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(54) Title: MODIFIED PLANTS AND PLANT CELLS

(57) Abstract: The present invention relates to modified plants, methods of preparing same, and methods of reducing methane emissions in animals, in particular in ruminant livestock. Provided are plants and plant cells comprising nucleic acid constructs for inducing expression of a polypeptide comprising a vanadate-dependent haloperoxidase (VHPO), or a functional fragment or homologue thereof.



MODIFIED PLANTS AND PLANT CELLS

TECHNICAL FIELD

[0001] The present invention relates to modified plants, methods of preparing same, and methods of reducing methane emissions in animals, in particular in ruminant livestock.

BACKGROUND

[0002] Ruminants are animals with multiple stomach compartments and include cows, sheep, goats, buffalo, deer, elk, giraffes and camels. While ruminants are important for ecological as well as human economic and cultural reasons, they are also associated with a number of environmental and economic difficulties.

[0003] Firstly, ruminants emit methane, a potent greenhouse gas, primarily via belches when digesting food during enteric fermentation, and also via excretion. This contributes towards climate change, with 6% of global greenhouse emissions estimated to result from ruminant methane emissions. It is also thought that methane contributes to the formation of ground level ozone, which is harmful both to humans, causing lung illnesses and deaths, and to ecology, inhibiting and destroying plants and crops.

[0004] Secondly, ruminants have a relatively low feed efficiency rate, due in part to the energy ruminants expend on belching. This results in ruminants requiring a lot of land space for crops grown to feed them and for grazing. Specifically, ruminants require approximately 30% of the earth's habitable land, which in the context of a growing global population places a growing pressure on land use. This can affect the sustenance of farmers, particularly in developing economies

[0005] Existing approaches to reducing ruminant methane emissions and land use requirements are limited in terms of worldwide scalability, effectiveness and financial viability for farmers. Such approaches include changing farming systems to improve feed efficiency and manure management, which is labour- and resource-intensive, and requires training, adoption by farmers and consistency in implementing; direct modification of the ruminants themselves through breeding and/or genetic modification; and vaccine-type treatments to generate antibodies in the saliva that suppress the growth of methanogens in the rumen.

[0006] In Winichayakul *et al* "In vitro gas production and rumen fermentation profile of fresh and ensiled genetically modified high-metabolizable energy ryegrass", Journal of Dairy Science, 2020, perennial ryegrass plants were genetically modified to increase leaf lipid content, leading to a decrease in methane proportion of the total gas production. However, the effects on plant viability and growth are not known.

[0007] Other approaches involve changing of ruminant diets through feed supplements, which can include methane-reducing inhibitor chemical compounds. Some of these approaches involve the chemical properties of certain seaweed species.

[0008] Studies have shown that red macroalgae *Asparagopsis* seaweed can reduce methane emissions and increase feed efficiency substantially when a small amount is added as a supplement (Abbott *et al* "Seaweed and Seaweed Bioactives for Mitigation of Enteric Methane: Challenges and Opportunities" Animals 2020). WO2021022341A1, WO2018018062A1, WO2020113279A1 and WO2020124167A1 describe the use of *Asparagopsis* seaweed for use as an animal feed supplement to reduce methane emissions and boost

immunity. However, it has also been identified that application of these inventions requires daily feeding of the supplements to ruminants, which is resource intensive and not practical for many farmers, especially if ruminants are grazing. Furthermore, growing *Asparagopsis* seaweed at scale can be difficult and potentially very damaging to surrounding ecosystems, while the processing and transportation of such seaweed and downstream products can also have environmental impacts.

[0009] WO2020243792A1 discusses a genetically modified yeast for use as a component of animal feed. The yeast are used to produce bromoform, which is thought to reduce methane production when consumed by ruminants. The application of this invention requires effort from farmers and feed crop suppliers in the addition of the yeast to the feed, separate production and quality control of the produced yeast, and monitoring of appropriate levels of the additive.

[0010] WO2020210074A1 discuss treating pasture with beneficial microbes and/or their growth by-products, to reduce greenhouse gas emissions in one or more ways. WO2019021250A1 describes treating plants or seeds with an algal granular composition. Applying these concepts poses similar problems as discussed above in terms of growing sufficient quantities of the microalgae, the pasture treatment itself, and the effectiveness of the approaches is also yet to be demonstrated.

[0011] Existing approaches to reducing ruminant land requirements include increasing efficiency through managing storage losses, inaccuracy in delivery of feed, animal feed waste, variation in feed nutrients, mould, pest damage, and bunk management. Bunk management involves improving consistency of feed intake through matching the amount of feed delivered to the amount of feed a ruminant can handle. Forage processing is also used, which can involve chopping and processing grains to reduce particle size and increase digestibility, which in turn can improve feed efficiency. Programme feeding involves feeding routines to achieve a specific rate of gain at a restricted feed intake, which can increase feed efficiency and reduce manure production, especially in growing rather than finishing diets. All of these approaches require effort on the part of farmers, and achieving lower land requirements at scale using these methods is not practical or economically viable for many farmers.

[0012] There is therefore a need to provide improved and more efficient ways to reduce methane production and other environmental damage by ruminants, and to improve feed efficiency, without the drawbacks associated with the existing methods.

SUMMARY OF THE INVENTION

[0013] In a first aspect, there is provided a nucleic acid construct for inducing expression of a polypeptide in a plant cell, the nucleic acid construct comprising a coding sequence encoding a polypeptide comprising a vanadate-dependent haloperoxidase (VHPO), or a functional fragment or homologue thereof. The coding sequence is operably linked to one or more regulatory elements, suitable to drive expression of the polypeptide in a plant cell.

[0014] Also provided herein is a modified plant cell comprising a nucleic acid coding sequence encoding a polypeptide comprising a vanadate-dependent haloperoxidase (VHPO), or a functional fragment or homologue thereof. In some embodiments, the modified plant cell comprises the construct described above.

[0015] Also provided herein is a plant comprising the modified plant cell as described. In some embodiments, the plant expresses VHPO in parts which are edible by livestock, suitably in its leaves and/or grains.

[0016] The plant or plant cells described may produce a brominated hydrocarbon, suitably bromoform. The VHPO may be monomeric. In some embodiments, the VHPO is a vanadate-dependent bromoperoxidase (VBPO).

[0017] The nucleic acid of the coding sequence may be DNA, which may be in the form of a plasmid.

[0018] The VHPO polypeptide may be derived from a species selected from *Asparagopsis* spp. (e.g. *A. taxiformis*, *A. armata*), *Acaryochloris marina*, *Alaria esculenta*, *Ascophyllum nodosum*, *Alteromonas naphthalenivorans*; *Caulerpa* spp. (e.g. *Caulerpa taxifolia*); *Chaetomorpha* spp. (e.g. *Chaetomorpha linum*), *Chondrus crispus*, *Colpomenia sinuosa*, *Corallina officinalis*, *Corallina pilulifera*, *Cystoseira trinodis*, *Furcellaria* spp. *Gracilaria* spp. (e.g. *Gracilaria changii*, *Gracilaria vermiculophylla*); *Hormophysa triquetra*, *Hypnea pannosa*, *Laminaria* spp. (e.g. *L. digitata*, *L. saccharina*), *Laurencia filiformis*, *Macrocystis pyrifera*, *Sargassum flavicans*, *Zonaria farlowii*, *Cladophora patentiramea*, *Dictyota bartayresii*, *Gigartina* spp. (e.g. *Gigartina stellata*), *Oedogonium* spp., *Padina* spp. (e.g. *Padina australis*), *Pterocladia capillacea* and *Ulva* spp. (e.g. *U. intestinalis*, *U. linza*, *U. lactuca*).

[0019] In some embodiments, the VHPO polypeptide is derived from a microalgal or macroalgal species. The microalgal species may be a member of the genus *Emiliana*, *Calcidiscus* or *Chaetocerus*. The macroalgal species may be a member of the genus *Asparagopsis* or *Chondrus*, and in some embodiments the VHPO polypeptide is derived from *Asparagopsis armata* or *Asparagopsis taxiformis*, and optionally from *Asparagopsis taxiformis* Azores, *Asparagopsis armata* Azores, or *Asparagopsis armata* Ireland. In some embodiments, the VBPO is selected from Mbb1, Mbb3 and Mbb4 of *A. taxiformis*.

[0020] In some embodiments, the coding sequence comprises a sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of SEQ ID NOs: 47, 49 to 54, 57 to 60, 64 to 67, 71 to 74, 77 to 80, and 82 to 87. In some embodiments, the nucleic acid construct, plant cell or plant of any preceding claim, wherein the coding sequence comprises a sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of SEQ ID NOs: 47, 49 and 50 (Mbb1, Mbb3 or Mbb4 of *A. taxiformis*). In some embodiments, the coding sequence comprises a sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of SEQ ID NOs: 54, 57 to 60, 64 to 67, 71 to 74, and 77 to 79 (VHPO of *A. armata*).

[0021] In some embodiments, the construct comprises a sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of SEQ ID NOs: 52, 58, or 80.

[0022] In some embodiments, the polypeptide comprising the VHPO comprises an amino acid sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to SEQ ID NOs: 1, 3 to 15, 18 to 21, 25 to 28, 32 to 35, 38 to 41, and 43 to 46. In some embodiments, the polypeptide comprising the VHPO comprises an amino acid sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of Mbb1, Mbb3 and Mbb4 of *A. taxiformis* (SEQ ID NOs: 1, 3 and 4).

[0023] In some embodiments, the polypeptide comprising the VHPO comprises an amino acid sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of SEQ ID NOs: 15, 18 to 21, 25 to 28, 32 to 35, and 38 to 40 (VHPO of *A. armata*). In some embodiments,

the polypeptide comprising the VHPO comprises an amino acid sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of *Chondrus crispus* vBPO (SEQ ID NOs: 5 to 7). In some embodiments, the polypeptide comprising the VHPO comprises a sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of *Acaryochloris marina* vBPO (SEQ ID NO: 8); *Alteromonas naphthalenivorans* vBPO (SEQ ID NO: 9), *Ascophyllum nodosum* vBPO (SEQ ID NO: 10), *Corallina officinalis* vBPO (SEQ ID NO: 11), *Corallina pilulifera* (SEQ ID NO: 12), *Gracilaria changii* vBPO (SEQ ID NO: 13), and *Laminaria digitata* vBPO (SEQ ID NO: 14).

[0024] The plant cell or plant may be a terrestrial plant. The plant or plant cell may be a monocotyledon, typically selected from corn, millet, sorghum or pasture grasses. The plant or plant cell may be a dicotyledon, suitably selected from alfalfa or clover.

[0025] In some embodiments, the coding sequence is operably linked to a promoter for driving expression of the polypeptide in a plant cell. The promoter may be a constitutive or inducible promoter. The promoter may be selected from AlcR/AlcA (ethanol inducible); GR fusions, GVG, and pOp/LhGR (dexamethasone inducible); XVE/OlexA (beta-estradiol inducible); and heat shock induction.

[0026] In some embodiments, the coding sequence is operably linked to a nucleic acid sequence encoding a targeting signal, and/or the polypeptide may include a targeting signal. The targeting signal may be a peroxisomal targeting signal, typically wherein the peroxisomal targeting signal is SEQ ID NO: 90. The targeting signal may be a mitochondrial targeting signal, suitably wherein the mitochondrial targeting signal is SEQ ID NO: 89. The targeting signal may be a chloroplast targeting signal, typically wherein the chloroplast targeting signal is SEQ ID NO: 88.

[0027] In a second aspect, there is provided an animal feed or animal supplement comprising the modified plant cell or plants of any described aspect or embodiment.

[0028] In a third aspect, there is provided a method for reducing methane production in an animal, comprising growing or culturing the modified plants or plant cells of any described aspect or embodiment under conditions suitable for the production of halogenated hydrocarbons, and feeding an effective amount of the modified plants or plant cells to the animal. A further method for reducing methane production in an animal comprises administering to the animal an effective amount of modified plant cells, plants, or animal feed of any described aspect or embodiment.

[0029] In some embodiments, the growing or culturing of the modified plant or plant cells does not include providing substrates or cofactors relevant to the production of a halogenated hydrocarbon. In some embodiments, where the halogenated hydrocarbon is bromoform, the substrates or cofactors relevant to the production of a halogenated hydrocarbon include at least one compound selected from the group consisting of KBr, sodium orthovanadate, pentane-2,4-dione, and H₂O₂.

[0030] The animal as described may be a ruminant, typically the animal is bovine. The animal may be a cow, sheep or goat.

[0031] In embodiments of the described methods, methane production may be reduced. In some embodiments, feed efficiency is increased.

[0032] In a fourth aspect, there is provided a method of preparing a modified plant cell, comprising transforming a plant cell with the nucleic acid construct of any described embodiment. The plant cell may be

transformed by *Agrobacterium*-mediated infiltration. The plant cell may be transformed by particle bombardment.

[0033] In a fifth aspect, there is provided a method of producing an animal feed for reduction of methane production in an animal, comprising growing the modified plant cell or plant of any described aspect or embodiment, and processing the modified plant cell or plant into an animal feed.

BRIEF DESCRIPTION OF THE DRAWINGS

[0034] Figures 1A to 1D show example constructs for driving expression of various genes in corn protoplasts, with associated reporters and targeting sequences where appropriate.

[0035] Figures 2A to 2D show example constructs for driving expression of *Asparagopsis taxiformis* Mbb1 in *Arabidopsis*, with associated reporters and targeting sequences where appropriate.

[0036] Figures 3A to 3D show fluorescence microscopy images of protoplasts transfected with AtMbb1 + GFP fusion constructs and an mCherry construct, as detailed in Example 1. Images were taken in GFP and mCherry channels at 20x magnification, under the same acquisition settings, and then merged. Figure 3A shows cells transfected with cytosol-targeting constructs; Figure 3B shows cells transfected with chloroplast-targeting constructs; Figure 3C shows cells transfected with mitochondria-targeting constructs; Figure 3D shows cells transfected with peroxisome-targeting constructs.

[0037] Figures 4A to 4D show fluorescence microscopy images of protoplasts transfected with CcMbb3 + GFP fusion constructs and an mCherry construct, as detailed in Example 1. Images were taken in GFP and mCherry channels at 20x magnification, under the same acquisition settings, and then merged. 4A shows cells transfected with cytosol-targeting constructs; 4B shows cells transfected with chloroplast-targeting constructs; 4C shows cells transfected with mitochondria-targeting constructs; 4D shows cells transfected with peroxisome-targeting constructs.

[0038] Figure 5 shows the morphology of transgenic plant lines 2007, 2011, and 2012 (labelled boxes) and six wild type *Arabidopsis* plants (not labelled), as described in Example 2.

[0039] Figures 6A to 6C show results of transcription analysis of transgenic plant lines according to Example 2. At-Mbb1 transcript levels were measured by qRT-PCR and then normalised to expression of a known wild-type gene. Figure 6A shows the results of Plate 1 also detailed in Table 3. Figure 6B shows the results of Plate 2 also detailed in Table 4. Figure 6C shows the results of Plate 1 also detailed in Table 5. Wild-type expression is on the far right of each of Figures 6A-C and has a normalized expression of zero.

[0040] Figures 7A to 7D show extracted ion chromatograms for transgenic plant material according to Example 5. Figure 7E is a chromatogram of the positive control: 0.25 µg/mL bromoform standard. Figure 7A is the chromatogram for the 2007 sample. Figure 7B is the chromatogram for the 2011 sample. Figure 7C is the chromatogram for the 2012 sample. Figure 7D is the gas chromatogram for the 2023 sample.

[0041] Figure 8 shows mass spectrometry results for material taken from the 2007 transgenic plant line, along with the NIST reference spectrum for bromoform, as detailed in Example 5. The 2007 sample mass spectrum is shown above, the NIST reference spectrum below.

DETAILED DESCRIPTION

[0042] Unless otherwise indicated, the practice of the present invention employs conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA technology, and chemical methods, which are within the capabilities of a person of ordinary skill in the art. Such techniques are also explained in the literature, for example, M.R. Green, J. Sambrook, 2012, *Molecular Cloning: A Laboratory Manual*, Fourth Edition, Books 1-3, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY; Ausubel, F. M. et al. (*Current Protocols in Molecular Biology*, John Wiley & Sons, Online ISSN:1934-3647); B. Roe, J. Crabtree, and A. Kahn, 1996, *DNA Isolation and Sequencing: Essential Techniques*, John Wiley & Sons; J. M. Polak and James O'D. McGee, 1990, *In Situ Hybridisation: Principles and Practice*, Oxford University Press; M. J. Gait (Editor), 1984, *Oligonucleotide Synthesis: A Practical Approach*, IRL Press; and D. M. J. Lilley and J. E. Dahlberg, 1992, *Methods of Enzymology: DNA Structure Part A: Synthesis and Physical Analysis of DNA Methods in Enzymology*, Academic Press; *Synthetic Biology, Part A, Methods in Enzymology*, Edited by Chris Voigt, Volume 497, Pages 2-662 (2011); *Synthetic Biology, Part B, Computer Aided Design and DNA Assembly, Methods in Enzymology*, Edited by Christopher Voigt, Volume 498, Pages 2-500 (2011); *RNA Interference, Methods in Enzymology*, David R. Engelke, and John J. Rossi, Volume 392, Pages 1-454 (2005). Each of these general texts is herein incorporated by reference.

[0043] Prior to setting forth the invention, a number of definitions are provided that will assist in the understanding of the invention. All references cited herein are incorporated by reference in their entirety. Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs.

[0044] As used herein, the term 'comprising' means any of the recited elements are necessarily included and other elements may optionally be included as well. 'Consisting essentially of' means any recited elements are necessarily included, elements that would materially affect the basic and novel characteristics of the listed elements are excluded, and other elements may optionally be included. 'Consisting of' means that all elements other than those listed are excluded. Embodiments defined by each of these terms are within the scope of this invention.

[0045] A 'polynucleotide' is a single or double stranded covalently linked sequence of nucleotides in which the 3' and 5' ends on each nucleotide are joined by phosphodiester bonds. The polynucleotide may be made up of deoxyribonucleotide bases or ribonucleotide bases. Polynucleotides include DNA and RNA, and may be manufactured synthetically *in vitro* or isolated from natural sources. Sizes of polynucleotides are typically expressed as the number of base pairs (bp) for double stranded polynucleotides, or in the case of single stranded polynucleotides as the number of nucleotides (nt). One thousand bp or nt equal a kilobase (kb). Polynucleotides of less than around 40 nucleotides in length are typically called 'oligonucleotides'. The term 'nucleic acid sequence' as used herein, is a single or double stranded covalently linked sequence of nucleotides in which the 3' and 5' ends on each nucleotide are joined by phosphodiester bonds. The polynucleotide may be made up of deoxyribonucleotide bases or ribonucleotide bases. Nucleic acid sequences may include DNA and RNA, and may be manufactured synthetically *in vitro* or isolated from natural sources.

[0046] Nucleic acids may further include modified DNA or RNA, for example DNA or RNA that has been methylated, or RNA that has been subject to post-translational modification, for example 5'-capping with 7-methylguanosine, 3'-processing such as cleavage and polyadenylation, and splicing. Nucleic acids may also

include synthetic nucleic acids (XNA), such as hexitol nucleic acid (HNA), cyclohexene nucleic acid (CeNA), threose nucleic acid (TNA), glycerol nucleic acid (GNA), locked nucleic acid (LNA) and peptide nucleic acid (PNA).

[0047] According to the present invention, similarity to the nucleic acid sequences described herein is not limited simply to 100% sequence identity. In this regard, the term “substantially similar”, relating to two sequences, means that the sequences have at least 70%, 80%, 90%, 95%, 98%, 99% or 100% similarity. Likewise, the term “substantially complementary”, relating to two sequences, means that the sequences are completely complementary, or that at least 70%, 80%, 90%, 95% or 99% of the bases are complementary. That is, mismatches can occur between the bases of the sequences which are intended to hybridise, which can occur between at least 1%, 5%, 10%, 20% or up to 30% of the bases.

[0048] The term ‘operably linked’, when applied to nucleic acid sequences, for example in an expression construct, indicates that the sequences are arranged so that they function cooperatively in order to achieve their intended purposes. By way of example, in a DNA vector a promoter sequence allows for initiation of transcription that proceeds through a linked coding sequence as far as a termination sequence. In the case of RNA sequences, one or more untranslated regions (UTRs) may be arranged in relation to a linked polypeptide coding sequence referred to as an open reading frame (ORF). A given mRNA as disclosed herein may comprise more than one ORFs, a so-called polycistronic RNA. An mRNA may encode more than one polypeptide, and may as a result include cleavage sites or other sequences necessary to result in the production of multiple functional products, as known in the art. A UTR may be located 5' or 3' in relation to an operatively linked coding sequence ORF. UTRs may comprise sequences typically found in mRNA sequences found in nature, such as any one or more of: Kozak consensus sequences, initiation codons, cis-acting translational regulatory elements, cap-independent translation initiator sequences, poly-A tails, internal ribosome entry sites (IRES), structures regulating mRNA stability and/or longevity, sequences directing the localisation of the mRNA, and so on.

[0049] The term ‘expressing a polypeptide’ in the context of the present invention refers to production of a polypeptide for which the polynucleotide sequences described herein code. Typically, this involves transcription of a DNA sequence comprised within a modified plant cell, followed by translation of the resultant mRNA sequence by the ribosomal machinery of the plant cell in which the sequence is comprised.

[0050] The term ‘polypeptide’ as used herein is a polymer of amino acid residues joined by peptide bonds, whether produced naturally or in vitro by synthetic means. Polypeptides of less than around 12 amino acid residues in length are typically referred to as “peptides” and those between about 12 and about 30 amino acid residues in length may be referred to as “oligopeptides”. The term “polypeptide” as used herein denotes the product of a naturally occurring polypeptide, precursor form or proprotein. Polypeptides can also undergo maturation or post-translational modification processes that may include, but are not limited to: glycosylation, proteolytic cleavage, lipidization, signal peptide cleavage, propeptide cleavage, phosphorylation, and such like. The term “protein” is used herein to refer to a macromolecule comprising one or more polypeptide chains. Some proteins are multimeric or involve complexes of polypeptide chains and other molecules such as cofactors. In such cases, polynucleotides coding for such proteins as described herein are intended to encompass the provision of multiple monomers such that a complete or functional resultant protein can be produced. Different monomers can be encoded on the same polynucleotide construct, or separately.

Transcription/translation of the coding polynucleotide sequence within a modified cell allows for localised post-translational modification appropriate to the cell type to be applied. Such modifications may regulate folding, localization, interactions, degradation, and activity of the gene product. Typical post translational modifications may include cleavage, refolding and/or chemical modification such as methylation, acetylation or glycosylation.

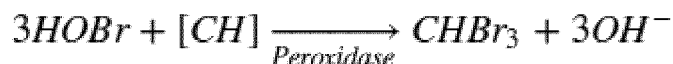
[0051] A 'promoter' is defined as an array of nucleic acid control sequences that direct transcription of an operably linked nucleic acid. Promoters include necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II-type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription.

[0052] The present invention seeks to alleviate the disadvantages of existing approaches of reducing ruminant methane emissions and land requirements by offering a solution that is globally scalable, economically advantageous for farmers and has potential to consistently reduce methane emissions and increase feed efficiency rates (and reduce total land requirements of ruminants).

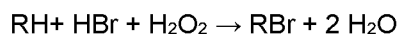
[0053] Methane is a greenhouse gas, which can be produced by methanogenic microbes, particularly methanogenic archaea. Without wishing to be bound by theory, it is thought that these microbes are not only present in the environment but also inhabit the gastrointestinal tract of ruminants, contributing to their production of methane. It is also thought that the presence of halogenated hydrocarbons, such as brominated hydrocarbons, can reduce methane production in this context. Brominated hydrocarbons are thought to prevent methane emission from ruminants by interfering with the vitamin B12 cofactor which is used by the methyltransferase enzymes of ruminant methanogenic archaea in the production of methane.

[0054] As mentioned, various macro algae have been shown to reduce methane emissions when fed to ruminants, with red macro alga *Asparagopsis* sp. being shown to be highly effective. These species produce halogenated compounds, including bromoform (CHBr_3) and polybromomethanes such as dibromomethane and chlorodibromomethane, which are thought to be synthesised by haloperoxidases catalysing the conversion of halide anions to hypohalous acid with hydrogen peroxide (H_2O_2) acting as the oxidant. The requirement for H_2O_2 links synthesis to the enzymatic production of reactive oxygen species (ROS).

[0055] Gene clusters in *Asparagopsis taxiformis* that contain reactive oxygen species (ROS)-producing enzymes together with bromoform-producing vanadium-dependent haloperoxidases (VHPOs) were identified in Thapa et al. "Genetic and biochemical reconstitution of bromoform biosynthesis in *Asparagopsis* lends insights into seaweed ROS enzymology" (ACS Chem Biol, 2020). They identified that Mbb1, Mbb3 and Mbb4 VHPOs can synthesise bromoform in an *in vitro* assay when the *E. coli* expressed recombinant proteins are provided sodium orthovanadate, potassium bromide, H_2O_2 and the artificial substrate monochlorodimedone (MCD), proposing the below equations. After testing a range of hydrocarbon substrates, they also proposed that acetoacetyl-S-ACP (an acyl-acyl carrier protein intermediate in plastidial fatty acid synthesis) is the likely physiological substrate for bromoform synthesis in *A. taxiformis*. The Thapa et al authors were unable to heterologously express the putative ROS-producing enzyme Mbb2 but did identify a *Chondrus crispus* homologue and demonstrate its NAD(P)H-oxidase (NOX) activity. They also demonstrated activity of homologous *C. crispus* VHPO proteins.



[0056] A more general alternative formula for the production of brominated organic compounds is



where RH is an organic substrate.

[0057] VHPO enzyme sources and uses

[0058] In embodiments of the present invention, plants or plant cells are modified to express substances which reduce methane production in animals, typically ruminants, which ingest the plants, plant cells, or feed prepared from these. In this context, plants are members of the Kingdom *Plantae*, typically terrestrial members thereof. Sources for genetic modification of such plants are frequently found in aquatic photosynthetic species, such as algal species and phytoplankton, several of which produce substances which reduce methane production in animals. It is contemplated to introduce the genetic basis for the production of these substances into plants, especially ruminant feed plants (forage) to enable efficient ingestion of appropriate amounts of these substances. Accordingly, the plants or plant cells of the present invention may be modified with a construct comprising a coding sequence (for example, a coding sequence encoding a VHPO) which is derived from an aquatic photosynthetic species such as a micro- or macroalgal species. In this context, 'derived from' means that the construct encodes a polypeptide similar in function and/or sequence to those produced by wild-type members of these species. Such constructs may differ from the original by the inclusion of codon optimisation, the presence of reporter sequences, targeting sequences, modified nucleobases, and so forth. It is contemplated that VHPO enzymes and other proteins as described herein may be engineered or modified to increase their activity, stability, or other properties, by any of a number of methods known in the art.

[0059] In some embodiments, the present invention provides plants and plant cells modified to express VHPO and/or otherwise to produce halogenated hydrocarbons, such as bromoform, in order to reduce methane production in animals. Again, suitable VHPO enzymes are present in a number of aquatic photosynthetic species. VHPO enzymes specialised to produce brominated hydrocarbons can be referred to as vanadium-dependent bromoperoxidases (VBPO), and references herein to VHPO are intended to encompass VBPO. It is expected that the presence of VHPO alone is sufficient for the production of halogenated hydrocarbons by modified plants and plant cells of the invention.

[0060] Species which have been determined to express VHPO and/or have methane reduction effects include *Asparagopsis* spp. (e.g. *A. taxiformis*, *A. armata*), *Acaryochloris marina*, *Alaria esculenta*, *Ascophyllum nodosum*, *Alteromonas naphthalenivorans*; *Caulerpa* spp. (e.g. *Caulerpa taxifolia*); *Chaetomorpha* spp. (e.g. *Chaetomorpha linum*), *Chondrus crispus*, *Colpomenia sinuosa*, *Corallina officinalis*, *Corallina pilulifera*, *Cystoseira trinodis*, *Furcellaria* spp. *Gracilaria* spp. (e.g. *Gracilaria changii*, *Gracilaria vermiculophylla*); *Hormophysa triquetra*, *Hypnea pannosa*, *Laminaria* spp. (e.g. *L. digitata*, *L. saccharina*), *Laurencia filiformis*,

Macrocystis pyrifera, *Sargassum flavicans*, *Zonaria farlowii*, *Cladophora patentiramea*, *Dictyota bartayresii*, *Gigartina* spp. (e.g. *Gigartina stellata*), *Oedogonium* spp., *Padina* spp. (e.g. *Padina australis*), *Pterocladia capillacea* and *Ulva* spp. (e.g. *U. intestinalis*, *U. linza*, *U. lactuca*) (see, for example, Thapa *et al* 2020, WO 2020/243792, Abbott *et al* 2020, Thapa, H. R., & Agarwal, V. (2021). Obligate Brominating Enzymes Underlie Bromoform Production by Marine Cyanobacteria. *Journal of Phycology*). Microalgal species determined to express VHPO include members of the genera *Emiliana*, *Calcidiscus* and *Chaetocerus*. Accordingly, nucleic acid sequences encoding polypeptides such as VHPO derived from any of these species may be used in the present context. The VHPOs may or may not be monomeric.

[0061] *A. taxiformis* preferentially grows in tropical to warm temperate waters, compared with *A. armata* which is adapted to cooler temperate waters, although the species overlap in some environments, such as the Mediterranean (Andreakis *et al* (2004) “*Asparagopsis taxiformis* and *Asparagopsis armata* (Bonnemaisoniales, Rhodophyta): genetic and morphological identification of Mediterranean populations” *European Journal of Phycology*). Indeed, subspecies or strains of each exist present in different locations, for example, *A. taxiformis* has an Atlantic and a Mediterranean strain, while *A. armata* has been isolated near Ireland and the Azores.

[0062] To identify further potential VHPO for use in the present context, genomic comparisons were made between the identified Mbb1, Mbb2, Mbb3 and Mbb4 polypeptides identified in *A. taxiformis* (SEQ ID NOs: 1 to 4) and *Chondrus crispus* (SEQ ID NOs: 5 to 7), and the related species *Asparagopsis armata*, isolated from strains in Ireland (*Asparagopsis armata* Ireland) and the Azores islands (*Asparagopsis armata* Azores), as well as a strain of *A. taxiformis* isolated from the Azores islands (*Asparagopsis taxiformis* Azores).

[0063] Multiple collections of macroalgae were made and DNA and RNA preparations generated for sequence analysis using Illumina sequencing technology. Library preparation for genomic DNA sequencing included DNA fragmentation, adapter ligation, size selection and amplification. It included unique dual indexing. The run type was paired end, with read lengths of 2 x 150 bp. More than 5 million read pairs (10 million reads) were obtained per sample (+/- 3%); Additionally, transcriptome sequencing was completed in triplicate using Illumina sequencing technology for each of the samples. The library preparation for RNA sequence analysis included strand-specific cDNA library preparation, purification of poly-A containing mRNA molecules, mRNA fragmentation, random primed cDNA synthesis (strand specific), adapter ligation and adapter specific PCR amplification. The run type was paired-end, with read lengths of 2 x 150 bp. 30 million read pairs were identified (+/- 3%). The approach included long and accurate read lengths to quantitatively evaluate common and rare transcripts. Genomic DNA and transcriptome sequencing data were mapped against taxonomically-distinct reference genome sequences and analysed in other ways for the identification and annotation of gene coding sequences, identification and quantification of transcripts, pairwise comparison of expression levels and determination of significant fold differences, alternative splicing analysis based on known/provided gene models for eukaryotes, and detection and annotation of SNPs and InDels. The transcriptome sequencing data also provided comprehensive information on gene expression, levels, sequence, structure and strand orientation of RNA types. The coding sequences identified in this analysis were searched using BLASTN to identify sequences related to Mbb1, 2, 3 and 4. This analysis resulted in the identification of Mbb1, 2, 3 and 4 coding sequences in *Asparagopsis taxiformis* Azores, and in *Asparagopsis armata* Ireland and Azores.

Additionally, both *Asparagopsis armata* strains were found to have a 2nd Mbb4 gene not present in *Asparagopsis taxiformis*. The identified polypeptide and nucleotide coding sequences are shown in Table 6.

[0064] Accordingly, the plant or plant cells described herein can be modified to express one or more proteins identified in *Asparagopsis taxiformis* and/or *Asparagopsis armata*, suitably VHPOs identified in one or both of these species. In some cases, the plant or plant cells are modified to express *A. armata* proteins selected from those identified as Mbb1 like, Mbb3 like, Mbb4 like, and Mbb4-2 like, and in particular, the Mbb4-2 like protein.

[0065] Inducible expression or activity of VHPO

[0066] In some instances, it can be advantageous to control the degree to which VHPO are expressed by the modified plant cells or plants, and/or the activity of the VHPO polypeptides synthesised by the plants or plant cells. Halogenated hydrocarbons can have toxic effects on the organisms which express them, and/or on the environment. For example, halogenated hydrocarbons are thought to play a role in ozone depletion.

[0067] Additionally, it can be beneficial to control expression of the encoded VHPO depending on the cell type and/or location of the cell within the plant. For example, it may be advantageous for efficiency to express the VHPO only in the parts of the plant which are eaten by a particular animal, such as the leaves or grains. This can also limit the impact of any toxicity of producing the VHPO or the subsequently produced halogenated hydrocarbon.

[0068] It is contemplated for the desired compounds such as bromoform to be produced in any plant tissue that is commonly fed to ruminant livestock. This can include, but is not limited to leaves and stems (for example from grasses/cereals, legumes, and brassicas), seeds (for example from cereal, pulse and oilseed crops) and roots/tubers (for example from turnip, swede, beet).

[0069] Plant gene promoters, including constitutive promoters; those for genes with tissue- or cell-specific or -enhanced expression; and those that are regulated in response to environmental, hormonal, chemical, and/or developmental signals, are discussed, for example, in US 9,556,102 B2, which is incorporated herein by reference.

[0070] Accordingly, it is contemplated for the nucleic acid coding sequences described herein to be operably linked to one or more promoters or other control sequences which permit control of the expression of the VHPO, for example, its transcription, translation, or otherwise. Such promoters are also known as 'inducible promoters', in contrast to 'constitutive promoters' which are active in all circumstances. In some instances, the inducible promoters permit expression only in the presence, or absence, of a particular condition, such as temperature, humidity, or the presence of one or more chemical signals. For example, inducible transgene expression which can be used in modified plant cells are discussed in Borghi "*Inducible gene expression systems for plants*". Methods Mol Biol. 2010, and Misra and Ganesan "The impact of inducible promoters in transgenic plant production and crop improvement" Plant Gene, 2021, and include AlcR/AlcA (ethanol inducible); GR fusions, GVG, and pOp/LhGR (dexamethasone inducible); XVE/OlexA (beta-estradiol inducible); and heat shock induction.

[0071] Other methods of controlling the expression of the provided polynucleotide coding sequence include the use of post-translational transcription control mechanisms. For example, the provided coding sequence may be operably linked to a microRNA sequence allowing for downregulation of expression in particular cell and/or tissue types and consequent expression in other cell and/or tissue types.

