

(12) STANDARD PATENT
(19) AUSTRALIAN PATENT OFFICE

(11) Application No. **AU 2013302536 B2**

- (54) Title
Lignin degrading enzymes from Macrophomina phaseolina and uses thereof
- (51) International Patent Classification(s)
C07K 14/37 (2006.01) **C12N 9/08** (2006.01)
C07H 21/04 (2006.01) **C12N 15/53** (2006.01)
- (21) Application No: **2013302536** (22) Date of Filing: **2013.08.15**
- (87) WIPO No: **WO14/028773**
- (30) Priority Data
- (31) Number (32) Date (33) Country
61/683,913 **2012.08.16** **US**
- (43) Publication Date: **2014.02.20**
(44) Accepted Journal Date: **2017.09.28**
- (71) Applicant(s)
Bangladesh Jute Research Institute
- (72) Inventor(s)
Alam, Maqsudul;Islam, Mohammed Shahidul;Hossen, Mohammed Mosaddeque;Haque, Mohammed Samiul;Alam, Mohammed Monjurul
- (74) Agent / Attorney
Shelston IP Pty Ltd., Level 21, 60 Margaret Street, Sydney, NSW, 2000, AU
- (56) Related Art
SCHALCH H ET AL, MOLECULAR CLONING AND SEQUENCES OF LIGNIN PEROXIDASE GENES OF PHANEROCHAETE-CHRYSOPOREUM, MOLECULAR AND CELLULAR BIOLOGY, VOL. 9, NR. 6, PAGE(S) 2743-2747.

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property
Organization
International Bureau



WIPO | PCT



(10) International Publication Number
WO 2014/028773 A3

(43) International Publication Date
20 February 2014 (20.02.2014)

(51) International Patent Classification:

C12N 9/08 (2006.01) C07H 21/04 (2006.01)
C12N 15/53 (2006.01) C07K 14/37 (2006.01)

(21) International Application Number:

PCT/US2013/055199

(22) International Filing Date:

15 August 2013 (15.08.2013)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

61/683,913 16 August 2012 (16.08.2012) US

(71) Applicant: BANGLADESH JUTE RESEARCH INSTITUTE [BD/BD]; Manik Mia Avenue, Dhaka, 1207 (BD).

(72) Inventors: ALAM, Maqsudul; 3138 Wailae Avenue, Apartment 605, Honolulu, HI 96816 (US). ISLAM, Mohammed, Shahidul; Bangladesh Jute Research Institute, Manik Mia Avenue, Dhaka, 1207 (BD). HOSSEN, Mohammed, Mosaddeque; Bangladesh Jute Research Institute, Manik Mia Avenue, Dhaka, 1207 (BD). HAQUE, Mohammed, Samiul; Bangladesh Jute Research Institute, Manik Mia Avenue, Dhaka, 1207 (BD). ALAM, Mohammed, Monjurul; Bangladesh Jute Research Institute, Manik Mia Avenue, Dhaka, 1207 (BD).

(74) Agents: GORDON, Dana, M. et al.; Foley Hoag LLP, Seaport West, 155 Seaport Blvd., Boston, MA 02210-2600 (US).

(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:

- with international search report (Art. 21(3))
- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))

(88) Date of publication of the international search report:

17 April 2014

(54) Title: LIGNIN DEGRADING ENZYMES FROM MACROPHOMINA PHASEOLINA AND USES THEREOF

(57) Abstract: The present invention relates to the field of plant breeding and disease resistance in respect of lignin degradation of plant by *Macrophomina phaseolina* ("M. phaseolina"). The present invention discloses isolated polynucleotide encoding of the lignin degrading enzymes, produced by *Macrophomina phaseolina*, comprising and consisting of nucleotide sequence set forth in SEQ. ID Nos. 2, 5, 8, 11, 14, 17, 20, 23, 26, 29, 32, 35, 38, 41, 44, 47, 50, 53, 56, 59, 62, 65, 68, 71, 74, 77, 80, 83, 86, 89, 92, 95, 98, 101, 104, 107, 110, 1, 4, 7, 10, 13, 16, 19, 22, 25, 28, 31, 34, 37, 40, 43, 46, 49, 52, 55, 58, 61, 64, 67, 70, 73, 76, 79, 82, 85, 88, 91, 94, 97, 100, 103, 106 and 109 or the complement of such sequences. The present invention also relates to isolated polypeptide encoded by the polynucleotide sequences set forth in SEQ ID Nos. 3, 6, 9, 12, 15, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45, 48, 51, 54, 57, 60, 63, 66, 69, 72, 75, 78, 81, 84, 87, 90, 93, 96, 99, 102, 105, 108 and 111; a recombinant gene construct comprising the polynucleotide; a transformant and a transgenic fungus comprising the recombinant gene construct, having enhanced production of lignin degrading enzyme. The invention provides polypeptides having an oligomerase activity, e.g., enzymes that convert recalcitrant soluble oligomerase to fermentable sugar in saccharification process of biomass.



WO 2014/028773 A3

Lignin degrading enzymes from *Macrophomina phaseolina* and uses thereof

RELATED APPLICATIONS

This application claims the benefit of priority to United States Provisional Patent Application serial number 61/683913, filed August 16, 2012; the contents of which are hereby incorporated by reference.

FIELD OF INVENTION

This invention relates to the lignin degrading proteins/enzymes and genes of *M. phaseolina*. More specifically, the present invention discloses nucleotide acid sequences of these proteins and facilitates the reduction lignin content of lignocellulosic materials. The present invention also relates to methods for selecting and isolating enzymes from *M. phaseolina* that are capable of degrading lignin, processes for cloning a gene segment from *M. phaseolina*, and methods of using the enzyme product of the gene segment. Particularly it can be used in the production or processing of pulps, woodpulp, methanol and textile.

BACKGROUND OF THE INVENTION

Any discussion of the prior art throughout the specification should in no way be considered as an admission that such prior art is widely known or forms part of the common general knowledge in the field.

Lignin is the second most abundant organic polymer, exceeded only by cellulose. It binds with cellulose fibres which make up approximately one-fourth of the weight of dry wood. This aromatic polymer is recalcitrant to degradation. Lignin is covalently associated with hemicelluloses in the cell wall via numerous types of linkage. Among the linkage, the most abundant lignin substructure is the p-aryl ether, which accounts for approximately 40% of the inter phenylpropane linkages (Higuchi T 1990. Lignin biochemistry: biosynthesis and biodegradation. Wood Sci. Technol. 24: 23-63). In addition lignin does not possess any repeating units like other biopolymer such as cellulose, protein, starch etc. Ether bonds are often prevalent, providing a variety of linkages to the numerous aromatic residues. These structural features dictate constraints on the degradation of the lignin. A portion of a typical structure is illustrated in Figure 1 and that the arylglycerol 3-aryl ether structure red color in the figure is quantitatively the most important linkage, constituting at least 40% of the polymer. But, biodegradation of lignin is a prerequisite for the processing of

biofuel, and wood pulp from plant raw materials. The improving of lignin degradation would drive the output from biofuel processing to better gain or better efficiency factor.

Lignin is a component of lignocellulose, which must be degraded to allow efficient use of cellulosic material for saccharification, paper production, biofuel production or upgradation of fodder. Lignocellulose degradation is a multienzymatic process involving both hydrolytic and oxidative enzymes. In general lignin composed of three principal building blocks namely, *p*-coumaryl alcohol, coniferyl alcohol and sinapyl alcohol. In addition, grass and dicot lignin also contain large amounts of phenolic acids such as *p*-coumaric and ferulic acid, which are esterified to alcohol groups.

- 10 Lignin peroxidases (LiP), manganese peroxidases (MnPs) and laccases are three families of enzymes that are involved in the biological degradation of lignin. LiP oxidizes nonphenolic lignin substructures by abstracting one electron and generating cation radicals (Kirk TK, Tien M, Kersten PJ, Mozuch MD and Kalyanaraman B 1986. Ligninase of *Phanerochaete chrysosporium*. Mechanism of its degradation of the non-phenolic arylglycerol β -aryl ether substructure of lignin. Biochem J 236: 279-287; Kirk TK and Farrell RL 1987. Enzymatic "combustion": The microbial degradation of lignin. Annu Rev Microbiol 41: 465-505) and MnP oxidizes phenolic rings to phenoxyl radicals which lead to decomposition of Lignin (Gold MH, Wariishi H and Valli K 1989. Extracellular peroxidases involved in lignin degradation by the white-rot basidiomycete *Phanerochaete chrysosporium*. In: Biocatalysis in Agricultural Biotechnology, pp. 127-140. Edited by Whitaker JR and Sonnet PE. American Chemical Society, Washington, DC). Whereas laccase is capable of oxidizing both phenolic and non-phenolic moieties of lignin but that the latter is dependent on the co-presence of primary laccase substrates (Bourbonnais R and Paice MG 1990. Oxidation of non-phenolic substrates. An expanded role for laccase in lignin biodegradation. FEBS Lett 267(1): 99-102). Figure 2 showed a dimeric model compounds that represent the major arylglycerol β -aryl ether lignin structure undergo $C\alpha$ - $C\beta$ cleavage upon oxidation by LiP (Kirk *et al.* 1986. Ligninase of *Phanerochaete chrysosporium*. Mechanism of its degradation of the non-phenolic arylglycerol β -aryl ether substructure of lignin. Biochem J 236: 279-287).

- Research on lignin biodegradation has increased enormously in recent years. Especially since the discovery of the first lignocellulose degrading fungus *Phanerochaete chrysosporium* genome was sequenced due to the interest on biological degradation of

lignin (Martínez *et al.* 2004. Genome sequence of the lignocellulose degrading fungus *Phanerochaete chrysosporium* strain RP78. *Nature Biotechnol* 22(6): 695-700). Perhaps the best studied, is the degradation of lignin in lignocellulose by white rot fungi, *Phanerochaete chrysosporium* (Aust SD 1995. Mechanisms of Degradation by White Rot Fungi. *Environ Health Perspect* 103:59-61; Leisola MSA, Ulmer D and Fiechter A 1984. Factors affecting lignin degradation in lignocellulose by *Phanerochaete chrysosporium*. *Arch Microbiol* 137: 171-175; Ulmer D, Leisola M, Puhakka J and Fiechter A 1983. *Phanerochaete chrysosporium*: Growth pattern and lignin degradation. *Appl Microbiol Biotechnol* 18: 153-157; Chua MGS, Chen CL, Chang HM and Kirk TK 1982. ¹³CNMR spectroscopic study of lignin degraded by *Phanerochaete chrysosporium*. I. New structures. *Holzforschung* 36: 165-172). White-rot fungi produce a range of extracellular lignolytic enzymes, including heme-dependent lignin peroxidases, manganese peroxidases, and versatile peroxidases and copper-dependent laccases (Sanchez C 2009. Lignocellulosic residues: biodegradation and bioconversion by fungi. *Biotechnol Adv* 27: 185-194; Ten Have R, Teunissen PJM 2001. Oxidative mechanisms involved in lignin degradation by white-rot fungi. *Chem Rev* 101: 3397-3413). With the aid of these extracellular peroxidase and laccase enzyme, white-rot fungi degrade lignin (Timothy DHB , Ahmad M, Hardiman EM and Rahmanpour R 2001. Pathways for degradation of lignin in bacteria and fungi. *Nat. Prod. Rep* 28: 1883-1896).

Increasing interest in the exploitation of plant biomass as a renewable resource has provided an impetus for research on microbial degradation of lignocellulose. Large quantity of biomass (mainly lignocellulosic materials) is generated from forestry, agriculture and food industry which are not used in byproduct processes. To effectively utilize this plant biomass as renewable resources, alternative means of degradation of lignocellulose need to be explored. It is desirable to identify new fungi capable of degrading lignin for use in the manufacture of cellulosic products from lignocellulosic materials.

In order to be efficient, the degradation of lignin requires several types of enzymes acting cooperatively. At least two categories of enzymes are necessary to degrade lignin: Lignin peroxidase that oxidizes nonphenolic lignin substructures and laccase that oxidize both phenolic and nonphenolic lignin substructure thus they can degrade cooperatively. To

realize and commercialize the mentioned enzymes, stable supply of various lignin degrading proteins are needed. Therefore, it is desirable for the industry to completely identify these lignin degrading genes and their encoded proteins, thus utilizing the genetic information for degradation of lignin from lignocellulosic materials.

SUMMARY OF THE INVENTION

According to a first aspect, the present invention relates to an isolated polypeptide having at least 80% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID No. 3, 6, and 9.

According to a second aspect, the present invention relates to an expression construct comprising a polynucleotide having at least 80% sequence identity to the nucleotide sequence selected from the group consisting of SEQ ID No. 1, 2, 4, 5, 7, and 8, wherein said polynucleotide is operably linked to at least one translational regulatory sequence, said translational regulatory sequence comprises a ribosomal binding site, translational start sequence, or translation stop sequence, or combination thereof.

According to a third aspect, the present invention relates to a recombinant gene construct comprising a polynucleotide having at least 80% sequence identity to the nucleotide sequence selected from the group consisting of SEQ ID No. 1, 2, 4, 5, 7, and 8, wherein the polynucleotide is expressible in a host cell to produce an enzyme which degrades lignin.

According to a fourth aspect, the present invention relates to a transformant comprising a polypeptide of any one of claims 1 to 7, an expression construct of the invention, a recombinant gene construct of the invention, or a polynucleotide having at least 80% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID No. 1, 2, 4, 5, 7, and 8, wherein said transformant produces an enzyme which accelerates lignin degradation.

According to a fifth aspect, the present invention relates to a transgenic fungi of *M. phaseolina* with enhanced lignin degradation, comprising a polypeptide of the invention, an expression construct of the invention, a recombinant gene construct of the invention, or a polynucleotide having at least 80% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID No. 1, 2, 4, 5, 7, and 8.

Unless the context clearly requires otherwise, throughout the description and the claims, the words "comprise", "comprising", and the like are to be construed in an inclusive sense as opposed to an exclusive or exhaustive sense; that is to say, in the sense of "including, but not limited to".

It has surprisingly been found that the fungi *M. phaseolina*, which are not closely related to either *Trichoderma reesi* or *Phanerochaete chrysosporium*, are capable of producing lignin degrading enzymes.

Accordingly, among other things, the present invention relates to the identification of lignin degrading enzymes, which are derivable from *M. phaseolina*, and their corresponding uses.

The present invention also relates to the use of *M. phaseolina* fungi in the degradation of lignin content of cellulosic materials.

The primary object of the present invention is to overcome or ameliorate at least one of the disadvantages of the prior art, or to provide a useful alternative.

In one aspect, the invention discloses sets of nucleotides sequences encoding lignin peroxidase (SEQ ID Nos. 1, 2, 4, 5, 7, 8, and/or any mixtures/combinations thereof), chloroperoxidase (SEQ ID Nos. 10, 11, 13, 14, 16, 17, 19, 20, 22, 23, 25, 26, and/or any

mixtures/combinations thereof) and haemperoxidase (SEQ ID Nos. 28, 29, 31, 32, 34, 35, 37, 38, 40, 41, 43, 44, and/or any mixtures/combinations thereof) of the fungi *M. phaseolina*.

The present invention also discloses sets of nucleotides sequences encoding multicopper oxidase (SEQ ID Nos. 46, 47, 49, 50, 52, 53, 55, 56, 58, 59, 61, 62, 64, 65, 67, 68, 70, 71, 73, 74, 76, 77, 79, 80, 82, 83, 85, 86, 88, 89, 91, 92, 94, 95, 97, 98, 100, 101, 103, 104, 106, 107, 109, 110, and/or any mixtures/combinations thereof) of the fungi *M. phaseolina*.

It is preferred that the isolated polynucleotide of the claimed invention consists and/or comprises of a nucleic acid sequence selected from the group comprising and/or consisting of SEQ ID Nos. 2, 5, 8, 11, 14, 17, 20, 23, 26, 29, 32, 35, 38, 41, 44, 47, 50, 53, 56, 59, 62, 65, 68, 71, 74, 77, 80, 83, 86, 89, 92, 95, 98, 101, 104, 107, 110, 1, 4, 7, 10, 13, 16, 19, 22, 25, 28, 31, 34, 37, 40, 43, 46, 49, 52, 55, 58, 61, 64, 67, 70, 73, 76, 79, 82, 85, 88, 91, 94, 97, 100, 103, 106 and 109, and/or any mixtures/combinations thereof, that codes for the polypeptide selected from the group comprising and/or consisting of SEQ ID Nos. 3, 6, 9, 12, 15, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45, 48, 51, 54, 57, 60, 63, 66, 69, 72, 75, 78, 81, 84, 87, 90, 93, 96, 99, 102, 105, 108 and 111, and/or any mixtures/combinations thereof. The present invention also relates to an isolated polynucleotide consisting and/or comprising the complement of the nucleotide sequences described above.

Another aspect of the present invention is to provide the molecular biology and genetic information of the genes and enzymes set forth in the above aspects to be utilized for the regulation and conversion of lignin degradation for the production of valuable products from lignocellulosic materials.

In another aspect, to facilitate *in vitro* production of the lignin degrading polypeptide, the present invention includes an expression construct capable of expressing polypeptide containing at least 70% sequential amino acids as set forth in SEQ ID Nos. 3, 6, 9, 12, 15, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45, 48, 51, 54, 57, 60, 63, 66, 69, 72, 75, 78, 81, 84, 87, 90, 93, 96, 99, 102, 105, 108 and 111. Preferably, the expression construct has inserted DNA or cDNA with sequential nucleotide as set forth in SEQ ID Nos. 2, 5, 8, 11, 14, 17, 20, 23, 26, 29, 32, 35, 38, 41, 44, 47, 50, 53, 56, 59, 62, 65, 68, 71, 74, 77, 80, 83, 86, 89, 92, 95, 98, 101, 104, 107, 110, 1, 4, 7, 10, 13, 16, 19, 22, 25, 28, 31, 34, 37, 40, 43, 46, 49, 52, 55, 58, 61, 64, 67, 70, 73, 76, 79, 82, 85, 88, 91, 94, 97, 100, 103, 106 and 109.

In yet another aspect, the present invention discloses a recombinant gene construct comprising a polynucleotide template having nucleotide sequence set forth in SEQ ID Nos. 2, 5, 8, 11, 14, 17, 20, 23, 26, 29, 32, 35, 38, 41, 44, 47, 50, 53, 56, 59, 62, 65, 68, 71, 74, 77, 80, 83, 86, 89, 92, 95, 98, 101, 104, 107, 110, 1, 4, 7, 10, 13, 16, 19, 22, 25, 28, 31, 34, 37, 40, 43, 46, 49, 52, 55, 58, 61, 64, 67, 70, 73, 76, 79, 82, 85, 88, 91, 94, 97, 100, 103, 106 and 109, wherein the polynucleotide template is expressible in a host cell to produce an enzyme

which oxidize lignin from lignocellulosic materials. Preferably, the recombinant gene construct further comprises a promoter region operably-linked to enhance expression of the polynucleotide template.

In accordance with one of the preferred embodiments of the present invention, the fungus *M. phaseolina* strain ms6 is isolated from infected jute plant. The isolated polypeptide is also preferably derived from this strain.

In another aspect, the present invention provides a potential commercially feasible way to isolate lignin degrading enzyme from *M. phaseolina* in order to keep up with the increasing global demand on exploitation/utilization of plant biomass as a renewable resource for the manufacture of cellulosic products.

In a further aspect, the invention is directed to utilization of the lignin degrading substances in animal feeds, biofuel, woodpulp, textile and paper industry.

One skilled in the art will readily appreciate that the present invention is well adapted to carry out the aspects and obtain the ends and advantages mentioned, as well as those inherent therein. The embodiments described herein are not intended as limitations on the scope of the present invention.

BRIEF DESCRIPTION OF THE DRAWINGS

The accompanying drawings, which are incorporated in and form a part of the specification, illustrate the embodiments of the present invention and, together with the description, serve to explain the principles of the invention.

Figure 1 Displays a common structure of softwood lignin. Major arylglycerol-P-aryl ether structure is shown in red color. The inset shows coniferyl alcohol, the phenylpropanoid building block of softwood lignin.

Figure 2 Displays a cleavage of internal an non-phenolic arylglycerol-P-aryl ether lignin structure **by** oxidized lignin peroxidase. **Figure 3** is the electrophoresed agarose gel image showing the PCR amplification result in which lane **1** is polynucleotides of lignin peroxidase of **SEQ ID NO. 1** and lane M is **DNA** molecular weight ladder.

Figure 4 is the electrophoresed agarose gel image showing the PCR amplification result in which lane **1** is polynucleotides of lignin peroxidase of **SEQ ID NO. 4** and lane M is **DNA** molecular weight ladder.

Figure **5** is the electrophoresed agarose gel image showing the PCR amplification result in which lane **1** is polynucleotides of lignin peroxidase of **SEQ ID NO. 7** and lane M is **DNA** molecular weight ladder.

Figure **6** is the electrophoresed agarose gel image showing the PCR amplification result in which lane **1** is polynucleotides of chloroperoxidase of **SEQ ID NO. 13** and lane M is **DNA** molecular weight ladder. _____

- Figure 7 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of chloroperoxidase of SEQ ID NO. 16 and lane M is DNA molecular weight ladder.
- 5 Figure 8 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of chloroperoxidase of SEQ ID NO. 19 and lane M is DNA molecular weight ladder.
- Figure 9 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of chloroperoxidase of SEQ ID NO. 22 and lane M is DNA molecular weight ladder.
- 10 Figure 10 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of chloroperoxidase of SEQ ID NO. 25 and lane M is DNA molecular weight ladder.
- Figure 11 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of haemperoxidase of SEQ ID NO. 28 and lane M is DNA molecular weight ladder.
- 15 Figure 12 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of haemperoxidase of SEQ ID NO. 31 and lane M is DNA molecular weight ladder.
- Figure 13 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of haemperoxidase of SEQ ID NO. 34 and lane M is DNA molecular weight ladder.
- 20 Figure 14 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of haemperoxidase of SEQ ID NO. 37 and lane M is DNA molecular weight ladder.
- 25 Figure 15 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of haemperoxidase of SEQ ID NO. 40 and lane M is DNA molecular weight ladder.

- Figure 16 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of haemperoxidase of SEQ ID NO. 43 and lane M is DNA molecular weight ladder.
- 5 Figure 17 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of multicopper oxidase of SEQ ID NO. 46 and lane M is DNA molecular weight ladder.
- Figure 18 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of multicopper oxidase of SEQ ID NO. 49 and lane M is DNA molecular weight ladder.
- 10 Figure 19 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of multicopper oxidase of SEQ ID NO. 52 and lane M is DNA molecular weight ladder.
- Figure 20 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of multicopper oxidase of SEQ ID NO. 55 and lane M is DNA molecular weight ladder.
- 15 Figure 21 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of multicopper oxidase of SEQ ID NO. 58 and lane M is DNA molecular weight ladder.
- Figure 22 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of multicopper oxidase of SEQ ID NO. 64 and lane M is DNA molecular weight ladder.
- 20 Figure 23 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of multicopper oxidase of SEQ ID NO. 67 and lane M is DNA molecular weight ladder.
- 25 Figure 24 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of multicopper oxidase of SEQ ID NO. 70 and lane M is DNA molecular weight ladder.

- Figure 25 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of multicopper oxidase of SEQ ID NO. 73 and lane M is DNA molecular weight ladder.
- 5 Figure 26 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of multicopper oxidase of SEQ ID NO. 76 and lane M is DNA molecular weight ladder.
- Figure 27 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of multicopper oxidase of SEQ ID NO. 79 and lane M is DNA molecular weight ladder.
- 10 Figure 28 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of multicopper oxidase of SEQ ID NO. 82 and lane M is DNA molecular weight ladder.
- Figure 29 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of multicopper oxidase of SEQ ID NO. 85 and lane M is DNA molecular weight ladder.
- 15 Figure 30 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of multicopper oxidase of SEQ ID NO. 88 and lane M is DNA molecular weight ladder.
- Figure 31 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of multicopper oxidase of SEQ ID NO. 91 and lane M is DNA molecular weight ladder.
- 20 Figure 32 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of multicopper oxidase of SEQ ID NO. 97 and lane M is DNA molecular weight ladder.
- 25 Figure 33 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of multicopper oxidase of SEQ ID NO. 100 and lane M is DNA molecular weight ladder.

Figure 34 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of multicopper oxidase of SEQ ID NO. 103 and lane M is DNA molecular weight ladder.

5 Figure 35 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of multicopper oxidase of SEQ ID NO. 106 and lane M is DNA molecular weight ladder.

Figure 36 is the electrophoresed agarose gel image showing the PCR amplification result in which lane 1 is polynucleotides of multicopper oxidase of SEQ ID NO. 109 and lane M is DNA molecular weight ladder.

10 DETAILED DESCRIPTION OF THE INVENTION

The definitions and/or methods provided herein define the present invention and guide those of ordinary skill in the art in the practice of the present invention. Except where otherwise stated, terms are to be understood according to conventional usage by those of ordinary skill in the relevant art. To the extent to which any of the definitions and/or methods is found to be inconsistent with any of the definitions and/or methods provided in any patent or non-patent reference incorporated herein or in any reference found elsewhere, it is understood that the said definition and/or method which has been expressly provided/adopted in this application will be used herein. The singular terms "a," "an," and "the" include plural referents unless context clearly indicates otherwise. Similarly, the word "or" is intended to include "and" unless the context clearly indicates otherwise. Hence, "comprising A or B" means including A, or B, or A and B. It is further to be understood that all base sizes or amino acid sizes, and all molecular weight or molecular mass values, given for nucleic acids or polypeptides are approximate, and are provided for description. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present disclosure, suitable methods and materials are described below.

The present invention provides the nucleotide sequences of *M. phaseolina* encoded protein/enzyme involved in lignin degradation. The genes encode proteins with an enzyme activity that is either in use in an industry or of interest to an industry. The genomic sequences of the invention that encode the enzymes are identified primarily by

comparison of nucleotide sequences of *M. phaseolina* genomic DNA and the nucleotide sequences of known enzyme genes of other microorganisms. Prior to this invention, the nucleotide sequences of these *M. phaseolina* genes, the reading frames, the positions of exons and introns, the structure of the enzymes, and their potential usefulness in various industries, such as those involved in the making of food and feed, beverages, textiles and detergents, were not known.

Analysis of the genome sequence of *M. phaseolina* reveals an abundance of genes coding for enzymes which degrade lignin in plant. The nucleotide sequences were initially annotated by software programs, such as Genescan and Glimmer M (The Institute of Genome Research, Rockville, NM), which can identify putative coding regions, introns, and splice junctions. Further automated and manual curation of the nucleotide sequences was performed to refine and establish precise characterization of the coding regions and other gene features.

Over 14000 cDNAs from *M. phaseolina* were partially or fully sequenced. Among them thirty-seven cDNAs encoding new enzymes with putative roles in lignin degradation were discovered.

Open reading frames (ORFs) are analyzed following full or partial sequencing of clones of cDNA libraries derived from *M. phaseolina* mRNA and are further analyzed using sequence analysis software, and by determining homology to known sequences in databases (public/private).

In the context of this disclosure, a number of terms used throughout the specification have the indicated meanings unless expressly indicated to have a different meaning.

As used herein, a "polynucleotide" is a nucleotide sequence such as a nucleic acid fragment. A polynucleotide may be a polymer of RNA or DNA that is single- or double-stranded, that optionally contains synthetic, non-natural or altered nucleotide bases. A polynucleotide in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA, synthetic DNA, or mixtures thereof. An isolated polynucleotide of the present invention may include at least one of 150 contiguous nucleotides (both upstream and downstream) derived from SEQ ID No. 1, 4, 7, 10, 13, 16,

19, 22, 25, 28, 31, 34, 37, 40, 43, 46, 49, 52, 55, 58, 61, 64, 67, 70, 73, 76, 79, 82, 85, 88, 91, 94, 97, 100, 103, 106 and 109, or the complement of such sequences.

"Polypeptide" as used herein, is a single linear chain of amino acids bonded together by peptide bonds, and having usually a sequence greater than 100 amino acids in length.

- 5 "Isolated" means altered "by the hand of man" from the natural state. If a composition or substance occurs in nature, it has been "isolated" if it has been changed or removed from its original environment, or both. For example, a polynucleotide or a polypeptide naturally present in a living plant or animal is not "isolated," but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated", as
10 the term is employed herein.

The term "gene", as used herein, is defined as the genomic sequences of the fungi *M. phaseolina*, particularly polynucleotide sequence encoding polypeptide of the series of enzymes involved in the lignin degradation pathway.

- A "coding sequence" or "coding region" refers to a nucleic acid molecule having sequence
15 information necessary to produce a gene product, such as an amino acid or polypeptide, when the sequence is expressed. The coding sequence may comprise untranslated sequences (e.g., introns or 5' or 3' untranslated regions) within translated regions, or may lack such intervening untranslated sequences (e.g., as in cDNA).

- The term "primer" as used herein, is an oligonucleotide capable of binding to a target
20 nucleic acid sequence and priming the nucleic acid synthesis. An amplification oligonucleotide as defined herein will preferably be 10 to 50, most preferably 15 to 25 nucleotides in length. While the amplification oligonucleotides of the present invention may be chemically synthesized and such oligonucleotides are not naturally occurring nucleic acids.

- 25 The abbreviation used throughout the specification to refer to nucleic acids comprising nucleotide sequences are the conventional one-letter abbreviations. Thus when included in a nucleic acid, the naturally occurring encoding nucleotides are abbreviated as follows: adenine (A), guanine (G), cytosine (C), thymine (T) and uracil (U). Also, unless otherwise specified, the nucleic acid sequences presented herein is the 5' → 3' direction.

As used herein, the term "complementary" and derivatives thereof are used in reference to pairing of nucleic acids by the well-known rules that A pairs with T or U and C pairs with G. Complement can be "partial" or "complete". In partial complement, only some of the nucleic acid bases are matched according to the base pairing rules; while in complete or
5 total complement, all the bases are matched according to the pairing rule. The degree of complement between the nucleic acid strands may have significant effects on the efficiency and strength of hybridization between nucleic acid strands as well known in the art. The efficiency and strength of said hybridization is depends upon in detection method.

The term "host cell", as used herein, includes any cell type which is susceptible to
10 transformation, transfection, transduction, expression and the like with a nucleic acid construct or expression vector comprising a polynucleotide of the present invention.

The term "operably linked" denotes herein a configuration in which a control sequence is placed at an appropriate position relative to the coding sequence of the polynucleotide sequence such that the control sequence directs the expression of the coding sequence of
15 a polypeptide.

A "vector" generally refers to a replicon, such as plasmid, phage, cosmid, yeast or virus to which another nucleic acid segment may be operably inserted so as to bring about the replication or expression of the segment. The term "vector" is also intended to refer to a nucleic acid molecule capable of transporting another nucleic acid to which it has been
20 linked. One type of vector is a "plasmid," which refers to a circular double-stranded DNA loop into which additional DNA segments may be ligated. Another type of vector is a viral vector, where additional DNA segments may be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal
25 mammalian vectors). Other vectors can be integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "recombinant expression vectors" (or simply, "expression vectors"). In general, expression vectors of utility in
30 recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" may be used interchangeably as the plasmid is the

most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

- 5 The term "nucleic acid construct" or "DNA construct" is sometimes used to refer to a coding sequence or sequences operably linked to appropriate regulatory sequences and inserted into a vector for transforming a cell. This term may be used interchangeably with the term "transforming DNA" or "transgene."

- 10 The term "promoter" as used herein, refers to a nucleic acid sequence that functions to direct transcription of a downstream gene. The promoter will generally be appropriate to the host cell in which the target gene is being expressed. The promoter together with other transcriptional and translational regulatory nucleic acid sequences (also termed "control sequences") is necessary to express a given gene. In general, the transcriptional and translational regulatory sequences include, but are not limited to, promoter
15 sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences.

- The term "*in vitro*" as used herein, refers to a biological reaction occurs in an artificial environment outside a living organism, which is usually conducted in a laboratory using components of an organism that have been isolated from their usual biological context in
20 order to permit a more detailed or more convenient analysis to be performed.

- The term "% homology" is used interchangeably herein with the term "% identity" herein and refers to the level of nucleic acid or amino acid sequence identity between the nucleic acid sequence that encodes any one of the inventive polypeptides or the inventive polypeptide's amino acid sequence, when aligned using a sequence alignment program.

- 25 For example, as used herein, 80% homology means the same thing as 80% sequence identity determined by a defined algorithm, and accordingly a homologue of a given sequence has greater than 80% sequence identity over a length of the given sequence. Exemplary levels of sequence identity include, but are not limited to, 80, 85, 90, 95, 98% or more sequence identity to a given sequence, e.g., the coding sequence for any one of
30 the inventive polypeptides, as described herein.

Exemplary computer programs which can be used to determine identity between two sequences include, but are not limited to, the suite of BLAST programs, *e.g.*, BLASTN, BLASTX, and TBLASTX, BLASTP and TBLASTN, publicly accessible at www.ncbi.nlm.nih.gov/BLAST.

- 5 Sequence searches are typically carried out using the BLASTN program, when evaluating a given nucleic acid sequence relative to nucleic acid sequences in the GenBank DNA Sequences and other public databases. The BLASTX program is preferred for searching nucleic acid sequences that have been translated in all reading frames against amino acid sequences in the GenBank Protein Sequences and other public databases.

- 10 A preferred alignment of selected sequences in order to determine "% identity" between two or more sequences is performed using for example, the CLUSTAL-W program.

As in setting forth, one embodiment of the present invention is an isolated polynucleotides encoding for lignin degrading polypeptide found in the fungi *M. phaseolina* comprising nucleotide sequence as setting forth in SEQ ID No. 2, 5, 8, 11, 14,
 15 17, 20, 23, 26, 29, 32, 35, 38, 41, 44, 47, 50, 53, 56, 59, 62, 65, 68, 71, 74, 77, 80, 83, 86, 89, 92, 95, 98, 101, 104, 107, 110, 1, 4, 7, 10, 13, 16, 19, 22, 25, 28, 31, 34, 37, 40, 43, 46, 49, 52, 55, 58, 61, 64, 67, 70, 73, 76, 79, 82, 85, 88, 91, 94, 97, 100, 103, 106 and 109. Correspondingly, the respective lignin degrading polypeptide encoded by these nucleotide sequences shall possess amino acid sequence as setting forth in SEQ ID Nos. 3, 6, 9, 12, 15,
 20 18, 21, 24, 27, 30, 33, 36, 39, 42, 45, 48, 51, 54, 57, 60, 63, 66, 69, 72, 75, 78, 81, 84, 87, 90, 93, 96, 99, 102, 105, 108 and 111.

In one embodiment, the 939 bp long polynucleotide illustrated in SEQ ID No. 2 is the full length cDNA clone encoded Lignin peroxidase protein exhibiting an open reading frame encoding a 312 amino acid polypeptide, as in SEQ ID No. 3, with a calculated molecular
 25 mass of about 32 kD. Through SMART analysis of SEQ ID No. 2, it reveals presence of Pfam peroxidase domain in the sequence. The protein family with the Pfam domain consists and/or comprises of secretory fungal peroxidases. These are monomeric glycoproteins involved in the degradation of lignin.

Preferably, the 1116 bp long polynucleotide illustrated in SEQ ID No. 5 is the full length
 30 cDNA clone encoded Lignin peroxidase protein exhibiting an open reading frame encoding

a 371 amino acid polypeptide, as in SEQ ID No. 6, with a calculated molecular mass of about 40 kD. Through SMART analysis of SEQ ID No. 5, it reveals presence of Pfam peroxidase domain in the sequence. The protein family with the Pfam domain consists and/or comprises of secretory fungal peroxidases. These are monomeric glycoproteins involved in the degradation of lignin.

Similarly, another aspect, the 1023 bp long polynucleotide illustrated in SEQ ID No. 8 is the full length cDNA clone encoded Lignin peroxidase protein exhibiting an open reading frame encoding a 340 amino acid polypeptide, as in SEQ ID No. 9, with a calculated molecular mass of about 35 kD. Through SMART analysis of SEQ ID No. 8, it reveals presence of Pfam peroxidase domain in the sequence. The protein family with the Pfam domain consists and/or comprises of secretory fungal peroxidases. These are monomeric glycoproteins involved in the degradation of lignin.

In another aspect, polynucleotides encoding for chloroperoxidase has 1260 bp as illustrated in SEQ ID No. 11 while the encoded protein is a 419 amino acid polypeptide with a calculated molecular mass of about 45 kD as illustrated in SEQ ID No. 12. The SEQ ID No. 11 contains a Pfam domain, namely peroxidase_2. The said domain involved in the lignin degradation.

In another aspect, polynucleotides encoding for chloroperoxidase has 690 bp as illustrated in SEQ ID No. 14 while the encoded protein is a 229 amino acid polypeptide with a calculated molecular mass of about 25 kD as illustrated in SEQ ID No. 15. The SEQ ID No. 14 contains a Pfam domain, namely peroxidase_2. The said domain involved in the lignin degradation.

In another aspect, polynucleotides encoding for chloroperoxidase has 1194 bp as illustrated in SEQ ID No. 17 while the encoded protein is a 397 amino acid polypeptide with a calculated molecular mass of about 43 kD as illustrated in SEQ ID No. 18. The SEQ ID No. 17 contains a Pfam domain, namely peroxidase_2. The said domain involved in the lignin degradation.

In another aspect, polynucleotides encoding for chloroperoxidase has 1317 bp as illustrated in SEQ ID No. 20 while the encoded protein is a 438 amino acid polypeptide with a calculated molecular mass of about 47 kD as illustrated in SEQ ID No. 21. The SEQ ID

No. 20 contains a Pfam domain, namely peroxidase_2. The said domain involved in the lignin degradation.

In another aspect, polynucleotides encoding for chloroperoxidase has 780 bp as illustrated in SEQ ID No. 23 while the encoded protein is a 259 amino acid polypeptide with a
5 calculated molecular mass of about 29 kD as illustrated in SEQ ID No. 24. The SEQ ID No. 23 contains a Pfam domain, namely peroxidase_2. The said domain involved in the lignin degradation.

In another aspect, polynucleotides encoding for chloroperoxidase has 951 bp as illustrated in SEQ ID No. 26 while the encoded protein is a 316 amino acid polypeptide with a
10 calculated molecular mass of about 35 kD as illustrated in SEQ ID No. 27. The SEQ ID No. 26 contains a Pfam domain, namely peroxidase_2. The said domain involved in the lignin degradation.

In another aspect, polynucleotides encoding for haemperoxidase has 1116 bp as illustrated in SEQ ID No. 29 while the encoded protein is a 371 amino acid polypeptide
15 with a calculated molecular mass of about 41 kD as illustrated in SEQ ID No. 30. The SEQ ID No. 29 contains a Pfam domain, namely peroxidase. Haemperoxidases oxidize lignin subunits using extracellular hydrogen peroxide generated by unrelated oxidases as a co-substrate. The said domain involved in the lignin degradation.

In another aspect, polynucleotides encoding for haemperoxidase has 1623 bp as
20 illustrated in SEQ ID No. 32 while the encoded protein is a 540 amino acid polypeptide with a calculated molecular mass of about 57 kD as illustrated in SEQ ID No. 33. The SEQ ID No. 32 contains a Pfam domain, namely peroxidase. Haemperoxidases oxidize lignin subunits using extracellular hydrogen peroxide generated by unrelated oxidases as a co-substrate. The said domain involved in the lignin degradation.

25 In another aspect, polynucleotides encoding for haemperoxidase has 1599 bp as illustrated in SEQ ID No. 35 while the encoded protein is a 532 amino acid polypeptide with a calculated molecular mass of about 57 kD as illustrated in SEQ ID No. 36. The SEQ ID No. 35 contains a Pfam domain, namely peroxidase. Haemperoxidases oxidize lignin subunits using extracellular hydrogen peroxide generated by unrelated oxidases as a co-
30 substrate. The said domain involved in the lignin degradation.

In another aspect, polynucleotides encoding for haemperoxidase has 2049 bp as illustrated in SEQ ID No. 38 while the encoded protein is a 682 amino acid polypeptide with a calculated molecular mass of about 70 kD as illustrated in SEQ ID No. 39. The SEQ ID No. 38 contains a Pfam domain, namely peroxidase. Haemperoxidases oxidize lignin subunits using extracellular hydrogen peroxide generated by unrelated oxidases as a co-substrate. The said domain involved in the lignin degradation.

In another aspect, polynucleotides encoding for haemperoxidase has 1605 bp as illustrated in SEQ ID No. 41 while the encoded protein is a 534 amino acid polypeptide with a calculated molecular mass of about 57 kD as illustrated in SEQ ID No. 42. The SEQ ID No. 41 contains a Pfam domain, namely peroxidase. Haemperoxidases oxidize lignin subunits using extracellular hydrogen peroxide generated by unrelated oxidases as a co-substrate. The said domain involved in the lignin degradation.

In another aspect, polynucleotides encoding for haemperoxidase has 960 bp as illustrated in SEQ ID No. 44 while the encoded protein is a 319 amino acid polypeptide with a calculated molecular mass of about 35 kD as illustrated in SEQ ID No. 45. The SEQ ID No. 44 contains a Pfam domain, namely peroxidase. Haemperoxidases oxidize lignin subunits using extracellular hydrogen peroxide generated by unrelated oxidases as a co-substrate. The said domain involved in the lignin degradation.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 1713 bp as illustrated in SEQ ID No. 47 while the encoded protein is a 570 amino acid polypeptide with a calculated molecular mass of about 64 kD as illustrated in SEQ ID No. 48. The SEQ ID No. 47 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 1860 bp as illustrated in SEQ ID No. 50 while the encoded protein is a 619 amino acid polypeptide with a calculated molecular mass of about 69 kD as illustrated in SEQ ID No. 51. The SEQ ID No. 50 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 1824 bp as illustrated in SEQ ID No. 53 while the encoded protein is a 607 amino acid polypeptide with a calculated molecular mass of about 67 kD as illustrated in SEQ ID No. 54. The SEQ ID No. 53 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 1737 bp as illustrated in SEQ ID No. 56 while the encoded protein is a 578 amino acid polypeptide with a calculated molecular mass of about 63 kD as illustrated in SEQ ID No. 57. The SEQ ID No. 56 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 1665 bp as illustrated in SEQ ID No. 59 while the encoded protein is a 554 amino acid polypeptide with a calculated molecular mass of about 61 kD as illustrated in SEQ ID No. 60. The SEQ ID No. 59 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 1803 bp as illustrated in SEQ ID No. 62 while the encoded protein is an 600 amino acid polypeptide with a calculated molecular mass of about 65 kD as illustrated in SEQ ID No. 63. The SEQ ID No. 62 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 1635 bp as illustrated in SEQ ID No. 65 while the encoded protein is a 544 amino acid polypeptide with a calculated molecular mass of about 61 kD as illustrated in SEQ ID No. 66. The SEQ ID No. 65 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 1743 bp as illustrated in SEQ ID No. 68 while the encoded protein is a 580 amino acid polypeptide with a calculated molecular mass of about 63 kD as illustrated in SEQ ID No. 69. The SEQ ID No. 68 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 1836 bp as illustrated in SEQ ID No. 71 while the encoded protein is a 611 amino acid polypeptide with a calculated molecular mass of about 67 kD as illustrated in SEQ ID No. 72. The SEQ ID No. 71 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 702 bp as illustrated in SEQ ID No. 74 while the encoded protein is a 233 amino acid polypeptide with a calculated molecular mass of about 26 kD as illustrated in SEQ ID No. 75. The SEQ ID No. 74 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 1854 bp as illustrated in SEQ ID No. 77 while the encoded protein is a 617 amino acid polypeptide with a calculated molecular mass of about 68 kD as illustrated in SEQ ID No. 78. The SEQ ID No. 77 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 2073 bp as illustrated in SEQ ID No. 80 while the encoded protein is a 690 amino acid polypeptide with a calculated molecular mass of about 77 kD as illustrated in SEQ ID No. 81. The SEQ ID No. 80 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 1824 bp as illustrated in SEQ ID No. 83 while the encoded protein is a 607 amino acid polypeptide with a calculated molecular mass of about 67 kD as illustrated in SEQ ID No. 84. The SEQ ID No. 83 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 1932 bp as illustrated in SEQ ID No. 86 while the encoded protein is a 643 amino acid polypeptide with a calculated molecular mass of about 72 kD as illustrated in SEQ ID No. 87. The SEQ ID No. 86 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 1950 bp as illustrated in SEQ ID No. 89 while the encoded protein is a 649 amino acid polypeptide with a calculated molecular mass of about 72 kD as illustrated in SEQ ID No. 90. The SEQ ID No. 89 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 2016 bp as illustrated in SEQ ID No. 92 while the encoded protein is a 671 amino acid polypeptide with a calculated molecular mass of about 74 kD as illustrated in SEQ ID No. 93. The SEQ ID No. 92 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 2085 bp as illustrated in SEQ ID No. 95 while the encoded protein is a 694 amino acid polypeptide with a calculated molecular mass of about 78 kD as illustrated in SEQ ID No. 96. The SEQ ID No. 95 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 1821 bp as illustrated in SEQ ID No. 98 while the encoded protein is a 606 amino acid polypeptide with a calculated molecular mass of about 68 kD as illustrated in SEQ ID No. 99. The SEQ ID No. 98 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 1854 bp as illustrated in SEQ ID No. 101 while the encoded protein is a 617 amino acid polypeptide with a calculated molecular mass of about 68 kD as illustrated in SEQ ID No. 102. The SEQ ID No. 101 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 1815 bp as illustrated in SEQ ID No. 104 while the encoded protein is a 604 amino acid polypeptide with a calculated molecular mass of about 67 kD as illustrated in SEQ ID No. 105. The SEQ ID No. 104 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 1632 bp as illustrated in SEQ ID No. 107 while the encoded protein is a 543 amino acid polypeptide with a calculated molecular mass of about 61 kD as illustrated in SEQ ID No. 108. The SEQ ID No. 107 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

In another aspect, polynucleotides encoding for multicopper oxidases (laccases) has 1752 bp as illustrated in SEQ ID No. 110 while the encoded protein is a 583 amino acid polypeptide with a calculated molecular mass of about 64 kD as illustrated in SEQ ID No. 111. The SEQ ID No. 110 contains a Pfam domain, namely multicopper oxidase. This multicopper oxidase (laccase) is extracellular, non-haem, copper containing proteins that catalyze the one-electron oxidation of phenols to phenoxy radicals.

The sequences provided by the present invention can also be used as preparatory materials for the rational modification or design of novel enzymes with characteristics that enable the enzymes to perform better in demanding processes.

5 The present disclosure includes as contained in the appended claims, as well as that of the foregoing description. Although this invention has been described in its preferred form with a degree of particularity, it is understood that the present disclosure of the preferred form has been made only by way of example and that numerous changes in the details of construction and the combination and arrangements of parts may be resorted to without departing from the scope of the invention and claims.

10 Various references are cited herein, the disclosures of which are incorporated by reference in their entirety.

EXAMPLE

The following example is intended to further illustrate the invention, without any intent for the invention to be limited to the specific embodiments described therein.

15 **Example 1 Designing and synthesis of primers**

The primers used in the study were either designed from the manually curated transcriptome and the “gene models” predicted from the genomic sequences of *M. phaseolina* ms6, by choosing the sequences manually with complete ORFs or using databases where similar genes have been successfully isolated from other plants.

20 Comparative bioinformatic analysis of the nucleotide sequences obtained from transcriptome were carried out using NCBI BLAST, BLASTP, RPS-BLAST, BLASTX and PSI-BLAST to identify homologues of the related genes and for the proper identification of gene. Nucleotide sequence alignments were performed through clustalW version 1.82 whenever multiple sequences were found from the “gene pool”. The alignment was then

25 edited. Gene specific primers (both forward and reverse) were selected manually or through Primer 3 plus tool and the primers were custom synthesized.

All oligonucleotides used in this study were synthesized and HPLC purified by the supplier and procured from Integrated DNA Technologies (IDT). Stock solution of 100 pmol were prepared in autoclaved ddH₂O and stored at -20°C, in aliquots for use.

Atty. Docket No. JGX-006.25

Oligonucleotides Sequences used as primers for PCR

Gene name	SEQ ID No.	Primer Sequence	Amplified product (bp)
lignin peroxidase	1	Forward GAGACCGCTACACCCACCCCT	1155
		Reverse CACCGCACTACGACCTCGCT	
lignin peroxidase	4	Forward GTCGTCGCGTGGCTGCTAGA	1276
		Reverse CCAGGCATCGGGGAACCTTCGG	
lignin peroxidase	7	Forward GGCGGCTCTCTCGCAGACGTA	1234
		Reverse GCCCTGCCCCAACCGATTCA	
Chloroperoxidase	10	Forward TGCTGCCTCCGCTCTGTCGC	1769
		Reverse CGCACCATGTCGCCTCTGCC	
Chloroperoxidase	13	Forward AACCGCTTTACCTGCCAGCCA	964
		Reverse ATTGGGGTTCGGTGCTCAGGAGT	
Chloroperoxidase	16	Forward ACGGAGCACATGAACACCGTCC	1777
		Reverse CTTCGCACCGCGAGCAGAGG	
Chloroperoxidase	19	Forward TCCCGCGAGCCCTTGGTCTG	1644
		Reverse GCCCTCGCTGGTTCCTTTGCT	
Chloroperoxidase	22	Forward ATGTTTTGTTTCGCGCCGCT	1265
		Reverse AATCTACCACTCCCGTCCCGC	
Chloroperoxidase	25	Forward ACCGCCGCTTCGTTTACGTC	475
		Reverse GCCCGCTTACTTTGCCGGTC	
Haem peroxidase	28	Forward TCGCCTGTGCTCACACCACG	1235
		Reverse TTAACGTCCGCCAAGCACGC	

Atty. Docket No. JGX-006.25

Gene name	SEQ ID No.	Primer Sequence	Amplified product (bp)
Haem peroxidase	31	Forward CGTTCCCAAGCCCGACGACTC	1177
		Reverse GGGCAAGTCCCAAGCCCATC	
Haem peroxidase	34	Forward AATGCGGTTTCTCGGGGGCT	1762
		Reverse TGTTGCTGGCCCTATGAAGGCAT	
Haem peroxidase	37	Forward CCATGGCAAGGCATCCCGGC	1172
		Reverse TGTGGCATCCCAACAGGGGC	
Haem peroxidase	40	Forward TGGACCTGGCCGTCAAACCG	1488
		Reverse GCCTCACAGAGCCGCACACTC	
Haem peroxidase	43	Forward CAGGCATGCGCTACGAGGCT	800
		Reverse ACCAGCTTACAGACGTGCCCTGA	
Multicopper oxidase	46	Forward TGGGCGGGCAGGTACGTGAAT	1935
		Reverse TCCGTGCTCTGGCCTCGCAT	
Multicopper oxidase	49	Forward GCTGGCGACGACAAGTGGCT	2033
		Reverse CCACAGAGTTCGCGAGGCCC	
Multicopper oxidase	52	Forward CATCCCACCGCGGGAAGCCT	2172
		Reverse ATCCCCGCCGTACGGTTTT	
Multicopper oxidase	55	Forward TCGTTGAAGTCGCTGTCCCGT	1944
		Reverse GCCCCGCACACCTGCCATAG	
Multicopper oxidase	58	Forward TGCTTGCTCAAGGGCGCTCA	2177
		Reverse TCAACTCAGACTACTGTCTGAAGTGC	

Atty. Docket No. JGX-006.25

Gene name	SEQ ID No.	Primer Sequence	Amplified product (bp)
Multicopper oxidase	61	Forward CACTGGCACGGCTTCACGCA	4930
		Reverse CCGCTACGCGGTCTGACTCCT	
Multicopper oxidase	64	Forward CACCCTCCGGTCGGGTAAGT	2116
		Reverse TACAGGTGCTATGCCAGCGTGC	
Multicopper oxidase	67	Forward TAGCATCGGCACAACGCCCAT	1246
		Reverse GAACCGGTGGCCGTGAAGGTG	
Multicopper oxidase	70	Forward ACCCACCCTCGCTCTCACA	2083
		Reverse TGGAAATGCGCAGAAGGACCGT	
Multicopper oxidase	73	Forward GCACGACATGTGGATTGCGGC	788
		Reverse TTGCCAGCCGTGCTCCGTCA	
Multicopper oxidase	76	Forward ACGACGTTGCAAGCTCCGCC	2022
		Reverse CCATCGGGCATAGAAGTCGCCG	
Multicopper oxidase	79	Forward TTCACCGGAGTCGCCTTCCCA	2249
		Reverse CGACGGGCTGCAGTACGAGA	
Multicopper oxidase	82	Forward AATCCCCTCTCACCTCGCCGC	2103
		Reverse GGCCACCCCTCAGAGACCGGA	
Multicopper oxidase	85	Forward CGCCGAACCAAAGCCTCCTCC	2858
		Reverse GCACAGGAGAAAGAGCTCACCCC	
Multicopper oxidase	88	Forward TCGCCCGTCCAGGAGAGATA	2208
		Reverse CCCCCATCTACCGGCCATTC	

Atty. Docket No. JGX-006.25

Gene name	SEQ ID No.	Primer Sequence	Amplified product (bp)
Multicopper oxidase	91	Forward ATGAGGGGTAATCGCGACGG	2382
		Reverse CCCTCTCACAACCTGACCCTGT	
Multicopper oxidase	94	Forward TCACTCAGTGCCCTACCGCTCC	1299
		Reverse CCGCAACGACTCCGTCCGGT	
Multicopper oxidase	97	Forward TGGGCTGATCCCGTTGCAGGA	1405
		Reverse GTAGCCGTGGCTGAGCGTGTT	
Multicopper oxidase	100	Forward TGCCGTTGCTGTAACATGCCGT	2099
		Reverse GACGGCGCTTTGCTCTTGCG	
Multicopper oxidase	103	Forward AGCATGCAATACTCGGTCGGTCT	633
		Reverse CGGGCAGCAGGATGTTTGCCAT	
Multicopper oxidase	106	Forward GGATACTCTCCGGGCACGTTCTG	1703
		Reverse ATGGCAGTGGACTGCGCGAC	
Multicopper oxidase	109	Forward GGAGGGAGCACTGATGCGCT	1873
		Reverse GGCTGCTCCTCCGCTCATGG	

Example 2 Amplification, cloning and sequencing of lignin peroxidase, chloroperoxidase, haemperoxidase and multicopper peroxidase from *M. phaseolina* ms6

Total RNA was isolated from three days old mycelium grown on liquid medium as previously described by Chomczynski P and Sacchi N, Single-step method of RNA isolation by acid guanidinium thiocyanate-phenol-chloroform extraction. (Anal Biochem 1987, 162: 156-159). The quality or the integrity of the RNA was checked by agarose gel electrophoresis and was quantified using Thermo Scientific Nano Drop 2000 as per standard procedures. cDNA first strand was synthesised using SuperScript III reverse

transcriptase (Invitrogen) following the manufacturer's instructions. The gene was amplified from the cDNA by PCR using the gene specific primers. The PCR reaction (50 μ L) contained 1 μ L of cDNA, 20 pmoles of each primers, 5 μ L of 10X PCR Buffer, 5 μ L of 2.5 mM dNTP mix and 1.0 unit of PfuTaq DNA polymerase. PCR was carried out in Thermal
 5 Cyclor (Applied Biosystems) using the following conditions: initial denaturation for 5 min at 95°C followed by 35 cycles of denaturation at 95°C for 30 sec, annealing at 59-61°C for 30 sec and extension at 72°C for 1 to 2.0 min depending on the length of the targeted gene, with a final extension at 72°C for 7 min. The PCR product was analyzed by 1% agarose gel using 1X TAE buffer and the amplicon was eluted from the gel using QIAGEN gel extraction
 10 kit following the manufacturer's instructions. The purified PCR product was ligated into pCR®8/GW/TOPO® TA cloning kit (Invitrogen) and transformed into competent *E. coli* cells (Invitrogen). Plasmids were isolated from putative colonies using QIAprep Spin Miniprep Kit (QIAGEN) following the manufacturer's instructions. The presence of the insert was checked by using the gene specific primers and positive plasmids were subjected to
 15 Sequencing.

Example 3 Analysis of the sequence

The nucleotide sequence and the amino acid sequence were analyzed by BLASTN and BLASTP programs respectively. The sequences reported from other plants were aligned with ClustalW. Phylogenetic analysis was carried out using the Neighbour Joining (NJ).

