cccttcaccg ataggaacaa tgttcaggtg 1140  
gcttctctcc tgcagactt tctgggtaaa cacggtgtgg atcaaaatgaa gagctga 1197
```

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<210> SEQ ID NO 18
<211> LENGTH: 1197
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT01M3-02 nucleotide sequence encoding the
      amino acid sequence corresponding to the herbicide tolerant
      protein ALT01M3 and based on the maize codon usage bias
```

<400> SEQUENCE: 18

atggagacac acaagaagac cggcacgtcc cgccaggagct tcgtgaaggc tgctggcacc
ggggctatcg ggattgctac gctccccactg tcgacagacta ctgccttcgc ggagactgat 120
aacgtggagc tggcgcagag caagaggaag gtggttctgg ctgagcaggg gtcgttctac 180
attggggggc ggactgtgac cggggccggc aagttcgacc catcgaagcc tgtcatcgg 240
gcgtctaacf agggcgctac gttctacatc aaccagatgt acgtgaattt ccaggctccc 300
gtccgcacaa ggggctccc actgggttgc tggcacggcg ggggctgac aggccatata 360
tgggagtcca ctccagatgg cggccccagg ttccagacac tcttcgttca ggacaggcac 420
acagtgtaca ctattgtatca gccagggagg ggcagggggg acatccctac cttcaatggc 480
ccattcgcc agctggagga ggagtccatc gtgaacaccg tcacggcgaa tggtagcaag 540
gagcgggctt gggtcagggg cggctcgcc cggccccagg ggcagtctt cgagaactct 600
cagttccccc ggggctacga ggataattac ttcaaggaga tgggcttctc accatccatc 660
tcgtctgacy agattgtcga tggcggttgc aagctcgta cccacatcg cccttgcgtt 720
ctggtgacgc atagcgcttc gggcgcttgc gggatgaggg ttgctacacaca tgcgaagaac 780
gttcggggca tggggcttca cgagccggcc acttccattt tcccaaggc caaggtgcca 840
gagatccac cactggccga caagaagtca cagatcttcc caccttcga gattcaggag 900
tcctacttca agaagctcgc taagatcccc attcagttcg tggcggttgc caacattct 960
aagaatccga agagcgctga ctgggttccgt gattgggtggc gcgtcacgcg ctacgcgcac 1020
tctctctcac tggaggctat caacaagtc gggggccagg cctcgcttgc ggacccctt 1080
accgctggcc tgagggggaa caccatc cgttacgg atcggaaacaa tggcagggtt 1140
gcgtcccccc tggcgatcc cctcggttgc cacgggttgc atcagaatga tgcgttgc 1197