[0072] Further methods of controlling the activity of the expressed VHPO include expressing the polypeptide in an inactive propeptide form, which is then activated under specific circumstances. Alternatively, substrates (such as carbon feedstocks), cofactors, and/or other compounds or conditions necessary for the VHPO to function can be withheld until halogenated hydrocarbon production is desired. In some embodiments, the modified plant cells or plants can be grown in the presence of vanadium or vanadium-containing compounds such as sodium orthovanadate, only when halogenated hydrocarbon production is desired. Similarly, the modified plant cells or plants can be grown in the presence of halogen or halides (suitably bromine or bromides such as sodium bromide or potassium bromide), only when halogenated hydrocarbon production is desired. In some embodiments, the modified plants or plant cells can produce or provide, or be modified to further produce or provide, substrates (such as hydrocarbon feedstocks), cofactors, and/or other compounds or conditions necessary for the VHPO to function. In such cases, the production of those secondary factors can alternatively or additionally be controlled by any suitable means, such as those described above.

[0073] In such cases, some embodiments of the methods described herein can involve providing necessary inducers, substrates or cofactors as indicated above only when VHPO expression and/or halogenated hydrocarbon production is desired. Similarly, inducers, substrates or cofactors can be depleted or removed when VHPO expression and/or halogenated hydrocarbon production is not desired. For example, vanadium compounds can be chelated to remove their availability.

[0074] It is contemplated that bromoform production may be induced in modified plants or plant cells as described herein by subjecting the plant or plant cell to one or more stressors (for example, heat or drought stress). Without being bound by theory, it is thought that levels of reactive oxygen species (ROS) may be increased in stressed plants and thereby more available to the VHPOs described herein.

As mentioned above, the modified plants or plant cells can be modified to further produce or provide, substrates (such as hydrocarbon feedstocks), cofactors, and/or other compounds or conditions necessary for the VHPO to function. For example, the plants or plant cells can be modified to produce further ROS, such as by modification to produce a protein that produces or increases production of ROS. Such a protein may be a NADPH_oxidase, for example, *A. taxiformis* NADPH_oxidase (Mbb2) or equivalents or homologues thereof. Conversely, when modification only to produce VHPO is desired, the plants or plant cells may not be modified to produce NADPH oxidase (such as Mbb2 and identified equivalents). Such modifications may be performed and controlled by any suitable means, such as those described herein.

[0075] Organelle-targeted expression

[0076] Since the VHPO proteins are peroxidases, they need H₂O₂, and potentially carbon feedstocks, in order to function. The availability of these substrates varies within the cell, and in particular, may be more abundant in the peroxisome, chloroplast and/or mitochondrion, since these organelles are particularly involved in the production and/or removal of reactive oxygen species. Thus, by targeting proteins such as VHPO to subcellular locations, the invention can reduce or eliminate the need for additional substrates and/or cofactors associated with halogenated hydrocarbon (e.g. bromoform) production to be provided to the plant or plant cell.

[0077] Additionally, targeting proteins such as VHPO to subcellular locations can act to protect the cell from any deleterious or toxic effects of any products, such as bromoform.

[0078] Accordingly, the polypeptides and/or encoding nucleic acid sequences of the invention may comprise or encode targeting sequences suitable to be targeted to particular cell locations, suitably to the peroxisome, chloroplast and/or mitochondrion. The targeting sequences may be selected to match those used by the species being modified, or may be chosen from another species, where appropriate. Targeting sequences may be located at the C-terminus, N-terminus, or elsewhere on the polypeptides.

Modification of plant cells and plants for use

[0079] The present invention is intended to encompass the modification of any suitable plant or plant cell, typically terrestrial plants or cells thereof which are suitable for feeding to ruminant animals. However, in some embodiments aquatic plants may be used. Depending on the animal, environment, climate and/or amounts needed to achieve methane reduction, the skilled person will be able to select a suitable candidate for modification.

[0080] In the context of this invention, references to plant cells herein are intended to encompass plant protoplasts, that is, plant cells lacking a cell wall, or which have been treated to remove the cell wall. Plant cells are often modified while in a protoplast state. It is envisioned that modified plant cells according to the invention may be cultured *in vitro*, as protoplasts or otherwise, and fed to the animals in processed or unprocessed form – that is, a process in which whole plants are never regenerated. Similar approaches are contemplated using callus cells or other plant cells grown in suspension.

[0081] The plant or plant cell may be a monocotyledon or a dicotyledon. Suitable monocotyledons include corn, millet, sorghum and pasture grasses. Suitable dicotyledons include alfalfa and clover.

[0082] Grasses which may be useful in the present context include *Agrostis* spp. (bentgrasses), *Agrostis capillaris* (common bentgrass), *Agrostis stolonifera* (creeping bentgrass), *Andropogon hallii* (sand bluestem), *Arrhenatherum elatius* (false oat-grass), *Bothriochloa bladhii* (Australian bluestem), *Bothriochloa pertusa* (hurricane grass), *Brachiaria decumbens* (Surinam grass), *Brachiaria humidicola* (koronivia grass), *Bromus* spp. (bromegrasses), *Cenchrus ciliaris* (buffelgrass), *Chloris gayana* (Rhodes grass), *Cynodon dactylon* (bermudagrass), *Dactylis glomerata* (orchard grass), *Echinochloa pyramidalis* (antelope grass), *Entolasia imbricata* (bungoma grass), *Festuca* spp. (fescues), *Festuca arundinacea* (tall fescue), *Festuca pratensis* (meadow fescue), *Festuca rubra* (red fescue), *Festulolium* (Festuca-Lolium hybrids), *Heteropogon contortus* (black spear grass), *Hymenachne amplexicaulis* (West Indian marsh grass), *Hyparrhenia rufa* (jaragua), *Leersia hexandra* (southern cutgrass), *Lolium* spp. (ryegrasses), *Lolium multiflorum* (Italian ryegrass), *Lolium perenne* (perennial ryegrass), *Megathyrsus maximus* (Guinea grass), *Melinis minutiflora* (molasses grass), *Paspalum conjugatum* (carabao grass), *Paspalum dilatatum* (dallisgrass), *Phalaris arundinacea* (reed canarygrass), *Phleum pratense* (timothy), *Poa* spp. (bluegrasses and meadow-grasses), *Poa arachnifera* (Texas bluegrass), *Poa pratensis* (Kentucky bluegrass), *Poa trivialis* (rough bluegrass), *Setaria sphacelata* (African bristlegrass), *Themeda triandra* (kangaroo grass), *Thinopyrum intermedium* (intermediate wheatgrass).

[0083] Legumes which may be useful in the present context include *Arachis pinto* (pinto peanut), *Astragalus cicer* (cicer milkvetch), *Chamaecrista rotundifolia* (roundleaf sensitive pea), *Clitoria ternatea* (butterfly-pea), *Kummerowia* (annual lespedezas), *Kummerowia stipulacea* (Korean clover, Korean lespedeza), *Kummerowia striata* (Japanese clover and common lespedeza), *Lotus corniculatus* (bird's-foot trefoil), *Macroptilium*

atropurpureum (purple bush-bean), *Macroptilium bracteatum* (burgundy bean), *Medicago* spp. (medics), *Medicago sativa* (alfalfa, lucerne), *Medicago truncatula* (barrel medic), *Melilotus* spp. (sweetclovers), *Neonotonia wightii* (perennial soybean), *Onobrychis viciifolia* (common sainfoin), *Stylosanthes* spp. (stylo), *Stylosanthes humilis* (Townsville stylo), *Stylosanthes scabra* (shrubby stylo), *Trifolium* spp. (clovers), *Trifolium hybridum* (alsike clover), *Trifolium incarnatum* (crimson clover), *Trifolium pratense* (red clover), *Trifolium repens* (white clover), *Vicia* spp. (vetches), *Vicia articulata* (oneflower vetch), *Vicia ervilia* (bitter vetch), *Vicia narbonensis* (narbon vetch), *Vicia sativa* (common vetch, tare), *Vicia villosa* (hairy vetch), *Vigna parkeri* (creeping vigna).

[0084] Cereals which may be useful in the present context include *Zea mays* (maize, corn) *Triticum* spp., *Triticum aestivum* (bread wheat), *Oryza sativa* (Asian rice), *Oryza glaberrima* (African rice), *Hordeum vulgare* (barley), *Avena sativa* (oats), *Secale cereale* (rye), *Sorghum* spp., *Sorghum bicolor*, Millets (e.g. *Panicum miliaceum*, *Panicum sumatrense*, *Panicum sonorum*, *Pennisetum glaucum*).

[0085] Root crops which may be useful in the present context include *Raphanus sativus* (Daikon, radish), *Brassica rapa* (turnip), *Brassica napus* (Rutabaga, Swede, forage rape), *Beta vulgaris* (sugar beet)

[0086] Pulses and oilseeds which may be useful in the present context include *Glycine max* (Soybean), *Phaseolus* spp., *Phaseolus vulgaris* (Kidney bean, navy bean, pinto bean, black turtle bean, haricot bean), *Vicia faba* (broad bean, field bean), *Pisum sativum* (garden pea), *Lupinus albus* (lupin), *Brassica napus* (oilseed rape, canola), *Helianthus annuus* (sunflower), *Arachis hypogaea* (peanut, groundnut).

[0087] In addition to forage plants for direct feeding to ruminant animals, it is also contemplated that plants and plant cells of other species may be transformed as discussed herein. For example, model plant species such as *Nicotiana benthamiana*, *Arabidopsis thaliana* (both eudicotyledons); and *Lemnoideae* (including *Lemna* spp.) or *Oryza sativa* (monocotyledons) may be used.

[0088] Any suitable method can be used to transiently and/or stably transform plant cells, as will be evident to the skilled person in context. For example, *Agrobacterium*-mediated transformation, chemical procedures, electroporation, and/or the use of high-velocity particles (particle bombardment) may be used. Genomic editing techniques as known in the art may also be used. For example, in US 9,556,102 B2, which is incorporated herein by reference, discusses methods for transformation of plants, plastid transformation; and the regeneration, development, and cultivation of plants from single plant protoplast transformants.

[0089] Similarly, the nucleic acid constructs of the invention or those comprised by the plant or plant cells of the invention can be of any suitable form. DNA or RNA sequences may be used. mRNA sequences may be used, suitably where short-term or transient production is preferred, as provided mRNA represents an exhaustible supply of genetic code for the production of a particular polypeptide. Circular RNA may also be used. DNA sequences may likewise be in any suitable form, such as a plasmid. The nucleic acid constructs and/or the method of transformation may be selected for stable transformation, such as by genomic integration.

[0090] The nucleic acid constructs may be modified to include one or more reporters by any suitable method, for example, by creating GFP fusions, which may aid in locating or identifying successful transformations.

[0091] The modified plants or plant cells are capable of producing halogenated hydrocarbons, such as bromoform.

Preparation and use of animal feed

[0092] The modified plants or plant cells produced can be expanded and propagated in any suitable way, such as by runners, cuttings, and the preparation of seed. The modified plants, whether or not subjected to further processing, can be used as an animal feed or feed supplement, and/or grown in a location where it can be eaten by said animal during normal feeding. As mentioned, the expression of the provided polypeptide can be induced by a suitable method. Where and when produced, the bromoform or other methane-reducing substance can inhibit the production of methane by the recipient animal, for example by inhibition of microbial production of methane.

[0093] Typically, the animal is a ruminant, and may be bovine, ovine, equine, camelid, or cervine. The animal may be a cow, sheep or goat. The feed efficiency may be increased, given that that energy-dense methane is not produced. The animal may be fed with the modified plant or derived feed intermittently or continuously, as appropriate.

[0094] The modified plant may be grown as an annual or perennial crop, depending on the species and cultivar, and either as a mixture together with other appropriate species or as a monoculture. Its tissues may be used as an agricultural foodstuff that livestock forage for themselves. Alternatively, the modified plants tissues may be harvested and processed in any way that is appropriate to provide fodder (or animal feed), which includes, but is not limited to, hay, straw, silage, cereal grains, pulses, oilseeds, tubers, mixed rations, compressed and pelleted rations. Extracts from the modified plants can also be fed to livestock in their drinking water or in licking blocks, or the like. Any means may be used that enables the modified plant material or an extract from that material to enter the rumen of the livestock. The content of bromoform, related halogenated compounds, or other components may be measured before feeding the modified plant material or extracts from that material to the animal, to determine an appropriate amount to be fed.

EXAMPLES

[0095] The invention is further illustrated by the following, non-limiting, examples. The below experiments demonstrate some embodiments of the invention in practice.

[0096] Example 1 – Transient Expression of AtMbb1, CcMbb3 and AaMbb4-2 in corn protoplasts

[0097] *Asparagopsis taxiformis* Mbb1 protein (AtMbb1, SEQ ID NO: 41), *Chondrus crispus* Mbb3 protein (CcMbb3 SEQ ID NO: 6) and *A. armata* Mbb4-2 protein (AaMbb4-2 SEQ ID NO: 19) were expressed in a corn protoplast system. Four green fluorescent protein (GFP) fusion constructs were designed for each gene, and signal peptides were added to direct the expressed fusion protein to the cytosol, chloroplast, mitochondria and peroxisome respectively. The gene sequences for AtMbb1 (SEQ ID NO: 80), AaMbb4-2 (SEQ ID NO: 58), and CcMbb3 (SEQ ID NO: 52) were codon optimized for expression in a corn system. Thus, a total of 12 vectors were designed and made as indicated below for transient expression in corn protoplasts.

[0098] Construct design: Chloroplast transit peptide (SEQ ID NO: 88), mitochondria targeting peptide (SEQ ID NO: 89), and peroxisome targeting peptide (SEQ ID NO: 90) were found from the typical maize chloroplast-localized protein (ribulose biphosphate carboxylase small subunit 2, GenBank accession: NP_001338725), mitochondria-localized protein (superoxide dismutase 3, GenBank accession: NP_001105742) and peroxisome-localized protein (silkless ears1, GenBank accession: NP_001131410). These signal peptides were fused to the N-terminus (chloroplast transit peptide, mitochondria targeting peptide) or C-terminus

(peroxisome targeting peptide) of AtMbb1, AaMbb4-2, and CcMbb3, while GFP (eGFP, SEQ ID NO: 97) was fused to the C-terminus of these genes.

[0099] Two linkers (Linker 1 (SEQ ID NO: 93) and 3XGGGGS (SEQ ID NO: 94)) were used between the domains of the fusion proteins. No signal peptide was found in AtMbb1, AaMbb4-2 and CcMbb3, indicating that they are cytosol-localized proteins, so AtMbb1-GFP, AaMbb4-2-GFP, and CcMbb3-GFP without additional signal peptide were considered as cytosol-localized. The chimeric genes were driven by a maize Ubi-1 promoter (SEQ ID NO: 91). The gene cassettes were cloned into a pUC57 vector. Example indications of how such constructs were structured can be seen in Figures 1A to 1D. Figure 1A shows a cytosol localised protein, the gene sequence fused with 3XG4S linker and GFP, and driven by a maize ubi-1 promoter and followed by a NOS terminator (SEQ ID NO: 96). The fragment was synthesized and cloned into pUC57. Figure 1B shows a chloroplast-localised protein, with a signal peptide from a maize RbcS protein fused to the N-terminus of the gene of interest, followed by GFP. The start codon (ATG) of the gene of interest was removed and two linkers added to improve protein expression. The chimeric gene was inserted between the maize ubi-1 promoter and the NOS terminator. Figure 1C shows a mitochondrion localised protein, with a mitochondrial targeting peptide from maize SOD3 fused to the N-terminus of the gene of interest, followed by GFP. The start codon (ATG) of the gene of interest was removed and two linkers added to improve protein expression. The chimeric gene was inserted between the maize ubi-1 promoter and the NOS terminator. Figure 1D shows a peroxisome localised protein, with the gene of interest fused with GFP, followed by a peroxisome targeting peptide. Two linkers were added to improve protein expression. The chimeric gene was inserted between the maize ubi-1 promoter and the NOS terminator. In the context of the invention, alternative reporters, genes (such as those described herein), promoters, terminators and linkers can of course be used where appropriate, and some components such as reporters can be omitted entirely if desired.

[0100] *Protoplast isolation and transfection:* Protoplasts were isolated from leaf tissues of 7-day-old etiolated corn seedlings (Coy et al., 2022. "Protoplast isolation and transfection in maize." *Methods Mol Biol.*). Briefly, the first true leaf was collected and the tip and the base removed. Leaf tissue was sliced into 0.5–1 mm slices using a new scalpel and distributed in Petri dishes containing digestion solution. The plates were placed in a vacuum chamber under house vacuum for 30 min, and then moved into an orbital shaking incubator at 28°C. Leaf tissue was incubated for 4 hr until protoplasts were released. The protoplast solution was collected using a 0.45 µm Steriflip filter device (Millipore), and was washed three times by adding 10 mL of the MMg solution. The protoplasts were counted by using a hemocytometer.

[0101] Plasmid DNA was received and transformed into *E. coli*, DNA was extracted and confirmed via PCR. To obtain the large amount of DNA required for protoplast transfection DNA maxi-preparation was carried out. For transfection, 40% polyethylene glycol (PEG) was added into the mixture of MMg solution, plasmid DNA, and protoplasts. Each plasmid was co-transfected with a reference plasmid expressing the fluorescent protein mCherry under the control of a constitutive promoter as a transfection efficiency control. mCherry was employed as a positive control for subcellular localisation. mCherry is a derivative of RFP, and used to co-localise GFP-fused proteins. For each target, there was an mCherry control associated with it.

[0102] Finally, the protoplasts were incubated at 28 °C overnight in dark. The cells were used for localization studies by a fluorescent microscope. Expression of the mCherry gene was used to determine transfection efficiency. Transfection efficiency may be calculated as the percentage of fluorescent protoplasts to the total

protoplasts, monitored under a fluorescent microscope. Detection of GFP by fluorescence microscopy confirmed successful transfection and expression of the fusion construct.

[0103] Fluorescence microscopy: In order to determine the expression of the AtMbb1 and CcMbb3 constructs, in the transfected corn protoplast cells, transient expression analysis by fluorescence microscopy analysis was carried out. The corn protoplasts were transfected as described above and then analysed to determine the subcellular localization of the expressed protein.

[0104] Imaging was performed 48 hours post-transfection and collected via stereoscope to determine proper subcellular localization. Images were taken in GFP and mCherry channels at 20x magnification, under the same acquisition settings, and then merged to produce Figures 3 and 4. Expression and localisation results of the fluorescence microscopy are summarised in Table 1.

[0105] Figure 3 depicts the resulting fluorescence microscopy images for AtMbb1 constructs. Figure 3A shows cells transfected with cytosol-targeting constructs; Figure 3B shows cells transfected with chloroplast-targeting constructs; Figure 3C shows cells transfected with mitochondria-targeting constructs; Figure 3D shows cells transfected with peroxisome-targeting constructs.

[0106] Figure 4 depicts the resulting fluorescence microscopy images for CcMbb3 constructs. 4A shows cells transfected with cytosol-targeting constructs; 4B shows cells transfected with chloroplast-targeting constructs; 4C shows cells transfected with mitochondria-targeting constructs; 4D shows cells transfected with peroxisome-targeting constructs.

Table 1: Fluorescence microscopy results

Gene of Interest	Cytosol	Chloroplast	Mitochondria	Peroxisome
AtMbb1	Strong expression, proper localization	Moderate expression, proper localization	Moderate expression, slight cytosolic localization	Weak expression, proper localization
CcMbb3	Strong expression, chloroplast localization	Weak, proper localization	Moderate, slight cytosolic localization	Weak expression, proper localization

[0107] Protein expression is confirmed in all AtMbb1 and CcMbb3 transfections. We have confirmed plasmid sequence via PCR and digestion for all 12 constructs. Targeting sequences are functioning for most constructs.

[0108] Example 2 – Expression of *Asparagopsis taxiformis* Mbb1 (AtMbb1) in *Arabidopsis*

[0109] Four vectors suitable for the stable transformation of *A. taxiformis* Mbb1 (AtMbb1, SEQ ID NO: 80) were designed and introduced into *Arabidopsis*. The gene sequence underwent codon optimisation for expression in *Arabidopsis*. A 3XHA epitope tag (SEQ ID NO: 95) was added to the gene to facilitate detection and quantification of the expressed protein. Signal peptides were added to direct Mbb1 expression to the chloroplast, mitochondria and peroxisome, respectively. Mbb1 expression was driven by a CaMV 35S promoter (SEQ ID NO: 92). Transgenic plants were further analysed by molecular analysis to determine

whether the plants had been successfully modified, whether the constructs were successfully transcribed into mRNA, and whether the constructs were successfully translated into mature protein, as described herein.

[0110] Construct design: For consistency with the transient expression experiment for the three proteins described in Example 1, the same signal peptides used in transient expression were utilized for making transgenic *Arabidopsis* plants expressing fusion proteins that are targeted into different organelles. These signal peptides were fused to the N- or C-terminus of AtMbb1, while 3XHA tag was fused to the C-terminus of this gene. Two linkers (Linker 1 (SEQ ID NO: 93) and 3XGGGGS (SEQ ID NO: 94)) were used for linking the different components (a signal peptide, AtMbb1 protein and the 3XHA tag) to make fusion proteins. No signal peptide was found in AtMbb1, suggesting that it is a cytosol-localized protein, so AtMbb1-HA without additional signal peptide was considered as cytosol-localized. The coding sequences were codon optimized for expression in *Arabidopsis*, the gene cassettes synthesized and cloned into pCAMBIA1300-35S vector where they are driven by an enhanced cauliflower mosaic virus 35S promoter.

[0111] Example indication of how such constructs may be structured can be seen in Figures 2A to 2D. In the context of the invention, alternative epitope tags, genes (such as those described herein), promoters, terminators and linkers can of course be used where appropriate, and some components such as epitope tags can be omitted entirely if desired. Figure 2A shows Chloroplast-localized AtMbb1. A signal peptide from maize RbcS protein was put in the N-terminus of AtMbb1, followed by 3XHA. ATG of AtMbb1 was removed and two linkers added to optimize protein expression. The cassette was synthesized and cloned into pCAMBIA1300-35S, where it is driven by an enhanced 35S promoter.

[0112] Figure 2B shows Mitochondria-localized AtMbb1. A mitochondrial targeting peptide from maize SOD3 was fused into the N-terminus of AtMbb1, followed by 3XHA. ATG of AtMbb1 was removed and two linkers added to improve protein expression. The cassette was synthesized and cloned into pCAMBIA1300-35S, where it is driven by an enhanced 35S promoter.

[0113] Figure 2C shows Peroxisome-localized AtMbb1. AtMbb1 was fused with 3XHA, followed by a peroxisome targeting peptide. Two linkers were added to improve protein expression. The cassette was synthesized and cloned into pCAMBIA1300-35S, where it is driven by an enhanced 35S promoter.

[0114] Figure 2D shows Cytosol-localized AtMbb1. No signal peptide was found in AtMbb1, indicating AtMbb1 is a cytosol localized protein. So AtMbb1 was fused with 3XG4S linker and 3XHA. The cassette was synthesized and cloned into pCAMBIA1300-35S, where it is driven by an enhanced 35S promoter.

[0115] Introduction of constructs into Agrobacterium: Plasmid DNA was transformed into *E. coli*, DNA was extracted and confirmed via PCR, and subsequently transformed into *Agrobacterium*. The finished constructs were introduced into *Agrobacterium* strain GV3101 by electroporation. The vector identity was confirmed by PCR after transformation.

[0116] Agrobacterium-mediated transformation in Arabidopsis: *Arabidopsis* ecotype Columbia (Col-0) was used in *Agrobacterium*-mediated transformation by using the floral dip approach (Clough and Bent, 1998. Floral dip: a simplified method for *Agrobacterium*-mediated transformation of *Arabidopsis thaliana*. *Plant J.*). Seeds were collected from mature plants after transformation. Seeds were harvested from the plants, sterilized, and plated on hygromycin selective growth media. Plants exhibiting an elongated hypocotyl after a prolonged dark treatment were transferred to soil for genotype analysis. Tissue was harvested from rosette

leaves of young plants and either DNA was isolated or the tissue was flash frozen for RNA and protein extraction for downstream assays.

[0117] *Plant growth phenotype:* Plants were grown and assessed for morphology and growth phenotype. Figure 5 shows transgenic plant lines 2007, 2011, and 2012 (labelled boxes) and six wild type *Arabidopsis* plants (not labelled). There is no discernible difference between the phenotypes of the plants, confirming that transgenic plants exhibit a normal phenotype and grow normally.

[0118] *Selection of transgenic Arabidopsis:* Screening of transgenic *Arabidopsis* was conducted by placing seeds on the selection medium (half-strength MS) with Hygromycin (50 mg/L). Two weeks later, the resistant seedlings were transferred into soil.

[0119] *Genotyping:* Genotyping of transgenic plants was conducted by PCR using primers specific to the selectable marker (*hyg* – hygromycin resistance gene) used for selection of transgenic events. A total of 74 plants tested positive for the presence of the *hyg* marker by PCR, with results visualised on agarose gel. 32 *hyg*-positive plant lines were carried forward for further analysis. The number of copies of the T-DNA present in the *Arabidopsis* genome in each event was determined by digital droplet PCR analysis, the results of which are set out in Table 2, below. DNA was isolated from the previous genotyping assay for copy number analysis. Probes targeting the transgene were compared to a gene with known copy number to arrive at a copy number variation (CNV) value which is relative to the copy number of the known gene. Plants are grouped by the target signal of the transfection construct. The results confirm that plants were successfully modified with the constructs.

Table 2: Plant copy number results

Plant ID (cyto)	Copy Number	Plant ID (chloro)	Copy Number	Plant ID (mito)	Copy Number	Plant ID (peroxi)	Copy Number
2007	0.98	2016	2.95	2027	4.23	2030	2.05
2008	12.5	2018	0.92	2344	3.98	2031	1.48
2010	11.2	2019	2.84	2345	30.7	2032	1.03
2011	3.51	2022	4.55	2346	31.1	2033	12.01
2012	4.49	2023	2.29	2347	7.8	2034	0.8
2013	35.4	2024	2.51	2348	5.2	2035	20.1
2014	2.2	2025	6.63	2349	0	2036	18.68
2015	7.6	2026	0.73	2350	20	2037	1.7

[0120] Genotyping was further carried out on T2 (second generation) plants descended from the above lines. PCR was carried out on T2 plant material using the same methods as described above. These results confirmed that the transgenes present in T1 (first generation) plants were inherited by T2 plants.

[0121] *Transcription analysis:* The levels of Mbb1 transcripts were then measured by qRT-PCR in each event. RNA was extracted from rosette leaves, and cDNA concentration was normalised across all samples. Gene of interest (AtMbb1) expression was normalized to WT-Actin using $\Delta\Delta C_q$ analysis. The results are shown in Figures 6A-C. Table 3 recites the results of Plate 1 depicted in Figure 6A; Table 4 recites the results of Plate

2 depicted in Figure 6B; Table 5 recites the results of Plate 3 depicted in Figure 6C. Samples were split across three different plates and cannot be directly compared. WT expression is on the far right of each of Figures 6A-C and has a normalized expression of zero. The results show that constructs are successfully transcribed by the plants.

Table 3: Plate 1 transcription results

Plant ID	Expression	Plant ID	Expression
2007	1.6813888	2014	0.0806747
2008	0.0093421	2015	0.0665885
2010	0.1086749	2016	0.1098342
2011	0.8176041	2018	1.4071898
2012	0.3359215	2019	0.0210561
2013	0.020181	2022	1.4357404

Table 4: Plate 2 transcription results

Plant ID	Expression	Plant ID	Expression
2023	0.17853	2345	0.02670
2024	0.22615	2346	0.00739
2025	0.03234	2347	0.10461
2026	0.83602	2348	0.03683
2027	0.01342	2349	0.18252
2344	0.19992	2350	1.47380

Table 5: Plate 3 transcription results

Plant ID	Expression	Plant ID	Expression
2030	0.16285	2034	0.41210
2031	0.10667	2035	0.05307
2032	1.00000	2036	0.09461
2033	0.06003	2037	0.41223

[0122] Translation analysis (T1): The production of the Mbb1 protein was analyzed by Western blotting using antibodies against the HA tag. Transgenic *Arabidopsis* previously identified as being selection marker-positive were grown in a growth chamber under long day conditions to increase leaf material for sampling, with seeds harvested and preserved. Leaf tissue was flash frozen in liquid nitrogen and stored at -80C until needed for total protein extraction. Frozen tissue was homogenized using a bead beater and protein extracted in an extraction buffer along with centrifugation to remove excess plant material. Protein concentrations were measured via Bradford assay against known BSA standards. Samples for Western blot analysis were normalized to 25 ug total protein, run on Tris-Glycine gels and transferred to PVDF. Equal loading was

determined by Ponceau staining. Antibodies raised against the HA-tag were used to detect protein, with a positive control confirming correct detection.

[0123] Presence of the transgene-encoded protein was confirmed by Western blot performed using the above procedure, confirming successful translation. Lines which tested positive for protein were: (Cytosol-targeting) 2007, 2011, 2012, 2331, 2332, 2333, 2335; (Chloroplast-targeting) 2018, 2023, 2026; (Mitochondria-targeting) 2350, 3652, 3657, 3660, 3664; (Peroxisome-targeting) 2030, 2032, 2038, 2353

[0124] Translation analysis (T2): Further analysis of protein expression in T2 (second generation) plants descended from selected plant lines tested above was conducted by Western blot using the same procedure as described above. Lines 2007, 2023, 2335, 2350, 2353 and 3652 were submitted for analysis. Pools of 10-day old T2 seedlings previously grown were subsequently frozen and stored at -80°C. Total protein was extracted under native conditions and Western blots performed to visualize transgene-encoded protein in the T2 generation. 75 ug of total extract was loaded for all T2 samples.

[0125] Presence of the transgene-encoded protein was confirmed in all lines tested except 2335, which was inconclusive. These results demonstrate that the transgene is heritable across generations and may be successfully translated in T2 generation transgenic plants.

[0126] Thus, successful transformation of *Arabidopsis* plants with vectors as described has been achieved. It has further been shown that transgenic *Arabidopsis* plants express the transgene of interest, and that mature protein encoded by the transgene has been detected by Western blot. It is therefore expected that plants expressing VHPO encoded by the transgene will produce bromoform when grown.

[0127] Example 3 – Liquid culture of Arabidopsis seedlings

[0128] Whilst it is expected that transgenic *Arabidopsis* plants of the invention, such as those described in Example 2 may produce bromoform without the addition of any additional substrates or cofactors, the plants may be grown in liquid culture with the addition of substrates and cofactors (such as KBr, Sodium orthovanadate, pentane-2,4-dione, and H₂O₂) to encourage and/or increase bromoform production further.

[0129] For each transgenic plant sample prepare approximately 100 seeds in a 1.5 mL Eppendorf tube, add 1 mL of sterile water and mix well. Put the tube upright at room temperature (23°C–25°C) for 10 min. Remove the water and add 1 mL of fresh sterilisation solution (5% (v/v) bleach, 0.01% (v/v) Tween 20 in sterile water). Gently mix on a shaker for 5–10 min. Discard the sterilisation solution and wash with 1 mL sterile water for 5 min. Repeat this step 3 times. This step should be performed in a laminar flow hood to avoid contamination.

[0130] Keep the surface-sterilized seeds in the closed tube with 1 mL sterile water at 4°C in the dark for 2–4 days to promote uniform germination prior to using the seeds in experiments. Prepare half strength Murashige and Skoog (1/2 MS) liquid growth medium (Sigma-Aldrich) containing 0.5% w/v glucose (or sucrose) and 0.1% w/v MES buffer. Adjust pH to 5.7 using 5M KOH. Autoclave to sterilise. For each sample transfer the 100 sterile seeds into a sterile 250 ml Erlenmeyer flask containing 50 ml of sterile ½ MS medium. Add lids and incubate the flasks on an orbital shaker at ~150 rpm placed in a growth chamber set to standard *Arabidopsis* growth conditions (20-22°C, 16h light [100 µmol m⁻² s⁻¹ PPFD], 8 h dark).

[0131] After 5-7 days there should be clumps of young seedlings growing in the flasks. Pour off the ½ MS media, then replace with fresh ½ MS media containing appropriate substrates and cofactors for bromoform production (50 mM KBr, 10 µM sodium orthovanadate, 1 mM pentane-2,4-dione and 2 mM H₂O₂) and incubate for up to 5 to 7 days. The seedlings can then be rinsed with sterile water, blotted dry on paper towel, weighed,

frozen in liquid nitrogen and stored at -80°C for analysis. Note the number of seeds per sample and medium incubation volumes can be scaled down to do cultures in smaller vessels such as multi-well plates - dependent on how much tissue is required for later extraction.

[0132] Example 4 – Soil culture of *Arabidopsis* with leaf spraying

[0133] Whilst it is expected that transgenic *Arabidopsis* plants of the invention, such as those described in Example 2, may produce bromoform without the addition of any additional substrates or cofactors, the plants may be grown in soil culture and additionally provided with substrates and cofactors (such as KBr, sodium orthovanadate, pentane-2,4-dione, and H₂O₂) to encourage and/or increase bromoform production further.

[0134] Transgenic *Arabidopsis* plants approximately 4-6 weeks old were grown in soil for 3 weeks. Substrates and cofactors were provided by spraying a solution of 50 mM KBr, 10µM sodium orthovanadate, 1 mM pentane-2,4-dione, and 2 mM H₂O₂ directly onto the rosette leaves of the plants. The leaves were sprayed with the solution three times per day for three days. A small amount of surfactant such as Tween 20 may be added to the solution to aid uptake as the leaf surface is hydrophobic.

[0135] Example 5 – In vivo production of bromoform by transgenic *Arabidopsis* lines

Seedlings or rosette leaf tissue from T2 *Arabidopsis* lines expressing AtMbb1 were tested for the *in vivo* production of bromoform. Bromoform was detected by GC-MS as described by Thapa *et al* (2020). Leaf tissue samples collected from transgenic plants were extracted with MeOH overnight. Following incubation, the samples were vigorously agitated on a vortex mixer, centrifuged at 16,000×g for 30 min to remove debris, and an aliquot of the supernatant was subsequently analyzed by GC-MS (1260G with 7890a MS; Agilent Technologies) in electron ionization (70 eV) mode using a DF-5ms ultra inert GC column (30 m length, 0.25 mm width and 0.5 µm film thickness). Frozen tissue samples were extracted in 300 µl / 100 mg tissue, the extract was centrifuged and then 50 µl used for GC/MS analysis. Bromoform production was quantified based on calibration curves generated from a bromoform standard. The column temperature conditions will be as follows: 40 °C for 3 min, increased to 200 °C at 10 °C/min and held for 1 min with a total run time of 20 min. Injection port, interface and ion source will be kept at 250 °C, 300 °C and 230 °C, respectively. Helium will be used as carrier gas at a flow rate of 0.9 mL/min.

Bromoform standards were tested against a known concentration of naphthalene (0.5 µg/mL, retention time of 10.263 minutes), and were detectable between 0.25 and 5 µg/mL with a retention time of 7.905 minutes. 0.5 µg/mL naphthalene was included in all test samples as an internal standard. Each sample was extracted in chloroform spiked with 0.5 µg/mL naphthalene, centrifuged, and 50 µL of the supernatant run through the GCMS.

[0136] T2 leaf samples: T2 plants for each of 19 different *Arabidopsis* events expressing AtMbb1 were grown in soil for three weeks. Leaves from these T2 plants, grown according to Example 4 were harvested, frozen and analyzed for the presence of bromoform by gas chromatography-mass spectrometry (GCMS). Samples underwent a double extraction and concentration process. They were initially extracted with chloroform as described above. Samples were then re-extracted with 150 µL saturated brine and 50 µL methanol, vortexed to separate the phases and the upper chloroform and methanol phase was transferred to a clean tube. This lower phase was reextracted with 300 µL of methyl tert-butyl ether and the top layer transferred to the chloroform/methanol. Samples were then dried under nitrogen gas and immediately redissolved in 50 µL methanol for GCMS injection. This resulted in the detection of bromoform from a total of 4 events (2007, 2011,

2012, and 2023) whereas no bromoform was detected from wild-type *Arabidopsis* plants. Peaks were detected at retention times of 7.922 (2007), 7.913 (2011), and 7.918 (2012 and 2023) minutes, consistent with bromoform elution. Some samples were reinjected in a different in order to confirm that positive results were not due to reagent contamination or carryover. Lines 2007, 2011, and 2012 express cytosolic AtMbb1 (no signal sequence) whereas the AtMbb1 is directed to the chloroplasts in the event 2023.