20 SEQ ID NO : 1
 LENGTH : 1379 (including 150 bp 5' UTR and 150 bp 3' UTR)
 TYPE : DNA
 ORGANISM : *M. phaseolina*
 25 CTGCTCAGCAGATCTTATCCCTCCAGAGCCAGAGCATCTTTAACTGACCAGCTTGCCTTCGTCCCAT
 CGTTTGCATTTTTTTTACACTTGACCAGTCAAGGCCCTCTTCCTTCTTTGAGACCGCTACACCCACC
 CCTTCGTACTGTCAAAATGTTATTCTCAAAGTCTTCCATCTTTCTCCTCTCCACTGCGGCCAGTGTG
 CAAGCACTCAGCCTCTCCGATGTCTCCTCTGCCGCCTCGGTCTGAAGCGTGAAGCTTCCGGCTTGG
 GGAACAACCTTCTATCTCTCGTTACCGTCGGGACTCTTGCCCTGATGTTTGGCAGAAAGTCGCATC
 CGAGCTGAAGGGCTGGTTCTTGATGGTTCCGTGTGCAGTGACGACGCACGCGCTGCCATCCGCCTC
 30 TCTTTCCACGACTGCTTTTCCGGCGGCTGCGATGGGTCCATCATCCTTGCCCACGAGTACACCCGCT
 CCGACAACGCTGGCTTAGCAGACTTTGCTATGAAGCTAGCGCCTCTCGCGGACCAGTACGAGGTGCG
 AACAGCTGACCTGATCCAATTCGCTGGCGGTAAGCCTTATCTATCCACCTTAAAAA
 aGGAAAAAAaGACTATCTCTAACACCTACCTCGACCAGCCCTCGCCACGGCCACCTGTCCCCTCGGC
 CCCCCCATAGCCGTCAAAGTCGGCCGCCAGGACTCGTCAACGCCCTCGGCAGAGGGACAGCTCCCCT
 35 CGTCGCGATCCTCGGCCTCCGTCTGATCGACCAGTTCGCGGCGAAGGGGTTCTCTGAGATAGACCT
 CGTCGCCCTCGTCGGTGCCACAGCACTGCCAAGCAGTTCTTCGATCAGCCCCACAAGGCCGGCCAA
 AGCCTCGACTCCACCCCCGCACTTGGGACACCAACTTTTACCGCCAGACGACGCTCGGCACTGCGC
 CCGTTACCCTCGAGAGCGATAAGAACCTCGCCACGGATCTGAGGACCGCGGTGCAGTGGACGGCGTT
 TAATGCCCAGGGCGTGTGGGCCGCGCGTATGTGAGCGCGTAAGTAGTGCATCATATGTTTCTTCTC

TGCTCTCAGATTGTTGAGAACTAATGGTCAATGTAGGATGAACAAGATGACCGTTTTGGGCAATGAT
GTCAGCAGCTTGACGGATTGCACGAGTGTTATCAGTGCGGCAACGAGCAAGCGCGACATCAAGGCCG
CACCTATTGCGGATAGGATTTGAGCTATGCAAGCAGTTCTGGGTGAGCGAGGTCGTAGTGCGGTGAC
TGGAGTTCTGTTTTTTTTTTTTTTtCTTAATTGGTAATGTCTGCTCTTGTGTTGATACCTGCCAGTATT
CGCGATTTATTCATCGGGAAGAGTTTAGAGAAGGGGGCA

SEQ ID NO : 2
LENGTH : 939
TYPE : DNA
ORGANISM : *M. phaseolina*
FEATURE NAME/KEY : CDS
LOCATION : (1).....(939)

atgttattctcaaagtcttccatctttctcctctccactgcgggccagtgtgcaagcactc
M L F S K S S I F L L S T A A S V Q A L
agcctctccgatgtctcctctgccgcctcggtcctgaagcgtgaagcttccggcttgggg
S L S D V S S A A S V L K R E A S G L G
aacaaccttctatctctcgttcaccgtcgggactcttgccctgatgttggcagaaagtc
N N L L S L V H R R D S C P D V W Q K V
gcatccgagctgaagggctggttcttgatggttccgtgtgcagtgacgacgcacgcgct
A S E L K G W F L D G S V C S D D A R A
gccatccgcctctctttccacgactgcttttccggcggtgcgatgggtccatcatcctt
A I R L S F H D C F S G G C D G S I I L
gcccacgagtagaccccgctccgacaacgctggcttagcagactttgctatgaagctagcg
A H E Y T R S D N A G L A D F A M K L A
cctctcgcgaccagtagcaggtcggaacagctgacctgatccaattcgctggcgccctc
P L A D Q Y E V G T A D L I Q F A G A L
gccacggccacctgtcccctcgggccccgcgcatagccgtcaaagtcggccgcccaggactcg
A T A T C P L G P R I A V K V G R Q D S
tcaacgccctcggcagagggacagctcccctcgctcgcgatcctcggcctccgtcctgatc
S T P S A E G Q L P S S R S S A S V L I
gaccagttcgcggcgaaggggttctctgagatagacctcgctcgccctcgctcggtgccac
D Q F A A K G F S E I D L V A L V G A H
agcactgccaaagcagttcttcgatcagccccgacaaggccggccaaagcctcgactccacc
S T A K Q F F D Q P D K A G Q S L D S T
cccggcacttgggacaccaacttttaccgccagacgacgctcggcactgcgcccgttacc
P G T W D T N F Y R Q T T L G T A P V T
ctcgagagcgataagaacctcgccacggatctgaggaccgcggtgcagtggacggcggtt
L E S D K N L A T D L R T A V Q W T A F
aatgccagggcggtgtggggccgcgcggtatgtgagcgcgatgaacaagatgaccgttttg
N A Q G V W A A A Y V S A M N K M T V L
ggcaatgatgtcagcagcttgacggattgcacgagtggttatcagtgcggaacgagcaag
G N D V S S L T D C T S V I S A A T S K
cgcgacatcaaggccgcacctattgcggataggatttga
R D I K A A P I A D R I -

SEQ ID NO : 3
LENGTH : 312
TYPE : PRT
ORGANISM : *M. phaseolina*

MLFSKSSI FLLSTAASVQALSLSLVSSAASVLKREASGLGNLLSLVHRRDSCPVDVWQKVASELKGW
FLDGSVCSDDARAARLSFHDCFSGGCDGSIILAHEYTRSDNAGLADFAFKLAPLADQYEVGTADLI
QFAGALATATCPLGPRIAVKVGQRQDSSTPSAEGQLPSSRSSASVLIDQFAAKGFSEIDLVALVGAHS
TAKQFFDQPDKAGQSLDSTPGTWDTNFYRQTTLGTAPVTLES DKNLATDLRTAVQWTAFAAQNQGVWAA
AYVSAMNKM T V L G N D V S S L T D C T S V I S A A T S K

SEQ ID NO : 4
 LENGTH : 1416 (including 150 bp 5' UTR and 150 bp 3' UTR)
 TYPE : DNA
 ORGANISM : *M. phaseolina*

5 TCTATATCTTGGCCCTTCGCCTGTTTCGCTTCAGGAGAACCCAACGCCAACATTCAATCTCAACCTCCT
 CTTTGAGTTACAATCGCTACTCTGGGAAATTTGTCCCAGCCTTTCATTCAACAACCTGTTTCTGTTTC
 AAACCAATCCGACGCCATGAAGTTCTCCACAGTCATCTCGAGCGTTGCTCTCACTTCTCTACTCCAG
 CCCGCCCTTGCCTACCTGGCATGGCAAATGTCGTCTCGGAGATCAAGGCCCGTCAAAACACCAATA
 ATGATGGTGACTCAAATCCCGAGATGATTGGCGATCTCGCCACCACCGGCCCAACCACCCCTGTGGG
 10 CCAAAGCATATACAACATCCTGATGGGGACCGAGTCGGCCGAGACCAAGCAGGCTGGCTACATCCCC
 CCTCTTATCGGCACCAACGCCTGCAAGAGGGACACCTGCTGCATCTGGGCCTACATCGCCGCCGAAC
 TGACCTCAATTTCAAGGGCATCACGGGCCGCTGCAACAAGAACGCGCGTGCCGCCATTTCGGCTCGG
 CTTCCACGACGCGGGGACTTGGTCCAAGAGCAGCAACGGCGCGGCGCGGACGGCTCGATCGCGCTG
 TCGGGCACGGAGATCAACAAGGCCGAGAACAACGGGCTGCAGGACATCATCGGCAAGATGATCACGT
 15 GGCAGAAGCGGTACGGGGTGGGCATGGCGGATCTGATCCAGTTCGCGGCCATCCACGCCGTGGTGAC
 GTGCCCCGCTGGGGCCGCGCATCCGCTTCTTCGTGCGGCGCAAGGACAGCAAAACGGCCAACGACGTC
 AGCCTGCTGCCGGGCGTCAACGATTTCGGCCGACAAGCTGATCGCGCTCTTCCAGGACAAGACCATCA
 CGCCGCACGAGCTCGCCGCCCTGCTCGGCGCCACACCACCTCACAGCAGTTCTTCGTGACACCAC
 CCGCGCCGGCGCCCCCAGGACAGCACCCCCGGCGTCTGGGACACCCGCTTCTACAACCAAACCACC
 20 TCCGACCAAGTTCCCAAGAAGGTCTTCCGCTTCGCCAGCGACGTTGTGCTGGCCAAGACCCGCGTA
 TGAGTGATGAGTGGGCGCCTTCGCCGACCCCGTCAAGGGCCAGAACCCTGGAATGAGGATTACGC
 CACCGCCTATACCCGCTCAGCCTGCTCGGCGTCAACAACATCAATAACTTGACTGAGTGCAGCAAG
 GTGCTGCCGTGGGCGCAACCGAAGTTCCCCGATGCCTGGAACCTGTTCTTGAGCAGTAGAGTGTAG
 TTTCTTCTTAATATCTGGCGTTCTTGGGGGTTTGGTCAAAAAGGAGAAAGATATTATTGTGATATT
 25 TGGTATACCCTAATGTTGGGAACATACATACGTATACAGGCTTCTTGTAATTACTCGGGCATCTTT
 TGCACAGAG

SEQ ID NO : 5
 LENGTH : 1116
 30 TYPE : DNA
 ORGANISM : *M. phaseolina*
 FEATURE NAME/KEY : CDS
 LOCATION : (1).....(1116)
 atgaagttctccacagtcattctcgagcggttgctctcacttctctactccagcccgccctt
 35 M K F S T V I S S V A L T S L L Q P A L
 gcctaccctggcatggcaaatgtcgtctcgagatcaaggcccggtcaaaacaccaataat
 A Y P G M A N V V S E I K A R Q N T N N
 gatgggtgactcaaatcccgagatgattggcgatctcgccaccaccggcccaaccaccctt
 D G D S N P E M I G D L A T T G P T T P
 40 gtgggccaagcatatacaacatcctgatggggaccgagtcggccgagaccaagcaggct
 V G Q S I Y N I L M G T E S A E T K Q A
 ggctacatccccctcttatcggcaccaacgcctgcaagaggacacctgctgcatctgg
 G Y I P P L I G T N A C K R D T C C I W
 gcctacatcgccgcccgaactgaccctcaatttcaagggcatcacgggcccgtgcaacaag
 45 A Y I A A E L T L N F K G I T G R C N K
 aacgcgcgtgccgccattcggtcggcttccacgacgcggggacttggtccaagagcagc
 N A R A A I R L G F H D A G T W S K S S
 aacggcggcgccgacggctcgatcgcgctgtcgggcacggagatcaacaaggccgag
 N G G G A D G S I A L S G T E I N K A E
 50 aacaacgggctgcaggacatcatcggaagatgatcacgtggcagaagcggtagcggggtg
 N N G L Q D I I G K M I T W Q K R Y G V
 ggcattggcgatctgatccagttcgcggccatccacgccgtggtgacgtgcccgtggtg
 G M A D L I Q F A A I H A V V T C P L G
 ccgcgcattccgcttcttcgtcgggcgcaaggacagcaaaacggccaacgacgtcagcctg
 55 P R I R F F V G R K D S K T A N D V S L

ctgccgggcggtcaacgattcgggccgacaagctgatcgcgctcttccaggacaagaccatc
L P G V N D S A D K L I A L F Q D K T I
acgccgcacgagctcgccgccctgctcgggcccccacaccacctcacagcagttcttcgctc
T P H E L A A L L G A H T T S Q Q F F V
5 gacaccacccgcgcccggcgccccccaggacagcacccccggcgctctgggacacccgcttc
D T T R A G A P Q D S T P G V W D T R F
tacaaccaaacacacctccgaccaagttcccaagaaggtcttccgcttcgccagcgacggtt
Y N Q T T S D Q V P K K V F R F A S D V
gtgctggccaaggaccgcgctatgagtgatgagtgggccgccttcgccgaccccgctcaag
10 V L A K D P R M S D E W A A F A D P V K
ggccagaaccactggaatgaggattacgccaccgcctatacccgccctcagcctgctcggc
G Q N H W N E D Y A T A Y T R L S L L G
gtcaacaacatcaataacttgactgagtgagcaaggtgctgccgtgggcgcaaccgaag
V N N I N N L T E C S K V L P W A Q P K
15 ttccccgatgcctggaacctgttcttgaccagtag
F P D A W N L F L D Q -

SEQ ID NO : 6
LENGTH : 371
20 TYPE : PRT
ORGANISM : *M. phaseolina*
MKFSTVISSVALTSLLQPALAYPGMANVVSEIKARQNTNNDGDSNPEMIGDLATTGPTTPVGQSIYN
ILMGTESAETKQAGYIPPLIGTNACKRDTCCIWAYIAAELTLNFKGITGRCNKNARAAIRLGFHDAG
TWSKSSNGGGADGSIALSGTEINKAENNGLDIIGKMITWQKRYGVGMADLIQFAAIHAVVTCPLGP
25 RIRFFVGRKDSKTANDVSLPGVNSADKLIALFQDKTITPHELAALLGAHTTSQQFFVDTTTRAGAP
QDSTPGVWDTRFYNQTTSDQVPKKVFRFASDVVLAKDPRMSDEWAAFADPVKGNHWNEDYATAYTR
LSLLGVNNINNLTECSKVLPAQPKFPDAWNLFLLDQ*

SEQ ID NO : 7
30 LENGTH : 1323 (including 150 bp 5' UTR and 150 bp 3' UTR)
TYPE : DNA
ORGANISM : *M. phaseolina*
TCGAGATGGCGGCTCTCTCGCAGACGTAAATCTATAAAGCCTTGCCGCGACTTTCTTTTGTGTATCT
CATCAGCATCGAGTTCCACAAGAGCTTGCTTCCTCTCCTCACTGAGCCTAGCGAGGAGCATCACTCA
35 GAACCTCCAATCACAATGCGGACCTCATCCCTGTTCTTGCTTCCGCATGCGGAACATCTGCTTAC
ACTCTCGTCTCGCTCGACTCTCTGCCAAGCACTCTTCATGACATAACCTCCCGCACCATCTCCAACC
TCGACCCCCGCAACCTCCTCTCCGCGCGCAAGACGCCCCGACTGCCCGGCCATCTGGAGGACCATCTC
AGCCGACCTGACCAAGAGCTTCCTCGCCAACGCGAGTGACCCGACCTCGCCCGCGCCGATCCGC
TACGCCTTCCACGACGCGGGCACCTTCTCGCTCAAGCTGCCACCTACGCGCCGGCCTCCGGCGGGCG
40 CCGACGGCTCGCTGCTGCTCGTTCGAGATCCAGCGGCCCGAGAACACGGGCTGCAGGCGTA
CAACGACTTCATCAAGGCCAAGTACAGCACGTACAAGTCTCGGGCGTTCGGCGCCGCCGACCTGATC
CAGTTCGCCGGCAACCACGCGTGGTGACGTGCCCGGGCGGGCCACGGTCAAGACGCTCGTTCGGCC
GCGGCGACAGCACGACCGCTCGCCGCTGAACGTGATGCCCGCGGGGTTTCGGCGCGGGCAGCGACCA
CGACTCGTCTGCTCCAGCTCTTCCAGGACAAGGGGTTTCAGCGCCGTTCGACCTGGCCGCGCTGATCGGC
45 GCCCCACACCACCTCCACGAACATCGCGGAGGCGCAGATCCCCGTTCGGCGCGCCCGCAGGACAGCACGC
CGGGCAGGTGGGACGTCAAGTACTACGCCGAGACGTACGCCCCGCGCGGGCGTCTCCCGCTTCGC
CTCCGACATCAACCTCTCCGACCCGACGAAAGCGGTTCGGCAAAGAGTTCCAGGGATTTCGTCAACAAC
CAGGGTAAGTGGACGGGCAAGTTTGCCGACGCCATGTTCCGTCTGAGTGTGTTGGGCATCCCGCCGG
CGACGTACAAGAATTTTCGCGACTGCACCGCTGCGCTGCCCAAGGGCACGAGCGCCAAGCGGGACAT
50 CCGCAGCGCCCCGATCAACGACCGCGCAAGGTAGAGGAGGGGAAAAGAAAGGAAGAAAAGAAAATAA
AAAGCGCAGCGAGGATGAATCGGTTGGGGCAGGGCGTTTCGGTTGAGGTTGTTTGTTCGCTCGCCTG
CCTTTTTTTTTTTTTTTtAATCCCTCTCATGATCCATCGAATGAGAACACTT

SEQ ID NO : 8
55 LENGTH : 1023

TYPE : DNA
ORGANISM : *M. phaseolina*
FEATURE NAME/KEY : CDS

LOCATION : (1).....(1023)

5 atgcggacctcatccctgttccttgcttccgcatgcggaacatctgcttacactctcgtc
M R T S S L F L A S A C G T S A Y T L V
tcgctcgactctctgccaaagcactcttcatgacataacctcccgcaccatctccaacctc
S L D S L P S T L H D I T S R T I S N L
gacccccgcaacctcctctccgcgcgcaagacgcccgaactgcccggccatctggaggacc
10 D P R N L L S A R K T P D C P A I W R T
atctcagccgacctgaccaagagcttccctcgccaacggcgagtgacccgacctcgcccg
I S A D L T K S F L A N G E C T D L A R
gcccggcatccgctacgccttcacgacgcgggcaccttctcgctcaagctgcccacctac
A A I R Y A F H D A G T F S L K L P T Y
15 ggcgcccgcctccggcgggcgccgacggctcgctgctgctcgctcgattcgagatccagcgg
A P A S G G A D G S L L L V D S E I Q R
cccgagaacaacgggctgcaggcggtacaacgacttcatcaaggccaagtacagcacgtac
P E N N G L Q A Y N D F I K A K Y S T Y
aagtcctcgggcgctcgggcgccgacgatccagttcgccggcaaccacgcccgtggtg
20 K S S G V G A A D L I Q F A G N H A V V
acgtgcccggggcgggccacgggtcaagacgctcgctcgggcgcgacagcacgaccg
T C P G G P T V K T L V G R G D S T T A
tcgcccgtgaacgtgatgccgcccggggttcggcgcgggcagcgaccacgactcgctgctc
S P L N V M P P G F G A G S D H D S L L
25 cagctcttccaggacaaggggttcagcgccgtcgacctggccgcgctgatcggcgcccac
Q L F Q D K G F S A V D L A A L I G A H
accacctccacgaacatcgcgaggcgagatccccgtcgggcgcgccgcaggacagcacg
T T S T N I A E A Q I P V G A P Q D S T
ccgggcaggtgggacgtcaagtactacgcccagacgtacgccccgcccgggctctcc
30 P G R W D V K Y Y A E T Y A P P A G V S
cgcttcgcctccgacatcaacctctccgacccgacgaaagcggtcggcaaagagttccag
R F A S D I N L S D P T K A V G K E F Q
ggattcgtcaacaaccagggttaagtggacgggcaagtttgccgacgccatgttccgtctg
G F V N N Q G K W T G K F A D A M F R L
35 agtgtgttgggcatcccgcggcgacgtacaagaatttcgcggaactgcaccgctgcgctg
S V L G I P P A T Y K N F A D C T A A L
cccaagggcacgagcgccaagcgggacatccgcagcgccccgatcaacgaccgcgcaagg
P K G T S A K R D I R S A P I N D R A R
tag
40 -

SEQ ID NO : 9
LENGTH : 340
TYPE : PRT

45 ORGANISM : *M. phaseolina*

MRTSSLFLASACGTSAYTLVSLDLPSTLHDITSRTISNLDPRNLLSARKTPDCPAIWRITISADLTK
SFLANGECTDLARAAIRYAFHDAGTFSLKLPTYAPASGGADGSLLLVDSEIQRPENNGLQAYNDFIK
AKYSTYKSSGVGAADLIQFAGNHAVVTCPPGPTVKTLVGRGDSTTASPLNVMPPGFGAGSDHDSLLQ
LFQDKGFSADVLAALIGAHTTSTNIAEAQIPVGAPQDSTPGRWDVKYYAETYAPPAGVSRFASDINL
50 SDPTKAVGKEFQGFVNNQGWTKGFADAMFRLSVLGIPPATYKNFADCTAALPKGTSAKRDIRSAPI
NDRAR*

SEQ ID NO : 10
LENGTH : 1930 (including 150 bp 5' UTR and 150 bp 3' UTR)

TYPE : DNA
ORGANISM : *M. phaseolina*
GAGCACGGCAGGTAGGTTGCATCCGAGAGGTCGTGGTAGGTAGGTATATATTGCTGCCTCCGCTCTG
TCGCTCTATAGAGGCAGGTCTTGGACATCTGTGAACAGGTTACCTTCTCATAATTTGATCCATTGGC
5 GAAGATATACTCAAGAATGCCGTCTACCTGGATGATTGCATTGGGCGCACTCACCcTTGCCGGCCAG
TCCGCAGCCTTTCTGCTGTGGCAGAACAATACGCTGCTCAGACATCTCACAAGGAGAAAAGAGTAA
ATGCAATTAGCCCCGGGTTCAATGCGGCGGCACAGAGGATTGACGTCTCGGGAGCTCACACTTTCTG
GCCCCCTGGCCCCGGTGACCAGAGAGGGCCCTGCCCGGGTCTGAATGCCTTAGCGAACCAGTAAGTG
10 CTCTGCAAGTCTCACAGGTCTTCTTGTACTGACAAAGTGTAGCAACTATTTGCCCCAGTGAGTTCTC
CACAACCTTATTCCCCGAAACCTTGTCACTGATTGTCTTCAGCAATGGCGTCGCAACAATCACGCAGT
TCGTCCAGGCCACAAACCAGGGTTAGTACAGCATCACCGCCACGGAAGCTACTACGTCTAGCTGAACC
ACATACGCAGTATACGGCATGGGTCTCGACCTTGGCACGTTCTGTCCGTCTACGGCGCGGTAATGG
ATGGCGACGGCCTCAGCTGGTCCATCGGCGGCGCGCCAGTACCGCAAACCTACTCAACCTCCTTAC
TCAGCCGCAAGGCCTCTCAGGTTTCGCACAACAAGTACGAGACAGATGCATCGCTACGCGCGGAGAC
15 CTGTACCAATAGTGCCTCTATCCCCCTTCTTCTGCCTCCCGCCACTCCGCTGACCTGCACCGCAGTGG
CGACAACCTCCCGGGTCGTCAATTCGCAATGGGACGCCCTCTTCGCGAAGCAAGCGGCACTGCCCAAT
GACCAGTCCAATTATGGCCTAGGTGTGCTGACCGACTTCCGAGTCGAGCGTTTCCAGCAGAGCGTCG
ATGAAAACCCCTACTTCTTCAACGCGCCCTTTTCCGGTGTGCTCGTGCAGCCTGCCGCGTACACATT
CATCTACCGCTTCATGGGCAACAAGAGCGCCGAGAAACCCGAGGGTGTGCTGACGAAAGAGGTGCTG
20 AAGAGCTTCTTCGGCTTCACTGGGCCTGACGACGACATGACATACGTGAGTCCCATCCCGCCGCTT
TCTCATTTCTTCCCACTCGAGTCTCCACATCCCCCCCCCCCCCCCCCCCCCCCCcACcATTTGTTG
TCGCCCTTCCCTCCAGCCACGCCACTGCCACAAACGCCACCGTCTGACCCACCGCAGAACCCCGGCC
ACGAGCGCATCCCCGAAAACCTGGTACAAGCGCGCCCCGGCGACGAATACACGATCCCCCTTCTACGC
ACTTGACCTCAACGCCGCGCGCTGCAGCACCCGCAATTCTGTCCGTTCGGCGGCAACACGGGCACC
25 ACCAACTCCTTCGCCGCGCTCGACCTGCAGGACCTGAGCGGCGGCCTGTACAACGCCGCCAGCCTGC
TCGAGGGCAACAACCTCGCCTGCTTCGGTTTCCAGGCGGCCGTCCTCAATTTCGCGCCGACCTGTTGAA
AGGGCTGGTGAGCGATTTGACCAAGCCGTTGGGTGTCTTGGGAGATGCGTTGGCGAGTGCCTTGAAT
GGATTAGGGTGTCCGCAGTTAGGCGGCCAGGCGTGGGATGATAGCGCGCTGGCGCAGTTTCCGGGGT
ATGCTAGGCTGAGGGCGGATGGGACGTACGGGAAGTAATGGACGCGGAGAAGTAGTGTGGCAGAGGC
30 GACATGGTGCATGGTGGACTGCGGCTTCAACGACAATGCAGAGATGATGGTATGAGGAACTGCA
CAGCAGTCTGCATGGATTGTCTAGACTAGACGAATTTTATGATTTTGAATGAAC

SEQ ID NO : 11
LENGTH : 1260
35 TYPE : DNA
ORGANISM : *M. phaseolina*
FEATURE NAME/KEY : CDS
LOCATION : (1).....(1260)

atgccgtctacctggatgattgcattgggcgcaactcacccttgccgggccagtcgcgcagcc
40 M P S T W M I A L G A L T L A G Q S A A
tttcctgctgtggcagaacaatacgtgctcagacatctcacaaggagaaaagagtaaat
F P A V A E Q Y A A Q T S H K E K R V N
gcaattagccccgggttcaatgcggcggcacagaggattgacgtctcgggagctcacact
A I S P G F N A A A Q R I D V S G A H T
45 ttcgtgccccctggccccgggtgaccagagagggccctgccccgggtctgaatgccttagcg
F V P P G P G D Q R G P C P G L N A L A
aaccacaatggcgctcgcaacaatcacgcagttcgtccaggccacaaaccagggtatacggc
N H N G V A T I T Q F V Q A T N Q V Y G
atgggtctcgaccttggcacgttcctgtccgtctacggcgcgtaatggatggcgacggc
50 M G L D L G T F L S V Y G A V M D G D G
ctcagctgggtccatcggcggcgccccagtagccgaaacctactcaacctccttactcag
L S W S I G G A P S T A N L L N L L T Q
ccgcaaggcctctcaggttcgcacaacaagtacgagacagatgcacgcctacgcgcgga
P Q G L S G S H N K Y E T D A S P T R G
55 gacctgtaccaatatggcgacaactccccgggtcgtcatttcgcaatgggacgcacctcttc

D L Y Q Y G D N S R V V I S Q W D A L F
 gcgaagcaagcggcactgcccaatgaccagtccaattatggcctaggtgtgctgaccgac
 A K Q A A L P N D Q S N Y G L G V L T D
 5 ttccgagtcgagcgtttccagcagagcgtcgatgaaaaccctacttcttcaacgcgccc
 F R V E R F Q Q S V D E N P Y F F N A P
 ttttccggtgtgctcgtgcagcctgccgcgtacacattcatctaccgcttcatgggcaac
 F S G V L V Q P A A Y T F I Y R F M G N
 aagagcgcgcgagaaacccgaggggtgtgctgacgaaagaggtgctgaagagcttcttcggc
 K S A E K P E G V L T K E V L K S F F G
 10 ttccactgggcctgacgacgacatgacatacaaccccgccacgagcgcacccccgaaaac
 F T G P D D D M T Y N P G H E R I P E N
 tgggtacaagcgcgcgcgcgcgcgaatacacgatcccccttctacgcacttgacctcaac
 W Y K R A P G D E Y T I P F Y A L D L N
 gccgcggcgcgtgcagcaccccgcaattcctgtccgtcggcggcaacacgggcaccaccaac
 15 A A A L Q H P Q F L S V G G N T G T T N
 tccttcgcggcgctgcacctgcaggacctgagcggcgccgtgtacaacgcgcgcagcctg
 S F A G V D L Q D L S G G L Y N A A S L
 ctcgagggcaacaacctcgctgcttcggtttccaggcggccgtccaattcgcgccggac
 L E G N N L A C F G F Q A A V Q F A P D
 20 ctggttgaaagggctgggtgagcgatttgaccaagccgttgggtgtcctgggagatgcgttg
 L L K G L V S D L T K P L G V L G D A L
 gcgagtgcggttgatgaggtggttcgcagttaggcggccaggcgtgggatgatagc
 A S A L N G L G C P Q L G G Q A W D D S
 gcgctggcgcagtttccggggtatgctaggctgagggcggatgggacgtacgggaagtaa
 25 A L A Q F P G Y A R L R A D G T Y G K -

SEQ ID NO : 12
 LENGTH : 419
 TYPE : PRT
 30 ORGANISM : *M. phaseolina*
 MPSTWMIALGALTLAGQSAAFPAVAEQYAAQTSHKEKRVNAISPGFNAAAQRIDVSGAHTFVPPGPG
 DQRGCPGLNALANHNGVATITQFVQATNQVYGMGLDLGTFLSVYGAVMDGDGLSWSIGGAPSTANL
 LNLLTQPQGLSGSHNKYETDASPTRGDLYQYGDNSRVVISQWDALFAKQAALPNDQSNYGLGVLTDF
 RVERFQQSVDENPYFFNAPFSGVLVQPAAYTFIYRFMGNKSAEKPEGVLTKEVLKSFFGFTGPDDDM
 35 TYNPGHERIPENWYKRAPGDEYTI PFYALDLNAAALQHPQFLSVGGNTGTTNSFAGVDLQDLSGGLY
 NAASLLEGNLACFGFQAAVQFAPDLLKGLVSDLT KPLGVLDALASALNGLGCPQLGGQAWDDSA
 AQFPGYARLRADGTYGK*

SEQ ID NO : 13
 LENGTH : 1108 (including 150 bp 5' UTR and 150 bp 3' UTR)
 40 TYPE : DNA
 ORGANISM : *M. phaseolina*
 CTGATGGTATGTACTTTGGTAAGCACGCCATTAACACTCGCTCCATCGCCTCGAGTTACCCTGTTG
 GAGCAGCAACCACAACCTTGAGCGAACAATTCGGCCATTAATACCATCGTACGAAGAAGGCTTAACC
 GCTTTACCTGCCAGCCATGAATCCAATCTGCTTTTTATCCCTGCTCACGGCCATGCTAGGCATGGCC
 45 ATGGGCGGTGGAACCCCTCTGAACCATGCTGAACCTTTTGATCCACGAACAGCTTGTGGGTGTGAC
 TGATGCGCATGAGCCCATTTCTTCTGATATCACCAACGCTCGCAGCCCCTGTCCCGGCCTTAACACG
 TTGGCGAACCAGGAAGCTCATTCGCCCCCTTGCTATGAAGAAAACCTGGAATTTACGCTCCTCCCGG
 TGGCTTCGACGGTGTTCGCGAACTACGATGAACCTTGTTAAGGCTCTGGTTGATAGTGTGTTGCTTTTG
 ATCGGGGGTCAACACCTTTTCGGTTGACGAGAACATCACGATTCGGCCTAATAATTTACACGCAGCC
 50 TCAGCGGCACACAAATCTCCCTAGATTCTGAGGCCTCGCCTACACGCCACGACGCGTACGACCCTCG
 GGCTTACTCCGGCTCGAGCAGCATCGAAATGAAGTGAACCTTCTTCAAACAGCTGTACGAGAAGCAG
 GCCGGGATCCACGCGATGCGGTAACTTTGCACTGGATGTTCTTGCTCAAAACATGTTGGAGCTGG
 TGGTGGTCAGCATCAAGAACAACCCGAACCTTCTTCTGAGCCCAACGCACATCGCATTTCGGACCATC
 GACGGCCACATGTGCATTCCCAACTTGTTTCGCGAACCACAGCACTGAGCATTGGCTGACCTCTCTC
 55 CTGAATAGAGAGGGGAGGGTCTCGCCATTCAATCCATGCTCAAACTATGACGCTTTGTAGTCTTCAGC

TCAGATTGTCACCAATCTGAAGGCGAGATCCCACCTTCTATACTCAGATTAAAGACCTAATAATACAA
TCGTATACTCAGCGAGAGAAGCACGAGAAGGACCGAGCCAACATTACCTCATCCTTCACACAACAC
ACTCCTGAGCACCGACCCCAATTCTAAATCAGCCCC

5 SEQ ID NO : 14
LENGTH : 690
TYPE : DNA
ORGANISM : *M. phaseolina*
FEATURE NAME/KEY : CDS

10 LOCATION : (1).....(690)

atgaatccaatctgctttttatccctgctcacggccatgctagggcatggccatgggcggt
M N P I C F L S L L T A M L G M A M G G
ggaaaccctctgaaccatgctgaaccttttgatccacgaacagcttaaacctggaatt
G N P L N H A E P F D P T N S L K P G I
15 tacgctcctcccggtggcttcgacgggtgctcggaactacgatgaacttgtaaaggctctg
Y A P P G G F D G V A N Y D E L V K A L
gttgatagtgtgttgcttttgatcggggggtcaccacctttcggttgacgagaacatcacg
V D S V L L L I G G H H L S V D E N I T
attccgcctaataatttcacacgcagcctcagcggcacacaaatctccctagattctgag
20 I P P N N F T R S L S G T Q I S L D S E
gcctcgctacacgccacgacgcgtacgacctcgggcctactccggctcgagcagcatc
A S P T R H D A Y D P R A Y S G S S S I
gaaatgaagtggaaacttcttcaaacagctgtacgagaagcaggccgggatccacgcgat
E M K W N F F K Q L Y E K Q A G I P R D
25 gcggttaactttgcaactggtgttcttgctcaaaacatggtggagctggtggtggtcagc
A V N F A L D V L A Q N M L E L V V V S
atcaagaacaacccgaacttcttccctgagcccaacgcacatcgcatcggaccatcgacg
I K N N P N F F L S P T H I A F G P S T
gccacatgtgcattcccaacttggttcggaaccacagcactgagcattgggtgacctct
30 A H M C I P N L F A N H S T E H W L T S
ctcctgaatagagagggaggggtctcgccattcattccatgctcaaactatgacgctttgt
L L N R E G G S R H S F H A Q T M T L C
agtcttcagctcagattgtcaccaatctga
S L Q L R L S P I -

35

SEQ ID NO : 15
LENGTH : 229
TYPE : PRT
40 ORGANISM : *M. phaseolina*
MNPICFLSLLTAMLGAMGGGNPLNHAEPFDPNTSLKPGIYAPPGGFDGVANYDELVKALVDSVLLL
IGGHHLSDENITIPPNNFTRSLSGTQISLDSEASPTRHDAYDPRAYSGSSSIEMKWNFFKQLYEKQ
AGIPRDAVNFDLVDLAQNMLELVVVSIIKNNPNFFLSPTHIAFGPSTAHMCIPNLFANHSTEHWLTSL
LNREGGSRHSFHAQTMTLCSLQLRLSPI*

45

SEQ ID NO : 16
LENGTH : 1554 (including 150 bp 5' UTR and 150 bp 3' UTR)
TYPE : DNA
ORGANISM : *M. phaseolina*

50 AAGCCTTGCTGGATCGACCTTTTTCAATTCGGCGAGATACACCCAAGTCATTGAACATCGAAACAGT
ACTTGCCTTCGTCAAATATGCGGTCACTCTTCCTTGCTTCCTTATTACTTTCTGCGGCGTCCGCTTT
CCCTTTCGTGGCAGATATGCCAGAGGTAGACTCTTCTCTCTTCCGTGAAGCACCCGTACGTAGGCAA
CAACCTGGCGGCAACCAACCTGGCGGAGCGGCGACTTGCCCTTTCAATGCCAACCACGTCCCCGCTG
CGCCAGTGACAGCTCGATTCCCTATAACAACGCAAAGAACGGAGTTCCCGGCAACGGAAAGGGCGG
55 TTACCAGGTTCCAGCGCCTGGTGACACGGCTCATCAGTTCATTGCACCAACAGCGCACGATATCCGT

GGGCCTTGCCCGGGCCTGAACGCTGCGGCCAATCACGGCGTGAGTCTTTCTGTAGTCCCCATTTCGA
 GTTTCAAGTCTCCTGACGGTGACCCTAAACAGTTCTCGCGCGGACGGCATAGTGACCTTCAACGA
 ACTGGTTCGACGCCCAGCAGAATGTCTACAATGTCGGCTACGACCTCTCTGTGCTGCTCGCCGTCTC
 5 GGCCTCACGCTCACCGACGGTGACCCCATCACCCAAAACTGTCTATCGGCTGCGACGCAACGACAC
 GCACATCTGTGGCCCCCTGCTGACTGGCAGTCAGCCCGGTCTGGATGGCCACAACAAGTTTCAAGC
 GGACACGTCGCTCACACGCAACGACTACTTCTGGCGGGCGGCGACAACCTCAACTTCAACGGCACG
 CTCTTCGGCATGATGGTGGATACGTGCCAGGGCAACTTCAACCGTGAGAACCTGGCGCTGTACCGCA
 AGCAGCGCTACGACCAGAGCCTACGCGACAACGAGAACTTCTACTTCGGCCCCGCTAAGCCTGCTGCT
 10 GTTCGGCGCCGCGCAGCTTCTTTTACGAGCTGATGCCAGCGGCACGCACAACCTACGCGCCCGATCTC
 GACACCATCTCGTCTCTTCTTCGGCGCCGAGCAGGCGCCCGATGGCTCCTGGCGCTTACCGCCGAGC
 GTATCCCGGACAACCTGGACCAACCGTGTGCTGCCGTACACCAATGAGGACGTGACGCGCGAAATCCT
 GGCTATGTACCTCCTCAACCCTGTGCTATTTGGCGGCGCCACAGGCGACGGCGGCTTCAACACGCTG
 CCGAAGTTTGGCTCCATCCAGGACGGCAAGATCGTTGAGGCACCCAATACGCTGTGCCTGCTGTACC
 15 AGCTGTGCGACGAGAGCGTGCCGAGCTCGCTGAATGGCATCATCACGCCGACTGTGGATGCGCTGAA
 CCTGGTTCGCGGATAAGCTAGCGCCGAGTTCAAGAACTTGGGGTGCCCGAATCCGTTGACTTGAATG
 AGTGATGGCCGTGTAGAGCCTCTGCTCGCGGTGCGAAGGAAAAAGAAAAAGTGAGGGGATTTTTGGC
 GAGAAATGAAATTCACGAAGATACTGCCCGGATGGTAGAGGGAACTTGGTCATGCATGTGCATGCG
 AAGGCGTTGATAT

20 **SEQ ID NO** : 17
LENGTH : 1194
TYPE : DNA
ORGANISM : *M. phaseolina*
FEATURE NAME/KEY : CDS

25 **LOCATION** : (1).....(1194)
 atgccagaggtagactcttctctcttccgtgaagcaccgcgtacgtaggcaacaacctggc
 M P E V D S S L F R E A P V R R Q Q P G
 ggcaaccaacctggcggagcggcgacttgccctttcaatgccaaccacgtccccgctgcg
 G N Q P G G A A T C P F N A N H V P A A
 30 ccagtgcagctcgatcttccctataacaacgcaaagaacggagttcccggaacggaaag
 P V T A R F P Y N N A K N G V P G N G K
 ggcggttaccaggttccagcgcctgggtgacacgggtcatcagttcattgcaccaacagcg
 G G Y Q V P A P G D T A H Q F I A P T A
 cacgatatccgtgggccttgcccgggcctgaacgctgcgcccaatcacggcttcctcgcg
 35 H D I R G P C P G L N A A A N H G F L A
 cgcgacggcatagtgccttcaacgaactggcgacgcccagcagaatgtctacaatgtc
 R D G I V T F N E L V D A Q Q N V Y N V
 ggctacgacctctctgtgctgctgcgcgctcctcggcctcacgctcaccgacgggtgacccc
 G Y D L S V L L A V L G L T L T D G D P
 40 atcaccccaaaaactgtctatcggtgcgacgcaacgacacgcacatctgtggccccctg
 I T Q K L S I G C D A T T R T S V A P L
 ctgactggcagtcagcccggtctggatggccacaacaagttcgaagcggacacgctcgctc
 L T G S Q P G L D G H N K F E A D T S L
 acacgcaacgactacttcttgccggggcggcgacaacttcaacttcaacggcacgctcttc
 45 T R N D Y F L A G G D N F N F N G T L F
 ggcgatgatggtggatacgtgccaggggaacttcaaccgtgagaacctggcgctgtaccgc
 G M M V D T C Q G N F N R E N L A L Y R
 aagcagcgctacgaccagagcctacgcgacaacgagaacttctacttcggcccgctaagc
 K Q R Y D Q S L R D N E N F Y F G P L S
 50 ctgctgctgttcggcgccgcccagcttccctttacgagctgatgccagcggcacgcacaaac
 L L L F G A A S F L Y E L M P S G T H N
 tacgcgcccgatctcgacaccatctcgtccttcttcggcgccgagcaggcgcccgatggc
 Y A P D L D T I S S F F G A E Q A P D G
 tcctggcgcttcaccgcccagcgtatcccggacaactggaccaaccgtgtgctgccgtac
 55 S W R F T A E R I P D N W T N R V L P Y

accaatgaggacgtgacgcgcgaaatcctggctatgtacctcctcaaccctgtgctattt
T N E D V T R E I L A M Y L L N P V L F
ggcggcgccacagggcgacggcggttcaacacgctgccgaagtttggctccatccaggac
G G A T G D G G F N T L P K F G S I Q D
5 ggcaagatcgttgaggcaccacaatcgtgtgcctgctgtaccagctgtcgacgcagagc
G K I V E A P N T L C L L Y Q L S T Q S
gtgccgagctcgctgaatggcatcatcacgccgactgtggatgcgctgaacctggcgcg
V P S S L N G I I T P T V D A L N L V A
gataagctagcgccgcagttcaagaacttggggtgcccgaatccgttgacttga
10 D K L A P Q F K N L G C P N P L T -

SEQ ID NO : 18
LENGTH : 397
TYPE : PRT

15 ORGANISM : *M. phaseolina*

MPEVDSSSLFREAPVRRQQPGGNQPGGAATCPFNNANHVPAAPVTARFPYNNAKNGVPGNGKGGYQVPA
PGDTAHQFIAPTAHDIRGPCPLNAAANHGFLLARDGIVTFNELVDAQNVYNVGYDLSVLLAVLGLT
LTDGDPITQKLSIGCDATTRTSVAPLLTGSQPGLDGHNKFEADTSLTRNDYFLAGGDNFNFNGLTFLG
MMVDTQCQGNFNRENLA LYRKQRYDQSLRDNENFYFGPLSLLLFGAASFLYELMPSTHNYAPDLDTI
20 SSFFGAEQAPDGSWRFTAERI PDNWTNRVLPYTNEDVTREILAMYLLNPVLFGGATGDGGFNTLPKF
GSIQDGKIVEAPNTLCLLYQLSTQSVPSLNGIITPTVDALNLVADKLAPQFKNLGCNPPLT*

SEQ ID NO : 19
LENGTH : 1792 (including 150 bp 5' UTR and 150 bp 3' UTR)
TYPE : DNA

25 ORGANISM : *M. phaseolina*

ACCGACCACCATCCATTGCTCTTTTCGCTGGCGGCTGGCGTCCAAGGCTCACTCTCACTCTAGTCAC
TCTTTGCAATCTCTGAATTCCCGCGAGCCCTTGGTCTGCGTTGTTAAGGATTTGTTGTCCGGGCATC
CCCTCTCTTTTCCGCAATGAAGTTCTCGTCCGCCCTTCTCCTGCTCTCCTCGAGCTCCCTTGTCGTC
GATGCCCTTCCCGCCCTCGGTGCGCAGAACCCTTGAGGGCCTCACTCCGAAAGGTTGACCGCTGCCC
30 TCAAGACGGTCGAGAAGTACAGGAAGGAGAAGCGCCTTATCATCGACTCCAGCAAGCCTATCGATAC
CACCGGCGACCACGCTTTCCAGCCACCCAGCGAAACCGACCAGCGCGGCCCTGTCTGGCTTGAAC
GCCCTGGCCAACCATGGCTACATCTCTCGCGACGGCATCACCAGCTTCGCCGAGGTTGTACCGCCA
TTAACCAAGGTTTCGTGCTGGATTTCGTGAGAGAAGGCGTGGCTTGGCACTGACAAGGATGTGAAGTG
ATGGGCATGGGCATCGAGCTCTCTGATTCTCGGTGTTATGGGTACCGTGTGGACGGGTAAACCCGC
35 TTTTCGCTGGACCCTGGCTTCTCTATCGGTGGGACCGCCCCCGGTGATGGCTCCGACAACATTCTGGG
CAACCTTGTGCGCCTGCTCGGTACGTAAGTGTCCCTCATCGGAGCCACGCCGCCGAGCTAAGCTGA
GACGTCTGCAGGTGACCTCTGTGGTCTGCAAGGCTCCCACTGGATTGAGTCTGACTCCTCTCTG
ACGCGTGATGATCTGTACCTCACCGGAGATGCCTGGACGATGAACATGACGCTCTTCCGCGACATCT
ACGACCGCGCGGATGAGGATGGCGTCATCTCCATGGATCTGCTCGCCGACCAGGCCGCCCGTCTGCTG
40 GGAGTACAGCATCGGCCACAACCCCACTTCTACTACGCCCTGTACCGGCATGGTCAGCCGTAAT
GCCGGCTACTTTTTCTCGGCCGCTGCTGTCAAACACACCGATGAACATCCGGACGGAATTCTCA
CTCAAGAAGTTTTCAAGAAGTTCTTCGCCGTCTACGAGGACGAGCAGGGCAACATGGAATACCGCAA
GGGCCACGAGACCTTCCCGACAACCTGGTACCGCAAGCCGGTCGAGTATGGCCTGGTCCCGCTCAAC
TTGGACCTCGTTGGCTGGGTCTTGAAGCACCTGAGCTGGGAAGGTACGTCTGCTCCCTTCTCACCCCA
45 AGATGGGAAGGCATGTGAAGTACTCGGCTTCCCACAGCATCGGCGGTAACACTGGCACCGTCAACT
CCTTCTCCGGCCTCGATCTGCACAGCATCACCGGCGGCGTCTCAATGCCACTTCGCTCCTCGAGAA
CAACAACCTGCTGTGTTTGTCTTTGAAGTTCTCAAGACCTTCGCCCCCACTCCCTCTCCCGCTC
CTGTGACGCTCGAAGTGCCGCTCAAGCTTATCGCCGACACCTGGCCACCCGCTCTTGAGCCTGG
CCTGCCCTGCCCTGGAAGGATATGACCGACGGTGGCGAGCCGCTGTGGGATGGCATTCAGAACAGGTT
50 CCCTGGCGGAGCAAGGCCGATCGAGTTTGTAGAGTTGCTCGAGAGGACACAGGACGTCTGGAGCA
TGACGTCTGGGTGAACGTACTGCGTGGAAGAAGAGCAAAGGAACCGAGGGCGAGAAATGATGTA
GTTAGCGTCTTGATTCTAATTTCGATACCATTTACATTCTTCGCCTTATCC

SEQ ID NO : 20
LENGTH : 1317
TYPE : DNA
ORGANISM : *M. phaseolina*
5 FEATURE NAME/KEY : CDS
LOCATION : (1).....(1317)
atgaagttctcgtccgccttctcctgctctcctcgagctcccttgctcgtcgatgccttc
M K F S S A L L L L S S S S L V V D A F
cccgcctcgggtgcgcagaaccttgagggcctcactccggaaagggttgaccgctgccttc
10 P A L G A Q N L E G L T P E R L T A A L
aagacggtcgagaagtaacaggaaggagaagcgccttatcatcgactccagcaagcctatc
K T V E K Y R K E K R L I I D S S K P I
gataccaccggcgaccacgctttccagccacccagcgaacccgaccagcgcgccctgt
D T T G D H A F Q P P S E T D Q R G P C
15 cctggcttgaaacgccttgcccaaccatggctacatctctcgcgacggcatcaccagcttc
P G L N A L A N H G Y I S R D G I T S F
gccgaggttgtcaccgcccattaaccaagtgatgggcatgggcatcgagctctctctgatt
A E V V T A I N Q V M G M G I E L S L I
ctcgggtgttatgggtaccgtgtggacgggtaaccgcttttcgctggaccctggcttctct
20 L G V M G T V W T G N P L S L D P G F S
atcgggtgggaccgcccccggtgatggctccgacaacattctgggcaaccttgctggcctg
I G G T A P G D G S D N I L G N L V G L
ctcgggtgacctcgtggtctgcaaggctcccacaactggattgagtctgactcctctctg
L G D P R G L Q G S H N W I E S D S S L
25 acgctgatgatctgtacctcaccggagatgcctggacgatgaacatgacgctcttccgc
T R D D L Y L T G D A W T M N M T L F R
gacatctacgaccgcgcggatgaggatggcgtcatctccatggatctgctcgccgaccag
D I Y D R A D E D G V I S M D L L A D Q
gccgcccgtcgtggtgggagtaacagcatcgccacaaccccaacttctactacggccctgtc
30 A A R R W E Y S I G H N P N F Y Y G P V
accggcatgggtcagccgtaatgccggctactttttcctcggccgctgctgtcaaaccac
T G M V S R N A G Y F F L G R L L S N H
accgatgaacatccggacggaattctcactcaagaagttttcaagaagttcttcgccgtc
T D E H P D G I L T Q E V F K K F F A V
35 tacgaggacgagcagggcaacatggaataaccgcaagggccacgagaccttcccgacaac
Y E D E Q G N M E Y R K G H E T F P D N
tggtaccgcaagccggctcgagtatggcctgggtcccgtcaacttgacactcggttggtgg
W Y R K P V E Y G L V P L N L D L V G W
gtcttgaagcaccctgagctgggaagcatcggcggtaaacactggcaccgtcaactccttc
40 V L K H P E L G S I G G N T G T V N S F
tccggcctcgatctgcacagcatcacccggcggtcctcaatgccacttcgctcctcgag
S G L D L H S I T G G V L N A T S L L E
aacaacaacctgctgtgttttgtctttgaagtctcaagaccttcgcccccaactccttc
N N N L L C F V F E V L K T F A P N S L
45 tccccgctcctgtcgacgctcgaagtggcgtcaagcttatcgccgacacctggccacc
S P L L S T L E V P L K L I A D T L A T
ccgctcttgagcctggcctgcctggaaggatatgaccgacgggtggcgagccgctg
P L L S L A C P A W K D M T D G G E P L
tgggatggcattcagaacaggttccctggcgcgagcaaggccggatcgagtttgtag
50 W D G I Q N R F P G A S K A G S S L -
SEQ ID NO : 21
LENGTH : 438
TYPE : PRT
55 ORGANISM : *M. phaseolina*

- MKFSSALLLLSSSSSLVVDAFPALGAQNLEGLTPERLTAALKTVEKYRKEKRLIIDSSKPIDTTGDHA
 FQPPSETDQRGPCPGLNALANHGYSIRDGITSFAEVVTAINQVMGMGIELSLILGVMGTVWTGNPLS
 LDPGFSIGGTAPGDGSDNILGNLVGLLDPRGLQGSNWI ESDSSLTRDDLYLTGDAWTMNMTLFRD
 IYDRADEDGVISMDDLADQAARRWEYSIGHNPNFYYPVTGMVSRNAGYFFLGRLLSNHTDEHPDGI
 5 LTQEVFKKFFAVYEDEQGNMEYRKGHETFPDNWYRKPV EYGLVPLNLDLVGWVLKHPELGSIGGNTG
 TVNSFSGLDLHSITGGVLNATSLENNNNLLCFVFEVLKTFAPNSLSPLLSTLEVPLKLIADTLATPL
 LSLACPAWKDMTDGGEPLWDGIQNRFP GASKAGSSL*
- SEQ ID NO : 22
 10 LENGTH : 1391 (including 150 bp 5' UTR and 150 bp 3' UTR)
 TYPE : DNA
 ORGANISM : *M. phaseolina*
 ATACTAACGCCGTGCAACCCCCGGGCAGCGCAGGTCTTGTTGATCGATATAAATGTTTTGTTTCGCG
 CCGCTATTGAAATTGGACACTCCAAGTCTTTCCATACATTCTTTCCCTATTGATCAATTGCTG
 15 CAAAAAACATTCCATCATGAAGCTCACCGTCTGTGCCACGACCCCTTTGCTTCGCTTTGGTTTATGGA
 CAAGGCTCCTACGAGGGGTGGAAGCCAGCTGGGCCAGACGACTGTATGTTAGTGAATTTCTACGT
 TTCTTTGATTTGCGCTGATGTACATCTACAGTTGCGGGCCCTTGCCCTATGATGAATACCTTGCC
 AACCATGGCTTTCTCCCCACGATGGCAGGAATATCACGAAAGCCAACGCAATCCACGCTCTCAACA
 CAGCTATCAACTTCAACACTTCCCTCGCTGCTATCATGTGGGAGCAGGCTATCATTGCAAACCCGGA
 20 GCCCAATGCTACGTTCTTCACTCTGTACGTGACTTCAAGCAAGCGTCTTTTGAGCTACCCTGAGTAG
 GGGGCTGCTCCGAAAGGCGACTTATCTAAACCTCCTCTTTCCACTATGTGAAGCTCTGACATTAAT
 AATATTGAACAGTGACCATCTTAATCGTCAACAGTCTTGAGCAGCATGCCAGCTTGAGGTGAGTG
 GAAGCCGCTTTCTCCAGCCTATTCCAACAAATCTCCTGACCAACACTCCTCTTCAGCCGATCCGAC
 GCCTTCTTCGGCAACAACACGCTCTTCAACCAAATCTCTCGACGTCTCTCGCGCGTGGTGGACGG
 25 AGGAAACCGTAGACGCCAAGATGCTGGCCAACAGCAAGTTGTTCCGGCAGATCGAGTCGCGAGCCGC
 CAACCCGAATTACACCTTCAACCAAATCTACCGAGGCCTTTAGCTTGGGCGAGGTGGCTGCTCCCATC
 ATCGTCTTCGGCGACACGCGCGCCGACCGTCAACAGGAGTCTGGTCGAGTACTTCTTCGGTGAGC
 CAAGACCTCAGAGACTTTGGTCTGCAAGGGTTCAAATTACTAATTATGGGGTGGTCTTGCAGAGAA
 CGAACGCTCCCCGACCGAGTTGGGCTGGACTAAGCAGGCTAATGATGTGTCTCTGGAGGTATCCTG
 30 GAGATCCAGGACCTCGTCCGCAACGCGACCAACCTGATCACCGATGCCCCGCTGCCGGCAGCGCCTC
 ACAAGCGGGACCTGCACGCCCCCTTACAGCCTCTAGATACGAATATAAAGCTGGCATGAAGATACCA
 GGGGTTTTTGAGAATTGTGTCTTCGGCGGGACGGGAGTGGTAGATTGAGCCTTGTGGGCTTCAGGT
 GTCTGGGGCATGTTTGTCTTGGTCTTTTACATGATTTCCCTAGCACGCC
- 35 SEQ ID NO : 23
 LENGTH : 780
 TYPE : DNA
 ORGANISM : *M. phaseolina*
 FEATURE NAME/KEY : CDS
- 40 LOCATION : (1).....(780)
 atgaagctcaccgtctgtgccacgaccttttgcttcgcttttggtttatggacaaggctcc
 M K L T V C A T T L C F A L V Y G Q G S
 tacgaggggtggaagccagctgggcccagacgacttttcgcgcccttgccctatgatgaat
 Y E G W K P A G P D D F R G P C P M M N
 45 accttgccaaccatggctttctccccacgatggcaggaatatcacgaaagccaacgca
 T L A N H G F L P H D G R N I T K A N A
 atccacgctctcaacacagctatcaacttcaacacttccctcgctgctatcatgtgggag
 I H A L N T A I N F N T S L A A I M W E
 caggctatcattgcaaaccggagcccaatgctacgttcttcactcttgaccatcttaat
 50 Q A I I A A N P E P N A T F F T L D H L N
 cgtcacaacgtcttgagcacgatgccagcttgagccgatccgacgccttcttcggcaac
 R H N V L E H D A S L S R S D A F F G N
 aaccacgtcttcaacaaactatcttcgacgtctctcgcgcggtggtagcggaggaaacc
 N H V F N Q T I F D V S R A W W T E E T
 55 gtagacgccaagatgctggccaacagcaagttgttcgggcagatcgagtcgcgagccgcc

V D A K M L A N S K L F R Q I E S R A A
aaccggaattacaccttcacccaaactaccgaggccttttagcttgggcgaggtggctgct
N P N Y T F T Q T T E A F S L G E V A A
cccatcatcgtcttcggcgaccacgcggccggcaccgtcaacaggagtctggtcaggtac
5 P I I V F G D H A A G T V N R S L V E Y
ttcttcgagaacgaacgcctcccgaccgagttgggctggactaagcaggctaataatgatgtg
F F E N E R L P T E L G W T K Q A N D V
tctctggaggtcatcctggagatccaggacctcgtccgcaacgcgaccaacctgatcacc
10 gatgccccgctgccggcagcgcctcacaagcgggacctgcacgcccccttacagcctctag
D A P L P A A P H K R D L H A P Y S L -

SEQ ID NO : 24
LENGTH : 259
15 TYPE : PRT
ORGANISM : *M. phaseolina*
MKLTVCATTLCFALVYGQGSYEGWKAPGDDFRGPCPMMNTLANHGFLPHDGRNITKANAIHALNTA
INFNTSLAAIMWEQAI IANPEPNATFFTL DHLNRHNVLEHDASLSRSDAFFGNHVFNQTI F DV SRA
WWTEETVDAKMLANSKLFRQIESRAANPNYFTTQTTEAFSLGEVA API IVFGDHAAGTVNRS LVEYF
20 FENERLPTELGWTKQANDVSLEVILEIQDLVRNATNLITDAPLPAAPHKRD L HAPYSL*

SEQ ID NO : 25
LENGTH : 1314 (including 150 bp 5' UTR and 150 bp 3' UTR)
TYPE : DNA
25 ORGANISM : *M. phaseolina*
GGCCCCGAAAGGGAGACAAAATACGAGATTCTCTATTACGCGCCCAAGAATCGACAACACCGCCC
ATCAGCTACCGCCGCCTTCGTTTACGTTCGTCCGCAGCAGCAACGCCCCGACGCTACAGTCAGTCAACA
GCCTCCAGCCGCCACGATGCCCAACGCAGTGCATCTGTCAATGCTCGTCTCACGCATGCGGTGCCG
ATCGCGGTTATCCGGGCTGGGAAGCGCAGCAAGTTGTGCGAGAAGCGCCCTCCAAGCACCACAACG
30 ACCTCTACGTGCCCAACCCAAGCCATCCGGTGCCGGGAAAGTGCCGTACATCCCGGACGAGGAAGA
GCACTACTTTGAGAAGCAGGTAAACGGCTCCGGCAATGGCTACTACCGGCGGTCTCTGCCCCGCA
GTCAACATCATGGCGAACAGGGGCTACATCAGCCGCTCGGGCCGGGACATCAGCTACGAGGAGATAG
CGATGGCATCGCGGGAGCTGTTCAACTTCGGCGACGACAACGTGAGCAGCGGCCCTGCAGACCGGC
AAAGTAAGCGGGCTCACCAACAATTCTTCTTGACAGATCATGATCGTGCTGGGGCCCAGCTTCGCG
35 GCGCACCCGGGCGCGAGCGCATCGACCTCGACATGCTGGCCGACGACGCGGTGCAGCACATCACCA
ACTGCCCTGCGGCGCCGACGCGGACGGACCGCGCTGGGCGACAACGTGAACCTGAACACGACGCT
GCTGGAGCAGCTGCTGGCGACGTCCAAGGACGGCGTCACGCTGACGCTCGAAGACGCGCCGAGCAC
CACCACTGCGGCACAACCAAGTCGCTGGCCGAGAACCCCGGCTTCCGCTTCAGCAACTCCGACGCCA
TCTGCTCGCTTGCGCAGTACGCCAACCTGTTTCGGTATCCTGGGCGGCGAGGGCAAGCATGGGCTCAA
40 CACGCTGTATGTGAAGACGTCAAGACCCTGTTTCGTGACGAAGACCTGCCGGACGGATACGGCCGG
AGGGAGCTGCCGTATTTCTCGACCGAGGCGAACAATACTACATCGACCGTATGGCCACCATCGGCT
TCGAGATCGAGCGGCCGTTCCCGGCCAACGACGCCGACCTGAAGGACATCGAGCCGGTGCAAGCCAG
ATTTGAAGTGGTGGACGGATGCTGAGCGGTGCAAAATTTAAAAAATTTTTTTTAGGCAGAAAGTC
AAGCATTTAATCGGGCTATACACATCATTCCTGTCAAACAAAATCATTTCTACAGCTGTACCGCC
45 TCGGAAAAGAATAACGGAGATTTAAAAAATTTTTTTTAC

SEQ ID NO : 26
LENGTH : 951
TYPE : DNA
50 ORGANISM : *M. phaseolina*
FEATURE NAME/KEY : CDS
LOCATION : (1).....(951)
atgccccaacgcagtgcatctgtcaatgctcgtcctcacgcgatgcggtgccgatcgcgggg
M P N A V H L S M L V L T H A V P I A G
55 tatccgggctgggaagcgcagcaagttgtcgcagaagcgcacctccaagcaccacaacgac