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<210> SEQ ID NO 19
<211> LENGTH: 369
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the amino acid sequence of ALT02
```

<400> SEQUENCE: 19

Met	Glu	Thr	Asp	Asn	Val	Glu	Leu	Ala	Gln	Ser	Lys	Arg	Lys	Val	Val
1					5					10					15

Leu Ala Glu Gln Gly Ser Phe Tyr Ile Gly Gly Arg Thr Val Thr Gly
 20 25 30

Pro Gly Lys Phe Asp Pro Ser Lys Pro Val Ile Pro Tyr Ser Asn Glu
 35 40 45

Gly Ala Thr Phe Tyr Ile Asn Gln Met Tyr Val Asn Phe Gln Ala Pro
50 55 60

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65	70	75	80
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Thr Gly His Ile Trp Glu Ser Thr Pro Asp Gly Arg Pro Gly Phe Gln 85	90	95
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Thr Leu Phe Val Gln Asp Arg His Thr Val Tyr Thr Ile Asp Gln Pro 100	105	110
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Gly Arg Gly Arg Gly Asn Ile Pro Thr Phe Asn Gly Pro Phe Gly Gln 115	120	125
--	-----	-----

Leu Glu Glu Glu Ser Ile Val Asn Thr Val Thr Gly Asn Ser Ser Lys 130	135	140
--	-----	-----

Glu Gly Ala Trp Val Arg Asp Arg Leu Gly Pro Ala Pro Gly Gln Phe 145	150	155	160
--	-----	-----	-----

Phe Glu Asn Ser Gln Phe Pro Arg Gly Tyr Glu Asp Asn Tyr Phe Lys 165	170	175
--	-----	-----

Glu Met Gly Phe Ser Pro Ser Ile Ser Ser Asp Glu Ile Val Asp Ala 180	185	190
--	-----	-----

Val Val Lys Leu Val Thr His Ile Gly Pro Cys Val Leu Val Thr His 195	200	205
--	-----	-----

Ser Ala Ser Gly Val Leu Gly Met Arg Val Ala Thr His Ala Lys Asn 210	215	220
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Val Arg Gly Ile Val Ala Tyr Glu Pro Ala Thr Ser Ile Phe Pro Lys 225	230	235	240
--	-----	-----	-----

Gly Lys Val Pro Glu Ile Pro Pro Leu Ala Asp Lys Lys Ser Gln Ile 245	250	255
--	-----	-----

Phe Pro Pro Phe Glu Ile Gln Glu Ser Tyr Phe Lys Lys Leu Ala Lys 260	265	270
--	-----	-----

Ile Pro Ile Gln Phe Val Phe Gly Asp Asn Ile Pro Lys Asn Pro Lys 275	280	285
--	-----	-----

Ser Ala Tyr Trp Phe Leu Asp Trp Trp Arg Val Thr Arg Tyr Ala His 290	295	300
--	-----	-----

Ser Leu Ser Leu Glu Ala Ile Asn Lys Leu Gly Gly Gln Ala Ser Leu 305	310	315	320
--	-----	-----	-----

Leu Asp Leu Pro Thr Ala Gly Leu Arg Gly Asn Thr His Phe Pro Phe 325	330	335
--	-----	-----

Thr Asp Arg Asn Asn Val Gln Val Ala Ser Leu Leu Ser Asp Phe Leu 340	345	350
--	-----	-----

Gly Lys His Gly Leu Asp Gln Asn Glu Ser Lys Leu Ala Ala Ala Leu 355	360	365
--	-----	-----

Glu

<210> SEQ ID NO 20
<211> LENGTH: 1110
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT02 nucleotide sequence encoding the amino acid sequence of ALT02

<400> SEQUENCE: 20

atggaaactg acaacgtgga gcttgcccaa tcgaagcgga aggttgtcct tgctgaacaa	60
ggcagtttct acatcgaaaa cagaacagta accgggcctg gaaaattcga tccgtcaaag	120
cccgtaattc catattccaa cgaagggtgcc acgtttata tcaatcaaat gtacgttaaac	180
tttcaagtc ctgtgcgccc tcgtggctg cctctagtct ttggcatgg gggcgacta	240
accggccata tctggaaatc tacccagac ggccgccccg gatttcagac cctctttgtt	300

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caagatcgcc atacggtctta cacgattgt cagccaggc gggaaagggg caatattct	360
acctttaatg gccctttgg gcagttggaa gaagagtcta ttgttaaacac tggttaccgg	420
aactccagta aagaaggagc gtgggttaga gatcgactag ggcccgcctcc cgccagtt	480
tttgagaaca gccaattccc acgtgggtat gaagacaact acttcaagga gatggggttc	540
agtccgtcga tctcatcaga tgagatagtc gacgctgttg ttaaactagt aactcacata	600
ggtccttgtt ttctgggtac ccattcggt tccggagtagt tggggatgc agtgcgaca	660
cacgccaaga acgtgagggg gategttgc tatgagcctg cgacaagtat ctccccaaa	720
ggaaaagtgc ctgagatacc gcctctcgcc gataaaaagt cgcaaatttt cccgggttc	780
gagatccagg agtcttactt taagaagctc gcgaagatac ccattcagtt tgtcttcgg	840
gataatatcc ccaagaaccc taaatccgcc tattgggtct tggactgggt gagagtca	900
cgctacgctc acagcttgc actcgaggt atcaataagc tcgggtgtca agcgctctt	960
ttggatttgc cgactgcggg acttcgcggc aacacgcatt ttccattcac cgaccggaa	1020
aacgtgcagg tgcgttctct gttatctgtat ttccctcgaa agcacggctt agatcagaac	1080
gaaagcaaac ttgctgtgc tcttgagtga	1110

<210> SEQ ID NO 21
<211> LENGTH: 1110
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT02-01 nucleotide sequence encoding the amino acid sequence corresponding to the ALT02 and based on the soybean codon usage bias

<400> SEQUENCE: 21

atggagactg ataacgtgga actcgccaa tctaagagaa aggtgggtct ggctgaacaa	60
gggtcatttt acataggggg taggactgtt actggtcctg gcaagttga tccatccaa	120
cctgtgatac cctacagtaa cgaaggagca acattctata ttaaccaa at gtatgttaac	180
ttccaggccc cagttagacc tagggactt ccattggttt tctggcatgg aggtggcttg	240
actggtcaca tctggagtc tacacctgac ggcagacccg ggtttcaaac cctttcg	300
caggataggc ataccgtgta cactattgac caacctggga gaggaagggg taacatcc	360
acttttaacg gaccttcgg acatgtggag gaagagtagt ttgttaaacac tgcacagga	420
aattcttcaa aggaagggtc ctgggtgaga gataggctt gccctgtcc cggcaattt	480
ttcgagaact ctcagttcc tagaggctat gaagacaattt actttaaggaa gatgggattc	540
agcccatcta tatccagtga tgaaattgtt gacgctgttg tgaaactcgt gacccatatt	600
ggtccttgtt ttctgggtac tcactcagca tccggcggtt ttgggtatgag agtggctaca	660
cacgcaaaga atgttagggg aattgtggcc tatgaaccag ctacctaattt cttccccaa	720
ggaaaagtgc cagagatacc acctctcggt gataagaaaa gccaatctt tccccatcc	780
gaaatacagg agtcttactt taagaaactt gccaagattt caatccattt tggttccgg	840
gataacatcc ccaagaatcc aaaatcagca tattgggtcc tggactgggt gagagtgaca	900
agatacgcac atagtctcag cctggaggcc ataaacaaat tggggggaca agcttccctt	960
ttggatctt ctaactgcagg attgagaggt aatacacact ttcccttcac cgataggaa	1020
aatgttcagg tggcttctct cctgtcagac ttccctggta aacacggctt ggatcaaaat	1080
gagagcaaac tcggccgcgc cctggaaatga	1110

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<210> SEQ ID NO 22
<211> LENGTH: 1110
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT02-02 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT02 and based on the maize codon usage bias

<400> SEQUENCE: 22

atggagactg ataacgtgga gctggcgca	60
gggtcggttct acattggggg gcgactgtg accggggccg gcaagttca cccatcgaa	120
cctgtcattc cgtactctaa cgaggggcgt acgttctaca tcaaccagat gtacgtaat	180
ttccagggtc ccgtccgccc aaggggccctc ccactggtgt tctggcacgg cgggggcctg	240
acaggccata tctgggagtc cactccagat ggccgccccag ggttccagac actttcgtt	300
caggacaggc acacagtgt a cactattgt cagccaggaa ggggcaggaa gaacatccct	360
accttcaatg gcccattcgg gcagctggag gaggagtcga tcgtgaacac cgtcacggc	420
aattccagca aggagggggc ttgggtcagg gaccggctcg gcccggcccc agggcagttc	480
ttagagaact ctcaaggccc cccgggctac gaggataatt acttcaagga gatgggcttc	540
tcaccatcca ttcgtctga cgagattgtc gatgccgtgg tcaagctgt tacccacatc	600
ggcccttgcg ttctggtgac gcatacgctc tcggggctc tcgggtatgg ggttgctaca	660
catgcgaaga acgttgcgg categtggcgt ttcggccgg ccacttccat tttccccaa	720
ggcaagggtgc cagagatccc accactggcc gacaagaagt cacagatctt cccaccttc	780
gagattcagg agtccctactt caagaagctc gctaagatcc ccattcagg tctgttccgc	840
gacaacatcc ctaagaatcc gaagagcgcg tactgggtcc tggattgggt ggcgcgtc	900
cgctacgcgc actctctctc actggaggct atcaacaagc tcgggggcca ggcctcgctc	960
ctggacccctc ctaccgctgg cctgaggggg aacacccatt tcccggtcac ggatcgaa	1020
aatgtccagg ttgcgtccct cctgagcgtat ttcctcgca agcacggct ggtatcagaat	1080
gagtctaaggc tcgctgcggc gctggagtga	1110

<210> SEQ ID NO 23
<211> LENGTH: 369
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the amino acid sequence of ALT02M1

<400> SEQUENCE: 23

Met Glu Thr Asp Asn Val Glu Leu Ala Gln Ser Lys Arg Lys Val Val			
1	5	10	15

Leu Ala Glu Gln Gly Ser Phe Tyr Ile Gly Gly Arg Thr Val Thr Gly		
20	25	30

Pro Gly Lys Phe Asp Pro Ser Lys Pro Val Ile Pro Tyr Ser Asn Glu		
35	40	45

Gly Ala Thr Phe Tyr Ile Asn Gln Met Tyr Val Asn Phe Gln Ala Pro		
50	55	60

Val Arg Pro Arg Gly Leu Pro Leu Val Phe Trp His Gly Gly Leu			
65	70	75	80

Thr Gly His Ile Trp Glu Ser Thr Pro Asp Gly Arg Pro Gly Phe Gln		
85	90	95

Thr Leu Phe Val Gln Asp Arg His Thr Val Tyr Thr Ile Asp Gln Pro		
100	105	110

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Gly Arg Gly Arg Gly Asn Ile Pro Thr Phe Asn Gly Pro Phe Gly Gln
115 120 125

Leu Glu Glu Glu Ser Ile Val Asn Thr Val Thr Ala Asn Ser Ser Lys
130 135 140

Glu Gly Ala Trp Val Arg Asp Arg Leu Gly Pro Ala Pro Gly Gln Phe
145 150 155 160

Phe Glu Asn Ser Gln Phe Pro Arg Gly Tyr Glu Asp Asn Tyr Phe Lys
165 170 175

Glu Met Gly Phe Ser Pro Ser Ile Ser Ser Asp Glu Ile Val Asp Ala
180 185 190

Val Val Lys Leu Val Thr His Ile Gly Pro Cys Val Leu Val Thr His
195 200 205

Ser Ala Ser Gly Val Leu Gly Met Arg Val Ala Thr His Ala Lys Asn
210 215 220

Val Arg Gly Ile Val Ala Tyr Glu Pro Ala Thr Ser Ile Phe Pro Lys
225 230 235 240

Gly Lys Val Pro Glu Ile Pro Pro Leu Ala Asp Lys Lys Ser Gln Ile
245 250 255

Phe Pro Pro Phe Glu Ile Gln Glu Ser Tyr Phe Lys Lys Leu Ala Lys
260 265 270

Ile Pro Ile Gln Phe Val Phe Gly Asp Asn Ile Pro Lys Asn Pro Lys
275 280 285

Ser Ala Tyr Trp Phe Leu Asp Trp Trp Arg Val Thr Arg Tyr Ala His
290 295 300

Ser Leu Ser Leu Glu Ala Ile Asn Lys Leu Gly Gly Gln Ala Ser Leu
305 310 315 320

Leu Asp Leu Pro Thr Ala Gly Leu Arg Gly Asn Thr His Phe Pro Phe
325 330 335

Thr Asp Arg Asn Asn Val Gln Val Ala Ser Leu Leu Ser Asp Phe Leu
340 345 350

Gly Lys His Gly Leu Asp Gln Asn Glu Ser Lys Leu Ala Ala Ala Leu
355 360 365

Glu

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<210> SEQ ID NO 24
<211> LENGTH: 1110
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT02M1 nucleotide sequence encoding the
      amino acid sequence of the herbicide tolerant protein ALT02M1

<400> SEQUENCE: 24

atggaaaactg acaacgtgga gcttgccaa tcgaagcgga aggttgtcct tgctgaacaa 60
ggcagttct acatcgaaaa cagaacagta accgggcctg gaaaattcga tccgtcaaag 120
ccggtaattc catattccaa cgaagggtgcc acgttttata tcaatcaaat gtacgtaaac 180
tttcaagctc ctgtgcgccc tcgtggctg cctcttagtc tttggcatgg gggcggacta 240
accggccata tctggaaatc taccccagac ggccggcccg gatttcagac cctctttgtt 300
caagatcgcc atacggtcta cacgattgat cagccaggcc gcggaaagggg caatattcct 360
acctttaatg gccctttgg gcagttggaa gaagagtcta ttgttaaacac tgttaccgca 420
aactccagta aagaaggagc gtgggttaga gatcgactag ggccccgtcc cggccagtt 480
tttggaaaaca gccaattccc acgtggttat gaagacaact acttcaagga gatggggttc 540

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agtccgtcga tctcatcaga tgagatagtc gacgctgttg ttaaactagt aactcacata	600
ggtccttgcg ttctggtgac ccattcggtc tccggaggac tgggcattgcg agtcgcgaca	660
cacggcaaga acgtgagggg gatcggtgct tatgagcctg cgacaagttt ctcccggaaa	720
ggaaaaagtgc ctgagatacc gcctctcgcc gataaaaaagt cgcaaatttt cccggcggtc	780
gagatccagg agtcttactt taagaagctc gcgaagatac ccattcagtt tgtcttcgga	840
gataatatcc ccaagaaccc taaatccgccc tattgggtct tggactgggtg gagagtca	900
cgctacgctc acagettgtc actcgaggct atcaataaggc tgggtggtca agcgtcttt	960
ttggatttgc cgactgcggg acttcgcggc aacacgcatt ttccattcac cgaccggaaat	1020
aacgtgcagg tcgcttctct gttatctgtt ttccctggaa agcacggctt agatcagaac	1080
gaaagcaaac ttgctgctgc tcttggatgtga	1110

<210> SEQ ID NO 25
<211> LENGTH: 1110
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT02M1-01 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT02M1 and based on the soybean codon usage bias

<400> SEQUENCE: 25

atggagactg ataacgtgga actcgccaa tctaagagaa aggtgggtc ggctgaacaa	60
gggtcattt acataggggg taggactgtt actggccttgc gcaagtttgc tccatccaaa	120
cctgtgatac cctacagtaa cgaaggagca acattctata ttaaccaat gtatgttaac	180
ttccaggcccc cagttagacc taggggactt ccattggttt tctggatgg aggtggcttgc	240
actggcaca tctgggagtc tacacctgac ggccagacccg ggtttcaac cctttcggtt	300
caggataggc ataccgtgta cactattgac caacctggg gaggaaaggaa taacatccca	360
acttttacg gacctttcggtt acagttggag gaagagatgtt ttgttacac tggacagcc	420
aattcttcaa aggaagggtgc ctgggtgaga gataggctt gccctgtcc cgggcaattt	480
ttcgagaact ctcagttcc tagaggctat gaagacaatt actttaaaggaa gatgggatttgc	540
agcccatcta tatccagtga tgaaattgtt gacgctgttgc tgaaactcgt gacccatatt	600
ggtccttgcg ttctggtgac tcactcagca tccggcggtt tggatgttgc agtggctaca	660
cacggcaaga atgttagggg aattgtggcc tatgaaccag ctacctcaat ctccccaaag	720
ggaaaaagtgc cagagatacc acctctcgct gataagaaaa gccaatctt tccccccattc	780
gaaaatacagg agtcttactt taagaaactt gccaagattt caatccatt tggatgttgc	840
gataacatcc ccaagaatcc aaaatcagca tattgggtcc tggactgggtg gagagtgaca	900
agatacgcac atagtctcag cctggaggcc ataaacaaat tggggggaca agttccctt	960
ttggatcttc ctactgcagg attggaggtt aatacacact ttcccttcac cgataggaaac	1020
aatgttcagg tggcttctct cctgtcagac ttctgggtt aacacggctt ggtcaaaat	1080
gagagcaaac tcggccggc cctggatgtga	1110

<210> SEQ ID NO 26
<211> LENGTH: 1110
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT02M1-02 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant

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protein ALT02M1 and based on the maize codon usage bias

<400> SEQUENCE: 26

atggagactg ataacgtgga	gctggcgacg	agcaagagga	aggtggttct	ggctgagcag	60
gggtcggttct acattggggg	gcggactgtg	accgggccc	gcaagttcga	cccatcgaag	120
cctgtcattc cgtactctaa	cgaggcgct	acgttctaca	tcaaccagat	gtacgtaat	180
ttccaggcgc	ccgtccgccc	aaggggcctc	ccactgggt	tctggcacgg	240
acaggccata tctgggagtc	cactccagat	ggccgcccag	ggttccagac	actcttcgtt	300
caggacaggc	acacagtgt	cactattgtat	cagccaggg	ggggcagggg	360
acottcaatg gcccattcg	gcagctggag	gaggagtcca	tcgtgaacac	cgtcacggcg	420
aattccagca aggagggggc	tttgggtcagg	gaccggctcg	ccccggcccc	agggcagttc	480
ttcgagaact ctca	ctcgttccc	ccggggctac	gaggataatt	acttcaagga	540
tcaccatcca tctcgctgt	cgagattgtc	gatgccgtgg	tcaagctcgt	tacccacatc	600
ggcccttgcg ttctgggt	gcatagcgct	tcggggctcc	tcgggatgag	ggttgctaca	660
catgcgaaga acgttgcgg	catecggt	tacgagccgg	ccacttccat	tttccccaa	720
ggcaagggtgc	cagagatccc	accactggcc	gacaagaagt	cacagatctt	780
gagattcagg agtcctactt	caagaagctc	gctaagatcc	ccattcagtt	cgtgttccgc	840
gacaacattc ctaagaatcc	gaagagcgcg	tactgggtcc	tggattgggt	gcccgtcact	900
cgctacgcgc	actctctctc	actggaggct	atcaacaacgc	tcggggccca	960
ctggacctcc	ctaccgctgg	cctgaggggg	aacacccatt	tcccggtcac	1020
aatgtccagg ttgcgtccct	cctgagcgt	ttccctcgcc	agcacgggct	ggatcagaat	1080
gagtctaagc tcgctgcggc	gctggagtga				1110

<210> SEQ ID NO 27

<211> LENGTH: 369

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: the amino acid sequence of the ALT02M2

<400> SEQUENCE: 27

Met	Glu	Thr	Asp	Asn	Val	Glu	Leu	Ala	Gln	Ser	Lys	Arg	Lys	Val	Val
1					5				10					15	

Leu	Ala	Glu	Gln	Gly	Ser	Phe	Tyr	Ile	Gly	Gly	Arg	Thr	Val	Thr	Gly
						20			25				30		

Pro	Gly	Lys	Phe	Asp	Pro	Ser	Lys	Pro	Val	Ile	Pro	Tyr	Ser	Asn	Glu
					35			40		45					

Gly	Ala	Thr	Phe	Tyr	Ile	Asn	Gln	Met	Tyr	Val	Asn	Phe	Gln	Ala	Pro
					50		55		60						

Val	Arg	Pro	Arg	Gly	Leu	Pro	Leu	Val	Phe	Trp	His	Gly	Gly	Ley
65					70			75		80				

Thr	Gly	His	Ile	Trp	Glu	Ser	Thr	Pro	Asp	Gly	Arg	Pro	Gly	Phe	Gln
					85			90		95					

Thr	Leu	Phe	Val	Gln	Asp	Arg	His	Thr	Val	Tyr	Thr	Ile	Asp	Gln	Pro
					100			105		110					

Gly	Arg	Gly	Arg	Gly	Asn	Ile	Pro	Thr	Phe	Asn	Gly	Pro	Phe	Gly	Gln
					115			120		125					

Leu	Glu	Glu	Glu	Ser	Ile	Val	Asn	Thr	Val	Thr	Gly	Asn	Val	Ser	Lys
					130			135		140					

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Glu Gly Ala Trp Val Arg Asp Arg Leu Gly Pro Ala Pro Gly Gln Phe
145 150 155 160

Phe Glu Asn Ser Gln Phe Pro Arg Gly Tyr Glu Asp Asn Tyr Phe Lys
165 170 175

Glu Met Gly Phe Ser Pro Ser Ile Ser Ser Asp Glu Ile Val Asp Ala
180 185 190

Val Val Lys Leu Val Thr His Ile Gly Pro Cys Val Leu Val Thr His
195 200 205

Ser Ala Ser Gly Val Leu Gly Met Arg Val Ala Thr His Ala Lys Asn
210 215 220

Val Arg Gly Ile Val Ala Tyr Glu Pro Ala Thr Ser Ile Phe Pro Lys
225 230 235 240

Gly Lys Val Pro Glu Ile Pro Pro Leu Ala Asp Lys Lys Ser Gln Ile
245 250 255

Phe Pro Pro Phe Glu Ile Gln Glu Ser Tyr Phe Lys Lys Leu Ala Lys
260 265 270

Ile Pro Ile Gln Phe Val Phe Gly Asp Asn Ile Pro Lys Asn Pro Lys
275 280 285

Ser Ala Tyr Trp Phe Leu Asp Trp Trp Arg Val Thr Arg Tyr Ala His
290 295 300

Ser Leu Ser Leu Glu Ala Ile Asn Lys Leu Gly Gly Gln Ala Ser Leu
305 310 315 320

Leu Asp Leu Pro Thr Ala Gly Leu Arg Gly Asn Thr His Phe Pro Phe
325 330 335

Thr Asp Arg Asn Asn Val Gln Val Ala Ser Leu Leu Ser Asp Phe Leu
340 345 350

Gly Lys His Gly Leu Asp Gln Asn Glu Ser Lys Leu Ala Ala Ala Leu
355 360 365

Glu

<210> SEQ ID NO 28
<211> LENGTH: 1110
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT02M2 nucleotide sequence encoding the amino acid sequence of the herbicide tolerant protein ALT02M2

<400> SEQUENCE: 28

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atggaaactg acaacgtgga gcttgcccaa tcgaagcggg aggttgtcct tgctgaacaa      60
ggcagttct acatcgaaaa cagaacagta accgggcctg gaaaattcga tccgtcaaag      120
ccggtaattc catattccaa cgaagggtgcc acgtttata tcaatcaaat gtacgtaaac      180
tttcaagtc ctgtgcggcc tcgtggctg cctctagtct ttggcatgg gggcgacta      240
accggccata tctggaaatc taccccagac ggccggcccc gatttcagac cctcttttt      300
caagatcgcc atacggtcta cacgattgtat cagccaggcc gcggaaagggg caatattcct      360
acctttaatg gccctttgg gcagttggaa gaagagtgcg ttgttaaacac tgttaccgga      420
aacgtcaga aagaaggaggc gtgggtaga gatcgactag ggcccgatcc cggccagtt      480
tttgagaaca gccaattccc acgtggatc gaagacaact acttcaagga gatggggttc      540
agtccgtcga tctcatcaga tgagatagtc gacgctgtt ttaaactagt aactcacata      600
ggtccttgcg ttctgggtac ccattcggtc tccggagttac tgggcattgcg agtcgcgaca      660
cacgccaaga acgtgagggg gatcggtgtc tatgagcctg cgacaagtat ctttccaaa      720

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ggaaaaagtgc ctgagatacc gcctctcgcc gataaaaagt cgcaaatttt cccgcccgttc	780
gagatccagg agtcttactt taagaagctc gcgaagatac ccattcagtt tgtcttcgga	840
gataatatcc ccaagaaccc taaatccgco tattggttct tggactggtg gagagtca	900
cgctacgctc acagcttgc actcgaggt atcaataaagc tcgggtggta agcgtcttt	960
ttggatttgc cgactcgccc acctcgccgc aacacgcattt ccatttcac cgaccggaaat	1020
aacgtgcagg tcgcttctct gttatctgtt ttccctcgaa agcacggctt agatcagaac	1080
gaaagcaaac ttgctgctgc tcttgagtga	1110

<210> SEQ ID NO 29
<211> LENGTH: 1110
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT02M2-01 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT02M2 and based on the soybean codon usage bias

<400> SEQUENCE: 29

atggagactg ataacgtgga actcgccaa tctaagagaa aggtgggtct ggctgaacaa	60
gggtcatttt acataggggg taggactgtt actggtcctg gcaagtttga tccatccaaa	120
cctgtgatac cctacagtaa cgaaggagca acattctata ttaaccaaat gtatgttaac	180
ttccaggccc cagttaggacc taggggactt ccattggttt tctggcatgg aggtggcttg	240
actggtcaca tctgggagtc tacacctgac ggcagacccc ggtttcaaac cctttcgtt	300
caggataggc ataccgtgta cactattgac caacctggaa gaggaagggg taacatccca	360
acttttaacg gaccttcgg acagttggag gaagagagta ttgttaacac tgtgacagga	420
aatgttatcaa aggaagggtc ctgggtgaga gataggcttg gcccgttcc cgggcaattt	480
ttcgagaact ctcagttcc tagaggctat gaagacaattt actttaagga gatgggattc	540
agcccatcta tatccagtga tgaaaattgtt gacgctgttg tgaaactcgt gacccatatt	600
ggtccttgc ttctggtgac tcactcagca tccggcgttc ttggatgag agtggctaca	660
cacgcaaaaga atgttagggg aattgtggcc tatgaaccag ctacctcaat cttccccaaag	720
ggaaaaagtcc cagagatacc acctctcgct gataagaaaa gccaaatctt tccccattc	780
gaaaatacagg agtcttactt taagaaactt gccaagattt caatccaaat tggggatgg	840
gataacatcc ccaagaatcc aaaatcagca tattggttcc tggactggtg gagagtgaca	900
agatacgcac atagtctcag cctggaggcc ataaacaaat tggggggaca agcttccctt	960
ttggatcttc ctactgcagg attgagaggt aatacacactt ttcccttcac cgataggAAC	1020
aatgttcagg tggcttctct cctgtcagac ttctggtaa aacacggctt ggatcaaaat	1080
gagagcaaac tcggccggccgc cctggaaatga	1110

<210> SEQ ID NO 30
<211> LENGTH: 1110
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT02M2-02 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT02M2 and based on the maize codon usage bias

<400> SEQUENCE: 30

atggagactg ataacgtgga gctggcgcag agcaagagga aggtggttct ggctgagcag	60
gggtcgttcc acattggggg gcgactgtg accggggcccg gcaagttcga cccatcgaag	120

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cctgtcattc	cgtactctaa	cgagggcgct	acgttctaca	tcaaccagat	gtacgtaat	180
ttccaggcgc	ccgtccgccc	aaggggcctc	ccactggtgt	tctggcacgg	cgggggcctg	240
acaggccata	tctgggagtc	cactccagat	ggccgcccag	ggttccagac	actcttcgtt	300
caggacaggc	acacagtgt	cactattgtat	cagccagggg	ggggcagggg	gaacatccct	360
accttcaatg	gccccattcgg	gcagctggag	gaggagtcca	tcgtgaacac	cgtcacggc	420
aatgtgagca	aggagggggc	ttgggtcagg	gaccggctcg	gcccgcccc	agggcagttc	480
ttcgagaact	ctcagttccc	ccggggctac	gaggataatt	acttcaagga	gatgggcttc	540
tcaccatcca	tctcgctctga	cgagattgtc	gatgcccgtgg	tcaagctgt	tacccacatc	600
ggcccttgcg	ttctggtgac	gcatacgct	tcgggctcc	tcgggatgag	ggttgctaca	660
catgcgaaga	acgttgcgg	categtggct	tacgagccgg	ccacttccat	tttccccaaag	720
ggcaagggtgc	cagagatccc	accactggcc	gacaagaagt	cacagatctt	cccaccttc	780
gagattcagg	agtcctactt	caagaagctc	gctaagatcc	ccattcagtt	cgtgttcggc	840
gacaacatcc	ctaagaatcc	gaagagcgcg	tactggttcc	tggattggtg	gchgctcacf	900
cgttacgcgc	actctctctc	actggaggt	atcaacaacg	tcggggccca	ggcctcgctc	960
ctggacatcc	ctaccgctgg	cctgaggggg	aacacccatt	tcccggttac	ggatcgaaac	1020
aatgtccagg	ttgcgtccct	cctgagcgat	ttccctcgga	agcacgggct	ggatcagaat	1080
gagtctaagc	tcgctgcggc	gctggagtga				1110

<210> SEQ ID NO 31

<211> LENGTH: 369

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: the amino acid sequence of the ALT02M3

<400> SEQUENCE: 31

Met	Glu	Thr	Asp	Asn	Val	Glu	Lle	Ala	Gln	Ser	Lys	Arg	Lys	Val	Val
1					5			10				15			

Lle	Ala	Glu	Gln	Gly	Ser	Phe	Tyr	Ile	Gly	Gly	Arg	Thr	Val	Thr	Gly
					20			25				30			

Pro	Gly	Lys	Phe	Asp	Pro	Ser	Lys	Pro	Val	Ile	Arg	Ala	Ser	Asn	Glu
		35				40				45					

Gly	Ala	Thr	Phe	Tyr	Ile	Asn	Gln	Met	Tyr	Val	Asn	Phe	Gln	Ala	Pro
		50				55			60						

Val	Arg	Pro	Arg	Gly	Lle	Pro	Leu	Val	Phe	Trp	His	Gly	Gly	Lle	
65					70			75			80				

Thr	Gly	His	Ile	Trp	Glu	Ser	Thr	Pro	Asp	Gly	Arg	Pro	Gly	Phe	Gln
		85				90				95					

Thr	Leu	Phe	Val	Gln	Asp	Arg	His	Thr	Val	Tyr	Thr	Ile	Asp	Gln	Pro
			100			105				110					

Gly	Arg	Gly	Arg	Gly	Asn	Ile	Pro	Thr	Phe	Asn	Gly	Pro	Phe	Gly	Gln
			115			120			125						

Leu	Glu	Glu	Ser	Ile	Val	Asn	Thr	Val	Thr	Ala	Asn	Val	Ser	Lys	
			130			135			140						

Glu	Arg	Ala	Trp	Val	Arg	Asp	Arg	Lle	Gly	Pro	Ala	Pro	Gly	Gln	Phe
145				150			155			160					

Phe	Glu	Asn	Ser	Gln	Phe	Pro	Arg	Gly	Tyr	Glu	Asp	Asn	Tyr	Phe	Lys
			165			170			175						

Glu	Met	Gly	Phe	Ser	Pro	Ser	Ile	Ser	Ser	Asp	Glu	Ile	Val	Asp	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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180	185	190	
Val Val Lys Leu Val Thr His Ile Gly Pro Cys Val	Leu Val Thr His		
195	200	205	
Ser Ala Ser Gly Val Leu Gly Met Arg Val Ala Thr His	Ala Lys Asn		
210	215	220	
Val Arg Gly Ile Val Ala Tyr Glu Pro Ala Thr Ser Ile Phe Pro Lys			
225	230	235	240
Gly Lys Val Pro Glu Ile Pro Pro Leu Ala Asp Lys Lys Ser Gln Ile			
245	250	255	
Phe Pro Pro Phe Glu Ile Gln Glu Ser Tyr Phe Lys Lys Leu Ala Lys			
260	265	270	
Ile Pro Ile Gln Phe Val Phe Gly Asp Asn Ile Pro Lys Asn Pro Lys			
275	280	285	
Ser Ala Tyr Trp Phe Leu Asp Trp Trp Arg Val Thr Arg Tyr Ala His			
290	295	300	
Ser Leu Ser Leu Glu Ala Ile Asn Lys Leu Gly Gly Gln Ala Ser Leu			
305	310	315	320
Leu Asp Leu Pro Thr Ala Gly Leu Arg Gly Asn Thr His Phe Pro Phe			
325	330	335	
Thr Asp Arg Asn Asn Val Gln Val Ala Ser Leu Leu Ser Asp Phe Leu			
340	345	350	
Gly Lys His Gly Leu Asp Gln Asn Glu Ser Lys Leu Ala Ala Ala Leu			
355	360	365	

Glu

<210> SEQ ID NO 32
 <211> LENGTH: 1110
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: the ALT02M3 nucleotide sequence encoding the amino acid sequence of the herbicide tolerant protein ALT02M3

<400> SEQUENCE: 32

atggaaactg acaacgtgga gcttgccaa tcgaagcggaa aggttgtcct tgctgaacaa	60
ggcagttct acatcgaaaa cagaacagta accgggcctg gaaaattcga tccgtcaaag	120
cccgtaattc gagcttccaa cgaagggtgcc acgaaaaata tcaatcaaat gtacgtaaac	180
tttcaagtc ctgtgcgccc tcgtggctg cctctagtct tttggcatgg gggcggacta	240
accggccata tctggaaatc tacccagac ggccggcccc gatttcagac cctctttgtt	300
caagatcggc atacggtcta cacgattgat cagccagggc gccaaggggg caatattcct	360
accttaatg gcccattttgg gcagttggaa gaagagtcta ttgttaaacac tttttccca	420
aacgtcagta aagaaagagc gtgggttaga gatcgactag ggcccgatcc cggccagtt	480
tttgagaaca gccaattccc acgtggttat gaagacaact acttcaagga gatggggttc	540
agtccgtcga tctcatcaga tgagatagtc gacgctgttg ttaaactagt aactcacata	600
ggtccttgtt ttctgggtac ccattcggt tccggagttac tggcatgct agtcgcgaca	660
cacgccaaga acgtggggg gatcggtct tatgagcctg cgacaagtat cttttccaaa	720
ggaaaaagtgc ctgagatacc gcctctcgcc gataaaaaagt cgccaaatttt cccgggttc	780
gagatccagg agtcttactt taagaagtc gccaagatac ccattcagtt tgtcttcgga	840
gataatatcc ccaagaaccc taaatccgccc tattggttct tggactggtg gagagtca	900
cgctacgctc acagcttgc actcgaggct atcaataagc tcgggtggta agcgtcttt	960

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ttggattgc cgactgcggg acttcgcggc aacacgcatt ttccattcac cgaccggaat 1020
aacgtgcagg tcgcttctct gttatctgtat ttccctcgaa agcacggctt agatcagaac 1080
qaaaqcaaac ttqctqctqc tcttqaqtqa 1110