[0137] Figures 7A-D are gas chromatograms of T2 leaf samples; for each sample two chromatograms are presented with x-axes of different scales in order to better visualize the data. Sample material was spiked with internal standard and as such peaks at elution times for bromoform and naphthalene are visible in each sample chromatogram. The peaks labelled with elution time relate to the sample material of the combined extracted ion chromatogram. Figure 7E is a chromatogram of the positive control: 0.25 µg/mL bromoform standard. Figure 7A is the chromatogram for the 2007 sample. Figure 7B is the chromatogram for the 2011 sample. Figure 7C is the chromatogram for the 2012 sample. Figure 7D is the gas chromatogram for the 2023 sample.

[0138] The mass spectra of samples were then analyzed to confirm the identity of the bromoform peak. As an example, the mass spectrum from event 2007 is shown in Figure 8, along with the NIST reference spectrum for bromoform. The 2007 sample mass spectrum is shown above, the NIST reference spectrum below. The 2007 sample spectrum shows a strong match to the expected spectrum for bromoform, with corresponding peaks for full and partial bromoform ions. This confirms the presence of bromoform in the 2007 sample, initially detected by gas chromatography.

[0139] T2 seedling samples: Bromoform was also detected in plant material taken from T2 seedlings grown according to Example 3 and tested according to the same protocol as described above in Example 5. In addition to the transgenic T2 seedlings, wild-type (non-transgenic) *Arabidopsis* seedlings were analyzed in parallel as a negative control. An extract of *A. taxiformis* algae was used as a positive control. Commercial bromoform was used as a standard. Bromoform peaks were observed by gas chromatography and peaks matching full bromoform ions detected by mass spectrometry in T2 seedling samples.

[0140] Taken together, in these examples we have shown that algal VHPO enzymes can be expressed in functional form in plant cells, and that transgenic plants expressing such VHPO enzymes are able to produce bromoform *in vivo*.

Table 6: List of Identified Sequences

SEQ ID NO	Description	Sequence
1	<i>A. taxiformis</i> Vanadium- dependent haloperoxidase Mbb1 [QKI80117.1]	MTDTQNPNAEVAFKVRVSAELARARGSPTHLSNNSESFRNPDPGTRSLLANFTKG LPHTKETALVVSAIDYDSFVRAIDSGDPRDFADLPLGPQGVEPRFTSGIASDPEVGTRA WESGGAGLVFDLEGPDAQAVTMPPAPELDSDELVTEVTECYWMSLLRDVPFPTFDS PHIQSAAESINNTQWQFKNNPPAHLTAAERSRLRGPITTANVFRGITPGDEVGPYLSQ FLLVGTGTGIANGNEVGDFIQYGGMRMDQVRVRAKSHIDYMTTFGAYLDVQNAANVS GRELYNEEPRFRFIHTPRDLATYVHFDALYQAYLNACIILLDIGAPFDSGIPFQLDNDID KQQGFATFGGPHILSLVTEVATRALKAVRFQKFNHRRRLRPEAIGARVDRYCATKAPE FAGAANKLSEALDKLLQKVHHDHKKQNLSDRGNPRANDFNPDGDVSKGNLLMPMAF PEGSPMHPAYGAGHATVAGACVTVLKAFFDGGYRLPFCYITDENGTLKAVEIDEPLT VDGELNKICSNISIGRNWAGVHYFTDYIESIRIGEEIAIGILQEQLTFSENFSMTLNKFD GSTIRI
2	<i>A. taxiformis</i> NAD(P)H oxidase Mbb2 [QKI80118.1]	MAKQKSLFTLLSATLESHLSTHAFQLLALIYALANALMFVWGAHDEFHHHTDANNLRW YICIARGAGYTLNLTALVILLAAARLFATYLRPLQHLPLDKSFPAFHVVAYTIAAAVVI HASFHLAWLVAYDMWETGMWGFTMSAATGVLLVVFVIMFISAMPKYRKKHFRIFYLI HVGALLFFGLLVFHGMYNRPETYKWIAAPLIYIDRVLRKYKISTAELELTGEHSSLK GSDILELRVPKPFQYAGQYAEVCVKINSEWHPFTIASSPHEDSMCFYIKALGDWTT NLRDAFEARVENDLYEPLKVQIRGPGAPAQHVSGYCRVVLISGGVGSTPFAAICKHL HHLNKSSENHSALESQVSSKRQSQVQWRIRDAISILFDVSLDDSRNDEAANQRRQQ LADMLNMSPKGDVHNVSFKRTQSKRSDDFDAVEDSKQMNFLSCRQDSKSSFNLDCC SDAIRYYNRPSFQFFSSSPRHVINWYERTRLLAFLHTTRFTFALLTLVARIVILCIVSIF NLGHIGLYNSHIDATWVIATNSILGLILGVALLTTILLEISFMRVRFYRVWRCVDFFIPLPI TFLCNISNFWNGHAQPKFLIFLDLIIVLPIMLLLLCHRMYSVSGSRNLLDDTAECRQG CKCNKTIPDVDFVWTTPRDSDDEWLRNELYPLATGTELRLHRYVTRENMADLEDPER FITTANAGRPQWDEIFAQIAEQTPSHSKIGVFFCGPHPMGAAVQKSMRKVEVMSNLRG SYLRKTESAVLVDDLILRDEGEVKLLREYGCNIRFVREENFS
3	<i>A. taxiformis</i> Vanadium- dependent haloperoxidase Mbb3 [QKI80119.1]	MTPPTRRQTALVKRIAAADLAANRHHPLHVRNADETTYKLPNHVCSYISAFKGLPHHL DGRLVSPHHFQLFVHAVQTGHVTDIAAIPLGPPHSSSFRSGIAKGAAVRAWESMAAGN TFDLQGPDAQAVTMPPCPRLNSHELVTETELYYMALLRDVPFTHFNKHHLVQSAVH DMNHTHWTRS NRCCLPERRRRHSKFTTDNIFRGVTPGDITGPYISQFLLVGTGKLG DAHEETEGYVQYGATRIDQVRVTEPKIDYMTTWAAYLDVQNGADLRRHSTYAKPPS YRFISTPRDLATYVHYDALYQAYLNACIILLDINAPYDGGLPFTADDAVDKQQGFATFGA PHVLTLVTEVATRALKAVRFQKYAVHRRRLRPEAVGGLLEQYRRYGGGHSGLAYIIRPIR HLADSLSSDLMFMVAKENGRQNSSITDNGHPRSHDEGSDDTHLLSMAYAEGLSPMHP SYGAGHATVAGACVTILKAFFDHTFKLPFAYVSSSDGRKLKTVKLSRKLTVDELNKL ANISIGRSWAGVHYSDYVESIRLGEVVAIGMLKEQKLTYSKFTMTIPKFDGGSVIEI
4	<i>A. taxiformis</i> Vanadium- dependent haloperoxidase Mbb4 [QKI80120.1]	MAEERRQNALDIRIQAARLAKKRDHPTEANGDEDRYPETLIGSFTKGLPHEKETGLLS NPADFADFVRAINTGAIKDIRRLKLGIDEDPRFISGIASKGDKHPFADTRAWE SMAAGLT YDLEGPDAQAVTMPPAPKGLSDDELVTEITESYWMALIRDVPFTEFERDGNATAAASIS RTRWWQFNEQPSQRPSTLTDEEIALRGRPYTKKNVFRGVTIGENVGPYLSQFLLVGTG GIGDVQQISDGYIQYGS MRMDQVRVRAAPKRDYMTTWASWLDVQNAAGDLRGREIYD DDTPFRFITTPRDLATWVHFDALYQAYLNACIILLDIKAPFDPHIPFQADDDVDKQQGFA TFGGPHILSLCTEVATRALKAVRFQKYNVHRRRLRPEAIGGLVERFKKTNGDAKFAPVKK LVNDLDGDMRLRRIEQHNCEQNKLSDDGHARRDDYSPEGESNQTYLLPMAFPEGSPM HPSYGAGHATVAGACVTVLKAFFDHEYELDFCYVPTTDGKRLEKVNINEKLTVEGELN KLCANICIGRNWAGVHYSDYFESIKVGEEIAIGILQEQLTYGEDFFMTLSKFDGEKIRI
5	XP_005714237.1 vanadium- dependent bromoperoxidase, vBPO [Chondrus crispus]	MSAARRQEAQTRVRAARLARDRDHGVFEPNGEEDRYFRPNSQIFS YLGSYTKGLPH NRRTALITSPNHFVRVRAIDSGEPADFIKVPPLGPRPALQFESEEEECRAANLFKSGIAG RNNTFPSSCLRAWESMGAGLVFDLEGPDAQAVGMPPAPTLDSELDVAEISEVYWMAL LRDVRFTDFTNPGPIGRAINTLNKTAWIRAARDPPDSLTPQERARLRGPFNP SNIFRG LPGDDVGYPYLSQFLLVGTGKIGGAQDMADGFISYGAHRIDQVRVHARKELDYMSTWE AFLDVQNGADVTGRDTFESGDAFRFITTTPRDLATYVHFDALYQAYLNACIILLDSGV RFDKGIPIFGEPDFKDHQGFAGHGGPHILSLVTEVATRALKAVRFQKFNHRRRLRPEA VGGLIERFNSNPDDPQFQDVKPLFEALDEDMRRVARHNREQNQSGDFGMPRADDF NPAGDTLETMLLPMAFPEGSPMHP SYGAGHATVAGACVTVLKAFFQHDTELD FCFVP SDDGSRLVDASHNMNKKLTVEGELNKVCSNISIGRNWAGVHYFTDYIESILLGEQIALGI LEEQMLTFPETFTMTVPFLSGELKVLIRST
6	XP_005719435.1 vanadium- dependent	MATPCFAQAPAPTLRRSPRRLPLTPTSFLPRPFLPKPFPRSPRHPHRLNAASARTSA AQPPDRAATPCATRQQQALELRAAAQLAHDRAHPAHVSNSEELHLHPKGTGAPLLL ANFTKGLPHERDTGLAADAHYDLFAAVHSGLPDDIRAIPLGPQAAPGVRPLRSLRF RSGIARSSHLPHTDVRVAWESMAAGNAFDLQGPDAQAVTMPPAPALASPELALEMTE NYWMALLRDVRFSSQFAADPTVAAAMESMNATEWWALACGDASAVAEERKRLRGPF

	bromoperoxidase, vBPO [Chondrus crispus]	TAQNVFRGNTQGDCKGPYISQFLLSGSAGLGQVNSGADGYIQYGAMRMDQVRVVAL EGLDYMTTWESWLDVQNGADLRGRELIEDGERFRFICTPRDLATYVHYDALYQAYLN ACIIMLNKKIPFDKGLPFQKDDDDIKQQGFALFGPPHILTLCTEVATRALKGIRFQKYNV HRRLRPEAVGGRVERYHHNCEDPLFADV KPLYDALDKDMLERVAAHNAEQNAKDDF GNSRFEDYSPTGSSGRTYLLPMAFPEGSPMHPAYGAGHAAVAGACTTILKAFFDHEH ELDFAVYPTADGSKLEDVVDLSGEKLTVEGELNKVCSNISVGRNWAGVHYFTDYRESII LGEKIALGLLEEQLTYAEFEFSMTIPLFDGSTVTI
7	XP_005710894.1 vanadium- dependent bromoperoxidase, vBPO [Chondrus crispus]	MSDMSTEISPRQGEAYDIRVAAATLALARDRKRKVFEPNGEEDRYFRPNSQILSYLGS YTKGLPHNRSTALVTSPNHFVRVQAI DSGEPADFIKVPLGPRPALEFTTEEECIAANLF KSGIATRNDSDPACLRWESMGAGLVFDLEGPDAQAVGMPPAPTLDSELDVAEISEL YWMALLRDVRFTDFTNPGPIRRRAINTLNRTTWIRAARDPPDSLTPQERARLRGPFNPS SIFRGTLPGDDVGPYLSQFLLVGTEGIGGAQDRADGFISYGAHRIDQVRVHATKELDY MTSWEAFLDVQNGADVAGRDTFESGSDAFRFTTTPRDLATYVHFDALYQAYLNACILIL DNKVKFDQGI PMGEPDFNGNQGIFFQDPDFKDHQRGFAHFGGPHILSLVTEVATRAL KAVRFQKFNTHRRLRPEAVGGLVFNFSNPDDPQFQDVKPLFEALDEDMLRRVASHN REQNERSDFGMPRADDFNPAGDTLETMLLPMAFPEGSPMHPYSGAGHATVAGACVT VLKAFFQHDA TLDFCYVPSDDGSRLDDASHTLNKKLTVEGELNKVCSNISIGRNWAGV HYFTDYIESILLGEQIALGILEEQMLTFPETFTMTVPLFSGGFRTLISTSDP
8	<i>Acaryochloris marina</i> vanadium- dependent bromoperoxidase	MTDRRQDSYAVRVEAAELARSNHPDHQANGDEERYAGAKYFMSFTKGLPHNEETG LLGDPKDFVEFRAIDDGFIDPFSSDLIRHGALYKVEGGEVKRVDREV DGDPPNNFRQ WEAPTAGVVF DLEGPDAQAVTMPPAPLLDGNGNPNPELVLEMAEVEYELAILRDQPF NDFENGSRNAAITQSIDRLNALSYSINQ TGRPRKVNTSGQLDAQTVFRGSSPGVEAGP YLSQFLLIGNTDLNRDADGIGGKVEDGLITYGALQINQRPVIAEPKGKDYMRSMSEYVE VQRGIRPPRETYGSTNGGSVAQPNRPPRRFISTPRDLSTYVHYDALY EAYLNACIILLE MGTPTDPGDFHLSGVGAAASSFESRRNAGGFALYGGPHILTLVTEVATRALKAVRFQK FNNHIRLRPEALAARIELVNSFDGLSQADKDTVPEVLKKYIGLFSNALKPTLNALGGNYL LPMFPEGSPMHPAYGAGHATVAGACVTILKAFFDTS AVLAKSGQSI AFKRL ENGDKPI AFRAPDLPGSGPGEGVPKDDLKPFKNHFLTLEGELNKLAANISIGRDMAGVHYFTDY YDSL RMGEEIAGILEEQALTYSTD PFLSVPTFDGDVRRIGRR
9	<i>Alteromonas naphthalenivorans</i> vanadium- dependent bromoperoxidase	MNETQNQRSKDSLDIRIRIASLNHRHQSIHSQVMHINNNGDEKSSINYAMSFTKGLEHNP ETGLVQNAETCEALIDAINGGEISPFHAIDVPTAEGKRRLWEAPTAGVFVDVQGPDAQE VTMAPPPGLGSSELT FEMAEVEYELAVLRDTALNKFSELSDEIAGPCERLNKLSYAMRG FCGRPRLTAKNACGDKVLTPTGTVFRGSSPGVGIGPYLSCFMLMGGGNTKSSVESGLI NYGAQTINQKVPKASDKNFMLEFDEWVAVQNGYSRNNTPKTGTGNYEENS GELKLT F IKTPRDLATYVHFDALYQAYLNACILILLSQKESQDFAPFDSNFVNLSGEFPNSRAGGFA LFGGPHILSLVTEVATRALKAVRYQKFQVHRRLRPEVLAARIAKSDNDAFKA AVGGAAS TNFENMKADLSDTLAKINELFHTEDDLPMFAEGSPMHPYSGAGHSTVAGACVTVLKA FFDNAQLARKGESVCFVKPEIAERDNWQPVKIVATDNDTLTIEDSDEVITLEAELNKL AANISIGRNMGGVHFFSDYYDSL RMGEEIALGILKDAQESYPYDAFTLSVKTFDGD EKLITRS
10	<i>Ascophyllum nodosum</i> vanadium- dependent bromoperoxidase	MMKASGGIITALLAAPPCLSQTVNELADMQTRPLLSGSVCRVRD TVDFLSPTKRAKIT FKRRIGIAAGELAVGPTCHLNNGDEANVPLFDGQFHKSLPHDDVGRVNPEAYQLLLDC IESNDINVC DQVPSGVESDGRKLVNPLGGGGHQVDGADSDNIFIKQPDNLLSERLAAQ QAEVYWMALLRDIPFSQFGTNTTVQMAAANLQGFDAFNGLSISR DADGNIDPMQDLF RTDWPGVSSGPMV SQFMLANFIDIGIVVEPKAKTLVPEMEYMTGVDTVLNIQNGGPP EDTLFVDEPLFIRNGRDLAALS FNDVLYTEAFRTILILFNESILAEAGPYGSSTRQEGFTT LGTSHYIHAMAAGSSSTRHAWYAKWQVHRVLRPEAYGGLLHFVINNLIDDVPLPASIVS NTELLNAVESLNQAQNGGTNQVFLLPMAVGE GSPVHPAYPSGHAINLGAYLTVLKAFL GFELGQRCFPSPMISNDAGTDRIPFVPSDGDVRVGT CINEDGEEVGLTYEGELNKVTS NVAIGRSHLG VHWRM DGVFGAEMGEAGAIRRLQQELGGLPEARDTEGPIPPASYKFR LYSGMTIELFPDNR YMLGDQMCKGFFT GDDFCVPADEEETAELDLVLGSSVVDQTCA EL
11	<i>Corallina officinalis</i> vanadium- dependent bromoperoxidase	MGIPADNLQSRKASFDTRVSAEALARGVVP SLANGEELLYRNPDPENGDPSPFIVS FTKGLPHDDNGAIIDPDDFLAFVRAINSGDEKEIADLT LGPARDPDTGLPIWRSDLANSL ELEVRGWENSSAGLTFDLEGPDAQSIAMPPAPVLTSPELIAEIAEL YLMALGREIEFSEF DSPKNAEYIQFAIDQLNGLEWFNTPAMLGDPPAEIRRRRGEVTVGNLFRGILPGSEVG PYLSQYIIVGSKQIGSATGGNKT LVSPNAADEFDGEIAYGSITISQVRVIATPGRDFMTD LKVFLDVQDAADFRGFESYEPGARLIRTIRDLATWVHFDALY EAYLNACILLANRVFPD PNIPFQQEDKLDNQDVFNFGDAHVLSLVTEVATRALKAVRYQKFNIHRRLRPEATGG LISVNKIAAEKGESVFPEVDLAVEELEDILEKAEISNRKQNIADGDPDPDP SFLLPQAF AE GSPFHPSYSGSHAVVAGACVTILKAFFDSNFQIDQVFEVDKDEDKLVKSSFKGTLTVA GELNKLADNIAIGRN MAGVHYFSDQFESILLGEQVAIGILEEQSLTYGENFFFFNLPKFDG TTIQI

12	<i>Corallina pilulifera</i> vanadium- dependent bromoperoxidase	MGIPADNLQSRKASFDTRVAAAELALARGVVPSPFANGEELLYRNCETGDPSPFIASFT KGLPHDDNGAIIDPDDFLAFVRAINSGDEKEIADLTGPARDPETGLPIWRSDLANSLEL EVRGWENSSAGLTFDLEGPDAQSVAMPPAPVLMSPELIAEMAELYLMALGRDIEFSEF ESPKNAAFIRSAIERLNGLEWFNTPAKLGDPAPAEIRRRRGEVTVGNLFRGILPGSEVGP YLSQYIIVGSKQIGSATVGNKTFVSPNADEFDGEIAYGSITISQVRVRIATPGRDFMTDL KVFLDVQDGADEFGRGFESYEPGARLIRTIRDLATWWHFDALYEAYLNACLILLANGVFPD PNLPFQQEDKLDNHDVFNFGSAHVLSLVTEVATRALKAVRYQKFNIHRRRLRPEATGG LISVNKKSFLAGSDIIFPEVSELVEELSSILDDVAESNEKQNRADGNVSPDKSFLLPMAFA EGSPFHPSYSGSHAVVAGACVTILKAFFDANFQIDKVFVDTDKLVKSSFKGTLTVA GELNKLADNVAIGRNMAGVHYFSDQFESLLLGEQIAIGILEEQSLTYGENFFFFNLPKFD GTTIQI
13	<i>Gracilaria changii</i> vanadium- dependent bromoperoxidase	MASHIPRFTKAYAVREQAALMAKSRPHPLHVSNNELRYRIPTSGEPHIGSYTKGLP HDRNTGVLSNPDDFQSFIRAMDAGDQFSIRDVPLGPQNEQQAFQSGIAKGV SARAW SMAAGLTYDLEGPDAQSVTMPPAPALDSELLTEVTELYWMALLRDVPFSEFNGDKN NDIQEAVDLSNSTPWQIAKNGVVPTTLDAERVRLRGPFTVMDVSPDKSFLLPMAFA YLSQFMLIGNTGIGNGNRIEDGFIRYGAHRVDQQRVRAEMGRDFMTTWSAFVDVQNG ADVRGREVYNNDVRYRFISTPRDLATYVHFDALYQAYLNACLILLGMRVPFDKGLPFQ REDDIDHQQTFATFGAPHILSLVTEVATRALKAVRFQKFNVHRRRLRPEAVGGLLHRYM QETTNDLYRGAKQLAENLDANLLDKVKRHNAKQNMKSDGDAPRANDLGECEDADEIT LLPMAFPEGSPMHPYSYGAGHATVAGACVTILKAFFDHGYELRMLDEDGETMIPFAFVP TADGSGLENRIGEYRNLTALTVEGELNKVCSNICIGRNWGGVHYFSDYRESIRVGEQV AIGLLEEQLTYGENFSMTVPLFDGGSVHRI
14	<i>Laminaria digitata</i> vanadium- dependent bromoperoxidase	MKISSLGLTALLAFAFCLGYEPEPTQPLLSGNVCRVRDSDLDFDPVPRAKVTLLKR LAIKDEISVGPTCHINNGDEENVPLFAGQYHKTLPDHFQVDEDAYKKLLECFTSD INECEKVP SGAGRRGGAKLTNPLGGTAHQVTGADSDNVFITTPDSLLSERLAAQQA EYWMALLRDIPFGEFAKNDYVRLAAENLQGLPAFKGLNIPRSEGGKIDPVTDLFRTTWP GVTTGPVVSQFMLSDFLIDSIVTPKADPLTPGVDMYTAQFQWLDVQNGASKLETTFD EENPRFIRNGRDLATIALRDQLYTEAFRAALILFTEGALGGEVGPYAEARQQGFATFG EPHILTAMASASSVTRHAWYAKWQVHRMLRPEAYGALVHNTLMRDVITPLPDSILRNT ELLNRVEVHNQRMNPDGEKTFLLPMAAQQGSPTHPAYPSGHAINNGAYITALKFLGY EAGQKCFPNPVSNDEGTAKRIKYPKSGREIVGECVNEKGKLEGLTYEGELNKISANV LLGRSHIGVHWRMDGVY GALMGETSCVRRLLQQLPEAREVEGKKRRGDIPPATY KFRLYSGKILELYGRNLYKLDGKLCGAFTGDDFCPIDEDDYSSFD DIVEEHAQFSLH GHTEL
15	<i>Asparagopsis armata</i> Azores – Mbb1_like	MATPDTQNP NRAEASF KIRLSAAELARSRGSPTHISNNSEARFRNP DGRSLLANFTK GLPHINETGLVQSALDYDQFVRAIDSGDARDFAALPLGPQNVTPRFTSGIATNPEQSG VRAWESMGAGRTFDLEGPDAQAVTMPPAPELDSEELVTEVTECYWMSLLRDVPFPT FHCDEDVAAA AKSINDTQWIKFKNPPTHTLSAERSRLRGPIDASNVRGITPGDDVGP YLSQFLLVGTGIANGNEVSDGFIQYGGMRMDQQRVVASPKVDYMTTFGSWLDVQN AADVTGRERYESDPGFRFIHTPRDLATYVHFDALYQAYLNACIILLDIGAPFD SGVFPQL DNDIDKQQA FAFATFGGPHILSLVTEVATRALKAVRFQKFNVHRRRLRPEAVGGLLHRYM TKAPEFSGAAKLVDSDLLDRVYYHNKKQNKLS DN GAPRSADFNPDGGLSEGNNL MPMAFPEGSPMHPAYGAGHATVAGACVTVLKAFFDGGFPLPFAYVTNENGCGLEPV EVSEPLTVDGELNKICSNISGRNWAGVHYFTDYIESIRIGEEIAGILQEQLTFSENFSM TLNKFDGSTIRI
16	<i>Asparagopsis armata</i> Azores – Mbb2-2_like	MNTAFPFRRKWSPSLWSARLESYLSTHAFELLTVITYITALSLMFVWGAHDEFHNQSP DTNLRWYIS IARGAGYTLNLTALVILLASRLFFTFIRDTP LHKILPVDKSFP AFHILVGYTI AASLFIHVPFHFTWIIAYDKWSAGLWDFMTSAVTGVVLLIFIMFMFALPFYRK YFRLF YISHMVGALLFFPLIFHGM YRRVPETYKWWALPLVIYILDRIARRFKISTVQLKLTSEHS ALKGKDILELRIPKPFYRAGQYAEIRVPSLSREWHPTIASAPHEKCMCFIKSLGNWT KELRGAFQNRMEGEDPNLLVQVRGPGFAPAHVSSYERVVLISGGVSGT PFAAISK SLHFLNKNKTCPSTDFSKTNLSEMKHIEQRISETISAVYDIDLANSSEPESEEQRKQYI TDMMNLT AQNSEELDVSTSR TSEQCVSSRSCPNIGDGLRILDVENQLEESSVSSMSTC DDEEDYSSDFSEEMRLEKELAAKRKMARQKIARLYERRSILFSFLHTRVTALQLSLI ARIVLCIVSIFNIGEFNFGDSRIGAKWWIGADAVLSVLHAVTLTLTILLEISFMGRFFRS SWQFMDFFVFPVLSILCSVSGVLSWTGTEMSGTLVFLHFIVLLPIMLIFMSARLYRSIGS LNLFHDRKCNPNACGKKIPDVDFIWTTRHTVDDQWLREELFPLEDGT KLRLHRYITG KESEDFESAETFITTSNIGRPPWDEIFAKIAQKSPSHAEIGVFCCGPHSMGAAVRKS MR KTEIRSNLRGAYLETTNVVDLVDLLRNTDHAELRRHGCNIRFVHSENFNG
17	<i>Asparagopsis armata</i> Azores – Mbb2_like	MPSPSSSTCPKSTQDLLTARLESHLSTHAFELLALVYATALLMFLWGAHDEFHHHT SDDNMRWYIS IARAAGYTLNLTALVILLAARLFSTYIRETPLHLIPLDKSFP AFHII VAYA IAISLVLHVAFHFAWIIAYDKWEPGLWGYTMSASTGSVLLIVFLVMFITALPTFRKKRFRF FYLTHMFGVILFFPLIFHGM YNRVPETYKWI TAPLIYIDRLLRRFKVSTVPLQLTSDHS SLKSADILELRVPKPFHYRAGQYAEVCVPSISSEWHPTIASAPHEETMTFFIKTLGNW TQALRHQFQTRMDSDDCKPLTVQIRGPYGAPAHVGRYQRVVLVSGGVGATPFAAIS

		KHLHHLNVAEHHKKTLDVDIPSKHTIQLGNRIRETISNMYGLGLGESGCAEDSNQQRRL QHLADMLNMSPDGAQVQKLGNESHPSPTGSSDVSSTCSSENVDLSSSSIGSQMATL GTYEKECSSRKGGREDKMGRSAYSKHNLMLFNGKRSRLLSLLHTTRITLLLLFTLIARL VLTVCVVSIFDLGHFSTTSGHIEAKWVIVTNVVLGLIVGLTLFTIIVLEVSMGTRFFHRNW RCVDFLVFVPLSFLCNLYGIVTWAGRDQSSSLTFVDYIITPIIFLLCHRLYRSIGTRNLF DDNGSCRGSEHSVPEVDFIWTVAHEGDDEWLREDLYTLATGTELRLHRYVTREKEVE VEGGEEFITSARAGRPKWDEIFLKIAEESRSCSEIGVFFCGPSGMGKQVRESLRRAEV FSSLRGSYLKRTGGGEVGVDEVRLLRFGSNVRFVFREEENFS
18	<i>Asparagopsis</i> <i>armata</i> Azores – Mbb3_like	MPPPTRRQSALVTRIAAADAANRSHPPHLRNGDETLYKTTSNALSYLATFTKGLPHH PDGRLVSAQHFLFARAVQTGTPQHADIPLGPPSTFSTFRSGIAKDAPLRAWESMAA GNTFDLQGPDPQSVTIPPCPRLESNELVTEMTLEYMALLRDVPFESHKSHHLVAAAV DDINHTHWQSHKCCPIELERHRHREPFSSSNVFRGTTTPGERNGPYISQFLVGTGKLG EIHDEADGYIQYGAIIRDQVRVSVETEIDYMTTWAFLDVQNAADLRRHSTYAKSSSYR FLYTPRDLATYVHHDSLYQAYLNACIILLDMKVPFDSGLPFTTEDHIDKQQGFVNFGGP HILTLVTEVATRALKAVRFQKYAVHRRLRPEAVGGLLEQYRRYGGGYSELANTIRPIRH LARSLSSNLMSLVAAANGHQATMSDNGFPRSHDTGSGETHLLPMAYPEGSPMHPS YGAGHATVAGACVTILKGFFDHTYKLPFAYVSSCNGKMLKKAKVAKKLSVEGELNKLA SNISIGRSWAGVHYYSYVESIRLGEEVAIGILKEQKLTYSKFSTIPKFDGTTIKI
19	<i>Asparagopsis</i> <i>armata</i> Azores – Mbb4-2_like	MSEERHASALRVRSEADLAASRPLPHTLANGDEHRYHDTHLASYTKGLPHEKDTGL SSSPDHFAAFVRAIETGAQEDITSLPLGIDEDPRFISAIASEGSDHPIADTRAWESMAAG NTYDLEGPDAQAVTMPPAPKIDSEELLTEITECYWMALLRDVPFTEFERDGTAAAAA SISRTRWWQFQEQQRPQPCDLSDAEIARLRGPFRKTNIFRGVTPGEQIGPYLSQFLLV GTKGIANIQEISDGFQYGGMRMDQVRVATPNRDYMTTWASWLDVQNAAGDVRGRE TYDNDTPFRFITTPRDLATYVHFDALYQAYLNACIILLDTKAPFDPEIPFVEDDDIDKQ GFATFGGPHILSLVTEVATRALKAVRFQKFGTHRRLRPEAVGGLIERYRKTEGAEPFEP IQKIATEIDNDLMTRISQHNAAQNELSDNGGARSGDYNPEGCEAETYLLPMAFPEG PMHPSYGAGHAAGVAGACVTILKAFFDHTHELEFCYVPSTDGQNLEEEVINEPLTVEHE LNKLCANISIGRNWAGVHYYSYDIESARLGEEVAIGILEEQSLTYGEEFSMTIPKFDGTTI KISNSK
20	<i>Asparagopsis</i> <i>armata</i> Azores – Mbb4_like	MSTTRQAALQVRTDAAKLAASRKLPTHTPNGDETRFSDSYASYTKGLPHDKKTGLL SSTDDFTAFVRAINTGAQEDIRSLRLGIDETPRFISGIASPALDLPIADTRAWESMAAGN TFDLEGPDAQAVTMPPAPKIDSEELLTEITECYWMALLRDVPFSEFHRNGTVAAAAASI SRTRWWQFQEQQRPQSDLTNAEIQLRGPFNKSNVFRGDMPEQVGPYLSQFLLV GTQGIGKMHQPEEGFIQYGGMRMDQVRVFATPNRDYMTTWASWLDVQNAAGDVRSR ETYDKDTPFRFITTPRDLATYVHFDALYQAYLNACIILLDTKAPFDHGLPFVQDDDDIDKQ QGATFGGPHILSLVTEVATRALKAVRFQKFGTHRRLRPEAVGGLIERYRKTNGAAPF AAAKKLATEIDNLMTRISRHNAAQNEFSDNGKARRNDFNPEGGASAETYLLPMAFPE GSPMHPSYGAGHAAGVAGACVTILKAFFDHKYKLKFCFEPSTDGRKLEKVNISEPLTVE HELNKLCANISIGRNWAGVHYYSYDIEESAKLGEEVAIGILQEQLTYGEKFSMTLPKFD GTCITISN
21	<i>Asparagopsis</i> <i>armata</i> Ireland – Mbb1_like	MATPDTQNPNAEASFIRLSAAELARSRGSPTHISNNSEARFRNPDGTRSLLANFTK GLPHINETGLVQSALDYDQFVRAIDSGDARDFAALPLGPQNVTPRFTSGIATNPEQSG VRAWESMGAGRTFDLEGPDAQAVTMPPAPELDSEELVTEVTECYWMSLLRDVPFPT FHCDEDVAAAASINDTQWIKFKNPPTHTLSAERSRLRGPIDASNVRFTGITPGDDVGP YLSQFLLVGTGIANNEVSDGFQYGGMRMDQVRVAVSPKVDYMTTFGSLWLDVGN AADVTGRERYESDPGFRFIHTPRDLATYVHFDALYQAYLNACIILLDIGAPFDSGVFPFQL DNDIDKQQAFAATFGGPHILSLVTEVATRALKAVRFQKFNHRRLRPETVGGRVDRYYK TKAPEFSGAAKLVDLSLDRVYYHNKKQKNLSDNGAPRSADFNPDGGLSEGNNL MPMAFPEGSPMHPAYGAGHATVAGACVTVLKAFFDGGFPLPFAYVTNENGCGLEPV EVSEPLTVDGELNKICSNISIGRNWAGVHYFTDYIESIRIGEEIAGILQEQLTFSENFSM TLNKFDGSTIRI
22	<i>Asparagopsis</i> <i>armata</i> Ireland – Mbb2-2_like	MNTAFPFRRKWSPSLWSARLESYLSTHAFELLTVITYITALSLMFVWGAHDEFHNQSP DTNLRWYISIRAGAGYTLNLTALVILLASRLFFTFIRDTPHLKILPVDKSFPAPFHLVGYTI AASLFIHVPHFTWIIAYDKWSAGLWDFMTSAVTGVVLLIFIMFMFALPFYRKKYFRLF YISHMVGALLFFPLIFHGMYYRVPETYKWWALPLVIYILDRIARRFKISTVQLKLTSEHS ALKGKDILELRIPKPTYRAGQYAEIRVPSLSREWHPFTIASAPHEKCMCFIKSLGNWT KELRGAFQNRMEGEDPNPLLQVRGPFQAPAHVSSYERVVLISGGVGSTPFAAISK SLHFLNKNKTCPSTDFSKTNLSEMKHIEQRISSETISAVYDIDLANSDEPESEEQRKQYI TDMNMLTAQNSEELDVSTSRSTSEQCVSSRSCPNIGDLRLDLANDESSVSSMSTC DDEEDYSSDFSEEMRLEKELAAKRKRMARQKIARLYERRSILFSFLHTTRVTLALQLSLI ARIVLVCIVSIFNIGEFNFGDSRIGAKWWIGADAVLSVLHAVTLTLILLEISFMGRPFRRS SWQFMDFFVPLSILCSVSGVLSWTGTEMSGTLVFLHFIVLLPIMLIFMSARLYRSIGS LNLFHDRKCNPNACGKKIPDVDFIWTTRHTVDDQWLREELFPLEDGTGLRLHRYITG KESEDFESAETFITTSNIGRPPWDEIFAKIAQKSPSHAEIGVFFCGPHSMGAAVRKSMR KTEIRSNLRGAYLETTNVVDLVADLLLRNTDHAAELRRHGCNIRFVFREEENFG