Y P G W E A Q Q V V A E A P S K H H N D
 ctctacgtgccccaaagccatccggtgccgggaaagtgccgtacatcccggagcag
 L Y V P N P S H P V P G K V P Y I P D E
 gaagagcactacttttgagaagcaggtaaacggctccggcaatggctactaccggcggtcg
 5 E E H Y F E K Q V N G S G N G Y Y R R S
 tcctgcccggcagtcacatcatggcgaacaggggctacatcagccgctcgggcccgggac
 S C P A V N I M A N R G Y I S R S G R D
 atcagctacgaggagatagcgatggcatcgcgaggctgttcaacttcggcgacgacaac
 I S Y E E I A M A S R E L F N F G D D N
 10 atcatgatcgtgctggggcccagcttcgcggcgcacccgggcccgcgagcgcacatcgacctc
 I M I V L G P S F A A H P G R E R I D L
 gacatgctggccgacgacgcggtgcagcacatcaccaactgccctgcggcgccgacgcgg
 D M L A D D A V Q H I T N C P A A P T R
 acggaccgcgcgctgggcgacaacgtgaacctgaacacgacgctgctggagcagctgctg
 15 T D R A L G D N V N L N T T L L E Q L L
 gcgacgtccaaggacggcggtcacgctgacgctcgaagacgcagccgagcaccaccacctg
 A T S K D G V T L T L E D A A E H H H L
 cggcacaaccagtcgctggccgagaacccccggcttcgcttcagcaactccgacgccatc
 R H N Q S L A E N P G F R F S N S D A I
 20 tgctcgcttgccgagtagcgaacctgttcggtatcctgggcccggcagggcaagcatggg
 C S L A Q Y A N L F G I L G R Q G K H G
 ctcaacacgctgtatgtggaagacgtcaagaccctgttcgctcgaagacctgccggac
 L N T L Y V E D V K T L F V D E D L P D
 ggatacggccggaggaggagctgccgtatttctcgaccgaggcgaacaactacatcgaccgt
 25 G Y G R R E L P Y F S T E A N N Y I D R
 atggcccaccacatcggttcgagatcgagcggcgttcccggccaacgacgcccacctg
 M A H H I G F E I E R P F P A N D A D L
 aaggacatcgagccggtgcaagccagatttgaagtggtagcgatgctga
 K D I E P V Q A R F E V V D G C -

30

SEQ ID NO : 27
 LENGTH : 316
 TYPE : PRT
 ORGANISM : *M. phaseolina*

35 MPNAVHLSMLVLTHAVPIAGYPGWAEQQVVAEAPSKHHNDLYVPNPSHPVPGKVPYIPDEEEHYFEK
 QVNGSGNGYYRRSSCPAVNIMANRGYISRSGRDISYEEIAMASRELNFNGDDNIMIVLGPSFAAHPG
 RERIDLDMLADDAVQHITNCPAAPTRTDRLGDNVNLNTTLLEQLLATSKDGVTLTLEDAAEHHHLR
 HNQSLAENPGFRFSNSDAICSLAQYANLFGILGRQKGHLNTLYVEDVKTLFVDEDLPDGYGRREL
 YFSTEANNYIDRMAHHIGFEIERPFPANDADLKDIEPVQARFEVVDGC*

40

SEQ ID NO : 28
 LENGTH : 1480 (including 150 bp 5' UTR and 150 bp 3' UTR)
 TYPE : DNA
 ORGANISM : *M. phaseolina*

45 ATCTGGCTTTTCTCTCTTCTGTGCGGGCGTCCCTTGCGCAACAGATACCCCATTCATCCCTTCAG
 TGCTTCTtCTTATCTCTTCGCGCGCTTTTCCCCAACACAGCCTCTTATCGCCTGTGCTCACACCAC
 GTTTCCCGCACACCCAATGGCTTCCACCGCCAGGTCCGTCTTCGCCCAGCGCGCTTCTGCGCTCC
 GCCCCGGCTCCATCAAGTCGAATGCCGCCGCTCATCTCGCTTCGCGCTCCCTACCCAAGCATTC
 GCCAGCAGTCTCGCCGCGGTACTCTTCCGAGGCCGGCTCCAAGTCTAACGGCCCCAACCCCGCCAT
 CTGGATTGGTGTCTCTCGCCGTCTGGGTGGCGCCGGGTACTATGCCTACAGCTCGGGTGGCGGCC
 50 CAGATCGCCTCCAAGGAACCTTCACCCCCAAGCCGAGGACTACCAGAAGGTCTACGACGCCATCG
 CCAAGGCCCTCGAAGAGCACGACTACGACGACGGCAGCTACGGCCCTGTCTGCTGAGACTGGC
 TTGGCACGCCAGCGGAACGTGAGTGACTTCCCCAACACTTCCAGCCCACATTGAACCACGCACTGA
 CGCCCTCCCTCACAGCTACGACAAGGAAACCGGCACCGGCGGCTCCAACGGCGCCACGATGCGCTTC
 GCGCCCGAGGCGGACCACGGCGCCAACGCCGGCTCAAGGCGGCCGCGACTTCTCGAGCCCATCA
 55 AGCAGCAGTTCCCGTGGATTACGTACTCGGACCTGTGGACGCTGGCAGGCGTCTGCGATCCAGGA

GATGCAGGGCCCCAAGGTGCCGTGGCGCCCCGGCCGCAGCGATCGCGACGTCTCCTTCTGCACGCCC
GACGGCCCGCCTGCCCCGACGCCTCCAAGGACCAGAACCACCTCCGCGCCATCTTCGGCCGCATGGGTT
GGAATGACCAGGAGATCGTGGCGCTGTTCGGCGCGCATGCGCTGGGGAGGTGCCATACGGATAGGAG
TGGATTTCGATGGCCCGTGGACCTTCAGCCCGACGACGCTGACGAACGATTATTTCAAGTTGTTGATC
5 GACGAGAAGTGGCAGTGGCGGAAGTGGGATGGACCTAAGCAGTTGGAGGACAAGAAGACGAAGAGCC
TGATGATGCTGCCGACGGATTACGCGTTGGTGCAGGACAAGAAGTTTAAGCCCTGGGTTCGAGAGGTA
CGCGAAGGATCAGGATGCCTTCTTCAAGGACTTCTCGAACGTGGTTATGAGGTTGTTTCGAGCTGGGC
GTGCCGTTCCAGAGTGGTGAGGACTCGAGGATTGTGTTTAAAGAGCAGCTTCGACTAGGCGTGCTTGG
CGGACGTTAATTCTGATCGACGGGGTTTGATGGGAAGTTGTAAAAGGTTCTATGACGATCAGTAAAG
10 AAGGGTTGTTTTTGCTTTTGAGTTTCGAGGACTAAAGACTAAGACAAGAGTAGCGCAAAGGTGGGAA
AGAATA

SEQ ID NO : 29
LENGTH : 1116
15 TYPE : DNA
ORGANISM : *M. phaseolina*
FEATURE NAME/KEY : CDS
LOCATION : (1).....(1116)

atggcttccaccgccaggtccgtcttcgcccgcagcgcgcttctgcgctccgccccggcc
20 M A S T A R S V F A R S A L L R S A P A
tccatcaagtccaatgccgcccgcctcatctcgcttcgccgtccctacccaagcattccgc
S I K S N A A R S S R F A V P T Q A F R
cagcagttctcgccgcggctactcttcgagggccggtccaagtctaacggccccaacccc
Q Q S R R G Y S S E A G S K S N G P N P
25 gccatctggattggtgctctcgccgtcctgggtggcgccgggtactatgcctacagctcg
A I W I G A L A V L G G A G Y Y A Y S S
ggtgccggcgcccagatcgctccaaggaacccttcaccccccaagcccaggactaccag
G A G A Q I A S K E P F T P K P E D Y Q
aaggtctacgacgccatcgccaaggccctcgaagagcacgacgactacgacgacggcagc
30 K V Y D A I A K A L E E H D D Y D D G S
tacggccctgtcctgctgagactggcttggcacgccagcggaacctacgacaaggaaacc
Y G P V L L R L A W H A S G T Y D K E T
ggcacccggcggtccaacggcgccacgatgcgcttcgcgcccagggcggaaccacggcgcc
G T G G S N G A T M R F A P E A D H G A
35 aacgccggcctcaaggcgcccgcgacttcctcgagcccacatcaagcagcagttcccgtgg
N A G L K A A R D F L E P I K Q Q F P W
attacgtactcggacctgtggacgctggcaggcgtcgctgcgatccaggagatgcagggc
I T Y S D L W T L A G V A A I Q E M Q G
cccaaggtgccgtggcgccccggcgcgacgacgacgtctccttctgcacgcccgcac
40 P K V P W R P G R S D R D V S F C T P D
ggccgcctgcccgcgcctccaaggaccagaaccacctccgcgcatcttcggccgcacg
G R L P D A S K D Q N H L R A I F G R M
ggttggaatgaccaggagatcggtggcgctgtcgggcgcgcatgcgctggggaggtgccat
G W N D Q E I V A L S G A H A L G R C H
45 acggataggagtggattcgatggcccgtggaccttcagcccgcgacgctgacgaacgat
T D R S G F D G P W T F S P T T L T N D
tatttcaagttgttgatcgacgagaagtggcagtgggcggaagtgggatggacctaagcag
Y F K L L I D E K W Q W R K W D G P K Q
ttggaggacaagaagacgaagagcctgatgatgctgccgacggattacgcgttggtgcag
50 L E D K K T K S L M M L P T D Y A L V Q
gacaagaagtttaagccctgggtcgagaggtacgcgaaggatcaggatgccttcttcaag
D K K F K P W V E R Y A K D Q D A F F K
gacttctcgaacgtggttatgaggttggttcgagctgggcgtgccgttcagagtggtgag
D F S N V V M R L F E L G V P F Q S G E
55 gactcgaggattgtgtttaagagcagcttcgactag

D S R I V F K S S F D -

SEQ ID NO : 30
LENGTH : 371
5 TYPE : PRT
ORGANISM : *M. phaseolina*
MASTARSVFARSALLRSAPASIKSNAARSSRFVPTQAFRQQSRRGYSSEAGSKSNGPNPAIWIGAL
AVLGGAGYYAYSSGAGAQIASKEPFTPKPEDYQKVYDAIAKALEEHDDYDDGSYGPVLLRLAWHASG
TYDKETGTGGSNGATMRFAPEADHGANAGLKAARDFLEPIKQQFPWITYSDLWTLAGVAAIQEMQGP
10 KVPWRPGRSDRDVSFCTPDGRLPDASKDQNLRLAIFGRMGWNDQEIVALSGAHALGRCHTDTRSGFDG
PWTFSPTTLTNDYFKLLIDKQWRKWDGPKQLEDKKTSLMMLPTDYALVQDKKFKPWVERYAKDQ
DAFFKDFSNVVMRLFELGVFPQSGEDSRIVFKSSFD*

SEQ ID NO : 31
15 LENGTH : 1981 (including 150 bp 5' UTR and 150 bp 3' UTR)
TYPE : DNA
ORGANISM : *M. phaseolina*
TAGAAGGCGCATGGAGTCGCACGCAGGGACCATGCGCAACACGGTGCCTGCAGAGAGGCGAAAGCCC
ATGCATATCACATTGATTTTTTAAAGAAGGAAGTGCAAGAAGCATTGAGACATCGCACTCACCTTCA
20 ACACCGCTATCGCGCGATGAAAGCCATCAGCATCGCCGTGTTGCGCCGCTCAGTGGTACCTCACACT
CTGGCAGACTATGTTTGGCCCTCGCAACATGACTTGTTGGAGGATATGTTGGCCATCCAACAAGGCT
ATATTTCGCATGGGCTTCACTGACTGTATGTCGACATTCACTTGAGCCTGAAGTAATGTCTCCCTACT
AAAGCATCGTCAAGTGTTGTTTCTTTCGGTTCACGGCAGCAACAGGCCCGGAGTAAACAACGCGGC
ACAATGGATTTCGACGGGTTTCCACGACTTCGCCACCCACGACTCGGCCGCTGGGACCGGCGGCTC
25 GATGCCCTCCCTCCTCTACGAGGTGCAACGGCCCGAGAACGAGGGCTCAGCCTTTAACGACACCTTCG
CCGACATGCACGACTTTATCAATCCCCGATCAAGCGCCTCGGATCTGATAGCGCTGGCCGTCGTGCG
ATCGGTTGCGGCTTGCGGCGGACCCAAAGATCCCCCTGCGAGCGGGACGAATTGATGCTGTGGAGGCG
GGCCCGGCCGCGGTTCCCAAGCCCGACGACTCACTGGAGAGCAGATCGATGCATTCGCGCGGACGG
GGTTCAACACCAGCGACATGATCGCCCTCGTTGCCCTGTGGCCATACCGTTCGGCGGCGTGCACAGCGT
30 AGATTTCCTCCGAGATCACCGGCGGCGAGAAAGACGTCTTGGACGTGCCGCAATTTGACAGCAGCGGC
ACCATCTTCGACACCGCAGTCGTGGACGAATACCTCGACAGCAACGGCGCCAACCCCTCGTCTTCG
GAGCCAACGACACCACGAACCTCGGACAAGCGCGTCTTCAGCGCCGACGGCAACAGCACCATGGCCAA
GCTCAAAGACCCCGCCACATTCAAAGCCACCTGCGCCGCCCTCTTCGAGCGTATGATCAACACCGTC
CCCTCATCCGTACCCCTCAGCGAACCCTCGAGCTGGCCGACATCAAGCCCTACATCGACAAGCTCG
35 AGCTCACACCCAACGCCTCCGCCCTCGCCTTCGAAGGCCGATCCGGCTGCGCACCTCCCCCGTCAC
CGGCCGCGACGCCGAGGGCACCAGCATCGCCCTCAATGTACCGACCGCGCTGGCGGGCGCAAGCTG
GTGCCGGCGCCGCGCGCGGTGTTGCGCGGCGGCACCTCGTACGGCTTCTTCGACGAGCAGTTAGCT
GGTTTCAATTTGCGACGCAGCTCGACGTGCGAGCCGCATCCAGGCCTTTGATATCCAGCTCACGAC
GGAGGCGACCGGACACGTGGAGACGTTGCAACGCTGGCACCGGCGGCTATCCTAGTCTCGACGAC
40 TTGCTATACTTGACGTGCAATCGTGCATGGACACGACTGCCACGGAGGGGAATATAACGGTGACGG
TTGCGGCGGCGGTGCGCGAGGATGCGGCGAAGGCGGGTGGCGGCCAGTGAGGATGGCGCATAA
GGTTTCAAGCAGATGGGTGTGATGTTGCCGAAGCTTGTGCTAGAGGCAGTGCCAATGGAGAGGTCAAAC
GTTTCGAGGGCGGGTATGTATTGTACGAGGTGGACATCCCAATCGATGCCGCTGGCTGGAGCACGA
AGTTTCGATGTTGTGTTGACGGCTGGGGGAGACGAGATTGTGTCTGGCCTGCACGGGACCAGCGATCT
45 TACCACATGTTTCGGGAACTGACCGGTTGATGGGCTTGGGGACTTGCCCTGAGTAGCATAGCATCGG
CGTGTTTTGGGTTTGTGTTTACAGGTGTGGAAGATCAGATGAAGGAAGAACCAACAGGTGATTGAACCT
ATGTCGCAAGTCAGCAATGCAGTGATGGTCTCGGCGTC

SEQ ID NO : 32
50 LENGTH : 1623
TYPE : DNA
ORGANISM : *M. phaseolina*
FEATURE NAME/KEY : CDS
LOCATION : (1).....(1623)
55 atgaaagccatcagcatcgccgtgttcgcccgtcagtggtacctcacactctggcagac

M K A I S I A V F A A S V V P H T L A D
 tatgtttggccctcgcaacatgacttgttgaggatatgttgccatccaacaaggctat
 Y V W P S Q H D L L E D M L A I Q Q G Y
 attcgcatgggcttcactgacttgggtgttccttgcggtcacggcagcaacaggcccgga
 5 I R M G F T D L V V P C G H G S N R P G
 gtaaacaacgcggcacaatggattcggacgggtttccacgacttcgccacccacgactcg
 V N N A A Q W I R T G F H D F A T H D S
 gccgctgggaccggcgccctcgatgcctccctcctctacgaggtcgaacggccccgagaac
 A A G T G G L D A S L L Y E V E R P E N
 10 gagggctcagcctttaacgacaccttcgccgacatgcacgactttatcaatccccgatca
 E G S A F N D T F A D M H D F I N P R S
 agcgctcggatctgatagcgctggcgctcgatcggttgcggttgcggttgcggttgcggttg
 S A S D L I A L A V V A S V A A C G G P
 aagatccccctgcgagcgggacgaattgatgctgtggaggcgggccccggcggttccc
 15 K I P L R A G R I D A V E A G P A G V P
 aagccccgacgactcactggagagcacgatcgatgcattcgcgcgacgggggttaacacc
 K P D D S L E S T I D A F A R T G F N T
 agcgacatgatcgccctcggttgctgtggccataccgtcgggcggtgcacagcgtagat
 S D M I A L V A C G H T V G G V H S V D
 20 ttccccgagatcacggcgggcgagaaagacgtcctggacgtgccgcaatttgacagcagc
 F P E I T G G E K D V L D V P Q F D S S
 ggcaccatcttcgacaccgcagtcgtggacgaatacctcgacagcaacggcgccaacccc
 G T I F D T A V V D E Y L D S N G A N P
 ctcgctcttcggagccaacgacaccacgaactcggacaagcgctcttcagcgccgacggc
 25 L V F G A N D T T N S D K R V F S A D G
 aacagcaccatggccaagctcaaagacccccgccacattcaaagccacctgcgcccgcctc
 N S T M A K L K D P A T F K A T C A A L
 ttcgagcgatgatcaacaccgtccccctcatccgtcaccctcagcgaacccatcgagctg
 F E R M I N T V P S S V T L S E P I E L
 30 gccgacatcaagccctacatcgacaagctcgagctcacacccaacgcctccgcccctcgcc
 A D I K P Y I D K L E L T P N A S A L A
 ttcgaaggccgcatccggctgcgcacctcccccgtcaccggcgcgacgccgagggcacc
 F E G R I R L R T S P V T G R D A E G T
 agcatcgccctcaatgtcaccgaccgcgctggcgggcgcaagctggtgccggcgccgcgc
 35 S I A L N V T D R A G G R K L V P A P R
 gccgtgttgcgggcgccacctcgtaaggcttcttcgacgagcagttcagctgggttcgaa
 A V L R G G T S Y G F F D E Q F S W F E
 tttgcgacgcagctcgacgtcgagccggcatccaggcctttgatatccagctcacgacg
 F A T Q L D V A A G I Q A F D I Q L T T
 40 gagggcaccggacacgtggagacgttcgacaacgctggcaccggcggtatcctagtctc
 E A T G H V E T F D N A G T G G Y P S L
 gacgacttgctatacttgacgtcgcaatcgatgcacgactgccacggaggggaat
 D D L L Y L Q S Q S C M D T T A T E G N
 ataacgggtgacggttgcgggcggtgcgcgaggatgcggcggaaggcggtgcgggcgcca
 45 I T V T V A A A V R E D A A K A G A A P
 gtggtgaggatggcgcataaggttcagcagatgggtgtgatgttgccgaagcttgtcgta
 V V R M A H K V Q Q M G V M L P K L V V
 gaggcagtgccaatggagaggtcaaacgtttcgcagggcggttatgtattgtacgaggtg
 E A V P M E R S N V S Q G G Y V L Y E V
 50 gacatcccaatcgatgccgctggctggagcacgaagttcgatgttggttgacggctggg
 D I P I D A A G W S T K F D V V L T A G
 ggagacgagattgtgtctggcctgcacgggaccagcgatcttaccacatgttcgggaaac
 G D E I V S G L H G T S D L T T C S G N
 tga
 55 -

SEQ ID NO : 33
LENGTH : 540
TYPE : PRT
5 ORGANISM : *M. phaseolina*
MKAISIAVFAASVVPHTLADYVWPSQHDLLLEDMLAIQQGYIRMGFTDLVVPCGHGNSRPGVNNAAQW
IRTGFHDFATHDSAAGTGGLDASLLYEVEPENECSAFNDTFADMHDFINPRSSASDLIALAVVASV
AACGGPKIPLRAGRIDAVEAGPAGVPKPDDSESTIDAFARTGFNTSDMIALVACGHTVGGVHSVDF
10 PEITGGEKDVLDVPQFDSSGTIFDTAVVDEYLDSENGANPLVFGANDTTNSDKRVFSADGNSTMAKLK
DPATFKATCAALFERMINTVPSSVTLSEPIELADIKPYIDKLELTPNASALAFEGRI RLRTSPVTGR
DAEGTSIALNVTDRAGGRKLVPAAPRAVLRGGTSYGFDEQFSWFEFATQLDVAAGIQAFDIQLTTEA
TGHVETFDNAGTGGYPSLDDLLYLQSQSCMDTTATEGNITVTVAADVREDAAKAGAAPVVRMAHKVQ
QMGVMLPKLVVEAVPMERSNVSQGGYVLYEVDIPIDAAGWSTKFDVVLTAGGDEIVSGLHGTSDLTT
CSGN*
15
SEQ ID NO : 34
LENGTH : 2012 (including 150 bp 5' UTR and 150 bp 3' UTR)
TYPE : DNA
ORGANISM : *M. phaseolina*
20 GGGGGAGGCCAATGCATGTCAGCAAAATACCTGTGGCTACCCCTGTTATGGCCACATCCAGCCCATT
TTGAATGGACGGTATAAAAATCTCTTCTGAAACCTTCAGAAAATTAAGGCAGGGACTATTGAAGGTTT
TGCCGTATCTGCCAAAATGCGGTTTCTCGGGGGCTTCTATCTACTCCTTGCTGCCACTCGCCACACA
CCTACGGCCAGAGCTGCGCTGCACTACCCAAATGCCCTCATTTCTCGCATGGAACACCTGCTGGTTG
ATACGGACGGCTCATTCAGGTCTGGTTTCAAGGACGCCATCAACCCCTGCACGAACCTACATTTTCAGG
25 TGCCCAAACGCTGGGGCGGCAGACCTCTGCACAGTGGCTCCGAGTTGCCTTCCATGATTTTCGTCACG
GCCCACGTCGACGAGGGCACTGGCGGGATCGACGCGTCCATCGGCTTCGAAACTCTCCGAGCAGAAG
ATTCGGGTCCGCATTCAATGACAGTTTTCGCTTCTTTGCTCCGTTTCGTGGATGCGCAAACCTTCAG
TATACCCATCGAGCCTTCCCCGTGAGGGCCGTGGCATGCGCTGACGTCCTTGCACTGGCCGACCT
CGTAGCCCTCTCTGTGGTGACTTCTCTGGGCCACTGCGGTGGTCTGCATGTCCCATATCGAGCGGGC
30 CGTATCGATGCTACGGGCGGAGGGCCGTTTCGGCGTTCCCGAACCCGAGACAAGCCTGGAAGAGACCC
TGGAAGAGTTTGCCAATGCTGGTTTCAATGCTGAAGATGCCATTGGATTAACGGCGTGCGGGCATTCT
TCTCGGCCGCGTCCATCACGGCGGGTTCCCCAACGTCGTGCCCGAATCGGCCATAGCACCAAACAAC
ACCGCGGGCGGCGTGAACCTGGACTCCACACGGGATAAATTCGACATCAGCATTGTCAAAGAATAACC
TCGGCAACTATGGGCAGCGCGGCGGACCTCTCGTTACCAAGTGACAACGTGACTGTCCGCTCGGATCT
35 TCGGCTGTACGAAAGCGATCAGAACAGGACAATGCAAGCTCTCGGTGAGTCAAAAGAATACTTCTTT
AGCACCTGTGGAATCTATTTGAGAGGATGATCAACACCGTTCCGCGCGAGGTCACTTTGTGATG
TCATCCATCCGATGACGGTGCAGCCGGTGAATTTACGTTTCGATATCATCAATGACCAGGCGCTGAG
GTTATCAGGAGTAGTGCGGTGAGCTTCCAAATAGAGCTGTTTCGGTCTGCACGCAACTGACCGAGC
CCCGCAGTATTTGCCCTCAGATAATGCTGCACCGTCGACGCTCGAGGTCTCACTCGCCGACAAAGCC
40 GGAAAGACTATGGCATCCATTACAGCAAGGGTTATTGAAGAGAAAGGGAATAGTTTCTGGGGGGCCA
CAGCTTACTACCCGGTCTTTTTGACATAAACCTTGCTGGGATTGCTTCTCGCAACAATCTTCCTGG
GAAGCTCCAGGTTTCGACAGCATCTCCTCAGACATTTGAGCTGCAACCGGAGCTGTTTTTTCATACCA
TCCCGTTCTAGCCCTGGCACGGGGATAAGTGTGGGGGCTGCCATAGGTGCTGCTGCGCGGTCCCGCA
ACTCGACTCTGAGTGTAGAGAGTGTGGAAGCCGTGGTCAGTGTGCCGATATCCAGACGGGAACACT
45 GGCACCGAAGGTCGAGAAGCATGAGTTGAATCTCGAAAGAGATCAAGATATTGGTTTGTACTCTATA
TTCAAGGGGAACCTAAGCGATGATTTGGCTTTCAACCTGCAGACGACCGTTGATATCACGGCAACTT
TTTCAGACGGCACTGTCTGGCAAGATAGTTACAACAGATTTGCAGTGCCGTAGAGCATCCTGAAAAT
GTCTTCGTCAAAATGCCCTTCATAGGGCCAGCAACAAATTTTCAGGCAGATATGTAGCTAGAGAGTCA
TTCAAAATACAAATGTCTTGGTTGTGCAACAAGTTTCGTGAGACGCTGCTCATGCACAATACAAGTGAG
50 CC
SEQ ID NO : 35
LENGTH : 1599
TYPE : DNA
55 ORGANISM : *M. phaseolina*

FEATURE NAME/KEY : CDS

LOCATION : (1).....(1599)

atgcggttttctcgggggcttctatctactccttgctgccactcgccacacacctacggcc
M R F L G G F Y L L L A A T R H T P T A
5 agagctgcgctgcactacccaaatgccctcatttctcgcatggaacacctgctggtgat
R A A L H Y P N A L I S R M E H L L V D
acggacggctcattcaggtctggtttcaaggacgccatcaaccctgcacgaactacatt
T D G S F R S G F K D A I N P C T N Y I
10 tcaggtgccc aaacgctggggcggcagacctctgcacagtggctccgagttgccttccat
S G A Q T L G R Q T S A Q W L R V A F H
gatttcgtcacggccacgtcgacgagggcactggcgggatcgacgcgtccatcggcttc
D F V T A H V D E G T G G I D A S I G F
gaaactctccgagcagaagattccgggtccgcattcaatgacagtttcgccttctttgct
E T L R A E D S G S A F N D S F A F F A
15 ccggttcgtggatgcgcaaacttccatggccgacctcgtagccctctctgtggtgacttct
P F V D A Q T S M A D L V A L S V V T S
ctgggccactgcgggtggtctgcatgtcccatatcgagcggggcgtatcgatgctacgggc
L G H C G G L H V P Y R A G R I D A T G
ggagggccggttcggcggttcccgaacccgagacaagcctggaagagaccctggaagagttt
20 G G P F G V P E P E T S L E E T L E E F
gccaatgctggtttcaatgctgaagatgccattggattaacggcgtgcgggcatttctctc
A N A G F N A E D A I G L T A C G H S L
ggccgcgtccatcacggcgggttccccaacgtcgtgcccgaatcggccatagcaccaaac
G R V H H G G F P N V V P E S A I A P N
25 aacaccgcggggcggcggtgaacctggactccacacgggataaattcgacatcagcattgtc
N T A G G V N L D S T R D K F D I S I V
aaagaatacctcggaactatgggcagcgcggcgacacctctcgttaccagtgacaacgtg
K E Y L G N Y G Q R G G P L V T S D N V
actgtccgctcggatcttcggctgtacgaaagcgatcagaacaggacaatgcaagctctc
30 T V R S D L R L Y E S D Q N R T M Q A L
ggtcagtcaaaagaatacttcttttagcacctgtggaaatctatttgagaggatgatcaac
G Q S K E Y F F S T C G N L F E R M I N
accgttccgcgcgaggtcactttgtcagatgtcatccatccgatgacggtgcagccggtg
T V P R E V T L S D V I H P M T V Q P V
35 aatttcacgttcgatatcatcaatgaccaggcgctgaggttatcaggagtagtgcggtat
N F T F D I I N D Q A L R L S G V V R Y
ttgccctcagataatgctgcaccgtcgacgctcgaggtctcactcgccgacaaagccgga
L P S D N A A P S T L E V S L A D K A G
aagactatggcatccattacagcaagggttattgaagagaaagggaatagtttctggggg
40 K T M A S I T A R V I E E K G N S F W G
gccacagcttactacccggtcggtttttgacataaaccttgctgggattgcttctcgcaac
A T A Y Y P V V F D I N L A G I A S R N
aatcttctcggaagctccaggttcgcacagcatctcctcagacatttgagctgcaaccg
N L P G K L Q V R T A S P Q T F E L Q P
45 gagctgtttttcataccatcccgttctagccctggcacggggataagtgtgggggctgcc
E L F F I P S R S S P G T G I S V G A A
ataggtgctgctgcgcggtcccgaactcgactctgagtgtagagagtgtggaagccgtg
I G A A A R S R N S T L S V E S V E A V
gtcagtggtgccggtatcccagacgggaacactggcaccgaaggctcgagaagcatgagttg
50 V S V P V S Q T G T L A P K V E K H E L
aatctcgaaagagatcaagatattgggttgactctatattcaaggggaacctaaagcgat
N L E R D Q D I G L Y S I F K G N L S D
gatttggtttcaacctgcagacgaccgttgatcacggcaactttttcagacggcact
D L A F N L Q T T V D I T A T F S D G T
55 gtctggcaagatagttacaacagatttgcagtgccgtag

V W Q D S Y N R F A V P -

SEQ ID NO : 36
LENGTH : 532
5 TYPE : PRT
ORGANISM : *M. phaseolina*
MRFLGGFYLLLLAATRHTPTARAALHYPNALISRMEHLLVDTDGSFRSGFKDAINPCTNYISGAQTLG
RQTSAQWLRVAFHDFVTAHVDEGTGGIDASIGFETLRAEDSGSAFNDSFAFFAPFVDAQTSMDLVA
LSVVTSLGHCGLHVPYRAGRIDATGGGPGFVPEPETSLEETLEEFANAGFNAEDAIGLTACGHSLG
10 RVHHGGFPNVVPESAIAPNNTAGGVNLDSTRDKFDISIVKEYLGNYGQRGGPLVTSDNVTVRSDLRL
YESDQNRMTQALGQSKEYFFSTCGNLFERMIN TVPREVTLSDVIHPMTVQPVNFTFDI INDQALRLS
GVVRYLPSDNAAPSTLEVSLADKAGKTMASITARVIEEKGNSFWGATAYYPVVFDINLAGIASRNNL
PGKLQVRTASPTFELQPELFFIPSRSSPGTGISVGAAIGAAARSRNSTLSVESVEAVSVPVVSQTG
TLAPKVEKHELNLERDQDIGLYSIFKGNLSDDLAFNLQTTVDITATFSDGTVWQDSYNRFAVP*

15 SEQ ID NO : 37
LENGTH : 2401 (including 150 bp 5' UTR and 150 bp 3' UTR)
TYPE : DNA
ORGANISM : *M. phaseolina*
TTTTAATATATTCTGCCGCTAAAACGTTGCCATGTGCTCCTGATTTTTCTCGACCGCCATTTCTCG
20 CCTCCGCATCGGCTCCCTGCTTCGGCGCGCTCGTCGCTAGCATCCAGTTTTCGCCAGTCCTTCCGTTT
CTCCCGCTCTTGAACCATGGCAAGGCATCCCGGCCTGACCTGGTGTGGGTTCGAGGCGTGGTCTAC
CACGCCATTGGCACCGCTGCTGCCCCGACATGGCCATCTTCCATGGATGAAGTGGAGGACATCATGG
TCCTCAACACCGGCTACCGCGCCCGCAGCTTCGCAGTGCCCGTCACACCCTGCGGCTTCTCGTCGCA
AGGCCCCGAGCGCTCCAAGCTGCCGAATGGATACGAACCGCCTTCCACGACATGGCTCCCGGCAGC
25 GTGTATACCGGCGTTCGAGGACTGGACGCATCGATAGCTTACGAAACACGGAGCTTGGAAAATCTCG
GCCCCGCTTCAACACCACACTAGCTACCTACGCGCCGTATCTGACAAGCAGATCTTCCATGGCTGA
CATCATTCGCTAGGAGTCTACACGGCGGTGCGGTTCATGCGGAGGTCCAATCGTGCCCTATCCGGACA
GGCAGAGTAGACGCAAAGGCAGCAGGCCCCGCAAGGTGTGCCTCTGCCGCAGAAATCTATCGGAACTT
TTCAAAACCAAGTTTCTCCGTACTGGCTTCAACACGACGGAGATGATCCAAGTGGTGGCGTGTGGCCA
30 CACTCTGGGCGGCGTGCACGCATCTGCCAACCCGGAGATCGTGCCCGTGGGGTTCGGCGGAGGACGGC
GTCGTCAAGTTCGACACGACGGACGCGTTTGACAACAAGGTTGTCAACGAGTACCTCTCGAATACAA
CCAAGAACTCGCTTGTGTGGGCCCCCTCTACTGCGAACGGCCGGAACCTCGGACGCTCGTGTCTTTCG
GGCGGATGGAATGCTACGGTCAGGGCTCTGGCTGACCCTGATACGTTCAACAGTGTTTGCCTAGG
ATGCTGCAGAAGATGATTGATGTTGTTCCAACGGGCGTGGTGTCTACTGACCCGATTTCAATCTATG
35 ATGTCAAACCCAGTGGGCTGCAGCTGACATTGCTTGGTGGAGGAGAGTCGGTAAAGCTTACGGGAGA
TATCCGTGTTAGGACTACGGAGCGCTCTGCGAGCCAGATTGAGAAGGTCGAGCTTGTCTACAAGGAC
CGCGAGGGGGCCGAATCCTCGACAGCTTTGAGCACCGAATCCTCAGGTTTCGGCCTCTGGGTTTCATG
ACAGCTTCGAGGTATAACTCATCCTAAGCCCCGTGTGGGATGCCACACTAACGGCCGAGAAAGTTCT
ACGGGGTCTCCGCAAACATCCCCACCGACTCCGGCATCTCCTCATTCAACGTCTCATACCCTCAC
40 CAGCGGCGAAACCGAACTTCACGACAATAATGGCAGCGGTTTCCCCCTCCAAGACACCGTCATCTTT
CAAAGCCCCGAGAGCTGCCTCAGCGGCACCACCATGACCGTCGCCGCCGCCGTCCTCAATACCGCCT
CCTCCGCCCCCACCTCAGCGTCACCCTCAAGGTCCCCAACTCCCGCTCCGTCTCCCGTCTCTCCA
GGTCAGCACAGTCGCCATGACGAAGAGCTCGTCTGTGCGCCCGTACGACCTCTACTCAACCACATAC
ACGCTAACCTCCGCCCCAACTCGCCGACACGCGCTTTGACGTCAAGCTCGGCGCTGCCGCCGCCGACG
45 CCTTCAAGTCTCTCCGCCGACCTCGGTGATGCTGCCAGGACCTGAGCCCCGAACCGCCCACTTCTTC
CAGCGCGCTAGCTCCTCGAGCACGGCTGCGCCGCCGGCCTCGTCTCTCTGCGGCACCAAGCTCC
TCTGACCTCCCGGCCCCCTCCCCCAGCACAAACACCCACGTCTCTCCACCCAATCTCCTCATCTACAA
CATTAGCATCATCGACCACCCCAACGCCCCAACACTCGCCTGCCCCGCCGCTGACGGCGCCACCTG
GACGCTATCCGGCGGCCAGAGTTGCGCGTCAAGTGCGGCAAGGACTACCAGGCCGGCCAGATCGGC
50 GTCACGTGGACGGCCAGCTTCGAGGCCTGTCTGCAGGCGTGCGTGGATACGGACACGTGCCAGGCGG
TCGCATTCTGTGGGGAGTGACAGGCGGGCGGGCAGTGCTACTTGAAGGACCAGAGCGCGGGCAGTGT
GGATGTTGAGGGGGTGTGGGGGGCGGTTCTGGAAAGCTGAGCGGTTCGGGCGATGGAGTAGGGGATAG

AGGGTTTGGGCTGGGGGGTAATGAATTACTTCTGATGAGCTTCTACTACTGCAGGTGGCACAAATCA
TGGCCTCTCATGGACCTCCGACGCCGATGCTGCCCCGCGTTTCAAGGTATTCTTGG

SEQ ID NO : 38
5 LENGTH : 2049
TYPE : DNA
ORGANISM : *M. phaseolina*
FEATURE NAME/KEY : CDS
LOCATION : (1).....(2049)
10 atggcaaggcatccccggcctgaccctgggtgtgggtcgcaggcgtggtctaccacgccatt
M A R H P G L T L V W V A G V V Y H A I
ggcaccgctgctgccccgacatggccatcttccatggatgaactggaggacatcatggtc
G T A A A P T W P S S M D E L E D I M V
ctcaacaccggctaccgcgcccgcagcttcgcagtgcccgtcacaccctgcggcttctcg
15 L N T G Y R A R S F A V P V T P C G F S
tcgcaaggccccggacgcgtccaagctgccgaatggatacgaaccgccttccacgacatg
S Q G P G R V Q A A E W I R T A F H D M
gctccccggcagcgtgtataccggcgctcggaggactggacgcacatcgatagcttacgaaaca
A P G S V Y T G V G G L D A S I A Y E T
20 cggagcttggaataatctcggccccgccttcaacaccacactagctacctacgcgcccgtat
R S L E N L G P A F N T T L A T Y A P Y
ctgacaagcagatcttccatggctgacatcattgcgctaggagtctacacggcggtgcgg
L T S R S S M A D I I A L G V Y T A V R
tcatgcggaggtccaatcgtgcctatccggacaggcagagtagacgcaaaggcagcaggc
25 S C G G P I V P I R T G R V D A K A A G
ccgcaagggtgtgcctctgccgcagaattctatcggaacttttcaaaaccagtttctccgt
P Q G V P L P Q N S I G T F Q N Q F L R
actggcttcaacacgacggagatgatccaagtgggtggcggtgtggccacactctggggggc
T G F N T T E M I Q V V A C G H T L G G
30 gtgcacgcacatctgccaaaccggagatcgtgcccggtgggggtcggcggaggacggcgctcgtc
V H A S A N P E I V P V G S A E D G V V
aagttcgacacgacggacgcgtttgacaacaagggtgtcaccgagtagctctcgaataca
K F D T T D A F D N K V V T E Y L S N T
accaagaactcgcttgttgtggggccctctactgcgaacggccggaactcggacgctcgt
35 T K N S L V V G P S T A N G R N S D A R
gtcttttgcggcggatggaaatgctacggtcagggctctggctgaccctgatacgttcaac
V F A A D G N A T V R A L A D P D T F N
agtgtttgcgctaggatgctgcagaagatgattgatgttgttccaacgggcgtggtgctc
S V C A R M L Q K M I D V V P T G V V L
40 actgacccgatttcaatctatgatgtcaaaccagtggtgctgcagctgacattgcttgggt
T D P I S I Y D V K P S G L Q L T L L G
ggaggagagtcggtaaagcttacgggagatatccgtgttaggactacggagcgtctcgcg
G G E S V K L T G D I R V R T T E R S A
agccagattgagaaggctcgagcttgtctacaaggaccgcgagggggccgaatcctcgaca
45 S Q I E K V E L V Y K D R E G A E S S T
gctttgagcaccgaatcctcaggttcggcctctgggttcgatgacagcttcgagttctac
A L S T E S S G S A S G F D D S F E F Y
ggggctctccgaaacatccccaccgactccggcatctcctcattcaacgtcctcatcacc
G V S A N I P T D S G I S S F N V L I T
50 ctccaccagcggcgaaaccgaacttcacgacaataatggcagcgggttccccctccaagac
L T S G E T E L H D N N G S G F P L Q D
accgtcatctttcaaagcccgagagctgcctcagcggcaccaccatgaccgtcgcggcc
T V I F Q S P Q S C L S G T T M T V A A
gccgtcctcaataccgcctcctccgccccaccctcagcgtcaccctcaagggtccccaac
55 A V L N T A S S A P T L S V T L K V P N

tccccgctccgctcctccccgtcctccaggtcagcacagtcgccatgacgaagagctcgtct
 S R S V L P V L Q V S T V A M T K S S S
 gtcggcccgtagcacctctactcaaccacatacacgctaacctccgccaactcgccgac
 V G P Y D L Y S T T Y T L T S A Q L A D
 5 acgcgctttgacgtcaagctcggcgctgccgccgacgccttcaagtcctccgcccac
 T R F D V K L G A A A A D A F K S S A D
 ctcggtgatgcctgccaggacctgagccccgaaccgcccacttcttccagcgcgcttagc
 L G D A C Q D L S P E P P T S S S A P S
 10 tcctcgagcacggctgcgcccgcggcctcgctcctcctctgccgcaccaagctcctctgac
 S S S T A A P P A S S S S A A P S S S D
 ctccccgccccctccccagcacaacacccacgtcctccacccaatctcctcatctaca
 L P A P S P S T T P T S S H P I S S S T
 acattagcatcatcgaccaccccaacgcccacaacactcgctgccccgcgctgacggc
 T L A S S T T P T P T T L A C P A A D G
 15 gccacctggacgtatccggcgccgaggaagttcgccgtcaagtgcggcaaggactaccag
 A T W T L S G G Q K F A V K C G K D Y Q
 gccggccagatcggcgtcacgtggacggccagcttcgaggcctgtctgcaggcggtgctg
 A G Q I G V T W T A S F E A C L Q A C V
 gatacgacacgtgccaggcggtcgcatctcggtggggagtgacagaggcgggcgggcagtg
 20 D T D T C Q A V A F V G S A E A G G Q C
 tacttgaaggaccagagcgcgggcagtggtgatgttgagggggtgtgggggcggttctg
 Y L K D Q S A G S V D V E G V W G A V L
 gaaagctga
 E S -

25
 SEQ ID NO : 39
 LENGTH : 682
 TYPE : PRT
 ORGANISM : *M. phaseolina*

30 MARHPGLTLVWVAGVVYHAIGTAAAPTWPSSMDELEDIMVLNTGYRARSFAVPVTPCGFSSQGPGRV
 QAAEWIRTAFHDMAPGSVYTGVGGLDASIAETRSLENLGPANFTTLATYAPYLTSRSSMADIIALG
 VYTAVRSCGGPIVPIRTGRVDAKAAGPQGVPLPQNSIGTFQNFQFLRTGFNTTEMIQVACGHTLGGV
 HASANPEIVPVGSAEDGVVKFDTTDAFDNKVVTEYLSNTTKNSLVVGPSTANGRNSDARVFAADGNA
 TVRALADPDTFNSVCARMLQKMIDVVPTGVVLTDPISIIYDVKPSGLQLTLGGGESVKLTGDIRVRT
 35 TERSASQIEKVELVYKDREGAESSTALSTESSGSASGFDDSFYFVGSANIPTDSGISSFNVLITLT
 SGETELHDNNGSGFPLQDTVIFQSPQSCLSGTTMTVAAVLNTASSAPTLVTLKVPNSRSVLPVLQ
 VSTVAMTKSSSVGPYDLYSTTYTLTSAQLADTRFDVKLGAAAADAFKSSADLGDACQDLSPEPPTSS
 SAPSSSSTAAPPASSSSAAPPSSDLPAPSPSTPTSSHPISSSTTLASSTPTPTTLACPAADGATW
 TLGGGQKFAVKCGKDYQAGQIGVTWTASFEACLQACVDTDCQAVAFVGSAGGQCYLKDQSAGSV
 40 DVEGVWGAVALS*

SEQ ID NO : 40
 LENGTH : 2004 (including 150 bp 5' UTR and 150 bp 3' UTR)
 TYPE : DNA
 45 ORGANISM : *M. phaseolina*

CCTTCTGAAATTTTCATGGCCAGCTTCTCGGTCTTTCTAATGAATTATAAGGCTATCTTCTGCAGC
 TTGTCGCTGCACGTTCTAGGATTCAACCAACCGTCATTCCTTCTCAAATCTCAGTCCAGTCGTTA
 CAGCTAATCACTTAATATGAAGCCCGCCGCTCTTGCCAGGCATTGGCCTGCTTAATGTCCTACCCATT
 ACCGCCGAATACGTCTGGCCTTCTAAATACGACTATTTGGAAGACCTGCTTTACCTTCAATCCGGTT
 50 ATCTGCGTGAGGGATTTGTGCGACGGTATGCATATATGAACAACTGCTGGTGTCCCCCACTAATGGC
 TTTTAGGTGTGGCTCCTTGTTCGTTTTCTCCGCTGGACCTGGCCGTCAAACCGCAGCGGAATGGGT
 CCGCACTGCATACCATGATATGGCCACTCATGATGCCGATGCTGGCACTGGTGGCTTGGACGCCTCT
 ATCATGTTTGAGACCGAGCGGGACGAAAACGTGGGCGATGCGTTCAATGGTACCTTCGGCTTTACAA
 ACAACTACTACAACATCAAAGCATCCGCTGCTGATCTTCTTGCACTCTCCACTGTCATCGCCGTTGG
 55 AACTGCGGTGGCCCGAAGATTCCTTTCCGTGTCGGTCGCGTGACGCCACGGAGGCTGGCCCTCTG

GGTGTTCCTCAAGCCGGATCAAGACGTTGATACGCACATTCAAATTTTTGCCAAGGCAGGCTTTAACA
 CCAGTAGGCCTTGAATTACCTGAGGTCCACCTACCAGCCGCTGACTAGAATAGGCGACATGATCACC
 ATGGTGGCCTGCGGCCACACCTTGGTGGCGTCCATGGCAAGGACTTCCCCGAGATCACTTTCAACG
 ACACGGAGACCAATTTCTGCAAGTTTGAAGGCAACAACCTCCTTCTCCAACCTTTGATAACACCGTCGT
 5 GACCGAGTATCTTGGCGGAAACCCCCCAACCCCTCGTCACCGGCAAGAACGAGACCAACAACAGC
 GATAAGCGCGTCTTTGGTGCCGACAACAACGCCACAATGCACTCCCTGTCGGACCCCTCCGTCTTCC
 AGTCCTCCTGCCAAGACATCCTCGCCCGCATGATCGACACCGTCCCCTCCAACGTCGCTCTCACC
 GCCTCTCGACCCAATCCTCATCAAGCCCTACATCCAAACCTTCTCCCTCGTCAACGCCACCCACCTC
 ACCCTGACCGGCCGCATCCGCGTCCGTACCGACTGGGACAGCTACACCGACCAGTCAGTCCACCTCA
 10 CCTACAACCCGCGCACAGCGCCCGCCAGAATGCGACCCTCAACACCACCATCCCCACCACCCGCGC
 CACCTTCCAGGGCGGCACCTCCAGCGGCATCTTTGGTGAAGTCTTCGCCTGGCAGAGTTCTCCGCC
 ACCCTCCCCACATCCAGCTCGATTACCGGCTTCACTGTACCGTCACGCGCGGCTCCACGGGCGAAT
 CCACCACCTACGACAACGCCGGCAGCACGAACGGCTACGCGCTCGACGACACGCTGCTCTACCAGAG
 CGCGCAGTCGTGCCGCGACGTCCGCCACCACAACCATACCGCTGCTGTGCGCAAGGACTTCCTCGCC
 15 CGAGGTGCAAAGGTGCGCGTCGAGATGGTGAACAGGGTGCCGCGCCAGGGCGTGACGTGCCGGCGC
 TAGAGGTGCAACCGTGGGGGGCGGAGACGGTCAAGGAGGTGGGCGAGTGGGTGTCGTGCAGGCTAA
 GGGTGAGTTGACGATGGAGAGCTTGAGCACAACGTTTGACGTCGTTGCGGGCGAGAAAAGGGTCGAG
 TTCCAAAGGACGAATGTGCTGGGGGAGGAGTGTGCGGCTCTGTGAGGCGTAACTTAAAAAAAAAAAA
 AAAGGAAGGATATATCAGTTTCTGGTACATACTTCGAATGAAAGTCTATGATTTCGTATGTCCATAAC
 20 ATTACTCTAGGCTTGAAACAACAATGCTGAATGTGCTTTATTGTGAGATAAAGAGTGTCTCT

SEQ ID NO : 41
 LENGTH : 1605
 TYPE : DNA
 25 ORGANISM : *M. phaseolina*
 FEATURE NAME/KEY : CDS
 LOCATION : (1).....(1605)
 atgaagcccgccgctcttgcaggcattggcctgcttaatgtcctacccattaccgcccga
 M K P A A L A G I G L L N V L P I T A E
 30 tacgtctggccttctaaatacgactatttggaagacctgctttaccttcaatccggttat
 Y V W P S K Y D Y L E D L L Y L Q S G Y
 ctgctgagggatttgcgacgggtgtggctccttgcttcttccgctggacctggc
 L R E G F V D G V A P C S F S S A G P G
 cgtcaaaccgcagcgaatgggtccgcactgcataccatgatatggccactcatgatgcc
 35 R Q T A A E W V R T A Y H D M A T H D A
 gatgctggcactggtggcttggacgcctctatcatgtttgagaccgagcgggacgaaaac
 D A G T G G L D A S I M F E T E R D E N
 gtgggcgatgcgttcaatggtaccttcggctttacaacaactactacaacatcaaagca
 V G D A F N G T F G F T N N Y Y N I K A
 40 tccgctgctgatcttcttgcactctccactgtcatcgccggttggaaactgcggtggcccg
 S A A D L L A L S T V I A V G N C G G P
 aagattcctttccgtgtcggtcgctggacgccacggaggtggccctctgggtgttccc
 K I P F R V G R V D A T E A G P L G V P
 aagccggatcaagacgttgatacgcacattcaaatttttgccaaggcaggctttaacacc
 45 K P D Q D V D T H I Q I F A K A G F N T
 agcgacatgatcaccatggtggcctgcggccacacccttggtggcgctccatggcaaggac
 S D M I T M V A C G H T L G G V H G K D
 ttccccgagatcactttcaacgacacggagaccaatttcgtcaagttcgaaggcaacaac
 F P E I T F N D T E T N F V K F E G N N
 50 tccttctccaactttgataacaccgtcgtgaccgagtatcttggcggaaccccccaac
 S F S N F D N T V V T E Y L G G N P P N
 cccctcgtcaccggcaagaacgagaccaacaacagcgataagcgctctttggtgccgac
 P L V T G K N E T N N S D K R V F G A D
 aacaacgccacaatgcactccctgtcggaccctccgtcttccagtcctcctgccaagac
 55 N N A T M H S L S D P S V F Q S S C Q D

atcctcgcccgcatgatcgacaccgtcccctccaacgtcgctctcaccgagcctctcgac
 I L A R M I D T V P S N V A L T E P L D
 ccaatcctcatcaagccctacatccaaaccttctccctcgtaacgccacccacctcacc
 P I L I K P Y I Q T F S L V N A T H L T
 5 ctgaccggccgcatccggtccgtaccgactgggacagctacaccgaccagtcagtccac
 L T G R I R V R T D W D S Y T D Q S V H
 ctcacctacaacccgcgcacagcgcccgccagaatgcgacctcaacaccaccatcccc
 L T Y N P R T A P A Q N A T L N T T I P
 10 accaccgcgccaccttccagggcgccacctccagcgccatcttgggtgaagtcttcgcc
 T T R A T F Q G G T S S G I F G E V F A
 tggcacgagttctccgccacccctccccacatccagctcgattaccggcttcaactgtcacc
 W H E F S A T L P T S S S I T G F T V T
 gtcacgcgcggctccacgggcgaatccaccacctacgacaacgccggcagcacgaacggc
 V T R G S T G E S T T Y D N A G S T N G
 15 tacgcgctcgacgacacgctgctctaccagagcgcgagtcgtgccgcgacgtcggcacc
 Y A L D D T L L Y Q S A Q S C R D V G T
 acaaccatcaccgctgctgtgcgcaaggacttctcgcccgaggtgcaaagggtcgccgtc
 T T I T A A V R K D F L A R G A K V A V
 gagatgggtgaacagggtgccgcgccaggcggtgtacgtgccggcgctagagggtcgaaccg
 20 E M V N R V P R Q G V Y V P A L E V E P
 tggggggcgagacgggtcaaggagggtcggcgagtggtcatcggtgcaggctaagggtgag
 W G A E T V K E V G E W V I V Q A K G E
 ttgacgatggagagcttgagcacaacgtttgacgtcgttgccggcgagaaaagggtcgag
 L T M E S L S T T F D V V A G E K R V E
 25 ttccaaaggacgaatgtgctgggggaggagtggtgcggctctgtga
 F Q R T N V L G E E C A A L -

SEQ ID NO : 42
 LENGTH : 534
 30 TYPE : PRT
 ORGANISM : *M. phaseolina*

MKPAALAGIGLLNLVLPITAEYVWPSKYDYLEDLLYLQSGYLREGFVDGVAPCSFSSAGPGRQTAAEWVRTAYH
 DMATHDADAGTGGLDASIMFETERDENVGDAFNCTFGFTNNYNIKASAADLLALSTVIAVGNCGPKIPFRV
 GRVDATEAGPLGVKPDQDQDTHIQIFAKAGFNTSDMITMVACGHTLGGVHGKDFPEITFNDTETNFKFEGN
 35 NSFSNFDNTVVTEYLGGNPPNPLVTGKNETNNSDKRVFGADNNATMHSLSDPVSFQSSCQDILARMIDTVPSN
 VALTEPLDPILIKPIYIQTFLVNATHLTGTGRIRVRTDWSYTDQSVHLTYNPRTPAQNATLNTTIPTTRAT
 FQGGTSSGIFGEVFAWHEFSATLPTSSSITGFTVTVTRGSTGESTTYDNAGSTNGYALDDTLTYQSAQSCRDV
 GTTTITAAVRKDFLARGAKVAVEMVNRVPRQGVVPALEVEPWGAETVKEVGEWVIVQAKGELTMESLSTTFD
 VVAGEKRVEFQRTNVLGEECAAL*

40 SEQ ID NO : 43
 LENGTH : 1414 (including 150 bp 5' UTR and 150 bp 3' UTR)
 TYPE : DNA
 ORGANISM : *M. phaseolina*

45 AGCTTGCTCTTCTTCTGTCTTTCTGCCCCCTTCTTCTCCAGACTCCTTTTCGCCGTAGATTTCTGCC
 TTTTGGACCTCGTTTTCTGCCCTCCACCAATAGCAAGCCAAGAGATTAGATTAGACATCGCCATCCC
 ATCGCCGACTCCAACAATGCCAGCAACCCAGGCGACTACGACGCCGTCCGCCACGACGTCAAGAAC
 CTCCTGCACCAGCCCGAGTACGACGACGGTTCCGCCGGGCCCCGTCTCGTCCGTCTCGCATGGTATG
 TTACGGCTACCCGCATCCTCCAGCCCAATCCGCCGTTTATCTGCTGTTCTGTTGCTCTGCCATCTTCT
 50 CTCCAGGGGCGAGCAAGTTTCCCAGCCTTTTTTTTTTGTCTTACGAACGGCATCTCGAACAGCCCCG
 TGACAACCACACCAGGCATTCGCGAGGGACCTACGACGCCCACTCTGACACAGGAGGCAGCAACGGT
 GCAGGCATGCGCTACGAGGCTGAAGGCGGCGACCCCGCCAATGCCGGCCTGCAGCACGCCCGCGTCT
 TCCTCGAGCCCATCAAGGCCGCGCACCCCTGGATAACCTACTCTGATCTGTGGACGCTGGCGGGCGT
 GGTGCCCATCAAGGAGATGGGCGGCCCGGACATCCCGTGGCAGCCCGGCCGACCGACTTCGTGAC
 55 GACAGCAAGCTGCCGCCGCGGGCGCCTGCCGGACGCCGCGCAGGGCGCTGACCACATCCGCTGGA

TTTTCTACCGCATGGGCTTCAACGATCAGGAAATTGTCGCCCTCAGCGGCGCCCACAACCTCGGCCG
CTGCCACGCCGACCGCTCCGGCTTCGACGGCGCCTGGGTCAACAACCCACCCGCTTCTCCAACCAG
TACTTTAAGCTCCTGACCTCGGTTCGAGTGGAAAGAGAAGACCTCCCCAGCGGCATCAAGCAGTTCG
CCTACTATGATGAGGACTCGGAGGAGGAGCTCATGATGCTGCCACCGATATCGCTCTCTTGACGA
5 CCCCTCCTTCGGCCGCTGGGTTCGAGAAGTATGCCGAGGACAAGGATGCCTTTTTTCGCAGACTTCTCA
AAGGTCTTTGCCAAGCTGATTGAGCTGGGCATAGTCAGAGATGAGAGCGGTGCGGTAATCAACACTG
ATAACGTCAAGGGCGGCTACATCTCTGCGCCCAAGAAGAGTGAGCTGCCTGGTGCTCCGGGTAAAGGC
TAATGAGGAGGCTGAGCCGCTCATGAAAGAGAATGAGAGGTTCAGGGCACGTCTGTAAGCTGGTTGG
TTTAGATTTCCTTTTTTTTTTTTTTTTCAAGACCGTTAGACTGCGCAAGCTAGAGGGGACGGATAGAT
10 GGACGATACCACCTAGATTCCTATGCCTTAAGAGGAGAAAGATAGTGCCTAGAGTTTTTCATAGAGAA
TGCAAAAC

SEQ ID NO : 44
LENGTH : 960
TYPE : DNA
15 ORGANISM : *M. phaseolina*
FEATURE NAME/KEY : CDS

LOCATION : (1).....(960)
atgccagcaacccaggcgactacgacgcccgtccgccacgacgtcaagaacctcctgcac
M P S N P G D Y D A V R H D V K N L L H
20 cagcccgagtacgacgacggttccgcgggcccgtcctcgctccgtctcgcatggcattcc
Q P E Y D D G S A G P V L V R L A W H S
gcagggacctacgacgcccactctgacacaggagcgacgaacggtgcaggcatgcgctac
A G T Y D A H S D T G G S N G A G M R Y
gaggctgaaggcggcgaccccgccaatgccggcctgcagcacgcccgcgtcttcctcgag
25 E A E G G D P A N A G L Q H A R V F L E
cccatcaaggccgcgcacccctggataacctactctgatctgtggacgctggcgggcggtg
P I K A A H P W I T Y S D L W T L A G V
gtcgccatcaaggagatggcgggcccgacatcccgtggcagcccggccgcaccgacttc
V A I K E M G G P D I P W Q P G R T D F
30 gtcgacgacagcaagctgccggcgggggccgctgccggacgcccgcgagggcgctgac
V D D S K L P P R G R L P D A A Q G A D
cacatccgctggattttctaccgcatgggcttcaacgatcaggaaattgtcgccctcagc
H I R W I F Y R M G F N D Q E I V A L S
ggcgcccaaacctcgccgctgccacgcccagccgctccggcttcgacggcgccctgggtc
35 G A H N L G R C H A D R S G F D G A W V
aacaacccccaccgcttctccaaccagtaactttaagctcctgacctcggtcgagtggaaa
N N P T R F S N Q Y F K L L T S V E W K
gagaagacctccccagcgcatcaagcagttcgctactatgatgaggactcggaggag
E K T L P S G I K Q F A Y Y D E D S E E
40 gagctcatgatgctgccaccgatatcgctctcttgacgacccctccttcgggcccgtgg
E L M M L P T D I A L L H D P S F R P W
gtcgagaagtatgccgaggacaaggatgccttttttcgcagacttctcaaaggtctttgcc
V E K Y A E D K D A F F A D F S K V F A
aagctgattgagctgggcatagtcagagatgagagcggtgcggtaatcaacactgataac
45 K L I E L G I V R D E S G A V I N T D N
gtcaagggcggtctacatctctgcgcccagaagagtgagctgcctggtgctccgggtaag
V K G G Y I S A P K K S E L P G A P G K
gctaattgaggaggctgagccgctcatgaaagagaatgagagggttcagggcacgtctgtaa
A N E E A E P L M K E N E R F R A R L -
50