```
<210> SEQ ID NO 33
<211> LENGTH: 1110
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT02M3-01 nucleotide sequence encoding the
      amino acid sequence corresponding to the herbicide tolerant
      protein ALT02M3 and based on the soybean codon usage bias
```

<400> SEQUENCE: 33

atggagactgataaacgtgga actcgccaa tctaagagaa aggtggtgct ggctgaacaa
gggtcattt acatagggg taggactgtt actggctcg gcaagttga tccatccaaa 120
cctgtgatac gagccgatggaa cgaaggagca acattctata ttaaccataat gtatgttaac
ttccaggccc cagtgagacc taggggactt ccattggttt tctggcatgg aggtggcttg 240
actggtcaca tctgggagtc tacacctgtac ggcagacccg ggtttcaaac cctctcggtt
caggataggc ataccgtgta cactattgtac caacctggga gaggaaaggaa taacatccca 360
acttttaacg gacccattcg acagttggag gaagagagta ttgttaacac tgtgcacagcc
aatgtatcaa aggaacgagc ctgggtgaga gataggcttgc cccctgtcc cgggcaattt
ttcgagaact ctcagttttcc tagaggctat gaagacaattt actttaaaggat gatgggattc
agcccatcta tatccagtgtat gaaattgtt gacgctgtt tgaaactcgt gaccatatt 600
ggtccttggttt ttctgggtgac tcacttcgca tccggcggttcc ttggatgag agtgtgctaca
cacgcaaaaga atgttagggg aattgtggcc tatgaaccag ctacccat cttccccaaag
ggaaaagttc cagatatacc acctctcgat gataaaaaaa gccaatctt tccccatcc
gaaatacagg agtcttactt taagaaactt gccaagattc caatccattt tgtttcggaa
gataacatcc ccaagaatcc aaaatcagca tattgggtcc tggactgggtg gagagtgaca
agataacgcac atagtctcag cctggaggccc ataaacaaat tggggggaca agcttccctt
ttggatcttc ctactgcagg attgagaggt aatacacact ttcccttcac cgatggaaac
aatgttcagg tggcttcctt cctgtcagac tttctgggtt aacacgggtct ggatccaaat
gagagcaacatc tccggccgc cctggaaatgtaa 1110

```
<210> SEQ ID NO 34
<211> LENGTH: 1110
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT02M3-02 nucleotide sequence encoding the
      amino acid sequence corresponding to the herbicide tolerant
      protein ALT02M3 and based on the maize codon usage bias
```

<400> SEQUENCE: 34

ataggagactg ataaacgttgg a gctggcgca g agcaagagg a aggtggttc t ggctgagcag	60
gggtcgttct acattgggg g cggactgtg accggggcccg g caagttcga cccatcgaag	120
cctgtcattc gggcgtctaa cgaggggcgc t acgttctaca t caaccagat gtaactgtaat	180
ttccagggctc ccgtccgccc a aaggggcctc ccactggtgt t ctggcacgg cgggggcctg	240
acaggccata tctgggagtc cactccagat ggccgcggc a ggttccagac actttcgtt	300

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87

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caggacaggc acacagtgtacactattgtat cagccaggaa ggggcagggg gaacatccct	360
accttcaatgcgccattcgcgacagctggag gaggagtccatcgtaaacac cgtcacggcg	420
aatgtgagca aggagcgggc ttgggtcagg gaccggctcg gcccggcccc agggcagttc	480
ttcgagaact ctcaaggccc ccggggctac gaggataatt acttcaagga gatggggcttc	540
tcaccatcca tctcgctgtatcgattgtatcgatgcccgttgc tcaagctcgatccacatc	600
ggcccttgcc ttctgggtgac gcatacgcttcgatgggtatcgatggatgag gggttgcata	660
catgcgaaga acgttgcggc catcgatgtatcgatggccggccacttccat tttcccaag	720
ggcaagggtgc cagagatccc accactggcc gacaagaagt cacagatctt cccaccttc	780
gagattcagg agtcctactt caagaagctc gctaagatcc ccattcaggatcgatccgttccgc	840
gacaacatcc ctaagaatcc gaagagcgcg tactggttcc tggatggatgcgcgtcacg	900
cgctacgcgc actctctctc actggaggtatcaacaacgc tcggggccca ggcctcgctc	960
ctggacacctcc taccgctgg cctgaggggg aacacccatt tcccgatccac ggatcggAAC	1020
aatgtccagg ttgcgtccct cctgagcgat ttccctcgca agcacgggttggatcagaat	1080
gagtctaagc tcgctgcggc gctggagtgtat	1110

<210> SEQ ID NO 35

<211> LENGTH: 362

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: the amino acid sequence of ALT03

<400> SEQUENCE: 35

Met Glu Thr Asp Asn Val Glu Leu Ala Gln Ser Lys Arg Lys Val Val			
1	5	10	15

Leu Ala Glu Gln Gly Ser Phe Tyr Ile Gly Gly Arg Thr Val Thr Gly		
20	25	30

Pro Gly Lys Phe Asp Pro Ser Lys Pro Val Ile Pro Tyr Ser Asn Glu		
35	40	45

Gly Ala Thr Phe Tyr Ile Asn Gln Met Tyr Val Asn Phe Gln Ala Pro		
50	55	60

Val Arg Pro Arg Gly Leu Pro Leu Val Phe Trp His Gly Gly Leu			
65	70	75	80

Thr Gly His Ile Trp Glu Ser Thr Pro Asp Gly Arg Pro Gly Phe Gln		
85	90	95

Thr Leu Phe Val Gln Asp Arg His Thr Val Tyr Thr Ile Asp Gln Pro		
100	105	110

Gly Arg Gly Arg Gly Asn Ile Pro Thr Phe Asn Gly Pro Phe Gly Gln		
115	120	125

Leu Glu Glu Ser Ile Val Asn Thr Val Thr Gly Asn Ser Ser Lys		
130	135	140

Glu Gly Ala Trp Val Arg Asp Arg Leu Gly Pro Ala Pro Gly Gln Phe			
145	150	155	160

Phe Glu Asn Ser Gln Phe Pro Arg Gly Tyr Glu Asp Asn Tyr Phe Lys		
165	170	175

Glu Met Gly Phe Ser Pro Ser Ile Ser Ser Asp Glu Ile Val Asp Ala		
180	185	190

Val Val Lys Leu Val Thr His Ile Gly Pro Cys Val Leu Val Thr His		
195	200	205

Ser Ala Ser Gly Val Leu Gly Met Arg Val Ala Thr His Ala Lys Asn		
210	215	220

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Val Arg Gly Ile Val Ala Tyr Glu Pro Ala Thr Ser Ile Phe Pro Lys
 225 230 235 240

Gly Lys Val Pro Glu Ile Pro Pro Leu Ala Asp Lys Lys Ser Gln Ile
 245 250 255

Phe Pro Pro Phe Glu Ile Gln Glu Ser Tyr Phe Lys Lys Leu Ala Lys
 260 265 270

Ile Pro Ile Gln Phe Val Phe Gly Asp Asn Ile Pro Lys Asn Pro Lys
 275 280 285

Ser Ala Tyr Trp Phe Leu Asp Trp Trp Arg Val Thr Arg Tyr Ala His
 290 295 300

Ser Leu Ser Leu Glu Ala Ile Asn Lys Leu Gly Gly Gln Ala Ser Leu
 305 310 315 320

Leu Asp Leu Pro Thr Ala Gly Leu Arg Gly Asn Thr His Phe Pro Phe
 325 330 335

Thr Asp Arg Asn Asn Val Gln Val Ala Ser Leu Leu Ser Asp Phe Leu
 340 345 350

Gly Lys His Gly Leu Asp Gln Asn Glu Ser
 355 360

<210> SEQ ID NO 36

<211> LENGTH: 1089

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: the ALT03 nucleotide sequence encoding the amino acid sequence of ALT03

<400> SEQUENCE: 36

atggaaactg acaacgtgga gcttgcccaa tcgaagcggaa aggttgtcct tgctgaacaa	60
ggcagtttct acatcgaaaa cagaacagta accgggcctg gaaaattcga tccgtcaag	120
ccggtaattc catattccaa cgaagggtgcc acgttttata tcaatcaaat gtacgtaaac	180
tttcaagtc ctgtcgcccc tcgtggctg cctctagtc ttggcatgg gggcgacta	240
accggccata tctggaaatc taccggcagac ggccggcccg gatttcagac cctctttgtt	300
caagatcgcc atacggtcta cacgattgtt cagccagggc gcggaaagggg caatattcct	360
acctttaatg gccctttgg gcagttggaa gaagagtctg ttgttaaacac tgttaccggaa	420
aactccagta aagaaggagc gtgggttaga gatcgactag ggcccgctcc cggccagttt	480
tttggaaaaca gccaattccc acgtgggttat gaagacaact acttcaagga gatggggttc	540
agtccgtcga tctcatcaga tgagatagtc gacgctgttg tttaaactagt aactcacata	600
ggtccttgcg ttctggtgac ccattcggtc tccggagttc tggcatgct agtgcgaca	660
cacggccaaac acgtggggg gategttgc tatgagcctg cgacaagtat cttttccaaa	720
ggaaaaatgc ctgagatacc gcctctcgcc gataaaaaatgc cgccaaatttt cccggccgttc	780
gagatccagg agtcttactt taagaagctc gcgaagatac ccattcagtt tgtcttcgga	840
gataatatcc ccaagaaccc taaatccggcc tattggttct tggactggtg gagagtcaact	900
cgtacgtc acagcttgc actcgaggct atcaataagc tcgggtgtca agcgtcttt	960
ttggatttgc cgactgcggg acttcgcggc aacacgcatt ttccattcac cgaccggaaat	1020
aacgtgcagg tcgcttctct gttatctgtt ttccctcgaa agcacggctt agatcagaac	1080
gaaagctga	1089

<210> SEQ ID NO 37

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<211> LENGTH: 1089
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT03-01 nucleotide sequence encoding the amino acid sequence corresponding to the ALT03 and based on the soybean codon usage bias

<400> SEQUENCE: 37

atggagactgataaacgtgga	actcgccaa	tctaagagaa	aggtgtgtct	ggctgaacaa	60	
gggtcattt	acataggggg	taggactgtt	actggtcctg	gcaagtttga	tccatccaaa	120
cctgtgatac	cctacagtaa	cgaaggagca	acattctata	ttaaccaa	at gtatgttaac	180
ttccaggccc	cagtgagacc	tagggactt	ccattggttt	tctggcatgg	aggtggttg	240
actggtcaca	tctggagtc	tacacctgac	ggcagacccc	ggtttcaaa	cctttcgtt	300
caggataggc	ataccgtgta	cactattgac	caacctggga	gaggaagggg	taacatccca	360
acttttaacg	gaccttcgg	acagttggag	gaagagagta	ttgttaacac	tgtgacagga	420
aattcttcaa	aggaagggtgc	ctgggtgaga	gataggcttg	gccctgctcc	cgggcaattt	480
ttcgagaact	ctcagttcc	tagaggctat	gaagacaatt	actttaaagg	gatgggattc	540
agccccatcta	tatccagtga	tgaaaattgtt	gacgctgttg	tgaaaactcgt	gacccatatt	600
ggtccttgg	ttctggtgac	tcactcagca	tccggcggttc	ttgggatgag	agtggctaca	660
cacgcaaaaga	atgttagggg	aattgtggcc	tatgaaccag	ctaccta	at ttcccaag	720
ggaaaagttc	cagagatacc	acctctcgct	gataagaaaa	gccaatctt	tccccatcc	780
gaaaatacagg	agtcttactt	taagaaactt	gccaagattc	caatccatt	tgttttccgga	840
gataacatcc	ccaagaatcc	aaaatcagca	tattggttcc	tggactggtg	gagagtgaca	900
agatacgcac	atagtctcag	cctggaggcc	ataaaacaat	tgggggggaca	agcttccctt	960
ttggatcttc	ctactgcagg	attgagaggt	aatacacact	ttcccttcac	cgataggaac	1020
aatgttcagg	tggcttctct	cctgtcagac	tttctgggta	aacacggct	ggatcaaaat	1080
gagagctga						1089

<210> SEQ ID NO 38
<211> LENGTH: 1089
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT03-02 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT03 and based on the maize codon usage bias

<400> SEQUENCE: 38

atggagactgataaacgtgga	gctggcgca	gcaagagga	aggtgtgtct	ggctgagcag	60	
gggtcgttct	acattggggg	gcggactgt	accggcccg	gcaagttcga	cccatcgaa	120
cctgtcatcc	cgtactctaa	cgaggcgct	acgttctaca	tcaaccagat	gtacgtgaat	180
ttccaggctc	ccgtccggcc	aaggggcctc	ccactggtgt	tctggcacgg	cgggggcctg	240
acaggccata	tctggagtc	cactccagat	ggccggccag	ggttccagac	actttcgtt	300
caggacagggc	acacagtgt	cactattgt	cagccaggg	ggggcagggg	gaacatccct	360
accttcaatg	gcccattcg	gcagctggag	gaggagtcca	tcgtgaacac	cgtcacggc	420
aattccagca	aggagggggc	ttgggtcagg	gaccggctcg	gcccggccccc	aggcagttc	480
ttcgagaact	ctcagttccc	ccggggctac	gaggataat	acttcaagga	gatgggcttc	540
tcaccatcca	tctcgctg	cgagattgtc	gatgccgtgg	tcaagtcgt	tacccacatc	600

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ggcccttgcg ttctggtgac gcatacgct tcgggcgtcc tcggatgag gggtgctaca   660
catgcgaaga acgttcgcgg cactgtggct tacgagccgg ccacttccat tttccccaaag   720
ggcaagggtgc cagagatccc accactggcc gacaagaagt cacagatctt cccaccttc   780
gagattcagg agtcctactt caagaagctc gctaagatcc ccattcagtt cgtgttccgc   840
gacaacatcc ctaagaatcc gaagagcgcg tactggttcc tggattgggt gcgcgtcacf   900
cgctacgcgc actctctctc actggaggct atcaacaagg tcgggggcca ggcctcgctc   960
ctggacactcc ctaccgctgg cctgaggggg aacacccatt tcccgttcac ggatcggAAC 1020
aatgtccagg ttgcgtccct cctgagcgtat ttccctggca agcacgggct ggatcagaat 1080
gagtcttga                                         1089

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<210> SEQ ID NO 39
<211> LENGTH: 362
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the amino acid sequence of the ALT03M1