23	<i>Asparagopsis armata</i> Ireland – Mbb2-3_like	MAPRSGKQRCSPSTSLTLLSARLESYSTNAFSLALFIYSLANILMFVWGAHDEFHHHT SQKNLRWYICARGAGYTLNLTALVILLAARLFATYIRETPLQHILPIDKSFPFHHIIVAYT IAAALFIHVSFHLVWIIAYDKWELGMWGFTMSATTGFALLTVFVVMFVSALPRFRKKQF RTFYLIHVMVGALLFFTLIFHGMYNRPETYKWAGPLAIYITIDRVLRFFKISTAKLELTG EHSSLKGSIDILELRVPKTFEYRAGQYAEVCVPSINNEWHPFTIASAPHEKSMCFYIKAIG DWTRHLRDAFEARIENDLYEPLKVQIRGPYGAPAQHVGRYRRVVLISGGVGSTPFAAI CKNLHHLNKSSENHSAKLESHGSSKRQSQIHWHIRDAISNLFVCLDDSRSDAASNQQ RIQQVADMLNMSPKGNVHNVSFKRNLSKTSDDCSSVEEITKQIRADEEISLSQKEKQS SYNLDACSESIRYYNRPSANVFNVAQRRIFNFYEYRSRLAFLHTTRFTFALLTLVARI VILCVVSIFNLGHIGISDSHIDAEEWIIATNSLLGLVLGIALLTTLLEISFMRLRFFYRGWR CVDFIFLPIITFLCNISNFMWSWGRQQAFLIFLDLIIVPIMFLLCHRLYRSIGARNLLD DTQCRQSCCTCNKTIPTDVFVWTTPRDSEDEWLRLSELYPLATGTDRLHRYVTREKDL DLEEPHFITTANTGRPQWDEIFAQIAEQTPSHNEVGVFVFCGPHPMGAAVQKSMRKV EVMSNLRGSYLKTDSELLVDLSRDEKEVKLLREHGCNIRFVLEENFS
24	<i>Asparagopsis armata</i> Ireland – Mbb2_like	MPSPSSSTCPKSTQDLLTARLESHTLHAFELLALVYATALLMFVWGAHDEFHHHT SDDNMRWYISIAAAGYTLNLTALVILLAARLFSTYIRETPLHLIPLDKSFPFHHIIVAYA IAISLVLHVAFHFAWIIAYDKWEPGLWGYTMSASTGSVLLIVFLVMFITALPTFRKKRFRF FYLTHTMFGVILFFPLIFHGMYNRPETYKWITAPLIYIIDRLRRFKVSTVPLQLTSDHS SLKSADILELRVPKPFHYRAGQYAEVCVPSISSEWHPFTIASAPHEETMTFFIKTLGNW TQALRHQFQTRMDSDDCKPLTVQIRGPYGAPAQHVGRYQRRVVLVSGGVGATPFAAIS KHLHHLNVAEHHKKTLDVDIPSKHITQLGNRIRETISNMYGLGLGESGCAEDSNQQR QHLADMLNMSPDGAVQKLGNESHPSPTGSSDVSDTCSSENVDFSSSSIGSQMATL GTYEKECSSRKGGREDMLGRSAYSKNLMLFLKGKRSRLLSLLHTTRITLTLFTLIARL VLTVCVSIFDLGHFSTTSGHIEAKWVIVTNVVLGLIVGLTLFTIIVLEVSFMGTRFFHRNW RCVDFLVFPVLSFLCNLYGIVTWAGRDQSSFLTVDYIITPIIFLLCHRLYRSIGTRNLF DDNGSCRGSEHSVPEVDFIWTVAHEGDDWLRREDLYTLATGTELRLHRYVTREKEVE VEGGEEFITSARAGRPKWDEIFLKIAEESRSCSEIGVFVFCGPGSGMGKQVRESLRRAEV FSSLRGSYLKRTGGGEVGVDEVRLLRFGSNVRVVFREENFS
25	<i>Asparagopsis armata</i> Ireland – Mbb3_like	MPPPTRRQSALVTRIAAADAANRSHPPHLRNGDETLYKTTSNALSYLATFTKGLPHH PDGRLVSAQHFLFARAVQTGTQHIADIPGPPSTFTSRSGIAKDAPLRAWESMAA GNTFDLQGPDPQSVTIPPCPRLESNELVTEMTELYMALLRDVPFHFHSHHLVAAAV DDINHTHWIQSHKCCPELERHRHREPSSSNVFRGTTTPGERNGPYISQFLIVGTGKLG EIHDEADGYIQYGAIRIDQVRVSVETEIDYMTTWAFLDVQNAADLRRHSTYAKSSSYR FLYTPRDLATYVHHDSLYQAYLNACIILLDMKVPFDSGLPFTTEDHIDKQQGFVNFGGP HILTLVTEVATRALKAVRFQKYAVHRRRLRPEAVGGLEQYRRYGGGYSELANTIRPIRH LARSLSSNLMSLVAAANGHQNATMSDNGFPRSHDTGSGETHLLPMAYPEGSPMHPS YGAGHATVAGACVTILKGFDDHTYKLPFAVYVSSCNGKMLKAKVAKKLSVEGELNKL SNISIGRSWAGVHYSDYVESIRLGEEVAIGILKEQKLTYSKFSMTIPKFDGTTIKI
26	<i>Asparagopsis armata</i> Ireland – Mbb4-2_like	MSEERHASALRVRSEAADLAASRPLPHTLANGDEHRYHDTHLASYTKGLPHEKDTGL SSSPDHFAAFVRAIETGAQEDITSPLGIDEDPRFISAIASEGSDHPIADTRAWESMAAG NTYDLEGPDAQAVTMPPAPKIDSEELLTEITECYWMALLRDVPFTEFERDGTAAAAA SISRTRWWQFQEQQPQRPCDLSDAEIALRGRPFRTKNIFRGVTPGEQIGPYLSQFLLV GTKGIANIQEISDGFQYGGMRMDQVRVATPNRDYMTTASWLDVQNAAGDVRSR TYDNDTPFRFITTTPRDLATYVHFDALYQAYLNACIILLDTKAPFDPEIPFVEDDDIDKQ GFATFGGPHILSLVTEVATRALKAVRFQKFGTHRRRLRPEAVGGLIERYRKTGEAEPFEP IQKIAEIDNDLMTRISQHNAAQNELSDNGGARSGDYNPEGCEAETYLLPMAFPEG PMHPSYGAGHAAVAGACVTILKAFFDHTHELEFCYVPSTDGQNLEEVEINEPLTVEHE LNKLCANISIGRNWAGVHYSDYIESARLGEEVAIGILEEQSLTYGEEFSMTIPKFDGTTI KISNSK
27	<i>Asparagopsis armata</i> Ireland – Mbb4_like	MSTTRQAAALQVRTDAAKLAASRKLPTHTPNGDETRFSDSYIASYTKGLPHDKKTGLL SSTDDFTAFVRAINTGAQEDIRSLRLGIDETPRFISGIASPALDPIADTRAWESMAAGN TFDLEGPDAQAVTMPPAPKIDSEELLTEITECYWMALLRDVPFSEFHRNGTVAAAAASI SRTRWWQFQEQQPQRPDLTNAEIQLRGPFNKSNVFRGDMPEGQVGPYLSQFLLV GTQGIGKMHQPEEGFIQYGGMRMDQVRVATPNRDYMTTASWLDVQNAAGDVRSR ETYDKDTDYRFITTTPRDLATYVHFDALYQAYLNACIILLDIKAPFDHGLPFVQDDDDIDKQ QGATFGGPHILSLVTEVATRALKAVRFQKFGTHRRRLRPEAVGGLIERYRKTNGAAPP AAAKKLATEIDNELMTRISRHNAKQNEFSNDNGKARRNDFNPEGGASAETYLLPMAFPE GSPMHPSYGAGHAAVAGACVTILKAFFDHKYKLFCEPSTDGRKLEKVNISEPLTVE HELNKLCANISIGRNWAGVHYSDYIESAKLGEEVAIGILQEQLTYGEKFSMTLPKFD GTCITISN
28	<i>Asparagopsis armata</i> Ireland 2 – Mbb1_like	MATPDTQNPNAEASFIRLSAAELARSRGSPTHISNNSEARFRNPDGTRSLLANFTK GLPQINETGLVQSALDYDQFVRAIDSGDARDFAALPLGPQNVTPRFTSGIATNPEQSG VRAWESMGAGRTFDLEGPDAQAVTMPPAPELDSEELVTEVTECYWMSLLRDVPFPT FHCDEDVAAAASINDTQWIKFKENPPHTLSAERSRLRGPIDASNVRGITPGDDVG PYLSQFLLVGTTGIANGNEVSDGFQYGGMRMDQVRVVASPKVDYMTTFGSWLDVQ

		NAADVTGRERYESDPGFRFIHTPRDLATYVHFDALYQAYLNACIILLDIGAPFDSGVVPF QLDNDIDKQQAFAFTGGPHILSLVTEVATRALKAVRFQKFNVHRRLRPETVGGRVDY YKTKAPEFSGAAKLVDSDLLDRVYYHNKKQNKLSDNAPRSADFNPDGGLSEGN LLMPMAFPEGSPMHPAYGAGHATVAGACVTVLKAFFDGGFPLPFAYVTNENGCGLEP VEVSEPLTVDGELNKCISNISIGRNWAGVHYFTDYIESIRIGEEIAGILQEQLTFSENFS MTLNKFDGSTIRI
29	<i>Asparagopsis</i> <i>armata</i> Ireland 2 – Mbb2-2_like	MNTAFPFRRKWSPSLWSARLESYLSHAFELLTVITYITALSLMFVWGAHDEFHNQSP DTNLRWYISIRGAGYTLNLTALVILLASRLFFTFIRDTPHKLIPVDKSFPAFHILVGTYI AASLFHVPFHFTWIIAYDKWSAGLWDFMTSAVTGVVLLIFIIMFMFALPFYRKKYFRLF YISHMVGALLFFPLLIHFGMYRRVPETYKWVALPLVIYILDRIARRFKISTVQLKLTSEHS ALKGKDILELRIPKPFYRAGQYAEIRVPSLSREWHPFTIASAPHEKCMCFIKSLGNWT KELRGAFQNRMEGEDPNPLLQVRGPFGAPAQHVSSYERVVLISGGVGSTPFAAISK SLHFLNKNKTCPSDFSKTNLSEMKHIEQRISSETISAVYDIDLANSSEPESEEQRKQYI TDMMNLT AQNSEELDVSTSRSTSEQCVRSCPNIGDGLRDVENKLEESSVSSMSTC DDEEDYSSDFSEEMRLEKELAAKRKRMARQKIARLYERRSILFSLHTTRVTALQLSLI ARIVLVCIVSIFNIGEFNFGDSRIGAKWWIGADAVLSVLHAVTLTLILLEISFMGRPFRRS SWQFMDFFVFPVPLSILCSVSGVLSWTGTEMSGTLVFLHFIVLLPIMLIFMSARLYRSIGS LNLFHDRKCNPNACGKKIPDVFIVTTRHTVDDQWLREELFPLEDGTGLRLHRYITG KESEDFESAETFITTSNIGRPPWDEIFAKIAQKSPSHAEIGVFFCGPHSMGAAVRKSMR KTEIRSNLRGAYLETTNVVDLVADLLLRNTDHAAELRRHGCNIRFVREENFG
30	<i>Asparagopsis</i> <i>armata</i> Ireland 2 – Mbb2-3_like	MAPRSGKQRCSPSTLTL SARLESYLSHAFELLALFIYSLANILMFVWGAHDEFHHHT SQKNLRWYICIRGAGYTLNLTALVILLAAARLFATYIRETPLQHILPIDKSFPFHHIIVAYT IAAALFIHVSFHLVWIIAYDKWELGMWGTMSATTGFALLTVFVVMFVSALPRFRKKQF RTFYLIHMVGALLFFTLFIHFGMYNRVPETYKWAGPLAIYIDRVLRRFKISTAKELTG EHSSLKGS DILELRVPKTFEYRAGQYAEVCVPSINNEWHPFTIASAPHEKSMCFYKAIG DWTRHLRDAFEARIENDLYEPLKVQIRGPYGAPAHVGRYRRVVLISGGVGSTPFAAI CKNLHHLNKS ENHSHKALES HGSSKRQSQIHWHIRDAISNLFVCLDDSRSDAASNQQ RIQQVADMLNMSPKGNVHNVSFKRNLSTSDDCSSVEEITKQIRADEEISLSQKEKQS SYNLDACSESIRYYNRPSANVFNVAQRRIFFYRSLLAFLHTTRFTFALLTLVARI VILCVVSIFNLGHIGISDSHIDAEWWIATNSLLGLVLGIALLTIVLFMFRLRRFFRGWR CVDFFIFLPITFLCNISNFMWSGRQQAFLIFLDLIIVPIMFLLLCHRLYRSIGARNLLD DTQCRQSCTCNKTIPDVFVWTTTPRDESEDEWLRSELYPLATGTDLRLHRYVTREKDL DLEPEHFITTANTGRPQWDEIFAQIAEQTPSHNEVG VFFCGPHPMGAAVQKSMRKV EVMSNLRGSYLKRTDSELLVEDLSLRDEKEVKLLREHGCNIRFVREENFS
31	<i>Asparagopsis</i> <i>armata</i> Ireland 2 – Mbb2_like	MPSPSSSTCPKSTQDLLTARLESHLSTHAFELLALVYATALLMFLWGAHDEFHHHT SDDNMRWYISIRARAAGYTLNLTALVILLAAARLFSTYIRETPLHLIPLDKSFPAFHIVAYA IAISLVLHVAFHFAWIIAYDKWEPGLWGTMSASTGSVLLIVLFVMFITALPTFRKKRFRF FYLTHMFGVILFFPLLIHFGMYNRVPETYKWITAPLIYIIDRLLRRFKVSTVPLQLTSDHS SLKSADILELRVPKPFHYRAGQYAEVCVPSISSEWHPFTIASAPHEETMTFFIKTLGNW TQALRHQFQTRMDSDDCKPLTVQIRGPYGAPAHVGRYQRRVVLVSGGVGATPFAAIS KHLHHLNVAEHHKKTLDVDIPSKHTIQLGNRIRETISNMYGLGLGESGCAEDSNQQR QHLADMLNMSPDGAVQKLGNESHPSPTGSSDVSDTCSSENVDLFSSSSIGSQMATL GTYEKECSSRKGGRDKMGRSAYSXKHNLMFLNGKRSRLLSLHHTTRITLTLFLLIARL VLTCCVVSIFDLGHFSTTSGHIEAKWIVTNVVLGLVGLTLFTIIVLEVSFMGRFFHRNW RCVDFLVFPVPLSFLCNLYGIVTWAGRDQSSFLTVDYIITPIIFLLCHRLYRSIGARNLLD DDNGSCRGSEHSVPEVDFIWTVAHGDDDEWLREDLYTLATGTGLRLHRYVTREKEVE VEGGEFIT SARAGRPKWDEIFLKIAEESRSCSEIGVFFCGPSGMGKQVRESLRAEV FSSLRGSYLKRTGGGEVGVDEVRLLRFGSNVRVFFREENFS
32	<i>Asparagopsis</i> <i>armata</i> Ireland 2 – Mbb3_like	MPPPTRRQSALVTRIAAADEAANRSHPPHLRNGDETLYKTTSNALSYLATFTKGLPHH PDGRLVSAQHFLFARAVQTGTPQHIADIPGPPSTFSTFRSGIAKDAPLRAWESMAA GNTFDLQGPDPQSVTIPPCPRLESNELVTEMTLEYMALLRDVPFHFHSHHLVAAV DDINHTHWIQSHKCCPELERHHRREPSSSNVFRGTTGPERNGPYISQFLIVGTGKLG EIHDEADGYIQYGAIQDQVRVSVETEIDYMTTWAFLDVQNAADLRRHSTYAKSSSYR FLYTPRDLATYVHHDLSYQAYLNACIILLDMKVPFDSGLPFTTEDHIDKQQGFVNFGGP HILTLVTEVATRALKAVRFQKYAVHRRLRPEAVGGLLEQYRRYGGGYSELANTIRPIRH LARSLSSNLM SLVAAAANGHQNATMSDNGFPRSHDTGSGETHLLPMAYPEGSPMHP YGAGHATVAGACVTILKGFFDHTYKLPFAYVSSCNGKMLKKAKVAKKLSVEGELNKL SNISIGRSWAGVHYYSYDYESIRLGEVAGILKEQKLTYSKFSMTIPKFDGTTIKI
33	<i>Asparagopsis</i> <i>armata</i> Ireland 2 – Mbb4-2_like	MSEERHASALRVSEAAADLAASRPLTHLANGDEHRYHDTLASHTYKGLPHEKDTGL SSSPDHFAAFVRAIETGAQEDITSLPLGIDEDPRFISAIASEGSDHIADTRAWESEMAAG NTYDLEGPDAAQAVTMPPAPKIDSEELLTEITECYWMALLRDVPFTEFERDGTAAAAA SISRTRWWQFQE QPGQRPCDLSAEIARLRGPFRKTNIFRGVTPGEQIGPYLSQFLLV GTKGIANIQEISDGFIIQYGGMRMDQVRVATPNRDYMTTWASWLDVQNAAGDVRGRE TYDNDTPFRFITTPRDLATYVHFDALYQAYLNACIILLDTKAPFDPEIPFVEDDDIDKQ GFATFGGPHILSLVTEVATRALKAVRFQKFGTHRRLRPEAVGGLIERYRKTEGAEPFEP

		IQKATEIDNDLMTRISQHNAAQNELSDNGGARSGDYNPEGCEAETYLPLMAFPEGSPMHPSYGAGHAAVAGACVTILKAFFDHTHELEFCYVPSTDGQNLEEVEINEPLTVEHELNKLCANISIGRNWAGVHYYSYDIESARLGEEVAIGILEEQSLTYGEEFSMTIPKFDGTTIKISNSK
34	<i>Asparagopsis armata</i> Ireland 2 – Mbb4_like	MSTTRQAAALQVRTDAAKLAASRKLPTHTPNGDETRFSDSYIASYTKGLPHDKKTGLL SSTDDFTAFVRAINTGAQEDIRSLRLGIDETPRFISGIASPALDLPIADTRAWESEMAAGN TFDLEGPDAQAVTMPPAPKIDSEELLTEITECYWMALLRDVPFSEFHRNGTVAAAAASI SRTRWWQFQEQPGQRPDLTNAEIQLRGPFNKSNVFRGDMPEQVGPYLSQFLLV GTQGIGKMHQPEEGFIQYGGMRMDQQRVRFATPNRDYMTTWASWLDVQNAAGDVRSR ETYDKDTEYRFITTPRDLATYVHFDALYQAYLNACILLLDIKAPFDHGLPFVQDDDDIDKQ QGFATFGGPHILSLVTEVATRALKAVRFQKFGTHRRRLRPEAVGGGLIERYRKTNGAAPP AAKKLATEIDNELMTRISRHNKQNEFSNDNGKARRNDFNPEGGASAETYLPLMAFPE GSPMHPSYAAGHAAVAGACVTILKAFFDHKYKLKFCFEPSTDGRKLEKVNISEPLTVEH ELNLCANISIGRNWAGVHYYSYDEESAKLGEEVAIGILQEQLTYGEKFSMTLPKFDG TCITISN
35	<i>Asparagopsis armata</i> Ireland 3 – Mbb1_like	MATPDTQNPNRAEASFIRLSAAELARSRGSPTHISNNSEARFRNPDGTRSLLANFTK GLPHINETGLVQSALDYDQFVRAIDSGDARDFAALPLGPQNVTPRFTSGIATNPEQSG VRAWESMGAGRTFDLEGPDAQAVTMPPAPELDSEELVTEVTECYWMSLLRDVPFPT FHCDEDVAAAASINDTQWIKFKENPPHTLTSASERSRLRGPIDASNVFRGITPGDDVGP YLSQFLLVGTGTGIANGNEVSDGFIQYGGMRMDQQRVVASPKVDYMTTFGSWLDVQN AADVTGRERYESDPGFRFIHTPRDLATYVHFDALYQAYLNACIILLDIGAPFDGSGVPFQL DNDIDKQAFATFGGPHILSLVTEVATRALKAVRFQKFNVHRRRLRPETVGGRVDRYYK TKAPEFSGAAKLVDLSLSDLLDRVYYHNKKQNKLSNDNGAPRSADFNPDGGLSEGNNL MPMAFPEGSPMHPAYGAGHATVAGACVTVLKAFFDGGFPLPFAYVTNENGCGLEPV EVSEPLTVDGELNKCISNISIGRNWAGVHYFTDYIESIRIGEEIAGILQEQLTFSENFSM TLNKFDGSTIRI
36	<i>Asparagopsis armata</i> Ireland 3 – Mbb2-2_like	MNTAFPFRRKWSPSLWSARLESYLSTHAFELLTVITYITALSLMFVWGAHDEFHNQSP DTNLRWYISIRAGAGYTLNLNTALVILLASRLFFTIFIRDTPLHKILPVDKSFPAPFHILVGYTI AASLFIHVPFHFTWIIAYDKWSAGLWDFMTSAVTGVVLLLIIFIMFMFALPFYRKKYFRL YISHMVGALLFFPLLIHFGMYRRVPETYKWWALPLVIYILDRIARRFKISTVQLKLTSEHS ALKGKDILELRIPKPFTYRAGQYAEIRVPSLSREWHPFTIASAPHEKCMCFIKSLGNWT KELRGAFQNRMEGEDPNPLLVQVRGPGGAPAHVSSYERVVLISGGVGSTPFAAISK SLHFLNKNKTCPSTDFSKTNLSEMKHIEQRISSETISAVYDIDLANSSDEPESEEQRKQYI TDMMNLTAAQNSEELDVSTSRSTSEQCVSSRSCPNIGDGLRILDVENQLEESSVSSMSTC DDEEDYSSDFSEEMRLEKELAAKRKMARQKIARLYERRSILFSFLHTTRVTALQLSLI ARIVLVCIVSIFNIGEFNFGDSRIGAKWWIGADAVLSVLHAVTLTLTILLEISFMGRPFRRS SWQFMDFFVFPVLSILCSVSGVLSWTGTEMSGTLVFLHFIVLLPIMLIFMSARLYRSIGS LNLFHDRKCNPNACGKKIPDVDFIWTTRHTVDDQWLREELFPLEDGTKLRLHRYITG KESEDFESAETFITTSNIGRPPWDEIFAKIAQKSPSHAEIGVFFCGPHSMGAAVRKSMR KTEIRSNLRGAYLETTNVVDLVADLLLRNTDHAAELRRHGCNIRFVREENFG
37	<i>Asparagopsis armata</i> Ireland 3 – Mbb2_like	MPSPSSSTCPKSTQDLLTARLESHLSTHAFELLALVYATALLMFLWGAHDEFHHHT SDDNMRWYISIRARAAGYTLNLNTALVILLAAARLFSTYIRETPLHLIPLDKSFPAPHIIVAYA IASLVLVHVAHFHAWIIAYDKWEPGLWGYTMSASTGSVLLIVFLVMFITALPTFRKKRFRF FYLTHMFGVILFFPLLIHFGMYRRVPETYKWIAPLIYIDRLRRFKVSTVPLQLTSDHS SLKSADILELRVPKPFHYRAGQYAEVCVPSISSEWHPFTIASAPHEETMTFFIKLTGNW TQALRHQFQTRMDSDDCKPLTVQIRGPYGAPAHVGRYQRRVVLVSGGVGATPFAAIS KHLHHLNVAEHHKKTLDVDIPSKHTIQLGNRIRETISNMYGLGLGESGCAEDSNQRR QHLADMLNMSPDGAVQKLGNESHPSPTGSSDVSOTCSSENVDSFSSSIGSQMATL GTYEKECSSRKGGREDKMGRSAYSXKHNLMFLNGKRSRLLSLLHTTRITLLLLFTLIARL VLTVCVSIFDLGHFSTTSGHIEAKWVIVTNVVLGLIVGLTFTIIVLEVSFMGTRFFHRNW RCVDFLVFVPLSFLCNLYGIVTWAGRDQSSFLTVDYIIITPIIFLLCHRLYRSIGTRNLF DDNGSCRGSEHSVPEVDFIWTVAHGDDDEWLREDLYLATGTLELRHRYVTRKEVE VEGGEEFITSARAGRPKWDEIFLKIAEESRSCSEIGVFFCGPSGMGKQVRESLRRAEV FSSLRGSYLKRTGGGEVGDDEVRLLRFGSNVRFVREENFS
38	<i>Asparagopsis armata</i> Ireland 3 – Mbb3_like	MPPPTRRQSALVTRIAAADEAANRSHPPHLRNGDETLYKTTSNALSYLATFTKGLPHH PDGRLVSAQHFLQFARAVQTGTQPHIADIPLGPPSTFTFRSGIAKDAPLRAWESMAA GNTFDLQGPDPQSVTIPPCPRLESNELVTEMETELYYMALLRDVPFESHKSHHLVAAV DDINHHTHWIQSHKCCIPELERHRHREPFSNNVFRGTTTPGERNGPYISQFLIVGTGKLG EIHDEADGYIQYGAIRIDQVRVSETEIDYMTTWAFLDVQNAADLRRHSTYAKSSYR FLYTPRDLATYVHHDSLYQAYLNACIILLDMKVPFDSGLPFTTEDHIDKQQGFVNFGGP HILTLVTEVATRALKAVRFQKYAVHRRRLRPEAVGGLEQYRRYGGGYSELANTIRPIRH LARSLSSNLMSLVAAANGHQNATMSDNGFPRSHDTGSGETHLLPMAYPEGSPMHPS YGAGHATVAGACVTILKGFFDHTYKLPFAYVSSCNGKMLKKAKVAKKLSVEGELNKLA SNISIGRSWAGVHYYSYVESIRLGEEVAIGILKEQKLTSEKFSMTIPKFDGTTIKI

39	<i>Asparagopsis armata</i> Ireland 3 – Mbb4-2_like	MSEERHASALRVRSEAADLAASRPLPHTLANGDEHRYHDTHLASYTKGLPHEKDTGLSSSPDHFAAFVRAIETGAQEDITSLPLGIDEDPRFISAIASEGSDHPIADTRAWESMAAGNTYDLEGPDAQAVTMPPAPKIDSEELLTEITECYWMALLRDVPFTEFERDGTAAAAAISRTRWWQFQEQQPGQRPCDLSDAEIARLRGPFRKTNIFRGVTPGEQIGPYLSQFLLVGTGKIANIQEISDGFIIQYGGMRMDQQRVVRVATPNRDYMTTWASWLDVQNAAGDVRGRETYDNDTPFRFITTTPRDLATYVHFDALYQAYLNACILLLDTKAPFDPEIPFVEDDDIDKQQGFATFGGPHILSLVTEVATRALKAVRFQKFGTHRRRLRPEAVGGGLIERYRKTGAEPPFIQKIATEIDNDLMTRISQHNAAQNELSDNGGARS GDYNPEGCESAETYLLPMAFPEGSPMHPSYGAGHAAVAGACVTILKAFFDHTHELEFCYVPSTDGQNLEEEVINEPLTVEHELNKLCANISIGRNWAGVHYYSYDIESARLGEEVAIGILEEQSLTYGEEFSMTIPKFDGTTIKISNSK
40	<i>Asparagopsis armata</i> Ireland 3 – Mbb4_like	MSTTRQAAALQVRTDAAKLAASRKLPTHTPNGDETRFSDSYIASYTKGLPHDKKTGLLSSDDFTAFVRAINTGAQEDIRSLRLGIDETPRFISGIASPALDLPIADTRAWESMAAGNTFDLEGPDAQAVTMPPAPKIDSEELLTEITECYWMALLRDVPFSEFHRNGTVAAAAASISRTRWWQFQEQQPGQRPCDLTNAEIQLRLGPFNKSNVFRGDMPEQVGPYLSQFLLVGTQGGIGKMHQPEEGFIQYGGMRMDQQRVRFATPNRDYMTTWASWLDVQNAAGDVRSEETDYDKDTPFRFITTTPRDLATYVHFDALYQAYLNACILLLDIKAPFDHGLPFVQDDDDIDKQQGFATFGGPHILSLVTEVATRALKAVRFQKFGTHRRRLRPEAVGGGLIERYRKTNGAAPPAAAKKLATEIDNLMTRISRHNAAQNEFSNGKARRNDFNPEGGASAETYLLPMAFPEGSPMHPSYGAGHAAVAGACVTILKAFFDHKYKLKFCFEPSTDGRKLEKVNISEPLTVEHELKLCANISIGRNWAGVHYYSYDIEESAKLGEEVAIGILQEQLTYGEKFSMTLPKFDGTCITISN
41	<i>Asparagopsis taxiformis</i> Azores – Mbb1_like	MTDTQNPNAEVAFAKVRVSAEELARARGSPHTLSNNSERFRNPDPGTRSLLANFTKGLPHTKETALVVSADYDSFVRAIDSGDPRDFADLPLGPQGVPRFTSGIASDPEVGTRAWESGGAGLVFDLEGPDAQAVTMPPAPELDSDELVTEVTECYWMSLLRDVPFPTFDSDPHIQSAAESINNTQWQFQKNPPAHLTAAERSRLRGPITANVFRGITPGDEVGPYLSQFLLVGTGTGIANGNEVGDFIIQYGGMRMDQQRVVRVAKSHIDYMTTFGAYLDVQNAANVSGRELYNEEPRFRFIHTPRDLATYVHFDALYQAYLNACIILLDIGAPFDSGIPFQLDNDIDKQQGFATFGGPHILSLVTEVATRALKAVRFQKFNHRRRLRPEAIGARVDRYCATKAPEFAGAANKLSEALDKLLQKLVHDHNKKQNLSDRGNPRANDFNPDGDVSKGNLLMPMAFPEGSPMHPAYGAGHATVAGACVTVLKAFFDGGYRLPFCYITDENGTLKAVEIDEPLTVDGELNKICSNISIGRNWAGVHYFTDYIESIRIGEEAIGILQEQLTFSENFSMTLNKFDGSTIRI
42	<i>Asparagopsis taxiformis</i> Azores – Mbb2_like	MDTVSPGDSRQKAQGGKMRPMRSFAILSANLEAFLSTHAFSLLFLIFYLTCTALMFVWGF TTQWKKT DNEAMIYFISIARGAGYSLNLTSLVILIAARLTFTLIRETPLQYILPLDKIFPLFHMFGYMI AFLVLHGT FHMTWIRFQGWNSGLWGFTMSFVTGFILPVFVVMLITSLPHFRKNKFR LFYLFHLYGALFFSILIFHGMYPETKYKWTGPSLIYLLDRKFIIRMKISSHDLDALEKSILKDG DILELRVPKPF DYRPGHYAEVMVPSINKEWHPFSIASAPHEETMCFYIKVLGDWTTTEVRNAFKARLDGTITEPLKVRVRGPYGAQCQDVGFKRVVLVSGGVGATPFSIAIVKELHYLKTQAKNKNDGPGRIARDIDVRIRDSIANLYDVEVQDMEKATHIAQQKSIYVTEMLELTARRTSSLHRVRSSVMDRMHGSSSTKTVLSTDAAIPLSLEDGPVGGGQPM SRMQRLSSSSLSKAGNIRRVMTLSENPTWQVMSAQNDPLTNTTDLRRQMARLYDKRGMLLAFMHTARFTFFLLTLIVRIIIISVAATLDSPYFQLNDQFDGYTRLWPVVVDA LFSVPVAAAALVVSITL EISFMRMR YFDTAARTFDALVLMPPAAVIGCVLAILTWAPQDPESVLVKVIEYVLFIPLLFLGLSWRLYRITRSRSLSDPACRCDNSDHPDVFDFIWSFPYEQSDQWLQDELGLAKGT ERLHRYVTREKELDVEAAKS FITSANTGRPKWDDIFQTIAEETPSNGAIGVFFCGPHVMGNQVRDAMLKVEVLSNLRAAYLRNTPDEVLMTDLNLPNAEAVERLRSLGCSVHFVYREENFG
43	<i>Asparagopsis taxiformis</i> Azores – Mbb3_like	MTPPTRRQTALVKRIAAADLAANRHHHPHVRNADESTYKLPNHVCSYISAF TKGLPHHLDGRLVSPHHFQLFVHAVQTGHVTDIAAIPLGPPHSSSFRSGIAKGA AVRAWESMAAGNTFDLQGPDAQAVTMPPCPRLNSHELVT EMTELYMALLRDVPFTHFNKHHLVQSAVHDMNHTHWTRS NRCCLP RPERRRRHRSKFTTDNIFRGVTPGDITGPYISQFLLVGTKGLGDAHEETEGYVQYGATR IDQRVRTVEPKIDYMTTWAAAYLDVQNGADLRRHSTYAKPPSYRFISTPRDLATYVHYDALYQAYLNACIILLDINAPYDGGLPFTADDAVDKQQGFATFGAPHVLT LVTEVATRALKAVRFQKYAVHRRRLRPEAVGGGLLEQYRRYGGGHSDLAYIIRPIRHLADSLSSDLMFVAKENG RQNSSITDNGHPRSHDEGSDDTHLLSMAYAEGSPMHPSYGAGHATVAGACVTILKAFFDHTFKLPFAYVSSSDGRKLKTVKLSRKL TVEDELNKL AANISIGRSWAGVHYYSYDYESIRLGEEVAIGMLKEQKLT YSEKFTMTIPKFDGVSVEI
44	<i>Asparagopsis taxiformis</i> Azores – Mbb4_like	MAEERRQNALDIRIQAARLAKKRDPHTHEANGDED RYPTKGLPHEKETGLLSNPADFADFVRAINTGAIKDIRRLKLGIDEDPRFISGIASKGDKHPFADTRAWESMAAGLTYDLEGPDAQAVTMPPAPKLDSDDELVTEITESYWMALIRDVPFTEFERDGTNTAAAAASISRTRWWQFNEQPSQRPSTLTDEE IARLRGPYTKKNVFRGV TIGENVGPYLSQFLLVGTKGIGDVQQISDGYIQYGS MRMDQQRVVAAPKRDYMTTWASWLDVQNAAGDLRGREIYDDTTPFRFITTTPRDLATWWHFDALYQAYLNACIILLDIKAPFDPHIPFQADDDVDKQQGFA TFGGPHILSLCTEVATRALKAVRFQKYNVHRRRLRPEAIGGLVERFKKTNGDAKFAPVKK