SEQ ID NO : 45
LENGTH : 319

TYPE : PRT

ORGANISM : *M. phaseolina*

5 MPSNPGDYDAVRHDKVNLHQPYYDDGSAGPVLVRLAWHSAGTYDAHSDTGGSNGAGMRYEAEAGGDPANAGLQ
HARVFLEPIKAAHPWITYSDLWTLAGVVAIKEMGGPDIPWQPGRTDFVDDSKLPGRGLPDAAQGADHIRWIF
YRMGFNDQEIVALSAGAHNLGRCHADRSFGDGAWVNNPTRFSNQYFKLLTSVEWKEKTLPSGIKQFAYYDEDSE
EELMMLPTDIALLDPSFRPWVEKYAEDKDAFFADFSKVFAKLIELGIVRDESGAVINTDNVKGYYISAPKKS
ELPGAPGKANEEAEPLMKENERFRARL*

SEQ ID NO : 46

10 LENGTH : 2160 (including 150 bp 5' UTR and 150 bp 3' UTR)

TYPE : DNA

ORGANISM : *M. phaseolina*

CAACTCTTTGGATCATTTCGCAGTTCTGCAGATTAGACTACTCTTTTCTCGCTCCACAATGAAGCTTG
CATCATGGCTGCTCCTCCCTCAAGTACTGGCAGCGCTGGGCGGCAGGTACGTGAATATAAATTGAC
15 TCTTGAGGCAAGCTGGATGGCTCAAGGTAGATGTCCCCGAAGAAACAAAGTGATAGTATCTCTGCTA
ACATGGACAGACGGGAACCCCTCGCGGTGTCTTAAGTATCAACGGCCAGACACCTGGTCCATTGATCT
GGGGATATGAAGGAGACACACTTCGCGTCACTGTGACCAATAAAATGTTTATTGAGGCTACTATGCA
TTGGTCAGAGTGAAGTCTGTCTGGACTGGGAGAATCAACTAACGGAAGCAGGCACGGTGTCTATCA
GGTCGACAAGTACTGGAACGACGGAGTACCTGGCGTGAAGTCAATGGCCATTGAATCCAGGGATTCTG
20 TATACTTACGAGTTTACTCTCACCAACCAAACTGGAAGCTACTTCTACCATGGCCACTTTGGACCCG
CATTTCGCGGACGGCCACGAGGCCCGCTGTGGATTGCACCGGCCCCCTGGAGACCCCGTCCGTATGA
GCTTGCGTCTGATGACCCGGCAGAGGTTGCAGCAATGCGCGCGGCCGAAGACAATCCGAGACACCTC
ATGGTTTCCGACTGGAAGTATGAGGGAATGGAAGTGTGATTGTGGGCTTCAGAGATGCAGGCATTG
CTCCGGCATGTTCTGCGTCCCTCGTGACAAATGGAAGGGCAGGACAACCTTGCTCGGCCAGATGA
25 TATCAAGAAATACGATCCCGAGGGTCGGAGGAATTCACCTGGGTGCCTTCCTCCTCCAGTCGGCGCT
GAGTTCACCAACAAGAGAGAATGCCGCGAGACTACCACCGACTTCGAGATCATTGAGCCGAAGAAG
GGGAGAAGTATATCTACATGAACCTTTATCCACCCTGGAGCCCACCATGAACTGCGAATCGCGGTGGA
CGAGCACGACATGATCATCGTGGCAGCTGACGGGGATTTTGTTCATGCCGAAAAAAGTCCAGGTACGT
TAATGCGAGAAGTTCGACTGAGCGGTGTGACCTATGGCTGCAGGCAATAAACCTCAACATGGGCGA
30 CAGGATCAGTGTCTGTTACCGCTAGACAAGAAGCCGGGGGAATACGCCATCCGCCTGTCTGTCATT
TCCGAGGAGCAATTGATTACGGGCTTGAGCATCTTGCGCTACCCCGGTGTGAGGAGCGCCGCAAAG
ACGGTATTATGCTGGCACCGGAAACAAAACCCCATATTGATCTGTTGGGGCGGATGGTCACTGAAGG
AGGTGTTCATGATGGATGAAATGACCGATTTGGCCCCCTTTCCGCCGCGCTCACCCCGAGCGACGTCT
GATCACACGTTTTCGGTTTTTATCAAACCGCACCGGCCGAGCACATGGATGCTGTGAGCGAGCCAC
35 ACCAAGGCTTCCGCCAGCAGATGCCTCCTATTATGTGGAACGAAGAGTCTCGTGCCCTACAACCAT
TCAGGGGATGAAGAATGGATCCACCGTAGACATCATCTTCGAGAGCCGCGCATACGCCATGCACCCCT
TTCCACAAACACAATCACAAGGCCTGGATTATTGGTAGAGGAAAGGGCTACTTCCGTTGGCCAGATG
TTGCTACTGCCATCTCGGAAGCTCCAGAGAATTTCAACCTGATCAACCCGCCGTTGCGAGATGGTGC
CCGGCTCGAAGCGGAAGAGGGATCCTGGACGGTGATCCGTTACACCATCACCTTTCTGCCATGAGC
40 ATGCTGCACTGCCATCGTATTCAGCACTTTGCGGTAAGTGTGTGATCTAGCCACCAACGAATGGTC
ACTGATTGAAACAGGCTGGACAACAGATAGTCCTTTTGGAGGGGAGGATGTGATGCAAAGCCCTCC
TGAGTACATCAAAAAATGACGCATGCGAGCTTTGTGCCGCACTCCGATACGGCCCCCTTGACTGA
GAGTTCCTCATGCGAGGCCAGAGCACGGAATGGGTAGTTGAAGTTAAACCTGCCACATAAAAAATA
GCTCGAATAACAGGATTTTGCTAGCTCATGGAAGTACCACTTGTTCTTTGCGTTTCACTTAATGG
45 CTGCGGTGAAAGCGAA

SEQ ID NO : 47

LENGTH : 1713

50 TYPE : DNA

ORGANISM : *M. phaseolina*

FEATURE NAME/KEY : CDS

LOCATION : (1).....(1713)

atggctcaaggtagatgtccccgaagaacaaagtgatagtatctctgctaacaatggaca
55 M A Q G R C P R R N K V I V S L L T W T

gacgggaaccctcgcggtgtcttaactatcaacggccagacacctgggtccattgatctgg
D G N P R G V L T I N G Q T P G P L I W
ggatatgaaggagacacacttcgcgctcactgtgaccaataaaatgtttattgaggctact
G Y E G D T L R V T V T N K M F I E A T
5 atgcattggcacggtgtctatcaggtcgacaagtactggaacgacggagtagctggcgtg
M H W H G V Y Q V D K Y W N D G V P G V
actcaatggccattgaatccagggattcgtatacttacgagtttactctcaccaaccaa
T Q W P I E S R D S Y T Y E F T L T N Q
10 actggaagctacttctaccatggccactttggacccgcatttcgcgacggccaacgaggg
T G S Y F Y H G H F G P A F A D G Q R G
ccgctgtggattgcaccggccccctggagaccccgctccgtatgagcttgctgctgatgac
P L W I A P A P W R P R P Y E L A S D D
ccggcagaggttgacgaatgcgcgcgccgaagacaatccgagacacctcatggtttcc
P A E V A A M R A A E D N P R H L M V S
15 gactggaactatgaggggaatggaagtgtgattgtgggcttcagagatgcaggcattgct
D W N Y E G M E V L I V G F R D A G I A
ccggcatgttctgcgtccctcgtgacaaatggaaagggcaggacaacttgccctcgccca
P A C S A S L V T N G K G R T T C L G P
gatgatatacaagaatacgcacccgaggggtcgagggaattcacttgggtgccttctcct
20 D D I K K Y D P E G R R N S L G C L P P
ccagtcggcgctgagttcaccaacaagagagaatgccgcgagactaccaccgacttcgag
P V G A E F T N K R E C R E T T T D F E
atcattcagggccaagaaggggagaagtatatctacatgaactttatccaccctggagcc
I I Q A E E G E K Y I Y M N F I H P G A
25 caccatgaactgcgaatcgcggtggacgagcagacatgatcatcgtggcagctgacggg
H H E L R I A V D E H D M I I V A A D G
gattttgtcatgccgaaaaaagtcaggcaataaacctcaacatggggcagacaggatcagt
D F V M P K K V Q A I N L N M G D R I S
30 gtccctggtagcgtacgacaagaagccgggggaatacgccatccgcctgtcgtccatttcc
V L V P L D K K P G E Y A I R L S S I S
gaggagcaattgattacgggcttgagcatcttgcgctaccccggtgtgcaggagcgccgc
E E Q L I T G L S I L R Y P G V Q E R R
aaagacggtattatgctggcaccggaacaaaaccccatattgatctgttggggcgatg
K D G I M L A P E T K P H I D L L G R M
35 gtcactgaaggaggtgtcatgatggatgaaatgaccgatttggccccctttccgccgcgc
V T E G G V M M D E M T D L A P F P P R
tcacccccagcgacgtctgatcacacgtttcggtttttatcaaaccgcaccggccccgagc
S P P A T S D H T F R F L S N R T G P S
acatggatgctgtcgagcgagccacaccaaggcttccgccagcagatgcctcctattatg
40 T W M L S S E P H Q G F R Q Q M P P I M
tggaacgaagagtctcgtggccctacaaccattcaggggatgaagaatggatccaccgta
W N E E S R G P T T I Q G M K N G S T V
gacatcatcttcgagagccgcgcatacgccatgcaccctttccacaaacacaatcacaag
D I I F E S R A Y A M H P F H K H N H K
45 gcctggattattggttagaggaagggtacttccgttggccagatgttgctactgccatc
A W I I G R G K G Y F R W P D V A T A I
tcggaagctccagagaatttcaacctgatcaaccgcggttgcgagatggtgcccggctc
S E A P E N F N L I N P P L R D G A R L
gaagcggaagagggatcctggacggtgatccgttacaccatcacctttcctgccatgagc
50 E A E E G S W T V I R Y T I T F P A M S
atgctgcactgccatcgtattcagcactttgcggctggacaacagatagtccttttggag
M L H C H R I Q H F A A G Q Q I V L L E
gggcaggatgtgatgcaaagccctcctgagtacatcaaaaaaatgacgcgatgcgagcttt
G Q D V M Q S P P E Y I K K M T H A S F
55 gtgccgcactccgatacgcccccttgactga

V P P L R Y G P L D -

SEQ ID NO : 48
LENGTH : 570
5 TYPE : PRT
ORGANISM : *M. phaseolina*

MAQGRCPRRNKVIVSLLTWTGDNPRGVLTINGQTPGPLIWGYEGDTLRVTVTNKMFIEATMHWHG
VYQVDKYWNDGVPVGTQWPIESRDSYTYEFTLTNQTSYFYHGHFGPAFADGQGRPLWIAPAPWRPRPY
ELASDDPAEVAAMRAAEDNPRHLMVSDWNYEGMEVLIVGFRDAGIAPACSASLVTNGKGRITCLGPD
10 DIKKYDPEGRNSLGCLPPPVGAEFTNKRECRETTTDFEIIQAEEGEKYIYMNFIHPGAHHELRIAV
DEHDMIIVAADGDFVMPKKVQAINLNMGDRISVLVPLDKKPGEYAIRLSSISEEQLITGLSILRYPG
VQERRKDGIMLAPETKPHIDLGRMVTEGGVMMDEMTDLAPFPSPSPATSDHTFRFLSNRTGPSTW
MLSSEPHQGFQRMPPIMWNEESRGPTTIQGMKNGSTVDIIFESRAYAMHPFHKNHKAWIIGRGKG
YFRWPDVATAISEAPENFNLINPLRDGARLEAEEGSWTVIRYITITFPAMSLHCHRIQHFAAGQQI
15 VLLEGQDVMQSPPEYIKKMTASFPVPLRYGPLD*

SEQ ID NO : 49
LENGTH : 2269 (including 150 bp 5' UTR and 150 bp 3' UTR)
20 TYPE : DNA

ORGANISM : *M. phaseolina*
AGTATGTGCGTTGATCCCGCTGTCTATTGAGCACCAGAGCACTGTCCAGCCACCTTGAGCTATCTC
AAGGGGCTATCTCATCTGGTCATCTTCGCTGGGGCATCGGTTGCCTTCTCAACCCTTCTCAATCCC
CTCACGCTTCTGCAACATGTTCTTCGGCTCCCTCCACTTGGGCATCGGCGCCCTATTGGTTGCCGGC
ACTCTTGCTGGCGACGACAAGTGGCTTAGCCCCGTCTACAAGAACTTTTACGAGTTCCCCCTACCTA
25 AGCCACCAATCAAGGAAGCGAAAGCGTAAGTCAACTGATATTTCTCTCGCTCGTCATTTGCATGCCT
AATCTTCGCAGGAAATATACCAACCCGACTACCGGTGCTGTGATCAACTACTACGAAATCACCATCT
CACCCCTGCAGCAACAGGTTTATCCTGGCCTTGGCAAGGCAAACCTCGTTGGCTACGATGGTATCTC
TCCCGGTCCCCTTTTAAAGATGGAGAGGGGAGAAGAGGCTGTCTGTTCTGTTTCAACAAGGCCTCC
ATTCCCAATTCCGTCCATCTTCACGGCTCCTACTCCTTTGCCCCCTTCGATGGCTGGGCGGAGGATA
30 CGACCAGCCCAGGCCAATACAAGGACTACTACTACCCCAATGCCAGTCTGCCCGTACCCTCTGGTA
CCACGACCATGCCGTCTTCCACACTGCCGAGAACGCCTACTACGGTCAGGCAGGTTTCTACATCCTG
CACGACTCGGCTGAGGATAGTCTGGGTCTCCCGTCTGGAGACTACGACATCCCGCTCGGTCTGAGCT
CGAAGCAATACCAGTCCAACGGTGACCTTTTACGCCCGAATGGCGAGACGGATAGCCTTTTGGCGA
TGTTATCCATGTCAACGGCCAGCCCTGGCCGTACCTCAAGGTCGAGCCAGGAAGTACCGCTTCCGC
35 CTGCTTGATAACAAGCATTTCCTCGCTTCCAGCTGTCACTCCAAGACGATAAGAGCAAGAAGATTG
ACTTTAACGTATCGCCTCCGATGCCGGCTCCTGTCCAGCCCTGTTCCGACCAACCTGCTACACAT
TTCCATGGCCGAACGCTGGGAAATTGTCTGCTGACTTCTCCAGTACGCTGGCAAGAACATCACCATG
AAGAACGAGCGTGACGTGACGGCCGATGAAGACTACAACAGCACTGACAAGGTCATGCGCTTCGTAG
TAGGCAACAAGGTTACCTCGACTGCCAACAAACCTGCCTGGCAGCCTCCGACGCTGCTTTCCC
40 GCCGAATAAGTCTGGTGTGACAGGAGCTTCAAGTTCGAGCGCAAAGGCGGTGAATGGACTATCAAC
GGCGTTACCTTTGCCGACGTGAGAACCGTATTTAGGCAAGCCCCAACGCGGACAGGTTGAGGTCT
GGGAGCTCGAGAACTCTTCGGCGGCTGGTCTCACCCCGTTACATCCATCTCATCGACTTCCAGGT
TATTTCTCGCACTGGTGGCAAGCGTGATGTCTGCCTTACGAGAAGAACGGTCTCAAAGATGTCTGTC
TTGCTTGGCGTGAACGAGAAGGTCAGAGTTGTCTGCTCGCTTCCAGCCCTGGGAAGGTGTCTACATGT
45 TCCATTGCCACAACCTGATCCACGAGGACCACGATATGGTGCCTCCAGCATTCTCTGATTACTC
GCAACAAAGACTGACAAATAATTACAGATGGCCGCTTTCAATGTATCCACCCTTTCAGACTACGGCT
ACGACCAGAAGGAGACCTTTTCATCGACCCGATGGAGTCCCGCTGGCGCGCAAAGGATGTCAAGAC
CGAAGACTTCACAACCGATGCCATCCAGTCAAGCTTGGCGCTTTCGCTGAAATAAATCGCTACAAG
GACGTTGCGAAGATCGAAAGTGCTCTTGAAAATTATTGGAAGACCGCTCCACCCGGGTTCAAGATTA
50 GCACCACCTCCTCAACTCCGAGCTCAACCGCCGCCACCTCCACCGCTTCCAGCAGTGGCTCAAACAC
CTCTATTACCGCCCCCATTCAGTCCCCGGCCACTACTTCACCCGCGACCACTTCGACCAAGGCGGAT
GACAAGGGCAAGGCTAAGACTTCTACGACCAAAACGAAGTAACGAAATGGCTTTTAGATCACGCTCA
TTATAGATAAACTTGGGAGAATTTGGGTGCGTGTCTTTTGGATAGTTTGGTTCGGAGGAGCGCTCTC
TGTAATATGGGCCTCGCGAACTCTGTGGATATTTGTTTCTCGGTGTCTGTTAATATC
55

SEQ ID NO : 50
LENGTH : 1860
TYPE : DNA
ORGANISM : *M. phaseolina*
5 FEATURE NAME/KEY : CDS
LOCATION : (1).....(1860)
atgttcttcggctccctccacttgggcatcggcgccctattggttgccggcactcttgct
M F F G S L H L G I G A L L V A G T L A
ggcgacgacaagtggcttagccccgtctacaagaacttttacgagttccccctacctaag
10 G D D K W L S P V Y K N F Y E F P L P K
ccaccaatcaaggaagcgaaagcgaaatataccaacccgactaccggtgctgtgatcaac
P P I K E A K A K Y T N P T T G A V I N
tactacgaaatcaccatctcaccctgcagcaacaggtttatcctggccttggaaggca
Y Y E I T I S P L Q Q Q V Y P G L G K A
15 aacctcgttggctacgatggtatctctcccggtcccacttttaagatggagaggggagaa
N L V G Y D G I S P G P T F K M E R G E
gaggctgtcgttcgtttcatcaacaaggcctccattcccaattccgtccatcttcacggc
E A V V R F I N K A S I P N S V H L H G
tcctactcctttgcccccttcgatggctggcgaggatacaccagcccaggccaatac
20 S Y S F A P F D G W A E D T T S P G Q Y
aaggactactactacccaatgcccgagtctgcccgtagccctctggtaccacgaccatgcc
K D Y Y Y P N A Q S A R T L W Y H D H A
gtcttccacactgccgagaacgcctactacggtcaggcaggtttctacatcctgcacgac
V F H T A E N A Y Y G Q A G F Y I L H D
25 tcggctgaggatagtctgggtctcccgctctggagactacgacatcccgctcggtctgagc
S A E D S L G L P S G D Y D I P L G L S
tcgaagcaataccagtcacaacggtgaccttttcagcccgaatggcgagacggatagcctt
S K Q Y Q S N G D L F S P N G E T D S L
tttggcgatgttatccatgtcaacggccagccctggccgtacctcaaggtcgagcccagg
30 F G D V I H V N G Q P W P Y L K V E P R
aagtaccgcttccgcctgcttgatacaagcatttcccggtgccttccagctgtcactccaa
K Y R F R L L D T S I S R A F Q L S L Q
gacgataagagcaagaagattgactttaacgtcatcgccctccgatgccggcctcctgtcc
D D K S K K I D F N V I A S D A G L L S
35 agccctgttccgaccaacctgctacacatttccatggccgaacgctgggaaattgtcgtc
S P V P T N L L H I S M A E R W E I V V
gacttctcccagtagctggcaagaacatcaccatgaagaacgagcgtgacgtgcaggcc
D F S Q Y A G K N I T M K N E R D V Q A
gatgaagactacaacagcactgacaaggctcatgcgcttcgtagtaggcaacaagggttacc
40 D E D Y N S T D K V M R F V V G N K V T
tcgactgccacaacaacctgcctggcagcctccgcagcgtgcctttcccgcgaataag
S T A N N N L P G S L R S V P F P P N K
tctggtgttgacaggagcttcaagttcgagcgcaaaggcggtgaatggactatcaacggc
S G V D R S F K F E R K G G E W T I N G
45 gttacctttgcccagctcgagaacgctattctaggcaagccccaacgcggacaggttgag
V T F A D V E N R I L G K P Q R G Q V E
gtctgggagctcgagaactcttccggcggtggtctcaccctgttcacatccatctcatc
V W E L E N S S G G W S H P V H I H L I
gacttccagggttatttctcgactggtggcaagcgtgatgtcctgccttacgagaagaac
50 D F Q V I S R T G G K R D V L P Y E K N
ggtctcaaagatgtcgtcttgccttggcggtgaacgagaaggctcagagttgtcgctcgcttc
G L K D V V L L G V N E K V R V A R F
cagccctgggaagggtgtctacatgttccattgccacaacctgatccacgaggaccacgat
Q P W E G V Y M F H C H N L I H E D H D
55 atgatggccgctttcaatgtatccaccctttcagactacggctacgaccagaaggagacc

M M A A F N V S T L S D Y G Y D Q K E T
 cttttcatcgacccgatggagtcgctggcgcgcaaaggatgtcaagaccgaagacttc
 L F I D P M E S R W R A K D V K T E D F
 acaaccgatgccatccagtcgaagcttgccgctttcgctgaaataaatcgctacaaggac
 5 T T D A I Q S K L A A F A E I N R Y K D
 gttgcaagatcgaaagtgtcttgaaaattattggaagaccgctcccaccgggttcaag
 V A K I E S A L E N Y W K T A P T G F K
 attagcaccacctcctcaactccgagctcaaccgccgccacctccaccgcttccagcagt
 I S T T S S T P S S T A A T S T A S S S
 10 ggctcaaacacctctattaccgccccattcagtcggccactacttccaccgcgacc
 G S N T S I T A P I Q S P A T T S P A T
 acttcgaccaaggcgatgacaagggaaggctaagacttctacgaccaaacgaagtaa
 T S T K A D D K G K A K T S T T K T K -
 15 **SEQ ID NO : 51**
LENGTH : 619
TYPE : PRT
ORGANISM : *M. phaseolina*
 MFFGSLHLGIGALLVAGTLAGDDKWLSPVYKNFYEFPLPKPPIKEAKAKYTNPTTGAVINYEITIS
 20 PLQQQVYPGLGKANLVGYDGISPGPTFKMERGEEAVVRFINKASIPNSVHLHGSYSFAPFDGWAEDT
 TSPGQYKDYYYPNQASARTLWYHDHAFVHTAENAYYGQAGFYILHDSAEDSLGLPSGDYDIPLGLSS
 KQYQSNGLFSPNGETDSLFGDVIHVNGQPWPYLKVEPRKYRFRLLDTSISRQSLQDDKSKKID
 FNVIASDAGLLSPVPTNLLHISMAERWEIVVDFSQYAGKNI TMKNERDVQADEDYNSTDKVMRFVV
 25 GNKVTSTANNLPGSLRSVPFPNKGSDRSFKFERKGGEWTINGVTADVENRILGKPKRGQVEVW
 ELENSSGWVSHPVHIHLIDFQVISRTGGKRDVLPYEKNGLDVLLGVNEKVRVVARFQPWEGVYMF
 HCHNLIHEDHDMMAAFNVSTLSYGYDQKETLFDPMESRWRAKDVKTEDFTTDAIQSKLAFAEIN
 RYKDVAKIESALENYWKTAPTGFKISTTSSTPSSTAATSTASSSGSNTSITAPIQSPATTSPATTST
 KADDKGKAKTSTTKTK*
 30 **SEQ ID NO : 52**
LENGTH : 2423 (including 150 bp 5' UTR and 150 bp 3' UTR)
TYPE : DNA
ORGANISM : *M. phaseolina*
 AAAGGCCTTTGGCTCCCGCCAAAATTGTTTCATCCTCACGCTCACTCCTGCGCTCTTCCCTACAGACC
 35 TTTTGCCTGTAGCTTTAGCTTCACGGTCTTTTCATTCCCCTTCTCTGGCATTTCATCCACCGCGGGA
 AGCCTCAATTACCACAATGGTGTCCCTTAAGCAAATCGGTGCCACTCTGTTGGCACTGACTGCTCAA
 ACCTTCGCTGCTGCCATCCCTGAGGCCGAACCGGTGGACCTCGTCGCGCCGTCAAGCCACGACCACTA
 CGTCCACCACCTCCTCAACCACCTCGAGGGTCCCGATTCCCGATGTACTTGGGGCCCTTCGAGCAG
 40 GGGTTGCTGGAAGAACGGCTTCAGCATTGCCACTGACTTTGACACGAAGTGGCCATCTACTGGCAAG
 ACTGTCTCATATCGCTTGAAGTTACGAATGTCACCAACTGCGAGGACTATCAAAGCAAGGGAATTG
 GAGATGGCTTCTGCGAGCCGATGCTGCTCATCAACAATCAGTTCCCAGGGCCTACCAGTCAGTTTTT
 CCCTCCTCGATGCCGGGTGACAAGGGCGTAATGACTCGTACTTTCCAGTCAATGCGGAATGGGGAG
 ACAACCTTGAGATTACTGTTGTCAATAGTATGCAAGACAACGGCACCTCATTCCACTGGCACGGCAT
 45 TCGTCAGCTGAACATCATGCCAAAACGATGGTGCCAACGGCGTCACCGAGTGCCCTATTCTCCCGGC
 GGAAGCTTCACTTATAAGTTCAAGGCTACACAGTATGGTGAGTCTTTGCCTTCTCTTCTACCTTTTC
 CATTTTCATGCAAGCATCTTCATGTGCGTTCTGTTGAGTTTTGAGGCGGAAATACTCTTGAGCTTGCC
 CCGTTCCGTTTGTGAGCCACGTGCAAGGCCACCTGCTCCCACTTGTGTCATAATACTGACCGGCCCT
 TcCAGGAACAACATGGTACCATAGCCATCACTCTGCTCAGTACGGCGATGGGATCCAAGGTGCCATC
 50 GTGATCAATGGCCCGGCAACCGCCAATTACGACGAGGATTTAGGCCCGGTTGCCCTCACCAGAACTT
 ACGATGAGACGGCATGGACGAAGAACTGGCTGGCGCTGCACGTGGCATTCCCTCCTCAGCCCCCTCAA
 CATTCTCTTCAATGGCTCCATGGTCAACAGCACCGGCGGCGCGCTACAACACCATCTCAGTCAAG
 CAAGGCAAGACTTACCGGCTGCGCCTGATTAACATGAGCGTCGACACTTTCTTCGTATTCTCCATGG
 ACGGGCACGAGTTCCAGATCATCACGGCCGACCTCGTCCCGTGCACCTTACAATGCGACCTCGAT
 55 CATGATCGGCATCGGCCAGCGCTACGACATCGTCTTCAAGGCCAACCAGCCCGCTGCCAACTACTGG
 CTGCGTACCGAGATCGCCAGCTGCAGTGCCAACGCCATCACGGCCGAAGCCGACATCGTCCCGGCG

GCATCCTGAACTACGACACCATCGACAAGACGGATCTGCCAGTCTCCACCAAGTCCGTTATCGAGAC
 GACCGACTGCGCCGCCGAGCCCTACGACAAGCTGGTCCCCTGGTGGGAGACGCAGGTCCCCAAGGAC
 CAGTTCCTGACCCAGCTCGAGGGCATCGACCTGACGTTTCGCGCGGGCGCCACGGTCGGCAGCGAGA
 CTGGTCTTGTGCAGTGGTACCTGAACGACAGCGCCATGGTCTGCTGACTGGGCCAAACCGACTCTGGA
 5 GTACTTCTCCGAGGGAGACACTAATACTATACGTCTTCAATGAACGTTTTCCAGATGCCCGCGGAGGGG
 AAGTGGTCGTTCTGGATCATCCACAACAACGCGGCCGCTCTGCTCGACCACCCGATCCATCTCCACG
 GCCACGACTTTTTTCCACCTGGGCGCCGGCACCGGCACCTGGGACGGCAACGTGGACTCCTTGATCTT
 CGACAATCCTATGCGCAGGGACGTGATGATCTTGCCACAGGATGGCTTATTATCGCCTTTCCAGCG
 10 GACAACCCCGCGCGTGGTTGATGCATTGCCACATCGTAAGTACCCAACAAGCCCCATCTCTCTCTC
 TCTCTCTCATCAAAGATGACGGCAACTGACAAGCAACCAGGCATGGCACGTTACCGACGGGCTTTCC
 TTGCAGTTCGTTGAAAACCCAGGCTCATTACGCAGGACCTCTCGGGCATGAAGAGCAACTGCGCCG
 CCTGGAAAGAGTACGAGGAGAAGGCTTACTATGAGAAGGAGGTTGGCGATTCCGGCTTGTAACCCG
 TGACGGCGGGGATGAGGAGTTTATGACGAGATGTTCACTTTATACCTTCTACCACCACCACCACCT
 TTTCTCTTTCTTTTACCGACGTAGGGCTGCACTATCTGGCGCGTCTGTGGTCTGCTTTGCATATGC
 15 ATAAATACCTT

SEQ ID NO : 53
 LENGTH : 1824
 TYPE : DNA
 20 ORGANISM : *M. phaseolina*
 FEATURE NAME/KEY : CDS
 LOCATION : (1).....(1824)
 atggtgtcccttaagcaaatcggtgccactctgttggcactgactgctcaaacccttcgct
 M V S L K Q I G A T L L A L T A Q T F A
 25 gctgccatccctgaggccgaaccggtggacctcgctcgcccgtaagccacgaccactacg
 A A I P E A E P V D L V A R Q A T T T T
 tccaccacctcctcaaccacctcgagggttcccgattcccgatgtacttggggcccttcg
 S T T S S T T S R V P D S R C T W G P S
 agcagggggttgctggaagaacggcttcagcattgccactgactttgacacgaagtggcca
 30 S R G C W K N G F S I A T D F D T K W P
 tctactggcaagactgtctcatatcgcttggaagttacgaatgtcaccaactgcgaggac
 S T G K T V S Y R L E V T N V T N C E D
 tatcaaagcaagggaattggagatggcttctgcaggccgatgctgctcatcaacaatcag
 Y Q S K G I G D G F C R P M L L I N N Q
 35 ttcccgaggcctaccatcaatgcggaatggggagacaaccttgagattactgttgatcaat
 F P G P T I N A E W G D N L E I T V V N
 agtatgcaagacaacggcacctcattccactggcacggcattcgctcagctgaactcatgc
 S M Q D N G T S F H W H G I R Q L N S C
 caaaacgatggtgccaacggcgctcacccagtgccctattcctcccggcggaagcttcact
 40 Q N D G A N G V T E C P I P P G G S F T
 tataagttcaaggctacacagtatggaacaacatggtaccatagccatcactctgctcag
 Y K F K A T Q Y G T T W Y H S H H S A Q
 tacggcgatgggatccaaggtgccatcgatgaatggcccggaaccgccaattacgac
 Y G D G I Q G A I V I N G P A T A N Y D
 45 gaggatttaggccccgttgccctcaccgaaacctacgatgagacggcatggacgaagaac
 E D L G P V A L T E T Y D E T A W T K N
 tggctggcgctgcacgtggcattccctcctcagccctcaacattctcttcaatggctcc
 W L A L H V A F P P Q P L N I L F N G S
 atggtcaacagcaccggcgggcgccgctacaacaccatctcagtaagcaaggcaagact
 50 M V N S T G G R Y N T I S V K Q G K T
 taccggctgcgcctgattaacatgagcgtcgacactttcttcgtattctccatggacggg
 Y R L R L I N M S V D T F F V F S M D G
 cagagttccagatcatcacggccgacctcgtccccgtgcacccttacaatgcgacctcg
 H E F Q I I T A D L V P V H P Y N A T S
 55 atcatgatcggcacggccagcgtacgacatcgctcttcaaggccaaccagccccgtgccc

I M I G I G Q R Y D I V F K A N Q P A A
 aactactggctgcgtaccgagatcgccagctgcagtgccaacgccatcacggccgaagcc
 N Y W L R T E I A S C S A N A I T A E A
 gacatcgtccccggcgccatcctgaactacgacaccatcgacaagacggatctgccagtc
 5 D I V P G G I L N Y D T I D K T D L P V
 tccaccaagtccgttatcgagacgaccgactgcgcccgcgagccctacgacaagctggtc
 S T K S V I E T T D C A A E P Y D K L V
 ccctgggtgggagacgcaggtccccaaggaccagttcctgaccagctcgagggcatcgac
 P W W E T Q V P K D Q F L T Q L E G I D
 10 ctgacgttcgcgccggcgccacggctcggcagcagagactggctctgtgcagtggtacctg
 L T F A A G A T V G S E T G L V Q W Y L
 aacgacagcgccatggctcgtcgactgggccaaccgactctggagtacttctccgagggga
 N D S A M V V D W A K P T L E Y F S E G
 gacactaactatacgtcttcaatgaacgttttccagatgcccgcgagggggaagtggctcg
 15 D T N Y T S S M N V F Q M P A E G K W S
 ttctggatcatccacaacaacgcggccgctctgctcgaccacccgatccatctccacggc
 F W I I H N N A A A L L D H P I H L H G
 cacgactttttccacctgggcgcggcgaccggcacctgggacggcaacgtggactccttg
 H D F F H L G A G T G T W D G N V D S L
 20 atcttcgacaatcctatgcgcagggacgtgatgatcttgcccacaggatggcttattatc
 I F D N P M R R D V M I L P T G W L I I
 gcctttccagcggacaaccccgcgcggtggttgatgcattgccacatcgcatggcacgtt
 A F P A D N P G A W L M H C H I A W H V
 accgacgggctttccttgagttcgttgaaaaccaggctcattcacgcaggacctctcg
 25 T D G L S L Q F V E N P G S F T Q D L S
 ggcataagagcaactgcgcgcctggaaagagtacgaggagaaggcttactatgagaag
 G M K S N C A A W K E Y E E K A Y Y E K
 gaggttggcgattccggctttaa
 E V G D S G L -

30

SEQ ID NO : 54
 LENGTH : 607
 TYPE : PRT
 ORGANISM : *M. phaseolina*

35 MVSLKQIGATLLALTAQTFAAAIPEAEFVDLVARQATTTTSTTSSTTSRVPDSRCTWGPSSRGCWKN
 GFSIATDFDTKWPSTGKTVSYRLEVNTVNCEDYQSKGIGDGFRCRPMLLINNQFPGPTINAEWGDNL
 EITVNSMQDNGTSFHWHGIRQLNSCQNDGANGVTECPIPPGGSFYKFKATQYGTWYHSHSAQY
 GDGIQGAIVINGPATANYDEDLGPVALTETYDETAWTKNWLALHVAFPQPLNILFNGSMVNSTGGG
 RYNTISVKQGKTYRLRLINMSVDTEFFVFSMDGHEFQIIITADLVPVHPYNATSIMIGIGQRYDIVFKA
 40 NQPAANYWLRTEIASCSANAITAEADIVPGGILNYDTIDKTDLPVSTKSVIETTDCAAEPYDKLVPW
 WETQVPKDQFLTQLEGIDLTFAGATVGSETGLVQWYLNDSAMVVDWAKPTLEYFSEGDTNYTSSMN
 VFQMPAEGKWSFWIIHNNAALLDHPHHLHGDFHFLGAGTGTWDGNVDSLIFDNPMMRDVMILPTG
 WLIIAFPADNPGAWLMHCHIAWHVTDGLSLQFVENPGSFTQDLSGMKSNCAAWKEYEKEKAYYEKEVG
 DSGL*

45

SEQ ID NO : 55
 LENGTH : 2147 (including 150 bp 5' UTR and 150 bp 3' UTR)
 TYPE : DNA
 ORGANISM : *M. phaseolina*

50

GCCACGGCTCCATTTGGATCGTCACTCACCACCACCACCACAACCACTCTCTACTCACCTCTTCACC
 AGCCCCCTCTTTCTCCTCACTGGCATCCATTCGTTGAAGTCGCTGTCCCGTTTTCTTGTCTTTTCGTC
 TTCTTCCACCGTCAGAATGAGGGCTTCTTACCTCTCTGCGGCTGCCTTCCTGGGCCTCTCGGCTGCC
 GCGCCGCAAGCCGCCAGCACTTCTTCTTCTCTGCTTCAGCCAACGCCAGTTCCACCAGCTCAGCAG
 55 CTACTTCCACTTGCACTGGCAACACTGCCGACGACCGCACTGTGTGGTGCGACTACGACATCAGCAC

CGACTACTACAACGACGGACCCGACACGGGGGTCACCCGCGAGTACTACTTCGTCTGTCAGCGACGTG
 ACCGTCTCGCCCGATGGCATCTCGCGCTCCGCTATGGCGGTGAACGGCAGCATCCCCGGCCCCACCA
 TTTTCGCCGACTGGGGTGACACAGTGAAAGTTACTGTCTACAACGACCTCACCACGAGCGGCAACGG
 CTCTTCCATCCATTGGCACGGTATCCGGCAGAATAACGAACCAGAATGATGGTGTGGTGTCTATT
 5 ACGCAATGCCCGATTGCGGTGCGCGAGACCTACACCTACGAGTGGAAGGCCACGCAGTACGGCTCTT
 CCTGGTACCCTCTCACATTGGCCTGCAGGCCTGGGAGGGTGTTTTCGGTGGTATCATTATCAACGG
 TCCCCGCTACTGCAAATTACGACGAGGACCTCGGCATCATGTTTCTCAATGATTGGGATCACTCGACT
 GTTGACGAGCTCTACGATTACGCTCAGAGCAGCGGTCTCTCTACGCTTGACACCGGTCTCATTAACG
 10 GAACCAACATCTACAATGACTCCGGAACAGTTACTGGATCTCGCTGGGAGGCCAGCCTGACCGAGGG
 TACCAGCTACCGGCTCCGTCTTGTCAACGCTGCTGTAGACTCGCACTTCAAATTTTCGATCGATAAC
 CACACCTCCAGGTTATCGCCATGGACCTGGTCCCCATTGAGCCCTACGAGACTACTGTTCTGGACA
 TTGGCATGGGTGAGCGCTACGACGTCATTGTTACGGCAGACCAGGCTTCTGTTGCTTCTGATTTCTG
 GCTTCGCGCAATTCCCCAGACCGCCTGCTCGGACAACGATAACGCAGATGATATCAAGGGCATAATC
 15 CACTACGGATCATCAACTGGTACTCCGGAACCACTGCTTAGTAAGTTCCGATGTCCACATCTTCCG
 AGCTCTCCGCTAATGATTCAACAGTGATTACACTGATGCCTGTGTGATGAGGACAGCTCTGATCTC
 GTAAGTGCTCGAGATTACGGTCTGCTGGAAGAGTAGGCGCGCTGACTGTGATCTTTAGGTCCCGT
 ATGTCTCTAAGACTGCCACCTCCGGTACCTCCCTGGCCGAGGCTGTTTCCGTGGCTACAACCTCGGA
 CAACCTCTTCCGCTGGTACATGAACGAGACCTCTATGGAGGTCGAGTGGGAGAATCCAACCTTCTG
 20 CAGGTCTACAACGACAATCTGACGTTCACTGACACATCGGGTGTTGTTCAACTTGACACCGCAGACC
 AATGGTACTTCTTCGTCTATCGAGACCGACAACGCTGTGCCACACCCAATCCATCTTCACGGCCACGA
 CTTCTTCGTCTCTGGCTGCGGGCACCAGGCTCTTACAGTTACAGCTTACTCTGACTCTGGATAACCTT
 CCCCCCGCGACACGGCTATGCTTGACTCCTCTGGCTACTTGGTCTCTGGCTTTCGAGACCGACAACC
 CAGGTGCGTGGTTGATGCACTGCCACATCGGCTGGCACACCAGCGAGGGCTTTGCCCTTCAGATCTT
 25 GGAGCGCTACACCGAGATCCAGGATAGCCTGATCGACTACGACGTCCTCAATGACACCTGCTCGACT
 TGGTCTACTTACTCCGAGGCAAACCTCGATCGAGGAGGAGGACTCTGGTGTGTAAGGAAAACCTGAG
 TGACAATCCGTCTATGGCAGGTGTGCGGGCGCTTTGGAGCTCTCTCTATCTCTGTGAAAGATCTTG
 TATATAACGTGATGCCAGCCTCTCCCTGACATTTGGTGCTTCGGTTGATCTACATATATTTCTTAT
 TTA

30

SEQ ID NO : 56
 LENGTH : 1737
 TYPE : DNA
 ORGANISM : *M. phaseolina*
 35 FEATURE NAME/KEY : CDS
 LOCATION : (1).....(1737)

atgagggtcttcttacctctctgcggtgccttctctgggcctctcggtctgcgcgcccga
 M R A S Y L S A A A F L G L S A A A P Q
 gccgccagcacttcttcttctctgcttcagccaacgccagttccaccagctcagcagct
 40 A A S T S S S S A S A N A S S T S S A A
 acttccacttgcaactggaacactgcccagcagccgactgtgtggtgcaactacgacatc
 T S T C T G N T A D D R T V W C D Y D I
 agcaccgactactacaacgacggacccgacacgggggtcaccgcgagtaactacttcgtc
 S T D Y Y N D G P D T G V T R E Y Y F V
 45 gtcagcgacgtgaccgtctcgcccgatggcatctcgcgctccgctatggcggtgaacggc
 V S D V T V S P D G I S R S A M A V N G
 agcatccccggccccaccattttcgccgactgggggtgacacagtgaagttactgtctac
 S I P G P T I F A D W G D T V K V T V Y
 aacgacctcaccacgagcggcaacggctcttccatccattggcacggtatccggcagaac
 50 N D L T T S G N G S S I H W H G I R Q N
 tacacgaaccagaatgatggtgtggtgtctattacgaatgccgattgcggtcggcgag
 Y T N Q N D G V V S I T Q C P I A V G E
 acctacacctacgagtgaaggccacgcagtagggctcttctgtgtaccactctcacatt
 T Y T Y E W K A T Q Y G S S W Y H S H I
 55 ggcctgcaggcctgggaggggtgttttcgggtggtatcattatcaacggtcccgtactgca

G L Q A W E G V F G G I I I N G P A T A
 aattacgacgaggacctcggcatcatgtttctcaatgattgggatcactcgactgttgac
 N Y D E D L G I M F L N D W D H S T V D
 gagctctacgattcagctcagagcagcggctcctcctacgcttgacaccgggtctcattaac
 5 E L Y D S A Q S S G P P T L D T G L I N
 ggaaccaacatctacaatgactccggaacagttactggatctcgctgggaggccagcctg
 G T N I Y N D S G T V T G S R W E A S L
 accgaggggtaccagctaccgggtccgtcttgtcaacgctgctgtagactcgcacttcaaa
 T E G T S Y R L R L V N A A V D S H F K
 10 ttttcgatcgataaccacacctccagggttatcgccatggacctgggtccccattgagccc
 F S I D N H T L Q V I A M D L V P I E P
 tacgagactactgttctggacattggcatgggtcagcgtacgacgtcattgttacggca
 Y E T T V L D I G M G Q R Y D V I V T A
 gaccaggtcttctgttcttctgatttctggcttcgcgcaattccccagaccgctgctcg
 15 D Q A S V A S D F W L R A I P Q T A C S
 gacaacgataacgcagatgatatcaagggcataatccactacggatcatcaactgggtact
 D N D N A D D I K G I I H Y G S S T G T
 ccggaaaccactgcttatgattacactgatgcctgtgtcgatgaggacagctctgatctc
 P E T T A Y D Y T D A C V D E D S S D L
 20 gtcccgatgtctctaagactgccacctccggtacctccctggccgagggtgtttccgctc
 V P Y V S K T A T S G T S L A E A V S V
 ggctacaactcggacaacctcttccgctgggtacatgaacgagacctctatggaggtcgag
 G Y N S D N L F R W Y M N E T S M E V E
 tgggagaatccaaccttctgcaggtctacaacgacaatctgacgttcactgacacatcg
 25 W E N P T L L Q V Y N D N L T F T D T S
 ggtgttgttcaacttgacaccgcagaccaatgggtacttcttcgtcatcgagaccgacaac
 G V V Q L D T A D Q W Y F F V I E T D N
 gctgtgccacaccaatccatcttcacggccacgacttcttcgtcctggctgcgggcacc
 A V P H P I H L H G H D F F V L A A G T
 30 ggctcttacagttcagacgttactctgactctggataaccctccccgcgcgacacggct
 G S Y S S D V T L T L D N P P R R D T A
 atgcttgactcctctgggtacttgggtcctggcttttcgagaccgacaaccaggtgcgtgg
 M L D S S G Y L V L A F E T D N P G A W
 ttgatgcactgccacatcggctggcacaccagcgagggctttgcccttcagatcttgag
 35 L M H C H I G W H T S E G F A L Q I L E
 cgctacaccgagatccaggatagcctgatcgactacgacgtcctcaatgacacctgctcg
 R Y T E I Q D S L I D Y D V L N D T C S
 acttgggtctacttactccgaggcaactcgatcgaggaggaggactctgggtgtgtaa
 T W S T Y S E A N S I E E E D S G V -
 40

SEQ ID NO : 57
 LENGTH : 578
 TYPE : PRT
 ORGANISM : *M. phaseolina*

45 MRASYLSAAFLGLSAAAPQAASTSSSSASANASSTSSAATSTCTGNTADDRTVWCDYDISTDYND
 GPDTGVTREYYFVVS DVTVPDGI SRSAMAVNGSIPGPTIFADWGD TVKVTVYNDLTTSGNGSSIHW
 HGIRQNYTNQNDGVVSITQCPIAVGETYTYEWKATQYGSSWYHSHIGLQAWEGVFGGIIINGPATAN
 YDEDLGIMFLNDWDHSTVDELYDSAQSSGPPTLDTGLINGTNIYNDSGTVTGSRWEASLTEGTSYRL
 RLVNAAVD SHFKFSIDNHTLQVIAMD LVPIEPYETTVLDIGMGQRYDVIVTADQASVASDFWLRAIP
 50 QTACSDNDNADDIKGIIHYGSSTGTPETTA YDYTDACVDEDSSDLVPYVSKTATSGTSLAEAVSVGY
 NSDNLFWRWYMNETSMEVEWENPTLLQVYNDNLFTDTSGVVQLD TADQWYFFVIETDNAVPHPIHLH
 GHDFVFLAAGTGSYSSDVTLTLDNPPRRDTAMLDSSGYLVLA FETDNPGAWLMHCHIGWHTSEGFAL
 QILERYTEIQDSLIDYDVLNDTCSTWSTYSEANSIEEEDSGV*

55 SEQ ID NO : 58

LENGTH : 2302 (including 150 bp 5' UTR and 150 bp 3' UTR)
 TYPE : DNA
 ORGANISM : *M. phaseolina*

5 TGCGCCCTCCCGCTGCTGGGCACTCTTTTATAAAGGCAGCTCTCCACTCCTGCCCTGTGAATGCT
 TGCTCAAGGGCGCTCAGGCATAGGTAAGTAGGGTAAGTATTGAGGCGTCTGGCTTTGCGGCCGAATCT
 TGGGACGATTTTCAGCCATGACTCGCCTTCCGTTCGTCTCGGGCTCGTGGCTACGGCTTTGGCCAAG
 ACGGTCACGTGTTGACTGGGACATTGGCTGGGTTTCCAGGGCTCCCGATGGATTTCGAGCGGCCTGTCA
 TCGCAATCAACGGCCAATGGCCGCTCCCTGTGCTGGAGGCCGACGTCAACGACACCATCATCGCCAC
 TGTCCACAATTCTCTTGGCAACGAAACGACCAGCATCCACTGGCACGGCATGTGGCAGAGAGGCACG
 10 CCGGAGCAAGACGGCGGGGCTGGCGTACGCAGTGTCCGATCCCGCCTGGCGAGACTTTTCAGTACG
 AGTTCAAAGCATACCCGGCCGGTACTTTCTGGTACCACTCGCATGACATGGGCCAGTATCCCGATGG
 CCTGCGCGACCCATGATCATCCATGACCCGACTCCGAAACCCAGAAGAGCAGTGATGGTGAAGTC
 GTGCTCTATGTGTCCGACTGGTACCACGACCAGATGCCGCCGCTTATCCACAGCTTCTTGACACCC
 CCAATTTCAACGGCGCGATGCCCAACCCGAACTCCAGCTTGATCAACGATCAGCAGTCCACGTCCAT
 15 CAACATCCGTCCCGGCGAGAAGAAATACGTGCGCATCATCAACACGTCCGCCCTCGCCACGTACTAC
 CTGCAGTTTGGTGGGTTCGCTTCAGCCACCCCTCCCCTGCGGAAGTGACTGACGATTTTCAGACCAA
 CACAACATCACCGTTGTGCGCAATTGACGGTGTGACGGTCCGTACTACCCCTGTGCTTATGCTGTG
 GCTTCGTGCATACCCGTGCGCAGCTTCCCGCCGTTGCATGCCCGAGGCGATACAAGGTTTTAGTGCT
 GACCGTAGTCGTGCAGTCGAACCGCAGAGCTGGAAGGCCCTGGAGATCGTCCCCGCCAGCGGTACG
 20 ACTTCATCATCGAAGGTCTCGAGAACCCCAAGGAACCTACGCATTTCATCAACAAGATGGCTGTTCT
 CGGTCTGCAGAACGTCAACAGCCTGGTCTACGACGAGTCCTTCGGCGAGCCGGAGTCGTTTCAGCCTG
 AGCTCTGGCGATCTCGGAAGTGATTTTACCCTGGTGCCTCTAGATCACGAGCCTCTCTTGAATCCG
 TGGACCACACCATCACGATGGAGGTCAATAATTTGAACATTGATGGCGTTGGCTTTTCGGTACGGCTG
 ATCCCGTGGCCGGGAGAAATCTTGCTCACATGTGCCACAGCATCACTCAAGGCCCGGACCCGTACAT
 25 TTCACCCCGCACGCCTACCCTGTACACAGCCCTCAGCACCGGCTTCAACGCCACCGACCCAGAAATC
 TACGGCCAGGTGAACCCCTACGTGCTCAACGCCGGTGAAGTCTCGCGGCTCGTCTCAACAGCAACG
 ATCTCGTCACCGCCAACAACCTCTGGCCGCGGGCACCCATGCATCTGCACGGCCACGTTTTTCAGGT
 GGTCCGTACGTTCTCCGAGCACTGGGACGGCAACACCTCGTCCTTCCCCGCCACGCCCATGAAGCGT
 GACACCACCGTCTTATTCGCTGGCGGCAGCCTGGTGTCTCCAGTTCGGTGCCGACAACCCCGGTGTTT
 30 GGCTGTGTAAGTATTTTTTTTCCGATGCCCATGGTGCCTGGACGTGAGCTGATGAGGATGGGCCTT
 GCAGTTCACTGCCATATTGAGTGGCACCTAGACGCCGGCATGTCCGCTACAATCATCGAGGCGCCGC
 TCGACTTGCAGCGCGAGGGCATCAAGATCCCCAGCAGCATCTTGAATCGTGACAGCCCTTGAACCT
 GACCACTCAAGGCAATTGCGCCGGCAACACCGCCAACCTGGATGACACTGCCGCCTGCAGGGTCTAC
 GACACCGATCCATGGGGGTAGGTTCATATCGGAGTTTAAATTGAGCTTGAAGGACATGTGCTGACCGTT
 35 GCGTTTAGTGCGCTTATCACGGATGACGGTGGTGGAATAGTACCCTGAACGGAACCACTTATAAGA
 GAATTTAGTGTAATCTTAATACGTCTTCACATGTACACAACCTATGCATTGTATTCAAATTCTAC
 ATAAGCACTTCGACAGTAGTCTGAGTTGACTGACTAGGCTCGTGGACGGAGGACGCCGTTTCTCGT
 CTTTGCCTGCTAAATTTTCGCGAT

40 SEQ ID NO : 59
 LENGTH : 1665
 TYPE : DNA
 ORGANISM : *M. phaseolina*
 FEATURE NAME/KEY : CDS

45 LOCATION : (1).....(1665)
 atgactcgcttccggttcgtcctcgggctcgtggctacggctttggccaagacgggtcact
 M T R L P F V L G L V A T A L A K T V T
 gttgactgggacattggctgggtttccagggtcccgatggattcgagcggcctgtcatc
 V D W D I G W V S R A P D G F E R P V I
 50 gcaatcaacggccaatggccgctccctgtgctggaggccgacgtcaacgacaccatcatc
 A I N G Q W P L P V L E A D V N D T I I
 gccactgtccacaattctcttggcaacgaaacgaccagcatccactggcagggcatgtgg
 A T V H N S L G N E T T S I H W H G M W
 cagagaggcagccccgagcaagacggcggggctggcgctcacgcagtggtccgatcccgccct
 55 Q R G T P E Q D G G A G V T Q C P I P P

ggcgagactttcacgtacgagttcaaagcatacccgccggtactttctggtaccactcg
 G E T F T Y E F K A Y P A G T F W Y H S
 catgacatgggccagtatcccgatggcctgcgcgccacccatgatcatccatgaccccgac
 H D M G Q Y P D G L R A P M I I H D P D
 5 tccgaaaccagaagagcagtgatgggtgaagtcgtgctctatgtgtccgactggtaccac
 S E T Q K S S D G E V V L Y V S D W Y H
 gaccagatgccgcgcgttatccacagcttcctgaccaccccccaatttcaacggcgcgatg
 D Q M P P L I H S F L T T P N F N G A M
 cccaacccgaactccagcttgatcaacgatcagcagtcacgtccatcaacatccgtccc
 10 P N P N S S L I N D Q Q S T S I N I R P
 ggcgagaagaaatacgtgcgcatcatcaacacgtccgcccctcgccacgtactacctgcag
 G E K K Y V R I I N T S A L A T Y Y L Q
 tttgaccaacacaacatcacgcttgctcgcaattgacgggtgttgacgtcgaaccgcagagc
 F D Q H N I T V V A I D G V D V E P Q S
 15 tggaaggccctggagatcgtccccggccagcggtagcacttcatcatcgaaggctctcgag
 W K A L E I V P G Q R Y D F I I E G L E
 aacccccacaaggaactacgcattcatcaacaagatggctgttctcggtctgcagaacgtc
 N P T R N Y A F I N K M A V L G L Q N V
 aacagcctgggtctacgacgagtccttcggcgagccggagtcgttcagcctgagctctggc
 20 N S L V Y D E S F G E P E S F S L S S G
 gatctcgggaagtgatttcaccctgggtgcctctagatcacgagcctctcttggaaatccgtg
 D L G S D F T L V P L D H E P L L E S V
 gaccacaccatcacgatggaggtcaataatttgaacattgatggcggttggtttcgcatc
 D H T I T M E V N N L N I D G V G F R I
 25 actcaaggcccgaccgctacatttcaccccgacgcctaccctgtacacagccctcagc
 T Q G P D P Y I S P R T P T L Y T A L S
 accggcttcaacgccaccgacccagaaatctacggccaggtgaaccctacgtcgtcaac
 T G F N A T D P E I Y G Q V N P Y V V N
 gccggtgaagtcgtccggctcgtcgtcaacagcaacgatctcgtcaccgccaacaactct
 30 A G E V V R L V V N S N D L V T A N N S
 ggccgcgggcaccccatgcatctgcacggccacggtttccaggtgggtcgggtcagttctcc
 G R G H P M H L H G H V F Q V V G Q F S
 gagcactgggacgggaacacctcgtccttccccgccacgcccataagcgtgacaccacc
 E H W D G N T S S F P A T P M K R D T T
 35 gtcctattcgctggcggcagcctgggtgctccagttccgtgcccgaacccccgggtgtttgg
 V L F A G G S L V L Q F R A D N P G V W
 ctgttttactgccatattgagtggcacctagacgccggcatgtccgctacaatcatcgag
 L F H C H I E W H L D A G M S A T I I E
 gcgccgctcgacttgcagcgcgagggcatcaagatccccagcagcatcttgaatcgtgc
 40 A P L D L Q R E G I K I P Q Q H L E S C
 agagccttgaacttgaccactcaaggcaattgcgccgggaacaccgccaacctggatgac
 R A L N L T T Q G N C A G N T A N L D D
 actgccgcctgcaggggtctacgacaccgatccatgggggtgcgcttatcacggatgacgggt
 T A A C R V Y D T D P W G A L I T D D G
 45 ggtggaaatagtagccctgaacggaaccacttataagagaatttag
 G G N S T L N G T T Y K R I -

SEQ ID NO : 60

LENGTH : 554

50 TYPE : PRT

ORGANISM : *M. phaseolina*

MTRLPFVLGLVATALAKTVTVDDWDIGWVSRAPDGFERPVIAINGQWPLPVLEADVNDTIIATVHNSL
 GNETTSIHWGHWQRTPEQDGGAGVTQCPIPPGETFTYEFKAYPAGTFWYHSHDMGQYPDGLRAPM
 I I H D P D S E T Q K S S D G E V V L Y V S D W Y H D Q M P P L I H S F L T T P N F N G A M P N P N S S L I N D Q Q S T S I N I R P G
 55 E K K Y V R I I N T S A L A T Y Y L Q F D Q H N I T V V A I D G V D V E P Q S W K A L E I V P G Q R Y D F I I E G L E N P T R N Y A F

INKMAVLGLQNVNSLVYDESFGEPEFSLSLSSGDLGSDFTLVPLDHEPLLESVDHTITMEVNNLNIDG
VGFRITQGPDPYISPRTPITYLTALSTGFNATDPEIYGQVNPYVYNAGEVVRLVVNSNDLVTANNNGR
GHPMHLHGHVFQVVGQFSEHWDGNTSSFPATPMKRDTTVLFAGGSLVLQFRADNPGVWLFHCHIEWH
LDAGMSATIIIEAPLDLQREGIKIPQQHLESCRALNLTTQGNCAAGNTANLDDTAACRVYDTPWGALI
5 TDDGGGNSTLNGTTYKRI*

SEQ ID NO : 61
LENGTH : 2460 (including 150 bp 5' UTR and 150 bp 3' UTR)
TYPE : DNA