```

<400> SEQUENCE: 39

```

Met Glu Thr Asp Asn Val Glu Leu Ala Gln Ser Lys Arg Lys Val Val
1           5          10          15

```

```

Leu Ala Glu Gln Gly Ser Phe Tyr Ile Gly Gly Arg Thr Val Thr Gly
20          25          30

```

```

Pro Gly Lys Phe Asp Pro Ser Lys Pro Val Ile Pro Tyr Ser Asn Glu
35          40          45

```

```

Gly Ala Thr Phe Tyr Ile Asn Gln Met Tyr Val Asn Phe Gln Ala Pro
50          55          60

```

```

Val Arg Pro Arg Gly Leu Pro Leu Val Phe Trp His Gly Gly Leu
65          70          75          80

```

```

Thr Gly His Ile Trp Glu Ser Thr Pro Asp Gly Arg Pro Gly Phe Gln
85          90          95

```

```

Thr Leu Phe Val Gln Asp Arg His Thr Val Tyr Thr Ile Asp Gln Pro
100         105         110

```

```

Gly Arg Gly Arg Gly Asn Ile Pro Thr Phe Asn Gly Pro Phe Gly Gln
115         120         125

```

```

Leu Glu Glu Ser Ile Val Asn Thr Val Thr Ala Asn Ser Ser Lys
130         135         140

```

```

Glu Gly Ala Trp Val Arg Asp Arg Leu Gly Pro Ala Pro Gly Gln Phe
145         150         155         160

```

```

Phe Glu Asn Ser Gln Phe Pro Arg Gly Tyr Glu Asp Asn Tyr Phe Lys
165         170         175

```

```

Glu Met Gly Phe Ser Pro Ser Ile Ser Ser Asp Glu Ile Val Asp Ala
180         185         190

```

```

Val Val Lys Leu Val Thr His Ile Gly Pro Cys Val Leu Val Thr His
195         200         205

```

```

Ser Ala Ser Gly Val Leu Gly Met Arg Val Ala Thr His Ala Lys Asn
210         215         220

```

```

Val Arg Gly Ile Val Ala Tyr Glu Pro Ala Thr Ser Ile Phe Pro Lys
225         230         235         240

```

```

Gly Lys Val Pro Glu Ile Pro Pro Leu Ala Asp Lys Lys Ser Gln Ile
245         250         255

```

```

Phe Pro Pro Phe Glu Ile Gln Glu Ser Tyr Phe Lys Lys Leu Ala Lys
260         265         270

```

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Ile	Pro	Ile	Gln	Phe	Val	Phe	Gly	Asp	Asn	Ile	Pro	Lys	Asn	Pro	Lys
275							280								285
Ser	Ala	Tyr	Trp	Phe	Leu	Asp	Trp	Trp	Arg	Val	Thr	Arg	Tyr	Ala	His
290							295								300
Ser	Leu	Ser	Leu	Glu	Ala	Ile	Asn	Lys	Leu	Gly	Gly	Gln	Ala	Ser	Leu
305							310								320
Leu	Asp	Leu	Pro	Thr	Ala	Gly	Leu	Arg	Gly	Asn	Thr	His	Phe	Pro	Phe
325															335
Thr	Asp	Arg	Asn	Asn	Val	Gln	Val	Ala	Ser	Leu	Leu	Ser	Asp	Phe	Leu
340								345							350
Gly	Lys	His	Gly	Leu	Asp	Gln	Asn	Glu	Ser						
355								360							

<210> SEQ ID NO 40
<211> LENGTH: 1089
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT03M1 nucleotide sequence encoding the amino acid sequence of the herbicide tolerant protein ALT03M1

<400> SEQUENCE: 40

atggaaactg acaaactgttgc gcttgccaa tcgaagcgga aggttgtcct tgctgaacaa 60
ggcagttctt acatcgaaaa cagaacagta accggggctg gaaaattcga tccgtcaaaag 120
ccggtaatttc cataattccaa cgaagggtgcc acgtttata tcaatcaaata gtacgtaaac 180
tttcaagotc ctgtgcgc ctc tggtggctg cctctatgtt ttggcatgg gggcgacta 240
accggccata tctggaaatc taccccagac ggccgcggg gatttcagac cctctttgtt 300
caagatcgcc atacggctta cacgattgtt cagccaggcc gcggaaggaa caatattcc 360
acctttaatg gccctttgg gcagttggaa gaagagtcga ttgttaaacac tgttaccgca 420
aactccagta aagaaggagc gtgggttaga gatcgacttag ggcggctcc cggccagttt 480
tttggagaaca gccaattccc acgtggttat gaagacaact acttcaagga gatggggttc 540
agtccgtcga tctcatcaga tgagatagtc gacgctgtt ttaaactagt aactcacata 600
ggtccttgcg ttcgtgtgac ccattcgct tccggagatc tggcatgcg agtgcgcaca 660
cacgccaaga acgtgaggaa gatcggtgt tatgagccctg cgacaagttat cttttccaaa 720
ggaaaaagtgc ctgagatacc gcctctcgcc gataaaaaagt cgccaaatttt cccggcggtt 780
gagatccagg agtcttactt taagaagctc gcaagatacc ccattcagtt tggatccggaa 840
gataaatcc ccaagaaccc taaatccgccc tattgggtt tggactgggtg gagagtcaact 900
cgctacgctc acagcttgc acgtcgaggct atcaataaagc tgggtggtca agcgtcttt 960
ttggatttgc cgactgcggg acttcgcggc aacacgcatt ttccattcactt cggccggat 1020
aacgtgcagg tggatccctt gttatctgtt ttccctggaa agcacggctt agatcagaac 1080
gaaaggctga 1089

<210> SEQ ID NO 41
<211> LENGTH: 1089
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT03M1-01 nucleotide sequence encoding the
amino acid sequence corresponding to the herbicide tolerant

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atggagactg ataacgtgga actcgccaa tctaagagaa aggtggtgct ggctgaacaa	60
gggtcattt acataggggg taggactgtt actggtcctg gcaagttga tccatccaaa	120
cctgtgatac cctacagtaa cgaaggagca acattctata ttaaccaa at gtatgttaac	180
ttccaggccc cagttaggacc taggggactt ccattggttt tctggcatgg aggtggcttg	240
actggtcaca tctgggagtc tacacctgac ggcagacccg ggtttcaa ac cctttcgtt	300
caggataggc ataccgtgta cactattgac caacctggga gaggaagggg taacatccca	360
acttttaacg gaccttcgg acagttggag gaagagagta ttgttaacac tgtgacagcc	420
aattcttcaa aggaagggtc ctgggtgaga gataggcttgc cccctgtcc cgggcaattt	480
ttcgagaact ctcagttcc tagaggctat gaagacaattt actttaaagga gatgggattc	540
agcccatcta tatccagtga tgaaaattgtt gacgctgtt tgaaaactcgt gacccatatt	600
ggtccttggtt ttctggtgac tcactcagca tccggcggtt ttggatgag agtggctaca	660
cacgcaaaga atgttagggg aattgtggcc tatgaaccag ctacctcaat cttccccaaag	720
ggaaaaagttc cagagatacc accttcgtt gataagaaaa gccaatctt tccccatcc	780
gaaatacagg agtcttactt taagaaactt gccaagattt caatccattt tggtttcgga	840
gataacatcc ccaagaatcc aaaatcagca tattggttcc tggactggtg gagagtgaca	900
agatacgcac atagtctcag cctggggccc ataaacaaat tggggggaca agcttccctt	960
ttggatcttc ctactgcagg attgagaggt aatacacact ttcccttac cgtataggAAC	1020
aatgttcagg tggcttctct cctgtcagac ttctgggtt aacacggctt ggtcaaaat	1080
gagagctga	1089

<210> SEQ ID NO 42
 <211> LENGTH: 1089
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: the ALT03M1-02 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT03M1 and based on the maize codon usage bias

<400> SEQUENCE: 42	
atggagactg ataacgtgga actcgccaa tctaagagaa aggtggtgct ggctgaacaa	60
gggtcattt acataggggg taggactgtt actggtcctg gcaagttga tccatccaaa	120
cctgtgatac cctacagtaa cgaaggagca acattctata ttaaccaa at gtatgttaac	180
ttccaggccc cagttaggacc taggggactt ccattggttt tctggcatgg aggtggcttg	240
actggtcaca tctgggagtc tacacctgac ggcagacccg ggtttcaa ac cctttcgtt	300
caggataggc ataccgtgta cactattgac caacctggga gaggaagggg taacatccca	360
acttttaacg gaccttcgg acagttggag gaagagagta ttgttaacac tgtgacagcc	420
aattcttcaa aggaagggtc ctgggtgaga gataggcttgc cccctgtcc cgggcaattt	480
ttcgagaact ctcagttcc tagaggctat gaagacaattt actttaaagga gatgggattc	540
agcccatcta tatccagtga tgaaaattgtt gacgctgtt tgaaaactcgt gacccatatt	600
ggtccttggtt ttctggtgac tcactcagca tccggcggtt ttggatgag agtggctaca	660
cacgcaaaga atgttagggg aattgtggcc tatgaaccag ctacctcaat cttccccaaag	720
ggaaaaagttc cagagatacc accttcgtt gataagaaaa gccaatctt tccccatcc	780
gaaatacagg agtcttactt taagaaactt gccaagattt caatccattt tggtttcgga	840

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gataacatcc ccaagaatcc aaaatcagca tattggttcc tggactggtg gagagtgaca	900
agatacgcac atagtctcgag cctggaggcc ataaacaaat tggggggaca agcttccctt	960
ttggatcttc ctactgcagg attgagaggt aatacacact ttcccttcac cgataggaac	1020
aatgttcagg tggcttctct cctgtcagac tttctgggta aacacggctct ggatcaaaat	1080
gagagctga	1089

<210> SEQ ID NO 43
<211> LENGTH: 362
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the amino acid sequence of the ALT03M2

<400> SEQUENCE: 43	
Met Glu Thr Asp Asn Val Glu Leu Ala Gln Ser Lys Arg Lys Val Val	
1 5 10 15	
Leu Ala Glu Gln Gly Ser Phe Tyr Ile Gly Gly Arg Thr Val Thr Gly	
20 25 30	
Pro Gly Lys Phe Asp Pro Ser Lys Pro Val Ile Pro Tyr Ser Asn Glu	
35 40 45	
Gly Ala Thr Phe Tyr Ile Asn Gln Met Tyr Val Asn Phe Gln Ala Pro	
50 55 60	
Val Arg Pro Arg Gly Leu Pro Leu Val Phe Trp His Gly Gly Leu	
65 70 75 80	
Thr Gly His Ile Trp Glu Ser Thr Pro Asp Gly Arg Pro Gly Phe Gln	
85 90 95	
Thr Leu Phe Val Gln Asp Arg His Thr Val Tyr Thr Ile Asp Gln Pro	
100 105 110	
Gly Arg Gly Arg Gly Asn Ile Pro Thr Phe Asn Gly Pro Phe Gly Gln	
115 120 125	
Leu Glu Glu Ser Ile Val Asn Thr Val Thr Gly Asn Val Ser Lys	
130 135 140	
Glu Gly Ala Trp Val Arg Asp Arg Leu Gly Pro Ala Pro Gly Gln Phe	
145 150 155 160	
Phe Glu Asn Ser Gln Phe Pro Arg Gly Tyr Glu Asp Asn Tyr Phe Lys	
165 170 175	
Glu Met Gly Phe Ser Pro Ser Ile Ser Ser Asp Glu Ile Val Asp Ala	
180 185 190	
Val Val Lys Leu Val Thr His Ile Gly Pro Cys Val Leu Val Thr His	
195 200 205	
Ser Ala Ser Gly Val Leu Gly Met Arg Val Ala Thr His Ala Lys Asn	
210 215 220	
Val Arg Gly Ile Val Ala Tyr Glu Pro Ala Thr Ser Ile Phe Pro Lys	
225 230 235 240	
Gly Lys Val Pro Glu Ile Pro Pro Leu Ala Asp Lys Lys Ser Gln Ile	
245 250 255	
Phe Pro Pro Phe Glu Ile Gln Glu Ser Tyr Phe Lys Lys Leu Ala Lys	
260 265 270	
Ile Pro Ile Gln Phe Val Phe Gly Asp Asn Ile Pro Lys Asn Pro Lys	
275 280 285	
Ser Ala Tyr Trp Phe Leu Asp Trp Trp Arg Val Thr Arg Tyr Ala His	
290 295 300	
Ser Leu Ser Leu Glu Ala Ile Asn Lys Leu Gly Gly Gln Ala Ser Leu	
305 310 315 320	

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Leu Asp Leu Pro Thr Ala Gly Leu Arg Gly Asn Thr His Phe Pro Phe
325 330 335

Thr Asp Arg Asn Asn Val Gln Val Ala Ser Leu Leu Ser Asp Phe Leu
340 345 350

Gly Lys His Gly Leu Asp Gln Asn Glu Ser
355 360

<210> SEQ ID NO 44

<211> LENGTH: 1089

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: the ALT03M2 nucleotide sequence encoding the amino acid sequence of the herbicide tolerant protein ALT03M2