		LVNDLDGDMRLRRIEQHNCEQNKLSDDGHARRDDYSPEGESNQTYLLPMAFPEGSPM HPSYGAGHATVAGACVTVLKAFFDHEYELDFCYVPTTDGKRLEKVNINEKLTVEGELN KLCANICIGRNWAGVHYYSDFYESIKVGEEIAIGILQEQLTYGEDFFMTLSKFDGEKIRI
45	<i>Asparagopsis taxiformis</i> Azores – Mbb_like	MFHNAFVASAPVGVARIRGASITTKHSPFNAFRRQSSAASVKMAQDNSDQEQRRKDA KQVRINAANLAFNRGVRPHKSNNGDESDFKETLIGTFTKGLRHNTETGQIFSRDLDFPFR ASLATGDPADFKIRLGPKLKPDTPGRWQSTLANGAPGLPFESQVKARAWESAGAGL AFDLEGPDAQAVTMPPAPKLASAELEFEIAELYFMALARDIPFSLWSDPTKAFFDNAI ATLSALPWVSEEFKGKLTDEERFRREGKLNLTGNIFRGYGAGVRDGPYISQYLIRGS QGLGTDGTATGQVMYGSGLDLRVRSEIEPRKDWMTTWAEFIDVQDGADVRQGEFPD YKCAPDGSPIFRFIADGRDLSTYVHYDALYEAYLNACFALLADGVGVDTGLPFRDDDE HDKQTAFATFGGPHILSLVCEVATRALKAVRYQKFQIHLRARPEAVGLIHAQKSERCD FGEEVRALVARLDGCGLLDLVADKNMQQNQTFADRVKDRSASSPSYLLPMAFPEGSP MHPSYGAGHGTVAGACTIILKAFFNTVQFDGKCAVKDAKPSNVEFTPLPNEIFEADAH GCLQPVCLPDGMTLTVDGELNKIANNVAFGRSLAGVHWSSDNIESLIGEEVARGILEE QVLTFAEQHSFTYVGFDDGHLNVIRSQPKHELNVDKRTVEVLRSDDPLVA
46	<i>Corallina officinalis</i> haloper oxidase pdb 1QHB A Chain A	MGIPADNLQSRKASFDTRVAAAELALARGAVPSFANGEELLYRNSETGDPSFIGSFT KGLPHDDNGAIIDPDDFLAFVRAINSGDEKEIAALTLPARDPETGLPIWRSDLANSIDL EVRGWENSSAGLTFDLEGPDAQSVAMPPAPVLTSPELIAEMAELYLMALGRDIEFSEF DSPKNAAFIRSAIERLNGLEWFNTPAKLGDPPEIRRRRGEVTVGNLFRGILPGSEVGP YLSQFIIVGSKQIGSATVGNKTLVSPNAADEFDGEIAYGSITISQVRRIATPGRDFMTDLK VFLDVQDAADFRGFESYEPGARLIRTIRDLATWWHFDLSYEAAYLNACLILLANGVPFDP NLPFQQEDKLDNQDVFNFGSAHVLSLVTEVATRALKAVRYQKFNIHRRRLREPEATGGL ISVNKNAFLKSESVFPEVDVLVEELSSILDDSSASSNEKQNIADGDVSPGKSFLLPMAFA EGSPFHPSYSGSHAVVAGACVTILKAFFDANFQIDQVFEVDTDKLVKSSFPGLTV AGELNKLADNVAIGRNMAGVHYFSDQFESLLLGEQIAIGILEEQSLTYGENFFFNLPKFD GTTIQI
47	A. taxiformis Vanadium- dependent haloperoxidase Mbb1 Coding sequence	ATGACCGACACACAGAATCCCAATCGTGCGAAGTGGCCTTCAAAGTCCGCGTAT CAGCAGCTGAGCTGGCACGCGCTCGTGGCTCCCCAACCCATCTATCCAACAACCTC GGAGAGTCGCTTCAGAAACCCGATGGTACCCGCTTCGCTGCTCGCCAAATTCACC AAGGGTCTCCCGCATACCAAGGAACCCGCTCTAGTGGTCCGCGCAATCGACTACG ATAGCTTTGTTCCGCGCAATTGACAGCGGTGATCCTCGTGATTTCGCGAGACCTCCCG CTCGGTCCGCGAGGTGTTGAGCCCAGATTACCTCCGGTATCGCTAGCGACCCAG AGGTCCGAACCCGTCCTGGGAAAGTGGTGGTGGTCTGCTGCTTGTCTTCGATCTCGA AGGTCCCGATGCTCAGGCTGTCACTATGCCGCCCGCGCCCGAGCTGGACAGCGA TGAATTGGTTACTGAAGTCACAGAATGCTACTGGATGTCTCTGCTGAGAGACGTTT CCTTCCCGACATTTGACAGTGATCCCCATATTCAGTCAGCTGCAGAGTCCATCAAT AACACCCAATGGATTCAATTCAGGAACACCCACCCAGCAGACATCGACTCGTGA GCGTTCCCGTCTCAGAGGCCCCATCACCACTGCCAACGTCTTCAGAGGTATCACA CCGGGAGACGAAGTCGGACCCTATCTGTACAGTTCTCTCTGTCGGTACCACCG GTATTGCCAATGGCAATGAAGTTGGCGACGGATTATCCAGTACGGTGGCATGCG TATGGACCAGCGCGTGCCTGTGCGCAAGTCACACATTGATTACATGACCACATTC GGCGCCTATCTCGACGTGCAAAATGCCGCCAACGTCTCCGGTCCGCAATTGTACA ATGAAGAGGAACCCCGTTTCCGCTTCATTACACTCCTCGTGATCTGGCCACTTAC GTGCATTTCCGACGCTTGTATCAGGCCTACCTCAACGCTGCATCATCTTGTCTCGA CATCGGTGCGCCATTGACTCTGGAATTCCTTCCAGCTCGATAACGACATTGATA AGCAGCAAGGATTTGCCACTTTCCGCGGTCCGCACATCCTCTCTAGTTACCGAA GTGGCCACCCGAGCCCTCAAGGCTGTTCCGCTTCCAGAAATTCACGTCATCGTC GTCTGCGTCCGGAGGCCATTGGTGCCCGAGTCGATCGATACTGCCAACAAGG CACCTGAATTTGCTGGCGCTGCCAAGCTCTCCGAAGCGCTGGACAAGAAGTTGTT GCAGAAGGTGCACGATCATAACAAGAAACAAAACCTGTTGAGCGATCGAGGAAAC CCGCGTGCAACGACTTCAACCCGACGGAGATGTGAGCAAGGTAATCTGCTGA TGCCCATGGCGTTCCAGAGGGAAGTCTATGCATCCCGCTACGGCGCTGGAC ATGCGACTGTTGACGGCGCTTGTGTACAGTGTTGAAGGCGTTCTTCGATGGTGG TTACAGGTTGCCGTTCTGCTACATCACCGACGAGAATGGAACAGGTCTTAAGGCA GTGGAAATTGACGAGCCGTTGACCGTCGACGGCGAGTTGAATAAGATTGCTCCA ATATTTGATTGGTCGCAATTGGGCTGGCGTGCATTACTTCACTGATTACATCGAG AGTATTCGATTGGTGAGGAGATTGCCATTGGTATTCTGCAGGAGCAAAAGCTGAC GTTCAGTGAAAACCTTCTCAATGACGCTGAACAAGTTTGACGGTTCGACCATCCGTA TCTAG
48	A. taxiformis NAD(P)H oxidase Mbb2 Coding sequence	ATGGCTAAGCAGAAGTCTCTCTTACGCTGCTCAGCGCCACACTAGAATCTCATCT CTCCACCCACGCTTTCCAACCTGCTCGCGCTGATCATCTATGCACTCGCCAACGCG CTCATGTTTGTCTGGGGCGCCCATGATGAATTCACCATCACACCGACGCCAATAA TCTGCGATGGTACATCTGTATCGCCCGCGGCGCAGGTTACACACTCAATCTCAAC ACGGCGCTCGTTATTCTGCTCGCCGCCGACTCTTTGCAACTTATCTTCGAGAAAC GCCCCTACAGCATATTCTGCCCTCGACAAGAGCTTTCCAGCTTTTCACATCGTTG

		TAGCCTACACTATTGCCGCCGCCGTTGTTATTACGCCCTCGTTTCATCTAGCCTGG CTCGTCGCCTATGACATGTGGGAACTGGCATGTGGGGATTTACGATGAGCGCCG CGACCGGAGTCGTCCTGCTCGTTGTCTTTATTGTCATGTTTATTTACGCGATGCC AAATACCGGAAAAAACATTTTCGCATCTTTTATCTTATTCATTCCGTTGGTGCTCTG CTCTTTTTCGGTCTGCTCGTATTTTCATGGAATGTACAACAGAGTACCGGAGACGTA CAAATGGATTGCTGCACCGCTTATCATCTATACCATTTGATAGAGTACTTCGACGGT ACAAGATATCCACCGCTGAGCTCGAATTAAGTGGAGAACATTCTCGCTGAAAGG GAGTGATATTCTGGAATTGCGAGTACCAAAGCCGTTTGATTATCAAGCTGGACAGT ATGCAGAAGTTTTCGCTCAAATCAATTAACAGTGAGTGGCATCCGTTTACAATTGCC AGTTTCGCCTCATGAGGACTCAATGTGCTTCTATATTAAGCGCTTGGTGATTGGAC AACAAATTTACGAGATGCTTTTGAAGCCCGAGTTGAGAATGATCTGTACGAACCAC TTAAGGTACAGATTCGAGGCCCATTCGGAGCTCCAGCTCAACATGTGAGTGGGTA TTGTCGAGTCGTGCTTATTTCCGGTGGTGTCGGCTCCACCCCATTCGCAGCTATTT GCAAGCATCTGCATCATTGAACAAGTCGGAATCATTCAAAGCTCTCGAATCG CAAGTTTCTCTCAAAGGCAGTCTCAAGTGCAATGGCGTATTCGAGATCGCTATTTTC CATACTTTTCGACGTCAGTCTGGATGATAGTCGAAATGATGAAGCCGCAAATCAGC AAAGACGACAGCAACTGGCTGATATGCTCAACATGTCGCCAAAGGGTGATGTGCA TAACGTTTCATTCAAACGCACTCAATCCAAGAGGTGAGATGACTTTGATGCCGTGG AGGACTCGAAACAAATGAATTTTTCATTGTGTCGCCAAGATAGCAAATCGAGTTTCA ATCTTGATGACTGTTCTGATGCCATCCGATACTACAATCGTCCTTCTTTTCAGTTCT TCAGTTTCATCCCCAAGGCATGTAATCAATTGGTATGAATACCGTACAAGGCTACTC GCATTTCTGCACACTACTCGGTTTACGTTTGCACCTTTTGTCTACGCTCGTCGCAAG AATTGTTATCTTGTGCATAGTGTCCATATTCAATCTCGGACACATTGGACTTTACAA TAGTCATATCGATGCTACGTGGGTGATTGCCACTAACTCCATATTGGGACTCATAC TTGGAGTCGCTCTGTTAACAACATATTCTATTGAAAATCAGTTTATGCGCGTGCGCT TCTTCTACCGAGTCTGGCGCTGTGTAGACTTTTTTCATCTTTCTACCTATAACTTTCC TGTGCAACATCAGCAATTTCCGCCAGCTGGAACGGTCATGCACAGCCGAAATTCCTA ATATTCCTGGATTTGATCATTGTACTGCCCATCATGCTGCTTTTGTATGCCATCGT ATGTACCGGAGCGTCGGGTACGAAACCTTCTGGACGACACGGCCGAATGTCTCGC CAGGGCTGTAAATGCAACAAACGATCCCGGATGTTGATTTTGTGTGGACGACGC CACGCGACAGCGACGACGAATGGCTGCGAAATGAACTGTATCCAATGGCCACGG GGACGGAGCTTCGGTTGCATCGGTATGTGACTCGCGAGAATATGGCCGACTTGGA GGACCCAGAGCGCTTCATTACAACGGCAAACGCTGGACGACCACAGTGGGACGA GATTTTCGCACAGATTGCAGAGCAAACGCCAAGTCACAGCAAGATCGGGGTGTTCT TTTTGGCGGCCGCATCCGATGGGTGCTGCCGTGCAAAGAGTATGCGCAAAGTGG AGGTCATGAGTAATCTGCGTGGGTCTGACCTGCGCAAGACGAGAGTGGCGGTTCT GGTCGATGATTTGATACTGAGGGATGAGGGGGAAGTGAAGTTATTGAGGGAATAT GGGTGTAATATTGATTTGTTTTCCGCGAGGAAAACCTTTAGCTAG
49	<i>A. taxiformis</i> Vanadium- dependent haloperoxidase Mbb3 Coding sequence	ATGACGCCGCCAACACGCCGCCAAACAGCGCTCGTCAAGCGCATTGCCGCCGCA GACCTGGCCGCCAATCGTCACCATCCGCTTCATGTGCGCAATGCCGACGAAACCA CCTACAAATTGCCAAACCATGTCTGTTCTACATATCCGCTTTCACCAAGGGTTTG CCCCATCATCTCGACGGCCGCTCGTTTCCCACACCACTTTCAACTCTTCGTCCA CGCCGTGCAAACTGGCCATGTCACAGACATTGCCGCCATTCCACTCGGACCCCCA CACTCCTCCTCCTTCCGTTCCGGCATCGCCAAGGGCGCCGCTGCGCGCATGG GAGTCCATGGCCGCGGGTAACACCTTTGATTTGCAAGGGCCTGATGCACAGGCCG TTACCATGCCCCCTTGTCCGCTCTCAATTCACACGAGCTCGTCACAGAGATGACA GAGCTTTATTATATGGCACTGTTGCGCGACGTGCCGTTTACGCATTTCAACAAACA TCATCTCGTTCACTCCGCTGTGCACGACATGAATCATACCCATTGGACTCGGTCCA ACAGATGCTGTTTACCTCGCCCCGAGCGCCGTCGACATCGCTCCAAATTCACCAC TGATAACATCTTCCGCGGTGTAACGCCCGGTGACATAACCGGTCCCTACATTTCCC AGTTTCTCCTTGTGCGGCACAAAGGGTCTCGGCGATGCACACGAAGAAACAGAAGG CTACGTTCAATACGGCGCCACAAGAATCGACCAGCGAGTGCGCACTGTGCAACCC AAAATTGACTACATGACGACATGGGCCGCTTATCTCGACGTGCAGAATGGTGCCG ACTTACGCCGTCACTCCACCTATGCCAAACCACCGTCTTACCGCTTCATTAGCACC CCGCGCGACCTCGCAACCTATGTGCATTACGACGCGTTGTATCAAGCGTATCTCA ACGCGTGATCATCTGCTCGACATCAACGCGCCATACGATGGCGGACTGCCCTT CACCGCCGACGATGCCGTGACAAAGCAGCAGGGCTTTGCGACATTTGGCGCGCC ACATGTGCTGACACTTGTGACAGAAAGTGGCGACACGCGCGCTGATGTCGCG TTTCAAAGTATGCCGTGCATCGGCGTCTGCGGCCGGAAGCTGTGCGCGGTCTAT TGGAGCAGTATAGACGCTACGGTGGTGACATTCCGATCTCGCATACATCATTCG TCCGATTCGTATCTCGCCGACTCGCTCAGTTCCGATCTGATGTTTCATGGTCGCCA AGGAGAACGGACGCCAGAATAGCTCGATTACGGATAACGGCCATCCGCGCTCGC ATGACGAAGGTTTCGGATGATACGCATCTGCTTTCCATGGCGTATGCGGAGGGAAG CCCGATGCATCCTAGTTATGGCGCGGGACATGCAACGGTTGCGGGCGCTTGTGTA ACAATCCTGAAAGCGTTCTTCGATCATACGTTCAAAGTGGCGTTTGCCTACGTGTC GTCGAGCGATGGGAGGAAATTGAAGACGGTCAAGTTGAGCAGGAAATTGACCGTG

		GAGGATGAGTTGAACAAGTTGGCAGCGAATATAAGCATTGGACGCAAGTTGGGCTG GCGTCCATTACTATTCGGATTATGTTGAGAGCATTGCGTTGGGCGAGGAGGTGGC CATCGGGATGCTCAAGGAGCAGAAGTTAACTTATTCGGAGAAATTCACGATGACAA TACCCAAATTTGACGGCTCCGTCATTGAAATTTAG
50	A.taxiformis Vanadium- dependent haloperoxidase Mbb4 Coding sequence	ATGGCAGAGGAACGTCGCCAAAACGCTCTAGACATCCGCATCCAAGCCGCCAGG CTTGCGAAGAAACGTGACCATCCAACCCATGAGGCAAACGGCGATGAGGATCGTT ACCCAGAAACACTCATCGGCTCCTTCACTAAAGGTCTTCCACATGAGAAAGAAACC GGTCTCTCTCCAACCCCGCCGATTTGCGCGACTTTGTTCCGCTATCAACACAG GCGCGATCAAAGACATAAGACGCCTCAAACCTTGAATCGATGAGGATCCTCGCTT CATATCTGGTATTGCCTCCAAGGGCGACAAGCATCCTTTCGCCGATACGCGCGCC TGGGAATCCATGGCCGCCGGTCTCACATACGATCTAGAAGGCCCTGATGCCCAAG CTGTACCATGCGCCGCCGCCGAAACTCGACAGTGATGAACTCGTCACAGAGAT TACGGAGAGCTATTGGATGGCTCTTATTCGTGATGTGCCGTTACAGAGTTTGAAC GTGATGAAATACAGCCGCAGCCGCAGCTTCCATCAGTCGCACCTCGTTGGGTACA ATTCAATGAGCAGCCTTACAGCGCTCCGTCAACATTGACCGATGAAGAGATTGCTA GATTGAGGGTCCGTATACCAAGAAAAATGTATTCCGTGGTGTGACGATCGGTGA GAACGTCCGCCCGTATCTGTCTCAGTTCTTACTGGTAGGCACGAAAGGTATCGGC GATGTACAGCAAATTTCCGATGGTTACATTCAGTACGGAAGTATGCGAATGGATCA GCGTGTCCGCGTCGACAGCGCCGAAACGCGATTATATGACAACCTTGGGCATCTTGG CTAGATGTGCAGAACGCTGGTGATTTACGTGGACGTGAAATTTACGATGATGATAC ACCGTTCCGCTTCATTACAACCCACGCGACCTTGCACATGGGTTCAATTCGACG CGTTATACCAGGCATATTTGAATGCTTGCAATCATCCTTCTCGACATCAAGCGCCG TTCGATCCACACATCCCGTTCCAGGCTGATGACGATGTAGATAAGCAGCAAGGATT TGCAACGTTTGGCGGCCCGCACATCCTATCATTGTGCACGGAAGTGGCTACGAGA GCACTCAAGGCAGTTCGCTTCCAAAAGTACAACGTGCATCGTCGTCTTCGTCCGG AGGCTATCGGCGGGCTTGTGGAACGCTTCAAGAAGACAAACGGAGATGCCAAGTT TGCCCCAGTGAAGAAGCTGGTGAATGACCTGGACGGCGATATGCTGCGACGCATT GAGCAGCACAACTGTGAGCAGAATAAGCTTTCAGATGATGGACATGCACGCCGAG ACGACTATTCACCGAGGGTGAGAGTAACAGACGTACCTTCTGCCATGGCGTT CCCGGAGGGGAGCCGATGCACCCGTATATGGTGACGGTCAAGCCACAGTTGC CGGTGCGTGTGTGACGGTGCTCAAGGCATTCTTCGACCATGAATACGAGCTGGAC TTCTGCTACGTACCGACACGGATGGCAAGCGTCTGGAGAAGGTAAATATCAATG AAAAATTGACAGTGGAAGGCGAACTGAACAAGCTGTGCGCTAATATCTGTATTGGT CGAAACTGGGCTGGCGTGCACTACTCGGACTACTTTGAGAGTATCAAAGTTGG TGAGGAGATTGCAATTGGTATTTTGCAAGAACAGAAGCTACGTATGGTGAAGACT TTTTCATGACGCTGTCCAAGTTTGACGGTGAAAAGATCCGTATCTAA
51	Chondrus crispus vanadium- dependent bromoperoxidase, vBPO_01 Coding sequence	ATGTCCGGCCCGCCGTAGACAGGAAGCCTTCCAGACCCGTGTCCTGCCGCCCGC CTGGCTCGCGACCGTGACCACCAAGTCTTCAACCCAACGGTGAGGAGGACCGC TACTCCGCCCCAACTCCCAGATCTTCAGCTACCTCGGCTCCTACACCAAGGGCTT GCCTCACAACCGCCGCACGGCCCTCATCACCTCGCCGAACCACTTCGTCCGCTTC GTCCGAGCCATCGACTCGGGCGAGCCAGCCGACTTCATCAAGGTCCCGCTCGGC CCGCGCCCGGCCCTCCAGTTCGAGTCCGAGGAAGAGTGCCGCGCCGCCAACCTC TTCAAATCCGGCATCGCCGCCGCCAACACCTTCCCGTCCCTCCTGCCGCGC CATGGGAGAGCATGGGCGCCGCTCGTCTTCGACCTGGAGGCTCCCGGACCGC CAGGCCGTCCGGATGCCGCCCGCCCCACGCTGGACAGCGACGAGCTCGTCGC CGAGATCTCCGAGGTCTACTGGATGGCCCTGCTGCGCGACGTCCGCTTCACTGAT TTCACCAACCCCGGCCGATCGGCAGGGCCATCAACACCCTCAACAAGACCGCCT GGATCCGGGCGGCACGGGACCCCCCGACTCGCTCACGCCGAGGAGCGCGCC CGCCTCCGCGGCCCGTTCAACCCGAGCAACATCTTCCGCGGAACCCTCCCCGGA GATGACGTCCGCCCGTACCTCTCCAGTTCTTGCTCGTGGAACAAAGGCGATTG GCGGCGCACAGGACATGGCTGACGGGTTTATTAGCTACGGCGCCACCGCATCG ACCAGCGCGTGCGTCACGCGAGGAAGGAGCTCGACTACATGACCTCTTGGGAGG CCTTCTTGACGTCCAGAACGGCGCCGATGTCACCGGTGCGGATACCTTTGAGTC GGGCTCTGACGCCTTCCGCTTCATCACAACCCCCCGTGATCTCGCCACGTACGTC CACTTTGACGCGCTCTACCAGGCCTACCTCAATGCCTGCCTGATCATGCTTGACAG CGGCGTGAGGTTTGATAAGGGTATTCCGTTTGGTGAGCCAGACTTCAAGGATCAT CAGAGAGGCTTCGCTCATTTCCGAGGACCGCATATTTTCCCTCGTCACAGAAGT TGCCACAAGGGCTTTGAAGGCTGTTGCTTCCAAAAGTTCAACACGATCGCCGT CTGCGTCCCGAGGCGTTGGTGCCGTGATCGAGCGCTTCAACAGCAACCCTGAC GACCCTCAGTTCAGGATGTGAAGCCGTTGTTCAAGCGCTGGATGAGGATATGA TGCGCCGCGTTGCTCGTCACAACAGGGAACAGAACCAAGGCTCTGACTTTGGCAT GCCGCGTGCCGACGACTTCAACCCCGCCGGTGACACTCTCGAGACGATGCTGTT GCCCATGGCTTTCCCGAGGGGAAGTCCGATGCATCCGTCGTACGGTGCCGGCCA TGCCACTGTGGCCGGGGCTTGTGTTACCGTGTTGAAGGCATTCTTCCAGCACGAC ACCGAGCTCGATTTCTGCTTCGTTCCAGTGATGACGGAAGCCGTCTTGTGACG CCAGCCACAACATGAATAAGAAATTGACTGTAGAGGGAGAGTTGAACAAAGTCTGC

		TCCAACATCAGCATTGGCCGCAACTGGGCTGGCGTTTCATTACTTTACCGATTACAT TGAGTCGATTCTCCTCGGGGAACAGATCGCGCTAGGCATCTTGAGGAGCAGATG TTGACTTTCCCCGAAACCTTCACAATGACCGTCCCTCTCTTCAGCGGCGAATTGAA GGTCTCCGCTCGACCTGA
52	Chondrus crispus vanadium- dependent bromoperoxidase, vBPO_02 Coding sequence	ATGGCAACCCCGTGCTTCGCCAGGCGCCGGCCCCCACCCTACGACGATCGCCG CGCCGTCTCCCCCTCACCCCGACCTCCTTCCTGCCGAGGCCGTTCTGCCAAAGC CCTTCCCCCGCTCCCCCGCCACCCGCGATCCGCGCCTAACGCCGCCCTCCGCGC GCACCTCCGCCGCCCAACCCCCGACCGCGCAGCCACGCCGTGCGCTACCCGC CAGCAGCAAGCGCTGGAGCTGCGCCGCGCGGGCGCAGCTCGCGCACGACCG TGCGCACCCCGCGCACGTGTGAACGGGTGGAGGAGCTTCACCTGCACCCGAA GACGGGCGCGCCGCTGCTGCTGGCCAACCTTCACGAAGGGGCTGCCGCACGAGC GCGACACGGGGCTGGCAGCCGACGCCGCGCACTACGACCTCTTCGTGGCGGGC GTCCATTCCGGCTTGCCGGACGACATCCGCGCCATCCCGCTCGGCCCGCAGGCC GCGCCCGGCGTCCGCTCCCGCGCTCGCTCCGCTTCCGCTCCGGCATCGCACGC AGCTCGACCTCTTCCCGCACACTGACGTCCGCGCTGGAGACCTGCGCGCG GGGAACGCGTTTCGACCTGCAGGGGGCCGGACGCGCAGGCCGTACCATGCCGCC CGCGCCCGCCCTCGCTCCCCGAGCTCGCGCTGGAGATGACGGAGAACTACTG GATGGCCCTGCTGCGCGACGTCCGCTTCTCGCAGTTTGCCGCGGACCCACCGT CGCCGCCGCCATGGAGAGCATGAACGCTACCGAGTGGGTGCCCTCGCGTGCGG CGACGCGTCGGCCGTGCGGGAGGAGGAGCGCAAGCGCCTGCGCGGGCCGTTTA CCGCGCAGAACGTGTTCCGTGGGAATACGCAAGGCGATTGCAAGGGGCCCTATAT CTCCAGTTTCTGCTGTCTGGAAGCGCGGGGCTGGGCCAAGTGAACAGCGCGC GGATGGATACATCCAGTACGGAGCAATGCGTATGGATCAGCGCGTTCTGTGCGC CTCGAGGGGCTTGACTATATGACCACGTGGGAGAGCTGGCTGGATGTGCAGAAC GGGGCCGACTTGCGGGGAAGGGAGTTGTATGAGGACGGCGAACGCTTTAGATTT ATTTGCACCCCGAGGGACTTGCCCACTTATGTCCATTATGATGCCCTGTATCAGGC TACTTGAACGCCTGCATTATCATGCTCAACAAGAAGATCCCCTTTGACAAGGGCC TGCCGTTCCAGAAGGATGACGACATCGACAAGCAGCAGGGCTTCGCCTTATTCGG CCCGCCGCACATTCTCACCTGTGACGCGAGGTGCGCACAGGGCCCTCAAGGG CATCCGCTTCCAAAAGTACAACGTCCACCGCCGTCTGCGTCCGGAGGCTGTGCGC GGCCGCGTGGAGCGCTACCACCACAACCTGCGAGGACCCGCTCTTCGCCGACGTC AAGCCGCTGTACGACGCCCTGGATAAGGACATGCTCGAGCGTGTGCGCGCAC AACGCCGAGCAGAACGCCAAGGACGACTTTGGGAACAGCCGTTTCAAGACTATT CCCCGACGGGTAGCTCCGGCAGGACCTATCTGCTGCCATGGCGTTTCCGGAGG GCAGCCCCATGCACCCGGCGTACGGCGCAGGGCATGCGGCAGTGGCCGGCGCG TGCACCACTATCCTCAAGGCGTTCTTCGACCACGACGACGAGCTTGACTTTGCGTA CGTGCCCAACCGGATGGCAGCAAATTGGAGGATGTTGTTGACTTTTGGGGAG AAGCTGACCGTCGAGGGAGAGCTCAACAAGGTCTGCTCGAATATCAGCGTCGGG CGCAACTGGGCTGGTGTGCACTACTTTACAGACTATCGCGAGTCCATCATCCTTG GGGAAAAGATTGCCCTCGGCCTGCTGGAGGAGCAGAAAGCTTACGTATGCTGAGG AGTTCTCCATGACGATTCTCTCTTTGATGGTTCCACTGTCACCATTAG
53	Chondrus crispus vanadium- dependent bromoperoxidase, vBPO_03 Coding sequence	ATGTCCGACATGTCGACTGAGATCAGCCCTAGACAACAGGAAGCCTACGATATCC GTGTCGCCGCCGCCACCCTGGCTCTGGCTCGCGACCGTAACAGCAAAAGTCTTCG AACCCAACGGTGAGGAGGACCGCTACTTCCGCCCAACTCCAGATCCCTCACTA CCTCGGCTCCTACACCAAGGGCCTGCCTCACAACCGCAGCAGGCCCTCGTCAC CTCGCCGAACCACTTCGTCCGCTTCGTCCAAGCCATCGACTCGGGCGAGCCAGC CGACTTCATCAAGGTCCCGCTCGGCCCGCGCCCGGCCCTCGAGTTCACGACCGA GGAAGAGTGATCGCCGCCAACCCTCTTCAAGTCCGGCATGCCACCCGCAACGA CAGCTTCGATCCCGCCTGCCTGCGCGCATGGGAGAGCATGGGCGCCGGTCTCGT CTTCGACCTGGAGGGCCCGGACGCCCAGGCCGTGGCATGCCGCCCGCCCCCA CGCTGGACAGCGACGAGCTCGTCGCCGAGATCTCCGAGCTGTACTGGATGGCCC TGCTGCGCGACGTCCGCTTCACTGACTTCACTAACCCTCGGCCGATCCGCAGGG CCATCAACACCCTCAACAGGACCACCTGGATCCGCGCGGCACGGGACCCCCCTG ACTCGCTCACGCCGAGGAGCGCGCCCGCCTCCGCGGCCCGTTCAACCCGAGCA GCATCTTCCGCGGAACACTCCCCGGAGATGACGTGCGCCCGTACCTCTCCAGTT CCTGCTCGTGGGAACCTGAGGGTATTGGCGGCGCGCAGGACAGGGCTGACGGGT TATTAGCTACGGTGCCCACCGCATCGACCAGCGCGTGGCTCAGCGACAAAGGA GCTCGACTACATGACCTCTTGGGAGGCCCTTTTTGACGCTCAGAACGGCGCTGAC GTTGCCGGTCGCGATACCTTTGAGTGGGGCTTGACGCGCTTCCGCTTACATTACGA CCCCCGTGATCTCGCCACGTATGTCCACTTTGACGCGCTCTACCAGGCCTACCT CAATGCCTGCCTGATCCTGCTCGACAACAAAGTAAAATTTGATCAGGGTATTCCGA TGGGTGAGCCAGACTTCAACGGTAATCAGGGTATTCCGTTTCAAGATCCAGACTTC AAGGATCATCAGCGAGGCTTTGCTCATTTCCGAGGACCGCATATTCTCTCCCTCGT CACAGAAGTTGCCACAAGGGCTTTGAAGGCCGTTTCGCTTCCAAAAGTTCAACACG CATCGCCGTCTGCGTCCCGAAGCCGTTGGTGGCCTGATCGAGCGCTTCAACAGCA ACCTGACGACCCTCAGTTCCAGGATGTGAAGCCGTTGTTTCAAGCGCTGGATGA

		GGATATGCTGCGCCGCGTTGCTAGTCACAACCGTGAACAGAACGAACGCTCTGAC TTTGGCATGCCGCGGGCCGACGACTTCAACCCCGCCGGTGACACTCTCGAGACG ATGCTGTTGCCCATGGCTTTCCCGAGGGAAAGTCCGATGCATCCGTCGTACGGTG CCGGCCATGCCACTGTGGCCGGGGCTTGTGTTACCGTGTGAAGGCATTCTTCCA ACATGACGCCACGCTCGACTTCTGCTACGTTCCCACTGATGACGGAAGCCGTCTT GACGACGCCAGCCACACCTTGAATAAGAAATTGACTGTAGAGGGAGAGTTGAACA AGGTCTGCTCCAACATCAGCATTGGCCGCAACTGGGCTGGCGTTCATTACTTTACC GACTACATTGAGTCGATTCTGCTCGGCCGAACAGATCGCGCTAGGCATCTTGGAGG AGCAGATGTTGACTTTCCCGAAACCTTCACAATGACCGTCCCTCTCTTCAGTGGC GGCTTCAGGACCCTCATCTCGACCTCTGATCCTTGA
54	<i>Asparagopsis armata</i> Azores – Mbb1_like coding sequence	TTAAATGCGAATTGTGCTTCCATCAAACCTTGTGAGGGTGCATCGAGAAATTCTCACT GAAGGTCAACTTCTGTTCCCTGAAGAATGCCAATAGCAATTTCCCTACCAATGCGGA TACTTTCAATGTAGTCAGTGAAGTAATGCACACCAGCCCAGTTACGTCCAATGGAA ATATTAGAGCAAATCTTGTTGAGCTCTCCGTCAACTGTGAGCGGCTCAGACACTTC AACC GGCTCGAGGCCGACGCCATTTTCGTTAGTGACGTGAACACGCGAGTGCCCA GAATCCACCATCAAAGAATGCCTTGAGAACAGTTACACAGGCTCCTGCAACAGTG GCATGTCCAGCACCATAAGCCGGATGCATCGGGCTTCCCTCTGGGAATGCCATTG GCATGAGAAGGTTGCCTTCGCTCAGGCCGCCATCAGGATTGAAATCTGCACTACG CGGAGCACCGTTGTGCTCAACTTATTTTGTCTTGTATGGTAATACACTCGATC CAACAGGTCAGAATCCAGGGAATCTACCAATTTAGCAGCTCCGGAAAATTCGGGT GCTTTGGTTTTGTAGTATCGGTGACACGACCGCCGACAGTCTCCGGGCGTAGAC GGCGATGGACGTTGAACCTTCTGGAAGCGCACTGCCTTGAGAGCGCGAGTGCCCA CCTCAGTAACGAGAGAGAGAATATGCGGTCCGCCAAACGTGGCAAATGCCTGCTG CTTATCTATATCATTGTGAGCTGGAACGGGACTCCGGAATCGAACGGTGCACCA ATGTGAGCAGAATGATGCAGGCGTTAAGATAGGCCTGGTACAGAGCGTCAAAAT GGACGTATGTGCGCAGATCACGCGGTGTGTGAATGAAGCGGAAACCAGGGTCTG ACTCGTATCGCTCACGCCCCGGTGACATCCGCAGCGTTCTGCACGTCAAGCCAGGA TCCAAAGGTGGTGCATGTAGTCAACCTTGGGGGATGCCACGCGTACCCGCTGGTCC ATGCGCATACCACCGTACTGGATGAAACCATCGCTGACCTCGTTCCGTTTGCGAT TCCTGTGGTACCGACCAAGAGGAATGGGACAAATATGGGCCTACATCATCTCCA GGAGTGATGCCCCCTGAAGACATTGGAGGCATCGATGGGGCCTCTGAGACGGGAG CGTTCGGCAGATGTGAGATGGGTGGGAGGGTTTTCTTGAATTTAATCCATTGAGT GTGTTGATACTCTTGGCAGCGGCTGCGACATCTTCGTGCAATGGAATGTTGGG AAGGGTACATCCCTGAGCAGGGACATCCAATAACATTCCGGTGACTTCAGTGACCA ACTCCTCGCTGTCTAGCTCTGGTGCGGGCGGCATAGTGACGGCCTGTGCATCAG GCCCTTCGAGATCGAATGTGCGTCCAGCACCCATACTTTCCAGGCACGAATCC CGACTGCTCTGGGTTGTGGCGATGCCGGATGTGAATCTGGGGGTGACATTCTGG GGGCCGAGTGGGAGAGCTGCGAAATCGCGGGCATCTCCGCTGTCAATAGCGCGT ACAAATTGGTCATAATCGAGGGCAGATTGAACCAGACCTGTTTCGTTGATATGGGG GAGACCTTTCTGTAAGTTAGCCAAGAGAGATCGTGTACCATCTGGGTTTCTGAAGC GAGCCTCTGAATTGTTGGAGATGTGAGTTGGAGAACCACGGGAGCGAGCAAGCTC GGCGGCAGAGGGCGAATCTTGAAGGAGGCCTCTGCGCGATTGGGATTCTGTGT GTCGGGGGTTGCCAT
55	<i>Asparagopsis armata</i> Azores – Mbb2-2_like coding sequence	ATGAACACAGCAATTTCCCTTCAGAAGAAAATGGTCCCCAAGTCTTTGAGTGCTCG CCTCGAGTCCTATCTCTCCACTCACGCCTTCGAGCTTCTCACAGTTATCACATACA TAACTGCACTCTCTCATGTTGCTATGGGGAGCTCACGATGAGTTCCACAATCAA TCTCCCGACACAAATCTCCGCTGGTACATTTCTATTGCTCGCGGAGCAGGTTACAC ACTCAACCTCAACACAGCACTTGTCATTCTACTTGATCTCGCCTCTTCTTCACATT CATCCGTGATACTCCCTGCACAAGATTCTTCTGTTGACAAAAGCTTCCCCGCCT TCCATATCCTTGTGGATATACGATAGCCGCATCTCTTTCATTATGTCCCGTTCC ATTTACATGGATCATTGCTTACGATAAATGGAGTGCAGGACTTTGGGATTTACCC ATGAGCGCTGTACAGGCGTCTGATTGTTACTTATCTTCATAATCATGTTTCATGTT GCTCTACCATTCTACAGAAAAAATATTTCCGGCTCTTCTACATTTCCACATGGTT GGAGCACTGCTGTTCTTCTCTCTCATCTTCCATGGTATGTACCGTCGTGTTCC GGAGACTTACAAGTGGGTTGCTCTACCTCTCGTGATCTACATTCTGGACAGAATCG CCGTCGCTTCAAAATCTCCACCGTTTCAGCTGAAGCTCACTTCCGAGCATTACGCT CTCAAAGGAAAAGACATTTTGAACCTTCGATTCCGAAACCCCTTCACATATCGCGC TGGTCAGTATGCAGAGATCCGTGTACCATCCTTGAGTAGGAGTGGCATCCCTTC ACAATTGCTAGTGCACCCCATGAAAAATGCATGTGCTTTTTTCATCAAATCACTCGG GAATTGGACCAAGGAGCTTCGAGGGGCATTTCAAACCGTATGGAAGGAGAAGAT CCGAACCCATTGCTAGTTCAAGTCCGTGGTCCATTTGGCGCTCCCGCTCAACATGT CTCTTCGTATGAAAGAGTGGTCCCTCATATCTGGCGGAGTTGGTTCAACGCCCTTCG CAGCCATCTCCAAAAGTTTGCATTTCTTGAACAAGAACAAACCTGCCCTTCTACTG ATTTTTCGAAAACCAATTTGTCTGAAATGAAGCATATTGAGCAGCGTATCTCGGAAA CTATTTCTGCTGTATATGATATCGATTTGGCAAACAGCTCCGATGAACCGGAATCT GAAGAACAAAGGAAGCAGTATATTACTGACATGATGAACCTTGACGGCCCAAAATTC