10 ORGANISM : *M. phaseolina*

CTCCGTATCTACTGCTGACTTCACATCCACAGCATGCAAGGACTCGAGGGCTTCTGATTAAACGAGC
ACTCACTTGGCTTTTGTCTGCGTTTTCTTTTCGTTTTCTACTATTTTCATCTTGATCCATTCTGTTCT
CGCCGTCGCTTTCCAGATGTCTTTTCGTTTCGAAAATTTTCACAGGCCTCATCGCTTTTACCCTGGC
TTAGGCCAAGATGAGACTAATGGGTGAGTATGCTGAACCTTGCGCAGGATATCTGAATAATAGTTGT
15 AGGGTTTCGAAATGGGGCACGTTTCGATGCACCGAGGCTCCAGAAGTTTCTGGATCGGGTGAGGTTAT
TCTGAAACATTACTGAGCTCGGCACTGATTGGTCGGCAGGGTCATGGCATTCCCTGGGGCGGTATGA
CTTGTAACCAACGCCAACCCGTATACTGAGTAGGACTCGGCCCGTGGTCCACAATCTTCTCTGCGCTG
ACGTTTCGGAAGAGCTCCAGACACAGGACAGACTGTGCGGTATGATTTACAGTCCAGCGGCATCCG
GTGTCTCCGGACGGCTACAAGAAGAACGTTTTGCTTGTGAACGGGCAATTTCCAGGCCCGCTCATGG
20 AAGCTAACTGGGGAGACACAATTGAAGGTAGGATGAGAGTAAATACGGGCAGCAACAACCTGCTGACA
GATACAGTGACTGTGCACAACAACATAGCCGGACCTGAGGAAGGCACACAACCTCCACTGGCACGGCT
TCACGCAGAGAGGGACGCCGTTTCATGGATGGTATCCCTTCCGTATCAAGCTGCCCATTTGCGCCCAA
CAATACCTTTGTGTATACCTTCAAGGCAGACCTTTACGGCACTGGCTGGTACCCTCTCATTACTCT
GGGCAATCCACCGGCGGCCTCCTCGGCCCAATCGTCGTCCATGGTCCCAGTGCCTTGACTATGATA
25 TTGACCTTGCCCTGTGTTTTTGAATGACTGGTACCACAAGGACTACTTGAGCTTATTGACGGTGG
TGAGACTTTCCCGTAGGTCAAAGGGCTCGATAGCTGAAACCTCCAACAGTCGTCGGAACGGACCCCA
GCCTATGGCATCCCAAGGCGGACAACAACATGATAAACGGGAAGATGGACTACGATTGCTCCCTTGT
CACTGACGGCACGCCTTGCGTCTCTAATGCCGGCTTGGCCACGTTTCAGCTTACCAAGGGCGCCACG
CACCGTCTCAGGCTCATAAACGGAGGATCCGCCTCCCTGCAGCACTTCAGTATCGATGGACACGAGA
30 TGACAGTCATTTCCAATGACTTCGTAGCCGTAGAGCCATACAGACGAAGACAGTGACTCTTGCAGT
AAGCCGCCCGATTTTTCCAGATATCCACATTACTAACACCCACCAGGTCCGCCAGCGGACAGACGT
CCTCGTCACGGCCAACGGCGACGCCACCGGCGCCTACTGGATGCGCAGCACCGTCGCGGACGATGAA
TCCTGCAACTGGTCCAACAGCCCCGCGCGCTCGCCGAGTCTACTACGACGCGCAAACCCCAACCG
TCAAGCCCAACAGCACCGGCTGGCCCCCGTCGCCAACAGCAAGGCAGCTGCGACAACGACCCGCT
35 TACCCAAACCATCCCCCTCTTCCCCATCCCCGCGGACCCAGCCCCCTCAACGACGCTTGAGCTCGAC
TTCGGCTGGACGCAAAACGCAACCGGACACCAAGTCTGGACGGTCAACGACCGCGGCTTCCGCGGCA
ACTACAACCGCCCCGTGCTGCAGCTCGCCGCGGGCTCGGACACCGCGTCGTCCGCGTACGCGTGGGA
GCCCCAATGGAACGTCTACGACACGGGCCGCAACCGCACCGTCCGCATCGTCATGCACAACAACCTCC
TCCATGTACCACGTACGTGAGCCCTTGTCTCCCCCCCCCCCCCCCCCTCCCTCTCGCTAATGGAAAG
40 ACACATGCAGCCCATGCACCTCCACGGGCACAACGCGCAGATCCTCGCCGCGGGCGCCAACGGCCCC
TGGGACGGCCGACCGTCGCGCGCCCCGCCAACCGGCCCGCGCGACGTCTACAGTCTCCCGCCGA
ACGGGCACCTGGTGATCCAGTACGCGCAGGACAACCGGGCGTGTGGCCGCTGCACTGCCACATCGC
GTGGCACGCGAGCGCGGGCATGTTTTCGAGCGTGTGAGCGGGCGGGGACATTGTGGGGAGCAGC
GGGGCCGCGGGGTGGAGGGAGGAGATGGCGGGCGTGTGTGCCGGGTGGGAGGCGTACACGCGGATGA
45 ACGTGGTGGAGCAGGTGGACAGTGGGGTGTGAGTTGGGAGCAAGGAGGGGGGTTTGTAGATGCGCGTA
TATGGTAAGCGGTTGGGGTTCTTGTGTTGACTCGATTTGCTCTGCAGGCGGTGTCTTTTTGCACTGT
GGCGCGTGCAATCTCGTTTTCTGTGCATCCTGGGTGGATAGGGAGCGGCG

SEQ ID NO : 62
50 LENGTH : 1803
TYPE : DNA
ORGANISM : *M. phaseolina*
FEATURE NAME/KEY : CDS
LOCATION : (1).....(1803)

55 atgtctttcgttttcgaaaattttcacaggcctcatcgcttttaccgctggcttaggcca

M S F V S K I F T G L I A F T A G L G Q
 gatgagactaatgggggttcgaaatggggcacgttcgatgcaccgagggtccagaagttt
 D E T N G V S K W G T F D A P R L Q K F
 ctggatcgggggtcatggcattccctggggcggtatgacttgtaccaacgccaacccgtat
 5 L D R G H G I P W G G M T C T N A N P Y
 actgaagctccagacacaggacagactgtgcggtatgatttcacagtccagcggcatccg
 T E A P D T G Q T V R Y D F T V Q R H P
 gtgtctccggacgggtacaagaagaacgttttgcttgtgaacgggcaatttcaggcccg
 V S P D G Y K K N V L L V N G Q F P G P
 10 ctcatggaagctaactggggagacacaattgaagtgactgtgcacaacaacatagccgga
 L M E A N W G D T I E V T V H N N I A G
 cctgaggaaggcacacaaatccactggcacggcttcacgcagagagggagccggttcatg
 P E E G T Q I H W H G F T Q R G T P F M
 gatggatcccttccgtatcaagctgccccattgcgcccacaataacctttgtgtatacc
 15 D G I P S V S S C P I A P N N T F V Y T
 ttcaaggcagacctttacggcactgggtgtaccactctcattactctgggcaatccacc
 F K A D L Y G T G W Y H S H Y S G Q S T
 ggcgccctcctcgcccacatcgctccatgggtcccagtgcgcttgactatgatattgac
 G G L L G P I V V H G P S A L D Y D I D
 20 cttggccctgtgtttttgaatgactgggtaccacaaggactacttgcagcttattgacggt
 L G P V F L N D W Y H K D Y L Q L I D G
 gtcgtcgggaacggaccccgacctatggcatcccaaggcggaacaacatgataaacggg
 V V G T D P S L W H P K A D N N M I N G
 aagatggactacgattgctcccttgtcactgacggcacgccttgctctctaatacgccgc
 25 K M D Y D C S L V T D G T P C V S N A G
 ttggccacgttcagcttcaccaagggcgccacgcaccgtctcagggtcataaacggagga
 L A T F S F T K G A T H R L R L I N G G
 tccgcctccctgcagcacttcagtatcgatggacacgagatgacagtcatttccaatgac
 S A S L Q H F S I D G H E M T V I S N D
 30 ttcgtagccgtagagccataaccagacgaagacagtgactccttgagtcggccagcggaca
 F V A V E P Y Q T K T V T L A V G Q R T
 gacgtcctcgtcacggccaacggcgacgccaccggcgccctactggatgcgacgaccgtc
 D V L V T A N G D A T G A Y W M R S T V
 gcggaacgatgaatcctgcaactgggtccaaccagcccgcgcgctcgccgcagtcactac
 35 A D D E S C N W S N Q P A A L A A V Y Y
 gacgcggcaaacccccaccgtcaagcccaacagcaccgggtggcccccgctcgccaaccag
 D A A N P T V K P N S T G W P P V A N Q
 caaggcagctgcgacaacgacccgcttacccaaaccatccccctcttccccatccccgcg
 Q G S C D N D P L T Q T I P L F P I P A
 40 gaccccagccccctcaacgacgcttgagctcgacttcgggtggacgcaaaacgcaaccgga
 D P S P S T T L E L D F G W T Q N A T G
 caccaagtctggacgggtcaacgaccgcgggttccgcggcaactacaaccgccccgtgctg
 H Q V W T V N D R G F R G N Y N R P V L
 cagctcgccgcggtcggacaccgcgtcggtccgcgtacgcgtgggagcccggaatggaac
 45 Q L A A G S D T A S S A Y A W E P E W N
 gtctacgacacgggcccgaaccgcaccgtccgcgtatgcacacaactcctccatg
 V Y D T G R N R T V R I V M H N N S S M
 taccaccccatgcacctccacgggcacaacgcgcagatcctcgccgcggggcgccaacggc
 Y H P M H L H G H N A Q I L A A G A N G
 50 ccctgggacggccgcaccgtcgcgcgccccgccaacccggcccgccgcgacgtctaccag
 P W D G R T V A R P A N P A R R D V Y Q
 ctcccgccgaacggggcacctgggtgatccagtacgcgcaggacaacccggggcggtgtggcg
 L P P N G H L V I Q Y A Q D N P G V W P
 ctgcactgccacatcggtggcacgcgagcgggcatgtttgcgagcgtgctggagcgg
 55 L H C H I A W H A S A G M F A S V L E R

gcgggggacattgtggggagcagcggggccggcggggtggagggaggagatggcgggcgtg
A G D I V G S S G A G G W R E E M A G V
tgtgccgggtgggagggcgtacacgcggatgaacgtgggtggagcaggtggacagtgggggtg
C A G W E A Y T R M N V V E Q V D S G V
5 tga
-
SEQ ID NO : 63
LENGTH : 600
TYPE : PRT
10 ORGANISM : *M. phaseolina*
MSFVSKI FTGLIAFTAGLGQDETNGVSKWGTFDAPRLQKFLDRGHGIPWGGMTCTNANPYTEAPDTG
QTVRYDFTVQRHPVSPDGYKKNVLLVNGQFPGPLMEANWGDTEVTVHNNIAGPEEGTQIHWGFTQ
RGTFPMDGIPSVSSCPIAPNNTFVYTFKADLYGTGWYHSHYSGQSTGGLLGPIVVHGPSALDYDIDL
GPVFLNDWYHKDYLLQIDGVVGTDPSSLWHPKADNNMINGKMDYDCSLVTDGTPCVSNAGLATFSFTK
15 GATHRLRLINGGSASLQHFSIDGHEMTVISNDFVAVEPYQTKTVTLAVGQRTDVLVTANGDATGAYW
MRSTVADDESNWSNQPAALAAVYYDAANPTVKPNSTGWPPVANQQGSCDNDPLTQTIPLFPIPADP
SPSTTLELDFGWTQONATGHQVWTVNDRGFRGNYNRPVLQLAAGSDTASSAYAWPEWNVYDTGRNRT
VRIVMHNNSSMYHPMHLHGHNQAQILAAGANGPWDGRTVARPANPARRDVYQLPPNGHLVIQYAQDNP
GVWPLHCHIAWHASAGMFASVLERAGDIVGSSGAGGWREEMAGVCAGWEAYTRMNVVEQVDSGV*
20
SEQ ID NO : 64
LENGTH : 2285 (including 150 bp 5' UTR and 150 bp 3' UTR)
TYPE : DNA
ORGANISM : *M. phaseolina*
25 TGAAGCCCTCTCTGACGCAGGTATCTATTTTATTAAACCAGTTTCACCCTCCGGTCGGGTAAAGTATT
TGCTCAAACAACTTGTCCAAGTGTCAAGTGTAGGTAAAGCTAGGAGGCTCACGAATCAAGAGACTCTC
CAGAGATATCTTCGCCATGATTCGCCTTTCTCTCGTGCTCGGCTTCATGGCCACGACACTGGCCAAG
ACCGTCACTCTTAACTGGGATATTGGGTGGGTTTCTGCGGCTCCAGATGGATTTACACGGCCCGTCA
TTGGCATCAACGGGGAGTGGCCGCCCCCGGTTTGGGAAGCCGACGTCAACGACACTATTATAGTAAT
30 TACGCGGAACCTCCTGCGTAACGAGACGACGAGCTTGCACGTGGCATGGTATGTGGCACTATAACTCG
ACCCACATGGACGGCGGAGCCAGGATTTACAGTGTGAAATCCCTCCGGGGGGGACATTACAGTACA
AGTTCAAGGCGTACCCGGCCGGCACCTTTTGGTATCATTCTCACGATATGGGCCAATATCCCGACGG
CCTGCGCGCCCAATGATCATTACGACCCTAAGGCTGCCGCGGAGCGGGACACTGATAAGGAGTAC
GTACTTACGGTCTCCGACTGGTACCGTGACCAGATGCCGTCACTTATCCACCGCTACTTGACAACTT
35 CCACTTATAATAGTACTATGCCAAATCCAACTCGAGCTTGATCAACGATCAGCAGTCTACAACGCT
AAACATCCGCCCCGGGCAGAAAGATATATGTTCCGATTATTAACATGTCAGCCCTCGCAACGTACTAT
CTACAGTTCGGTAGGTGTATCCATATGGCCCTGTTACACGGACGAAGCTAACGATTAAGATCAACAC
CACTTGACTGTTATTGCCATTGACGGTGTGACGGTTGGTAACTCTATTACCTATTCTGCGCTAAGA
TGCATGTCGGCATATGTGCCGTTAGCTGCATGCAAACGCGTTACAAGGTTAAGTGCTAACAAACGGGC
40 AGTCGATCCCCAGACTTGGGAGGCTCTGGAGATTATCCCTGGACAGCGGTACGACGTCAATTATCACC
GGCCTAGAGAACCCCGAAAGGAAGTATGCATTTATCAACAAGATGGCTACTCTTGGCTTCCAGAAC
ATAACGTCCTTAGTTACGATTTCGTCTGCGCTGTCCCGGAGCCGTTGAACGTGGGCAGCTTCAATCT
TAGAAGCGATTTCAACCTGACCCCGCTTGATGAGGAGCTACTACTGGAGCCCGTGGACCACACCTTC
ACCATGGAGGTCAATAACGTGAACGTGACGGCGTAGGCTCCCGGTGAGATATTCCCTACCCCCCGG
45 GCCCCCGGGGCGGGTCCCGAAGTCGGTATGAGGCTTACTCACTCCAATCCGCAGCATCACGCAGGGA
CCGGACCTTACATCGCCCCGCGTACGCCACCTTATACACCACCTGAGCACCGGCTCTAATGCTA
TTAACCCCGCCATATACGGCCAGGCGAACGCTTACGTAGTGAAGCCGGCGATATTGTCCAGCTTGT
CGTCAATAGTAACGAACCCGTCACTACCAACACTTCCGGTCTGTTGGGCACCTATGCACCTGCACGGC
CACACCTTCCAAGTGGTTGGCCAATATGGCAGCCCTTGGGACGGCGATGCCTCTAAATTCCTGCTG
50 TTCTATGAAGCGGGATACCACTGTTCTGTTTACTGGCGGGAGCTTGGTGATCCGGTTCCGCGCGGA
CAATCCTGGAGTTTGGATGTGTACGGCTCCGCTTTGCTCGAAGACCCGCGTTTGAAAGCGTTGACTG
ACCTGTAACCTCGCAGTCCATTGCCACAACGAATGGCACCTTGACGCCGGCATGGCTGGAACGATTAT
CGAAGCGCCACTCGAGCTTCAACAAAGCGGTCTGACGATTCCGCCGAGCACCTCGCGTCGTGCAGG
GCGTTAACTTAAACGACCCGGGGCAATTGTGCCGGTAATACTGCGAACCTAGAGGATACGGCTGCAT
55 GCAGAGTCTACGACACTGAGCCTTGGGGGTGAGTTACTCCATTATTGTTTTGTTGTTATAACCCCTTG

CTGATGACAATACTTCTCTAGTGCACCTTATCAAGAGAGATGAGGAAACAGCATATTAAATAGCACGC
TGGCATAGCACCTGTAGATGTAGACTGATTCTAGTATTTATTACCTGTGTACACTTGAAGAAAATT
GTTGTAAAATGATATGTCCCATGCAACTGAACATGGCCTACGTGGCGAGAGTTTATCAGGCGCCTT
CTGCTCC

5

SEQ ID NO : 65
LENGTH : 1635
TYPE : DNA
ORGANISM : *M. phaseolina*

10

FEATURE NAME/KEY : CDS

LOCATION : (1).....(1635)

15

atgattcgcttttctctcgtgctcggttcatggccacgacactggccaagaccgtcact
M I R L S L V L G F M A T T L A K T V T
cttaactgggatattgggtgggtttctgcggctccagatggatttacacggccccgtcatt

20

L N W D I G W V S A A P D G F T R P V I
ggcatcaacggggagtgggcgcccccggttttggaagccgacgtcaacgacactattata
G I N G E W P P P V L E A D V N D T I I
gtaattacgcggaacctcctgcgtaacgagacgacgagcttgactggcatgggtatgtgg
V I T R N L L R N E T T S L H W H G M W

25

cactataactcgacccacatggacggcgaggccaggatttcacagtgtgaaatccctccg
H Y N S T H M D G G A R I S Q C E I P P
ggggggacattcacgtacaagttcaaggcggtaccggcgccgaccttttggtatcattct
G G T F T Y K F K A Y P A G T F W Y H S
cacgatatgggccaatatcccgacggcctgcgcgccccaatgatcattcacgaccctaag

30

H D M G Q Y P D G L R A P M I I H D P K
gctgccgaggagcgggacactgataaggagtagctacttacggtctccgactggtaccgt
A A A E R D T D K E Y V L T V S D W Y R
gaccagatgccgtcacttatccaccgctacttgacaacttccacttataatagtactatg
D Q M P S L I H R Y L T T S T Y N S T M

35

ccaaatccaaactcgagcttgatcaacgatcagcagctctacaacgctaatacatccgcccc
P N P N S S L I N D Q Q S T T L N I R P
gggcagaagatatatgttcggattattaacatgtcagccctcgcaacgtactatctacag
G Q K I Y V R I I N M S A L A T Y Y L Q
ttcgatcaacaccacttgactgttattgccattgacgggtgtcgacgtcgatccccagact

40

F D Q H H L T V I A I D G V D V D P Q T
tgggaggctctggagattatccctggacagcggtagcagctcattatcacggccttagag
W E A L E I I P G Q R Y D V I I T G L E
aaccccgaaaggaactatgcatttatcaacaagatggctactcttggttccagaacaat
N P E R N Y A F I N K M A T L G F Q N N
aacgtccttagttacgattcgtcctggcctgtcccggagccggttgaaactgggcagcttc

45

N V L S Y D S S W P V P E P L N V G S F
aatcttagaagcgatttcaacctgaccccgcttgatgaggagctactactggagcccgtg
N L R S D F N L T P L D E E L L L E P V
gaccacaccttcaccatggaggtcaataacgtgaacgtcgacggcgtaggctcccgcatc
D H T F T M E V N N V N V D G V G S R I
acgcagggaccggacccttacatcgcccccggtacgcccaccctatacaccaccctgagc

50

T Q G P D P Y I A P R T P T L Y T T L S
accggctctaattgctattaaccccgccatatacggccaggcgaacgcttacgtagtggaa
T G S N A I N P A I Y G Q A N A Y V V E
gccggcgatattgtccagcttgcgtcaatagtaacgaacccgtcactaccaacacttcc
A G D I V Q L V V N S N E P V T T N T S
ggctcgtgggcaccctatgcacttgcacggccacaccttccaagtgggtggccaatatggc

55

G R G H P M H L H G H T F Q V V G Q Y G
agcccttgggacggcgatgcctctaattccctgctgttccctatgaagcgggataccact
S P W D G D A S K F P A V P M K R D T T

gttctgtttactggcgaggagcttggtgatccggttccgcgcggacaatcctggagtttgg
V L F T G G S L V I R F R A D N P G V W
atgttccattgccacaacgaatggcaccttgacgccggcatggctggaacgattatcgaa
M F H C H N E W H L D A G M A G T I I E
5 gcgccactcgagcttcaacaaagcggcttgacgattccgccgcagcacctcgcgctcgtgc
A P L E L Q Q S G L T I P P Q H L A S C
agggcgtaaacttaacgacccggggcaattgtgccggtaatactgcaacctagaggat
R A L N L T T R G N C A G N T A N L E D
10 acggctgcatgcagagtctacgacactgagccttgggggtgcacttatcaagagagatgag
T A A C R V Y D T E P W G A L I K R D E
gaaacagcatattaa
E T A Y -

SEQ ID NO : 66
15 LENGTH : 544
TYPE : PRT
ORGANISM : *M. phaseolina*
MIRLSVLGFMATTLAKTVTLNWDIGWVSAAPDGFTRPVIINGEWPPPVLADVNDTIIVITRNL
RNETTSLHWHGMWHYNSTHMDGGARISQCEIPPGGTFTYKFKAYPAGTFWYHSHDMGQYPDGLRAPM
20 I I HDPKAAAERD TDKEYVLT VSDWYRDQMPSLIHRYLTSTYNSTMPNPNSSLINDQQSTTLNIRPG
QKIYVRIINMSALATYYLQFDQHHLTVIAIDGVDVDPQTWEALEIIPGQRYDVIITGLENPERNYAF
INKMATLGFQNNNVLSYDSSWPVPEPLNVGSFNLRSDFNLTPLEELLLEPVDHTFTMEVNNVNVDG
VGSRITQGPDPYIAPRTPTLTYTTLSTGSNAINPAIYGQANAYVVEAGDIVQLVNSNEPVTNTSGR
GHPMHLHGHTFQVVGQYGSPPWDGDASKFPAVPMKRDTTVLFTGGSVLIRFRADNPGVWMFHCHNEWH
25 LDAGMAGTII EAPLELQQSGLTI PPQHLASCRALNLTTRGNCAGNTANLEDTAACRVYDTEPWGALI
KRDEETAY*

SEQ ID NO : 67
30 LENGTH : 2412 (including 150 bp 5' UTR and 150 bp 3' UTR)
TYPE : DNA
ORGANISM : *M. phaseolina*
GGGAGACGATCTGGAAGTGTTTGTTTCAGAAATGATTTGGCCGTTGAAACCACCATTCATTGGCACGGT
CGGTATCCATGGTATACTTTTTACGAAGGCTAGTCAGCTGAAGGAGAAGTTCGGCAGGCATCCTTCA
GCAAGGAACACCACACATGGACGGAGTTCGGGAGTAACACAGGTTGGTTGATGACCTTCTATCGGG
35 ATGACTAGGGCCTAACTTTTGGCGCAGGAGCCGATCCCACCAGGAGGAACTTCACGTACCGCTTCT
CGCTCAAAAACGAATACGGCTTCTACTGGTATCACTCGCATTTCGAGCATACTCGGACGACGCCAT
CCGCGGACCACTAGTCATCCATCCATCCTCACAACGCCCGGCCATACGAGACTCTCGCGAGGAAC
CAGACTGAGCTTACTGCTTTGCAAGAAGCTGAACGCGAAGCGGTGCCTATCCTCCTATCTGACTGGT
40 ACCATCGCGTTTCGGACGACATCTTCAACGAATACCTAACAAACAGGCGCGTTCCCGAGTTGCGTGGA
CAGTCTCCTCGCCAATGGATACGGAAGGGTGCAGTGTCTACCGGAATACATTCTGGCAGCCGGAGCT
GGGCTAGGCATGGAGCCTGCACCTGTCAATGCTACCGCGACTAGCATCGGCACAACGCCCATGTCTT
CCATGGCGATGGGTACAAAGTACATGGAGACCAATACCAAGGAGTCGATGCGTATGGAGTCTATGGC
ACTAGACACTACGTCCATGGAGCATCACATGCGACGCATGGATTCCATGTGAGCGGAGGATATGTCC
ATGAATACGATGACTGCTCATTCTACGCCTGCGGCTGCGCCCGACTCAGGCATGCCGATGGGCTCCA
45 TGTCAATGGCTTCTCTACCCGTATCAGGCATATCGGGCACGTGCGGCCTGTGCGGCATGTCAAATAT
GGCGAGCGGTCCCCTTGGTCTCGCGGCTGCAGTGTCTCCCATGATGTTGAGACCGGGCTACAACATC
AGCTCTCTCCCGCCAGAGACTTGACACAGACACGTGAGCGCCGCTGCTGACTGTGATGCAAATATA
CACGAGGCTGGCTTGCAATTAACCTAGTCAACTCCGGTTTCAGTAACCAAGCTCAGCGTCTCACTAGA
CGCCCATTCGATGTTTGTCTATGCGGCCGACGGATTCTTTGTGAAACCCCAAGAAGTAGAAGTAAGT
50 TGCACCTCCCCCTAACTTGTGTCGGAAGACTTACCGCGTCTAGGTATTACAAATCTCAATCGGGCA
ACGGTACTCAGTAATGATCAAACCTTAATCAACGGCCCGGAACTACACTCTACGGTTTTCGTCGTAT
CCCTACGCGCATATGCAACAGGTTATCGAAGGCCAAGCGACCGTCTCATATAAGGTAAGCAGCAAGC
TTTTCCCCCACTCGGTATAGAACTAACTTCGTTAGGTTGATGCCGCAGAGGACATTATGCCGGTGGA
CTTGACAAACGACCCTACTGCAACGTGGATGCTTGTCAACGGTTCGGCAAAGTCGAACGCTTCTGAA
55 TTGAAGACGGACATGCTCGCCCCGTTGAGGCAATTGCGCCGCCATCCCAAGCGGATATAACTTACG

ACTTCACGATCAGTCAGACAGAGATCGTAACTTGGGTGTTAAACGGATATCCCTATTCGGAACCTTC
 GACGCCTATTATCTACGGCAATGCGTCGGAAGCGTGGAACGCAAATACTACAATCCGCATTCTTCC
 AACTCGACCGTAGACATTATAATGCGGATTGCCAACGACTCAATGGATACGGCAAGTTGCAGTCCAG
 GCCGCCGTCAAAACGCCTGCATAAGCTAACCCGATAATGCCGTAGATGGGTTCATCCTATGCACCTTC
 5 ACGGCCACCGGTTCTTCGCCCTCGGCTCTGGATCGGGCTCCTTCCCATATCAGAACGCCGTGACGC
 GCCTCCATCCCTCATTAACCTCGAAAACCTCCGTACCGGGACACAACCGATTTACCACCTTCAGGC
 TGGGCAGTCATTTCGTATGTAGCCAACAATCCAGGCGCATGGATGTTTCACTGCCACATCCAGTGGC
 ACCTCGTGAGCGGCATGGCATTGGTGTGTTGTCGAAGGAGAAGAGCAGCTGCCTGGTTTGGTGGGTGC
 GGCTGCGAACGGAACAAGCAATGCGAATAGCGCGTCACCGGCGCGTAGCACTCGAGAGCATGCGGCC
 10 TTTGCCGTTGTTGCTACCTAAGCACTGTTTTCTTCGCGTATGGCTACTAATGCGCGAAGCGCCATG
 TAAGAGCGCGCCTGAGGTAATAAAGGTGGCGACTGCAAAAAGCTCATGTCCCGCAATGATGGGAGT
 TCTTTGGAGATTCTGAATCAAAGACGTCGATATTCTGGGTCCAGTCGGTGCAGAACAGACCCCATGG

SEQ ID NO : 68
 15 LENGTH : 1743
 TYPE : DNA
 ORGANISM : *M. phaseolina*
 FEATURE NAME/KEY : CDS

LOCATION : (1).....(1743)
 20 atggacggagttccgggagtaacacaggagccgatcccaccaggaggaaacttcacgtac
 M D G V P G V T Q E P I P P G G N F T Y
 cgcttctcgctcaaaaacgaatacggcttctactggtatcactcgcatttccgagcatatc
 R F S L K N E Y G F Y W Y H S H F R A Y
 tcggacgacgccatccgcggaaccactagtcacatccatcctcacaacgcccccgcca
 25 S D D A I R G P L V I H P S S Q R P R P
 tacgagactctcgcgaggaaccagactgagcttactgctttgcaagaagctgaacgcgaa
 Y E T L A R N Q T E L T A L Q E A E R E
 gcggtgcctatcctcctatctgactggtaccatcgcggttccggacgacatcttcaacgaa
 A V P I L L S D W Y H R V S D D I F N E
 30 tacctaacaacaggcggttccccagttgctggtgacagtcctcctcgccaatggatacggaa
 Y L T T G A F P S C V D S L L A N G Y G
 aggggtgcggtgtctaccggaatacattctggcagccggagctgggctaggcatggagcct
 R V R C L P E Y I L A A G A G L G M E P
 gcacctgtcaatgctaccgcgactagcatcggcacaacgcccattgtcttccatggcgatg
 35 A P V N A T A T S I G T T P M S S M A M
 ggtacaaagtacatggagaccaataccaaggagtcgatgcgtatggagtctatggcacta
 G T K Y M E T N T K E S M R M E S M A L
 gacactacgtccatggagcatcacatgcgacgcatggattccatgtcagcggaggatag
 D T T S M E H H M R R M D S M S A E D M
 40 tccatgaatacgtatgactgctcattctacgcctgcggtgctgcgcccactcaggcatgccg
 S M N T M T A H S T P A A A P D S G M P
 atgggctccatgtcaatggcttctctacccgtatcaggcatatcgggcacgtcgggcctg
 M G S M S M A S L P V S G I S G T S G L
 tcgggcatgtcaaatatggcgagcggtcccccttggtcctcgcggtgcagtgtcccatg
 45 S G M S N M A S G P L G P R G C S A P M
 atgttcagaccggggtacaacatcagctctctcccgcagagacttgacagacacgtca
 M F R P G Y N I S S L P P E T C T D T S
 gcgcccgtgctgactgtcgatgcaaactatacacagggtggcttgcattaaacttagtc
 A P L L T V D A N Y T R G W L A L N L V
 50 aactccggttcagtaaccaagctcagcgtctcactagacgcccattcgatgtttgtctat
 N S G S V T K L S V S L D A H S M F V Y
 gcggccgacggattctttgtgaaaccccaagaagtagaagtattacaaatctcaatcggg
 A A D G F F V K P Q E V E V L Q I S I G
 caacggtactcagtaatgatcaaacttaataacggcccggaaactacactctacggttt
 55 Q R Y S V M I K L N Q R P G N Y T L R F

gcgtcgatccctacggcgatatgcaacaggttatcgaaggccaagcgaccgtctcatat
 A S Y P Y G D M Q Q V I E G Q A T V S Y
 aaggttgatgccgcagaggacattatgccggtggacttgacaaacgaccctactgcaacg
 K V D A A E D I M P V D L T N D P T A T
 5 tggatgcttgtcaacggttcggcaaagtcgaacgcttctgaattgaagacggacatgctc
 W M L V N G S A K S N A S E L K T D M L
 gccccgttcgaggcaattgcgccgccatcccaagcggatataacttacgacttcacgac
 A P F E A I A P P S Q A D I T Y D F T I
 agtcagacagagatcatgggtcatcctatgcaccttcacggccaccggttcttcgccctc
 10 S Q T E I M G H P M H L H G H R F F A L
 ggctctggatcgggctccttcccatatcagaacgccgtcgacgcgcctccatccctcatt
 G S G S G S F P Y Q N A V D A P P S L I
 aacctcgaaaaccctccgtaccgggacacaaccgatttaccaccttcaggctgggcagtc
 N L E N P P Y R D T T D L P P S G W A V
 15 attcgctatgtagccaacaatccaggcgcatggatgtttcactgccacatccagtggcac
 I R Y V A N N P G A W M F H C H I Q W H
 ctcgtagcgccatggcattgggtgtttgtcgaaggagaagagcagctgcctgggttggtg
 L V S G M A L V F V E G E E Q L P G L V
 ggtgcggctgcgaacggaacaagcaatgcgaatagcgcgtcaccggcgcgtagcactcga
 20 G A A A N G T S N A N S A S P A R S T R
 gagcatgcggcctttgccgttgttgctaccctaagcactgttttcttcgcgtatggctac
 E H A A F A V V A T L S T V F F A Y G Y
 taa

25

SEQ ID NO : 69
 LENGTH : 580
 TYPE : PRT
 ORGANISM : *M. phaseolina*

30 MDGVPGVTQEPIPPGGNFTYRFLKNEYGFYWHSHFRAYSDDAIRGPLVIHPSSQRPRPYETLARN
 QTELTALEAEREAVPILLSDWYHRVSDDIFNEYLTGTGAFPSCVDSLLANGYGRVRCLEPYILAAGA
 GLGMEPAPVNATATSIGTTPMSSMAMGTKYMETNTKESMRMESMALDTTSMHHMRRMDSMSAEDMS
 MNTMTAHSTPAAAPDSGMPMGSMASLPVSGISGTSGLSGMSNMASGPLGPRGCSAPMMFRPGYNI
 SSLPPETCTDTSAPLLTVDANYTRGWLALNLVNSGVS TKLSVSLDAHSMFVYAADGFFVKPQEVEVL
 35 QISIGQRYSVMIKLNQRPGNYTLRFASYPYGDMQQVIEGQATVS YKVDAEDIMPVDLTNDPTATWM
 LVNGSAKSNASELKTDLAPFEAIAPPSQADITYDFTISQTEIMGHPMHLHGHRFFALGSGSGSFPY
 QNAVDAPPSLINLENPPYRD TDLPPSGWAVIRYVANNPGAWMFHCHI QWHLVSGMALVFVEGEEQL
 PGLVGAAANGTSNANSASPARSTREHAFAVVATLSTVFFAYGY*

40

SEQ ID NO : 70
 LENGTH : 2242 (including 150 bp 5' UTR and 150 bp 3' UTR)
 TYPE : DNA
 ORGANISM : *M. phaseolina*

AGTCCACCCTTTCTATTTCTTTCTCCTCACGTCACATTCAGATACCCGGGCTCCTTTCAACTGCCAAA
 45 TTTCTTTTCCCGGGACTCATTCCTCCCCGACTCTCTTACTCTTCTCTCAATTTCTTACCACCC
 ACCGCTCGCTCTCACAATGTCTTTTCGTTGCCAGGTCCGTAGTAAGCGGCCTCGCCAGCAGAGCCGCC
 TTTACTAATGGATCATGGACCGGTGCCTGGGAGACTCATGGCTCCACCCAAGGTTCCATCTCACCGC
 AACTACGCAACGGTACGTACCAGGTTTCACTTGTAAATCCCAAATTTGACTGATCTTTGTTGCAGG
 CGGCGGGCCTCTTGGTACCTTGGACGCTCCAACTTGCCTGGCTGTATTGGTTCTCCACCGTGGGGC
 50 AACCATGACTCTCATGACCCTTTCCGCATGCCTGATACTGGCATTACTCGGGAGTATGACTTTACTC
 TCACTTATCAAGACATCGCTCCCGATGGCGTCACTAAGAGGGGCGTCGTTGTCAATGGTCAATATCC
 CGGGCCACGATCGAGGCCAACTGGTGCCTACATCACTACATCACGCACATGACATCAGGCTAACAC
 TTCGTTTCAAGGGCGACTGGATCCAGGTACGCTCCACAACGGTCTAGGCGAGGACGAAGGTGAGGGT
 ACCGCGATGCACTGGCACGGCTTTTTCAGAAAGGAGAGCCAGTGGATGGATGGTGTCCCCGGTGTTC
 55 AACAATGTCCTATTCTCTCCGGAGAGAGCTTCACCTACCGCTTCCGCGCTGAGCAGTATGGCACTTC

TTGGTACCACAGCCACTACAGCGCGCAGTACTCGGGCGGTGCTGCTGGTCCTCTCATCGTATACGGT
 CCGGACAGCCAGAGTTACGACGTTGACCTCGGTCCCGTCATGGTATCTGACTGGTACCACTCGCAAT
 ACTACGATATTGTCAAGCAGACCATGCAGGCCGACCCACGGGCACCACCCCTCCGCCGCCGCCTCA
 GTCCGACAACAACCTGATCCAGGGCTTTGGCGAATTGACTGCTCGCTGACGACGAAGCCCTGCATT
 5 CCTGACGCCGGTGTAGCCAAGTTCAAGTTCACTTCCGGCAAGAAGCATCGCCTCAGGCTCATCAACT
 CCGGCTCCGAGGCGATGCAGAGGTTCTCTATCGACGGCCACACCATGAAGATCATCGCACACGACTT
 CGTCCCGATCGAGCCCTACGAGGTACGGCCCTGACCCTTGGCGTCGGACAGCGGGCCGACGTGGTT
 GTCGAAGCCACGGGCAAGCCCTCGGACGCGTACTGGATGCGCTCAGAGATCGGGCTCAACAAGTGCA
 ACGTCTTCAATGCGAACGCCCTCCGAGGCCCTCGCCGTCATCCTCTACGAGGATGCAGACCTGCTGGC
 10 CGTGCCAGCTCCTCCGCCAGCCGATGCGGAGCTGACATCGTGCACCAACGACGACATCTCCGTC
 GGCTGCCGCTCCAGCACATCTGCCCGACCCCAACCCGTCCGTACGACCGAGCTGCACATCGAGA
 ACAAGTACAACGGCACGCACTGGCTCTGGCACTTCGGCGGCCCCAGCTACCGCGCCGACTTCAACGA
 CGCCCTCCTCTACCAGCTCCAACAGGGCACGCCCCGACTTCGGCCCGCAGTCCAACGTGCACGACTTC
 GGCGCCAACAATCCGTCCGCTTCGTCTCTACAACCAGTCCCGGCTCAGCATCCCATGCACTTGC
 15 ATGGCCACAACCTTCTGGGTCTCGCCGACGGCGTCGGCACCTGGGACGGCGCCATCGCCAACCCGCA
 GAACCCCGAGCGCCGCGACGTGCACGTCTTCAGCCCGCCAGGGCAGCACCCCGTCTGTACATGGTC
 GTACAGATTGAGCTGGACAACCCGGGCTGTGGCCGTTCCACTGCCACATCGCGTGGCACGTCTCGG
 CGGGGTTGTATTTGAACGTGCTGGAGCGCCCGACGACATCAAGGCGCTGCAGATTCCGGCCGCGGT
 TGGTGATCAGTGCAGGGCGTGGGCGGACTACACGGCAAAGAATACGGTGGATCAGATCGACTCGGGG
 20 TTGAAGAAGGAGTAGAAGGCGTGATAGTTTGCTATTGTTCTTTCTCTCTCTCTTTTTTTTTTTTTT
 TTTTACACCTTCCCTTCTTGATACCAGCATGTTTTTGGGCGTTATTTACGGTCCCTTCTGCGCATTTT
 CAAGGCGTTATGTCTTTCCCTTGGCGATAAG

SEQ ID NO : 71
 25 LENGTH : 1836
 TYPE : DNA
 ORGANISM : *M. phaseolina*
 FEATURE NAME/KEY : CDS

LOCATION : (1).....(1836)
 30 atgtctttcggttgccaggtccgtagtaagcggcctcgccagcagagccgcctttactaat
 M S F V A R S V V S G L A S R A A F T N
 ggatcatggaccggtgcctgggagactcatggctccaccaaggttccatctcaccgcaa
 G S W T G A W E T H G S T Q G S I S P Q
 ctacgcaacggcgggcggtccttggtagcttggacgctccaaacttgctggtgtatt
 35 L R N G G G P L G T L D A P N L P G C I
 ggttctccaccgtggggcaaccatgactctcatgaccctttcggcattgctgatactggc
 G S P P W G N H D S H D P F G M P D T G
 attactcgggagtatgactttactctcacttatcaagacatcgctcccgatggcgctcact
 I T R E Y D F T L T Y Q D I A P D G V T
 40 aagagggggtcggttgcaatgggtcaatatcccgggccacgatcgaggccaactggggc
 K R G V V V N G Q Y P G P T I E A N W G
 gactggatccaggtcacggtccacaacggtctaggcgaggacgaaggtgaggggtaccgcg
 D W I Q V T V H N G L G E D E G E G T A
 atgcactggcacggctttttgcagaaggagagccagtggtggtggtgtccccgggtgtt
 45 M H W H G F L Q K E S Q W M D G V P G V
 caacaatgtcctattcctcccgagagagcttcacctaccgcttccgcgctgagcagtat
 Q Q C P I P P G E S F T Y R F R A E Q Y
 ggcacttcttggtagccactacagcgcgagtagctcgggcggtgctgctggtcct
 G T S W Y H S H Y S A Q Y S G G A A G P
 50 ctcatcgatatacgggtccggacagccagaggttacgacgttgacctcggtcccgatcatggta
 L I V Y G P D S Q S Y D V D L G P V M V
 tctgactggtagcactcgcaataactacgatattgtcaagcagaccatgcaggccgacccc
 S D W Y H S Q Y Y D I V K Q T M Q A D P
 acgggcaccacccctccgcccgcctcagtcggacaacaacctgatccagggttttggc
 55 T G T T P P P P P Q S D N N L I Q G F G

gaattcgactgctcgctgacgacgaagccctgcattcctgacgcccgggtgtagccaagtcc
 E F D C S L T T K P C I P D A G V A K F
 aagttcacttccggcaagaagcatcgctcaggtcatcaactccgggtccgagggcgatg
 K F T S G K K H R L R L I N S G S E A M
 5 cagaggttctctatcgacggccacaccatgaagatcatcgacacgacttcgtcccgatc
 Q R F S I D G H T M K I I A H D F V P I
 gagccctacgaggtcacggccctgacccttggcgctcggacagcgggcccgcgtggtgtc
 E P Y E V T A L T L G V G Q R A D V V V
 gaagccacgggcaagccctcggacgcgtactggatgcgctcagagatcggggtcaacaag
 10 E A T G K P S D A Y W M R S E I G L N K
 tgcaacgtcttcaatgcgaacgcctccgagggcctcgcgctcatcctctacgaggatgca
 C N V F N A N A S E A L A V I L Y E D A
 gacctgctggccgtgccagctcctccgcccagcccgatgcggagctgacatcgatgcacc
 D L L A V P S S S A Q P D A E L T S C T
 15 aacgacgacatctcgcgtcggcctgccgctccagcacatcctgcccgaacccaacccgtcc
 N D D I S V G L P L Q H I L P D P N P S
 gtcacgaccgagctgcacatcgagaacaagtacaacggcacgcactggctctggcacttc
 V T T E L H I E N K Y N G T H W L W H F
 ggcgccccagctaccgcgccgacttcaacgacgcccctcctctaccagctccaacagggc
 20 G G P S Y R A D F N D A L L Y Q L Q Q G
 acgccccgacttcggccccgcagtcgaacgtgcacgacttcggcgccaacaaatccgtccgc
 T P D F G P Q S N V H D F G A N K S V R
 ttcgctcgtctacaaccacgtcccgggtcagcatcccatgcacttgcattggccacaacttc
 F V V Y N H V P A Q H P M H L H G H N F
 25 tgggtcctcgccgacggcgtcggcacctgggacggcgccatcgccaacccgcagaacccc
 W V L A D G V G T W D G A I A N P Q N P
 cagcgcgcgacgtgcacgtccttcagcccgcagggcagcaccctcgatcatggtc
 Q R R D V H V L Q P A Q G S T P S Y M V
 gtacagattgagctggacaacccgggctgtggcgttccactgccacatcgcggtggcac
 30 V Q I E L D N P G L W P F H C H I A W H
 gtctcggcggggttgatattgaacgtgctggagcggcggacgacatcaaggcgctgcag
 V S A G L Y L N V L E R P D D I K A L Q
 attccggccgcggttggtgatcagtgaggcggtggcgggactacacggcaaagaatacg
 I P A A V G D Q C R A W A D Y T A K N T
 35 gtggatcagatcgactcggggttgaagaaggagtag
 V D Q I D S G L K K E -

SEQ ID NO : 72
 LENGTH : 611
 40 TYPE : PRT
 ORGANISM : *M. phaseolina*
 MSFVARSVVSGLASRAAFTNGSWTGAWETHGSTQGSISPQLRNGGGPLGTLADPNLPGCIGSPWGN
 HDSDHPFGMPDTGITREYDFTLTYQDIAPDGVTKRGVVVNGQYPGPTIEANWGDWVQVTVHNLGEGD
 EGEGTAMHWHGFLQKESQWMDGVPGVQQCPPIPGESFTYRFRAEQYGTSWYHSHYSAQYSGGAAGPL
 45 IVYGPDSQSYDVLGPVMVSDWYHSQYYDIVKQTMQADPTGTTPPPPQSDNNLIQGFGEFDCSLTT
 KPCIPDAGVAKFKFTSGKKHRLRLINSNGSEAMQRFSDGHTMKIIAHDFVPIEPYEVLTALTLGVGQR
 ADVVVEATGKPSDAYWMRSEIGLNKCNVFNANASEALAVILYEDADLLAVPSSSAQPDALTSCTND
 DISVGLPLQHILPDPNPSVTTELHIENKYNTHWLWHFGGPSYRADFNALLYQLQQGTPDFGPQSN
 VHDFGANKSVRFVYVNHVPAQHFMHLHGHNFVVLADGVGTWDGAIANPQNPNQRRDVHVLQPAQGSTP
 50 SYMVVQIELDNPLWPFHCHIAWHVSAGLYLNVLERPDDIKALQIPAAVGDCRAWADYTAKNTVDQ
 IDSGLKKE*

SEQ ID NO : 73
 LENGTH : 1048 (including 150 bp 5' UTR and 150 bp 3' UTR)
 55 TYPE : DNA

ORGANISM : *M. phaseolina*

GGACCGTTGCGGCGTTACTGATCTTCGGGTGAACGTCTCTCTTCGTACCAGGAAGCCGCCAACGCCG
AAGAAAGGGAGAAATACGTGTGGCTCAACTTTATCCACCCTGGCGCCCATCATGAGCTGCGGATCTC
CGTTGACGAGCACGACATGTGGATTGCGGCCGAGATGGAGACTTCGTA AAAACCaAGAAAGTCCAA
5 GTAAGTTTCCACGTCTCGGTTTCGAGCACGCGCTGACAATCTCAAGGCCATCAATGTCAACATGGGC
GAGAGGATAAGCGTCCTTATTCCTCTTACCCAAAGTCCTGGAGAGTACGCCATCCGCATGGTCTCTC
TCGCGGAAGAGCAGCTCATCTGGGGCTTGGAATTCTCCGGTACCCCGGTGTTCAAGAGAGACGAGA
TGAGAATGGCATAATGATCCTGCCAGAAAGCCAGCCACACATTGATGTTTCAAGGATAACCTGTTGACT
GACGGAATTGTGATGGACGAAATGACCGACCTGATCCCGTTTCCCGCGCGCCGTCTCCAGCCAAGG
10 CCCACCACACCTTTTCGCTTCGCCATCAAGCGGCCGAATCCAAGCACGTGGATTTTGGCATCGGAGCC
GCATCAAGGATTCAAGAACAGCTTCCGCCGTGCTTTGGAACAAGGATTCCCGTGGCCCTACGACG
TTCGGCGGAATGAAGAACGGCTCGGTTGTGGACATCATTTATGAAAACGGAGCATTTGGGATGCATC
CGTTTCACCACTGGATGAACGAATCGCATCACAGTATGGCAACTGCTGACATTTATGCACAACCAC
AAAGCGTTCATCATCGGCATGGGGATGGGTTCTCCGGTGGCCAGACGTTGCCTCGGCCCTCAAGG
15 AGGCCCCGTGAAAACCTTTAACATGGTGAACCTCTCTCCGTGACGGAGCACGGCTGGCAAAGGGAGA
AGGATCGTGGACTGTAATCCGCTACCAGATCACCTCTCCCGCAATGTCCATGTTACACTGTAAGCAG
CTCTCTGCAAAGTGCCTGACGGTGTAAGCACTGACGACCTCTC

20 **SEQ ID NO : 74**
LENGTH : 702
TYPE : DNA
ORGANISM : *M. phaseolina*
FEATURE NAME/KEY : CDS

LOCATION : (1).....(702)
25 atgtggattgcgggccgcagatggagacttcgtaaaaccaaagaaagtccaagccatcaat
M W I A A A D G D F V K P K K V Q A I N
gtcaacatgggagagaggataagcgctccttattcctcttacccaaagtcctggagagtag
V N M G E R I S V L I P L T Q S P G E Y
gccatccgcgatggtctctctcgcggaagagcagctcatctggggcttggaattctccgg
30 A I R M V S L A E E Q L I W G L G I L R
taccgccgtgttcaagagagacgagatgagaatggcataatgatcctgccagaaagccag
Y P G V Q E R R D E N G I M I L P E S Q
ccacacattgatgttcaggataacctgttgactgacggaattgtgatggacgaaatgacc
P H I D V Q D N L L T D G I V M D E M T
35 gacctgatcccggtttcccgcgcgccgtcctccagccaaggccgaccacacctttcgcttc
D L I P F P A R R P P A K A D H T F R F
gccatcaagcgccgaatccaagcacgtggattttggcatcggagccgcgatcaaggattc
A I K R P N P S T W I L A S E P H Q G F
agacaacagcttccgcccgtgctttggaacaaggattcccggtggccctacgacgttcggc
40 R Q Q L P P V L W N K D S R G P T T F G
ggaatgaagaacggctcggttgtggacatcatttatgaaaacggagcatttgggatgcat
G M K N G S V V D I I Y E N G A F G M H
ccgtttcaccagtggatgaacgaatcgcatcacagtatggcaactgctgacatttcatgc
P F H Q W M N E S H H S M A T A D I S C
45 acaaccacaaagcggttcacatcgccatgggggatgggttcttccggtggccagacgttg
T T T K R S S S A W G M G S S G G Q T L
cctcgccctcaaggaggccctgaaaactttaacatggtga
P R P S R R P L K T L T W -

50 **SEQ ID NO : 75**
LENGTH : 233
TYPE : PRT
ORGANISM : *M. phaseolina*

MWIAAADGDFVKPKKVQAINVNMGERISVLIPLTQSPGEYAIRMVSLAEEQLIWGLGILRYPGVQER
RDENGIMILPESQPHIDVQDNLITDGI VMD EMTDLIPFPARRPPAKADHTFRFAIKRPNPSTWILAS
EPHQGFRQQLPPVLWNKDSRGPTTFGGMKNGSVVDIIYENGAFGMHPFHQWMNESHHSMATADISCT
TTKRSSSAWGMGSSGGQTLPRPSRRPLKTLTW*

5

SEQ ID NO : 76
LENGTH : 2269 (including 150 bp 5' UTR and 150 bp 3' UTR)
TYPE : DNA
ORGANISM : *M. phaseolina*

10 GCTGCGAGGCATTTCGAGAGGATTACCGAGTATTGGAGAGGCCGCGTGAAGGCAGCAGAGCATTAAAT
ACGTGCTTTGGAGCACGCGAATTACTTTCAAGTTGAACAAGATATCACCTGTCTGCACGACGTTGC
AAGCTCCGCCGAGCCATGAAGTGTGCAACTCTTTGGAGCTATCTTGCCTCTGTCTGACCGTCGGC
GCTTCTGCGAGGTATTCCATTTCAGCATAGACTTCAAACATTACCTAAATGCTGACAACTCATTTACA
GAAGCTTGACGCGGTCTTGCCTCAGCACAAAGACCAACGGAGGGTCCAATTGGGGAACCTTTGGACTG
15 TCCAAAGTTACCCGATTTTTTTGACCTCGAACCCGCTGCCCGCGGCTTCCCGTGGGGTGACAGAAGC
GGCCTAAGCAACGATCCCTACACTGATGTGCCGAACACCGGGGTGACGAGGTACTACGATTTTCAGCG
TCGCACGTGGCTATCTCGCTCCAGATGGCTACAACAAAAGTGGCATCTTCATCAACGCGAGTTCCC
TGGGCTGCCATTGAGGCCAATTGGGGCGACATGATTGAAGTACGAGTGCACAACAACATCGTCGGC
CCTGAAGAAGGCACTGCGTTCCACTGGCATGGCATTACTCAGAAGGGCAGCAATGGTTTTGACGGCG
20 TTCCCGCGGTGTCCCAATGCCCATTTGCCCTGGATCCTCTTTTACCTACCGCTTCCGTGCCGACGT
CTACGGCACTTCTTGGTGGCACTCGCACTTCTCTGCGCAATATACCGCTGGTGTCTTTGGGCCCCCTC
ATTATCTACGGCCCCAAGCATGTTCTTACGATGTTGATGTGCGCCCTGTAATTCTCGGTGATTACT
ACCACCGTGACTACTTTGATGTTCTGAGGATGCTGCCAGCAACACCACTGACTTCAACATCTACGT
CCCTTGGTCCGACAACAATCTGATCAATGGCAAGAACAACTATAATTGCTCCATGGTAGCTGGAAAC
25 TCTACGAGCTTCGCCAACGCTACAAGCTCCTCGAACGCCACGTGCTTCTCCAACGCTGGCCTTGCCC
AGTTCCGTTTTGAGCCAGGCAAAGTGCACCGCCTGCGTCTGATGAACGTGGGCGCAGCAGCACTGCT
GCACTTCTCAATCGACGGGCACAAAATGCAAGTCATCGCCACGACTTGAACCTGTTGTCCCGTAC
GAGGACAGCTCATCACGTGGGCGCCGCCAACGCACCGACATCCTCGTCACTGCAGATGCCAACCC
CCAACGAGACATACTGGATCCGCTCCACCATCTCGCTCAACTGCTCTGTCTCGCACAACACCAACGC
30 GCTGGCCGTTCTCTCCTACGAAGGCAATGACCACATAGAAGAGCCACGCAGCCGATTAGCGCCGCC
GCGGCCGCTGCTGACGAGAAGAGCTTCTCTGCAAGAACGACGACCTGTCCCAGACGGTGCCCTTCT
TCCCCAAGCCCGTCGCCGAGCCCGATGTGACCGAGACGATCGAAGTCGACCTCTTCACCAATGCGAC
CGGCCACCATGTGTGGATCATGAACAACCGCACGCAGCGCACGAACTACAACGAGCCCGTCTTGCTG
CTCGCCAACCAGGGCAACAGCACCTTCCCGGACGAGTGGAACGTTTACGACTTTGGGCGCAACAAGA
35 CCATCCGCATCGTCTCTCAACACCGTCTACAGTCCGCCACCCGATGCACTTGCACGGCCACTCTTT
CGTAAGACCCCTTCATCCCTTCGCCACGCATGTGTGCCCACTCTGACCTCTTCCTCGCAGCAAGTCTT
CGCCGAAGGCCCCGGCGCTGGGACGGCACGACCATCACCAACCCATCCAATCCCGCCCGCCGCGAC
ACGCACATGCAGCGCCGGTACGGGCACCTGGTAATCCAGTTCGAGGCCGACAACCCGGGCGCGTGGA
GCTACCACTGCCACATCGCTGGCACGCCAGCATGGGCTACAACATCGAGATCCTCGAGCGCGGCGA
40 CGAGCTGGCGGCCGCCGGCGCTATTCTATGGTCATGCAGCAGACGTGTGATGATTGGAAGGAGTGG
AGCGGCAGGAATGTGGTCAATCAGATCGACGCGGGCATTTAGATTATCGGCGACTTCTATGCCCGAT
GGTATAATGTTTTTACCAGCGTGGGATGATGTGGGTTTGGGGTCGGAATTTGTAGATATGGGCGGG
GGATTGCTGCACAAAATAGACCGATGCACATGTTTATAAAGCAAAAACCTCTTCCCAT

45 SEQ ID NO : 77
LENGTH : 1854
TYPE : DNA
ORGANISM : *M. phaseolina*
FEATURE NAME/KEY : CDS

50 LOCATION : (1).....(1854)

atgaagtgtgcaactctttggagctatcttgcctctgtcctgaccgtcggcgcttctgcg
M K C A T L W S Y L A S V L T V G A S A
agaagcttgacgcggtccttgccctcagcacaagaccaacggagggtccaattggggaact
R S L T R S L P Q H K T N G G S N W G T
55 ttggactgtccaaagtaccgcgattttttgacctcgaacccgctgcccggcggttcccg

L D C P K L P D F L T S N P L P G G F P
 tggggtgacagaagcggcctaagcaacgatccctacactgatgtgccgaacaccggggtg
 W G D R S G L S N D P Y T D V P N T G V
 acgaggtactacgatttcagcgtcgcacgtggctatctcgctccagatggctacaacaaa
 5 T R Y Y D F S V A R G Y L A P D G Y N K
 agtggcatcttcatcaacggcgagttccctgggcctgccattgaggccaattggggcgac
 S G I F I N G E F P G P A I E A N W G D
 atgattgaagtacgagtgcacaacaacatcgtcgccctgaagaaggcactgcgttccac
 M I E V R V H N N I V G P E E G T A F H
 10 tggcatggcattactcagaagggcacgcaatggtttgacggcggtcccgcggtgtcccaa
 W H G I T Q K G T Q W F D G V P G V S Q
 tgccccattgccccctggatcctcttttacctaccgcttcggtgccgacgtctacggcact
 C P I A P G S S F T Y R F R A D V Y G T
 tcttggtggcactcgcacttctctgcgcaataaccgctgggtgcttttgggccccctcatt
 15 S W W H S H F S A Q Y T A G A F G P L I
 atctacggccccaagcatgttccttacgatgttgatgtcgccctgtaattctcggtgat
 I Y G P K H V P Y D V D V G P V I L G D
 tactaccaccgtgactactttgatgttctggaggatgctgccagcaacaccactgacttc
 Y Y H R D Y F D V L E D A A S N T T D F
 20 aacatctacgtcccttggtccgacaacaatctgatcaatggcaagaacaactataattgc
 N I Y V P W S D N N L I N G K N N Y N C
 tccatggtagctggaaactctacgagcttcgccaacgctacaagctcctcgaacgccacg
 S M V A G N S T S F A N A T S S S N A T
 tgcttctccaacgctggccttgcccagttccggttcgagccaggcaaagtgcaccgcctg
 25 C F S N A G L A Q F R F E P G K V H R L
 cgtctgatgaacgtgggcgagcagcactgctgcacttctcaatcgacgggcacaaaatg
 R L M N V G A A A L L H F S I D G H K M
 caagtcatcgcccagacttcgaacctgttgccttcgtaggagcagacgtcatcacgctg
 Q V I A H D F E P V V P Y E A D V I T L
 30 ggcgcccgaacgcaccgacatcctcgtcactgcagatgccaaccccaacgagacatac
 G A A Q R T D I L V T A D A N P N E T Y
 tggatccgctccaccatctcgtcactgctctgtctcgcacaacaccaacgcgctggcc
 W I R S T I S L N C S V S H N T N A L A
 gttctctcctacgaaggcaatgaccacatagaagagccacgcagccgcatttagcgccgcc
 35 V L S Y E G N D H I E E P R S R I S A A
 ggggcccgtgctgacgagaagagcttcctctgcaagaacgacgacctgtcccagacggtg
 A A A A D E K S F L C K N D D L S Q T V
 cccttcttccccaagcccgtcgccgagcccgatgtgaccgagacgatcgaagtgcacctc
 P F F P K P V A E P D V T E T I E V D L
 40 ttcaccaatgcgacggccaccatgtgtggatcatgaacaaccgcacgcagcgcacgaac
 F T N A T G H H V W I M N N R T Q R T N
 tacaacgagcccgtcttgctgctcgccaaccagggaacagcaccttcccggacgagtgg
 Y N E P V L L L A N Q G N S T F P D E W
 aacgtttacgacttttgggcgcaacaagaccatccgcatcgctcctcaacaccgtctaccag
 45 N V Y D F G R N K T I R I V L N T V Y Q
 tccgcccaccgatgcacttgacggccactctttccaagtccctcgccgaaggccccggc
 S A H P M H L H G H S F Q V L A E G P G
 gcctgggacggcacgaccatcaccaaccatccaatcccgcggcgacacgcacatg
 A W D G T T I T N P S N P A R R D T H M
 50 cagcgccggtacgggacacgtggaatccagttcgaggccgacaacccgggcgcggtggagc
 Q R R Y G H L V I Q F E A D N P G A W S
 taccactgccacatcgcttgacggcagcatgggctacaacatcgagatcctcgagcgc
 Y H C H I A W H A S M G Y N I E I L E R
 ggcgacgagctggcgccgcccggcgctattcctatggtcatgcagcagacgtgtgatgat
 55 G D E L A A A G A I P M V M Q Q T C D D

tggaaggagtggagcggcaggaatgtggtcaatcagatcgacgcgggcatttag
W K E W S G R N V V N Q I D A G I -