<400> SEQUENCE: 44

atggaaaactg acaacgtgga gcttgccaa tcgaagcggaa aggttgtcct tgctgaacaa	60
ggcagtttct acatcgaaaa cagaacagta accgggcctg gaaaattcga tccgtcaaag	120
ccggtaattc catattccaa cgaagggtgcc acgttttata tcaatcaaat gtacgtaaac	180
tttcaagtc ctgtgcgccc tcgtggctg cctctagtct ttggcatgg gggcgacta	240
acccggccata tctggaaatc taccocagac ggccggcccg gatttcagac cctctttgtt	300
caagatcgcc atacgggtcta cacgattgtat cagccaggcc gcggaaagggg caatattcct	360
acctttaatg gccctttgg gcagttggaa gaagagtcga ttgttaacac tggttaccgga	420
aacgtcagta aagaaggaggc gtgggttaga gatcgactag ggcccgctcc cggccagttt	480
tttgagaaca gccaattccc acgtggttat gaagacaact acttcaagga gatggggttc	540
agtccgtcga tctcatcaga tgagatagtc gacgctgttt ttaaactagt aactcacata	600
ggtccttgc ttctggtgac ccattcggt tccggagtagc tggcatgcg agtcgcgaca	660
cacggcaaga acgtgagggg gategttgc tatgagcctg cgacaagtat cttcccaaa	720
ggaaaaagtgc ctgagatacc gcctctcgcc gataaaaagt cgccaaatttt cccggcgttc	780
gagatccagg agtcttactt taagaagtc gcgaagatac ccattcagg tgccttcggaa	840
gataatatcc ccaagaaccc taaatccgcc tattggttct tggactggtg gagagtcaact	900
cgctacgctc acagcttgc actcgaggt atcaataagc tcgggtgtca agcgtcttt	960
ttggatttgc cgactgcggg acttcgcggc aacacgcatt ttccattcac cgaccggaaat	1020
aacgtgcagg tcgcttctct gttatctgtat ttccctcgaa agcacggctt agatcagaac	1080
gaaagctga	1089

<210> SEQ ID NO 45

<211> LENGTH: 1089

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: the ALT03M2-01 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT03M2 and based on the soybean codon usage bias

<400> SEQUENCE: 45

atggagactg ataacgtgga actcgccaa tctaagagaa aggtgggtct ggctgaacaa	60
gggtcatttt acataggggg taggactgtt actgggtcctg gcaagtttga tccatccaaa	120
cctgtgatac cctacagtaa cgaaggagca acattctata ttaaccaaattt gtatgttaac	180
ttccaggccc cagtgagacc tagggactt ccattgggtt tctggcatgg aggtggctt	240

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actggtcaca tctgggagtc tacacctgac ggcagacccg ggtttcaaac cctttcggt	300
caggataggc ataccgtgta cactattgac caacctggga gaggaagggg taacatccca	360
acttttaacg gacctttcggt acagttggag gaagagagta ttgttaacac tgtgacagga	420
aatgttatcaa aggaagggtgc ctgggtgaga gataggcttg gccctgctcc cgggcaattt	480
ttcgagaact ctcagttcc tagaggctat gaagacaattt actttaaggaa gatgggattc	540
agcccatcta tatccagtga tgaaaattgtt gacgctgtt tgaaactcgt gacccatatt	600
ggtccttggg ttctggtgac tcactcagca tccggcggtt ttggatgag agtggctaca	660
cacgcaaaga atgttagggg aatttgtggcc tatgaaccag ctacctcaat cttccccaaag	720
ggaaaaagttc cagagatacc acctctcgct gataagaaaa gccaaatctt tccccccattc	780
gaaaatacagg agtcttactt taagaaacctt gccaagattt caatccaatt tgtttccgaa	840
gataacatcc ccaagaatcc aaaatcagca tattggtcc tggactgggag gagagtgaca	900
agataacgcac atagtctcag cctggaggcc ataaacaaat tggggggaca agttccctt	960
ttggatcttc ctactgcagg attgagaggt aatacacact ttcccttcac cgataggAAC	1020
aatgttcagg tggcttctct cctgtcagac tttctgggta aacacgggtct ggatcaaaat	1080
gagagctga	1089

<210> SEQ ID NO 46
 <211> LENGTH: 1089
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: the ALT03M2-02 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT03M2 and based on the maize codon usage bias

<400> SEQUENCE: 46

atggagactg ataacgtgga gctggcgca gcaagaggg aagggtggttct ggctgagcag	60
gggtcggtct acattggggg gcggactgtg accggggccg gcaagttcgaa cccatcgaa	120
cctgtcattt cgtactctaa cgagggcgct acgttctaca tcaaccagat gtacgtaa	180
ttccaggctt ccgtccgccc aaggggcctt ccactgggtt tctggcacgg cgggggcctg	240
acaggccata tctgggagtc cactccagat ggccgcccgg ggttccagac actttcggt	300
caggacaggc acacagtgtt cactattgtt cagccagggg gggggcagggg gaacatccct	360
accttcaatg gcccatttcgg gcagctggag gaggagtcca tcgtgaacac cgtcacggc	420
aatgtgagca aggagggggc ttgggtcagg gaccggctcg gcccggccccc agggcagttc	480
tttcgagaact ctcagttccc ccggggctac gaggataattt acttcaagga gatgggttc	540
tcaccatcca tctcgctgtt ctagatgttgc gatgccgtgg tcaagctgtt taccacatc	600
ggcccttgcg ttctggtgac gcatagcgct tcggcggtcc tcggatgag gggtgtaca	660
catgcgaaga acgttgcgg catcggttgc ttcggcggtt ccacttccat tttccccaaag	720
ggcaagggtgc cagagatccc accactggcc gacaagaagt cacagatctt cccacccctt	780
gagattcagg agtcttactt caagaagctc gctaagatcc ccattcagg tctgttccggc	840
gacaacatcc ctaagaatcc gaagagcgcc tactgggtcc tggattgggtt ggcgttacgg	900
cgctacgcgc actctctctc actggaggct atcaacaaggc tcggggccca ggcctcgctc	960
ctggacccctt ctaccgttgg cctggggggg aacacccattt tcccttcac ggatggaaac	1020
aatgtccagg ttgcgtccct cctgagcgat ttctcggttca agcacgggtt ggatcagaat	1080
gagtcttga	1089

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<210> SEQ ID NO 47
<211> LENGTH: 362
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: The amino acid sequence of the ALT03M3
<400> SEQUENCE: 47

Met Glu Thr Asp Asn Val Glu Leu Ala Gln Ser Lys Arg Lys Val Val
1 5 10 15

Leu Ala Glu Gln Gly Ser Phe Tyr Ile Gly Gly Arg Thr Val Thr Gly
20 25 30

Pro Gly Lys Phe Asp Pro Ser Lys Pro Val Ile Arg Ala Ser Asn Glu
35 40 45

Gly Ala Thr Phe Tyr Ile Asn Gln Met Tyr Val Asn Phe Gln Ala Pro
50 55 60

Val Arg Pro Arg Gly Leu Pro Leu Val Phe Trp His Gly Gly Leu
65 70 75 80

Thr Gly His Ile Trp Glu Ser Thr Pro Asp Gly Arg Pro Gly Phe Gln
85 90 95

Thr Leu Phe Val Gln Asp Arg His Thr Val Tyr Thr Ile Asp Gln Pro
100 105 110

Gly Arg Gly Arg Gly Asn Ile Pro Thr Phe Asn Gly Pro Phe Gly Gln
115 120 125

Leu Glu Glu Ser Ile Val Asn Thr Val Thr Ala Asn Val Ser Lys
130 135 140

Glu Arg Ala Trp Val Arg Asp Arg Leu Gly Pro Ala Pro Gly Gln Phe
145 150 155 160

Phe Glu Asn Ser Gln Phe Pro Arg Gly Tyr Glu Asp Asn Tyr Phe Lys
165 170 175

Glu Met Gly Phe Ser Pro Ser Ile Ser Ser Asp Glu Ile Val Asp Ala
180 185 190

Val Val Lys Leu Val Thr His Ile Gly Pro Cys Val Leu Val Thr His
195 200 205

Ser Ala Ser Gly Val Leu Gly Met Arg Val Ala Thr His Ala Lys Asn
210 215 220

Val Arg Gly Ile Val Ala Tyr Glu Pro Ala Thr Ser Ile Phe Pro Lys
225 230 235 240

Gly Lys Val Pro Glu Ile Pro Pro Leu Ala Asp Lys Lys Ser Gln Ile
245 250 255

Phe Pro Pro Phe Glu Ile Gln Glu Ser Tyr Phe Lys Lys Leu Ala Lys
260 265 270

Ile Pro Ile Gln Phe Val Phe Gly Asp Asn Ile Pro Lys Asn Pro Lys
275 280 285

Ser Ala Tyr Trp Phe Leu Asp Trp Trp Arg Val Thr Arg Tyr Ala His
290 295 300

Ser Leu Ser Leu Glu Ala Ile Asn Lys Leu Gly Gly Gln Ala Ser Leu
305 310 315 320

Leu Asp Leu Pro Thr Ala Gly Leu Arg Gly Asn Thr His Phe Pro Phe
325 330 335

Thr Asp Arg Asn Asn Val Gln Val Ala Ser Leu Leu Ser Asp Phe Leu
340 345 350

Gly Lys His Gly Leu Asp Gln Asn Glu Ser
355 360

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<210> SEQ ID NO 48
 <211> LENGTH: 1089
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: the ALT03M3 nucleotide sequence encoding the amino acid sequence of the herbicide tolerant protein ALT03M3

<400> SEQUENCE: 48

atggaaaactg acaacgtgga gcttgcccaa tcgaagcggaa	60
agggttgtcct tgctgaacaa	
ggcagttct acatcgaaaa cagaacagta accgggcctg	120
gaaaattcga tccgtcaaag	
ccggtaattc gagcttccaa cgaagggtgcc acgttttata	180
tcaatcaaattt gtacgtaaac	
tttcaagctc ctgtgcggcc tcgtgggctg cctcttagtct	240
tttggcatgg gggcgacta	
accggccata tctggaaatc taccccagac ggccggcccg	300
gatttcagac cctctttgtt	
caagatcgcc atacggtcta cacgattgat cagccaggc	360
cgccaaagggg caatattcct	
acctttaatg gcccctttgg gcagttggaa gaagagtgcgtt	420
ttgttaaacac tgttaccgca	
aacgtcagta aagaaagagc gtgggtttaga gatcgactag	480
ggcccgctcc cggccagttt	
tttgagaaca gccaattccc acgtggttat gaagacaact	540
acttcaagga gatggggttc	
agtccgtcgtc tctcatcaga tgagatagtc gacgctgttgc	600
ttaaactagt aactcacata	
ggtccttgcgt ttctgggtgac ccattcggct tccggagtagc	660
ttggcatgctcg agtccgtcgtc	
cacggcaaga acgtggggg gatcggtgt tatgagcctg	720
cgacaagttat ctttccccaaa	
ggaaaaagtgc ctgagatacc gcctctcgcc gataaaaagt	780
cgcaaaatttt cccgcggc	
gagatccagg agtcttactt taagaagctc gcgaagatac	840
ccattcagtt tgtcttcgga	
gataatatcc ccaagaaccc taaatccgccc tattgggtct	900
ttggactgggtg gagagtcaact	
cgctacgctc acagcttgc actcgaggct atcaataagc	960
tcgggtggta agcgtcttt	
ttggatttgc cgactgcggg acttcgcggc aacacgcatt	1020
ttccattcac cgaccggaaat	
aacgtgcagg tcgcttctct gttatctgat ttccctcgaa	1080
agcacggctt agatcagaac	
gaaagctga	1089

<210> SEQ ID NO 49
 <211> LENGTH: 1089
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: the ALT03M3-01 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT03M3 and based on the soybean codon usage bias

<400> SEQUENCE: 49

atggagactg ataacgtgga actcgcccaa tctaagagaa	60
agggtgggtct ggctgaacaa	
gggtcatttt acatagggggg taggactgtt actggcctgt	120
gcaagtttga tccatccaaa	
cctgtgatac gagccagtaa cgaaggagca acattctata	180
ttaaccaaattt gtatgttaac	
ttccaggccc cagttagacc tagggactt ccattggttt	240
tctggcatgg aggtggcttgc	
actggtcaca tctgggagtc tacacctgac ggcagaccccg	300
ggtttcaaac cctcttcgtt	
caggataggc ataccgtgta cactattgac caacctggaa	360
gaggaagggg taacatccca	
acttttaacg gaccttcgg acatggtaga gaagagtagt	420
ttgttaaacac tgcgtacagcc	
aatgtatcaa aggaacgagc ctgggtgaga gataggcttgc	480
ccctgtcc cgggcatttt	
ttcggagaact ctcagttcc tagaggctat gaagacaattt	540
actttaagga gatgggattc	

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agcccatcta tatccagtga taaaattgtt gacgctgttg tgaaactcgt gaccatatt    600
ggtccttgta ttctggtgac tcactcagca tccggcggtc ttggatgag agtggctaca    660
cacgcaaaga atgttagggg aattgtggcc tatgaaccag ctacctaatt cttccccaaag    720
ggaaaatgtc cagagatacc acctctcgct gataagaaaa gccaaatctt tccccccattc    780
gaaatacagg agtcttactt taagaaactt gccaagattt caatccaatt tggtttcgga    840
gataacatcc ccaagaatcc aaaatcagca tattgggtcc tggactgggt gagagtgaca    900
agataacgcac atagtcctcgctt cctggaggcc ataaacaaat tggggggaca agttccctt    960
ttggatcttc ctactgcagg attgagaggt aatacacact ttcccttcac cgataggAAC    1020
aatgttcagg tggcttcctt cctgtcagac tttctggta aacacggctt ggatcaaaat    1080
gagagctga                                         1089

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<210> SEQ ID NO 50
<211> LENGTH: 1089
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT03M3-02 nucleotide sequence encoding the
      amino acid sequence corresponding to the herbicide tolerant
      protein ALT03M3 and based on the maize codon usage bias

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<400> SEQUENCE: 50
atggagactg ataacgtgga gctggcgac agcaagagga aggtggttct ggctgagcag    60
gggtcggttcc acattggggg gcgactgtg accggggccc gcaagttcga cccatcgaa    120
cctgtcatcc gggcgctaa cgagggcgct acgttctaca tcaaccatgt gtacgtaaat    180
ttccaggctc ccgtccggcc aaggggccctc ccactgggtt tctggcacgg cggggggctg    240
acaggccata tctgggagtc cactccagat ggccggccag ggttccagac actttcggtt    300
caggacaggc acacagtgtt cactattgtt cagccaggaa ggggcaggaa gaacatccct    360
accttcaatg gcccattcg gcaactggag gaggagtcac tcgtgaacac cgtcacggcg    420
aatgtgagca aggagggggc ttgggtcagg gaccggctcg gcccggccccc agggcaggctc    480
ttcgagaact ctcagttccc ccggggctac gaggataatt acttcaaggaa gatggggcttc    540
tcaccatcca tctcgctgtt cggatgttc gatggcggtt tcaagtcgt tacccacatc    600
ggcccttgcg ttctggtgac gcatacgctt tcggggcgctt tcggatgag gggttgcata    660
catcgcaaga acgttgcggg catcggttgc ttcggcgccg ccacttccat tttccccaaag    720
ggcaagggtgc cagagatccc accactggcc gacaagaagt cacagatctt cccaccttc    780
gagattcagg agtcttactt caagaagctc gctaagatcc ccatttcgtt cgtttccggc    840
gacaacattc ctaagaatcc gaagagcgac tactgggtcc tggattgggt ggcgtcactg    900
cgctacgcgc actctctctc actggaggtt atcaacaagg tcggggggcca ggcctcgctc    960
ctggacctcc ctaccgttgg cctggggggg aacacccattt tcccttcac ggatcgaaac    1020
aatgtccagg ttgcgtccctt ccttgagcgat ttccctggca agcacgggtt ggatcagaat    1080
gagtcttga                                         1089

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<210> SEQ ID NO 51
<211> LENGTH: 350
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the amino acid sequence of ALT04

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<400> SEQUENCE: 51

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Met Ser Lys Arg Lys Val Val Leu Ala Glu Gln Gly Ser Phe Tyr Ile
1           5          10          15

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

Val Ile Pro Tyr Ser Asn Glu Gly Ala Thr Phe Tyr Ile Asn Gln Met
35          40          45

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

Phe Trp His Gly Gly Leu Thr Gly His Ile Trp Glu Ser Thr Pro
65          70          75          80

Asp Gly Arg Pro Gly Phe Gln Thr Leu Phe Val Gln Asp Arg His Thr
85          90          95

Val Tyr Thr Ile Asp Gln Pro Gly Arg Gly Arg Asn Ile Pro Thr
100         105         110

Phe Asn Gly Pro Phe Gly Gln Leu Glu Glu Ser Ile Val Asn Thr
115         120         125

Val Thr Gly Asn Ser Ser Lys Glu Gly Ala Trp Val Arg Asp Arg Leu
130         135         140

Gly Pro Ala Pro Gly Gln Phe Phe Glu Asn Ser Gln Phe Pro Arg Gly
145         150         155         160

Tyr Glu Asp Asn Tyr Phe Lys Glu Met Gly Phe Ser Pro Ser Ile Ser
165         170         175

Ser Asp Glu Ile Val Asp Ala Val Val Lys Leu Val Thr His Ile Gly
180         185         190