		CGAAGAACTCGATGTTTCCACTTCAAGAACAAGTGAACAATGTGTATCATCGAGGA GCTGCCCCAAATATTGGAGATGGTCTCCGGATATTGGATGTGCAAAATCAATTAGAA GAATCTTCAGTGAGCAGCATGTCTACATGCGACGATGAAGAAGATTATTCATCAGA TTTCAGTGAAGAAATGAGACTTGAAAAGGAACTTGCCGCCAGGAAACGTAAGATG GCTCGCCAAAAAATTGCCCCTCTCTATGAGAGACGTTCAATATTATTCTCTTTTCTT CATACCACTCGGGTAACTCTGGCACTTCAACTCTCTCTAATTGCACGCATTGTTCTT GTGTGCATTGTATCAATCTTCAACATTGGTGAATTCAACTTTGGGGACAGCCGCAT AGGTGCCAAATGGGTTATAGGTGCCGATGCGAGTGTGAGTGTGTTGCATGCAGTC ACTCTAACTTTGACCATACTCTTGAAATTAGCTTCATGGGACCCCGCTTCTTCCGT TCTTCTTGGCAGTTTATGGACTTTTTCTGTTTTCTGCCGCTCAGTATTCTGTGCAGC GTCAGTGGTGTACTATCTTGGACTGGGACGGAAATGTCAGGAACATTAGTTTTTCT TCACTTCATTGTATTGCTGCCAATTATGCTTATTTTCATGAGTGCTCGTCTGTATCG GAGTATTGGGTCCCTGAATCTATTTTCATGATCGGAAGTGTAACCCAAACTGCGCAT GCGGAAAGAAAAATCCAGACGTTGACTTTATCTGGACAACACGTCACACCCGTAGAT GACCAATGGTTACGAGAAGAAGCTTTCTCTAGAGGACGGCACAACAACTCCGTCT TCACCGATATATTACAGGCAAGGAAAGTGAAGACTTTGAAAGTGCTGAGACCTTTA TTACTACAAGCAACATTGGAAGACCGCCCTGGGACGAAATATTCGCCAAAAATTGCC CAAAAGTCACCAAGTCACGCAGAAATCGGAGTGTGTTTTCTGCCGACCACACTCAAT GGGAGCAGCTGTGAGGAAAAGCATGCGAAAAACTGAAATACGGAGTAACTTGCGT GGGGCATATCTGGAGACAATAATGTTGTGCATCTTGTTGCCGATCTTCTTCTGAG AAATACTGACCATGCAGCAGACTTCGGAGGCATGGGTGCAATATTGATTTGTAT TTCGTGAAGAGAAGCTTCGGTTGA
56	<i>Asparagopsis armata</i> Azores – Mbb2_like coding sequence	TCAGCTAAAGTTCTCTCCCGAAATACGAATCGAACATTGCTTCCAAACCGTTCA GTAATCTTACCTCGTCCCCAACCTCCCCTCCACCCGTTTTCTCAAGTATGATCCC CTCAAACACTGAAAACCTCCGCCCGCCGCAAACCTCTCCCGAACCTGCTTCCCCAT CCCCTGGGTCCACAGAAGAACACCCCGATCTCACTGCAGCTCCGCGACTCCTCC GCGATCTTCAAAAATATTTTCATCCCACTTCGGACGCCCCCGCCCTAGCAGATGTGAT AACTCCTCCCTCCCTCCACCTCCACTTCTTCTCCCGTGTACGTACCGATGCA GTCGCAGCTCCGTCCCGTCGCAAGCGGTACAGATCTTCGCGAAGCCACTCGTC GTCCCCCTCGTGCGCGACCGTCCAGATAAAGTCCACTTCCGGAACGCTGTGTTCT GACCCCCGGCAACTCCCGTTATCGTCGAAAAGGTTTCGCGTCCCAATGCTTCGGT ATAATCGATGACAGAGAAGTAGGAAGATAATCGGTGTGATAATAATATAGTCGACA AATGTCAGGAAGGACGATTGGTCTCGTCCAGCCACGTTACAATTCCGTATAGATT GCACAGAAATGACAGAGGAACGAACACCAAAAAGTCAACGCATCGCCAATTCTTG TGGAAGAATCGCGTCCCCATAAACTCACTTCCAGCACAATTATTGTGAATAGAGT CAATCCAACAATTAGTCCCAGAACGACGTTTGTACAGATAACCCACTAGCCCTCTA TGTGTCCGCTGGTTGTGCTGAAATGACCAAGATCGAAGATAGATACAACACACGTC AGCACTAATCGCGCAATTAGTGTGAACAGCAGCAGCAATGTTATTCGAGTCGTGTG AAGTAAGGAAAGAAAGTCTAGAGCGCTTTCCATTGAGAAACATCAAATTATGCTTCG AGTACGCAGATCGCCCCATCTTATCTTCTCTCCCGCCTTTTCTAGAGCTGCACTCT TTCTCGTATGTTCCAGCGTGCCATTTGACTCCCAATACTTGATGAAAACGAGAG ATCGACATTTTCCGAAGTGCACGTATCACTCACATCAGAAGAGCCTGTCCGGAGACG GATGAGAGATTTTCAATTTCTAATTTCTGCACCGCTCCATCCGGGACATGTTCCAGC ATATCCGCCAGATGCTGTCTTCTTTGTTGTTGGAATCTCTGCGCAGCCGCTTTC ACCCAACCCCAAGCCGTACATATTGGAGATCGTTTCTCTGATCCGGTTCCCGAGTT GTATTGTATGCTTAGATGGAATGTCAACATCGAGCGTCTTTTTGTGATGTTTCAGCG ACATTCAGGTGGTGCAGATGTTTCGAGATGGCGGCAAAAGGGGTGGCGCCAACA CCTCCTGACACCAACACTACCCGTTGATATCTGCCGACGTGCTGAGCGGGAGCGC CGTACGGTCCGCGGATCTGTACCGTAAGTGGTTTGCAGTCGTCTGAATCCATGCG TGTTTGAATTGGTGGCGCAGTGCTTGAGTCCAATTGCCAAGAGTTTTGATGAAGA AGGTCATGGTTTTCTCGTGGGTGCGCTTGCGATTGTGAATGGATGCCACTCTGA ACTGATCGAAGGGACACAGACCTCTGCATATTGCCCGCTCTGTAATGGAAGGGC TTTGGGACTCGGAGTTTCGAGAATGTCAGCACTCTTGAGAGAAGAATGATCGCTGG TGAGCTGCAAGGGAAGTGTGGACACTTTGAAACGACGAAGAAGTCTATCAATAATG TAGATGATGAGTGGGGCGGTGATCCATTTGTAAGTTTCTGGAACGCGGTTGTACAT TCCATGAAAGATTAGTAGAGGGAAGAAGAGTATCACTCCGAACATATGTGTGAGAT AGAAGAATCGGAAGCGTTTCTTCCGAAATGTTGGGAGGGCAGTTATGAACATGACT AGAAACACAATGAGGAGGACAGATCCTGTGATGCGCTCATAGTATCCCCAAA GGCCTGGTTCCCATTTATCGTAGGCAATAATCCACGCGAAATGGAAGCGACATG GAGGACGAGGGAGATGGCAATAGCGTAAGCGACAATAATATGGAAGGCTGGGAA GCTTTTGTCAAGAGGAATGATTAGATGCAATGGGGTCTCGCGAATATAAGTTGAAA AGAGTCTGGCAGCGAGAAGAATGACCAATGCAGTATTGAGATTTAGGGTGTAACC TGCTGCGCGGGCGATGGAGATGTACCATCGCATGTTATCATCGGAAGTGTGGTGA TGGAATTCGTATGGGCTCCCCATAGGAACATGAGGAGGAGTGCGGTGGCATACA CGACGAGAGCGAGAAGTTTGAAGGATGTGTGGAGAGTGGGACTCGAGTCGAG CGGTGAGGAGATCTTGAGTGGACTTTGGACATGTGGATGAGGATGGAGAGGGCAT

57	<i>Asparagopsis armata</i> Azores – Mbb3_like coding sequence	ATGCCTCCCCCAACTCGTCGTCAATCCGCTCTCGTCACTCGCATTGCAGCTGCAG ATGAAGCCGCAAAACCGTTCACATCCTCCTCATCTAAGAAATGGCGATGAGACGCT GTACAAGACTACCTCAAATGCTCTCTCCTACCTCGCGACCTTCACAAAAGGTCTCC CTCATCATCCCCGACGGTCTGTCTAGTCTCCGCACAGCATTTCCTCAACTCTTCGCCCGT GCTGTCCAAACAGGAACTCCACAGCACATTGCAGATATTCCTCCTCGGACCTCCATC CACCTTTTCCACATTCCGCTCCGGAATTGCAAAGGATGCCCACTCCGCGCTTGG GAATCCATGGCCGCTGGAAATACATTGACCTTCAAGGGCCTGATCCCCAATCAG TCACAATACCCCCATGTCCACGTCTCGAATCCAATGAGCTCGTCACAGAGATGACA GAGCTTTACTACATGGCACTCCTCAGGGATGTCCATTCTCTCATTTCAAAAGTCAT CACCTCGTCGCCGCTGCCGTGACGATATCAATCACACCCATTGGATTCAATCCCA TAAATGTTGCATCCCAGAACTGGAACGTACAGACACAGAGAACCCTTCTCATCCT CTAATGTCTTCCGTGGCACCCACACCAGGCGAGCGCAATGGTCTTACATCTCACA ATTCCTCATTGTTGGAACCAAAGGGCTCGGAGAAATCCACGACGAGGCAGATGGC TACATCCAATACGGTGCCATCCGAATCGATCAGAGAGTTCGATCAGTCGAGACAG AAATCGACTACATGACCACCTGGGCGGCTTCCCTTGACGTCCAGAATGCCGCGAGA TTTGCGCAGACATTCTACATATGCCAAATCAAGCTCCTATCGCTTCTGTACACAC CACGCGACCTCGCTACCTACGTTTCATCATGACTCGCTCTACCAAGCCTATCTCAAC GCATGCATCATCCTCCTCGACATGAAAGTCCCATTGACTCCGGTCTCCCTTCAC CACGGAAGACCACATCGACAAACAACAGGGCTTTGTAAACTTTGGAGGCCCCCAT ATCCTCACACTCGTCACAGAGGTTGCTACCCGAGCCCTCAAGGCAGTCCGTTTCC AAAAATACGCCGTCCACAGACGTCTTCGCCAGAGGCTGTCCGCGGCTCTTAGA ACAATACAGACGATACGGTGGCGGATATTACAGAGCTAGCAAATACTATTCGTCCCA TACGCCATCTCGCCCGTTCTCTAAGTTCAAACCTCATGTGCTCGTCGCAGCAGC GAACGGCCATCAGAACGCAACAATGAGCGACAACGGATTTCCACGCTCCCATGAT ACAGGCTCCGGTGAGACTCATTTGCTGCCAATGGCCTATCCGGAGGGAAGTCCGA TGCACCCTAGCTATGGTGCCGGGCATGCCACAGTGGCCGGGGCGTGCGTAACGA TATTGAAAGGCTTTTTCGATCACACCTACAAGCTCCCGTTCCGCTATGTCTCATCCT GCAATGGGAAGATGCTGAAGAAGGCAAAGTCCGGAAGAACTTTCCGGTGAAG GAGAGCTGAATAAACTGGCGTCTAATATCAGTATTGGACGTAGCTGGGCTGGCGT ACACTACTACTCCGACTATGTGGAGAGTATTGATTGGGAGAGGAAGTGGCGATT GGAATCCTGAAAGAGCAAAAGTTAACTTATTCGGAATAATTCTCAATGACAATTCCC AAATTTGATGGCACAACCATCAAAATATAG
58	<i>Asparagopsis armata</i> Azores – Mbb4-2_like coding sequence	ATGTCCGAAGAACGCCATGCATCCGCCTTGAGAGTCCGTAGTGAAGCCGCAGATC TCGCTGCTTCACGCCCCCTCCCCACCCACCTTGCAAACGGCGATGAGCATCGCTA CCACGACACCCACCTCGCCTCCTACACGAAAGGTCTTCCACACGAAAAGGATACC GGCCTCTCCTCCTCTCCAGATCACTTCGCAGCCTTTGTACGCGCCATCGAAACAG GCGCTCAAGAAGATATTACAAAGTCTCCCCCTAGGTATCGATGAAGACCCCGTTTC ATATCCGCCATCGCTTCAGAGGGCTCCGACCATCCCATAGCCGACACTAGAGCGT GGGAATCCATGGCAGCTGGTAATACATACGATCTGGAGGGACCGGACGCTCAGG CAGTCACCATGCCGCCTGCCCAAAAATCGATAGTGAAGAACTCTTGACGGAGAT CACCGAGTGCTACTGGATGGCCCTTCTTCGCGACGTCCCGTTTCACAGAGTTCGAA AGGGATGGCACTACCGCTGCCGCAGCCGCTTCGATCAGCCGAACGCGCTGGGTG CAGTTCCAAGAGCAGCCCGGGCAACGCCCTGCGATCTGTCTGATGCAGAAATTG CACGTTTGCGAGGTCCATTACAGGAAAACAACATCTTCGCGGCGTGAACCCCTGG TGAACAAATCGGTCCCTATCTCTCTCAGTTCCCTTCTCGTTGGCACAAGGGTATCG CGAACATTACAGGAAATTTAGATGGATTCAATACGGAGGTATGCGTATGGAC CAACGTGTTGTTGTTGGCAACCCCAATAGGGACTACATGACCACCTGGGCATCCT GGCTCGACGTGCAGAACGCAGGTGATGTACGAGGACGTGAAACGTACGACAACG ACACTCCATTCCGTTTCATTACTACACCGCGCGATCTTGCCACCTACGTCCATTTT GATGCACTTTACCAGGCATACCTGAACGCATGTCTCATTCTTCTCGACACCAAGGC CCCTTTTCGATCCAGAAATCCCTTTTGTGGAAGATGATGACATCGATAAAACAACAGG GATTGCTACCTTTGGAGGTCCCCATATCCTCTCGCTTGTACAGAGGTGCGAACT AGGGCATTGAAGGCTGTGCGCTTCCAGAAGTTTGGTACCCACCGCCGTCTACGCC CCGAGGCTGTCCGGCGTCTTATCGAGCGATACCGAAAGACGGAGGGAGCAGAGC CCTTTGAGCCCATCCAGAAAATCGCCACTGAGATCGACAATGACCTTATGACACGA ATCTCGCAGCACAACGCCGCGCAGAATGAACTTTCCGACAACGGTGGTGCCCGAA GCGGCGATTATAATCCTGAGGGCTGCGAAAGCGCAGAACTTATCTTCTCCCGAT GGCATTCCCGGAGGGTAGCCCAATGCATCCAGCTATGGTGAGGGCATGCTGCG TGTTGCGGGTGATGTGTGACGATCCTAAAGGCGTTCTTCGACCACACTCACGAG CTTGAATTCTGTTATGTGCCAGCACAGACGGCCAGAATCTTGAGGAGGTGGA TCAATGAACCGCTCACAGTGGAGCATGAGCTCAACAAGCTTTGTGCCAACATCAGT ATTGGTAGGAATTGGGCTGGTGTGCACTATTACTCGGATTACATAGAGAGCGCAA GGTTGGGTGAAGAGGTTGCAATTGGTATTCTAGAAGAACAGAGTCTGACGTACGG TGAGGAGTTCTCCATGACTATTCCCAAGTTTGTGGTACGACTATCAAGATTTCAA CTCAAAGTAA

59	<i>Asparagopsis armata</i> Azores – Mbb4_like coding sequence	TCAGTTGGAGATCGTAATGCACGTTCCATCAAACCTTGGGGAGGGTCATGGAGAAC TTCTCACCATACGTCAAGCTCTGTTCTTGCAAAAATACCGATGGCAACCTCTTCACC CAACCTTGCACCTCTCTTCGTAATCCGAGTAGTAGTGCACACCGGCCAGTTTCTTC CAATACTGATGTTGGCACACAACTTGTTCAAGCTCGTGTTCAACTGTGAGCGGTTCA CTGATGTTAACCTTCTCTAGCTTCTGCGCTGTGTGCTGGGTTCAAAGCAGAACTT TAACTTGTATTTGTGATCAAAGAAGGCCTTGAGGATCGTGACACAGGCGCCAGCG ACAGCGCGGTGTCCAGCACCGTAGCTGGGATGCATTGGGCTTCCCTCCGGGAAC GCCATTGGAAGAAGGTAGGTTTCTGCGCTTGCGCCACCCTCGGGGTTGAAATCAT TTCTTCGTGCTTTACCGTTGTGCGAAAACTCATTCTGCTTGGCGTTGTGACGCGAG ATGCGCGTCATAAGCTCATTGTGCGATCTCGGTAGCGAGCTTCTTAGCGGCTGCGA ATGGCGCTGCGCCGTTCTGCTTGCGGTAGCGCTCGATGAGTCCGCCGACAGCTT CGGGGCGTAGGCGACGATGCGTACCGAACTTCTGGAAGCGCACAGCCTTAAGTG CTCTGGTTGCAACCTCTGTGACAAGAGAAAGGATGTGAGGCCCCGCCAAAGGTGGC AAATCCCTGTTGTTTATCGATGTGCTGCTCTGCACAAAAGGAAGGCCATGATCGA AGGGAGCCTTTATGTCGAGAAGAATGAGACAGGCAATTGAGTATGCTTGATGATAG GCGTCGAAATGGACGTAGGTTGCGAGATCGCGCGGGGTGGTAATGAAACGGTA ATCAGTATCTTTGTCGTATGTTTCACGTGAGCGGACGTCCCTGCATTCTGTACGT CGAGCCAGGAGGCCAAGTAGTCATATAGTCGCGGTTGGGAGTCGCAAAGCGAA CGCGCTGGTCCATTTCGCATACCTCCGTATTGAATGAAACCTTCTTCTGGCTGGTGC ATTTTCCCGATACCCTGTGTACCGACAAGCAAGAACTGGGAGAGGTAGGGGCCCTA CCTGTTTACCAGGCATGTCGCCGCGGAAGACGTTTGATTTGTTGAAGGGCCGCG CAGACGTTGGATTTTACGCAATTTGTGAGATCGGATGGCGCTGCCGGGCTGCTCC TGAAACTGTACCCAGCGTGTACGACTAATCGATGCGGCTGCGGCAGCAACTGTTT CGTTTCGATGAAATTCTGAGAAGGGCACGTGCGCAAGAAGGGCCATCCAATAGCA TTCTGTGATCTCTGTCAAGAGCTCTTCGCTGTGATTTTAGGTGCAGGAGGCATGG TGACTGCCTGTGCATCAGGCCCTTCGAGATCGAAGGTATTGCCTGCGGCCATGGA TTCCCAGGCGCGAGTGTGAGCGATGGGGAGGTGAGTGTGCTGGGGATGCGATGCC GGAGATGAAACGAGGTGTTTCATCAATACCTAGGCGGAGGCTCCTGATGTCTTCC TGTGCGCCTGTGTTGATAGCACGCACAAAGGCAGTGAAGTCATCTGTAGATGAGA GAAGGCCTGTCTTTTGTGCTGTGGTAAACCCTTTGTGTAGGATGCGATGTATGAA TCTGAGAAACGGGTCTCATCGCCATTGGGGGTGTGGGTAGGGAGTTTTCGGGAG GCTGCTAGTTTTGCGGCATCTGTGCGTACTTGTAGTGCAGGCTGCTTGACGTGTGG TAGACAT
60	<i>Asparagopsis armata</i> Ireland – Mbb1_like coding sequence	TTAAATGCGAATTGTGCTTCCATCAAACCTTGTGAGGGTCATCGAGAAATTCTCACT GAAGGTCAACTTCTGTTCTGAAGAATGCCAATAGCAATTTCTCACCATGCGGA TACTTTCAATGTAGTCAGTGAAGTAATGCACACCAGCCAGTTACGTCCAATGGAA ATATTAGAGCAAATCTTGTTCAGCTCTCCGTCAAAGTGTGAGCGGCTCAGACACTTC AACCGGCTCGAGGCGCGAGCCATTTTCGTTAGTGACGTATGCAAACGGCAGGGG GAATCCACCATCAAAGAATGCCTTGAGAACAGTTACACAGGCTCCTGCAACAGTG GCATGTCCAGCACCATAAGCCGGATGCATCGGGCTTCCCTCTGGGAATGCCATTG GCATGAGAAGGTTGCCTTCGCTCAGGCCGCCATCAGGATTGAAATCTGCACTACG CGGAGCACCGTTGTGCTCAACTTATTTTGCTTCTTGTATGGTAATACACTCGATC CAACAGGTCAGAAATCAGGGAATCTACCAATTTAGCAGCTCCGAAAATTCGGGT GCTTTGGTTTTGTAGTATCGGTGACACGACCGCCGACAGTCTCCGGCGTAGAC GGCGATGGACGTTGAACTTCTGGAAGCGCACTGCCTTGAGAGCGCGAGTGGCCA CCTCAGTAACGAGAGAGAGAATATGCGGTCCGCCAAACGTGGCAAATGCCTGCTG CTTATCTATATCATTGTGAGCTGGAACGGGACTCCGGAATCGAACGGTGCACCA ATGTGAGCAGAAATGATGCAGGCGTTAAGATAGGCCTGGTACAGAGCGTCAAAAT GGACGTATGTGCGCAGATCACGCGGTGTGTGAATGAAGCGGAAACCAGGGTCTG ACTCGTATCGCTCACGCCCGGTGACATCCGACGCTTCTGCAGTCAAGCCAGGA TCCAAAGGTGGTCATGTAGTCAACCTTGGGGGATGCCACGCGTACCCGCTGGTCC ATGCGCATACCACCGTACTGGATGAAACCATCGCTGACCTCGTTTCCGTTTTCGAT TCCTGTGGTACCGACCAAGAGGAACTGGGACAAATATGGGCCTACATCATCTCCA GGAGTGATGCCCCTGAAGACATTGGAGGCATCGATGGGGCCTCTGAGACGGGAG CGTTCCGGCAGATGTGAGATGGGTGGGAGGGTTTTCTTGAATTTAATCCATTGAGT GTCGTTGATACTCTTGGCAGCGGCTGCGACATCTTCGTCGCAATGGAATGTTGGG AAGGGTACATCCCTGAGCAGGGACATCCAATAACATTCCGTGACTTCAGTGACCA ACTCCTCGCTGTCTAGCTCTGGTGCGGGCGGCATAGTGACGCTTGTCATCAG GCCCTTCGAGATCGAATGTGCGTCCAGCACCCATACTTTCCAGGCACGAACTCC CGACTGCTCTGGGTTTGTGGCGATGCCGGATGTGAATCTGGGGGTGACATTCTGG GGGCCGAGTGGGAGAGCTGCGAAATCGCGGGCATCTCCGCTGTCAATAGCGCGT ACAAATTGGTCATAATCGAGGGCAGATTGAACCAGACCTGTTTCGTTGATATGGGG GAGACCTTTTCGTGAAGTTAGCCAAGAGAGATCGTGTACCATCTGGGTTTCTGAAGC GAGCCTCTGAATTGTTGGAGATGTGAGTTGGAGAACCACGGGAGCGAGCAAGCTC GGCGGCAGAGAGGCGAATCTTGAAGGAGGCCCTGCGCGATTGGGATTCTGTGT GTCGGGGGTTGCCAT

61	<i>Asparagopsis armata</i> Ireland – Mbb2-2_like coding sequence	ATGAACACAGCATTTCCTTCAGAAAGAAAATGGTCCCCAAGTCTTTGGAGTGCTCG CCTCGAGTCCTATCTCTCCACTCACGCCCTTCGAGCTTCTCACAGTTATCACATACA TAACTGCACTCTCTCATGTTTCGTATGGGGAGCTCACGATGAGTCCACAATCAA TCTCCCGACACAAATCTCCGCTGGTACATTTCTATTGCTCGCGGAGCAGGTTACAC ACTCAACCTCAACACAGCACTTGTCACTTCTACTTGCATCTCGCCTCTTCTTACATT CATCCGTGATACTCCCCTGCACAAGATTCTTCTGTTGACAAAAGCTTCCCCGCCT TCCATATCCTTGTGGATATACGATAGCCGCATCTCTTTCATTATGTCCCGTTCC ATTTACATGGATCATTGCTTACGATAAATGGAGTGCAGGACTTTGGGATTTCCACC ATGAGCGCTGTCACAGGCGTCGTATTGTTACTTATCTTCATAATCATGTTTCATGTT GCTCTACCATTCTACAGAAAAAATATTTCCGGCTCTTCTACATTTCCCATGTTT GGAGCACTGCTGTTCTTCTCTCTCATCTTCCATGGTATGTACCGTCGTGTTCC GGAGACTTACAAGTGGGTTGCTCTACCTCTCGTGATCTACATTCTGGACAGAATCG CCCGTCGCTTCAAAATCTCCACCGTTCAGCTGAAGCTCACTTCCGAGCATTGAGCT CTCAAAGGAAAAGACATTTTGAACCTCGTATTCGAAACCCCTTACATATCGCGC TGGTCAGTATGCAGAGATCCGTGTACCATCCTTGAGTAGGAGTTGGCATCCGCTT ACAATTGCTAGTGCACCCCATGAAAAATGCATGTGCTTTTTTTCATCAAATCACTCGG GAATTGGACCAAGGAGCTTCGAGGGGCATTTCAAACCGTATGGAAGGAGAAGAT CCGAACCCATTGCTAGTTCAAGTCCGTGGTCCATTTGGCGCTCCCGCTCAACATGT CTCTTCGTATGAAAGAGTGGTCCATATCTGGCGGAGTTGTTCAACGCCCTTCCG CAGCCATCTCCAAAAGTTTGCATTTCTTGAACAAGAACAAAACCTGCCCTTCTACTG ATTTTTCGAAAACCAATTTGTCTGAAATGAAGCATATTGAGCAGCGTATCTCGGAAA CTATTTCTGCTGTATATGATATCGATTGCGAAACAGCTCCGATGAACCGGAATCT GAAGAACAAGGAAGCAGTATATTACTGACATGATGAACCTTGACGGCCCAAAATTC CGAAGAACTCGATGTTTCCACTTCAAGAACAAGTGAACAATGTGTATCATCGAGGA GCTGCCCAAAATATTGGAGATGGTCTCCGGATATTGGATGTGCAAAATCAATTAGAA GAATCTTCAGTGAGCAGCATGTCTACATGCGACGATGAAGAAGATTATTCATCAGA TTTCAGTGAAGAAATGAGACTTGAAAAGGAACTTGCCGCCAGGAAACGTAAGATG GCTCGCCAAAAAATTGCCGTCTCTATGAGAGACGTTCAATATTATTCTCTTTTCTT CATACCACTCGGGTAACTCTGGCACTTCAACTCTCTCTAATTGCACGCATTGTTCTT GTGTGCATTGTATCAATCTTCAACATTGGTGAATTCAACTTTGGGGACAGCCGCAT AGGTGCCAAATGGGTTATAGGTGCCGATGCAGTGTGAGTGTGTTTGCATGCAGTC ACTCTAACTTTGACCATACTCTTGGAAATTAGCTTCATGGGACCCCGCTTCTTCCGT TCTTCTTGGCAGTTTATGGACTTTTTCGTTTTCGTCCCGCTCAGTATTCTGTGCAGC GTCAGTGGTGTACTATCTTGGACTGGGACGGAAATGTCAGGAACATTAGTTTTTCT TCACTTCATTGTATTGCTGCCAATTATGCTTATTTTCATGAGTGCTCGTCTGTATCG GAGTATTGGGTCCCTGAATCTATTTTCATGATCGGAAGTGAACCGTACCGCAT GCGGAAAGAAAATCCCAGACGTTGACTTTATCTGGACAACACGTCACACCGTAGAT GACCAATGGTTACGAGAAGAATCTTCTCTAGAGGACGGCACAAAACCTCCGTCT TCACCGATATATTACAGGCAAGGAAAGTGAAGACTTTGAAAGTGCTGAGACCTTTA TACTACAAGCAACATTGGAAGACCGCCCTGGGACGAAATATTCGCCAAAATTGCC CAAAAGTCACCAAGTCACGCAGAAATCGGAGTGTGTTTCTGCGGACCACACTCAAT GGGAGCAGCTGTGAGGAAAAGCATGCGAAAAACTGAAATACGGAGTAACTTGCCT GGGGCATATCTGGAGACAATAATGTTGTCGATCTTGTGCGGATCTTCTTCTGAG AAATACTGACCATGCAGCAGAGCTTCGGAGGCATGGGTGCAATATTCGATTTGTAT TTCGTGAAGAGAATTCGGTTGA
62	<i>Asparagopsis armata</i> Ireland – Mbb2-3_like coding sequence	CTAACTAAAGTTTTCTCTCGAAAGACAAACCGAATATTGCATCCGTGTTCTCTCAA TAACTTAACCTCCTTTTCATCCCTCAATGACAAGTCTTCCACTAACAATTCAGTGTC AGTCTTTTCGAAATACGATCCTCGGAGGTTGCTCATCACTTCAACTTTCTCATACT CTTCTGAAGTGTGACCCCATAGGATGTGGCCCGCAGAAGAACTCCAACCTTCAT TGTGGCTAGGAGTTTGTTCGGCAATTTGTGCGAAAATCTCATCCCACTGAGGCCGT CCAGTATTTCGAGTAGTGATGAAATGTTCAAGTTCTTCCAGGTCCAAGTCTTTTTC ACGTGTTACATATCGGTGCAATCGTAGATCAGTTCCTGTGGCCAGCGGGTACAGC TCACTCCGCAGCCACTCATCCTCACTATCACGAGGAGTAGTCCATACAAAGTCAAC GTCTGGAATAGTTTTGTACAGGTGCAACTCTGACGACATTGTGTGTCATCCAAAA GGTTGCGTGCGCCAATACTTCGGTACAGGCGATGGCAAAGCAAGAGGAACATGAT TGGAACGACAATAATCAAGTCCAGAAAAATAAGAAATTTCTGCTTGTGACGTCCAC TCCAACCTCATGAAATGCTGATATTACAGAGAAAGGTAATAGGGAGAAAGATAAAG AAGTCGACGCAACGCCAACCCTGTGAGAAGAAGCGCAGTCGATGAACTGATTT CCAGTAGAACGGTAGTCAACAGCGCAATCCCGAGTACGAGTCCCAATAAGGAATT AGTGGCAATGACCCATTCCGGCATCAATATGACTGTCACTGATTCCAATATGCCCAA GATTGAAAATAGATACAACGCACAAAAATAACAATTCTTGCAACCAGAGTGAGAAGA AGAGCAAATGTGAATCTTGTGTATGCAGAAAAGCGAGCAGTCTTGAGCGGTACTC ATAGAAATTGAAAATCCTCCGCTGCGCAACATTGAAGACGTTGGCTGAAGGTGCGAT TATAATATCGAATAGATTGAGAACATGCATCAAGATTATAACTGCTTTGCTTCTCTT CTGAGACAGCGATATTTCTCATCCGCTGATCTGCTTGTGTTATTTCTCAACCGA ACTGCAATCATCAGACGCTTTTGATAGATTGCGTTTTAAAGAAACGTTATGGACGTT