5 SEQ ID NO : 78
LENGTH : 617
TYPE : PRT
ORGANISM : *M. phaseolina*
MKCATLWSYLASVLTVGASARSLTRSLPQHKTNGGSNWGTLDCPKLPDFLTSNPLPGGFPWGDRSGL
SNDPYTDVPNTGVTRYDFSVARGYLAPDGYNKSIGIFINGEFPGPAIEANWGDMEVVRVHNNIVGPE
10 EGTAHFWHGITQKGTQWFDGVPVVSQCPIAPGSSFTYRFRADVGTSSWWSHFSQAQYTAGAFGLII
YGPKHVPYDVPVILGDYHRDYFDVLEDAASNTTDFNIYVPWSDNNLINGKNNYNCMSVAGNST
SFANATSSSNATCFSNAGLAQFRFEPGKVHRLRLMNVGAAALLHFSIDGHKMQVIAHDFEPVVPYEA
DVITLGAAQRTDILVTADANPNETYWIRSTISLNCVSHNTNALAVLSYEGNDHIEEPRSRIASAAA
AADEKSFLCKNDDLSQTVPFPPKPAEPDVTETIEVDLFTNATGHHVWIMNNRTQRTNYNEPVLALLA
15 NQGNSTFPDEWNVYDFGRNKTIRIVLNTVYQSAHPMLHGHFSFQVLAEGPGAWDGTITNPSNPARR
DTHMQRRYGHLLVIQFEADNPGAWSYHCHIAWHASMGYNIEILERGDELAAGAI PMVMQQTCDWKE
WSGRNVVNQIDAGI*

20 SEQ ID NO : 79
LENGTH : 2373 (including 150 bp 5' UTR and 150 bp 3' UTR)
TYPE : DNA
ORGANISM : *M. phaseolina*
GACAATCCCTCCGCTAAATCCGACATCCGGTACTCTCGCCTCCCGGATCCCGAGCGGACACACAGCT
TCGCCTGTATACCACTTTCACCGGAGTCGCCTTCCACCCCCCTATAATTCTTTTCTGTGAGTCTA
25 CTCCGCGCGCGGTATCATGATAGATACCAAGAGCACAGGGTCCGCGCGAGACGGCGGTCTTACGCC
GCCTTAAGGCAAGACGAGTCAGAGCTATACGAGCAGAAAGAACATACGCAGTGTACACAGCCCTCCG
GCGCCGCTACCTCGGTGGAATGGCAGAGAAGAAGCCCTGGGATTGATCGACGAAAATGTCGTCGC
TCGAACAAAAGACGCTGTGGACCCACCCGCGGTACTCTGTCTTCCTTGAATTTGCCATCCTCGGT
CTGGTACTCATAATCGCTCTACTCGGCGCTCTCGCTTGGTCCAGAGGCTCTCATCATACACGACC
30 CGGTATCTGGCAGTTCACAACCATCGTCCAAGGGTCGCGCGGAAAGTATGTCTTGACCCCTGCCTG
GGATTTCTGCTGCACCGCCGAGGTCCGCAAATACCACTGGACGATCAGGGACATCGAGCTTCGCCCA
GACGGCGTGAAGCGGCCGCTGATCACCATCAATAACGAGTTCCCGGGGCCGACCATCGAATGCAACC
AGGGGGATACCGTGCGGGTTGAGGTTATAACGAAGCCGTCAATTCAACTTCCTTTACTGGCACGG
CATTTACCAGAACGGAACACGTACATGGATGGCACGGTCGGCATCAGCCAGTGTCTTATCACGTCT
35 GGGTCTAGCATGACATATGAGTTCAAAGTCGACAGAGAATCCGGCACCTATTGGTATCATGCGCACA
TGGCTATGCAGGGCTCAGATGGTCTTTTGGTCTCTGATCGTCCATTGAAAAATGAGCGGAAGCT
GCAGCAACTCGAATATGCCTCCGATCAAGTCATCATGGTCCACGATTACTACCACGATCTGACCAGC
GCGCTGATAACCACTACTTAGCGCCGGATAACGAGAACACAGAGCCTGTCCCTGACGGAGGTCTCA
TCAACGGAATGAATAAGAGAAATTGCGAGCTCCTCCGTGGTCGAGACTGTGATGCCACTGATGCACA
40 GCTTGCCACATTGGCCCTCGAACCGAACAAAGAACACCGTCTTCGAATTATCAATACTGGAGCATTT
GCTGAATTCCAGGTGAAGATTGACGAGCACACGTTCTGCTGTGACGGAGGTGGATGGGACCGAAGTTG
CTCCCGCTACTACCACAGGCTCAACATCAATCCCGACAGCGCTACAGCATCGTAATAAACACCAA
TGTCACGGATCGTGAATCTTCTGGCTGAGAGCTAAGATGATTGAGGCCTGTTTCGCTGAGGAGAAC
CCAAATCTGGATCCCGAAGTGCGCGCCATTATCCAATATACTCGCAAGGACGAGGATACCCAGCCCA
45 AGGAACCTTCGAGCAGAGACTGGGACGACATCGTGGACATGCAGTGTCTCGACATGAACGTGACAGA
GCTCCAGCCCGTAGAGAAGGCAACACCTCCACCTGCAGACACCACACTATACCTCCGCTCCAACCTTC
GAGATCGGCAACTGGCGTCTGAGCCGCGGCTTCTTCAACAGCTCGTCTGGCGTCCAACACTCTCAT
CCCCAAGCCTGCACCGCATGATCGACGGCTCCACAGCCAAAACGCCAGCTTCTCCCGACCGAGC
GTACCCCTTCAGATCAACTCGGCCGGCTTCGACACTGGGCCCCGAGCTGGTCTACCAGACCAGCGGC
50 ATCCGCACCATCGACATCCTCGTTTCCAACCTTCGACGACGGCAACCACCCGCTCCACCTGCACGGCT
ACAAGTACTTTCGTCTTTCGCTCGGGCCACGGCTACCCGCCCCGCGACCTCTACGCGCATCTCGACAT
CTCGAACCCTGCGCCGCGACACCGCTCGATCGAGGCGTTTCGCTGGATCCTACTGCGTCTCGTC
GCCGACAACCCGGGCGTCTGGGCCTTCCACTGCCACATCGGCTGGCACACCGAGGCCGGCATGCTGA
TGCAGTTCGCCACGCGCTCGACGTGCTCGCATCCAGCCAAATCCCGGATACGCACCTCGCGCTCTG
55 CGCGGCCGACGGGCTCGACCGCGGCGCTCGCCGCCAGACTCGACGTGGTTTGGGGATTTTGGGGAT

CTAGATCCTTGAAAAGTTCTGGAGAGGAGTGGGAGTTTCACCTGGCATGCAAGCGTCTCCGTTTCTT
CAGGCCAGGCTGACCCACTTCCCGCGCACGCCGATCTCGTACTGCAGCCCGTCGCCTTCCATGTTTA
GGTCCCACCTGCGGTACTCATCTTCGAC

5 SEQ ID NO : 80
 LENGTH : 2073
 TYPE : DNA
 ORGANISM : *M. phaseolina*
 FEATURE NAME/KEY : CDS

10 LOCATION : (1).....(2073)
 atgatagataccaagagcacagggtccggcgcagacggcggtcgttacgcgcgcttaagg
 M I D T K S T G S G A D G G R Y A A L R
 caagacgagtcagagctatacgagcagaaagaacatacgagtgtagacagccctccggc
 Q D E S E L Y E Q K E H T Q C T Q P S G
15 gccgcgtacctcggtggaaatggcagagaagaagccctgggattgatcgacgaaaatgtc
 A A Y L G G N G R E E A L G L I D E N V
 gtcgctcgaacaaaaagacgctgtggacccacccggcggtactctgtcttccttgaattt
 V A R T K R R C G P T R R Y S V F L E F
 gccatcctcggtctggtactcataatcgctctactcggcgctctcgcttggtccagaggc
20 A I L G L V L I I A L L G A L A W S R G
 tctcatcatcataccgacccgggtatctggcagttcacaaccatcgccaaggggtcgccgc
 S H H H T D P V S G S S Q P S S K G R R
 ggaaagtatgtcctggaccctgcctgggatttcgctgcaccgccgcaggtccgcaaatac
 G K Y V L D P A W D F A A P P Q V R K Y
25 cactggacgatcagggacatcgagcttcgccagacggcggtgaagcggccgctgatcacc
 H W T I R D I E L R P D G V K R P L I T
 atcaataacgagttcccggggcccaccatcgaatgcaaccagggggataaccgtgcggggtt
 I N N E F P G P T I E C N Q G D T V R V
 gaggttcataacgaagccgtcaattcaacttcctttcactggcacggcatttaccagaac
30 E V H N E A V N S T S F H W H G I Y Q N
 ggaaccacgtacatggatggcacgggtcggcatcagccagtgctcctatcacgtctgggtct
 G T T Y M D G T V G I S Q C P I T S G S
 agcatgacatatgagttcaaagtcgacagagaatccggcacctattggtatcatgcgcac
 S M T Y E F K V D R E S G T Y W Y H A H
35 atggctatgcagggctcagatgggtcttttgggtcctctgatcgctccattcgaaaaatgag
 M A M Q G S D G L F G P L I V H S K N E
 cggaagctgcagcaactcgaatatgcctccgatcaagtcacatggtccacgattactac
 R K L Q Q L E Y A S D Q V I M V H D Y Y
 cacgatctgaccagcgcgctgataccacactacttagcgccggataacgagaacacagag
40 H D L T S A L I P H Y L A P D N E N T E
 cctgtccctgacggaggtctcatcaacgggaatgaataagagaaattgagagctcctccgt
 P V P D G G L I N G M N K R N C E L L R
 ggtcgagactgtgatgccactgatgcacagcttgccacattcggcctcgaaccgaacaag
 G R D C D A T D A Q L A T F G L E P N K
45 aaccaccgtcttcgaattatcaatactggagcatttgctgaattccaggtgaagattgac
 N H R L R I I N T G A F A E F Q V K I D
 gagcacacgttcgctgtgacggaggtggatgggaccgaagttgctcccgccctactaccac
 E H T F A V T E V D G T E V A P A Y Y H
 aggtcaacatcaatcccgacagcgctacagcatcgtaataaacaccaatgtcacggat
50 R L N I N P G Q R Y S I V I N T N V T D
 cgtgactccttctggctgagagctaagatgattgaggcctgtttcgctgaggagaaccca
 R D S F W L R A K M I E A C F A E E N P
 aatctggatcccgaagtgcgcgccattatccaatatactcgcaaggacgaggatacccag
 N L D P E V R A I I Q Y T R K D E D T Q
55 cccaaggaaccttcgagcagagactgggacgacatcggtggacatgcagtgctcgacatg

P K E P S S R D W D D I V D M Q C L D M
 aacgtgacagagctccagcccgtagagaaggcaacacctccacctgcagacaccacacta
 N V T E L Q P V E K A T P P P A D T T L
 tacctccgctccaacttcgagatcggcaactggcgtctgagccgcggttcttcaacagc
 5 Y L R S N F E I G N W R L S R G F F N S
 tcgtcctggcgtccaacactctcatccccaagcctgcaccgcatgatcgacggcctccac
 S S W R P T L S S P S L H R M I D G L H
 agccaaaacgccagcttctccccgaccgagcgtaccccttccagatcaactcggccggc
 S Q N A S F L P D R A Y P F Q I N S A G
 10 ttcgacactgggccccgagctgggtctaccagaccagcggcatccgcaccatcgacatcctc
 F D T G P E L V Y Q T S G I R T I D I L
 gtttccaacttcgacgacggcaaccacccgctccacctgcacggctacaagtacttcgtc
 V S N F D D G N H P L H L H G Y K Y F V
 cttgcgtcggggccacggctacccgcccggcaccctctacgcgcacatctcgacatctcgaac
 15 L A S G H G Y P P A D L Y A H L D I S N
 ccgctgcgcgcgacaccgctcgatcgaggcgttcggctggatcctactgcgtctcgtc
 P L R R D T A S I E A F G W I L L R L V
 gccgacaacccgggctctgggccttccactgccacatcggttgccacaccgagggccggc
 A D N P G V W A F H C H I G W H T E A G
 20 atgctgatgcagttcgccacgcgcgtcgacgtgctcgcatccagccaaatcccggatacg
 M L M Q F A T R V D V L A S S Q I P D T
 cacctcgcgctctgcgcggccgacgggctcgaccgcggcgcgtcgccgccagactcgacg
 H L A L C A A D G L D R G A S P P D S T
 tggtttgggattttggggatctagatccttga
 25 W F G D F G D L D P -

SEQ ID NO : 81
 LENGTH : 690
 TYPE : PRT
 30 ORGANISM : *M. phaseolina*
 MIDTKSTGSGADGGRYAALRQDESELYEQKEHTQCTQPSGAAYLGNGREEALGLIDENNVARTKRR
 CGPTRRYSVFLEFAILGLVLIIALLGALAWSRGSHHTDPVSGSSQPSSKGRRGKYVLDPAWDFAAP
 PQVRKYHWTIRDIELRPDGVKRPLITINNEFPGPTIECNQGDTVREVEVHNEAVNSTSFHWGIIYQNG
 TTYMDGTVGISQCPITSGSSMTYEFKVDRESGTYYWYHAHMAMQGS DGLFGLIIVHSKNERKLQOLEY
 35 ASDQVIMVHDYYHDLTSALI PHY LAPDNENTEFPVDPGGLINGMNRKNCCELLRGRDCDATDAQLATFG
 LEPNKNHRLRIINTGAFAEFQVKIDEHTFAVTEVDGTEVAPAYYHRLNINPGQRYISIVINTNVTDRD
 SFWLRAKMI EACFAEENPNLDPEVRAIIQYTRKDEDTQPKEPSSRDWDDIVDMQCLDMNVTELQPVE
 KATPPPADTTLYLRNFEIGNWRLSRGFFNSSWRPTLSSPSLHRMIDGLHSQNASFLPDRAYPFQI
 NSAGFDTGPELVYQTS GIRTIDILVSNFDDGNHPLHLHGKYFVLASGHGYPPADLYAHLDISNPLR
 40 RDTASIEAFGWILLRLVADNPGVWAFHCHIGWHT EAGMLMQFATRV DVLASSQIPDTHLALCAADGL
 DRGASPPDSTWFGDFGDLDP*

SEQ ID NO : 82
 LENGTH : 2372 (including 150 bp 5' UTR and 150 bp 3' UTR)
 45 TYPE : DNA
 ORGANISM : *M. phaseolina*
 TATATGTTCCCTCCGTCTCAACGGAAATCCGGCAGTGC GCAAGACGAGCCCCCTTTCTCTTCTGCTT
 CGCCTGCTTTTCGTAGTCTCGTCTCCGCCCTAGACGTCTGCTCTCTCAGACAATTTGCTCAAATCCC
 CTCTCACCTCGCCGCCATGCGCTTCGCGAGCCTCGCCGTGGCATGGCTCACAACGTGCGTTGTCCAA
 50 TCACTTGCCAACGAGCCCATCCCGTTTCGACAGGATCCTCTGGGGTGAGAATGGCCCCGCCGGTAACC
 ATATGGTGAAGCGTCAGGCCAGCTCCAGCTCCCCTGCCTCATCCACCACAAGGGCCCCGATTCCGC
 CTGCACAAACGGCCCTTTGACGAGGAGCTGCTGGTCCAATGGCTTTTCCATAGCCACTGACTTTGAC
 GCCAAGTGGCCCAATACCGGAAAGACCGTCCATGTAAGCGCGCCTGCAGATATGCATCCGTCCTGCT
 GCTGACGTGCAGCCCATAGTATGACCTGACCATCAACAACGCCACCTGCAGCCCCGACGGCGGGCCC
 55 AGCCGCCCGTGCCTGATGTTCAACAACAAGATCCCTGGGCCTACGCTTTACGCCAATTGGGGCGACA

TGATCTCCGTTACCATCACCAACAAGATGCCCAACAACGGCACCAGCGTGCACTGGCATGGTCTGCG
 TCAGTACAATACAAACACCCAGGATGGCGTCAACGGAATCACGGAATGCCCTCTGGCTCCCGGCGAT
 TCCAAGACCTACCTATTCCAGGCTACACAGTTCGGCACGACCTGGTTCCACAGCCATTTCTCTGCGC
 AGTATGGCGACGGTGCCGTCGGCCAGCTCATCATCAATGGCCCCGCCTCGGCGAATTACGATTTGGA
 5 TCTCGGCACCTACACTATGACCGACTGGTACTACAGCACTGCGTTCCAGGTGCAAGATCAATTTGAT
 GCCGCCCTTCAGAGGAAGGCCCCCGCCGCGGAGGTGACACCATCCTGGTGAACGGTACGATGAAGT
 CTCCGGATGGCTCTGCTGGTAGCTACAGCCAAGTCAAGGGCCTTGTCAAGGGAAAGAAGTACCGCCT
 GCGTCTCATCAACACCTCGGTGGACAACAACATCCGCGTCTCGCTGGACAACCACCCATTACCGTC
 10 GTCACTTCCGACTTCGTCCCGAGCAAGCCTTGGACTACTGACTGGCTTCTCTTAGCCATCGGCCAGC
 GCTACGATGTCATCTTCACGGCCAATCAACCCGCGGCCAATTATTGGTTCCGTGCAGAAGTTGCCAC
 CGCATGTGCTAGCGCCAACAAGTACCGCGGCCGCGGTATATTAGCTACGTTGGTGCCGATGGCAGC
 GCTCCCCCAGAGACCGCGGTGACTGTTCCAGGTGGCTGTACCGAGCCTCTGCCTGCGCCTTTCTGTCG
 CAAACCAGGTTCCAAGCCAAGTCTTCCTCGACCAAGTGAAGACCCTTAGCGTCGATGTTTATGCGGC
 AAACGTCTCGACCAACCAGAAGAACATTGTCTTCTGGGGCATCAACATGACTGCCATTGACATTGAT
 15 TGGGAGAAGCCGACGCTGGAATACGTGAGGACAAAAAATACCAGCTACCCCCACGTTTACAACCTTGA
 TCGAGTTGCCACAGAGAACATTGTAAGCGGAGTTAAGCTTCAACCCCGAGAAATGTTATTAACGAT
 CGCAACAGTGGACCTACTGGATCATCCAAGAACTCCCGGCACTCCCCCAATTCCGCATCCAATTCA
 CTTGCACGGTAAGCTGCAGGTCTCAACCTTGCAACCCCGTAGAGATACTGATGGTCGCCTCTGTCCA
 GGCCACGACTTCTACATCCTCGGAACCGGCTCTGGTGCCTTCGACCGCAGCACCTCGCCGTCCTCCC
 20 TCAATTTCAATAACCCCAACCCGCGCGACGTCGCACTGGTTCCCGGCGGCGGTTGGTTGGCCATTGC
 CTTCCCGACCGACAACCCAGGCGCTTGGCTCATGCACTGCCATATCGTAAGTTTACCTATCTCTCCG
 ACTACGATCAATTGTGTATATTTCATGCGCACGGCGCTGACACGTGGATTTCCCTCGCCACAGGCTTG
 GCACATTAGCGAAGGTCTCGGAGTTTCAGTTCTCGAGGGCAAGGATAAGATCAATCTTCCCGACGCT
 GCGTGGGAGACGACCTGCTCGAATTGGGACAAGTACTGGGACACCACTATCTACCCCAAGCAGGATT
 25 CCGGTCTCTGAGGGGTGGCCGTTTTTTTTTCTTCTTTACGGGCCTGAGTTTAAGGGGGGTTTGATGT
 TTTGCTGAAAAAAGACCCGTAGTGATTCTTGATTATACTTTTCGTTTTATTTCATATTGATAGGAAG
 CAACCTGATCGCACTTCGTAAACCGCA

SEQ ID NO : 83
 30 LENGTH : 1824
 TYPE : DNA
 ORGANISM : *M. phaseolina*
 FEATURE NAME/KEY : CDS
 LOCATION : (1).....(1824)
 35 atgcgcttcgcgagcctcgccgtggcatggctcacaacgtgcgctgtccaatcacttgcc
 M R F A S L A V A W L T T C V V Q S L A
 aacgagcccatcccgcttcgacaggatcctctgggggtgagaatggccccgcggtaaccat
 N E P I P F D R I L W G E N G P A G N H
 atggtgaagcgtcaggccagctccagctccctgcctcatccaccacaagggccccggat
 40 M V K R Q A S S S S P A S S T T R A P D
 tccgcctgcacaaacggccctttgacgaggagctgctgggtccaatggctttttccatagcc
 S A C T N G P L T R S C W S N G F S I A
 actgactttgacgccaagtggcccaataaccggaagaccgtccattatgacctgaccatc
 T D F D A K W P N T G K T V H Y D L T I
 45 aacaacgccacctgcagccccgacggcgggcccagccgcccgtgcctgatgttcaacaac
 N N A T C S P D G G P S R P C L M F N N
 aagatccctgggcctacgctttacgccaattggggcgacatgatctccgttaccatcacc
 K I P G P T L Y A N W G D M I S V T I T
 aacaagatgccccacaacggcaccagcgtgcactggcatgggtctgcgtcagtacaatata
 50 N K M P N N G T S V H W H G L R Q Y N T
 aacacccaggatggcgtcaacggaatcacggaatgccctctggctccccggcgattccaag
 N T Q D G V N G I T E C P L A P G D S K
 acctacctattccaggctacacagttcggcacgacctgggtccacagccattttctctgcg
 T Y L F Q A T Q F G T T W F H S H F S A
 55 cagtatggcgacgggtgccgtcggccagctcatcatcaatggccccgcctcggcgcaattac

Q Y G D G A V G Q L I I N G P A S A N Y
 gatttcgatctcggcacctacactatgaccgactgggtactacagcactgcgttccaggtc
 D F D L G T Y T M T D W Y Y S T A F Q V
 gaagatcaatttgatgccgcccttcagaggaaggcccccgcccgccaggtgacaccatc
 5 E D Q F D A A L Q R K A P G P P G D T I
 ctggtgaacggtacgatgaagtctccggatggctctgctggttagctacagccaagtcaag
 L V N G T M K S P D G S A G S Y S Q V K
 ggccttgtcaagggaaagaagtaccgcctgcgtctcatcaacacctcgggtggacaacaac
 G L V K G K K Y R L R L I N T S V D N N
 10 atccgcgtctcgcgtggacaaccacccattcaccgtcgtcacttccgacttcgtcccagagc
 I R V S L D N H P F T V V T S D F V P S
 aagccttggactactgactggcttctcttagccatcgccagcgctacgatgtcatcttc
 K P W T T D W L L L A I G Q R Y D V I F
 acggccaatcaaccgcggccaattattgggtccgtgcagaagttgccaccgcatgtgct
 15 T A N Q P A A N Y W F R A E V A T A C A
 agcgccaacaagtaccgcggccggtatattcagctacggttggtgccgatggcagcgct
 S A N K Y R G R G I F S Y V G A D G S A
 cccccagagaccgcgctgactgttccaggtggctgtaccgagcctctgcctgcgcctttc
 P P E T A V T V P G G C T E P L P A P F
 20 gtcgcaaaccaggttccaagccaagtcttcctcgaccaagtgaagacccttagcgctcgat
 V A N Q V P S Q V F L D Q V K T L S V D
 gtttatgcggcaaacgtctcgcaccaaccagaagaacattgtcttctggggcatcaacatg
 V Y A A N V S T N Q K N I V F W G I N M
 actgccattgacattgattgggagaagccgacgctggaatacgtcaggacaaaaaataacc
 25 T A I D I D W E K P T L E Y V R T K N T
 agctacccccacgtttacaacttgatcgagttgcccacagagaacatttggacctactgg
 S Y P H V Y N L I E L P T E N I W T Y W
 atcatccaagaaactcccggcactcccccaattccgcacccaattcacttgcacggccac
 I I Q E T P G T P P I P H P I H L H G H
 30 gacttctacatcctcggaaaccggctctggtgccttcgaccgcagcacctcgcgcctcctcc
 D F Y I L G T G S G A F D R S T S P S S
 ctcaatttcaataacccccacccggcgacgtcgactggttcccgccggcggttggttg
 L N F N N P T R R D V A L V P G G G W L
 gccattgccttcccgaccgacaaccagcgcttggtcatgcactgccatatcgcttg
 35 A I A F P T D N P G A W L M H C H I A W
 cacattagcgaaggtctcggagttcagttcctcgaggggaaggataagatcaatcttccc
 H I S E G L G V Q F L E G K D K I N L P
 gacgctgcgtgggagacgacctgctcgaattgggacaagtactgggacaccactatctac
 D A A W E T T C S N W D K Y W D T T I Y
 40 cccaagcaggattccggtctctga
 P K Q D S G L -

SEQ ID NO : 84

LENGTH : 607

45 TYPE : PRT

ORGANISM : *M. phaseolina*

MRFASLAVAWLTTCVVQSLANEPI PFDRILWGENGPAGNHMVKRQASSSSPASSTTRAPDSACTNGP
 LTRSCWSNGFSIATDFDAKWPN TGKT VHYDLTINNATCSPDGGPSR PCLMFNNKI PGPTLYANW GDM
 ISVTITNKMPNNGTSVHWHGLRQYNTNTQDGVNGITECPLAPGDSKTYLFQATQFGTTWFHSHFSAQ
 50 YGDGAVGQLI INGPASANYDFDLGTYTMTDWYYSTAFQVEDQFDAALQRKAPGPPGDTILVNGTMKS
 PDGSAGSYSQVKGLVKGKKYRLRLINTSV DNNIRVSLDNHPFTVVTSD FVPSKPWTTDWLLLAIGQR
 YDVI FTANQPAANYWFRAEVATACASANKYRGRGIFS YVGADGSAPPETAVTVPGCTEPLPAPFVA
 NQVPSQVFLDQVKTLSDVYAANVSTNQNIVFWGINMTAIDIDWEKPTLEYVR TKNTSYPHVYNLI
 ELPTENIWTYWI IQETPGTPPI PHPIHLHGHD FYILGTGSGAFDRSTSPSSLNFNPNPTRRDVALVPG

GGWLAI AFPTDNPGAWLMHCHIAWHI SEGLGVQFLEGKDKINLPDAAWETTCSNWDKYWDTTIYPKQ
DSGL*

5 SEQ ID NO : 85
LENGTH : 3008 (including 150 bp 5' UTR and 150 bp 3' UTR)
TYPE : DNA
ORGANISM : *M. phaseolina*
10 GAGAAGAGCTTTTTCGAAGCCATGTCAGCAGGATTAGCTCCTGAGACAGCCCTGCCCCAAAGTCCCGT
ATTTCTATGGCCGCAGTTCTCTCTCCTCGCCGAACCAAGCCTCCTCCAGTACTTTCTTCTCAAACC
TGCTCATACAAGTGCAATGGGGTTCTTCAATGCCTGCTGGGACTTGCTGCTCCACCTCCCTTTCTTT
GCTCCGCGGGGCGGCGGCTTCGAGCGGGATCGCTCGCAGCTTCCGATCTCCTCCGTCGAGTGGCG
GCGTAGTCATCCACCCGGAGAATGCTTCCCCTGGCTTACCTGCTCTTACCCGAGCATGGAAGGGTG
GGAAAGCTGCAACTACCCGACGACAGGAGCTGCTGGCTTAAAGATGGGAGGGCGAGTCAGCCTTAC
15 TTCTCTCAATACGATATCCACACAGACTGTAAGTCTCGATATGGTTGCCCGCATTCATGCTTTCA
GCTTTACCAGGCCTTCGTGCTAAATTTATGAAGACGAGACCGTCTGGCCTCAGGGTGTAACCAGAGA
AGTAAGTGTGGAATAAAGCCCTGGGGCGCGGGGAACCCGGCCTCTGAGCCTTCATCTATGGCAG
CCCGTACACATCGAGAGACGAAGTATTTATCGCGAAGAGAATGCCCTGATCTCTTTAAGCACATAC
ATCTGCATGAATATTTCAATTCCCCTTGTTCATCAGGGATGATCAAGGGGCCATGCCGTTACAAAAAT
20 GTCTGGGCAGAGTCCCTTCTTTTACGCTGCAGCAGATTTGCTTACTCGGTGTTTACTGAACATTTG
CAGTACTGGATCAACCTCAAGGACCAAGTGTAAGTGTGCTGCCATTCCCTTGAGTCCGCTGTAGCTGC
TCATACGCCCAGCTTTTCCCGACGGTTATTCCAAGCCTTATGGCAAAGTAATCAACGACACCTACC
CAGGTCCTTTAATCGAGGCTTGCTGGGGCGATGAAGTAGTTGTTTCATGTGACAACTACCTGCAGAC
GAATGGCACTACGTATTCACACGTCTATATCAGTTGTGCCGCGTATGAGCTGATGATGGGGCAGTA
25 TTCCTGACGCGGTGTGAGACAGCAGTTAGCAACGAAATGGACGGAGTCAACGGTTTGTCTGCAA
GATCCCACTATTTACCTCCTCGGCTCACGTCTAGTATTACACAGTGTCTATCGCTTATGGTG
ACACCTTACCTACCGCTTTCGTGTTACTCAATATGGAACCTACGTGTAAGTGTTCGACTCCTGAT
CTGGTCTCAGCCATTGACACGGAAGTAGGGTACCATTACACTACTCGCTCCAATACCCAGATGGCG
TTGCTGGCCCTCTCGTATTTACGGCCCTACAGCAGCCGATTGGGATGAAGAGTGGGAGACCCCGCT
30 GATGATCACTGATTGGGTTCACGATTCCGCTTTTGGGGTCTTCTCCAGGAACTCCTCGCGTCGGAT
CCTGCCAACCGGAACGTACACCACCCGTGGGGGACAGCATTCTGCTTAACGGACACGGACATTACA
ACTGCAGCCTTTCTCAGGACCAAAACCGCTGCGCGCCGGGATATGGATCTTACTACACGCAAAGATT
CCAAAAGGGTAAAAGGTACTTGATCAGGCTAATTAACCTCCTCAGCTGGAGCAGCATTTATCTTCTCC
ATAGACGGACACAAAATGAAGGTCATCTCCACGGATCTCGTTCCTTCCATTGAGCCGTACGAGACAAATG
35 CAGTGCTCCTCAACATAGGTATATAGCGTTTGGTGCTCGTCTTAGCATGTCTCCAGACACTAACTT
CCCGCAGGCCAACGCTACAACATCATCGTCGAAGCCAAACGCCGAACCCGGCGACTACTGGATCCGTA
CCGAGATACCCGGCGGGCCAGGCGGCTGTGGCAGCGTGACGACCGGGCCGGTAACGTGACGGGCAT
CCTGCGCTACGACGGACGAGTACCGCGCTACCGACCTCATCGAAGAATGACTACCCGTGCGACTGC
CACGATGAGCCAGCGGAGCTGCTGCACCCAATCCTGCGGTGGACGGTGGATCCGCACCCGCAGAACG
40 ACGTACACAACAACACGTACGAGGTGGCATTTTCAGACGCCAGTTCCACAAGGCCCTTCCGCTGGGA
CCTGACCGACACGCCCATGTGGCTCGACTTCTCAAACCCGACCATCCTCAACCTGTACAACACCACC
TGGAACCCGGAGTACGCCGTCTCGACTGTGAGTTGTCTTCTTACCTCCCGTTCTCCCCAAAAAAC
ACTAGCAACGAGTGGATGAAGACTGACAGGTACGAAAACAGACAACCTATGACCGCGGCTTCTGTCTAC
CTCGTCATCACGGCCAACCTGACACGGCTGGGCGACAACAAGCGCGAGATCCCCGCGGCCACCCCA
45 TCCACCTGCACGGCCACGACTTCGCCGTCTCGCCAGTCCAACCTCGACCTATGACGAGCGCTCCGA
CCCGCTCAATTTACCCCTCGCCAACCCGCCGCGCGATGTCTTCTTCTGCGGAGCAACGGCTAC
GTCGCGCTGGCGTTCAAGCCGGACAATCCCGGCATATGGTTGGTGCATTGCCATATCGCTTGGCATG
CCAGTTCTGGTGAGTGTCTTTCTTTTCTTTTGGTAACTTTGTTTTCTGTGGCTTTTTTAAAGT
GTGTGAATGCATGCTGATGATTTTTATACGATGCACAGGCCTGGCACTGCAGATTCTGGAGAGGCAG
50 CCAGATATCCTGGATTGATTTGGCAGCTCGAGGCGACGAATAAGACGTGTGCTGGATGGGATACGT
ACGAGAGGGCGCATCCGATCGAGCAAGACGACAGCGGTATCTGATTAGACGTACCTCTGCGTCAGAT
CCGACGAGTTGGGAGTGAATGATGCCCTCTGGAAGGATTGTGAAGGATGGGGTGAGCTCTTCTCCT
GTGCATTTTCTCTCATGTTGAGGAGCTCTGTTCTGATGCTGAGTACGCTCATTTATTTCC

55

SEQ ID NO : 86
LENGTH : 1932
TYPE : DNA
ORGANISM : *M. phaseolina*
5 FEATURE NAME/KEY : CDS
LOCATION : (1).....(1932)
atgggggttcttcaatgcctgctgggaacttgctgctccacctccctttctttgctccgcgg
M G F F N A C W D L L L H L P F F A P R
ggcggcggttctcgagcgggatcgctcgcagcttccgatctcctccgggtccgagtggcggc
10 G G G F E R D R S Q L P I S S G P S G G
gtagtcacccacccggagaatgcttccccctggcttcacctgctcttaccgagcatggaa
V V I H P E N A S P G F T C S Y P S M E
gggtgggaaagctgcaactcacccgacgacaggagctgctggcttaaagatgggagggcg
G W E S C N S P D D R S C W L K D G R A
15 agtcagccttacttctctcaatacgatatccacacagactacgagaccgtctggcctcag
S Q P Y F S Q Y D I H T D Y E T V W P Q
ggtgtaaccagagaatactggatcaacctcaaggaccaagtgcttttccccgacgggtat
G V T R E Y W I N L K D Q V L F P D G Y
tccaagccttatggcaaagtaataacgacacctacccagggtcctttaatcgaggcttgc
20 S K P Y G K V I N D T Y P G P L I E A C
tggggcgatgaagtagttgttcatgtgacaaactacctgcagacgaatggcactactatt
W G D E V V V H V T N Y L Q T N G T T I
cactggcacggtgtgagacagcagttcagcaacgaaatggacggagtcaacgggtattaca
H W H G V R Q Q F S N E M D G V N G I T
25 cagtgtcctatcgcttatggtgacaccttcacctaccgctttcgtgttactcaatatgga
Q C P I A Y G D T F T Y R F R V T Q Y G
actacgtggtaccattcacactactcgtccaataccagatggcgttgctggccctctc
T T W Y H S H Y S L Q Y P D G V A G P L
gtattttcacggccctacagcagccgattgggatgaagagtgggagacccccgctgatgatc
30 V F H G P T A A D W D E E W E T P L M I
actgattgggttcacgattcggcttttggggcttctctcccaggaactcctcgctcggat
T D W V H D S A F G V F S Q E L L A S D
cctgccaaaccggaacgtcacaccacccgtgggggacagcattctgcttaacggacacgga
P A N R N V T P P V G D S I L L N G H G
35 cattacaactgcagcctttctcaggacccaaaaccgctgcgcgcccgggatatggatcttac
H Y N C S L S Q D Q N R C A P G Y G S Y
tacacgcaaagattccaaaagggtaaaagggtacttgatcaggctaattaactcctcagct
Y T Q R F Q K G K R Y L I R L I N S S A
ggagcagcatttatcttctccatagacggacacaaaatgaaggctcatctccacggatctc
40 G A A F I F S I D G H K M K V I S T D L
gttcccattgagccgtacgagacaaatgcagtgtcctcaacataggccaacgctacaac
V P I E P Y E T N A V L L N I G Q R Y N
atcatcgtcgaagccaacgcggaacccggcgactactggatccgtaccgagatacccggc
I I V E A N A E P G D Y W I R T E I P G
45 gggccaggcggctgtggcagcgtgcacgaccgggcccggtaacgtgacgggcatcctgcgc
G P G G C G S V H D R A G N V T G I L R
tacgacggacgcagttaccgctaccgacctcatcgaagaatgactaccgctcgactgc
Y D G R S T A L P T S S K N D Y P S D C
cacgatgagccagcggagctgctgcacccaatcctgccgtggacgggtggatccgcacccg
50 H D E P A E L L H P I L P W T V D P H P
cagaacgacgtacacaacaacacgtacgaggtcggcatttcagacgcccagttccacaag
Q N D V H N N T Y E V G I S D A Q F H K
gccttccgctgggacctgaccgacacgcccattgtggctcgacttctcaaaccgaccatc
A F R W D L T D T P M W L D F S N P T I
55 ctcaacctgtacaacaccacctggaacccggagtagcgcgtcatcgactacaactatgac

L N L Y N T T W N P E Y A V I D Y N Y D
 cgcggcttcgtctacctcgtcatcacggccaacctgacacggctgggcgacaacaagcgc
 R G F V Y L V I T A N L T R L G D N K R
 gagatccccgcccggccaccccatccacctgcacggccacgacttcgccgtcctcgcccag
 5 E I P A G H P I H L H G H D F A V L A Q
 tccaactcgacctatgacgagcgctccgacccgctcaatttcaccctcgccaacccgccc
 S N S T Y D E R S D P L N F T L A N P P
 cgccgcgatgtcgtcttcctgcccagcaacggctacgtcgcgctggcggttcaagccggac
 R R D V V F L P S N G Y V A L A F K P D
 10 aatccccggcatatggttggtgcattgccatatcgcttgccatgccagttctggcctggca
 N P G I W L V H C H I A W H A S S G L A
 ctgcagattctggagaggcagccagatatcctggattcgattggcacgctcgaggcgacg
 L Q I L E R Q P D I L D S I G T L E A T
 aataagacgtgtgctggatgggatacgtacgagagggcgcatccgatcgagcaagacgac
 15 N K T C A G W D T Y E R A H P I E Q D D
 agcggatatctga
 S G I -

SEQ ID NO : 87
 20 LENGTH : 643
 TYPE : PRT
 ORGANISM : *M. phaseolina*
 MGFFNACWDL L L L H L P F F A P R G G G F E R D R S Q L P I S S G P S G G V V I H P E N A S P G F T C S Y P S M E G W E S C N S
 P D D R S C W L K D G R A S Q P Y F S Q Y D I H T D Y E T V W P Q G V T R E Y W I N L K D Q V L F P D G Y S K P Y G K V I N D T Y P G
 25 P L I E A C W G D E V V V H V T N Y L Q T N G T T I H W H G V R Q Q F S N E M D G V N G I T Q C P I A Y G D T F T Y R F R V T Q Y G T
 T W Y H S H Y S L Q Y P D G V A G P L V F H G P T A A D W D E E W E T P L M I T D W V H D S A F G V F S Q E L L A S D P A N R N V T P
 P V G D S I L L N G H G H Y N C S L S Q D Q N R C A P G Y G S Y Y T Q R F Q K G K R Y L I R L I N S S A G A A F I F S I D G H K M K V
 I S T D L V P I E P Y E T N A V L L N I G Q R Y N I I V E A N A E P G D Y W I R T E I P G G P G G C G S V H D R A G N V T G I L R Y D
 G R S T A L P T S S K N D Y P S D C H D E P A E L L H P I L P W T V D P H P Q N D V H N N T Y E V G I S D A Q F H K A F R W D L T D T
 30 P M W L D F S N P T I L N L Y N T T W N P E Y A V I D Y N D R G F V Y L V I T A N L T R L G D N K R E I P A G H P I H L H G H D F A
 V L A Q S N S T Y D E R S D P L N F T L A N P P R R D V V F L P S N G Y V A L A F K P D N P G I W L V H C H I A W H A S S G L A L Q I
 L E R Q P D I L D S I G T L E A T N K T C A G W D T Y E R A H P I E Q D D S G I *

SEQ ID NO : 88
 35 LENGTH : 2404 (including 150 bp 5' UTR and 150 bp 3' UTR)
 TYPE : DNA
 ORGANISM : *M. phaseolina*
 A A A T G C C A T G G A C A G C T C G C C C G G G A T C G A T G T C C T T T C T C C C C G A G C C C C G T C G C C C G T C C A G G A
 G A G A T A A A C C T T C T C A T A G G C C T C A T T C C T A C T C T C C T T C C C T T T T C G T T A C C C T C C C C G A C C
 40 G C G G T C C A C C T T C G A C A T G T G G T G G T T G G C A T T G T T C A T T G C T T G T G G C C G C C A C G G C C T G G G C C
 A A G G A G C C C T A C C T C A A G G T C C A C G A T G A T A C C T T T A T T C C A G A T G C C G T G T T G C G G G T A A C A G A G G
 A G A G T G C C T C A T T G G T T G C A T C G A G A G G A C C T C C G C C G T G G T C A A C G G C A C A G T T C C G G G G C C G A T
 T T T G G A A T T C C A A T C C G G C A G C G T G G T A T G G G T T C G T G T T T A C A A T G A T A T G G C A G A C A A A A C C T C
 A C C A T G G T A A G C C C C G A C G A T A T G C C T G C G G T G A A T C A G A C T A G T C A A T T A A C T T C T C G G T C C A C A G
 45 C A T T G G C A T G G C C T C A C C A T G G C A G C C G C T C C A T T C G C C G A C G G T T C C G T T G C A G C C A G C C A G T G G G
 C G A T C G A G C C G T T C A A A T T C T T C G A C T A C G A G C T C A A C C T A T T C G A C A T C A A G C C T G G G A C G T A T T T
 C T A C C A C T C C C A T G T C G G A T T C C A G G C A A T T A C T G C C A C G G G T C C C C T G C T C A T T A C C A A A A G C C G
 G G A G A G G A G C C G C C G T A T G A G T A C G A G G A G G A A C G C A T C G T C C T C T T T T C C G A C C T T T A C A A C A C G A
 C G G A C C A C G A C A T T G A A A C C G G A C T G G T A G C C A G C C T T T C A A A T G G A G C G G T G A G G T C G G A G A C G T
 50 C C T C G T C A A C G G A T A T G G C A T A T C G C A G T A C C G G C C A C G A A C G A C G C C G A G A G T T G C A A C C T T G C A
 C A G A T T C C C G T G A A G C T G G G A A G A C G T A C C G T T T G C G T T T C A T T G G T G C C A C T G C C T T T C T T T C C
 T C T C C G T T G G C T T T G A G A A G C A A T C T T A C C A T C A T C G A G G C G G A T G G C C A C T A C A C G G A A C C T G C
 A G A A A T C A G C T T C C T T C A A A T C G G C G G C G G C C A A C G G T A T T C T G C T C T C T A A A G A C A T G G A C T T G C
 G A G G A G C T C G C C G C C A A G A C T G C T G G T C G A A A C C A G T T C T A C A T C C A A A T C G A G A C T C G T G A C A G G C
 55 C C A A G A A C C T A C C A C C T A C G C C A T T C T G G A C T A C A G C G A C A G C T G C G C C A C C A A T A G C A T C A G C G T

CGAGGCCACCATCGGCAAGGACTCAACATCGCCCCCTTCTACGCCCCCTCCTTCGCTCAGCAAACCC
 GGCAACAACAACAAAAACAACAACACCACGCTCTCCCGCAAGACGCCGCCCAAGACCCACCGC
 TGCACCTCCCGCCACCGTGCAAGGCTGGCTCGACCATGACCTCCACCCGCTCGAAACCTACACGGA
 CTTCCCGACGGCGGACGAGGTCACGCGCACCGTCTACATGGACATCTTCCAGCTAGGGCAGGACGGC
 5 TACGTCAAGTGGGCGCAGAACAACCTGTCTGTGGTACGAGCACACGCCCAAGGTTCCCTACCTCGTCG
 CGCTCTACACCAACAGCACGCAGTACCTGCCCCGACTACGACTATGCCGTTCGCATCGGGGACGGGCCA
 CGACGACCGCGTTCGGTGCCTGGCCCGCAAGATGGGCGAGGTGCTCGAGATCATCGTCGTCAACACG
 GGCAGCTACAGCGGCGGCATGGACGTGCATCCCATGCACCTGCACGGCGCGCACCCGTTCTATTTGG
 GGAGTGGGAAGGGCACGTACAACAGAGAGGAGAACGAGAAGAAGTTGGCGGGGAGGGTGCCGGTCAC
 10 GAGGGATTTCGATGATGCTGTATCGGTATGGCGAGAAGGAGGAGCCGCACAAGGATAATAGCTGGATT
 GCGCTGAGGATAAGGGTGACGCAGCCGGGGGTGTGGATGTTCCATTGCCATACGCTGGCGCATATGA
 TTATGGGTGAGTTTGACCTTTTTtCCCTTTTTTTTTTTTTTTTTtCTtATTGCGCATGTTGGTTTGAT
 GAAAACCATGGTGTGATGTGATTTGGAACAGGTATGCAAACGGTCTGGGTGTTTGGCGATTTCGAAG
 GATATCCTCACGCTGCCGCTGCCGATGGTGGAAGGTTACTTGGTGCCTGGCGGAGATGTGTTCCGGTG
 15 ATGATGATCATGATCCGGTGGTGGTGCACCTTCTTTGACCTGGACGACGACGACGATGATGATGA
 TGCCAATAAGACCGACGGGAACGGCGGGAAGAATGGCCGGTAGATGGGGGGAGGAGATTACTTGAT
 TCGCAATGGAAGAGGTTACTGCGGAGGGGATTTGTAATGCATGCTACAGTTTTTATGTTATATGCCA
 GGTATAACCAGAAGGAAAGCCGGATGATTAATCGTGGAACAAGAGAAAGAAGCATTTA

20 **SEQ ID NO** : 89
LENGTH : 1950
TYPE : DNA
ORGANISM : *M. phaseolina*
FEATURE NAME/KEY : CDS

25 **LOCATION** : (1).....(1950)
 atgtggtggttggcattgttctcattgcttgtggccgcccacggcctgggccaaggagccc
 M W W L A L F S L L V A A T A W A K E P
 tacctcaaggtccacgatgatacctttattccagatgccgtgttgcggttaacagaggag
 Y L K V H D D T F I P D A V L R V T E E
 30 agtgcctccattggttgcacgagaggacctccgccgtggtcaacggcacagttccgggg
 S A S I G C I E R T S A V V N G T V P G
 ccgatttttgaattccaatccggcagcgtggtatgggttcgtgtttacaatgatatggca
 P I L E F Q S G S V V W V R V Y N D M A
 gacaaaaacctcaccatgcattggcatggcctcaccatggcagccgctccattcgccgac
 35 D K N L T M H W H G L T M A A A P F A D
 ggttccgttgcagccagccagtggtggcgatcgagccgttcaaattcttcgactacgagctc
 G S V A A S Q W A I E P F K F F D Y E L
 aacctattcgacatcaagcctgggacgtatttctaccactcccatgtcggattccaggca
 N L F D I K P G T Y F Y H S H V G F Q A
 40 attactgccacgggtccctgctcattaccaaaaagccgggagaggagccgccgtatgag
 I T A T G P L L I T K K P G E E P P Y E
 tacgaggaggaacgcacgtcctcttttccgacctttacaacacgacgaccacgacatt
 Y E E E R I V L F S D L Y N T T D H D I
 gaaaccggactggttagccagccctttcaaattggagcgggtgaggtcggagacgtcctcgtc
 45 E T G L V A S P F K W S G E V G D V L V
 aacggatatggcatatcgagtagccgacccgacgaacgacgcccagaggttgcaaccttgca
 N G Y G I S Q Y P A T N D A E S C N L A
 cagattcccgtggaagctgggaagacgtaccgtttgctttcattggtgccactgccctt
 Q I P V E A G K T Y R L R F I G A T A L
 50 tctttcctctccgttggctttgagaagcacaatcttaccatcatcgaggcggatggccac
 S F L S V G F E K H N L T I I E A D G H
 tacacggaacctgcagaaatcagcttcccttcaaattcggcgggcgccaacgggtattctgct
 Y T E P A E I S F L Q I G G G Q R Y S A
 ctccataagacatggacttgcgaggagctcgccgccaagactgctggtcgaaaccagttc
 55 L L K T W T C E E L A A K T A G R N Q F

tacatccaaatcgagactcgtgacaggcccaagaacctcaccacctacgccattctggac
 Y I Q I E T R D R P K N L T T Y A I L D
 tacagcgacagctgcgccaccaatagcatcagcgtcgaggccaccatcggcaaggactca
 Y S D S C A T N S I S V E A T I G K D S
 5 acatcgcccccttctacgccccctcttcgctcagcaaaccggcaacaacaacaaaaac
 T S P P S Y A P P S L S K P G N N N K N
 aacaacaacaccacgctctcccgaagacgcccgaagacccaccgctgcacctccc
 N N N T T L S R K T P P K T P P L H L P
 10 cccaccgtgcaaggctggctcgaccatgacctccaccgctcgaaacctacacggacttc
 P T V Q G W L D H D L H P L E T Y T D F
 ccgacggcgggacgaggtcacgcgacacgctctacatggacatcttccagctagggcaggac
 P T A D E V T R T V Y M D I F Q L G Q D
 ggctacgtcaagtgggcgagaacaacctgtcgtggtacgagcacacgcccgaaggttccc
 G Y V K W A Q N N L S W Y E H T P K V P
 15 tacctcgtcgcgctctacaccaacagcacgcagctacctgcccgactacgactatgccgtc
 Y L V A L Y T N S T Q Y L P D Y D Y A V
 gcatcggggacggggccacgacgaccgctcggtgcctggcccgccaagatgggacgaggtg
 A S G T G H D D R V G A W P A K M G E V
 ctcgagatcatcgtcgtcaacacgggcagctacagcggcgccatggacgtgcatcccatg
 20 L E I I V V N T G S Y S G G M D V H P M
 cacctgcacggcgcgccaccggttctatttggggagtggggaaggcacgtacaacagagag
 H L H G A H P F Y L G S G K G T Y N R E
 gagaacgagaagaagtggcggggaggggtgccgggtcacgagggattcgatgatgctgtat
 E N E K K L A G R V P V T R D S M M L Y
 25 cggtatggcgagaaggaggagccgcacaaggataatagctggattgcgctgaggataagg
 R Y G E K E E P H K D N S W I A L R I R
 gtgacgcagccgggggtgtggatgttccattgccatcgctggcgcatatgattatgggt
 V T Q P G V W M F H C H T L A H M I M G
 atgcaaacgggtctgggtgtttggcgattcgaaggatatcctcacgctgccgctgccgatg
 30 M Q T V W V F G D S K D I L T L P L P M
 gtggaagggttacttgggtgcctggcgagatgtgttcgggtgatgatgatcatgatccgggt
 V E G Y L V P G G D V F G D D D H D P V
 gtggtgcacttctttgacctggacgacgacgacgatgatgatgccaataagacc
 V V H F F D L D D D D D D D D A N K T
 35 gacgggaacggcggaagaatggccggtag
 D G N G G K N G R -

SEQ ID NO : 90
 LENGTH : 649
 40 TYPE : PRT
 ORGANISM : *M. phaseolina*
 MWLALFSLVAATAWAKEPYLKVHDDTFIPDAVLRVTEESASIGCIERTSAVVNGTVPGPILEFQS
 GSVVWVRVYNDMADKNLTMHWHGLTMAAAPFADGSVAASQWAI EPFKFFDYELNLFDIKPGTYFYHS
 HVGFAQITATGPLLITKKPGEEPPEYEEERIVLFSDLNTTDHDIETGLVASPFKWSGEVGDVLVN
 45 GYGISQYPATNDAESC NLAQIPVEAGKTYRLRFIGATALSFLSVGF EKHNLTIIEADGHYTEPAEIS
 FLQIGGGQRY SALLKTWTCEELAAKTAGRNQFYI QIETRDRPKNLTTYAILDYS DSCATNSISVEAT
 IGKDSTSPPSYAPPSLSKPGNNNNNNNTLSRKTPPKTPPLHLPPTVQGWLDHDLHPLETYTDFPT
 ADEVTRTVYMDIFQLGQDGYV KWAQN NLSWYEHTPKVPYLVALYTNSTQYLPDYDYAVASGTGHDDR
 VGAWPAKMGEVLEIIVVNTGSYSGGMDVHPMHLHGAHPFYL GSGKGTYNRENEKKLAGRVPVTRDS
 50 MMLYRYGEKEEPPHKDNSWIALRIRVTQPGVWMFCHTLAHMIMGMQTVVWVFGDSKDILTLPMPVEG
 YLVPBGDVF GDDDHDPVVVHFFDLDDDDDDDDANKTDGNGGKNGR*

SEQ ID NO : 91
 LENGTH : 2569 (including 150 bp 5' UTR and 150 bp 3' UTR)
 55 TYPE : DNA

ORGANISM : *M. phaseolina*

CGCCCGATTACACCATTCCTCTGACACTCTCCTCCGGAGCTCGCATCAGGGCGCTCTCTCGCCCTC
 CTGACCTTCCGTCCGGCGCCGATATCGTCTGTTCCTGATATGAGGGGTAATCGCGACGGTGCTCCC
 GCCCACACTCTCAGCCATGGCCAGTCTCTGTTCCTCCTGCTTGCTGCTGCCCTGTGCAGCCGCGCT
 5 GCCACAGTCACGTATGACTTTAACGTGACCTGGGTACCGCCAACCCTGATGCTGCTTTTCGTGCA
 CTACCATTTGGCATCAATGGCCAGTGGCCGCTCCCTGCAATCGACGTCACCAAGGGCGACCGGTTGT
 CATCAACGTCAACAACCAGCTGGAAACGGAGAGTACCAGTTTGCATTTCCATGGAATCTACATGAAT
 GGCACCAACCACATGGATGGCCGACTGGCGTGACCCAGTGCGAGATACCGCCCGGGAGCTCATTCA
 10 CATACAATTTTACGGTATAGCACGATCCACCCCTTGTTTACTTATAGCTAACCGCACGCAGGTCTGA
 CCAACCGGGAACCTTACTGGTGAGTAGCCAGCTGTTGGCGTCAAGACTGGGAAAGCTGACGTAGCTTC
 AGGTATCATTCTCACAACCGCGCCAGTATCCCGATGGATTGCGAGGGCCTTTTATTGTGAGAGACC
 CCGACAATCCGTTCAAGGATGACTATGATGAGGAAGTCGTCTGACATTCTCCGACTGGTACCACGA
 CCGGATCCCCACCCTCATGAAGAGTTTCATTAGTGTCAAAACCCACCGGCGCGGAGCCTGTCCCG
 15 AACGCGGCACTGATGAATGACACTCAGAACCTCACCTTCCAGATGACTCCCGGGCGGAGATACATGT
 TCCGACTAATAAACATTGGTGCATTTGCTGCTCAATACGTCTGGTTCGAAGGCCATACCATGCGTAT
 CGTAGAAGTCGACGGCGTGTACACCGAAGCCGCGAGATGCAGAGCGAATTTACATGACTGCCGCTCAA
 CGCTACAGCGTAATCATCACGCAAGAACGAATCTACCTCAAACCTTCGCCTTTGTTGGAAGCATGG
 ATCAGGTCAGCTATCCTTTTACTGGGCCGACATTTTCTTCTTAACATAATGCAGGATCTCTTTTG
 20 ATACTATTCCAGCAGGCCTTAATAATAACGTGACCGGGTGGCTTGTCTACAATCAACAGAACGGCTT
 GTTGCCACCTTTAGCTATCGGGGACTACGATCCGTTTCGATGACTTCACACTTGTGCCTCAAGATGGT
 ATGGAGCTCTACGATCACGTCGATCATTCCATCACCTTCGATATGAAGATGGACAATCTCGGGGACG
 GAGCAAATTAGTATGTTGACTGTAGTTGACAACGGCCAAATGCCATGACTGACGAGCGCAGTGCCCTT
 TTTCAACGACGTGACCTACGTCGAGCCCCAAGTGCCGACTCTGTACACGGTGTGTTCTACTGGCAAT
 25 AATGCCACAGACTCGAGAATCTACGGTAGCAACACCAACAGCTTCATATTGGCTAAGGACGAAGTCG
 TCGAGATCATCCTCAACAACAATGATCCGGGAAAGCACCTTTCCATCTGCATGGGCACGCATTCCA
 AGCAATCGTTTCGTCCGAAGAAGAAGCCGGCGCGTACGTGGCAAACGAAACCTTCCCCCAGACGCCA
 ATGCGCCGCGATACAATTCTTGTCCGGCCCAATGGCAATATAGTACTGAGATTCAAGGCTGACAATC
 CTGGTGTCTGGGCTGTTCCATTGTTCATATTGAATGGTATGCTCCTTGGTATCTTTTATCCTAGCTCTA
 30 CTGACCTCTTACTGTTAGGCATGTTGCGTCGGGCCCTTATTGCCACCATGATAGAGGCACCGCTTGAC
 CTGCAATCTTCTCTCGGCAACAGCATTCTGCTGATCACTGGCGAGCTTGTGCCGCCGCCGCGCACAC
 CTACTGCAGGCAACGCAGCAGGCAACACGATTGATTATCTTGACCTGACTGGTGAAAACAAGAGCCC
 CGGCCCGCTTCCCTCTGGCTTTGAAGCGAAAGGCATTGTGCGGCTTGTCTTCAGTTGTATTGCTGCT
 GTCTTGGGCATGGCAGCCATCGTATGGTACGGGATGGCGCCTCTGACAGATGGAACGGTGCAGCAAC
 35 AACACGTTGTGGATCAACAGCCGCAAGGACGCTCCGCACAAGTTGGCGTCATGCCCTTAGCGGTGCG
 GGCAAAACGTGAGCAAAGGATGGCCAGCCGACTGATTTGGAGGCAGAGATGCGGCAAGAAAAGAGC
 GGAGAAATTACCATGGTGGAGCAGAGGAGGAGCAGCCGTGGGTATCGAACATGCTGGATGTCAGGA
 GGAGTAGCCGCGGTTTCGTCTAACATGCTAGAGACCAGAAGAAGCAGTCGTGGCAGTGAGCAGATGCT
 GTCATGAGGACCAACATCATGGTAGCAAGGTAAGTGGAATCGGCTGTGAAGAAATACAGGGTCAGT
 40 TGTGAGAGGGAAAGCTATCACGAATGGCTGAAGAGCTTTGGGCCTTGTTACGATGTAATGTTGTCCG
 GAAATGTTGTGGTAATTATTGTA