Pro Cys Val Leu Val Thr His Ser Ala Ser Gly Val Leu Gly Met Arg
195         200         205

Val Ala Thr His Ala Lys Asn Val Arg Gly Ile Val Ala Tyr Glu Pro
210         215         220

Ala Thr Ser Ile Phe Pro Lys Gly Lys Val Pro Glu Ile Pro Pro Leu
225         230         235         240

Ala Asp Lys Lys Ser Gln Ile Phe Pro Pro Phe Glu Ile Gln Glu Ser
245         250         255

Tyr Phe Lys Leu Ala Lys Ile Pro Ile Gln Phe Val Phe Gly Asp
260         265         270

Asn Ile Pro Lys Asn Pro Lys Ser Ala Tyr Trp Phe Leu Asp Trp Trp
275         280         285

Arg Val Thr Arg Tyr Ala His Ser Leu Ser Leu Glu Ala Ile Asn Lys
290         295         300

Leu Gly Gly Gln Ala Ser Leu Leu Asp Leu Pro Thr Ala Gly Leu Arg
305         310         315         320

Gly Asn Thr His Phe Pro Phe Thr Asp Arg Asn Asn Val Gln Val Ala
325         330         335

Ser Leu Leu Ser Asp Phe Leu Gly Lys His Gly Leu Asp Gln
340         345         350

```

<210> SEQ ID NO 52

<211> LENGTH: 1053

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: the ALT04 nucleotide sequence encoding the amino acid sequence of ALT04

<400> SEQUENCE: 52

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atgtcgaagc ggaagggttgt ccttgctgaa caaggcagtt tctacatcggtt gggcagaaca	60
gttaaccgggc ctggaaaatt cgatccgtca aagccggtaa ttccatatttc caacgaaggt	120
gccacgtttt atatcaatca aatgtacgta aactttcaag ctccctgtgcg ccctctgtggg	180
ctgcctctag tcttttggca tggggggcga ctaaccggcc atatctggaa atctacccca	240
gacggccccc ccggatttca gaccctctt gttcaagatc ggcatacggtt ctacacgatt	300
gatcagecag ggcgcggaaag gggcaatattt cctaccttta atggccctt tggcagttt	360
gaagaagagt cgattgttaa cactgttacc ggaaactcca gttaaagaagg agcgtgggtt	420
agagatcgcac tagggccgc tcccgccag ttttttggaa acagccaattt cccacgtgggt	480
tatgaagaca actacttcaa ggagatgggg tttagtccgtt cgatctcatc agatgagata	540
gtcgacgctc ttgttaaact agtaactcac ataggtcctt gtgttctggt gacccatcg	600
gcttccggag tactgggcat gcgagtcgcg acacacgcca agaacgtgag gggatcggt	660
gcttatgagc ctgcgacaag tatcttccc aaaggaaaag tgccctgagat accgccttc	720
gcccataaaaa agtcgaaat ttccccgcgg tttagatccagg aggagtctttaaagaag	780
ctcgcgaaga tacccattca gtttgcgttcc ggagataata tcccaagaa ccctaaatcc	840
gcctattggt tcttggactg gtggagagtc actcgctacg ctcacagctt gtcactcgag	900
gctatcaata agtcgggtgg tcaagcgtct ctttggatt tgccgactgc gggacttcgc	960
ggcaacacgc attttccattt caccgaccgg aataacgtgc aggtcgctt tctgttatct	1020
gatttcctcg gaaagcacgg ctttagatcgt tga	1053

<210> SEQ ID NO 53
 <211> LENGTH: 1053
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: the ALT04-01 nucleotide sequence encoding the
 amino acid sequence corresponding to the ALT04 and based on the
 soybean codon usage bias

<400> SEQUENCE: 53

atgtctaaga gaaagggttgt gctggctgaa caagggtcat tttacatagg gggtaggact	60
tttaactggtc ctggcaagtt tgatccatcc aaacctgtga taccctacag taacgaagga	120
gcaacattct atattaacca aatgtatgtt aacttccagg ccccaactgtgag accttagggaa	180
cttccattgg ttttctggca tggaggtggc ttgactggc acatctggaa gtctacacct	240
gacggcagac ccgggttca aacccttcc gttcaggata ggcatacggtt gtacactatt	300
gaccaacactg ggagaggaag gggtaacatc ccaacttttta acggacctt cggacagttt	360
gaggaagaga gtattgttaa cactgtgaca ggaaatttttta caaaggaaagg tgccctgggt	420
agagataggc ttggccctgc tcccgccaa tttttcgaga actctcagg ttcctagaggc	480
tatgaagaca attactttaa ggagatggga tttagcccat ctatatccag ttagaaattt	540
gttgcacgtt ttgtgaaact cgtgacccat attggcctt gtgttctggt gactcactca	600
gcatccggcg ttcttggat gagagtggctt acacacgcaaa agaatgttag gggattgtg	660
gcctatgaac cagctacccatc aatcttccc aaggaaaag ttccagagat accacccctc	720
gctgataaga aaagccaaat ctttccca ttcgaaatac aggagtcttta ctttaagaaa	780
cttgccaaaga ttccaaatcca atttttttcc ggagataaca tcccaagaa tccaaatca	840
gcataattggt tcttggactg gtggagagtg acaagatacg cacatagttt cagcctggag	900
gccataaaaca aattgggggg acaagcttcc ctttggatc ttcctactgc aggattggaa	960

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ggttaatacac acttccctt caccgatagg aacaatgttc aggtggctc tctcctgtca    1020
gactttctgg gttaaacacgg tctggatcaa tga                                1053
```

<210> SEQ ID NO 54
<211> LENGTH: 1053
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT04-02 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT04 and based on the maize codon usage bias

<400> SEQUENCE: 54

```
atgagcaaga ggaaggtgg tctggctag caggggtcg tctacattgg gggggggact      60
gtgaccgggc cggcaagtt cgaccatcg aagcctgtca ttccgtactc taacgagggc     120
gctacgttct acatcaacca gatgtacgtg aatttccagg ctcccgtccg cccaaaggggc   180
ctccccactgg tgttctggca cggggggggc ctgacaggcc atatctggga gtccactcca   240
gatggccgcc cagggttcca gacactcttc gttcaggaca ggcacacagt gtacactatt  300
gtcagcccg ggagggggcag gggaaacatc cttaccttca atggccatt cggcagctg     360
gaggaggagt ccatctgtaa caccgtcaag ggcaatttcca gcaaggaggg ggcttgggc   420
agggacccggc tcggccggc cccagggcag ttcttcgaga actctcagtt ccccccgggc   480
tacgaggata attacttcaa ggagatgggc ttctcaccat ccattctcg tcgacgagatt  540
gtcgatgccg tggcaagct cgatccccac atcgccctt gcgttctgg tgcgtatgc     600
gcttcggcg tcctcggat gaggggttget acacatgca agaacgttc cggcatcg     660
gtttacgagc cggccacttc catttcccc aaggcgaagg tgccagagat cccaccactg   720
gccgacaaga agtcacagat ctccccaccc ttcgagattc aggagtccca cttcaagaag  780
ctcgctaaga tccccattca gtctgttgc ggccacaaca ttccctaagaa tccgaagac   840
gcgtactgt tcctggattt gtggcgcgtc acgcgtacg cgcactct ctcactggag   900
gctatcaaca agctcggggg ccaggccctcg ctctggacc tccctaccgc tggctgagg  960
ggaaacaccc attccccgtt cacggatcg aacaatgtcc aggttgctc ctcctgagc  1020
gatttcctcg gcaagcacgg gctggatcag tga                                1053
```

<210> SEQ ID NO 55
<211> LENGTH: 350
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the amino acid sequence of the ALT04M1