		TCCCTTTGGAGACATATTGAGCATATCGGCGCACTTGTGTATTCCGCTGTTGGTTCCG ATGCAGCATCACTGCGGCTATCATCCAGACATACATCGAAGAGATTGGAAATGGCA TCACGGATGTGCCAATGAATTTGAGACTGTCTTTTCGAAGATCCATGTGATTCCAA AGCTTTTCGAATGGTTTTGAGACTTGTGTGAGATGGTGTAGGTTTTTGCAGATTGCTG CGAAAGGTGTTGAACCGACCCCTCCGGAGATAAGAACGACGCGACGATATCCTCT CAGTGCTGGGCTGGAGCACCATATGGTCCGCGGATCTGGACTTTGAGCGGTTCA TATAGGTCATTCTCAATTCGAGCTTCGAACGCATCTCGAAGATGTCTAGTCCAATC ACCAATCGCCTTGATGTAGAAGCACATAGATTTCTCATGAGGTGCACTTGCATTTG TAAAAGGATGCCACTCATTATTTATTGAAGGCACGCATACCTCTGCATATTGACCA GCACGGTATTTCGAACGTTTTTGGGACTCGCAGCTCCAGAATATCACTTCCCTTCAG GGAAGAGTGCTCACCAGTGAGTTCGAGCTTCGCTGTTGAAATCTTGAATCGTCTCA GAACCCTATCAATTGTGTAGATAGCGAGAGGTCCGGCAATCCATTTGTACGTTTCG GGGACTCTGTTGTACATGCCGTGAAAGATAAGCAGAGTGGAAGAATAGTAATGCAC CAACCATATGGATGAGGTAGAAGGTACGGAATTGCTTCTTCGAAATCTAGGAAGA GCAGAGACGAACATGACGACAAATACTGTGAGAAGAGCAAAACCTGTAGTGGCAC TCATAGTAAACCCCCACATGCCTAATTCCCATTATCATAGGCAATGATCCACACGA GATGGAAGGAAACATGTATGAAGAGTGCGGCTGCAATGGTGTAGGCCACGATGAT GTGGAAGCTGGGAAACTTTTGTGATTGGGAGGATGTGTTGCAGAGGAGTTTCA CGGATGTAGGTGCGGAAAAGTCCGGCGGCGGAGAAGGATGACGAGAGCGGTATTG AGATTGAGTGTGTATCCAGCACCACGGGCAATGCAGATGTACCATCGTAGATTTTT TTGCAAGTATGGTGATGAAATTCGTCATGGGCACCCAGACGAACATGAGAATGT TTGCGAGTAGTAGATGAAAAGTGCAGAAAGCGAGAATGCAATTTGTTGATAGATAG GATTCTAGGCGTGCGCTGAGGAGAGTGAGAGAGGTGGGAGAGCATCGTTGCTTG CCGGAGCGGGGAGCCAT
63	<i>Asparagopsis</i> <i>armata</i> Ireland – Mbb2_like coding sequence	ATGCCCTCTCCATCCTCATCCACATGTCCAAAGTCCACTCAAGATCTCCTCACCGC TCGACTCGAGTCCCACCTCTCCACACATGCCTTCGAACTTCTCGCTCTCGTCGTGT ATGCCACCGCACTCCTCCTCATGTTTCTATGGGGAGCCCATGACGAATCCATCAC CACACTTCCGATGATAAACATGCGATGGTACATCTCCATCGCCCGCGCAGCAGGTT ACACCTTAAATCTCAATACTGATTGGTCATTCTTCTCGCTGCCAGAACTCTTTCAA CTTATATTTCGCGAGACCCCATTTGCATCTAATCATTTCTCTTTCGAGAAAGCTTCCAG CCTTCCATATTATTGTCGCTTACGCTATTGCCATCTCCCTCGTCTCCATGTCGCTT TCCATTTTCGCGTGATTATTGCCCTACGATAAATGGGAACCAGGCCTTTGGGGATAC ACTATGAGCGCATCGACAGGATCTGTCTCCTCATTGTGTTTCTAGTCATGTTTCATA ACTGCCCTCCCAACATTTTCGGAAGAAACGCTTCCGATTCTTCTATCTCACACATAT GTTTCGGAGTGATACTCTTCTTCCCTCTACTAATCTTTTCATGGAATGTACAACCGCGT TCCAGGAACTTACAAATGGATCACCGCCCCACTCATCATCATATTATTGATAGACT TCTTCGTCGTTTTCAAAGTGTCACAGTTCCCTTTCGAGCTCACCAGCGATCATTCTT CTCTCAAGAGTGCTGACATTCTCGAACTCCGAGTCCCAAAGCCCTTCCATTACAGA GCGGGGCAATATGCAGAGGTCTGTGTCCCTTCGATCAGTTTCAGAGTGGCATCCAT TCACAATCGCAAGCGCACCCACGAAGAAACCATGACCTTCTTCATCAAAACTCTT GGCAATTGGACTCAAGCACTGCGCCACCAATTCCAAACACGCATGGATTTCAGACG ACTGCAAACCACTTACGGTACAGATCCGCGGACCGTACGGCGCTCCCGCTCAGCA CGTCGGCAGATATCAACGGGTAGTGTGGTGTGTCAGGAGGTGTTGGCGCCACCCCT TTTGCGGCCATCTCGAAACATCTGCACCACCTGAATGTCGCTGCAACATCACAAAA GACGCTCGATGTTGACATTCCATCTAAGCATACAATACTCGGGAACCGGATCA GAGAAACGATCTCCAATATGTACGGCTTGGGGTTGGGTGAAAGCGGCTGCGCAGA GGATTCCAACCAACAAAGAAGACAGCATCTGGCGGATATGCTGAACATGTCCCCG GATGGAGCGGTGCAGAAATTAGGAAATGAAATCTCTCATCCGTCTCCGACAGGCT CTTCTGATGTGAGTGATACGTGCAGTTCGGAATGTCGATCTCTCGTTTTTCATCA AGTATTGGGAGTCAAATGGCCACGCTGGGAACATACGAGAAGAGTGCAGCTCTA GAAAAGCGGGAGAGAAAGATATGCTGGGCGCATCGCTAGATCGAAGAATAATTT GATGTTTTCTTAAGGGAAAGCGCTCTAGACTTCTTCTTCTTCTCACACGACTCGAAT AACATTGCTGCTGCTGTTCCACACTAATTGCGCGATTAGTGCTGACGTGTGTTGTAT CTATCTTCGATCTTGGTCATTTTCAGCACAACCAGCGGACACATAGAGGCTAAGTGG GTTATCGTGACAAACGTCGTTCTGGGACTAATTGTTGGATTGACTCTATTACAATA ATTGTGCTGGAAGTGAGTTTTATGGGGACGCGATTCTTCCACAGGAATTGGCGAT GCGTTGACTTTTTTGGTGTTTCGTTCTCTGTCATTTCTGTGCAATCTATACGGAATTG TAACGTGGCTGGACGAGACCAATCGTCTTCTGACATTTCTGACTATATTATT ATCACACCGATTATCTTCTACTTCTCTGTATCGATTATACCGAAGCATTGGGACG CGAAACCTTTTCGACGATAACGGGAGTTGCCGGGGGTGAGAACACAGCGTTCCGG AAGTGGACTTTATCTGGACGGTCGCGCACGAGGGGGACGACGAGTGGCTTCGCG AAGATCTGTACACGCTTGCAGCGGGGACGGAGCTGCGACTGCATCGGTACGTGA CACGGGAGAAGGAAGTGGAGGTGGAGGGAGGGGAGGAGTTATCACATCTGCTA GGGCGGGGGCGTCCGAAGTGGGATGAAATATTTTTGAAGATCGCGGAGGAGTCCG GGAGCTGCAGTGAGATCGGGGTGTTCTTCTGTGGACCCAGTGGGATGGGAAGC AGGTTTCGGGAGAGTTTTGCGGCGGGCGGAAGTTTTTCAGTAGTTTGGGGGATCATA

		CTTGAGGAAAACGGGTGGAGGGGAGGTTGGGGACGAGGTAAGATTACTGAAGCG GTTTGAAGCAATGTTTCGATTCTGATTTTCGGGAGGAGAACTTTAGCTGA
64	<i>Asparagopsis armata</i> Ireland – Mbb3_like coding sequence	ATGCCTCCCCAACTCGTCGTCAATCCGCTCTCGTCACTCGCATTGCAGCTGCAG ATGAAGCCGCAAAACCGTTCACATCCTCCTCATCTAAGAAATGGCGATGAGACGCT GTACAAGACTACCTCAAATGCTCTCTCCTACCTCGCGACCTTCACAAAGGGTCTCC CTCATCATCCCCGACGGTCTGTCTAGTCTCCGCACAGCATTTTCAACTCTTCGCCCCG GCTGTCCAAACAGGAATCCACAGCACATTGCAGATATCCCCTCGACCTCCATC CACCTTTTCCACATTCCGCTCCGGAATTGCAAAGGATGCCCCACTCCGCGCTTGG GAATCCATGGCCGCTGGAAATACATTGACCTTCAAGGGCCTGATCCCCAATCAG TCACAATACCCCCATGTCCACGTCTCGAATCCAATGAGCTCGTCACAGAGATGACA GAGCTTTACTACATGGCACTCCTCAGGGATGTCCATTCTCTCATTTCAAAAGTCAT CACCTCGTCGCCGCTGCCGTCGACGATATCAATCACACCCATTGGATTCAATCCCA TAAATGTTGCATCCCAGAACTGGAACGTCACAGACACAGAGAACCCTTCTCATCCT CTAATGTCTTCCGTGGCACCACACAGGCGAGCGCAATGGTCCTTACATCTCACA ATTCCTCATTGTTGGAACCAAGGGCTCGGAGAAATCCAGGCAGTCCGCTTTCC TACATCCAATACGGTGCCATCCGAATCGATCAGAGAGTTTCGATCAGTCGAGACAG AAATCGACTACATGACCACCTGGGCGCGCTTCCCTTGACGTCCAGAATGCCGCAGA TTTGCGCAGACATTCTACATATGCCAAATCAAGCTCCTATCGCTTCCCTGTACACAC CACGCGACCTCGCTACCTACGTTTCATCATGACTCGCTCTACCAAGCCTATCTCAAC GCATGCATCATCCTCCTCGACATGAAAGTCCCATTGCACTCCGGTCTCCCCCTTAC CACGGAAGACCACATCGACAAACAACAGGGCTTTGTAACCTTTGGAGGCCCCCAT ATCCTCACACTCGTCACAGAGGTTGCTACCCGAGCCCTCAAGGCAGTCCGCTTTCC AAAAATACGCCGTCCACAGACGTCTTCGCCAGAGGCTGTGGCGGCCTCTTAGA ACAATACAGACGATACGGTGGCGGATATTAGAGCTAGCAAATACTATTCGTCCCA TACGCCATCTCGCCCGTTCTCTAAGTTCAAACCTCATGTGCTCGTCGCAGCAGC GAACGGCCATCAGAACGCAACAATGAGCGACAACGGATTTCCACGCTCCCATGAT ACAGGCTCCGGTGAGACTCATTTGCTGCCAATGGCCTATCCGGAGGGAAGTCCGA TGCACCCTAGCTATGGTGCCGGGCATGCCACAGTGGCCGGGGCGGTGCGTAACGA TATTGAAAGGCTTTTTTCGATCACACCTACAAGCTCCCGTTCCGCTATGTCTCATCCT GCAATGGGAAGATGCTGAAGAAGGCAAAGGTGCGGAAGAACTTTTCGGTGGAAAG GAGAGCTGAATAAACTGGCGTCTAATATCAGTATTGGACGTAGCTGGGCTGGCGT ACACTACTACTCCGACTATGTGGAGAGTATTGATTGGGAGAGGAAGTGGCGATT GGAATCCTGAAAGAGCAAAAGTTAACTTATTCGGAATAATTCTCAATGACAATTCCC AAATTTGATGGCACAACCATCAAAATATAG
65	<i>Asparagopsis armata</i> Ireland – Mbb4-2_like coding sequence	TTACTTTGAGTTTGAAATCTTGATAGTCGTACCATCAAACCTTGGGAATAGTCATGGA GAACTCCTCACCCTACGTCAGACTCTGTTCTTCTAGAATACCAATTGCAACCTCTTC ACCCAACCTTGCCTCTCTATGTAAATCCGAGTAATAGTGACACACAGCCCAATTCC TACCAATACTGATGTTGGCACAAGCTTGTGAGCTCATGCTCCACTGTGAGCGGT TCATTGATTTCCACCTCCTCAAGATTCTGGCCGTCTGTGCTGGGCACATAACAGAA TTCAAGCTCGTGAGTGTGGTCTGAAGAAGCCTTTAGGATCGTCACACATGCACCC GCAACAGCAGCATGCCCTGCACCATAGCTGGGATGCATTGGGCTACCCTCCGGG AATGCCATCGGGAGAAGATAAGTTTCTGCGCTTTCGCAGCCCTCAGGATTATAATC GCCGCTTTCGGGCACCACCGTTGTGCGAAAGTTTATTCTGCGCGCGCTTGTGCTGC GAGATTCTGTGTCATAAGGTCATTGTGCTCATCTCAGTGGCGATTTTCTGATGGGCTC AAAGGGCTCTGCTCCCTCCGTCTTTCGGTATCGCTCGATAAGACCGCCGACAGCC TCGGGGCGTAGACGGCGGTGGGTACCAAACCTTCTGGAAGCGCACAGCCTTCAAT GCCCTAGTTGCGACCTCTGTGACAAGCGAGAGGATATGGGGACCTCCAAAGGTAG CGAATCCCTGTTGTTTATCGATGTCATCATCTTCCACAAAAGGGATTTCTGGATCGA AAGGGGCCTTGGTGTGAGAGAAGATGAGACATGCGTTTCAGGTATGCCTGGTAAAG TGCATCGAAATGGACGTAGGTGGCAAGATCGCGCGGTGTAGTAATGAAACGGAAT GGAGTGTGTTGTGCTACGTTTACGTCCTCGTACATCACCTGCGTTCTGCACGTC GAGCCAGGATGCCAGGTGGTCATGTAGTCCCTATTTGGGGTTGCCACACGAACA CGTTGGTCCATACGCATACCTCCGTATTGAATGAATCCATCTGAAATTTCTGAATG TTCGCGATACCCTTTGTGCCAACGAGAAGGAACTGAGAGAGATAGGGACCGATTT GTTACCAGGGGTACGCGCGGGAAGATGTTTGTTCCTGAATGGACCTCGCAA ACGTGCAATTTCTGCATCAGACAGATCGCAGGGGGCGTTGCCCGGGCTGCTCTTGG AACTGCACCCAGCGCGTTTCGGCTGATCGAAGCGGCTGCGGCAGCGGTAGTGCCA TCCCTTTGAACTCTGTGAACGGGACGTCGGAAGAAGGCCATCCAGTAGCACT CGGTGATCTCCGTCAAGAGTTCTTCACTATCGATTTTTGGGGCAGCGGCATGCT GACTGCCTGAGCGTCCGGTCCCTCCAGATCGTATGTATTACCAGCTGCCATGGAT TCCCACGCTCTAGTGTGCGCTATGGGATGGTCGGAGCCCTCTGAAGCGATGGCG GATATGAAACGGGGGTCTTCATCGATACCTAGGGGGAGACTTGTAAATATCTTCTTG AGCGCCTGTTTCGATGGCGCGTACAAAGGCTGCGAAGTGATCTGGAGAGGAGGA GAGGCCGGTATCCTTTTCGTGTGGAAGACCTTTCGTGTAGGAGGCGAGGTGGGTG TCGTGGTAGCGATGCTCATCGCCGTTTGAAGGTGGGTGGGGAGGGGGCGTGAA

		GCAGCGAGATCTGCGGCTTCACTACGGACTCTCAAGGCGGATGCATGGCGTTCTT CGGACAT
66	<i>Asparagopsis armata</i> Ireland – Mbb4_like coding sequence	TCAGTTGGAGATCGTAATGCACGTTCCATCAAACCTTGGGGAGGGTCATGGAGAAC TTCTCACCATACGTCAAGCTCTGTTCTTGCAAAATACCGATGGCAACCTCTTCACC CAACTTTGCACTCTCTTCGTAATCCGAGTAGTAGTGACACCCGGCCAGTTTCTTC CAATACTGATGTTGGCACACAACCTTGTTTCAGCTCGTGTTCAACTGTGAGCGGTTCA CTGATGTTAACCTTCTCTAGCTTCCCTGCCGTCTGTGCTGGGTTCAAAGCAGAACCT TAACCTGTATTGTGATCAAAGAAGGCCCTTGAGGATCGTGACACAGCGCCAGCG ACAGCGGCGGTGTCCAGCACCGTAGCTGGGATGCATTGGGCTTCCCTCCGGGAAC GCCATTGGAAGAAGGTAGGTTTTCTGCGCTTGCGCCACCCTCGGGGTTGAAATCAT TTCTTCGTGCTTTACCGTTGTGCGAAAACCTCATTCTGCTTGGCGTTGTGACGCGAG ATGCGCGTCATAAGCTCATTGTGCGATCTCGGTAGCGAGCTTCTTAGCGGCTGCGA ATGGCGCTGCGCCGTTCTGTTGCGGTAGCGCTCGATGAGTCCGCCGACAGCTT CGGGGCGTAGGCGACGATGCGTACCGAACTTCTGGAAGCGCACGCCCTTAAGTG CTCTGGTTGCAACCTCTGTGACAAGAGAAAGGATGTGAGGCCGCCAAAGGTTGGC AAATCCCTGTTGTTTATCGATGTGCTGCTCCTGCACAAAAGGAAGGCCATGATCGA AGGGAGCCTTTATGTGAGAAGAATGAGACAGGCATTGAGGTATGCTTGATAGAG GGCGTCGAAATGGACGTAGGTTGCGAGATCGCGCGGGGTGGTAATGAAACGGTA ATCAGTATCTTTGTGCGATGTTTCACGTGAGCGGACGTCCCTGCATTCTGTACGT CGAGCCAGGAGGCCCAAGTAGTCATATAGTCGCGGTTGGGAGTCGCAAAGCGAA CGCGCTGGTCCATTTCGCATACCTCCGTATTGAATGAAACCTTCTTCTGGCTGGTGC ATTTTCCCGATACCCTGTGTACCGACAAGCAAGAACTGGAGAGGTAGGGGCTTA CCTGTTACACAGGCATGTCGCGCGGGAAGACGTTTGATTGTTGAAGGGGCCGCG CAGACGTTGGATTTACGATTTGTGAGATCGGATGGGCGCTGGCCGGGCTGCTCC TGAAACTGTACCCAGCGGTGACGACTAATCGATGCGGCTGCGGCAGCAACTGTTT CGTTTCGATGAAATTCTGAGAAGGGCACGTGCGCAAGAAGGGCCATCCAATAGCA TTCTGTGATCTCTGTCAAGAGCTCTTCGCTGTCGATTTTAGGTGCAGGAGGCATGG TGACTGCCTGTGCATCAGGCCCTTCGAGATCGAAGGTATTGCCTGCGGCCATGGA TTCCAGGCGCGAGTGTGACGCGATGGGGAGGTCGAGTGCTGGGGATGCGATGCC GGAGATGAAACGAGGTGTTTCATCAATACCTAGGCGGAGGCTCCTGATGCTTCC TGTGCGCCTGTGTTGATAGCACGCACAAAGGCAGTGAAGTCATCTGTAGATGAGA GAAGGCCTGTCTTTTGTGCTGTGGTAAACCCTTTGTGTAGGATGCGATGTATGAA TCTGAGAAACGGGTCTCATCGCCATTGGGGGTGTGGGTAGGGAGTTTGCGGGAG GCTGCTAGTTTTGCGGCATCTGTGCGTACTTGTAGTGCGGCTGCTTGACGTGTGG TAGACAT
67	<i>Asparagopsis armata</i> Ireland 2 – Mbb1_like coding sequence	ATGGCAACCCCCGACACACAGAATCCCAATCGCGCAGAGGCCTCCTTCAAGATTG GCCTCTCTGCCGCCGAGCTTGCTGCTCCCGTGGTTCTCCAACTCACATCTCCAA CAATTCAGAGGCTCGCTTCAGAAACCCAGATGGTACACGATCTCTCTTGCTAACT TCACGAAAGGTCTCCCCCAGATCAACGAAACAGGTCTGGTTCAATCTGCCCTCGAT TATGACCAATTTGTACGCGCTATTGACAGCGGAGATGCCCGCGATTTGCGAGCTCT CCCCTCGGCCCCCCAGAATGTACCCCCAGATTACATCCGGCATCGCCACAAAC CCAGAGCAGTCGGGAGTTCTGTGCTGGGAAAGTATGGGTGCTGGACGCACATTC GATCTCGAAGGGCCTGATGCACAGGCCGTCACTATGCCGCCGACACAGAGCTA GACAGCGAGGAGTTGGTCACTGAAGTCACCGAATGTTATTGGATGTCCCTGCTCA GGGATGTACCTTCCCAACATTCCATTGCGACGAAGATGTCGACAGCCGCTGCCAA GAGTATCAACGACACTCAATGGATTAAATTCAAGGAAAACCTCCACCCATCTCA CATCTGCCGAACGCTCCCGTCTCAGAGGCCCATCGATGCCTCCAATGTCGTCAG GGGCATCACTCCTGGAGATGATGTAGGCCCATATTTGTCCAGTTCTCTTGGTGG GTACCACAGGAATCGCAAACGGAACGAGGTGACGCGATGGTTTCATCCAGTACGG TGGTATGCGCATGGACCAGCGGGTACGCGTGGCATCCCCAAGGTTGACTACATG ACCACCTTTGGATCCTGGCTTGACGTGCAGAACGCTGCGGATGTACCGGGGCGTG AGCGATACGAGTCAGACCCTGGTTTCCGCTTCATTACACACCCGCGTGATCTGGC GACATACGTCCATTTGACGCTCTGTACCAGGCCTATCTTAACGCCTGCATCATT TGCTCGACATTGGTGCACCGTTGATTCCGGAGTCCCGTTCCAGCTCGACAATGA TATAGATAAGCAGCAGGCATTTGCCACGTTTGGCGGACCGCATATTCTCTCTCG TTACTGAGGTGGCCACTCGCGCTCTCAAGGCAGTGCGCTTCCAGAAGTTCAACGT CCATCGCCGTCTACGCCCGGAGACTGTCGGCGGTCGTGTGACCGGATACTACAAA ACCAAAGCACCCGAATTTTCCGGAGCTGCTAAATTGGTAGATTCCCTGGATTGGA CCTGTTGGATCGAGTGATTACCATAACAAGAAGCAAAATAAGTTGAGCGACAACG GTGCTCCGCGTAGTGACGATTTCAATCCTGATGGCGGCCTGAGCGAAGGCAACCT TCTCATGCCAATGGCATTCCCAGAGGGAAGCCCGATGCATCCGGCTTATGGTGCT GGACATGCCACTGTTGCAGGAGCCTGTGTAACCTGTTCTCAAGGCATTCTTTGATGG TGGATTCCCCCTGCCGTTTGCATACGTCACTAACGAAAATGGCTGCGGCCTCGAG CCGGTTGAAGTGTCTGAGCCGCTCACAGTTGACGGAGAGCTGAACAAGATTGCT CTAATATTTCCATTGGACGTAACCTGGGCTGGTGTGATTACTTCACTGACTACATTG AAAGTATCCGCATTGGTGAGGAAATTGCTATTGGCATTCTTCAGGAACAGAAGTTG

		ACCTTCAGTGAGAATTTCTCGATGACCCTCAACAAGTTTGATGGAAGCACAATTGCG CATTTAA
68	<i>Asparagopsis armata</i> Ireland 2 – Mbb2-2_like coding sequence	ATGAACACAGCATTTCCCTTCAGAAGAAAATGGTCCCCAAGTCTTTGGAGTGCTCG CCTCGAGTCCTATCTCTCCACTCACGCCCTTCGAGCTTCTCACAGTTATCACATACA TAACTGCACTCTCTCTCATGTTTCGTATGGGGAGCTCACGATGAGTTCCACAATCAA TCTCCCGACACAAATCTCCGCTGGTACATTTCTATTGCTCGCGGAGCAGGTTACAC ACTCAACCTCAACACAGCACTTGTCATTCTACTTGCACTCTGCCTCTTCTTCACATT CATCCGTGATACTCCCCTGACACAAGATTCTTCTGTTGACAAAAGCTTCCCCGCCT TCCATATCCTTGTGGATATACGATAGCCGCATCTCTCTTCATTTCATGTCCCGTTCC ATTTACATGGATCATTGCTTACGATAAATGGAGTGCAGGACTTTGGGATTTACC ATGAGCGCTGTCACAGGCGTCGTATTGTTACTTATCTTCATAATCATGTTTCATGTT GCTCTACCATTCTACAGAAAAAATATTTCCGGCTCTTCTACATTTCCACATGGTT GGAGCACTGCTGTTCTTCTCTCTCATCTTCCATGGTATGTACCGTCGTGTTCC GGAGACTTACAAGTGGGTTGCTCTACCTCTCGTGATCTACATTCTGGACAGAATCG CCCGTCGCTTCAAAATCTCCACCGTTACAGCTGAAGCTCATCCGAGCTCCGAGCT CTCAAAGGAAAAGACATTTTGAACCTCGTATTCCGAAACCCTTCACATATCGCGC TGGTCAGTATGCAGAGATCCGTGTACCATCCTTGAGTAGGGAGTGGCATCCCTTC ACAATTGCTAGTGCACCCCATGAAAAATGCATGTGCTTTTTTCATCAATCACTCGG GAATTGGACCAAGGAGCTTCGAGGGGCATTTCAAACCGTATGGAAGGAGAAGAT CCGAACCCATTGCTAGTTCAAGTCCGTGGTCCATTTGGCGCTCCCGCTCAACATGT CTCTTCGTATGAAAGAGTGGTCCCTCATATCTGGCGGAGTTGGTTCAACGCCCTTCG CAGCCATCTCCAAAAGTTTGATTTCTTGAACAAGAACAACCTCCCTCTACTG ATTTTTCGAAAACCAATTTGTCTGAAATGAAGCATATTGAGCAGCGTATCTCGGAAA CTATTTCTGCTGTATATGATATCGATTTGGCAAACAGCTCCGATGAACCGGAATCT GAAGAACAAGGAAGCAGTATATTACTGACATGATGAACCTGACGGCCCAAAATTC CGAAGAAGCTGATGTTTCCACTTCAAGAACAAGTGAACAATGTGTATCATCGAGGA GCTGCCCAAAATATTGGAGATGGTCTCCGGATATTGGATGTGCAAAATCAATTAGAA GAATCTTCAGTGAGCAGCATGTCTACATGCGACGATGAAGAAGATTATTCATCAGA TTTCAGTGAAGAAATGAGACTTGAAAAGGAACTTGCCGCCAGGAAACGTAAGAT GCTCGCCAAAAAATTGCCGTCTCTATGAGAGACGTTCAATATTATTCTCTTTTCTT CATACCACTCGGGTAACTCTGGCACTTCAACTCTCTCTAATTGCACGCATTGTTCTT GTGTGCATTGTATCAATCTTCAACATTGGTGAATTCAACTTTGGGACAGCCGCAT AGGTGCCAAATGGGTTATAGGTGCCGATGCAGTGTTGAGTGTTTTGCATGCAGTC ACTCTAACTTTGACCATACTCTTGGAAATTAGCTTCATGGGACCCCGCTTCTTCCGT TCTTCTTGGCAGTTTATGGACTTTTTCTGTTTTCTGCCGCTCAGTATTCTGTGCAGC GTCAGTGGTGACTATCTTGGACTGGGACGGAAATGTCAGGAACATTAGTTTTCT TCACTTCATTGTATTGCTGCCAATTATGCTTATTTTCATGAGTCTCGTGTATCG GAGTATTGGGTCCCTGAATCTATTTTCATGATCGGAAGTGTAACCCAAACTGCGCAT GCGGAAAGAAAAATCCCAGACGTTGACTTTATCTGGACAACACGTCACACCGTAGAT GACCAATGGTTACGAGAAGAACTCTTTCCTCTAGAGGACGGCACAACAACTCCGTCT TCACCGATATATTACAGGCAAGGAAAGTGAAGACTTTGAAAGTGCTGAGACCTTTA TACTACAAGCAACATTGGAAGACCGCCCTGGGACGAAATATTCGCCAAAATTGCC CAAAAGTCACCAAGTCACGCAGAAATCGGAGTGTTTTCTGCGGACCACACTCAAT GGGAGCAGCTGTGAGGAAAAGCATGCGAAAAACTGAAATACGGAGTAACCTTCGT GGGGCATATCTGGAGACAATAATGTTGTGATCTTGTGCGGATCTTCTTCTGAG AAATACTGACCATGCAGCAGAGCTTCGGAGGCATGGGTGCAATATTGATTTGTAT TTCGTGAAGAGAAGCTTCGGTTGA
69	<i>Asparagopsis armata</i> Ireland 2 – Mbb2-3_like coding sequence	ATGGCTCCCCGCTCCGGCAAGCAACGATGCTCTCCACCTCTCTCACTCTCCTCA GCGCACGCCTAGAATCCTATCTATCAACAAATGCATTCTCGCTTCTCGCACTTTTCA TCTACTCACTCGCAAACATTCTCATGTTTCGTCTGGGGTGCCCATGACGAATTTCT CACCATACTTCTCAAAAAAATCTACGATGGTACATCTGCATTGCCCGTGCTGG ATACACACTCAATCTCAATACCGCTCTCGTCATCCTTCTCGCCGCCCGACTTTTCG CGACCTACATCCGTGAAACTCCTCTGCAACACATCCTCCCAATCGACAAAAGTTTC CCAGCTTTCCACATCATCGTGGCCTACACCATTGCAGCCGCACTCTTCATACATGT TTCTTCCATCTCGTGTGGATCATTGCCTATGATAAATGGGAATTAGGCATGTGGG GGTTTACTATGAGTGCCACTACAGGTTTTGCTCTTCTCACAGTATTTGTCGTATGT TCGTCTCTGCTCTTCTAGATTTGAAAGAAGCAATTCCTGACCTTCTACCTCATCC ATATGGTTGGTGCACTTACTATTCTCACTCTGCTTATCTTTCAGGCATGTACAACA GAGTCCCCGAAACGTACAAATGGATTGCCGGACCTCTCGCTATCTACACAATTGAT AGGGTTCTGAGACGATTCAAGATTTCAACAGCGAAGCTCGAACTCACTGGTGAGC ACTCTTCCCTGAAGGGAAGTGATATTCTGGAGCTGCGAGTCCCAAAAACGTTTCGAA TACCGTGCTGGTCAATATGCAGAGGTATGCGTGCCCTCAATAAATAATGAGTGGCA TCCTTTTACAATTGCAAGTGACCTCATGAGAAATCTATGTGCTTCTACATCAAGGC GATTGGTGATTGGACTAGACATCTTCGAGATGCGTTCGAAGCTCGAATTGAGAATG ACCTATATGAACCGCTCAAAGTCCAGATCCGCGGACCATATGGTGCTCCAGCCCA GCACGTGAGAGGATATCGTCCGCTCGTTCTTATCTCCGGAGGGGTCGGTTCAACA

		CCTTTTCGCAGCAATCTGCAAAAACCTACACCATCTCAACAAGTCTGAAAACCATTC GAAAGCTTTGGAATCACATGGATCTTCGAAAAGACAGTCTCAAATTCATTGGCACA TCCGTGATGCCATTTCCAATCTCTTCGATGTATGTCTGGATGATAGCCGCAGTGAT GCTGCATCGAACCACAGCGAATACAACAAGTCGCCGATATGCTCAATATGTCTCC AAAGGGAAACGTCCATAACGTTTCTTTTAAACGCAATCTATCAAAGACGTCTGATGA TTGCAGTTCGGTTGAAGAAATAACCAAGCAGATCAGAGCGGATGAGGAAATATCG CTGTCTCAGAAAGAGAAGCAAAGCAGTTATAATCTTGATGCATGTTCTGAATCTATT CGATATTATAATCGACCTTCAGCCAACGTCTTCAATGTTGCGCAGCGGAGGATTTT CAATTTCTATGAGTACCGCTCAAGACTGCTCGCTTTTCTGCATACAACAAGATTCAC ATTTGCTCTTCTTCTCACTCTGGTTGCAAGAATTGTTATTTTGTGCGTTGTATCTATT TTCAATCTTGGGCATATTGGAATCAGTGACAGTCATATTGATGCCGAATGGGTCAT TGCCACTAATTCCTTATTGGGACTCGTACTCGGGATTGCGCTGTTGACTACCGTTC TACTGGAAATCAGTTTCATGCGACTGCGCTTCTTCTACAGAGGTTGGCGTTGCGTC GACTTCTTTATCTTTCTCCCTATTACCTTTCTCTGTAATATCAGCAATTTATGAGTT GGAGTGGACGTCAACAAGCGAAATTTCTTATTTTCTGGAGTTGATTATTGTCTGTTT CAATCATGTTCTCTTGTCTTTGCCATCGCCTGTACCGAAGTATTGGCGCACGCAAC CTTTTGGATGACACACAATGTCGTGAGAGTTGCACCTGTAACAAAATCTTCCAGA CGTTGACTTTGTATGGACTACTCCTCGTGATAGTGAGGATGAGTGGCTGCGGAGT GAGCTGTACCCGCTGGCCACAGGAACCTGATCTACGATTGCACCGATATGTAACAC GTGAAAAGGACTTGGACCTGGAAGAACCTGAACATTTCACTACTGCGAATACT GGACGGCCTCAGTGGGATGAGATTTTCGCACAAATTGCCGAACAAATCCTAGCC ACAATGAAGTTGGAGTGTTCTTCTGCGGGCCACATCCTATGGGTGCAGCAGTTCA GAAGAGTATGAGGAAAGTTGAAGTGATGAGCAACCTCCGAGGATCGTATTTGCGA AAGACTGACAGTGAATTGTTAGTGAAGACTTGTATTGAGGGATGAAAAGGAGGT TAAGTTATTGAGAGAACACGGATGCAATATTCGGTTTGTCTTTTCGAGAGGAAAAT TTAGTTAG
70	<i>Asparagopsis armata</i> Ireland 2 – Mbb2_like coding sequence	ATGCCCTCTCCATCCTCATCCACATGTCCAAAGTCCACTCAAGATCTCCTCACCGC TCGACTCGAGTCCCACCTCTCCACACATGCCTTCGAACCTCTCGCTCTCGTCGTGT ATGCCACCGCACTCCTCCTCATGTTCCATATGGGGAGCCCATGACGAATTCATCAC CACACTTCCGATGATAACATGCGATGGTACATCTCCATCGCCCGCGCAGCAGGTT ACACCCTAAATCTCAATACTGCATTGGTCATTCTTCTCGCTGCCAGACTCTTTTCAA CTTATATTGCGGAGACCCCATTCATCTAATCATTCTCTTGACAAAAGCTTCCAG CCTTCCATATTATTGTCGCTTACGCTATTGCCATCTCCCTCGTCTCCATGTGCGCTT TCCATTTGCGGTGGATTATTGCCACGATAAATGGGAACAGGCCCTTTGGGGATAC ACTATGAGCGCATCGACAGGATCTGTCTCTCCTCATTGTGTTTCTAGTCATGTTTCATA ACTGCCCTCCCAACATTTTCGGAAGAACGCTTCGATTCTTCTATCTCACACATAT GTTGCGAGTGATACTCTTCTTCCCTCTACTAATCTTTTCATGGAATGTACAACCGCGT TCCAGAACTTACAAATGGATCACCGCCCCACTCATCATCTACATTATTGATAGACT TCTTCGTCGTTTCAAAGTGTCACAGTTCCCTTGACGCTCACCAGCGATCATTCTT CTCTCAAGAGTGCTGACATTCTCGAACTCCGAGTCCCAAAGCCCTTCCATTACAGA GCGGGGCAATATGCAGAGGTCTGTGTCCCTTCGATCAGTTTCAGAGTGGCATCCAT TCACAATCGCAAGCGCACCCACGAAGAAACCATGACCTTCTTCATCAAAACTCTT GGCAATTGGAATCAAGCACTGCGCCACCAATTCCAAACACGCATGGATTTCAGACG ACTGCAAAACCACTTACGGTACAGATCCGCGGACCGTACGGCGTCCCGCTCAGCA CGTCGGCAGATATCAACGGGTAGTGTTGGTGTGAGGAGGTGTTGGCGCCACCCCT TTTGCCGCCATCTCGAAACATCTGCACCACCTGAATGTGCTGAACATCACAAAAA GACGCTCGATGTTGACATTCCATCTAAGCATACAATACTCGGGAACCGGATCA GAGAAACGATCTCCAATATGTACGGCTTGGGGTTGGGTGAAAGCGGCTGCGCAGA GGATTCCAACCAACAAAGAAGACAGCATCTGGCGGATATGCTGAACATGTCCCCG GATGGAGCGGTGCAGAAATTAGGAAATGAAATCTCTCATCCGTCTCCGACAGGCT CTTCTGATGTGAGTGATACGTGCAAGTTCGGAATAATGTGATCTCTCGTTTTTCATCA AGTATTGGGAGTCAAATGGCCACGCTGGGAACATACGAGAAAGAGTGCAGCTCTA GAAAAGGCGGGAGAGAAGATAAGATGGGGCGATCTGCGTACTCGAAGCATAATTT GATGTTTCTGAATGGAAGCGCTCTAGACTTCTTTCTTACTTCACACGACTCGAAT AACATTGCTGCTGCTGTTTCACACTAATTGCGCGATTAGTGCTGACGTGTGTTGTAT CTATCTTCGATCTTGGTCATTTTACGACAACAGCGGACACATAGAGGGCTAAGTGG GTTATCGTGACAAACGTCGTTCTGGGACTAATTGTTGGATTGACTCTATTACAATA ATTGTGCTGGAAGTGAGTTTTATGGGGACGCGATTCTTCCACGAATTTGGCGAT GCGTTGACTTTTTTGGTGTTCGTTCTCTGTGCAATCTATACGGAATTG TAACGTGGGCTGGACGAGACCAATCGTCCTTCTGACATTTGTGACTATATTATT ATCACACCGATTATCTTCTACTTCTCTGTGATCGATTATACCGAAGCATTGGGACG CGAAACCTTTTCGACGATAACGGGAGTTGCCGGGGGTGAGAACACAGCGTTCCGG AAGTGGACTTTATCTGGACGTCGCGCACGAGGGGGACGACGAGTGGCTTCGCG AAGATCTGTACACGCTTGCACGGGGACGAGCTGCGACTGCATCGGTACGTGA CACGGGAGAAGGAAGTGAGGTGGAGGGAGGGGAGGATTTATCACATCTGCTA GGGCGGGGCGTCCGAAGTGGGATGAAATATTTTGAAGATCGCGGAGGAGTGC