SEQ ID NO : 92**LENGTH : 2016****TYPE : DNA****45 ORGANISM : *M. phaseolina*****FEATURE NAME/KEY : CDS****LOCATION : (1).....(2016)**

atggcccagtcctctgttcctcctgcttgctgctgcccctgtgcagccgcgctgccacagtc
 M A Q S L F L L L A A A L C S R A A T V
 50 acgtatgactttaacgtgacctgggtcaccgccaaccctgatgctgcttttcgtcgact
 T Y D F N V T W V T A N P D A A F R R T
 accattggcatcaatggccagtgcccgctccctgcaatcgacgtcaccaagggcgaccgc
 T I G I N G Q W P L P A I D V T K G D R
 gttgtcatcaacgtcaacaaccagctggaaacggagagtaccagtttgcatttccatgga
 55 V V I N V N N Q L E T E S T S L H F H G

atctacatgaatggcaccaaccacatggatggcccgactggcggtgacccagtgcgagata
 I Y M N G T N H M D G P T G V T Q C E I
 ccgcccgggagctcattcacatacaattttacggctcgaccaaccgggaacttactggtat
 P P G S S F T Y N F T V D Q P G T Y W Y
 5 cattctcacaaccgcggccagtatcccgatggattgagggccttttattgtcagagac
 H S H N R G Q Y P D G L R G P F I V R D
 cccgacaatccggttaaggatgactatgatgaggaagtcgtcctgacattctccgactgg
 P D N P F K D D Y D E E V V L T F S D W
 taccacgaccggatccccaccctcatgaagagtttcattagtggtcacaaacccccaccggc
 10 Y H D R I P T L M K S F I S V T N P T G
 gcgagcctgtcccgaaacgcggcactgatgaatgacactcagaacctcaccttcagatg
 A E P V P N A A L M N D T Q N L T F Q M
 actccccgggagagatacatgttccgactaataaacattgggtgcatttgctgctcaatac
 T P G R R Y M F R L I N I G A F A A Q Y
 15 gtctggttcgaaggccataccatgcgtatcgtagaagtcgacggcgtgtacaccgaagcc
 V W F E G H T M R I V E V D G V Y T E A
 gcagatgcagagcgaattttacatgactgccgctcaacgctacagcgaatcatcacccga
 A D A E R I Y M T A A Q R Y S V I I T A
 aagaacgaatctacctcaaacttcgcctttgttggaagcatggatcaggatctctttgat
 20 K N E S T S N F A F V G S M D Q D L F D
 actattccagcaggccttaataataacgtgaccgggtggccttgcttacaatcaacagaac
 T I P A G L N N N V T G W L V Y N Q Q N
 ggcttggtgccaccttttagctatcggggactacgatccggttcgatgacttcacacttggt
 G L L P P L A I G D Y D P F D D F T L V
 25 cctcaagatggatggagctctacgatcacgtcgatcattccatcacctcgatatgaag
 P Q D G M E L Y D H V D H S I T L D M K
 atggacaatctcggggacggagcaaattatgcctttttcaacgacgtgacctacgtcgag
 M D N L G D G A N Y A F F N D V T Y V E
 cccaagtgccgactctgtacacgggtgtgtctactggcaataatgccacagactcgaga
 30 P K V P T L Y T V L S T G N N A T D S R
 atctacggtagcaacaccaacagcttcatttggttaaggacgaagtcgtcgagatcatc
 I Y G S N T N S F I L A K D E V V E I I
 ctcaacaacaatgatccgggaagcaccctttccatctgcatgggcacgcattccaagca
 L N N N D P G K H P F H L H G H A F Q A
 35 atcggttcgctccgaagaagaagccggcgctacgtggcaaacgaaaccttccccagacg
 I V R S E E E A G A Y V A N E T F P Q T
 ccaatgcgcccgcatacaattcttggtccggcccaatggcaatatagtactgagattcaag
 P M R R D T I L V R P N G N I V L R F K
 gctgacaatcctggtgtctggtgttccattgtcatattgaatggcatggtgctcgggc
 40 A D N P G V W L F H C H I E W H V A S G
 cttattgccaccatgatagaggcaccgcttgacctgcaatcttctctcggcaacagcatt
 L I A T M I E A P L D L Q S S L G N S I
 cctgctgatcactggcgagcttggtgcccgcggccacacactactgcaggcaacgcagca
 P A D H W R A C A A A G T P T A G N A A
 45 ggcaacacgattgattatcttgacctgactggtgaaaacaagagccccggccccgcttccc
 G N T I D Y L D L T G E N K S P G P L P
 tctggcctttgaagcgaaaggcattgtcgcgcttgctcttcagttgtattgctgctgtcttg
 S G F E A K G I V A L V F S C I A A V L
 ggcattggcagccatcgatgggtacgggatggcgccctctgacagatggaactgggtcagca
 50 G M A A I V W Y G M A P L T D G T G Q Q
 caacacgttggtgatcaacagccgcaaggacgctccgcacaagttggcgtcatgcccta
 Q H V V D Q Q P Q G R S A Q V G V M P L
 gcggtcgcggaacacgtgagcaaaggatggccagccggactgatttgaggagcagagatg
 A V A A K R E Q R M A S R T D L E A E M
 55 cggcaagaaaagagcggagaaattaccatggtggagcagaggaggagcagccgtgggtca

R Q E K S G E I T M V E Q R R S S R G S
tcgaacatgctggatgtcaggaggagtagccgcggttcgtctaacatgctagagaccaga
S N M L D V R R S S R G S S N M L E T R
agaagcagtcgtggcagtgagcagatgctgtcatga
5 R S S R G S E Q M L S -

SEQ ID NO : 93
LENGTH : 671
TYPE : PRT

10 ORGANISM : *M. phaseolina*

MAQSLFLLLAALCSRAATVTYDFNVTWVTANPDAAFRRRTTIGINGQWPLPAIDVTKGDRVVINNN
QLETESTSLHFHGIYMNGTNHMDGPTGVTQCEIPPGSSFTYNFTVDQPGTYWYHSHNRGQYPDGLRG
PFIVRDPNPNFKDDYDEEVVLTFSWDYHDIRIPTLMKSFISVTNPTGAEPVPNAALMNDTQNLTFQMT
PGRRYMFRLINIGAFAAQYVWFEGHTMRIVEVDGVYTEADAERIYMTAAQRYSVIITAKNESTSNF
15 AFVGSMDQDLFDTI PAGLNNNV TGWL VYNQQNGLLPPLAIGDYDPFDDFTLVPQDGMELYDHVDHSI
TLDMKMDNLGDGANYAFFNDVTYVEPKVPTLYTVLSTGN NATDSRIYGSNTNSFILAKDEVVEIILN
NNDPGKHPFHLHGHAFAQIAVRSEEEAGAYVANETFPQTPMRRDTILVRPNGNIVLRFKADNPGVWLF
HCHIEWHVASGLIATMIEAPLDLQSSLGNSIPADHWRACAAAGTPTAGNAAGNTIDYLDLTGENKSP
GPLPSGF EAKGIVALVFSCIAAVLGMAAIVWYGMAPLTDGTGQQQHVVDDQQPQGRSAQVGVMPPLAVA
20 AKREQRMASRTDLEAEMRQEKSGEITMVEQRRSSRGSSNMLDVRSSRGSSNMLETRSSRGSEQMLS*

SEQ ID NO : 94
LENGTH : 3063 (including 150 bp 5' UTR and 150 bp 3' UTR)
25 TYPE : DNA

ORGANISM : *M. phaseolina*

ACGCCTCGCCAACCTCATCTTCGTGGAACAGGCTTAGGTATCAAGCCTCCTTTGCAATCACTTACGC
GGCCCTCTCTACCTCCTGCTCATGTTTGAACAAATCACACCTCTTTGAAACGCTAGAAACACACTGT
TTCTATACCGTCGAGAATGGCCTGGACCTCAGCTCTAGATCGATCCTCGTGGCTTGCCCCAGCTTCC
30 CCACCAAGGGGGTTTGGTAAGTCGTAAAAGTTTCTCACAGTTCGCAAATTCAGAGTACCGGTTT CAG
CCTCTGATCTTTGCCACTGTACGGCGGCAGCTGAAGCCGCGTGACGTGCAATCTCCCCCTGAATA
CGTATGTGCCGACTTGTATTTCTTACATCCAGCCGTCTAGGATCGTTCCGTATCGGTCTCTGCAA
CGACTACCACTACGACCACTGGGAAATCCTCCACGTTCTCTACGCTGACCAGCACTTCATCTTCGTC
TACAGCGAAGACTAGCTCGGCCAGCTCGGCATCGCTTTCACGCACTACTCCTTCACCTGCCAGCTCT
35 TCTTCCGTGAGCTCTTCGTGATCAGATCCTCTTCTGGCGGATCTTCATCTGCTGGTACTTCTTCTG
CCCGCTCATCATATGT CAGCTCTTCTTTGAGCTCGCGTTCTGCTGTTTCTTCCCTAGTGACCAGCAT
ATCCTCTTCTCTACCTCAACTGGCACGGTATCGTCTCGCCGCTTCGAAGAGCTCCAGCTCTTCA
TCTTCCACTCTTTT CAGCCTCTTCAACCACAAAGTTGCTACTGGTACCCCGTGTGCTGGAACACTG
CGGCTTCCAGGACAGCCTGGTGCATCACACCATGACGATGACTACTATCCCATATCCAGATAC
40 CGGAGTCACACGCAATACTGGTTCGACCTTGTGAGGTGACTGTTGCCCTGATGGCATTGAGAGA
GCTGCCATGGCGGTCAACGGCAGCATCCCTGGACCCACCATGAGGCGGATTGGGGCGATATCGCCG
TCATGCATGTGACCAACAGCTTGATCTCGAGCAAGAACGGCACTAGCATTCAATTCACGGTATCCA
GCAGAACTTCACAAATCAAACGGACGGTGTATTTCCATCACTCAGTGCCCTACCGCTCCTGGCGAG
AACTACACGTATACCTGGAGGGCTGAGCAGTACGGAATACTATGGTGAGCTTGATCCGAGGATACAG
45 ATGTAAAGGAGATGCTAAGATATCACAGGTACCATTTCTCACTTTGCGCTTCAAGCTTGGGAAGGTGT
CTTTGGAGGTACATACATCCCCGCTCCAGGACCTCCAACATTTATTAACGAAGCCCTGCAGGTATCA
AGATCAATGGTCCGGCGAGTGCCAACTACGATTACGATCTTGGCCATGTCTTCTGTGAGTTTTCGAC
GCCCCCTTTTCCACTCATTGTATAAAGTAAGCTTATGCGACAAAAGCCAACGATTGGAGCCACGAGAC
TTGAGCTCTCTCGAGATCGTTTCTGCAATTCGAGGTCCGCCAACACTTGAGAATGCCCTTATCAAC
50 GGTACCAACGTGTACAACAACCTCGGGAACCATAACGGGCTCTCGTTTTTGAGACAACATTTGAGGAAG
GCAAATCCTACAGTTGAGGTTGGTCAGCGCGCCATCGACACGCATTTCAAGGTGTCATTGGGTAA
GTTGAGCCAAAACATTGAGATTTCTGAGATCTAAAGCTGATTGTGTTGCAGATAACCACAGCATGC
TTGT CATAGCCAACGACCTTGTACCCATCGTGCCGTACAACACGACCGTCTGAACATCGGAATGGG
TCATCCACTTTCTATCAGGAACCTGGCCATCAAACCTGACACTGAACCCAGGCCAACGCTACGATGTA
55 ATCATCACCGCCAACCAAGCCGTAGTCGCCACCGACTTCTGGCTGCGTGCCGTCCCGCAGACGGCCT

GCTCCAATAACGCCAACCCAGACAATATCAAAGGAATAATCCGGTACAGCACCTCCACCTCCGCCTA
 CGACTGGACGAACGAATGCGTTCGACGAGGCCCTCACCAACCTCGTGCCATGGGTGACTAAGAACGCG
 GCCTCGGGCAGCAGTCTATCTGAAGTGGTGACGCTGGGTGCGAACGTTGACAACCTCAACCGCTGGA
 TGATGAACAGCACATCGATGGTTGTTCGAGTGAATGATCCCTCGTTGCTGCAGGTTTGAATAATGA
 5 TACCAATTTTACGGATACGAGCGGCGTGGTACAGGCTTGGTACGGCGGACGAGTGGGTCATGTTTGT
 ATCGAGATGACGCTGCCGATTCCGCGTCCCATCCATCTTCACGGGCATGATGTAGATTTCTTCCAGC
 CGCCCCCCCCCCCCCTTTTTTTTGGGCTCTACTTCTAGAAATACCGGACGGAGTCGTTGCGGAGC
 GCGCCTTCGCCGACTTTTTCGCTTCCGATGTCTCAAGAAAGGTGTCCATGTTGTAATGTGTATCCCAG
 AGGCTTCCCGGCTGACTTGTGTTTGTCAACACAGTTCAACATCCTCGCCCAAGGGACCGGCACGTACG
 10 ATTCATCCGTGTGCTCACCCTGTCAAACCCGCCGCGGAGGGACGTTGCGCTGCTGCCCGCAGCCGG
 GTACTTGGTGATTGCATTGCCACCGATAACCCTGGAGCCTGTGAGGACTTCTCTTTTTCTTGTGCA
 TCCCTGGATGTATCCTTGCTGTGAAATTTTGGCTGACGCATTCGTCTCAATGCAGGGCTCATGCA
 CTGCCACATCGGCCGGCGCACTACGAGGGCTTCGCAATCCAGATCCTCGAGCGCTGGGACGAGATC
 TCGCCGCTTATCGACTACGAGACGCTTGAAGGCAACTGCAACAGATGGGACGCGTACGTGTGGTCA
 15 GCGATGTCTGACAGGACGATTCTGGCGTATGAGCAATGAAGGTTAGAGTATTTGCGACGTGTTTTAT
 CATATATAAACCTTTTAAATCGTAGTCGCTCCTTAACCATAATGTTAATCCATCACTTGGGCCATC
 CAAGCACCAACAAAACATTTGAGCCTTCCCAATCAGGACTGGCACAAG

SEQ ID NO : 95
 20 LENGTH : 2085
 TYPE : DNA
 ORGANISM : *M. phaseolina*
 FEATURE NAME/KEY : CDS
 LOCATION : (1).....(2085)
 25 atggccttgacctcagctctagatcgatcctcgtggcttgccccagcttccccaccaagg
 M A W T S A L D R S S W L A P A S P P R
 gggtttgctgaagccgctgtacgtcgaattctcccctgaatacgtatgtgccggacttg
 G F A E A A C T S N S P L N T Y V P D L
 tatttcttcatacccagccgtctaggatcggttcggtatcggtctctgcaacgactaccac
 30 Y F F I P S R L G S F G I G L C N D Y H
 tacgaccactgggaaatcctccacgttctctacgtgaccagcacttcatcttctcttc
 Y D H W E I L H V L Y A D Q H F I F L F
 ttccgtgagctcttcgtcgatcagatcctcttctggcggtatcttcatctgctggtacttc
 F R E L F V D Q I L F W R I F I C W Y F
 35 ttctgcccgtcatcatatgtcagctcttctttgagctcgcggtctgctgtttcttccct
 F C P L I I C Q L F F E L A F C C F F P
 agtgaccagcatatcctcttctctcacctcaactggcacggtatcgctcctcgcccgcttc
 S D Q H I L F S H L N W H G I V L A R F
 gaagagctccagctcttcatcttccactctttcagcctcttcaaccacaaagcctggtgc
 40 E E L Q L F I F H S F S L F N H K A W C
 gatcacaccattgacgatgactactatcccattatcccagataccggagtcacacgcgaa
 D H T I D D D Y Y P I I P D T G V T R E
 tactggttcgaccttgctcgaggtgactggtgcccctgatggcattgagagagctgccatg
 Y W F D L V E V T V A P D G I E R A A M
 45 gcggtcaacggcagcatccctggacccaccattgaggcggattggggcgatatcgccgtc
 A V N G S I P G P T I E A D W G D I A V
 atgcatgtgaccaacagcttgatctcgagcaagaacggcactagcattcatttccacggt
 M H V T N S L I S S K N G T S I H F H G
 atccagcagaacttcacaaatcaaacggacggtgttatttccatcactcagtgccctacc
 50 I Q Q N F T N Q T D G V I S I T Q C P T
 gctcctggcgagaactacacgtatacctggagggtgagcagtacggaactacatggtac
 A P G E N Y T Y T W R A E Q Y G T T W Y
 cattctcactttgcgcttcaagcttgggaaggtgtctttggaggtacatacatccccgct
 H S H F A L Q A W E G V F G G T Y I P A
 55 ccaggacctccaacatttattaacgaagccctgcaggtatcaagatcaatggtccggcga

P G P P T F I N E A L Q V S R S M V R R
gtgccaaactacgattacgatcttggccatgtcttccccaacgattggagccacgagact
V P T T I T I L A M S S S N D W S H E T
tcgagctctctcgagatcgtttctgcaattcgaggtccgccaacacttgagaatgccctt
5 S S S L E I V S A I R G P P T L E N A L
atcaacggtaccaacgtgtacaacaactcggaaccataacgggctctcgttttgagaca
I N G T N V Y N N S G T I T G S R F E T
acatttgaggaaggcaaactcctacaggttgaggttggtcagcggcgccatcgacacgcat
T F E E G K S Y R L R L V S G A I D T H
10 ttcaaggtgtcattggataaccacagcatgcttgtcatagccaacgaccttgtaaccatc
F K V S L D N H S M L V I A N D L V P I
gtgccgtacaacacgaccgtcctgaacatcggaatgggccaacgctacgatgtaatcatc
V P Y N T T V L N I G M G Q R Y D V I I
accgccaaccaagcgtagtcgccaccgacttctggctgcgtgccgtcccgcagacggcc
15 T A N Q A V V A T D F W L R A V P Q T A
tgctccaataacgccaaccagacaatatcaaaggaataatccggtacagcacctccacc
C S N N A N P D N I K G I I R Y S T S T
tccgcctacgactggacgaacgaatgcgtcgacgagggccctcaccaacctcgtagccatgg
S A Y D W T N E C V D E A L T N L V P W
20 gtgactaagaacgcggcctcgggcacgagtcctatctgaagtggtagcgtgggtcgcaac
V T K N A A S G T S L S E V V T L G R N
gttgacaacctcaaccgctggatgatgaacagcacatcgatggttgtagcgtggaatgat
V D N L N R W M M N S T S M V V E W N D
ccctcggttgctgcaggtttggaataatgataccaatttcacggatacagagcggcggtggtc
25 P S L L Q V W N N D T N F T D T S G V V
aggcttggtacggcggacgagtggtcatgtttgttatcgagatgacgctgccgattccg
R L G T A D E W V M F V I E M T L P I P
cgtcccatccatcttcacgggcacgatttcaacatcctcgccaagggaccggcacgtac
R P I H L H G H D F N I L A Q G T G T Y
30 gattcatccgtgtcgtcaccctgtcaaaccgcgcggaggacggttgcgctgctgccc
D S S V S L T L S N P P R R D V A L L P
gcagccgggtacttggtgattgcattcgccaccgataaccctggagcctgggtcatgcac
A A G Y L V I A F A T D N P G A W L M H
tgccacatcgccggcgccactacggaggggttcgcaatccagatcctcgagcgtgggac
35 C H I G R R T T E G F A I Q I L E R W D
gagatctcgccgcttatcgactacgagacgcttgaaggcaactgcaacagatgggacgcg
E I S P L I D Y E T L E G N C N R W D A
tacgtgtcggtcagcgatgtcgtacaggacgattctggcgatatga
Y V S V S D V V Q D D S G V -
40

SEQ ID NO : 96
LENGTH : 694
TYPE : PRT
ORGANISM : *M. phaseolina*

45 MAWTSALDRSSWLAPASPPRGFAEAACTSN SPLNTYVPDLYFFIP SRLGSFGIGLCNDYHYDHWEILHVLYAD
QHFI LFFREL FVDQILFWRIFICWYFFCPLIICQLFFELAFCCFFPSDQHILFSLNWHGIVLARFEELQLF
IFHSFSLFNHKA WCDHTIDDDYPIIPDTGVTREYWF DLVEVT VAPDGI ERAAMAVNGSIPGPTIEADWG DIA
VMHVTNSLISSKNGTSIH FHGIQQNFTNQT DGVISITQCPTAPGENYTYTWRAEQYGT TWYHSHFALQAWEGV
FGGTIIPAPGPPTFINEALQVSRSMVRRVPTTITILAMSSSNDWSHETSSSLEIVSAIRGPPTLENALINGTN
50 VYNSGTITGSRFETTFEEGKSYRLRLVSGAIDTHFKVSLDNHSM LVIANDLVPIVPYNTTVLNIGMQRYDV
IITANQAVVATDFWLRAVPQTACSNNANPDNIKGIIRYSTST SAYDWTNECVDEALTNLVPVWTKNAASGTS L
SEVVTLGRNVDNLNRWMMNSTSMVVEWNDPSLLQVWNNDTNFTDTSGVVRLGTAD EWVMFVIEMTLPIPRPIH
LHGHD FNILAQGTGT YDSSVSLT LSNPPRRDVAL LPAAGYLVI AFATDNPGAWLMHCHIGRRTTEGFAIQILE
RWDEISPLIDYETLEGNCNRWDAYVSVDVQDDSGV*

55

SEQ ID NO : 97
LENGTH : 2449 (including 150 bp 5' UTR and 150 bp 3' UTR)
TYPE : DNA
ORGANISM : *M. phaseolina*

5 GCGCACCCCCGAATTTTCATGTGGCACTTTGCTGGTGGCGATGCATAAAGTCTCCCAAACCTTGATCT
TCAGCGTCGAGAGCAGCTCAACGTCCGATCCGATTTTTTCGTTACCGCGCTTCTTGTCCTCAAGCC
CCCAATACAATTCAACATGTTTTCTTTTGTCTCCAGAAGCCTCAACTGCCGCTATGGCTGGACTTT
GGCCTTTCATATGGTCAATGTTTCGGCGGAAACAGTCAAGACTGCGTACACTCGCCCCAGAGCAGAC
10 ACTGCTGGCATGATGGGTTCGATATCAACACCGATTATGAAGCTAAGATACCGCCAGGGAAGCTCGT
GGAGGTAAGATAACCCAGCCACAGACGGCTCAGGCCATCGCAACTCACCTCCCTTAGTACGATTTCA
CTATCTCGGAAGCAGTCCTTGCTCCGGACGGATACTTGACGAATGTCACTCTGGTAAATGGAGTATT
CCCTGGTCCAACCCTCGAAGCTGAATGGGGAGATACGATCAGTATGCCTTCTTCATATGAAATCTTT
CTGTGTGCCTTTTGACGTGATTGCTGACATTTCTGCCAGGGATAACGATCCACAACAACCTCACAA
15 ACCACAATGGCACATCCATACATTGGCATGGAATTCGCCAATTCGAGACCAATTGGCTTGATGGTGT
TCCCCGCGTCACTCAATGCCCGTCAAAGGTACTACGGCTGGTTTGTCTTGGGAGAGAAACAGGGGAG
CTAAGTGTCAACGAGCCTGGAGACTCGCAAGTTGTGAATTCCGAGCGATGCAATATGGGACCGCATG
GTATCATTCACACTACAGTCTTCAGTGTGAGTATCAATCACAGAGCTCTTGAGCGGCACTTACGCTA
ACCATGATTAGATACAAACGGAGTTCTCGGTATTTGCTATCTCCCTTCCATACAGTTCCACAACCTGT
GGGCTGATCCCGTTGCAGGACCCATTACATCAAGGGACCTCGAGCATGAACTACGACGTGGATCT
20 CGGGCCACTGTTGATCAGTGATTGGTATCACACGATGCCTTCGGCCTATTCCATTATGAGATCGCT
TCACCGCACGCGCCGCTTCGGGTACAACTATCTTGAATGGCAAGGGAGTCTTTGATTGCGATCCAG
CCAGCGATGCTCGTTGTACGGGAGAGCACCAACGGCACGAGATAGTGTTCGAAGAGGGTAAAGATA
CAAAATTGGACTAATAAATACCGGCAGCCTTCTGACATACAAGTTCTGGATCGATGGCCATAATTTT
ACAGTTGTGCAGACGGATTTCGTTCCCATCAAACCATACGTCACCGACGTTCTGATCGTCGGGATAG
25 GTATGTTTCAGTGCCTACAAAGAATTGGCGGTAAACTGATCATTCAGCTCAACGATACGAGATCAT
TATCGAAGCAAATGTGACATTCACACGTGGTCCAACCTTCTGGATTACGCAACGTACTGTGACGAT
GATGACATGTTGGACTCGAGAGTTGGCATAGTCCGCTACGACGGCAGCGAGGTCGTGATCCGCACA
CGCCGCCAAGAGTGAGCAACACCCCGGATACGGGTGTCTGATCCAGCCACGGAGAATCTTGTTCC
CATCGTGAAGAGGGAAGTAGGCAAGAGAGTGAACGGGCTCAGCCCTGCTGATTACCTCAGGATCGGC
30 CTGCAGGGCTGGCCCAACATCTCGGACACAGATTGCTCGTACACAAATGGACACTTACCAACAGAA
CCCAGTACATTGATTGGAGGGAGCCAACAATCAAGGCGCTCACTTCGGATGTGCGGGCTGATTTTGC
GGATGAGACATGCCCCATATACCTGGACTACGAGACTGGCGAGTGGGTGTACTTCGTCATCGAGAAC
AACTACACGCTGAGCGACGCCAACACGCCCCGACCATCCCCGCTCGGTCCATCCCATCCACTTAC
ACGGGCATGACTTCGTGATCCTCGCCAGGGTGACGGCATGTTGACCCCGTCGACGTGGTGCCGAA
35 CCTCCACAACCCAAACAGGAGGGACGTGGTCAATTGCCCGATTGGCGGCTACGTATGGATCGCATTC
CAGGTCAACAATCCAGGAGCGTGGCTGATGCATTGCCATATCGCCTGGCATGCCAGCGCCGACTCT
CACTGCAGTTCATTGAGCAACCTGGCCTGATCAAGGGGTTAATGGAGCAGGCAGGAGCCTTGCCGGA
GCTTGCTGATCGATGCGAGGACTGGACTGAGTACTACAATACTGTAAACATACCAAAAGGCGCACTG
CAAGATGATTGGGCATATGAGTTGGTATTGAACCTCCGGCTGAACACGCTCAGCCACGGCTACTTG
40 CTTGGCCAAGATTGAGGGTTGGCCGAGAAATGAGTAGTGGGGATTATCACTTTCTTAGAATGTGCAC
GAAAGGGTAGTGTTCGGTCATGTCTCTTAGCTTGAAA

SEQ ID NO : 98
LENGTH : 1821
45 TYPE : DNA
ORGANISM : *M. phaseolina*
FEATURE NAME/KEY : CDS

LOCATION : (1).....(1821)
atgttttcttttgcgtccagaagcctcaactgccgctatggctggactttggcctttca
50 M F S F V V Q K P Q L P L W L D F G L S
atatgggtcaatgttcggcggaacagtcgaagactgcgtacactcgccccagagcagacac
I W S M F G G N S Q D C V H S P Q S R H
tgctggcatgatgggttcgatatcaacacccgattatgaagctaagataaccgccagggaag
C W H D G F D I N T D Y E A K I P P G K
55 ctctggagtagcatttcactatctcgaagcagtccttgctccggacggatacttgacg

L V E Y D F T I S E A V L A P D G Y L T
 aatgtcactctggttaaattggagtattccctggtccaaccctcgaagctgaatggggagat
 N V T L V N G V F P G P T L E A E W G D
 acgatcaggataacgatccacaacaacctcacaaccacaatggcacatccatacattgg
 5 T I R I T I H N N L T N H N G T S I H W
 catggaattcgccaattcgagaccaattggcttgatggtggttcccggtcactcaatgc
 H G I R Q F E T N W L D G V P G V T Q C
 ccgtcaaagcctggagactcgcaagttgtcgaattccgagcgatgcaatatgggaccgca
 P S K P G D S Q V V E F R A M Q Y G T A
 10 tggatatcattcacactacagtcttcagtatacaaaccggagttctcggacccattcacatc
 W Y H S H Y S L Q Y T N G V L G P I H I
 aagggacccctcgagcatgaactacgacgtggatctcggggccactgttgatcagtgattgg
 K G P S S M N Y D V D L G P L L I S D W
 tatcaccacgatgccttcggcctattccattatgagatcgcttcaccgcacgcgcccgtt
 15 Y H H D A F G L F H Y E I A S P H A P L
 ccggtcacaactatcttgaatggcaagggtctttgattgcatccagccagcgatgct
 P V T T I L N G K G V F D C D P A S D A
 cgttgtacgggagagcaccaacggcacgagatagtggttcgaagagggtaaaagatacaaa
 R C T G E H Q R H E I V F E E G K R Y K
 20 attggactaataaataaccggcagccttctgacatacaagttctggatcgatggccataat
 I G L I N T G S L L T Y K F W I D G H N
 ttacagttgtgcagacggatttcgttcccatcaaaccatacgtcacccgacgttctgatc
 F T V V Q T D F V P I K P Y V T D V L I
 gtcgggatagctcaacgatacagagatcattatcgaagcaaattgtgacattcacacgtggc
 25 V G I A Q R Y E I I I E A N V T F T R G
 tccaacttctggattcacgcaacgtactgtgacgatgatgacatgttgactcgagagtt
 S N F W I H A T Y C D D D D M L D S R V
 ggcatagtccgctacgacggcagcgacggctcgtgatccgcacacgcccgaagagtga
 G I V R Y D G S D G R D P H T P P K S E
 30 caacaccccgatacgggtgtcgtgatccagccacggagaatcttggttcccatcgtgaag
 Q H P G Y G C R D P A T E N L V P I V K
 agggaagtaggcaagagagtgaacgggctcagccctgctgattacctcaggatcggcctg
 R E V G K R V N G L S P A D Y L R I G L
 cagggtggcccaacatctcggacacagattcgtcgtacacaaatggacacttaccaac
 35 Q G W P N I S D T D S L V H K W T L T N
 agaaccagtagattgattggagggagccaacaatcaaggcgctcacttcggatgtcggg
 R T Q Y I D W R E P T I K A L T S D V G
 gctgatttttcggatgagacatgccccatatacctggactacgagactggcgagtgggtg
 A D F A D E T C P I Y L D Y E T G E W V
 40 tacttcgtcatcgagaacaactacacgctgagcgacgccaacacgccccgcaccatcccc
 Y F V I E N N Y T L S D A N T P R T I P
 cgctcgggtccatcccatccacttacacgggcatgacttcgtgatcctcgccccaggggtgac
 R S V H P I H L H G H D F V I L A Q G D
 ggcattgttcgaccccgctcgacgtggtgcccgaacctccacaacccaaccaggagggtg
 45 G M F D P V D V V P N L H N P T R R D V
 gtcaattgcccgatggcggtacgtatggatcgcatccaggtcaacaatccaggagcg
 V N C P I G G Y V W I A F Q V N N P G A
 tggtgatgcattgccatatcgccctggcatgccagcgccggactctcactgcagttcatt
 W L M H C H I A W H A S A G L S L Q F I
 50 gagcaacctggcctgatcaaggggttaatggagcaggcaggagccttgccggagcttgct
 E Q P G L I K G L M E Q A G A L P E L A
 gatcgatgcgaggactggactgagtactacaatactgtaaacataccaaaaggcgactg
 D R C E D W T E Y Y N T V N I P K G A L
 caagatgattcgggcatatga
 55 Q D D S G I -

SEQ ID NO : 99
LENGTH : 606
TYPE : PRT
5 ORGANISM : *M. phaseolina*
MFSFVVQKPQLPLWLD FGLS IWSMFGGNSQDCVHSPQSRHCWHDGFDINTDYEAKI PPGKLVEYDFT
I SEAVLAPDGYLTNVTLVNGVFP GPTLEAEWGD TIRITI HNNLTNHN GTSI HWHGIRQFETNWL DGV
PGVTQCPSKPGDSQVVEFRAMQYGTAWYHSHYSLQYTNGVLGPIHI KGPSSMNYD VDLGPLLI SDWY
HHD AFGLFHYEIAS PHAPLPVTTILNGKGVFDCDPASDARCTGEHQ RHEIVFE EGKRYKIGLINTGS
10 LLTYKFWIDGHNFTVVQTD FVPIKPYVTDVLI VGIAQRYEII IEANVTFT RGSNFWIHATYCD DDDM
LDSRVGIVRYDGS DGRDPHTPPKSEQHPGYGCRDPATENLVPIVKREVGKRVNGLSPADYLRIGLQG
WPNISD TDSL VHKT LTNRTQYIDWREPTIKALTS DVGADFADETCPIYLDYETGEWVYFVIENNYT
LSDANTPR TI PRSVHPIHLHGHD FVILAQGDGMFDPVDVVPNLHNPTRRDV VNCPIGGYVWIAFQVN
NPGAWLMHCHIAWHASAGLSLQFIEQPGLIKGLMEQAGALPELADRCEDWTEYYNTVNI PKGALQDD
15 SGI*

SEQ ID NO : 100
LENGTH : 2347 (including 150 bp 5' UTR and 150 bp 3' UTR)
TYPE : DNA
20 ORGANISM : *M. phaseolina*
GATACAACTCTTCTCCCCGCCTCTCTTTCA CAACTGTCTATCGCTCCTTTGTTTTCTGTCCCTCC
TTAAGGTCACATACTACTGAGACTATTTCGTGTCTCGTGCCTCTCATTAGTTT TAGTTGATTCATC
TTGCCGTTGCTGTAACATGCCGTTTTCTCCACGCCTAAGTATATGCCTTTTAGCATTTTGCTCTCAC
ATTGTGTTTCGCACTTTTCGATACCAAATGTAAAGGATAGGACCCCCACTTAAGCCCGCGCAATTACG
25 GATTTTCGTTTCGGCAACCTGTCTTGGGGCGGGCGGAGCCTTCCGACCCACTCGCACAAGGTGCAGA
ACGTTTGGATGACATCAGTCTCCCGGCCCTGAAGATGGCTGTCTTTTCTCAAAGATGCTCGGAAC
TGCTGGCGCGATAACTTCAACATCGACACCGATTTCGACGAGCGCTTCCCCACGACCGGGAAGACGG
TCACTGTAAGGAATCATCGCACCTCTTGGAACCTTACGCTAATACCGAGGGCAGTATAATCTGGAG
ATCACAACACTACCATGGCCCCGTGACGGAATCGAACGCGTCGTCATGGCCGTGAATGGCCAATATC
30 CCGGCCCGACCTTATTGCTGATTGGGGGGACACGATGGTTATCAACGTCAAGAATAGCCTGGACCA
CAACGGTACGGGTCTCCATTTCCATGGACTGCGCCAATACAAAAGCAACGGCGCCGATGGGGCGAAC
GGTATCACAGAA TGCCCAATTGCCCCCGGCGAGACCAAGACCTACACCTTTCAATGTACCCAGCACG
GTAGCTCGTGGTACCACTCGCATTACTCTGTCCAGTACTCCGACGGCGTTCTCGGCGGCATTATCAT
CAACGGCCCCCGCGACGCGCACTACGACCACGATCTTGGTGTGTACATGCTTTCTGACTGGTACCAC
35 ACTCCAATGTTTGA ACTAGCCGAAGCTGCCAGGCATTTCGACAAGGGGGCCACCGAAGGCGGATAACG
GACTCATCAACGGGACGATGAAGAGCCCTGACGGTTCTCTTGGAGCCTATGGCCAGATCCATGTGAA
GAAGGGTCTGCGGTACAGGATTTCGCGTAATGAATGTTGGCACTAACGACCACTACCTCTTCTGTGTT
GATGGGCACAACCTCACCGTGATCGCAAGTGATTTCGTGCCGGTCGTGCCCTTTTCGGCGTCCAGCA
40 TTTCCCTCGGTGTTGGTGAGATATCCGATCTTTATGTTGTTATTTTCGTGCTGACCGTCACTTTAGG
ACAGAGGTACGACGTGATCCTTATCGCCGACCAAGACATTGACAAC TACTGGATCCGCTCCGACCCG
GACTCTGCCTGTAGCGTTAACGGCAACGCCGGCAACATAAAAGCCATCCTCTCGTATGACACGGCTC
CCGCGGACGCTCAGCCGAATAGCAGCGCCACAGCATCTCCTCGGGCTGCAAGGACATGGCAGTCGT
GCCAAGAGTTGCTAATAACCGTGCCCTCTGATCGCTTCGCGGACGCGCTCCAGAGCCTGGCGATGAGC
45 GTCAATATCACGCAGCAGAACGGCCCCGCTCGTCCAGTGGTATATCAACGGCTCGGCTATGGAGGTCG
ACTGGAGCTACCCGACGGTCCAATATGTCTTAGATGGGAACACGTGCTACCCGCGTGAGCTGAACCT
AGTCCAGCTGGATGAGGCGGACCAGTGGTACTACTTCGTATCCAGACCGTGCAAGGCTTGCGTGTC
AACCTGCCGCACCCAATTCATCTTCATGGCCACGTACGTTCCCTCCTTTCCCTTCTCCCTAAACGA
AACAGTAAAAGAGGGACAAGTGAATGCGACGTACTGATTTGTTGTCCAATTGGTCCAGGACTTCTAC
ATCCTCGGCGCCGGTCCCGGCGAGTGGGACGGCAACATCGATGGCCTGCAGTTCGACAACCTCCCGC
50 GGCGCGATACGGCAATGCTACCTGCGGGTGGCTACCTCATCCTCGCCTTTCCGGCCGACAACCTGG
CGCCTGGCTCATGCATTGCCACATCCCGTTCCACGTCCAGCAGGGCTTCGGGCTGCAGTTCTTGAG
CGGCCGGATGAGATTGAGGGCGTCATGGGCGATACGAGCCCGTTTACAACGAGTGTGCGGCTTGA
AGGACTACTATGGTGGGGGCCAGGCTTTTCAGCAGTCCGATTCCGGGCTTGTAATTGGTGTGGTGGC
TTGCGCAAGAGCAAAGCGCCGTGGTGTCTGGCGGTGATTTT TAGTGGCACGGTTTTTGTACTCAT

CAACTCCTAATCACTAAGTCAGCCACCCTCGTTTCCGCCCACCCTGTACAGTCAGCATCATAACGTA
AC

SEQ ID NO : 101
5 LENGTH : 1854
TYPE : DNA
ORGANISM : M. phaseolina
FEATURE NAME/KEY : CDS
LOCATION : (1).....(1854)

10 atgccgttttctccacgcctaagtatatgccttttagcattttgctctcacattgtgttc
M P F S P R L S I C L L A F C S H I V F
gcacttttcgataccaaatgtaaaggataggacccccacttaagcccgcgcaattacgga
A L S I P N V K D R T P H L S P R N Y G
tttcgttttcggcaacctgtcttggggcgggcgaggccttccgacccactcgcacaaagg
15 F R F G N L S W G G A E P S D P L A Q G
gcagaacgtttggatgacatcagtcctcccgccccctgaagatggctgtcttttctccaaa
A E R L D D I S L P A P E D G C L F S K
gatgctcggaactgctggcgcgataaacttaacatcgacaccgatttcgacgagcgcttc
D A R N C W R D N F N I D T D F D E R F
20 cccacgaccgggaagacggtcacttataatctggagatcacaaacactaccatggccccct
P T T G K T V T Y N L E I T N T T M A P
gacggaatcgaacgcgtcgtcatggccgtgaatggccaatatcccgccccgacccttatt
D G I E R V V M A V N G Q Y P G P T L I
gctgattgggggggacacgatgggttatcaacgtcaagaatagcctggaccacaacggtacg
25 A D W G D T M V I N V K N S L D H N G T
ggtctccatttccatggactgcgccaatacaaaaagcaacggcgccgatggggcgaaacggt
G L H F H G L R Q Y K S N G A D G A N G
atcacagaatgcccaattgccccggcgagaccaagacctacacctttcaatgtaccag
I T E C P I A P G E T K T Y T F Q C T Q
30 cacggtagctcgtgggtaccactcgcttactctgtccagtactccgacggcggttctcggc
H G S S W Y H S H Y S V Q Y S D G V L G
ggcattatcatcaacggccccgcccgcgcactacgaccacgatcttgggtgtgtacatg
G I I I N G P A D A H Y D H D L G V Y M
ctttctgactgggtaccacactccaatgtttgaactagccgaagctgccaggcattcgaca
35 L S D W Y H T P M F E L A E A A R H S T
aggggcccaccgaaggcgggataacggactcatcaacgggacgatgaagagccctgacggt
R G P P K A D N G L I N G T M K S P D G
tctcttggagcctatggccagatccatgtgaagaagggtctgcggtacaggattcgcgta
S L G A Y G Q I H V K K G L R Y R I R V
40 atgaatgttggcactaacgaccactacctcttctctgttgatgggcacaacctcaccgtg
M N V G T N D H Y L F S V D G H N L T V
atcgcaagtgatttcgtgccggtcgtgcccttttccggcggtccagcatttccctcggtgtt
I A S D F V P V V P F S A S S I S L G V
ggacagaggtacgacgtgatccttatcgccgaccaagacattgacaactactggatccgc
45 G Q R Y D V I L I A D Q D I D N Y W I R
tccgacccggactctgcctgtagcgttaacggcaacgcggcaacataaaaagccatcctc
S D P D S A C S V N G N A G N I K A I L
tcgtatgacacggctcccgcgagcgtcagccgaatagcacgcgccacagcatctcctcg
S Y D T A P A D A Q P N S T R H S I S S
50 ggctgcaaggacatggcagtcgtgccaaagagttgctaataccgtgccctctgatcgcttc
G C K D M A V V P R V A N T V P S D R F
gcggaacggcgtccagagcctggcgatgagcgtcaatatcacgcagcagaacggccccgctc
A D A V Q S L A M S V N I T Q Q N G P L
gtccagtggtatatcaacggctcgggtatggaggtcgactggagctacccgacgggtccaa
55 V Q W Y I N G S A M E V D W S Y P T V Q

tatgtcctagatgggaacacgtcgtacccgcgtgagctgaacctagtccagctggatgag
 Y V L D G N T S Y P R E L N L V Q L D E
 gcggaaccagtgggtactacttcgtcatccagaccgtgcaaggcttgctgtcaacctgccg
 A D Q W Y Y F V I Q T V Q G L R V N L P
 5 cacccaattcatcttcatggccacgacttctacatcctcggcgccggtcccggcgagtgg
 H P I H L H G H D F Y I L G A G P G E W
 gacggcaacatcgatggcctgcagttcgacaaccctccgcggcgcgatacggcaatgcta
 D G N I D G L Q F D N P P R R D T A M L
 cctgcgggtgggtacctcatcctcgctttccggccgacaaccctggcgctggctcatg
 10 P A G G Y L I L A F P A D N P G A W L M
 cattgccacatcccggttcacgtccagcagggcttcgggctgcagttcttgagcgccg
 H C H I P F H V Q Q G F G L Q F L E R P
 gatgagattgagggcgctcatggcgatacagagcccgttttacaacgagtgtgcggcttgg
 D E I E G V M G D T S P F Y N E C A A W
 15 aaggactactatgggtgggggcccaggtttttcagcagtcggattcgggcttgttaa
 K D Y Y G G G Q A F Q Q S D S G L -

SEQ ID NO : 102
 LENGTH : 617
 20 TYPE : PRT
 ORGANISM : *M. phaseolina*
 MPFSPRLSICLLAFCSHIVFALSI PNVKDRTPHLSPRNYGFRFGNLSWGGAEPSDPLAQQGAERLDDI
 SLPAPEdGCLFSKDARNCWDRDNFNIDTDFDERFPTTGKTVTYNLEITNTTMAPDGIERVVMAVNGQY
 PGPTLIADWGD TMVINVKNSLDHNGTGLHFHGLRQYKSNAGDANGITECPIAPGETKTYTFQCTQH
 25 GSSWYHSHYSVQYSDGVLGGII INGPADAHYDHLGVYMLSDWYHTPMFELAEAAHRHSTRGPPKADN
 GLINGTMKSPDGLGAYGQIHVKKGLRYRIRVMNVGTNDHYLFSVDGHNLTVIASDFVPVVPFSASS
 ISLGVGQRYDVILIADQDIDNYWIRSDPDSACSVNGNAGNIKAILS YDTAPADAQPNSTRHSISSGC
 KDMVVPRVANTVPSDRFADAVQSLAMSVNITQQNGPLVQWYINGSAMEVDWSYPTVQYVLDGNTSY
 PRELNLVQLDEADQWYFVIQTVQGLRVNLPHPIHLHGHDIFYILGAGPGEWDGNIDGLQFDNPPRRD
 30 TAMPLPAGGYLILAFPADNPGAWLMHCHIPFHVQQGFGLQFLERPDEIEGVMGDTSPFYNECAAWKDY
 YGGGQAFQQSDSGL*

SEQ ID NO : 103
 LENGTH : 2415 (including 150 bp 5' UTR and 150 bp 3' UTR)
 35 TYPE : DNA
 ORGANISM : *M. phaseolina*
 TCGAGCAAGATGAATGTATCCTCCGTGGAAAGTCTTTTTTCTCAGGGCGGCCGTCCGCTTTGACCTC
 TGCCCTCTTGCTGGATTATAGAATACCCAGACGCCCATGTAGTGCATGGCCTTGTAACCTTACCCAC
 CACCTCTCTCGGAAGATGATTGGCCATTCTCTCGTAGCTGTAGCACTCGGCAGCGCAGCCATGGCA
 40 CTGGCTCTTCCTCAGAGCCACGTCCCCGCTGCTTGATGAACGGTCCGCACTCTCGGAAGTGCTGGG
 GCAACTACTCCATCGACACGGACTGGTACACCGAACTCCATACACGGGCGTGGTGAGAGAATACTG
 GTTCCTGGTCGAGAATAACACCGTAGCACCAGATGTACACGCCCCCTCTGGGTTGCGCCATTGGCAAC
 GCATGGCAGGCTGACTTGGGGTGGCAGGGATATGAGACATGGGCTCTCACGGTAAACCGCTCGATTCT
 CTGGACCAACAATCGAGGCCAACTGGGGCGACGAAGGTAAAGTTGTTTCGACTGGGATTGCGCCGCC
 45 GATAATGCTTACTGCTACGCAGTAATCGTTTATGTACCAATGGCATGGAGCGGAATGGTACCGCAA
 TCCATTTCCACGGCCTAAGGCAGCTGGGAGCCACGAAATGGATGGTGTCCCTGGGGTTACGCAGTG
 TCCTATAGTACGCCCCGTACCCTCTCTCTCTCGCACTGCTGCGCGCAAGCTATTGATACTTCTCAGGC
 TCCCCGACACTCCTACACATACAAGTGGCGAGCTACTCAATACGGAACGGTGAATCCCCCTCGAGG
 CAGAATCGGCCATACTTTAACTGACGGGTCTGAAAGAGCTGGTATCATTCCCACTTCAGCATGCAAT
 50 ACTCGGTCTGGTCTACAGGGCCCGATCGTCAATCACGGACCTGCTACGGCAGACTATGACGAGGACCT
 GGGAACGGTCTGCTTGACGAGTGGAGTACACCTCTCCGTTTCCCATGTGGTGGTACGCACGTGTG
 CCTTCCGACCGCCCTCGCTCTCAAACTCGCTCATCAACGGCAAAAACGTCTTCTATTGCGACAGTA
 CGACCGATTGAGATGCTACGGTAACGGCACACGGTGGAGTGGCGCTTTGAGCAGGGGAAAAAGTA
 TCGAATGAGGCTCATCAATACAGGCCTCTACTCAAACTTCCGTTTTGCCATTGACAACCACAACCTC
 55 ACCGTTATTGCGACCGACTTTGTTCTATCAAACCCTACACCACAGATAACGTGAGTACCAACCCC

TTGCTTTCGTGCACTCTAACGAGACATTTCTCCCAGGTGGCAATTTCAATGGGGCAACGCTACGACA
 TCGTCGTTGAGGCAAATCAACCGGAAGGTGATTACTGGCTGCGGTAAGGCTCTAATGAATTGATCAG
 ACATTGAAAAAAGGGGGCGGGGGGAACCCCATCAACTGACATTCAACCCTACCTAGGGCTATAT
 5 GGCAAACATCCTGCTGCCCAGCACTACTCAAACAATACCCTTGGCATAATCCGCTACACAGCAAA
 CTCCACTGCCGAACCAACAACAAGTCTGCACTATCCTACCCGGACACATGCGGCGACGAGCCG
 GCAGCGAGCCTCGTGCCGCACCTGGCCCTCAACGCGAGCACGCCGCCGTCGTGCGCACCTACGACC
 TGTCCAAAGTCACACTCGAGCTGCCAAAGGGCTTCTCTGGACACTGAACGACACCTACCTCTGGAT
 CAACTGGTTCGTGCGCAACGAACCTTGAGGCTGGCCGAGGGCGGCCGCCGCTGCGGCGAGCCTGCCC
 10 GCCGAATATCTCGCCGTCGACAGCCGGGCCGGCAACGAGGGACGCTGGGCGTATCTCGTGTTCAACG
 ACGTCTCCGCCCCGAATCGCTCGCACCCGATGCACCTGCACGCCACGACTTCTTCTGCTCGGCAC
 CGGCCCTGGCTATTTTGTAGTACGGCAGCAACAGCAGCAGCCTGGCGATGCTCAACCTGCACAACCCG
 CCTCGTCGCGACACGGCGACCTGGCCCGAGTCTGGCTGGATGGTCGTGCGGTTCTCATGGACAACC
 CGGGGAGCTGGCTGATCCACTGCCACATCGCCTGGCACTCGAGCGAGTCGCTCGGCCTGCAGTTCCT
 15 GGAGAGCCCTGAGACGTATGTCCCTCGATTGGAAGGCCAGAGATTGCGGGAGACGTGCGAGGCGTGG
 GATGCATTCTGGAATCGCCACGACTCATAACGAGCAAGAGGATGCGGGGATATAAGGGCCGCGAGGAC
 TGCATGAACGCATGCTTTGGTCTGTCATGGAGGCTTCGTGAATTGGCGGGAAAGATGTGACTAACTT
 CTTCTCGCATGTTCTTGGCTCTCTCCTTCTCTACACTCTCTAAATAATCCGCAAATTTCCATGTGC
 GTA

20 **SEQ ID NO** : 104
LENGTH : 1815
TYPE : DNA
ORGANISM : *M. phaseolina*
FEATURE NAME/KEY : CDS

25 **LOCATION** : (1).....(1815)
 atgattggccattctctctgtagctgtagcactcggcagcgcagccatggcactggctctt
 M I G H S L V A V A L G S A A M A L A L
 cctcagagccacgtccccgctgcttgcataaacggtccgcactctcggaagtgtggggc
 P Q S H V P A A C M N G P H S R K C W G
 30 aactactccatcgacacggactggtagaccgaaactccatacacgggctggtgagagaa
 N Y S I D T D W Y T E T P Y T G V V R E
 tactggttctggtcgagaataaccacgtagcaccagatgtacacgccccctctgggttgc
 Y W F L V E N T T V A P D V H A P L G C
 gccattggcaacgcatggcaggctgacttggggtggcagggatagagacatgggctctc
 35 A I G N A W Q A D L G W Q G Y E T W A L
 acggtaaaccgctcgattcctggaccaacaatcgaggccaactggggcgacgaagtaac
 T V N R S I P G P T I E A N W G D E V I
 gttcatgtcaccaatggcatggagcgggaatggtaccgcaatccatttccacggcctaagg
 V H V T N G M E R N G T A I H F H G L R
 40 cagctgggagcccacgaaatggatggtgtccctggggttacgcagtgtcctatagctccc
 Q L G A H E M D G V P G V T Q C P I A P
 ggacactcctacacatacaagtggcgagctactcaatacggaaacgagctggtatcattcc
 G H S Y T Y K W R A T Q Y G T S W Y H S
 cacttcagcatgcaataactcggctcgtctacagggcccgatcgtcattcacggacctgct
 45 H F S M Q Y S V G L Q G P I V I H G P A
 acggcagactatgacgaggacctgggaacggctcgtcttgacaggactggagtcacacctct
 T A D Y D E D L G T V V L Q D W S H T S
 ccggttcgcatgtggtggtacgcacgtgtgccttccggaccgcccctcgctctcaaactcg
 P F A M W W Y A R V P S G P P S L S N S
 50 ctcatcaacggcaaaaacgtcttctattgacagctacgaccgattcgagatgctacggt
 L I N G K N V F Y C D S T T D S R C Y G
 aacggcacacggctcggagtggtgctttgagcaggggaaaaagtatcgaatgaggctcatc
 N G T R S E W R F E Q G K K Y R M R L I
 aatacaggcctctactcaaacttccgttttgccattgacaaccacaacctcaccggttatt
 55 N T G L Y S N F R F A I D N H N L T V I

gcgaccgactttgttcctatcaaaccctacaccacagataacgtggcaatttcaatgggg
 A T D F V P I K P Y T T D N V A I S M G
 caacgctacgacatcgtcgttgaggcaaatacaaccggaaggtgattactggctgcgggct
 Q R Y D I V V E A N Q P E G D Y W L R A
 5 atatggcaaacatcctgctgcccgaacgactactcaaacaatacccttggcataatccgc
 I W Q T S C C P N D Y S N N T L G I I R
 tacacagcaaactccactgccgaaccaaacaacaagtccctgcactatcctaccggac
 Y T A N S T A E P N T T S P A L S Y P D
 10 acatgcggcgacgagccggcagcgagcctcgtgccgcacctggccctcaacgcgagcagc
 T C G D E P A A S L V P H L A L N A S T
 ccggccgtcgtgccgcacctacgacctgtccaaagtcacactcgagctgccaaagggcttc
 P A V V R T Y D L S K V T L E L P K G F
 ctctggacactgaacgacacctacctctggatcaactggtcgtcgccaacgaacttgagg
 L W T L N D T Y L W I N W S S P T N L R
 15 ctggccgagggcgccgagcctgcccgcgaatatctcgccgtcgac
 L A E G G A A A A S L P A E Y L A V D
 agccgggcccgaacgagggacgctgggctatctcgtgttcaacgacgtctccgcccgc
 S R A G N E G R W A Y L V F N D V S A R
 aatcgctcgacccgatgcacctgcacggccacgacttcttcctgctcggcaccggccct
 20 N R S H P M H L H G H D F F L L G T G P
 ggctattttgagtacggcagcaacagcagcagcctggcgatgctcaacctgcacaaccgc
 G Y F E Y G S N S S S L A M L N L H N P
 cctcgtcgcgacacggcgacctggcccgagtctggctggatggtcgtcgcggttcctcatg
 P R R D T A T W P E S G W M V V A F L M
 25 gacaaccggggagctggctgatccactgccacatcgccctggcactcgagcgagtcgctc
 D N P G S W L I H C H I A W H S S E S L
 ggccctgcagttcctggagagccctgagacgtatgtccctcgattggaaggccagagattg
 G L Q F L E S P E T Y V P R L E G Q R L
 cgggagacgtgcgagggcgtgggatgcattctggaatcgccacgactcatacgagcaagag
 30 R E T C E A W D A F W N R H D S Y E Q E
 gatgcggggatataa
 D A G I -

SEQ ID NO : 105
 35 LENGTH : 604
 TYPE : PRT
 ORGANISM : *M. phaseolina*
 MIGHSLVAVALGSAAMALALPQSHVPAACMNGPHSRKWCWGNYSIDTDWYTETPYTGVVREYWFLVEN
 TTVAPDVHAPLGAIGNAWQADLGWQGYETWALTVNRSIPGPTIEANWGDEVIVHVTNGMERNGTAI
 40 HFHGLRQLGAHEMDGVPGVTQCPIAPGHSYTYKWRATQYGTSWYHSHFSMQYSVGLQGPIVIHGPAT
 ADYDEDLGTVVLQDWSHTSPFAMWWYARVPSGPPSLSNSLINGKNVFCSTTDSRCYGNNGTRSEWR
 FEQGGKYRMLINTGLYSNFRFAIDNHNLTVIATDFVPIKPYTTDNVAISMGQRYDIVVEANQPEGD
 YWLRAIWQTSCCPNDYSNNTLGIIRYTANSTAEPNNTSPALSYPDTCGDEPAASLVPHLALNASTPA
 45 VVRTYDLSKVTLELPKGFLWTLNDTYLWINWSSPTNLRLAEGGAAAAASLPAEYLAVDSRAGNEGRW
 AYLVDNDVSARNRSHPMHLHGHDFFLLGTGPGYFEYGSNSSLAMLNLHNPPRRDTATWPESGWMVV
 AFLMDNPGSWLIHCHIAWHSSSESLGLQFLESPETYVPRLEGQRLRETCEAWDAFWNRHDSYEQEDAG
 I*

SEQ ID NO : 106
 50 LENGTH : 2275 (including 150 bp 5' UTR and 150 bp 3' UTR)
 TYPE : DNA
 ORGANISM : *M. phaseolina*
 TCGATGCATCCCTCTCTGACGCAGATCTCTTTTATAAAACCGACTGTCATCCTCGATTGAGTCAGTC
 TTTGCTCAAACGGACTTATTCAAAGGTCAGTTGGGTGAGTTGGGAGGCTGATGGATTTCAGGATACTC
 55 TCCGGGCACGTTGCCATGATTCGCCTTTTCTCGTGCTCGGCTTTGTGGCCACGACATTGGCCAAG