<400> SEQUENCE: 55

```
Met Ser Lys Arg Lys Val Val Leu Ala Glu Gln Gly Ser Phe Tyr Ile
1           5          10          15

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

Val Ile Pro Tyr Ser Asn Glu Gly Ala Thr Phe Tyr Ile Asn Gln Met
35          40          45

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

Phe Trp His Gly Gly Leu Thr Gly His Ile Trp Glu Ser Thr Pro
65          70          75          80

Asp Gly Arg Pro Gly Phe Gln Thr Leu Phe Val Gln Asp Arg His Thr
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85	90	95
Val Tyr Thr Ile Asp Gln Pro Gly Arg Gly Arg Gly Asn Ile Pro Thr		
100	105	110
Phe Asn Gly Pro Phe Gly Gln Leu Glu Glu Ser Ile Val Asn Thr		
115	120	125
Val Thr Ala Asn Ser Ser Lys Glu Gly Ala Trp Val Arg Asp Arg Leu		
130	135	140
Gly Pro Ala Pro Gly Gln Phe Phe Glu Asn Ser Gln Phe Pro Arg Gly		
145	150	155
Tyr Glu Asp Asn Tyr Phe Lys Glu Met Gly Phe Ser Pro Ser Ile Ser		
165	170	175
Ser Asp Glu Ile Val Asp Ala Val Lys Leu Val Thr His Ile Gly		
180	185	190
Pro Cys Val Leu Val Thr His Ser Ala Ser Gly Val Leu Gly Met Arg		
195	200	205
Val Ala Thr His Ala Lys Asn Val Arg Gly Ile Val Ala Tyr Glu Pro		
210	215	220
Ala Thr Ser Ile Phe Pro Lys Gly Lys Val Pro Glu Ile Pro Pro Leu		
225	230	235
Ala Asp Lys Lys Ser Gln Ile Phe Pro Pro Phe Glu Ile Gln Glu Ser		
245	250	255
Tyr Phe Lys Lys Leu Ala Lys Ile Pro Ile Gln Phe Val Phe Gly Asp		
260	265	270
Asn Ile Pro Lys Asn Pro Lys Ser Ala Tyr Trp Phe Leu Asp Trp Trp		
275	280	285
Arg Val Thr Arg Tyr Ala His Ser Leu Ser Leu Glu Ala Ile Asn Lys		
290	295	300
Leu Gly Gly Gln Ala Ser Leu Leu Asp Leu Pro Thr Ala Gly Leu Arg		
305	310	315
Gly Asn Thr His Phe Pro Phe Thr Asp Arg Asn Asn Val Gln Val Ala		
325	330	335
Ser Leu Leu Ser Asp Phe Leu Gly Lys His Gly Leu Asp Gln		
340	345	350

<210> SEQ ID NO 56
 <211> LENGTH: 1053
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: the ALT04M1 nucleotide sequence encoding the
 amino acid sequence of the herbicide tolerant protein ALT04M1

<400> SEQUENCE: 56

atgtcgaagc ggaagggtgt ccttgctgaa caaggcagt tctacatcg ggccagaaca	60
gttaaccgggc ctggaaaatt cgatccgtca aagccggtaa ttccatatcc caacgaaggt	120
gccacgtttt atatcaatca aatgtacgta aactttcaag ctccctgtgcg ccctcgtggg	180
ctgcctctag tcttttggca tggggccgga ctaaccggcc atatctggga atctacccca	240
gacggccgccc cgggatttca gaccctttt gttcaagatc ggcatacggt ctacacgatt	300
gatcagccag ggcgcggaag gggcaatatt cctaccttta atggcccttt tgggcaggtt	360
gaagaagagt cgattgttaa cactgttacc gcaaactcca gtaaagaagg agcgtgggtt	420
agagatcgac tagggccgcg tcccgccag tttttgaga acagccaatt cccacgtgggt	480
tatgaagaca actacttcaa ggagatgggg ttcagtcgtcgatctcatc agatgagata	540

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gtcgacgctg ttgttaact agtaactcac ataggtcctt gtgttctgg gaccatcg	600
gcttcggag tactggcat gcgagtcgcg acacacgcca agaacgtgag ggggatcgtt	660
gcttatgagc ctgcgacaag tatcttccc aaaggaaaag tgcctgagat accgcctctc	720
gccgataaaa agtcgaaat ttcccccg ttcgagatcc aggagtctta ctttagaag	780
ctcgcgaaga tacccattca gtttgtctt ggagataata tcccaagaa ccctaaatcc	840
gcctattgg tcttgactg gtggagatgc actcgctacg ctcacagctt gtcactcgag	900
gctatcaata agctcggtgg tcaagcgtct ctttggatt tgccgactgc gggacttgc	960
ggcaacacgc atttccatt caccgaccgg aataacgtgc aggtcgcttc tctgttatct	1020
gatttcctcg gaaagcacgg ctttagatcag tga	1053

<210> SEQ ID NO 57
<211> LENGTH: 1053
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT04M1-01 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT04M1 and based on the soybean codon usage bias

<400> SEQUENCE: 57

atgtctaaga gaaaggtgg gctggctgaa caagggtcat tttacatagg gggtaggact	60
gttactggtc ctggcaagtt tgatccatcc aaacctgtga taccctacag taacgaagga	120
gcaacattct atattaacca aatgtatgtt aacttccagg ccccaagtgg acctagggg	180
cttccattgg ttttctggca tggaggtggc ttgactggc acatctggg gtctcacacct	240
gacggcagac ccgggtttca aaccctcttc gttcaggata ggcataccgt gtacactatt	300
gaccaacctg ggagaggaag gggtaacatc ccaacttttta acggacacctt cgacagg	360
gaggaagaga gtattgttaa cactgtgaca gccaattttt caaaggaaagg tgcctgggt	420
agagataggc ttggccctgc tccggggcaa ttttcgaga actctcagtt tcctagaggc	480
tatgaagaca attactttaa ggagatggg ttcagccat ctatatccag tgatgaaatt	540
gttgacgctg ttgtgaaact cgtgacccat attggtcctt gtgttctgg gactcactca	600
gcatccggcg ttctggat gagagtggct acacacgcaa agaatgttag gggattgt	660
gcctatgaac cagctacctc aatctcccc aaggaaaag ttccagagat accacctctc	720
gctgataaga aaagccaaat ctttccccca ttcgaaatac aggagtctta ctttggaaa	780
cttgccaaga ttccaaatcca atttttttc ggagataaca tcccaagaa tccaaatca	840
gcatattggt tcctggactg gtggagatgt acaagatacg cacatagttt cagcctggag	900
gccataaaaca aattgggggg acaagcttcc ctttggatcc ttccactgc aggattgaga	960
ggtaatacac acttccctt caccgatagg aacaatgttc aggtggatcc ttcctgtca	1020
gactttctgg gtaaacacgg tctggatcaa tga	1053

<210> SEQ ID NO 58
<211> LENGTH: 1053
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT04M1-02 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT04M1 and based on the maize codon usage bias

<400> SEQUENCE: 58

atgagcaaga ggaaggtgg tctggctgag caggggtcg tctacattgg gggggcggact	60
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gtgaccgggc ccggcaagtt cgaccatcg aaggctgtca ttccgtactc taacgagggc	120
gctacgttct acatcaacca gatgtacgt aatttccagg ctcccggtccg cccaaaggggc	180
ctccccactgg tgttctggca cggcgggggc ctgacaggcc atatctggga gtccactcca	240
gatggccgcc cagggttcca gacactttc gttcaggaca ggcacacagt gtacactatt	300
gatcagccag ggagggcag ggggaacata cctacattca atggcccatt cgggcagctg	360
gaggaggagt ccatcgtaa caccgtcagc gcaattcca gcaaggaggg ggcttggtc	420
agggacccgc tcggccggc cccaggcag ttctcgaga actctcagg tccccgggc	480
tacgaggata attactcaa ggagatgggc ttctcacat ccatctcg tcgacgagatt	540
gtcgatgccc tggtaagct cgtaaccac atcgccctt gcttcttgt gacgcatagc	600
gcttcgggcg tcctcggtat gaggggtgtt acacatgcga agaacgttcg cggcatcg	660
gcttacgagc cggccacttc cattttcccc aaggcaagg tgccagagat cccaccactg	720
gcccacaaga agtcacagat cttcccacct ttcgagattc aggagtccta cttcaagaag	780
ctcgctaaga tccccattca gttcgtgttc ggccacaaca ttccctaagaa tccgaagagc	840
gcgtactgtt tcctggattt gtggcgcttc acgcgtacg cgcactctt ctcactggag	900
gctatcaaca agctcggggg ccaggcctcg ctccctggacc tccctaccgc tggcttgagg	960
ggaaacaccc atttcccggtt cacggatcg aacaatgtcc aggttgcgtc ctcctgagc	1020
gatttcctcg gcaagcacgg gctggatcg tga	1053

<210> SEQ ID NO 59

<211> LENGTH: 350

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: the amino acid sequence of the ALT04M2

<400> SEQUENCE: 59

Met Ser Lys Arg Lys Val Val Leu Ala Glu Gln Gly Ser Phe Tyr Ile			
1	5	10	15

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

Val Ile Pro Tyr Ser Asn Glu Gly Ala Thr Phe Tyr Ile Asn Gln Met			
35	40	45	

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

Phe Trp His Gly Gly Leu Thr Gly His Ile Trp Glu Ser Thr Pro			
65	70	75	80

Asp Gly Arg Pro Gly Phe Gln Thr Leu Phe Val Gln Asp Arg His Thr			
85	90	95	

Val Tyr Thr Ile Asp Gln Pro Gly Arg Gly Arg Asn Ile Pro Thr			
100	105	110	

Phe Asn Gly Pro Phe Gly Gln Leu Glu Glu Ser Ile Val Asn Thr			
115	120	125	

Val Thr Gly Asn Val Ser Lys Glu Gly Ala Trp Val Arg Asp Arg Leu			
130	135	140	

Gly Pro Ala Pro Gly Gln Phe Phe Glu Asn Ser Gln Phe Pro Arg Gly			
145	150	155	160

Tyr Glu Asp Asn Tyr Phe Lys Glu Met Gly Phe Ser Pro Ser Ile Ser			
165	170	175	

Ser Asp Glu Ile Val Asp Ala Val Val Lys Leu Val Thr His Ile Gly	
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180	185	190
Pro Cys Val Leu Val Thr His Ser Ala Ser Gly Val		
195	200	205
Leu Gly Met Arg		
Val Ala Thr His Ala Lys Asn Val Arg Gly Ile Val		
210	215	220
Ala Tyr Glu Pro		
Ala Thr Ser Ile Phe Pro Lys Gly Lys Val Pro		
225	230	235
Glu Ile Pro Pro Leu		240
Ala Asp Lys Lys Ser Gln Ile Phe Pro Pro Phe		
245	250	255
Glu Ile Gln Glu Ser		
Tyr Phe Lys Lys Leu Ala Lys Ile Pro Ile Gln Phe		
260	265	270
Gly Val Phe Gly Asp		
Asn Ile Pro Lys Asn Pro Lys Ser Ala Tyr Trp		
275	280	285
Phe Leu Asp Trp Trp		
Arg Val Thr Arg Tyr Ala His Ser Leu Ser Leu		
290	295	300
Glu Ala Ile Asn Lys		
Leu Gly Gly Gln Ala Ser Leu Leu Asp Leu Pro		
305	310	315
Thr Ala Gly Leu Arg		320
Gly Asn Thr His Phe Pro Phe Thr Asp Arg Asn Asn		
325	330	335
Val Gln Val Ala		
Ser Leu Leu Ser Asp Phe Leu Gly Lys His Gly		
340	345	350
Leu Asp Gln		

<210> SEQ ID NO 60

<211> LENGTH: 1053

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: the ALT04M2 nucleotide sequence encoding the amino acid sequence of the herbicide tolerant protein ALT04M2

<400> SEQUENCE: 60

atgtcgaagc ggaagggtgt ctttgctgaa caaggcagg tctacatcg ggccagaaca	60
gttaaccgggc ctggaaaatt cgatccgtca aagccggtaa ttccatatttc caacgaagg	120
gccacgtttt atatcaatca aatgtacgta aactttcaag ctccctgtgc ccctcggtgg	180
ctgcctctag tcttttggca tggggccgga ctaaccggcc atatctggga atctacc	240
gacggccgccc ccggatttca gacectcttt gttcaagatc ggcatacgg ctacacgatt	300
gatcagccag ggcgcggaag gggcaatatt cctaccttta atggcccttt tggcagtt	360
gaagaagagt cgattgttaa cactgttacc gaaaaacgtca gtaaagaagg agcgtgg	420
agagatcgac tagggccccgc tccccggccag tttttgaga acagccaatt cccacgttgt	480
tatgaagaca actacttcaa ggagatgggg ttcatgtccgt cgatctcatc agatgagata	540
gtcgacgctg ttgttaact agtaactcac ataggctctt gtgttgtgt gaccatc	600
gcttcggag tactggcat gcgagtcgcg acacacgcca agaacgtgag gggatcg	660
gcttatgagc ctgcgacaag tatcttccc aaaggaaaag tgcctgagat accgcctc	720
gccgataaaa agtcgcaaat ttccccggc ttcgagatcc aggagtctt ctttaagaag	780
ctcgcaaga tacccattca gtttgtctt ggagataata tcccaagaa ccctaattcc	840
gcctatttgt tcttgactg gtggagagtc actcgctacg ctcacagctt gtcactcg	900
gctatcaata agctcggtgg tcaagcgtct ctttggatt tgccgactgc gggacttc	960
ggcaacacgc attttccatt caccgaccgg aataacgtgc aggtcgctc tctgttatct	1020
gatttcctcg gaaagcacgg ctttagatcg tga	1053

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<210> SEQ ID NO 61
<211> LENGTH: 1053
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT04M2-01 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT04M2 and based on the soybean codon usage bias;

<400> SEQUENCE: 61

atgtctaga	gaaagggttgt	gctggctgaa	caagggtcat	tttacatagg	gggttaggact	60
gttactggc	ctggcaagtt	tgtatccatcc	aaacctgtgta	taccctacag	taacgaagga	120
gcaacattct	atattaacca	aatgtatgtt	aacttccagg	ccccagttag	accttagggga	180
cttccattgg	ttttctggca	tggaggtggc	ttgactggtc	acatctggga	gtctcacacct	240
gacggcagac	cggggttca	aaccctcttc	gttcaggata	ggcataaccgt	gtacactatt	300
gaccaacctg	ggagaggaag	gggtaacatc	ccaacttttta	acggacacctt	cggacagttg	360
gaggaagaga	gtattgttaa	cactgtgaca	ggaaatgtat	caaaggaaagg	tgcctgggtg	420
agagataggc	ttggccctgc	tcccggcaaa	ttttcgaga	actctcagtt	tcctagaggc	480
tatgaagaca	attacttaa	ggagatggga	ttcagcccat	ctatatccag	tgtatgaaatt	540
gttgacgctg	ttgtgaaact	cgtgacccat	attggtcctt	gtgttctgg	gactcactca	600
gcatccggcg	ttcttggat	gagagtggct	acacacgcaa	agaatgttag	ggaaattgtg	660
gcctatgaac	cagctacctc	aatttcccc	aaggaaaaa	ttccagagat	accacacctc	720
gctgataaga	aaagccaaat	ctttcccca	ttcgaaatac	aggagtcttta	ctttaagaaa	780
cttgccaaga	ttccaatcca	atttgtttt	ggagataaca	tcccaagaa	tccaaaatca	840
gcataattgt	tcctggactg	gtggagagtg	acaagatacg	cacatagttct	cagcctggag	900
gccataaaca	aattgggggg	acaagcttc	ctttggatc	tccctactgc	aggattgaga	960
ggttaatacac	actttccctt	caccgatagg	aacaatgttc	aggtggcttc	tctcctgtca	1020
gactttctgg	gttaaacacgg	tctggatcaa	tga			1053

<210> SEQ ID NO 62
<211> LENGTH: 1053
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the ALT04M2-02 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT04M2 and based on the maize codon usage bias

<400> SEQUENCE: 62

atgagcaaga	ggaagggttgt	tctggctgag	caggggtcgt	tctacattgg	ggggcggact	60
gtgaccgggc	cggcaagtt	cgaccatcg	aagcctgtca	ttccgtactc	taacgagggc	120
gctacgttct	acatcaacca	gatgtacgt	aatttccagg	ctccctgtcg	cccaaggggc	180
ctccccactgg	tgttctggca	cggcgggggc	ctgacaggcc	atatctggta	gtccactcca	240
gatggccgcc	cagggttcca	gacacttttc	gttcaggaca	ggcacacagt	gtacactatt	300
gatcagccag	ggagggggcag	gggaaacatc	cctaccttca	atggcccatt	cggcagctg	360
gaggaggagt	ccatcgtgaa	caccgtcact	ggcaatgtga	gcaaggagg	ggcttgggtc	420
agggacccgc	tggcccccgc	cccaggccag	ttcttcgaga	actctcagtt	ccccggggc	480
tacgaggata	attacttcaa	ggagatgggc	ttctcaccat	ccatctcgct	tgacgagatt	540
gtcgatgccc	tggtaagct	cgttacccac	atcgccctt	gcgttctgg	gacgcatacg	600

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gcttcggcg tcctcggtat gagggttgct acacatgcga agaacgttcg cggcatcgtg	660
gcttacgagc cggccacttc cattttcccc aaggggcaagg tgccagagat cccaccactg	720
gcccacaaga agtcacagat cttcccacct ttcgagattc aggagtccata cttcaagaag	780
ctcgctaaga tccccattca gttcgtgttc ggccacaaca ttccataagaa tccgaagagc	840
gcgtactggc tcctggattt gtggcgcgta acgcgtacg cgactctct ctcactggag	900
gctatcaaca agctcgcccc ccaggccctcg ctctggacc tccctaccgc tggccctgagg	960
gggaacacccc atttcccggtt cacggategg aacaatgtcc aggttgcgtc cctctgagc	1020
gatttcctcg gcaaggcacgg gctggatcag tga	1053

<210> SEQ ID NO 63
<211> LENGTH: 350
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the amino acid sequence of the ALT04M3

<400> SEQUENCE: 63

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

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275 280 285

Arg Val Thr Arg Tyr Ala His Ser Leu Ser Leu Glu Ala Ile Asn Lys
 290 295 300

Leu Gly Gly Gln Ala Ser Leu Leu Asp Leu Pro Thr Ala Gly Leu Arg
 305 310 315 320

Gly Asn Thr His Phe Pro Phe Thr Asp Arg Asn Asn Val Gln Val Ala
 325 330 335

Ser Leu Leu Ser Asp Phe Leu Gly Lys His Gly Leu Asp Gln
 340 345 350

<210> SEQ ID NO 64

<211> LENGTH: 1053

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: the ALT04M3 nucleotide sequence encoding the amino acid sequence of the herbicide tolerant protein ALT04M3

<400> SEQUENCE: 64

atgtcgaagc ggaagggttgt ccttgctgaa caaggcagtt totacatcggttggcagaaca	60
gttaaccgggc ctggaaaatt cgatccgtca aagccggtaa ttcgagotttc caacgaaggtt	120
ggcacgtttt atatcaatca aatgtacgta aactttcaag ctccctgtgcgc ccctctgtggg	180
ctgcctcttag tcttttggca tggggggcga ctaaccggcc atatctggga atctacccca	240
gacggccgccc ccggatttca gaccctcttt gttcaagatc ggcatacggcttacacgatt	300
gatcagcccg ggccgcggaaag gggcaatatt cctaccttta atggcccttt tggcagtttgc	360
gaagaagagt cgattgttaa cactgttacc gcaaacctgtca gtaaagaag agcgtgggtt	420
agagatcgac tagggccgc tccccggccag ttttttgaga acagccaaatttccacgtgg	480
tatgaagaca actacttcaa ggagatgggg ttcaagtcgtt cgtatctcatc agatgagata	540
gtcgacgctg ttgttaaact agtaactcac ataggtcctt gtgttctggt gaccctatcg	600
gcttccggag tactggcat gcgagtcgcg acacacgcca agaacgtgag ggggatcgtt	660
gcttatgagc ctgcgacaag tatcttccc aaaggaaaag tgcctgagat accgcctctc	720
gccgataaaaa agtcgcaaat ttccccggc ttcgagatcc aggagtctta cttaagaag	780
ctcgcgaaaga tacccattca gtttgtcttggagataata tccccaaagaa ccctaaatcc	840
gcctattgggt tcttggactg gtggagagtc actcgctacg ctcacagctt gtcactcgag	900
gctatcaata agctcggtgg tcaaacgtctt ctttggatt tgccgactgc gggacttcgc	960
ggcaacacgc atttccattt caccgaccgg aataaacgtgc aggtcgcttc tctgttatct	1020
gatttcctcg gaaagcacgg ctttagatcgtt gta	1053

<210> SEQ ID NO 65

<211> LENGTH: 1053

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: the ALT04M3-01 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT04M3 and based on the soybean codon usage bias;

<400> SEQUENCE: 65

atgtctaaga gaaagggttgt gctggctgaa caagggtcat tttacatagg gggtaggact	60
gttactggtc ctggcaagtt tgatccatcc aaacctgtga tacgagccag taacgaagga	120
gcaacattct atattaacca aatgtatgtt aacttccagg ccccaagtggac accttagggaa	180

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cttccatgg ttttctggca tggaggtggc ttgactggtc acatctggga gtctacacct	240
gacggcagac cggggtttca aacccttcc gttcaggata ggcataccgt gtacactatt	300
gaccaacctg ggagaggaag gggtaacato ccaacttttca acggacctt cggacagttg	360
gaggaagaga gtattgttaa cactgtgaca gccaatgtat caaaggaacg agcctgggtg	420
agagataggc ttggccctgc tccccggcaa ttttcgaga actctcagggt tccttagaggc	480
tatgaagaca attacttaa ggagatggga ttcaagccat ctatatccag tcatgaaatt	540
gttgacgctg ttgtaaaact cgtgacccat attggctt gtttctgggt gactcactca	600
gcattccggcg ttcttggat gagagtggct acacacgc当地 aagatgttag gggatttg	660
gcctatgaac cagctacctc aatttcccc aaggaaaag ttccagagat accaccttc	720
gctgataaga aaagccaaat ctttccccca ttcgaaatac aggagtctt cttttagaaa	780
cttgccaaga ttccaatcca atttgttttca ggagataaca tcccaagaa tccaaatca	840
gcataatttgtt tcctggactg gtggagagtg acaagatacg cacatagtct cagcctggag	900
gccataaaaca aattgggggg acaagcttcc cttttggatc ttccactgac aggattgaga	960
ggtaatacac actttccctt caccgatagg aacaatgttc aggtggctt cttctgtca	1020
gactttctgg gtaaacacgg tctggatcaa tga	1053

<210> SEQ ID NO 66

<211> LENGTH: 1053

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: the ALT04M3-02 nucleotide sequence encoding the amino acid sequence corresponding to the herbicide tolerant protein ALT04M3 and based on the maize codon usage bias

<400> SEQUENCE: 66

atgagcaaga ggaaggtggc tctggcttag caggggtcg tctacattgg gggggggact	60
gtgaccgggc cggcaagtt cgaccatcg aagcctgtca ttccggcgctc taacgaggc	120
gtacgttct acatcaacca gatgtacgtg aatttcagg ctcccgtccg cccaaaggggc	180
ctcccaactgg tgttctggca cggcgggggc ctgacaggcc atatctgggaa ttccactcca	240
gtatggccca cagggttcca gacacttttc gttcaggaca ggcacacagt gtacactatt	300
gtatcggccg ggagggggcag ggggaacatc cttacccatc atggccattt cgggcagctg	360
gaggaggagt ccattgtgaa caccgtcactg gcaatgtga gcaaggagcg ggcttgggtc	420
aggggaccggc tcggcccgcc cccaggggcag ttcttcgaga actctcagggt ccccccgggc	480
tacggaggata attacttcaa ggagatgggc ttctcaccat ccattctcgac tgacgagatt	540
gtcgatggcg tggtaagct cgttacccac atcggccctt gcttctgggt gacgatagc	600
gtttcggcgcc ttctcggat gagggttgc acacatgcga agaacgttcg cggcatcg	660
gttttacggc cggccacttc cattttcccc aaggcaagg tgccagagat cccaccactg	720
ggccgacaaga agtcacagat ctccccaccc ttctggatcc aggagtccctt cttcaagaag	780
ctcgctaaga tccccattca ttctgtgttc ggcacaaca ttccataagaa tccgaagac	840
gctgtactggt ttctggattt gttggcgctc acgcgtacg cgcactctt ctcactggag	900
gctatcaaca agtcgggggg ccaggcctcg ctccctggacc tccctaccgc tggcctgagg	960
ggaaacaccc atttcccggtt cacggatgg aacaatgtcc aggttgcttc cttctgtac	1020
gatttcctcg gcaagcacgg gctggatcg tga	1053

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<210> SEQ ID NO 67
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the primer 3 for PCR amplification of the ALT01M1 gene

<400> SEQUENCE: 67

tgccagacata tggaaaccga taaaaaaac

29

<210> SEQ ID NO 68
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the primer 4 for PCR amplification of the ALT01M1 gene

<400> SEQUENCE: 68

ccccaaagcttc tagcttcgt tctgatctaa gcccgtgc

37

<210> SEQ ID NO 69
<211> LENGTH: 1322
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 69

gtcgacacctgc aggtcaacgg atcaggatat tcttgtttaa gatgttgaac tctatggagg	60
tttgttatgaa ctgtatgtatct aggaccggat aagttccctt cttcatagcg aacttattca	120
aagaatgttt tgtgtatcat tcttgttaca ttgttattaa tgaaaaata ttattggtca	180
ttggactgaa cacgagtgtt aaatatggac caggccccaa ataagatcca ttgatataatg	240
aattaaataaa caagaataaa tcgagtcacc aaaccacttg cttttttaa cgagacttgt	300
tcaccaactt gatacaaaaag tcattatcct atgcaaatac ataatcatac aaaaatatcc	360
aataaacacta aaaaattaaa agaaatggat aatttcacaa tatgttatac gataaagaag	420
ttactttcc aagaaattca ctgattttat aagcccactt gcattagata aatggcaaaa	480
aaaaacaaaaa aggaaaagaa ataaagcacg aagaattcta gaaaatacga aatacgcttc	540
aatgcagtgg gacccacggt tcaattattt ccaattttca gctccaccgt atattnaaaa	600
aataaaacga taatgtctaaa aaaatataaa tcgtaacgat cgtaaatctt caacggctgg	660
atcttatgac gaccgttaga aattgtgggtt gtgcacgagt cagtaataaa cggcgtcaaa	720
gtggttgcag ccggcacaca cgagtcgtgt ttatcaactc aaagcacaaa tactttcct	780
caacctaaaa ataaggcaat tagccaaaaa caactttgcg tggtaacaaac gctcaataca	840
cgtgtcattt tattattagc tattgtttca ccgccttagc ttctctgtga cctagtgc	900
ctcgtctttt cttcttccttc ttctataaaa caatacccaa agcttcttct tcacaattca	960
gatttcaatt tctcaaaatc ttaaaaactt tctctcaattt ctctctaccg tggatcaaggt	1020
aaatttctgt gttccttattt ctctcaaaat cttcgatttt gtttcgttc gatcccaattt	1080
tctgtatgtt tctttgggtt agattctgtt aatcttagat cgaagacgt tttctgggtt	1140
tgtatcgtag atatcatctt aattctcgat tagggttca taaatatcat ccgatttggtt	1200
caaataattt gagtttgcg gaataattac tcttcgattt gtgatttcta tcttagatctg	1260
gtgttagttt ctatgttgcg cgtatcgattt tggatgggtt tctgatcaac	1320
ag	1322

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<210> SEQ ID NO 70
<211> LENGTH: 253
<212> TYPE: DNA
<213> ORGANISM: Agrobacterium tumefaciens

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<400> SEQUENCE: 70

gatcgttcaa acattggca ataaagttc ttaagattga atcctgtgc cggtttgcg 60
atgattatca tataatttct gttgaattac gttaaaggatc taataattaa catgtaatgc 120
atgacgttat ttatgagatg ggttttatg attagagtcg cgcattata catttaatac 180
gcgatagaaa acaaataatac ggcgcggaaac taggataaat tatcgcgcgc ggtgtcatct 240
atgttactatc atc 253
```

<210> SEQ ID NO 71
<211> LENGTH: 1534
<212> TYPE: DNA
<213> ORGANISM: *Brassica napus*

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<210> SEQ ID NO 72
<211> LENGTH: 228
<212> TYPE: DNA
<213> ORGANISM: *Arabidopsis thaliana*
<400> SEQUENCE: 72

```
atggcgcaag ttagcagaat ctgcaatggt gtgcagaacc catctttat ctccaatctc      60
tcgaaatcca gtcaacgcaa atctccctta tcggtttctc tgaagacgca gcagcatcca     120
cgagcttatac cgatttcgtc gtcgtggga ttgaagaaga gtggatgac gttattggc     180
tctgagttc gtcctttaa ggtatgtct tctgtttcca cggcgtgc     228
```

<210> SEQ ID NO 73
<211> LENGTH: 1368
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: EPSPS: the 5-enolpyruvylshikimate-3-phosphate synthase gene

<400> SEQUENCE: 73

```
atgcttcacg gtgcaaggcag cggccccgca accggcccga aatcctctgg cctttccgga      60
accgtccgca ttcccgccga caagtcgatc tcccaccggc cttcatgtt cggcggtctc     120
gcgagcggtg aaacgcgcac caccggccctt ctggaaggcg aggacgtcat caatacggc     180
aaggccatgc aggcgatggg cggccgcata cgtaaggaaag ggcacacctg gatcatcgat    240
ggcgtcggca atggcggcctt cctggcgcctt gaggcgccgc tcgatttcgg caatgccgc    300
acgggctgccc gcctgacgat gggcctcgatc ggggtctacg atttcgacag cacccatc      360
ggcgcacgcct cgctcacaaa gcccgcgtatc ggccgcgtgt tgaacccgtc ggcgaaatg    420
ggcgtcggagg tgaaatcgga agacgggtac cgtcttcccg ttaccttgcg cggccgaaag    480
acgcgcacgc cgatcaccta ccgcgtgcgc atggcctccg cacaggtgaa gtccgcgtg     540
ctgctcgcgc gcctcaacac gcccgcata acgacggtca tcgagccgtat catgacgcgc    600
gatcatacgg aaaagatgtc gcagggtttt ggcccaacc ttaccgtcga gacggatgcg     660
gacggcgtgc gcaccatccg cctggaaaggc cggccgcata tcaccggca agtcatcgac    720
gtgccggcgc acccgcttcc gacggccctt cctgggtttt cggccctgtc tggtccggc     780
tccgacgtca ccatctcaa cgtgtgtatc aacccaccc gcacccgcctt catctgacg     840
ctgcaggaaa tggcgccga catcgaagtca atcaacccgc gccttgcgg cggcgaagac    900
gtggcgacc tgccgcgttcg ctccctccacg ctgaaggccgc tcacgggtcc ggaagaccgc    960
gcgccttcga tgatcgacga atatccgatt ctgcgtgtcg cccgcgcctt cggccgtgc    1020
gcgaccgtga tgaacgggtctt ggaagaactc cgcgtcaagg aaagcgaccgc cctctggcc    1080
gtcgccaaatg gcctcaagct caatggcgatc gattgcgtatc agggcgagac gtgcgtcg     1140
gtgcgtggcc gcctgacgg caaggccgcgg ggcaacgcgc cggccgcgc cgtcgccacc    1200
catctcgatc accgcacgcg catgagctt ctcgtcatgg gcctcgatc ggaaacccct     1260
gtcacgggtgg acgatgccac gatgtcgcc acgagcttcc cggagttcat ggacctgtatc    1320
gccgggctgg ggcgcaagat cgaactctcc gatacgaagg ctgcctga     1368
```

<210> SEQ ID NO 74
<211> LENGTH: 643
<212> TYPE: DNA
<213> ORGANISM: *Pisum sativum*

<400> SEQUENCE: 74

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agctttcggt cgtatcatcg gtttcgacaa cgttcgtcaa gttcaatgca tcagttcat	60
tgcgcacaca ccagaatccct acttagatgg agtattatgg cattggaaa actgttttc	120
ttgttaccatt tggttgctt gtaatttact gtgttttta ttcggtttc gctatcgAAC	180
tgtgaaatgg aaatggatgg agaagagttt atgaatgata tggccctttt gttcatttc	240
aaatataat tatttggttt ttcttcttatt tggttggtgt tgaatttggaa attataagag	300
atatgcAAAC attttggttt gagtaaaaat gtgtcaatc gtggcctcta atgaccgaag	360
ttaatatgag gagtaaaaaca ctgttagttt taccattatg cttattcaat aggcaacaaa	420
tatattttca gacctgaaaa agctgcaaat gttactgaat acaagtatgt cctttgtgt	480
tttagacatt tatgaacttt cctttatgtt atttccaga atccttgta gattctaattc	540
attgcattttt aattatagtt atactcatgg atttggtagt gaggatgaaa atattttta	600
atgcattttt aacttgcata attgattgac aacatgcata aat	643

<210> SEQ ID NO 75
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the primer 5 for detecting the EPSPS gene sequence

<400> SEQUENCE: 75

ctggaaaggcg aggacgtcat caata	25
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<210> SEQ ID NO 76
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the primer 6 for detecting the EPSPS gene sequence

<400> SEQUENCE: 76

tggccggcatt gccgaaatcg ag	22
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<210> SEQ ID NO 77
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the probe 1 for detecting the EPSPS gene sequence

<400> SEQUENCE: 77

atgcaggcga tggcgcccc catccgtt	28
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<210> SEQ ID NO 78
<211> LENGTH: 1992
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 78

ctgcagtgcg ggcgtgacccg gtcgtgcccc tctctagaga taatgaggcat tgcgtgtcta	60
agttataaaa aattaccaca tattttttt gtcacacttg tttgaagtgc agtttatcta	120
tctttataca tatattttaa cttaactcta cgaataat aatctatagt actacaataa	180
tatcagtgtt ttagagaatc atataaatga acagtttagac atggctaaa ggacaatgt	240
gtatTTTgac aacaggactc tacagttta tcttttagt gtgcgtgt tctccctttt	300

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tttgcaaat agttcacct atataatact tcattcattt tattagtaca tccattnagg	360
gttaggggtt aatgggtttt atagactaat ttttttagta catctatTTT attctatTTT	420
agcctctaaa ttaagaaaaac taaaactcta ttttagttt ttatTTAAT aatTTAGATA	480
taaaatagaa taaaataaaag tgactaaaaa taaaacAAAT accCTTAAg aaatTTAAAA	540
aactaaggaa acatTTTCT tggTTcgagt agataatGCC agcCTGTTAA acGCCGTCGA	600
cgaGTCTAAC ggacaccaac cagcgaacca gcagcgtcgc gtcgggccaA gCGAAGCAGA	660
cgccacggca tctctgtcgc tgccTCTGGA cccCTCTGGA gagTTCCGCT ccaccGTGG	720
actTGCTCCG CTGTCGGCAT CCAGAAATTG CGTGGCGGAG CGGCAGACGT GAGCCGGCAC	780
ggcagggggc ctccTCTCC tctcacggca cggcagCTAC gggggattcc tttcccACCG	840
ctccTTCGCT ttccCTTCCt CGCCCGCCGT aataaATAGA cACCCCTCC ACACCCCTTT	900
tcccccaacct cgtgttGTTc ggagOGCACA cacacacaAC cAGATCTCCC CCAAATCCAC	960
ccgtcggcAc ctccGTTCA aggtacGCGC CTCGTCCTCC CCCCCCCCCC CTCTCTACCT	1020
tctctagatc ggCGTTCCGG TCCATGGTTA gggccccggta gttctacttc tggTcatGTT	1080
tgtgttagat ccgtgtttgt gttagatccg tgctgtacG gttcgtacAC ggatGCGAcc	1140
tgtacgtcAG acacGTTCTG attgotaACT tgccAGTGTt totCTTGGG gaATCTGGG	1200
atggctCTAG CGGTCCGCA gacGGGATEG atttcatGAT ttttttGTT tcgttGcATA	1260
gggtttGGTT tgccCTTTc CTttatTTCA atatatGccG tgcaCTTGTt tgctGGGTCA	1320
tcttttcatG ctTTTTTG tctGGTTGT gatGATGTT tctGGTTGGG CGGTGTTCT	1380
agatcggagt agaattCTGT ttCAAActAC ctggTGGATT tattaATTT ggatCTGTat	1440
gtgtgtGcCA tacatATTCA tagTTACGAA ttGAAGATGA tggatGGAAA tatcGATCTA	1500
ggatAGGTat acatGTTGAT gCGGGTTTA ctGATGcATA tacAGAGATG ctTTTGTc	1560
gcttGGTTGT gatGATGTTG TGtGGTTGGG CGGTGTTCA ttGTTCTAG atCGGAGTAG	1620
aataCTGTT caaACTACCT ggtGTATTA ttaATTTGt aactGTatGT gtGTGTCATA	1680
catCTTCATA gttacGAGTT taAGATGGAT ggaAAATATCG atCTAGGATA ggtataACATG	1740
ttGATGTGGG ttTTACTGAT GcATAcAtGAT GATGGCAtAT GcAGCAtCTA ttCATATGCT	1800
ctaaccTTGA GTACCTATCT attataATAA ACAAGTATGT ttTATAATTA ttTTGATCTT	1860
gataACTTG gatGATGGCA tatGcAGCAG ctATATGTGG atTTTTTAG CCCTGCCTC	1920
atacGCTATT tattGCTTG gtACTGTTc ttTTGTCGAT GTCACCCCTG ttGTTGGTG	1980
ttacttCTGC AG	1992

<210> SEQ ID NO 79

<211> LENGTH: 1176

<212> TYPE: DNA

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 79

atgcaaaaac tcattaACTC agtgcAAAC tatGCTGGG gcagcAAAC ggcGTTGACT	60
gaactttatG gtatGGAAA tccgtccAGC cAGCCGATGG CGAGCTGTG gatGGGCGCA	120
catccgAAA gcaGTTcACG agtgcAGAAT gCcGCCGGAG atATGTTc ACTGCGTGT	180
gtgattGAGA gtGATAAATC gACTCTGCTC ggAGAGGCCG ttGCCAACG CTtGGCGAA	240
ctgcCTTCC tGTTCAAAGT attatGCGCA gcACAGCCAC tctccATTCA gttcATCCA	300
aacAAACACA attCTGAAAT CGGTTTGCc AAAGAAAATG CGCAGGTAT CCCGATGGAT	360

-continued

ggccggcggc gtaactataa agatcctaac cacaagccgg agctgggtt tgcgctgacg	420
ccttccttg ccatgaacgc gtttcgtgaa ttttccgaga ttgtctccct actccagccg	480
gtcgcaaggc cacatccggc gattgctcac ttttacaac agcctgatgc cgaacgttta	540
agcgaactgt tcgccagcct gttgaatatg cagggtgaag aaaaatcccg cgcgctggcg	600
attttaaat cggccctcga tagccagcag ggtgaaccgt ggcaaacgat tcgtttaatt	660
tctgaatttt acccggagaaga cageggctctg ttctccccgc tattgtgaa tgtggtgaaa	720
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gccatttgt tctgcgtcga aggcgatgca acgttggaa aaggttctca gcagttacag	1080
cttaaacccgg gtgaatcagc gtttattgcc gccaacgaaat caccgggtgac tgtcaaaggc	1140
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<210> SEQ ID NO 80
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the primer 7 for detecting the PMI gene sequence

<400> SEQUENCE: 80

gctgttaagag cttaactgaaa aaattaaca 29

<210> SEQ ID NO 81
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the primer 8 for detecting the PMI gene sequence

<400> SEQUENCE: 81

cgcatctgcag gtgcacgg 18

<210> SEQ ID NO 82
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the probe 2 for detecting the PMI gene sequence

<400> SEQUENCE: 82

tctcttgcttta agctggggagc tcgatcc 27

The invention claimed is:

1. An herbicide tolerance protein, comprising:
the amino acid sequence as shown in SEQ ID NO: 27.
2. The herbicide tolerance protein according to claim 1,
wherein the herbicide tolerance protein consists of
the amino acid sequence as shown in SEQ ID NO: 27.
3. An herbicide tolerance protein, comprising
the amino acid sequence as shown in SEQ ID NO: 31.
4. The herbicide tolerance protein according to claim 3,
wherein the herbicide tolerance protein consists of
the amino acid sequence as shown in SEQ ID NO: 31.

5. A method of making an herbicide tolerant plant, comprising: co-expressing the herbicide tolerance protein of

claim 2 in said plant together with at least one additional

protein which is different from the herbicide tolerance

protein of claim 2.

6. A method of making an herbicide tolerant plant, comprising: co-expressing the herbicide tolerance protein of

claim 3 in said plant together with at least one additional

protein which is different from the herbicide tolerance

protein of claim 3.

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7. A method of making an herbicide tolerant plant, comprising: co-expressing the herbicide tolerance protein of claim 4 in said plant together with at least one additional protein which is different from the herbicide tolerance protein of claim 4.

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8. The method according to claim 5, wherein the additional protein is 5-enolpyruvylshikimate-3-phosphate synthase, glyphosate oxidoreductase, glyphosate-N-acetyltransferase, glyphosate decarboxylase, glufosinate acetyltransferase, α -ketoglutarate-dependent dioxygenase, dicamba monooxygenase, 4-hydroxyphenylpyruvate dioxygenase, acetolactate synthase, cytochrome-like proteins or protoporphyrinogen oxidase.

9. A method of making an herbicide tolerant plant, comprising: co-expressing the herbicide tolerance protein of claim 1 in said plant together with at least one additional protein which is different from the herbicide tolerance protein of claim 1.

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