ACTGTTACTTTTAACTGGAACATCGGCTGGGTTTCTGCGGCTCCAGATGGATTTACACGGCCCGTCA
 TCGGCATCAACGGGCTGTGGCCGCCTCCCGTCTTAGAAGCCGACGTTAACGACACCATTATCGTAAC
 CGCGCATAACTCGCTAGGCAATGAGACGACGAGCTTGCACTGGCATGGCATGTGGCAGAACAACCTCG
 ACTCATATAGACGGCGGAAGTAGAGTCTCGCAGTGCAGAAATCCCTCTAGGGGGCACCTTTACGTACA
 5 GGTTTAAGGCATACCCGGCAGGCACCTTTTGGTACCATTCTCACGCTATGGGCCAATATCCCGACGG
 CCTACGGGCCCCGATGATTATTACGACCCTGATTCTGCTGCGGAGCAGGACGCCGATGAGCAGCAT
 ATACTTACGGTCTCGGACTGGTACCGTAACCAGATGCCGCCGCTTATCCACCGCTATCTAACTACTC
 CTAACTATAACGGCGCCATGCCGAAACCCAACTCGAGCTTAGTTAACGACCAGCAGTCCAAGAGGCT
 10 AAACATCCGCCCCGGGGCAGAAGAGCTATATCCGCATTATTAATATATCAGCGCTAGCAACGTTCTAT
 CTACAGTTCGGTAGGTACATCCCCCTTGTGTACAGACAAAGCTAACGATTTAGATCAACACAACAT
 GACTGTCTGTTTCTATCGACGATGTTAACGGTTGGTAATCCTGTTACTTATGCTACGCTAAGATGCAT
 GTCGGCATATAAGCCGTAGTCGTATGCAAACACGTAAGATTAAAGTGCTAACGACAGGTAGTCGAGC
 CCCAGAGTTGGGAGGCCCTAGAGATTACCCCGGACAACGGTACGACGTTATCATCACCGGTCTAGA
 GAACCCCCAAAGAACTATGCATTTATCAATAAGATGGCCGTTCTCGGCTTGCAAGAACAACATC
 15 CTCAGTTATAATTCTGTCCTGGCCTGACCCAGAGCCATTGGCCGTGAGTAGGTTCAACCTCGGAAGCG
 ATATCAATCTAACTCCGCTTGACCACGAGCCACTGCTGGAGCCCCGTGGACAAAACCTTCACCATGGA
 GGTCAACAACCTCAACATCGACGGCGTAGGCTACCGGTGAGATTGCCCCGCGGCCCTTAATCCGCAT
 GCCGCTTGCTAACTTCGATACACAGCATCACGCAAGGCCCGTACCCCTACATTACCCCGCGCACACC
 CACTCTGTACACTGCCCTAACCCACCGGCTTTAATGCTACCAACCCCGCCATCTACGGCCAGACCAAC
 20 TCTTACATCGTAGAAGCCGGCGATATCGTCCAGCTCGTTGTCAACAGCAACGACCTTGTCAACAATA
 ACACCTCCGGCCGCGGGCACCCCATGCACCTGCACGGCCACACCTTCCAAGTCGTGGGCCAATACGG
 CACCCACTGGGACGGCGACACCGCAAAATTCCCTACCGTTCCAATGAAGCGGGACACGACCGTTCTC
 TTCGCCGCGGGGAGCTTGGTCAATTCGTTCCAGGCGAACAATCCTGGTGTCTGGATGTGTACGGCTC
 TCCTCCACTTTGCACGAAAACCCAGTCCCCCGGCTGCTTGAAAAGCTTTTTTGAACGTACCTTGTGA
 25 GTCGCGCAGTCCACTGCCATATCGAATGGCATCTCGACGCCGCGCATGGCCGCCACAATCATCGAAGC
 GCCGCTCGAGTTCCAGCGAAGCGGTCTGCGGATCCCGCCACAGCACCTCGCGGCGTGCCGGGCATTA
 AACTTAACGACCCGGGGCAATTGTGCCGGCAACACCGTTAACCTGGAGGATACGGCTGCGTGCAGAA
 TCTACGACACTGATCCTTGGGGGTGAGTTGCTCTGATTTTCGCGTTAACGCAGCCTTTGCTGACGACT
 ACCGCTTTCTGCAGTGCCTTATCGGGGAACGTGAGACAGCACGTTGAATAACACGCTGGCGTAGCA
 30 CCGTATTTTGTATAGACTACTTTTCCATGTTAAATTTTCTGTATACAGTTCGAAATAGATTCAATT
 AGGGACAAATACCAGAAACAGGCTCATCCGCAACTCATGTGCACCCTGCGTAGATCGTTATGCT

SEQ ID NO : 107
 LENGTH : 1632
 35 TYPE : DNA
 ORGANISM : *M. phaseolina*
 FEATURE NAME/KEY : CDS
 LOCATION : (1).....(1632)

atgattcgccctttttctcgtgctcggtttgtggccacgacattggccaagactgttact
 40 M I R L F L V L G F V A T T L A K T V T
 ttttaactggaacatcggtggttttctgcggtccagatggatttacacggcccgctcatc
 F N W N I G W V S A A P D G F T R P V I
 ggcatacaacgggtgtggccgcctcccgctcttagaagccgacgttaacgacaccattatc
 G I N G L W P P P V L E A D V N D T I I
 45 gtaaccgcgcataactcgctaggcaatgagacgacgagcttgcaactggcatggcatgtgg
 V T A H N S L G N E T T S L H W H G M W
 cagaacaactcgactcatatagacggcggaagtagagtctcgagtgcgaaatccctcta
 Q N N S T H I D G G S R V S Q C E I P L
 gggggcaccttttacgtacaggtttaaggcatacccggcaggcacttttttggtaccattct
 50 G G T F T Y R F K A Y P A G T F W Y H S
 cacgctatgggccaatatcccgacggcctacgggccccgatgattattcacgaccctgat
 H A M G Q Y P D G L R A P M I I H D P D
 tctgctgcgagcaggacgccgatgagcagcatatacttacggtctcggactggtaccgt
 S A A E Q D A D E Q H I L T V S D W Y R
 55 aaccagatgccgcccgttatccaccgctatctaactactcctaactataacggcgccatg

N Q M P P L I H R Y L T T P N Y N G A M
 ccgaaacccaactcgagcttagttaacgaccagcagtcgaagaggctaatacatccgccc
 P K P N S S L V N D Q Q S K R L N I R P
 5 gggcagaagagctatatccgcattattaatatcagcgctagcaacggttctatctacag
 G Q K S Y I R I I N I S A L A T F Y L Q
 ttcgatcaacacaacatgactgtcgtttctatcgacgatgttaacgctcgagccccagagt
 F D Q H N M T V V S I D D V N V E P Q S
 tgggagggcctagagattacccccggacaacgggtacgacggttatcatcaccgggtctagag
 10 W E A L E I T P G Q R Y D V I I T G L E
 aacccccaaagaaactatgcatttatcaataagatggccggttctcggttgacagaacaac
 N P Q R N Y A F I N K M A V L G L Q N N
 aacatcctcagttataattcgtcctggcctgacccagagccattggccgtgagtaggttc
 N I L S Y N S S W P D P E P L A V S R F
 15 aacctcgggaagcgatatcaatctaactccgcttgaccacgagccactgctggagccccgtg
 N L G S D I N L T P L D H E P L L E P V
 gacaaaaccttcaccatggaggtcaacaacctcaacatcgacggcgtaggctaccgcatc
 D K T F T M E V N N L N I D G V G Y R I
 acgcaaggccccgtacccctacattacccccgcgacacccactctgtacactgccctaacc
 T Q G P Y P Y I T P R T P T L Y T A L T
 20 accggctttaaagctaccaacccccgccatctacggccagaccaactcttacatcgtagaa
 T G F N A T N P A I Y G Q T N S Y I V E
 gccggcgatatcgtccagctcgttggtcaacagcaacgaccttgtcacaactaacacctcc
 A G D I V Q L V V N S N D L V T T N T S
 25 gggcgcgggcaccatgcacttgacggccacaccttccaagtcgtgggccaatacggc
 G R G H P M H L H G H T F Q V V G Q Y G
 acccactgggacggcgacaccgcaaaattccctaccggttccaatgaagcgggacacgacc
 T H W D G D T A K F P T V P M K R D T T
 gttctcttcgcccggcgaggcttggtcattcggttcaggcgacaatcctggtgtctgg
 V L F A G G S L V I R F Q A N N P G V W
 30 atgttccactgccatatcgaatggcatctcgacggcgcatggccgccacaatcatcgaa
 M F H C H I E W H L D A G M A A T I I E
 gcgcccgtcgcagttccagcgaagcgggtctgcggatccccgccacagcacctcgcggcgtgc
 A P L E F Q R S G L R I P P Q H L A A C
 cgggcattaaacttaacgacccgggggaattgtgccgggaacaccgttaacctggaggat
 35 R A L N L T T R G N C A G N T V N L E D
 acggctgcgtgcagaatctacgacactgatccttgggggtgcgcttatcggggaacgtgag
 T A A C R I Y D T D P W G A L I G E R E
 acagcacgttga
 T A R -
 40

SEQ ID NO : 108
 LENGTH : 543
 TYPE : PRT
 ORGANISM : *M. phaseolina*

45 MIRLFLVLGFVATTLAKTVTFNWNIGWVSAAPDGFTRPVIGINGLWPPPVLEADVNDTIIVTAHNSL
 GNETTSLHWHGMWQNNSTHIDGGSRVSQCEIPLGGTFTYRFKAYPAGTFWYHSHAMGQYPDGLRAPM
 I IHDPDSAAEQDADEQHILTVSDWYRNQMPPLIHRYLTTPNYNGAMPKPNSSLVNDQQSKRLNIRPG
 QKSYIRIINISALATFYLQFDQHNMTVVSIDDVNVEPQSWEALEITPGQRYDVIITGLENPQRNYAF
 INKMAVLGLQNNNLSYNSSWPDPEPLAVSRFNLGSDINLTPLDHEPLLEPVDKFTTMEVNNLNIDG
 50 VGYRITQGPYPYITPRTPTLYTALTTFGNATNPAYIGQTNSYIVEAGDIVQLVVNSNDLVTTNTSGR
 GHMHLHGHTFQVVGQYGTHWDGDTAKFPTVPMKRDTTVLFAGGSLVIRFQANNPGVWMFHCHIEWH
 LDAGMAATIIIEAPLEFQRSGLRIPPQHIAACRALNLTTRGNCAGNTVNLEDTAACRIYDTPWGALI
 GERETAR*

55

SEQ ID NO : 109
LENGTH : 2052 (including 150 bp 5' UTR and 150 bp 3' UTR)
TYPE : DNA
ORGANISM : *M. phaseolina*

5 GCAGCAACTACATCCGGGTAGGCATCAAACGCAAAGATGGTACGGAGGGAGCACTGATGCGCTTTTA
TAGCTCATATCAGCACAGCTGCGTGTAGTTGAATGGGACCGACCGAGTTTTTTTGTAGCCTCAATCT
TTCCACGCTCCGAACCATGTCCTCAGATTCTCAGAAGCATGGCGCTGTGCTCCGTAGGCGCAGCATA
CCACAGCAACCAGAAGAAGAAACCCCGCCTTCAACAACCCGGAAGTCATCGGAAAATCGACATAGCG
10 TTCTATCATGGTTTCTCTTTGTCTTTTCATGCGCCATCTTCGCGACGTTTATTTCTTATCTCAATAG
CGCAACGGCATAACAACTGCGGGGTCTTATTACACAATAACTGGCCTCAAGGCTTTTCTGTCCCAT
GGGAACCTCTGACAACAATTTGACAGTCATCTGGCAAGGGCCATACGGCGGATCTCTGGGCCAGA
ACTTGCATCCTCGAGAGCACGTGGTCCGTGCTCCTAGTGTGAGGCACTACAGTTGGAAGGTTACCAA
GGCTTTTCGATAACCCAGATGGGGTGAAAAAGGCTGTTTATCTGATTAACGACGGCTTTCTGGGACCC
ACAGTCGAAGCTCGTTCTGGCGATAGACTGGTGATTGAGGTCCAAAATGCGTTGGAAGACGAAGGTC
15 TCTCCTTCCACTGGCACGGTCTTTTAATGAGAGGTGCCAACTACATGGACGGTGCCGTGCGATTAC
GCAAGACGCCATTACCCGGGCGCCAACCTTCACGTATGAGTTTCGATATCGCGGATGACCAAGCCGGC
ACATTTTGGTATCACGCTCATGACCAAGTGACGCGGGCGGATGGCCTGTTGCGAGGACTGATCATCC
ATCGCCCGGAAACCGCAACTGGAGTCGCCGATTTGGATAGATATGGGTACGATGAAGAGAGATTGCT
GCTTATCGGACACTGGTACCATCGTTCCGCACAAGATGTCTTAGCGTGGTACATCAGTGCTGGGTCC
20 TTTGGAATGAGCCTGTGCGGATTCACTCCTCATCAATGGAATGGGAGCATTCAATTGCTCAAAAAG
CTATTCCTGCGAGACCTGTGGAATGCATTAACCTTTGAAGGAACTGCCACACCTAATCTACAGTTCAA
CTTCACCAGACGTACCCGGCTGAGACTCGTCAACACTGGTACATTGGCTGGATTACCTTGAGCATT
CCGGGTGCGGCCATGCAGGTCATCGAAGTTGACGGCGGCAATGCCGTTACCAGCGACTCTGAGAACG
ACACTTCAGTAGGGAGCTTATATCCAGGCCAACGTGCCGACCTAATCCTCTCTTGCCAGAGGATAC
25 TCTAGAAGCCTCAAAAATTTCAATCACCTTGACGGGGAGGACTTCAAGTACCCCAATCCAGCCCTG
ACTCGCACTCAGCACTTCTCCATATTTTCGCTCTGCCCCTGTCCCGAAGGAAAAGAGCGAAGCCTCTG
CCTCTTCGGAACAAGGCAGGCCAGAAAGCCACGCACCACAAACCCTCATCGACCTCAATGCCCTTGT
CAGCGCAGATATCATCACCCCATCACTGCCCCCTGCCACTGAACACACTCTCGTTCTATACGCCAAC
ACCTCAAACCTCTCCACCCGCGGCAACAAACCCACGGCTACATGAACCAAACAGCTGGTCCGCCG
30 AATCCTCTCCGCCCCGTCCGCTCATCGCGCTGCCGCGCTCCTCTTGGGACGCCAACCAGTTCTGTCCC
GCGCATCCCTCTTCCCAACGGCACCTCAGACGCGCCCTGGGTACCATCGTCCTCAACAACCTGGAC
GACGGCTCGCACCCCTTCCACCTACATGGCCACGCGTTCTGGGTGCTCCAAACCCACGCCGCGAGGT
GGGGCTGGGGGTGCTGGAATCCATGAGCGGAGGAGCAGCCGCCGGGCGGCCACTGGAGCTGCAGCG
CGCGGTGACGAGGGATACGGTCATGGTGCCGCGAGGGGGTATGCGGTGCTGCGATTTAGAGCGGAC
35 AATGAGGGGCTCTGGATGCTGCACTGCCACAATTTGTGGCAT

SEQ ID NO : 110
LENGTH : 1752
TYPE : DNA
40 ORGANISM : *M. phaseolina*
FEATURE NAME/KEY : CDS
LOCATION : (1).....(1752)

atgtcctcagattctcagaagcatggcgctgtgctccgtaggcgcagcataccacagcaa
M S S D S Q K H G A V L R R R S I P Q Q
45 ccagaagaagaacccccgccttcaacaacccggaagtcacatcggaataatcgacatagcggt
P E E E T P P S T T R K S S E N R H S V
ctatcatggtttctctttgtcctttcatgcgccatcttcgcgacgtttatctcctatctc
L S W F L F V L S C A I F A T F I S Y L
aatagcgcaacggcataccaaactgcggggctcttattacacaataactggcctcaaggct
50 N S A T A Y Q T A G S Y Y T I T G L K A
tttctgtcccatgggaactctgacaacaatttcgacagtcacatcctggcaaggggccatac
F L S H G N S D N N F D S H P G K G P Y
ggcggatctctgggcccagaacttgcatcctcgagagcacgtggtccgtgctcctagtgtc
G G S L G Q N L H P R E H V V R A P S V
55 aggcactacagttggaagggtaccaaggcttttcgataccacagatgggggtgaaaaaggct

R H Y S W K V T K A F R Y P D G V K K A
 gtttatctgattaacgacggctttctgggacccacagtcgaagctcgttctggcgataga
 V Y L I N D G F L G P T V E A R S G D R
 ctggtgattgaggtccaaaatgcggttgaagacgaaggtctctccttccactggcaggt
 5 L V I E V Q N A L E D E G L S F H W H G
 cttttaatgagaggtgccaaactacatggacggtgccgtcggatttacgcaagacgccatt
 L L M R G A N Y M D G A V G F T Q D A I
 caccggggcgccaacttcacgtatgagttcgatatcgcggtatgaccaagccggcacattt
 H P G A N F T Y E F D I A D D Q A G T F
 10 tgggtatcacgctcatgaccaagtgcagcgggcggtatggcctgttcggaggactgatcatc
 W Y H A H D Q V Q R A D G L F G G L I I
 catcgcccgaaaccgcaactggagtcgcccgatttgatagatatgggtacgatgaagag
 H R P E T A T G V A D L D R Y G Y D E E
 agattgctgcttatcgacactggtagcatcggtccgcacaagatgtcctagcgtggtac
 15 R L L L I G H W Y H R S A Q D V L A W Y
 atcagtgctgggtcctttggaaatgagcctgtgccggttccactcctcatcaatggaatg
 I S A G S F G N E P V P D S L L I N G M
 ggagcattcaattgctcaaaaagctatttcctgcgagacctgtggaatgcattaactttgaa
 G A F N C S K A I P A R P V E C I N F E
 20 ggaactgccacacctaatactacagttcaacttcaccagacgtcaccgggtgagactcgtc
 G T A T P N L Q F N F T R R H R L R L V
 aacactggtacattggctgggttccacttgagcattccgggtgcccgcacatgcaggtcatc
 N T G T L A G F T L S I P G A A M Q V I
 gaagttgacggcggaatgccgttaccagcgcactctgagaacgacacttcagtagggagc
 25 E V D G G N A V T S D S E N D T S V G S
 ttatatccaggccaacgtgccgacctaatactctcttggccagaggataactctagaagcc
 L Y P G Q R A D L I L S W P E D T L E A
 tcaaaaatttcaatcaccttgacggggaggacttcaagtacccaatccagccctgact
 S K I S I T L D G E D F K Y P N P A L T
 30 cgcactcagcacttctccatatttcgctctgcccctgtcccgaaggaaaagagcgaagcc
 R T Q H F S I F R S A P V P K E K S E A
 tctgcctcttcggaacaaggcaggccagaaagccacgcaccacaaaccctcatcgacctc
 S A S S E Q G R P E S H A P Q T L I D L
 aatgcccttgtcagcgcagatatcatcaccccatcactgccccctgccactgaacacact
 35 N A L V S A D I I T P S L P P A T E H T
 ctcgttctatagccaacacccctcaaactctcccaccgcggaacaaacccacgggtac
 L V L Y A N T L K L S H R G N K P H G Y
 atgaaccaaaccagctggctcgccgcaatcctctccgccccgtccgctcatcgcgctgccg
 M N Q T S W S P Q S S P P R P L I A L P
 40 cgctcctcttgggacgccaaccagttcgctcccgcgcatccctcttcccaacggcacctca
 R S S W D A N Q F V P R I P L P N G T S
 gacgcgccttgggtcaccatcgctcctcaacaacctggacgacggctcgcaccccttccac
 D A P W V T I V L N N L D D G S H P F H
 ctacatggccacgcggttctgggtgctccaaaccacgcgcgaggggtgggggtgggggtcg
 45 L H G H A F W V L Q T H A A G W G W G S
 tggaatccatga
 W N P -

SEQ ID NO : 111
 50 LENGTH : 583
 TYPE : PRT
 ORGANISM : *M. phaseolina*
 MSSDSQKHGAVLRRRSIPQQPEETPPSTTRKSENHRHSVLSWFLVLSCAIFATFISYLN SATAYQTAGSYTITGL
 KAFLSHGNSDNNFSDHPGKGPYGGSLGQNLHPREHVVRAPSVRHYSWKVTKAFRYPDGVKKAVYLINDGFLGP
 55 TVEARSGDRLVIEVQNALEDEGLSFHWHGLLMRGAN YMDGAVGFTQDAIHPGANFTYEFDIADDQAGTFWY

HAHDQVQRADGLFGGLIHRPETATGVADLDTRYGYDEERLLIGHWYHRSAQDVLAWYISAGSFGNEPVPDSLLI
NGMGAFNC SKAIPARPVECFINFE GTATPNLQFNFTRRHRLRVNTGTLAGFTLSIPGAAMQVIEVDGGNAVTS
SENDTSVGS LYPGQRADLILSWPEDTLEASKISITLDGEDFKYPNPALTRTQHFSIFRSAPVPKEKSEASASSEQGRP
ESHAPQTLIDLNALVSADIITPSLPPATEHTLVLYANTLKLSHRGNKPHGYMNQTSWSPQSSPPRPLIALPRSSWD
5 ANQFVPRIPLPNGTSDAPWVTIVLNNLDDGSHPFHLHGHAFWVLQTHAAGWGWGSWNP*

INCORPORATION BY REFERENCE

All of the U.S. patents, U.S. published patent applications, and published PCT applications that cited herein are hereby incorporated by reference.

10 EQUIVALENTS

While several embodiments of the present invention have been described and illustrated herein, those of ordinary skill in the art will readily envision a variety of other means and/or structures for performing the functions and/or obtaining the results and/or one or more of the advantages described herein, and each of such variations and/or modifications
15 is deemed to be within the scope of the present invention. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. It is, therefore, to be understood that the foregoing embodiments are presented by way of example only and that, within the scope of the appended claims and equivalents thereto; the invention
20 may be practiced otherwise than as specifically described and claimed.

What is claimed is:

1. An isolated polypeptide having at least 80% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID No. 3, 6, and 9.
2. The isolated polypeptide of claim 1, wherein said polypeptide has at least 85% sequence identity to the amino acid sequence selected from the group consisting of SEQ ID No. 3, 6, and 9.
3. The isolated polypeptide of claim 1, wherein said polypeptide has at least 90% sequence identity to the amino acid sequence selected from the group consisting of SEQ ID No. 3, 6 and 9.
4. The isolated polypeptide of claim 1, wherein said polypeptide has at least 95% sequence identity to the amino acid sequence selected from the group consisting of SEQ ID No. 3, 6 and 9.
5. The isolated polypeptide of claim 1, wherein said polypeptide has at least 98% sequence identity to the amino acid sequence selected from the group consisting of SEQ ID No. 3, 6 and 9.
6. The isolated polypeptide of claim 1, wherein said polypeptide has at least 99% sequence identity to the amino acid sequence selected from the group consisting of SEQ ID No. 3, 6 and 9.
7. The isolated polypeptide of claim 1, wherein said polypeptide has 100% sequence identity to the amino acid sequence selected from the group consisting of SEQ ID No. 3, 6 and 9.
8. An expression construct comprising a polynucleotide having at least 80% sequence identity to the nucleotide sequence selected from the group consisting of SEQ ID No. 1, 2, 4, 5, 7, and 8, wherein said polynucleotide is operably linked to at least one translational regulatory sequence, said translational regulatory sequence comprises a ribosomal binding site, translational start sequence, or translation stop sequence, or combination thereof.

9. The expression construct of claim 8, wherein said polynucleotide has at least 85% sequence identity to the nucleotide sequence selected from the group consisting of SEQ ID No. 1, 2, 4, 5, 7, and 8.
10. The expression construct of claim 8, wherein said polynucleotide has at least 90% sequence identity to the nucleotide sequence selected from the group consisting of SEQ ID No. 1, 2, 4, 5, 7, and 8.
11. The expression construct of claim 8, wherein said polynucleotide has at least 95% sequence identity to the nucleotide sequence selected from the group consisting of SEQ ID No. 1, 2, 4, 5, 7, and 8.
12. The expression construct of claim 8, wherein said polynucleotide has at least 98% sequence identity to the nucleotide sequence selected from the group consisting of SEQ ID No. 1, 2, 4, 5, 7, and 8.
13. The expression construct of claim 8, wherein said polynucleotide has at least 99% sequence identity to the nucleotide sequence selected from the group consisting of SEQ ID No. 1, 2, 4, 5, 7, and 8.
14. The expression construct of claim 8, wherein said polynucleotide has 100% sequence identity to the nucleotide sequence selected from the group consisting of SEQ ID No. 1, 2, 4, 5, 7, and 8.
15. A recombinant gene construct comprising a polynucleotide having at least 80% sequence identity to the nucleotide sequence selected from the group consisting of SEQ ID No. 1, 2, 4, 5, 7, and 8, wherein the polynucleotide is expressible in a host cell to produce an enzyme which degrades lignin.
16. The recombinant gene construct of claim 15, further comprising a promoter region operably-linked to enhance expression of the polynucleotide template.
17. The recombinant gene construct of claim 15, wherein said polynucleotide has at least 85% sequence identity to the nucleotide sequence selected from the group consisting of SEQ ID No. 1, 2, 4, 5, 7, and 8.

18. The recombinant gene construct of claim 15, wherein said polynucleotide has at least 90% sequence identity to the nucleotide sequence selected from the group consisting of SEQ ID No. 1, 2, 4, 5, 7, and 8.

19. The recombinant gene construct of claim 15, wherein said polynucleotide has at least 95% sequence identity to the nucleotide sequence selected from the group consisting of SEQ ID No. 1, 2, 4, 5, 7, and 8.

20. The recombinant gene construct of claim 15, wherein said polynucleotide has at least 98% sequence identity to the nucleotide sequence selected from the group consisting of SEQ ID No. 1, 2, 4, 5, 7, and 8.

21. The recombinant gene construct of claim 15, wherein said polynucleotide has at least 99% sequence identity to the nucleotide sequence selected from the group consisting of SEQ ID No. 1, 2, 4, 5, 7, and 8.

22. The recombinant gene construct of claim 15, wherein said polynucleotide has 100% sequence identity to the nucleotide sequence selected from the group consisting of SEQ ID No. 1, 2, 4, 5, 7, and 8.

23. A transformant comprising a polypeptide of any one of claims 1 to 7, an expression construct of any one of claims 8 to 14, a recombinant gene construct of any one of claims 15 to 22, or a polynucleotide having at least 80% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID No. 1, 2, 4, 5, 7, and 8, wherein said transformant produces an enzyme which accelerates lignin degradation.

24. A transgenic fungi of *M. phaseolina* with enhanced lignin degradation, comprising a polypeptide of any one of claims 1 to 7, an expression construct of any one of claims 8 to 14, a recombinant gene construct of any one of claims 15 to 22, or a polynucleotide having at least 80% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID No. 1, 2, 4, 5, 7, and 8.

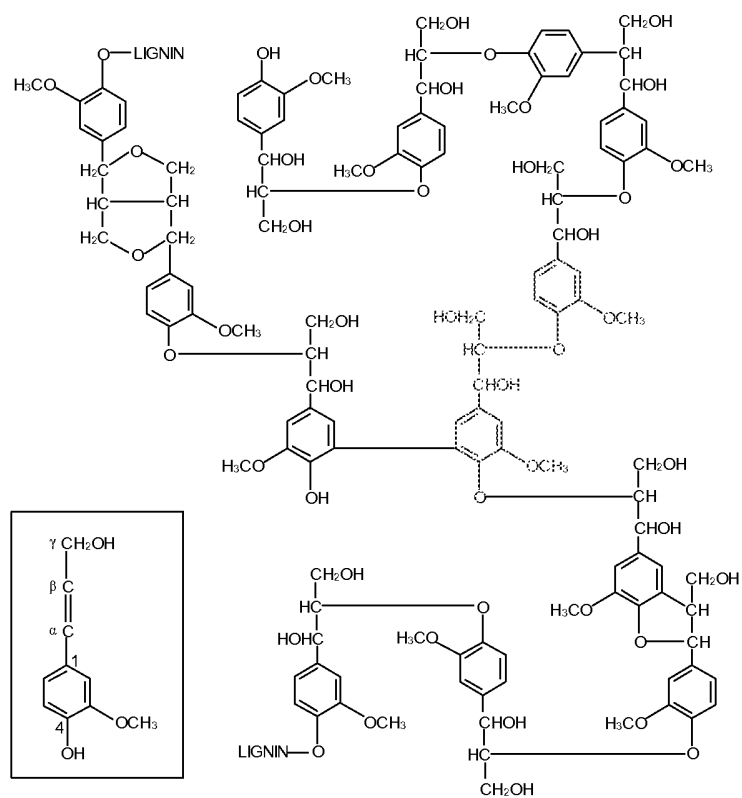


Figure 1

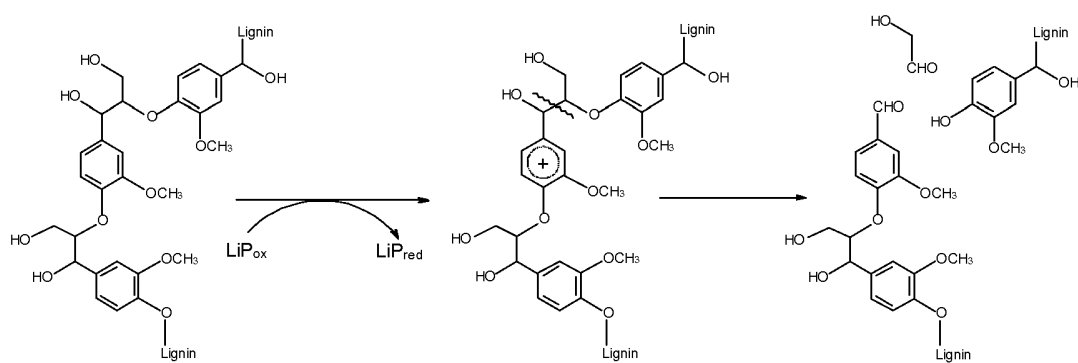
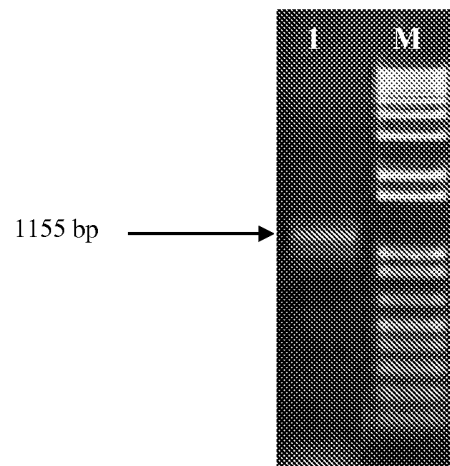
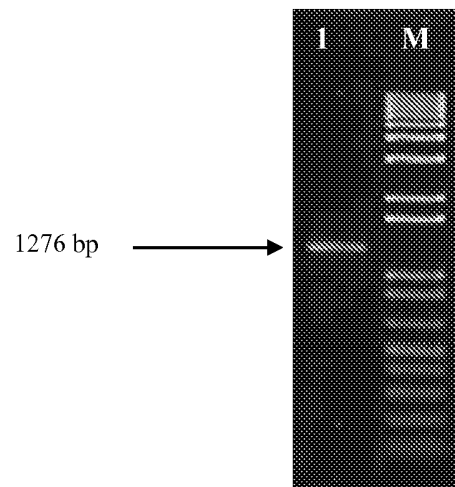
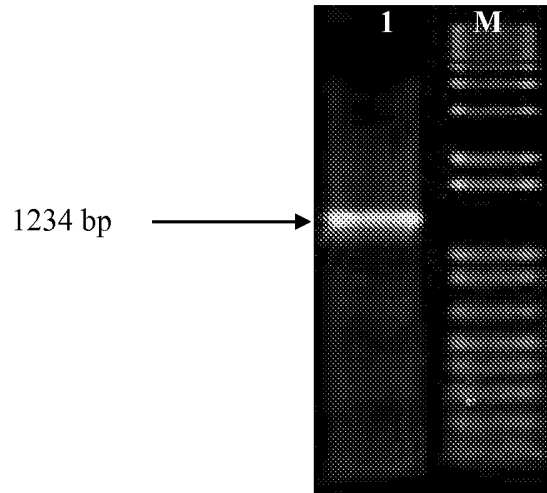
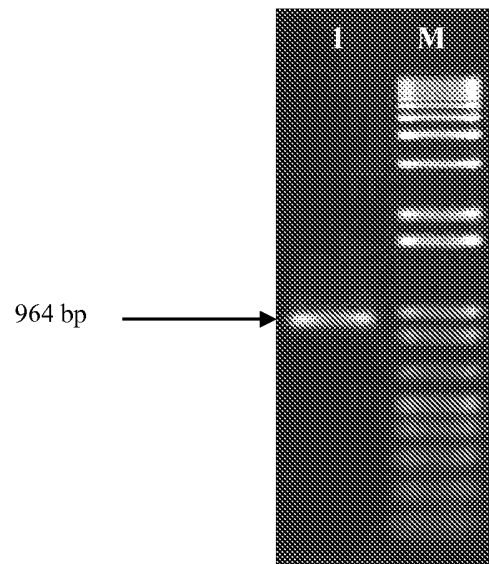
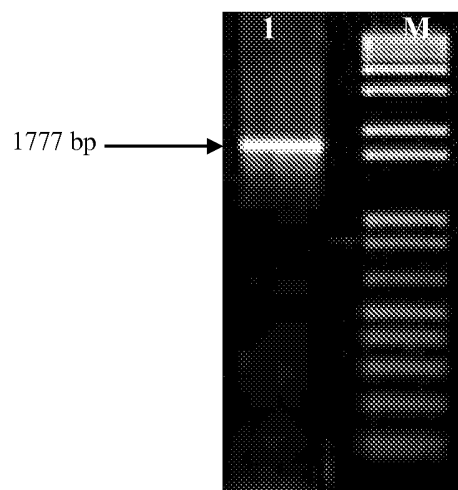
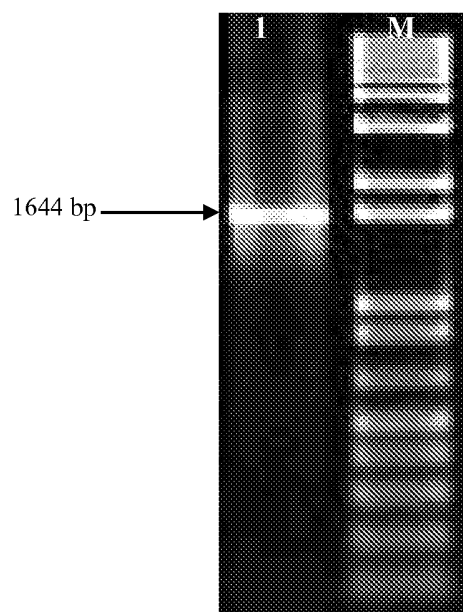
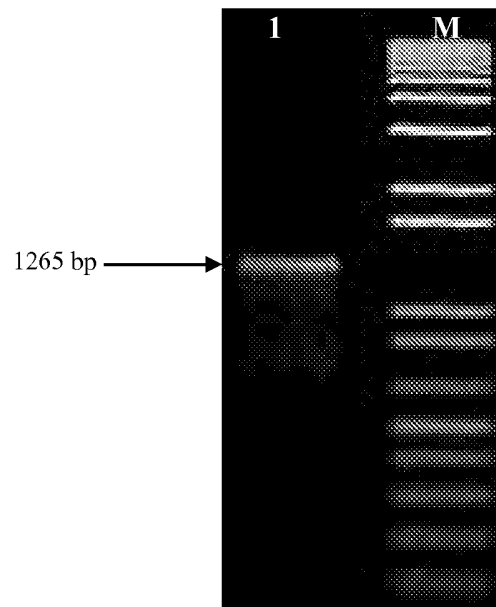
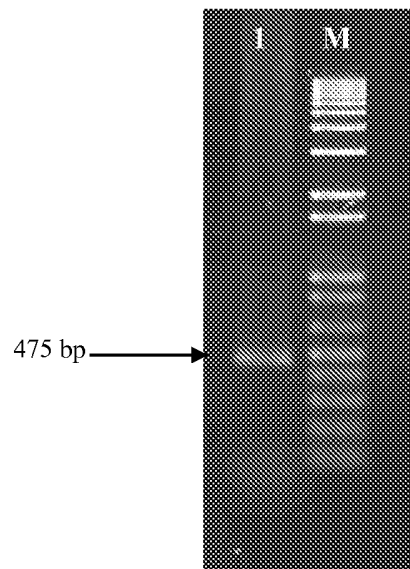


Figure 2

**Figure 3****Figure 4**

**Figure 5****Figure 6**

**Figure 7****Figure 8**

**Figure 9****Figure 10**

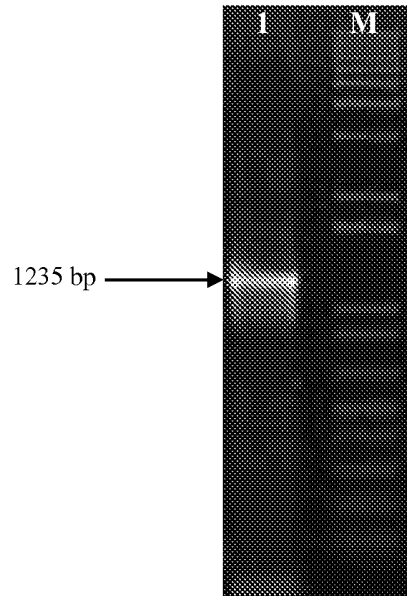


Figure 11

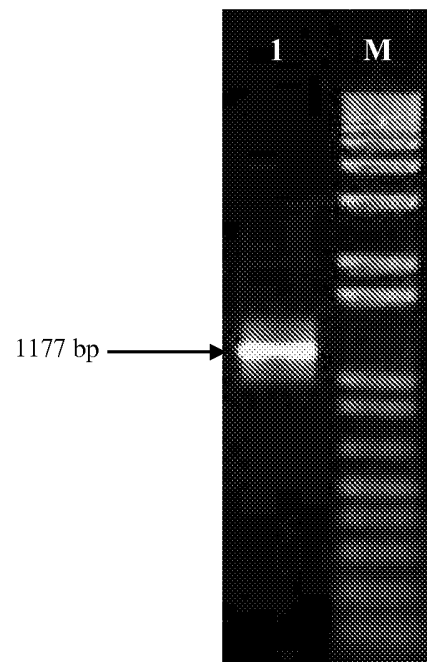


Figure 12

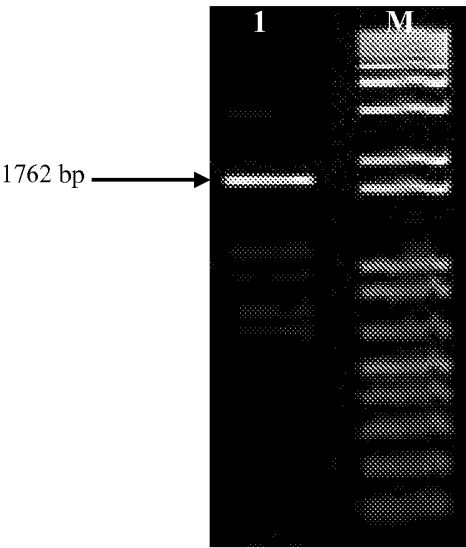


Figure 13

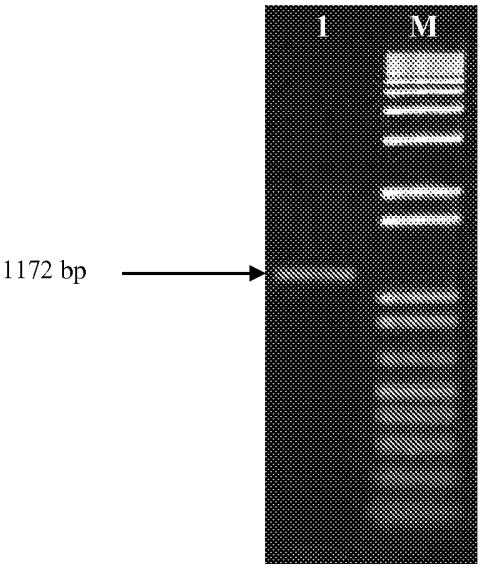


Figure 14

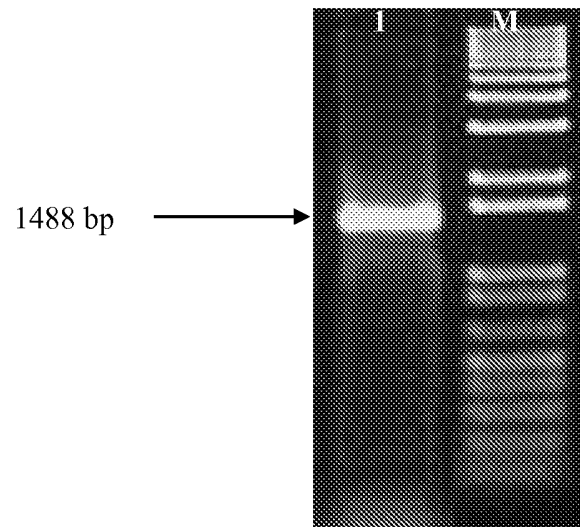


Figure 15

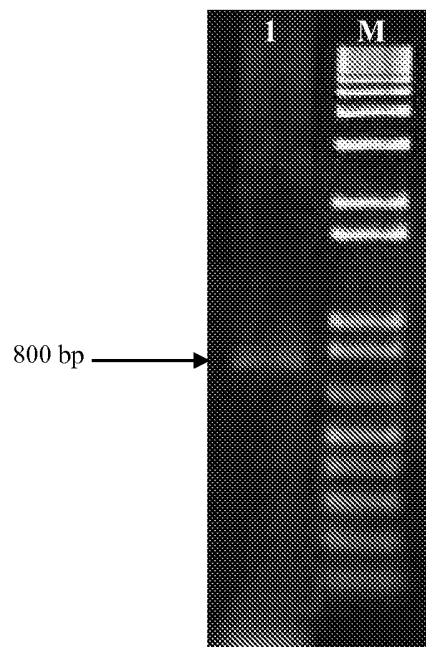


Figure 16

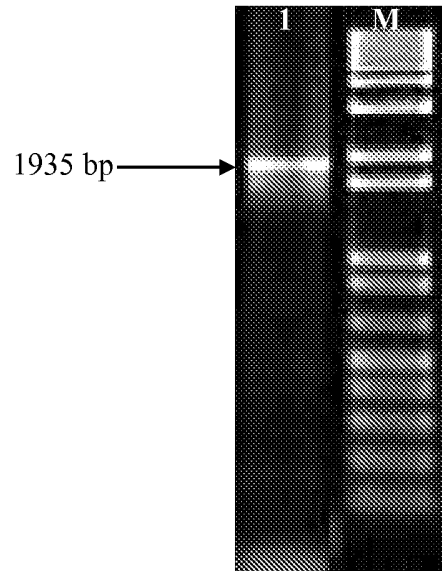


Figure 17

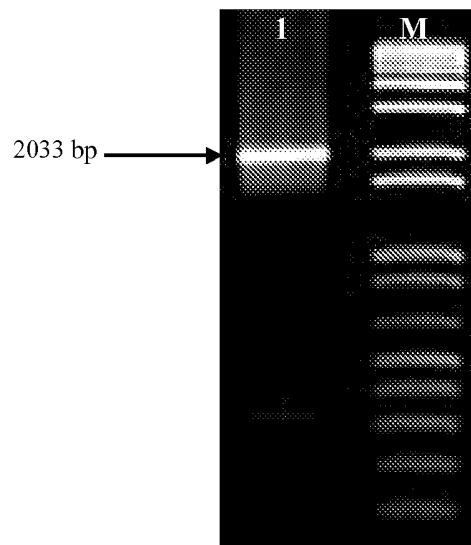


Figure 18

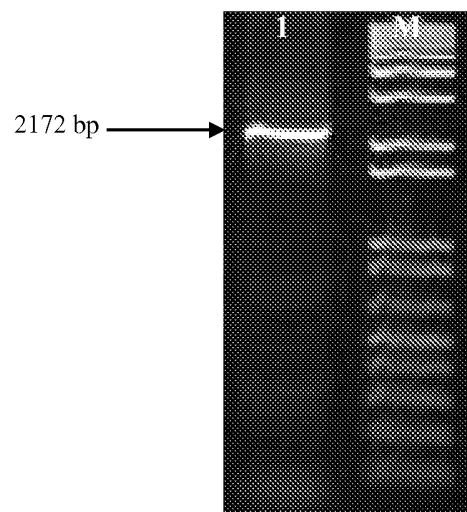


Figure 19

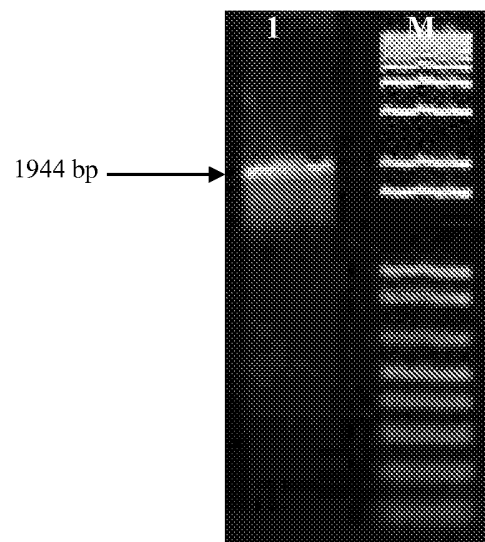


Figure 20

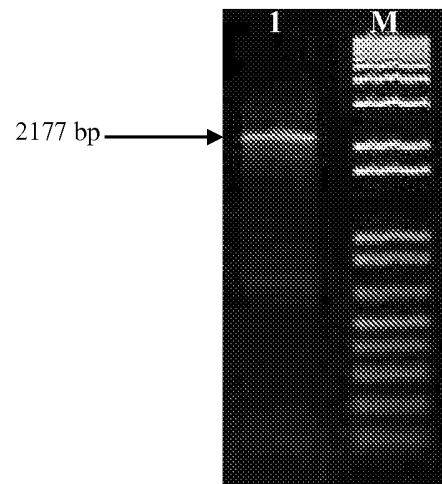


Figure 21

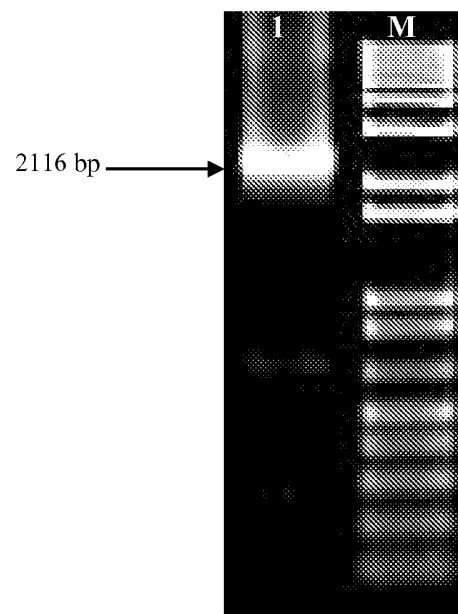


Figure 22

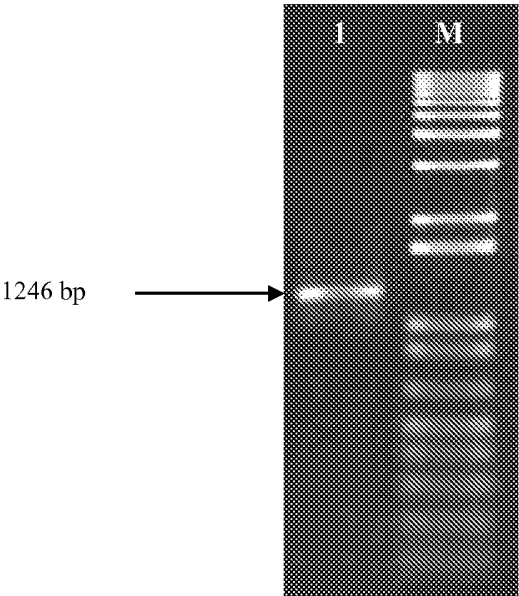


Figure 23

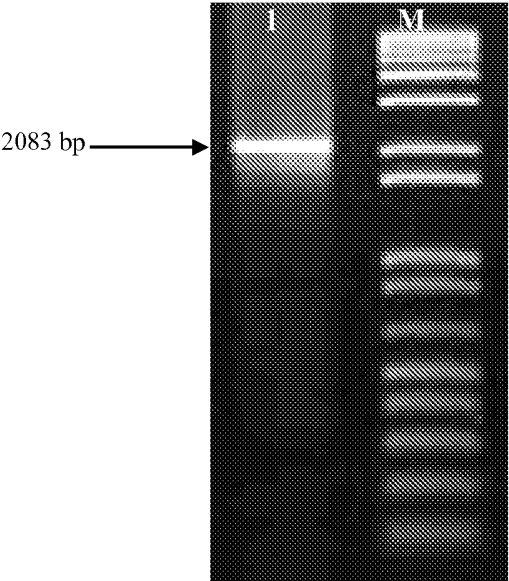


Figure 24

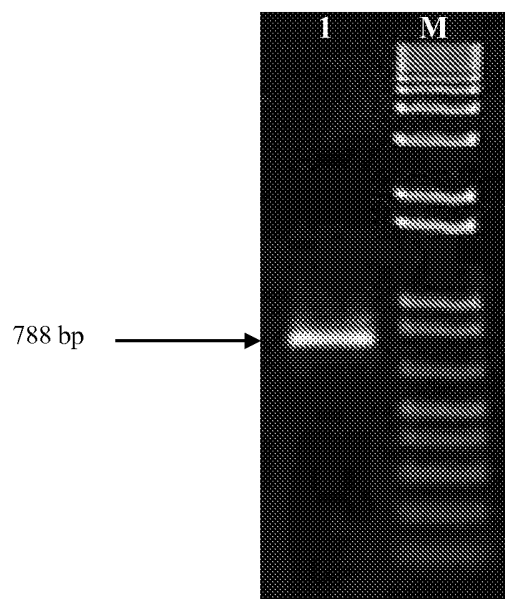


Figure 25

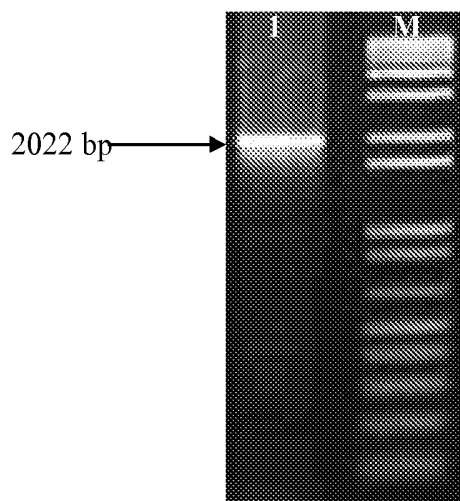
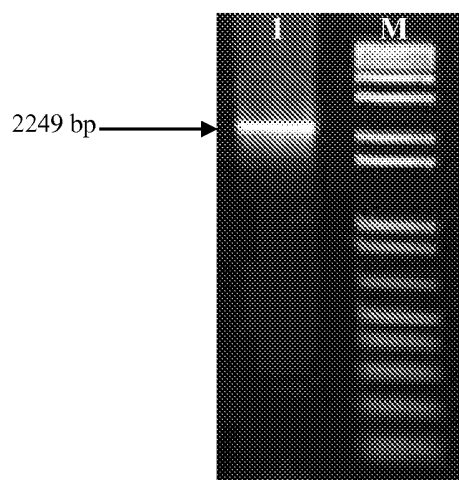
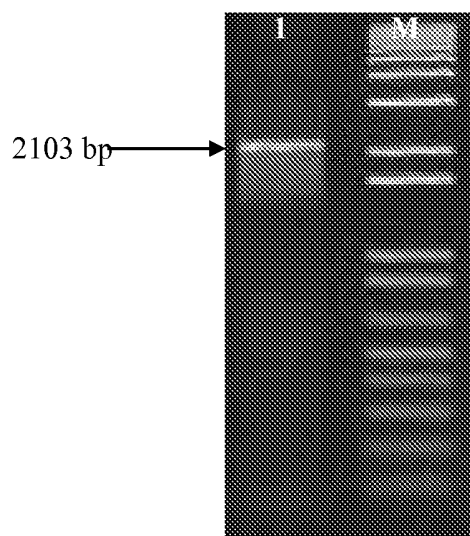


Figure 26

**Figure 27****Figure 28**

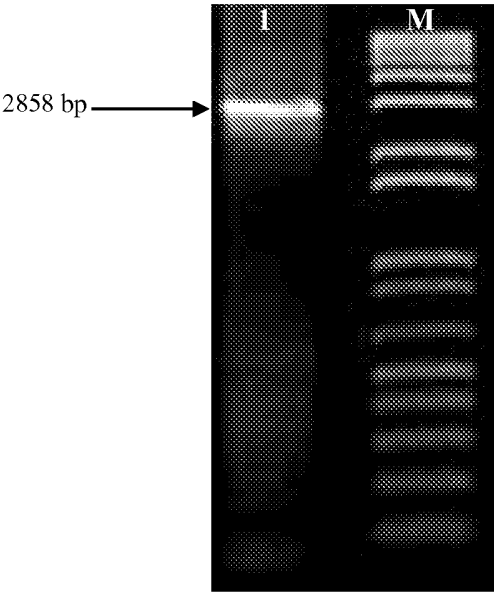


Figure 29

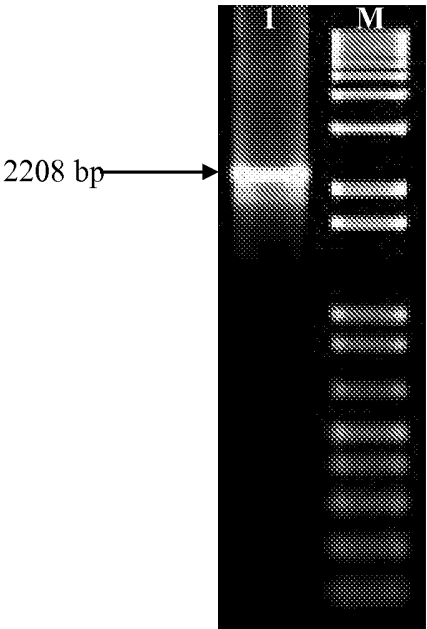


Figure 30

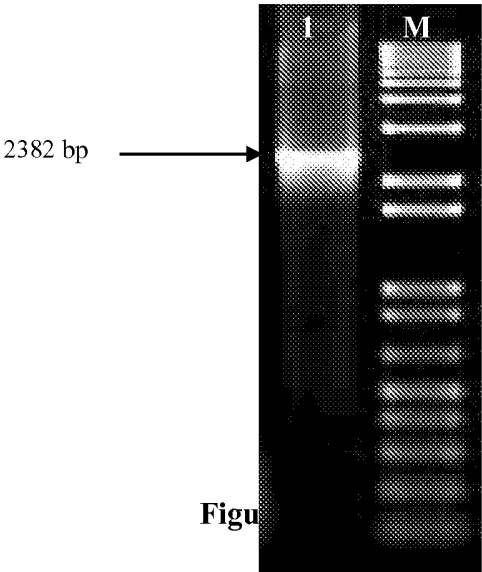


Figure 31

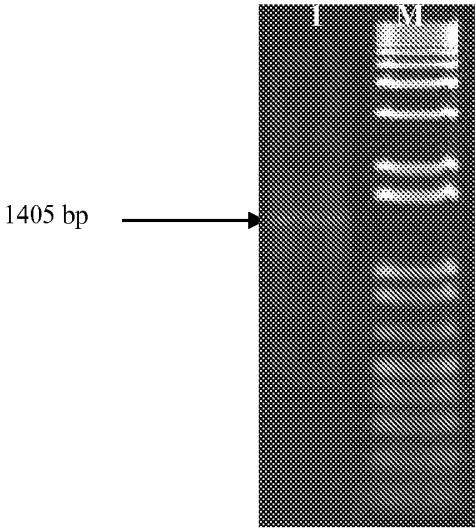
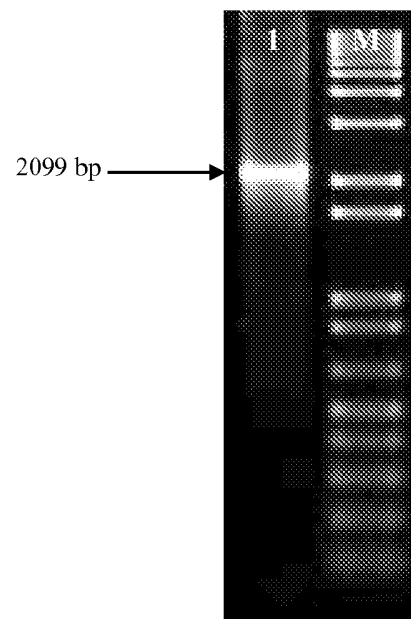
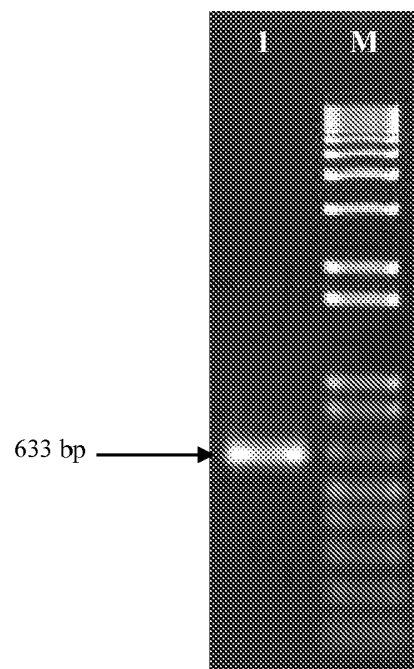
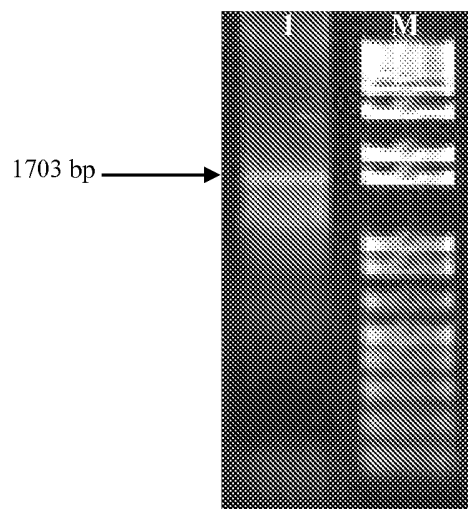
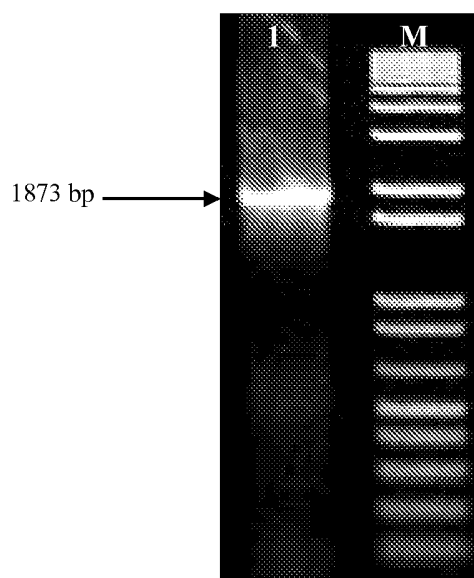


Figure 32

**Figure 33****Figure 34**

**Figure 35****Figure 36**