		GGAGCTGCAGTGAGATCGGGGTGTTCTTCTGTGGACCCAGTGGGATGGGGAAGC AGGTTTCGGGAGAGTTTTCGGCGGGCGGAAGTTTTTCAGTAGTTTGAGGGGATCATA CTTGAGGAAAACGGGTGGAGGGGAGGTTGGGGACGAGGTAAGATTACTGAAGCG GTTTGGAAGCAATGTTTCGATTCTGATTTCGGGAGGAGAACTTTAGCTGA
71	<i>Asparagopsis armata</i> Ireland 2 – Mbb3_like coding sequence	CTATATTTTGATGGTTGTGCCATCAAATTTGGGAATTGTCATTGAGAATTTTTCCGA ATAAGTTAACTTTTGCTCTTTCAGGATTCCAATCGCCACTTCCTCTCCCAATCGAAT ACTCTCCACATAGTCGGAGTAGTAGTGTACGCCAGCCCAGCTACGTCCAATACTG ATATTAGACGCCAGTTTATTCAGCTCTCCTTCCACCGAAAAGTTTCTCGCGACCTTT GCCTTCTTCAGCATCTTCCATTGCAGGATGAGACATAGGCGAACGGGAGCTTGT AGGTGTGATCGAAAAAGCCTTTCAATATCGTTACGCACGCCCCGGCCACTGTGGC ATGCCCCGCCACCATAGCTAGGGTGCATCGGACTTCCCTCCGGATAGGCCATTGGC AGCAAATGAGTCTCACCGGAGCCTGTATCATGGGAGCGTGGAAATCCGTTGTCGC TCATTGTTGCGTTCTGATGGCCGTTCTGCTGCTGCGACGAGCGACATGAGGTTTGA ACTTAGAGAACGGGCGAGATGGCGTATGGGACGAATAGTATTTGCTAGCTCTGAA TATCCGCCACCGTATCGTCTGTATTGTTCTAAGAGGCCGCGACGACCTCTGGGC GAAGACGTCTGTGGACGGCGTATTTTTGGAAACGGACTGCCTTGAGGGCTCGGGT AGCAACCTCTGTGACGAGTGTGAGGATATGGGGGCCTCCAAAGTTTACAAAGCCC TGTTGTTTGTGATGTGGTCTTCCGTGGTGAAGGGGAGACCCGAGTCGAATGGGA CTTTCATGTCGAGGAGGATGATGCATGCGTTGAGATAGGCTTGGTAGAGCGAGTC ATGATGAACGTAGGTAGCGAGGTGCGGTGGTGTGTACAGGAAGCGATAGGAGCTT GATTTGGCATATGTAGAATGTCTGCGCAAATCTGCGGCATTCTGGACGTCAAGGAA GGCGGCCAGGTGGTCATGTAGTCGATTTCTGTCTCGACTGACTCGAACTCTCTGA TCGATTCCGATGGCACCCTATTGGATGTAGCCATCTGCCTCGTCTGATTTCTCC GAGCCCTTTGGTTCCAACAATGAGGAATTGTGAGATGTAAGGACCATTGCGCTCG CCTGGTGTGGTGCCACGGAAGACATTAGAGGATGAGAAGGGTTCTCTGTGTCTGT GACGTTCCAGTTCTGGGATGCAACATTTATGGGATTGAATCCAATGGGTGTGATTG ATATCGTCGACGGCAGCGGCGACGAGGTGATGACTTTTGAATGAGAGAATGGGA CATCCCTGAGGAGTGCCATGTAGTAAAGCTCTGTCTCTGTGACGAGCTCATTG GATTCGAGACGTGGACATGGGGTATTGTGACTGATTGGGGATCAGGCCCTTGAA GGTCGAATGTATTTCCAGCGGCCATGGATTCCCAAGCGCGGAGTGGGGCATCCTT TGCAATCCGGAGCGGAATGTGGAAAAGGTGGATGGAGGTCCGAGGGGAATATCT GCAATGTGCTGTGGAGTTCTGTTTGGACAGCACGGGCGAAGAGTTGAAAATGCT GTGCGGAGACTAGACGACCGTCGGGATGATGAGGGAGACCCTTTGTGAAGGTGCG CGAGGTAGGAGAGAGCATTTGAGGTAGTCTTGTACAGCGTCTCATCGCCATTTCTT AGATGAGGAGGATGTGAACGGTTTTCGGCTTCATCTGCAGCTGCAATGCGAGTGA CGAGAGCGGATTGACGACGAGTTGGGGGAGGCAT
72	<i>Asparagopsis armata</i> Ireland 2 – Mbb4-2_like coding sequence	TTACTTTGAGTTTGAAATCTTGATAGTCGTACCATCAAACCTTGGGAATAGTCATGGA GAACCTCTCACCCTACGTACGACTCTGTTCTTCTAGAATACCAATTGCAACCTCTTC ACCCAACCTTTCGCTCTCTATGTAATCCGAGTAATAGTGCACACCAGCCCAATTCC TACCAATACTGATGTTGGCACAAGCTTGTGAGCTCATGCTCCACTGTGAGCGGT TCATTGATTTCCACCTCTCAAGATTCTGGCCGTCTGTGCTGGGCACATAACAGAA TTCAAGCTCGTGAGTGTGGTCAAGAACGCCTTTAGGATCGTCACACATGCACCC GCAACAGCAGCATGCCCTGCACCATAGCTGGGATGCATTGGCTACCCCTCCGGG AATGCCATCGGGAGAAGATAAGTTTCTGCGCTTTCGACGCCCTCAGGATTATAATC GCCGCTTCGGGCACCACCGTTGTGCGAAAGTTTATTCTGCGCGCGCTTGTGCTGC GAGATTCTGTGCATAAGGTCATTGTGATCTCAGTGGCGATTTTCTGGATGGGCTC AAAGGGCTCTGCTCCCTCCGTCTTTCGGTATCGCTCGATAAGACCGCCGACAGCC TCGGGGCGTAGACGGCGGTGGGTACCAAACCTTCTGGAAGCGCACAGCCTTCAAT GCCCTAGTTGCGACCTCTGTGACAAGCGAGAGGATATGGGGACCTCCAAAGGTAG CGAATCCCTGTTGTTTATCGATGTCATCATCTTCCACAAAAGGGATTTCTGGATCGA AAGGGGCCCTTGGTGTGCGAGAAGAATGAGACATGCGTTTCAGGTATGCCTGGTAAAG TGATCGAAATGGACGTAGGTGGCAAGATCGCGCGGTGTAGTAATGAAACGGAAT GGAGTGTGCTTGTGCTACGTTTCACGTCCTCGTACATCACCTGCGTTCTGCACGTC GAGCCAGGATGCCAGGTGGTCATGTAGTCCCTATTTGGGGTTGCCACACGAACA CGTTGGTCCATACGCATACCTCCGTATTGAATGAATCCATCTGAAATTTCTGAATG TTCGCGATACCTTTGTGCCAACGAGAAGGAAGTGAAGAGATAGGGACCGATTT GTTACCAAGGGGTACGCCCGCGGAAGATGTTTGTTCCTGAATGGACCTCGCAA ACGTGCAATTTCTGCATCAGACAGATCGCAGGGGCGTTGCCCGGCTGCTCTTGG AACTGCACCCAGCGCGTTTCGGCTGATCGAAGCGGCTGCGGCAGCGGTAGTGCCA TCCCTTTTCAACTCTGTGAACGGGACGTCGCGAAGAAGGGCCATCCAGTAGCACT CGGTGATCTCCGTCAAGAGTTCTTCACTATCGATTTTGGGGCAGGCGGCATGGT GACTGCCTGAGCGTCCGGTCCCTCCAGATCGTATGATTACCAGCTGCCATGGAT TCCCACGCTCTAGTGTGCGCTATGGGATGGTCCGAGCCCTCTGAAGCGATGGCG GATATGAAACGGGGGTCTTCATCGATACCTAGGGGGAGACTTGAATATCTTCTTG AGCGCCTGTTTCGATGGCGCGTACAAAGGCTGCGAAGTGATCTGGAGAGGAGGA GAGGCCGGTATCCTTTTCGTGTGGAAGACCTTTCGTGTAGGAGGCGAGGTGGGTG

		TCGTGGTAGCGATGCTCATCGCCGTTTGCAAGGTGGGTGGGGAGGGGGCGTGAA GCAGCGAGATCTGCGGCTTCACTACGGACTCTCAAGGCGGATGCATGGCGTTCTT CGGACAT
73	<i>Asparagopsis armata</i> Ireland 2 – Mbb4_like coding sequence	ATGTCTACCACACGTCAAGCAGCCGCACTACAAGTACGCACAGATGCCGCAAAAC TAGCAGCCTCCCGCAAACCTCCCTACCCACACCCCCAATGGCGATGAGACCCGTTT CTCAGATTCATACATCGCATCCTACACAAAGGGTTTACCACACGACAAAAAGACAG GCCTTCTCTCATCTACAGATGACTTCACTGCCTTTGTGCGTGCTATCAACACAGGC GCACAGGAAGACATCAGGAGCCTCCGCGCTAGGTATTGATGAAACACCTCGTTTCA TCTCCGGCATCGCATCCCCAGCACTCGACCTCCCCATCGCTGACACTCGCGCCTG GGAATCCATGGCCGAGGCAATACCTTCGATCTCGAAGGGCCTGATGCACAGGCA GTCACCATGCCTCCTGCACCTAAAATCGACAGCGAAGAGCTCTTGACAGAGATCA CAGAATGCTATTGGATGGCCCTTCTTCGCGACGTGCCCTTCTCAGAATTTTCATCGA AACGGAACAGTTGCTGCCGAGCCGCATCGATTAGTCGTACACGCTGGGTACAGT TTCAGGAGCAGCCCGGCCAGCGCCCATCCGATCTCAGAAATGCTGAAATCCAACG TCTGCGCGGCCCTTCAACAAATCAAACGTCTTCCGCGGACATCGATAAACACAGCTGAA CAGGTAGGCCCTACCTCTCCAGTTCTTGCTTGTGCGGTACACAGGGTATCGGGA AAATGCACCAGCCAGAAGAAGGTTTCATTCAATACGGAGGTATGCGAATGGACCA GCGCGTTCGCTTTGCGACTCCCAACCGCGACTATATGACTACTTGGGCCCTCCTGG CTCGACGTACAGAATGCAGGGGACGTCCGCTCACGTGAAACATACGACAAAGATA CTGAGTACCGTTTTATTACCACCCCGCGCGATCTCGCAACCTACGTCCATTTTCGAC GCCCTCTATCAAGCATACCTCAATGCCTGTCTCATTCTTCTCGACATAAAGGCTCC CTTCGATCATGGCCTTCTCTTTTGTGACGAGCAGCAGACATCGATAAACACAGCTGAT TTGCCACCTTTGGCGGGCCTCACATCCTTTCTTTGTACAGAGGTTGCAACCAGA GCACTTAAGGCTGTGCGCTTCCAGAAGTTTCGGTACGCATCGTCGCCTACGCCCCG AAGCTGTGCGCGGACTCATCGAGCGCTACCGCAAGACGAACGGCGCAGCGCCAT TCGCGAGCCGCTAAGAAGCTCGCTACCGAGATCGACAATGAGCTTATGACGCGCAT CTCGCGTCACAACGCCAAGCAGAATGAGTTTTCCGACAACGGTAAAGCACGAAGA AATGATTTCAACCCCGAGGGTGGCGCAAGCGCAGAAACCTACCTTCTTCCAATGG CGTTCCCGGAGGGAAGCCCAATGCATCCAGCTACGCTGCTGGACACGCCGCTG TCGCTGGCGCCTGTGTACGATCCTCAAGGCCTTCTTTGATCACAATACAAGTTA AAGTTCTGCTTTGAACCCAGCACAGACGGCAGGAAGCTAGAGAAGGTTAACATCA GTGAACCGCTCACAGTTGAACACGAGCTGAACAAGTTGTGTGCCAACATCAGTATT GGAAGAAACTGGGCCGGTGTGCACTACTACTCGGATTACGAAGAGAGTGCAAAGT TGGGTGAAGAGGTTGCCATCGGTATTTTGAAGAACAGAGCTTGACGTATGGTGA GAAGTTCTCCATGACCTCCCCAAGTTTGATGGAACGTGCATTACGATCTCCAAC GA
74	<i>Asparagopsis armata</i> Ireland 3 – Mbb1_like coding sequence	TTAAATGCGAATTGTGCTTCCATCAAACCTTGTGAGGGTCATCGAGAAATTCTCACT GAAGGTCAACTTCTGTTCCCTGAAGAATGCCAATAGCAATTTCTCACCAATGCGGA TACTTTCAATGTAGTCAGTGAAGTAATGCACACCAGCCAGTTACGTCCAATGGAA ATATTAGAGCAAATCTTGTTCACTCTCCGTCAACTGTGAGCGGCTCAGACACTTC AACC GGCTCGAGGGCCGAGCCATTTTCGTTAGTGACGTATGCAAACGGCAGGGG GAATCCACCATCAAAGAATGCCTTGAGAACAGTTACACAGGCTCCTGCAACAGTG GCATGTCCAGCACCATAAGCCGGATGCATCGGGCTTCCCTCTGGGAATGCCATTG GCATGAGAAGGTTGCCTTCGCTCAGGCCGCCATCAGGATTGAAATCTGCATACG CGGAGCACCGTTGTGCTCAACTTATTTTGCTTCTTGTTATGGTAATACACTCGATC CAACAGGTCAGAATCCAGGGAATCTACCAATTTAGCAGCTCCGGAAAATTCGGGT GCTTTGGTTTTGTAGTATCGGTGACACGACCGCCGACAGTCTCCGGGCGTAGAC GGCGATGGACGTTGAACTTCTGGAAGCGCACTGCCTTGAGAGCGCGAGTGGCCA CCTCAGTAACGAGAGAGAGAATATGCGGTCCGCCAAACGTGGCAAATGCCTGCTG CTTATCTATATCATTGTGAGCTGGAACGGGACTCCGGAATCGAACGGTGCACCA ATGTCGAGCAGAATGATGCAGGCGTTAAGATAGGCCTGGTACAGAGCGTCCGAAAT GGACGTATGTGCGCAGATCACGCGGTGTGTGAATGAAGCGGAAACCAGGGTCTG ACTCGTATCGCTCACGCCGGTGACATCCGCAGCGTTCTGCACGTCAAGCCAGGA TCCAAAGGTGGTCATGTAGTCAACCTTGGGGGATGCCACGCGTACCCGCTGGTCC ATGCGCATACCACCGTACTGGATGAAACCATCGCTGACCTCGTTTCCGTTTGCGAT TCCTGTGGTACCGACCAAGAGGAACTGGGACAAATATGGGCCTACATCATCTCCA GGAGTGATGCCCTGAAGACATTGGAGGCATCGATGGGGCCTCTGAGACGGGAG CGTTCCGCGAGATGTGAGATGGGTGGGAGGGTTTTCTTGAATTTAATCCATTGAGT GTCGTTGATACTCTTGGCAGCGGCTGCGACATCTTCGTCGAATGGAATGTTGGG AAGGGTACATCCCTGAGCAGGGACATCCAATAACATTCCGGTGACTTCAGTGACCA ACTCCTCGCTGTCTAGCTCTGGTGCGGGCGGCATAGTGACGGCCTGTGCATCAG GCCCTTCGAGATCGAATGTGCGTCCAGCACCCATACTTTCCAGGCACGAACTCC CGACTGCTCTGGGTTTGTGGCGATGCCGGATGTGAATCTGGGGGTGACATTCTGG GGGCCGAGTGGGAGAGCTGCGAAATCGCGGGCATCTCCGCTGTCAATAGCGCGT ACAAATTGGTCATAATCGAGGGCAGATTGAACCAGACCTGTTTCGTTGATATGGGG GAGACCTTTCGTGAAGTTAGCCAAGAGAGATCGTGACCATCTGGGTTTCTGAAGC

		GAGCCTCTGAATTGTTGGAGATGTGAGTTGGAGAACCACGGGAGCGAGCAAGCTC GGCGGCAGAGAGGCGAATCTTGAAGGAGGCCTCTGCGCGATTGGGATTCTGTGT GTCGGGGGTTGCCAT
75	<i>Asparagopsis armata</i> Ireland 3 – Mbb2-2_like coding sequence	TCAACCGAAGTTCTCTTCACGAAATACAAATCGAATATTGCACCCATGCCTCCGAA GCTCTGCTGCATGGTCAGTATTTCTCAGAAGAAGATCGGCAACAAGATCGACAACA TTAGTTGTCTCCAGATATGCCCCACGCAAGTTACTCCGTATTTCAGTTTTTCGCATG CTTTTCCTCACAGCTGCTCCCATTGAGTGTGGTCCGCAGAAAAAACTCCGATTTTC TGCGTGACTTGGTGACTTTTGGGCAATTTTGGCGAATATTTTCGTCCCAGGGCGGTC TTCCAATGTTGCTTGTAGTAATAAAGGTCTCAGCACTTTCAAAGTCTTCACTTTCCT TGCTGTAAATATATCGGTGAAGACGGAGTTTTGTGCCGTCTCTAGAGGAAAGAGT TCTTCTCGTAACCATTGGTCATCTACGGTGTGACGTGTTGTCCAGATAAAGTCAAC GTCTGGGATTTTCTTTCCGCATGCGCAGTTTGGGTTACACTTCCGATCATGAAATA GATTCAGGGACCCAATACTCCGATACAGACGAGCACTCATGAAATAAAGCATAATT GGCAGCAATACAATGAAGTGAAGAAAACTAATGTTCTGACATTTCCGTCCCAGT CCAAGATAGTACACCCTGACGCTGCACAGAATACTGACGGGAGCGGAGAAA AAGTCCATAAACTGCCAAGAAGAACGGAAGAAGCGGGGTCCCATGAAGCTAATTT CCAAGAGTATGGTCAAAGTTAGAGTGAAGTGCATGCAAAACACTCAACACTGCATCG GCACCTATAACCCATTTGGCACCTATGCGGCTGTCCCCAAAGTTGAATTCACCAAT GTTGAAGATTGATACAATGCACACAAGAACAATGCGTGCAATTAGAGAGAGTTGAA GTGCCAGAGTTACCCGAGTGGTATGAAGAAAAGAGAATAATATTGAACGTCTCTCA TAGAGACGGGCAATTTTGGCGAGCCATCTTACGTTTCTGCGGCAAGTTCCCTT TTCAAGTCTCATTCTTCACTGAAATCTGATGAATAATCTTCTTCATCGTCGCATGTA GACATGCTGCTCACTGAAGATTCTTCTAATTGATTTTCGACATCCAATATCCGGAGA CCATCTCCAATATTTGGGCAGCTCCTCGATGATACACATTGTTCACTTGTTCTTGAA GTGGAAACATCGAGTTCTTCGGAATTTTGGGCGTCAAGTTCATCATGTCAGTAAT ATACTGCTTCCTTTGTTCTTCAGATTCCGGTTCATCGGAGCTGTTTGCCAAATCGAT ATCATATACAGCAGAAATAGTTTTCCGAGATACGCTGCTCAATATGCTTCATTTTCA CAAATTGGTTTTCGAAAAATCAGTAGAAGGGCAGGTTTTGTTCTTGTTCAAGAAATG CAAACTTTTGGAGATGGCTGCGAAGGGCGTTGAACCAACTCCGCCAGATATGAGG ACCACTCTTTCATACGAAGAGACATGTTGAGCGGGAGCGCCAAATGGACCACGGA CTTGAAGTGAATGGGTTCCGATCTTCTCCTTCCATACGGTTTTGAAATGCCCT CGAAGCTCCTTGGTCCAATCCCGAGTGATTTGATGAAAAAGCACATGCATTTTTTC ATGGGGTGCACTAGCAATTGTGAAGGGATGCCACTCCCTACTCAAGGATGGTACA CGGATCTCTGCATACTGACCAGCGCGATATGTGAAGGGTTTTCGGAATACGAAGTT CCAAAATGTCTTTTCTTTGAGAGCTGAATGCTCGGAAGTGAGCTTCAGCTGAACG GTGGAGATTTTGAAGCGACGGGCGATTCTGTCCAGAATGTAGATCAGGAGAGGTGA GAGCAACCCACTTTGTAAGTCTCCGGAACACGACGGTACATACCATCGAGAGGTGAG AAGAGGAAAGAACAGCAGTGCTCCAACCATGTGGGAAATGTAGAAGAGCCGGA TATTTTTTTCTGTAGAATGGTAGAGCGAACATGAACATGATTATGAAGATAAGTAAC AATACGACGCCTGTGACAGCGCTCATGGTGAAATCCCAAAGTCTGCACTCCATTT ATCGTAAGCAATGATCCATGTGAAATGGAACGGGACATGAATGAAGAGAGATGCG GCTATCGTATATCCAACAAGGATATGGAAGGCGGGGAAGCTTTGTCAACAGGAA GAATCTTGTGAGGGGAGTATCACGGATGAATGTGAAGAAGAGGCGAGATGCAAG TAGAATGACAAGTGCTGTGTTGAGGTTGAGTGTAACCTGCTCCGCGAGCAATA GAAATGTACCAGCGGAGATTTGTGTCGGGAGATTGATTGTGGAAGTCACTCGTGAG CTCCCCATACGAACATGAGAGAGAGTGACGTTATGTATGTGATAACTGTGAGAAGC TCGAAGGCGTGAGTGGAGAGATAGGACTCGAGGCGAGCACTCCAAGACTTGGG GACCATTTTCTTCTGAAGGGAAATGCTGTGTTTCAT
76	<i>Asparagopsis armata</i> Ireland 3 – Mbb2_like coding sequence	ATGCCCTCTCCATCCTCATCCACATGTCCAAAGTCCACTCAAGATCTCCTCACCGC TCGACTCGAGTCCCACCTCTCCACACATGCCTTCGAACTTCTCGCTCTCGTCTGT ATGCCACCGCACTCCTCCTCATGTTCCATATGGGGAGCCCATGACGAATTCATCAC CACACTTCCGATGATAACATGCGATGGTACATCTCCATCGCCCGCGCAGCAGGTT ACACCCTAAATCTCAATACTGCATTGGTCATTCTTCTCGCTGCCAGACTCTTTTCAA CTTATATTCGCGAGACCCCATTCATCTAATCATTCTTCTGACAAAAGCTTCCAG CCTTCCATATTATTGTCGCTTACGCTATTGCCATCTCCCTCGTCTCCATGTGCGCTT TCCATTTGCGGTGGATTATTGCCACGATAAATGGGAACAGGCCCTTTGGGGATAC ACTATGAGCGCATCGACAGGATCTGTCTCCTCATTGTGTTTCTAGTCATGTTTCATA ACTGCCCTCCCAACATTTTCGGAAGAAACGCTTCGATTCTTCTATCTACACATAT GTTTCGAGTGATACTCTTCTTCCCTCTACTAATCTTTTCATGGAATGTACAACCGCT TCCAGAACTTACAAATGGATCACCGCCCCACTCATCATCTACATTATTGATAGACT TCTTCGTCTGTTTCAAAGTGTCCACAGTTCCTTGCAGCTCACCAGCGATCATTCTT CTCTCAAGAGTGCTGACATTCTCGAACTCCGAGTCCCAAAGCCCTTCCATTACAGA GCGGGGCAATATGCAGAGGTCTGTGTCCCTTCGATCAGTTTCAGAGTGGCATCCAT TCACAATCGCAAGCGCACCCACGAAGAAACCATGACCTTCTTCATCAAACTCTT GGCAATTGGACTCAAGCACTGCGCCACCAATTCCAAACACGCATGGATTTCAGACG ACTGCAAACCACTTACGGTACAGATCCGCGGACCGTACGGCGCTCCCGCTCAGCA

		CGTCGGCAGATATCAACGGGTAGTGTTGGTGTGAGGAGGTGTTGGCGCCACCCCT TTTGCCGCCATCTCGAAACATCTGCACCACCTGAATGTCGCTGAACATCACAAAA GACGCTCGATGTTGACATTCCATCTAAGCATACAATACTCGGGAACCGGATCA GAGAAACGATCTCCAATATGTACGGCTTGGGGTTGGGTGAAAGCGGCTGCGCAGA GGATTCCAACCAACAAAGAAGACAGCATCTGGCGGATATGCTGAACATGTCCCCG GATGGAGCGGTGCAGAAATTAGGAAATGAAATCTCTCATCCGCTCTCCGACAGGCT CTTCTGATGTGAGTGATCGTGCAGTTCGGAAAATGTCGATCTCTCGTTTTTCATCA AGTATTGGGAGTCAAATGGCCACGCTGGGAACATACGAGAAAGAGTGCAGCTCTA GAAAAGGCGGGAGAGAAGATAAGATGGGGCGATCTGCGTACTCGAAGCATAATTT GATGTTTCTGAATGAAAGCGCTCTAGACTTCTTTCCTTACTTCACACGACTCGAAT AACATTGCTGCTGCTGTTCCACACTAATTGCGCGATTAGTGCTGACGTGTGTTGTAT CTATCTTCGATCTTGGTCATTTACAGCACAACCAGCGGACACATAGAGGGCTAAGTGG GTTATCGTGACAAACGTCGTTCTGGGACTAATTGTTGGATTGACTCTATTCAACA ATTGTGCTGGAAGTGAGTTTTATGGGACGCGATTCTTCCACAGGAATTTGGCGAT GCGTTGACTTTTTGGTGTTCGTTCTCTGTCATTTCTGTCAATCTATACGGAATTG TAACGTGGGCTGGACGAGACCAATCGTCCTTCTGACATTTGTCGACTATATTATT ATCACACCGATTATCTTCTACTTCTCTGTGTCGATTATACCGAAGCATTGGGACG CGAAACCTTTTCGACGATAACGGGAGTTGCCGGGGGTGAGAACACAGCGTTCCGG AAGTGGACTTTATCTGGACGTCGCGCACAGGGGGACGACGAGTGGCTTCGCG AAGATCTGTACACGCTTTCGACGGGGACGGAGCTGCGACTGCATCGGTACGTGA CACGGGAGAAGGAAGTGAGGTGGAGGGAGGGAGGAGTTTATCACATCTGCTA GGGCGGGGCGTCCGAAGTGGGATGAAATATTTTTGAAGATCGCGGAGGAGTCCG GGAGCTGCAGTGAGATCGGGGTGTTCTTCTGTGGACCCAGTGGGATGGGGAAGC AGGTTCCGGAGAGTTTTCGGCGGGCGGAAGTTTTCAGTAGTTTGAGGGGATCATA CTTGAGGAAAACGGGTGGAGGGGAGGTTGGGACGAGGTAAGATTACTGAAGCG GTTTGGAAGCAATGTTTCGATTCGTATTTTCGGGAGGAGAACTTTAGCTGA
77	<i>Asparagopsis armata</i> Ireland 3 – Mbb3_like coding sequence	ATGCCTCCCCCAACTCGTCGTCAATCCGCTCTCGTCACTCGCATTGCAGCTGCAG ATGAAGCCGCAACCGTTACATCCTCCTCATCTAAGAAATGGCGATGAGACGCT GTACAAGACTACCTCAAATGCTCTCTCCTACCTCGCGACCTTCACAAAGGGTCTCC CTCATCATCCCAGCGTCTGCTAGTCTCCGCACAGCATTTCAACTCTTCGCCCGT GCTGTCCAAACAGGAACCTCCACAGCAGATTGCAGATATTTCCCTCGGACCTCCATC CACCTTTTCCACATTCCGCTCCGGAATTGCAAAGGATGCCCACTCCGCGCTTGG GAATCCATGGCCGCTGGAAATACATTGACCTTCAAGGGCCTGATCCCCAATCAG TCACAATACCCCCATGTCCACGTCTCGAATCCAATGAGCTCGTCACAGAGATGACA GAGCTTTACTACATGGCACTCCTCAGGGATGTCCCATTTCTCTCATTTCAAAAGTCA CACCTCGTCGCCGCTGCCGTCGACGATATCAATCACACCCATTGGATTCAATCCCA TAAATGTTGCATCCCAGAACTGGAACGTACAGACACAGAGAACCCTTCTCATCCT CTAATGTCTTCCGTGGCACCACACCAGGCGAGCGCAATGGTCCTTACATCTCACA ATTCTCATTGTTGGAACCAAGGGCTCGGAGAAATCCACGACGAGGCAGATGGC TACATCCAATACGGTGCCATCCGAATCGATCAGAGAGTTTCGATCAGTCGAGACAG AAATCGACTACATGACCACCTGGGCCGCCCTTCTTGACGTCCAGAATGCCGCAGA TTTGCGCAGACATTCTACATATGCCAAATCAAGCTCCTATCGCTTCTGTACACAC CACGCGACCTCGCTACCTACGTTTCATCATGACTCGCTCTACCAAGCCTATCTCAAC GCATGCATCATCCTCCTCGACATGAAAGTCCCATTGACCTCCGCTTCCCTTCCAC CACGGAAGACCACATCGACAAACAACAGGGCTTTGTAACTTTGGAGGCCCCCAT ATCCTCACACTCGTCACAGAGGTTGCTACCCGAGCCCTCAAGGCAGTCCGTTTCC AAAAATACGCCGTCCACAGACGTCTTCGCCAGAGGCTGTGCGCGGCCTCTTAGA ACAATACAGACGATACGGTGGCGGATATTCAGAGCTAGCAAATACTATTCGTCCCA TACGCCATCTCGCCCGTTCTCTAAGTTCAAACCTCATGTGCTCGTCGACGACAGC GAACGGCCATCAGAACGCAACAATGAGCGACAACGGATTTCCACGCTCCCATGAT ACAGGCTCCGGTGAGACTCATTGCTGCCAATGGCCTATCCGGAGGGAAGTCCGA TGCACCCTAGCTATGGTGCCGGGCATGCCACAGTGGCCGGGGCGTGCCTAACGA TATTGAAAGGCTTTTTTCGATCACACCTACAAGCTCCCGTTTCGCTATGTCTCATCCT GCAATGGGAAGATGCTGAAGAAGGCAAAGGTCGCGAAGAACTTTCCGGTGGGAAG GAGAGCTGAATAAACTGGCGTCTAATATCAGTATTGGACGTAGCTGGGCTGGCGT ACACTACTACTCCGACTATGTGGAGAGTATTGATTGGGAGAGGAAGTGGCGATT GGAATCCTGAAAGAGCAAAAGTTAACTTATTCGGAATAATTCTCAATGACAATTCCC AAATTTGATGGCACAACCATAAAATATAG
78	<i>Asparagopsis armata</i> Ireland 3 – Mbb4-2_like coding sequence	TTACTTTGAGTTTGAAATCTTGATAGTCGTACCATCAAACCTTGGGAATAGTCATGGA GAACCTCTACCGTACGTGAGACTCTGTTCTTCTAGAATACCAATTGCAACCTCTTC ACCAACCTTTCGCTCTCTATGTAATCCGAGTAATAGTGCACACCAGCCCAATTCC TACCAATACTGATGTTGGCACAAAGCTTGTGAGCTCATGCTCCACTGTGAGCGGT TCATTGATTTCCACCTCCTCAAGATTCTGGCCGTCTGTGCTGGGCACATAACAGAA TTCAAGCTCGTGAGTGTGGTCAAGAACGCCTTTAGGATCGTCACACATGCACCC GCAACAGCAGCATGCCCTGCACCATAGCTGGGATGCATTGGGCTACCCTCCGGG AATGCCATCGGGAGAAGATAAGTTTCTGCGCTTTCGCGCCCTCAGGATTATAATC

		GCCGCTTCGGGACCAACCGTTGTCGGAAAGTTCACTTCTGCGCGGCGTTGTGCTGC GAGATTCGTGTCATAAGGTCATTGTGCGATCTCAGTGGCGATTTTCTGGATGGGCTC AAAGGGCTCTGCTCCCTCCGTCTTTCCGTATCGCTCGATAAGACCGCCGACAGCC TCGGGGCGTAGACGGCGGTGGGTACCAAACCTTCTGGAAGCGCACAGCCTTCAAT GCCCTAGTTGCGACCTCTGTGACAAGCGAGAGGATATGGGGACCTCCAAAGGTAG CGAATCCCTGTTGTTTATCGATGTCATCATCTTCCACAAAAGGGATTTCTGGATCGA AAGGGCCCTTGGTGTGCGAGAAGAATGAGACATGCGTTTCAGGTATGCCTGGTAAAG TGCATCGAAATGGACGTAGGTGGCAAGATCGCGCGGTGTAGTAATGAAACGGAAT GGAGTGTGCTTGTGCTACGTTTTCACGTCCTCGTACATCACCTGCGTTCTGCACGTC GAGCCAGGATGCCAGGTGGTCATGTAGTCCCTATTTGGGGTTGCCACACGAACA CGTTGGTCCATACGCATACCTCCGTATTGAATGAATCCATCTGAAATTTCTGAATG TTCGCGATACCTTTGTGCCAACGAGAAGGAACTGAGAGAGATAGGGACCGATTT GTTCACCAGGGGTCACGCCGCGGAAGATGTTTGTTCCTGAATGGACCTCGCAA ACGTGCAATTTCTGCATCAGACAGATCGCAGGGGCGTTGCCCGGGCTGCTCTTGG AACTGCACCCAGCGCGTTCCGGCTGATCGAAGCGGCTGCCAGCGGTAGTGCCA TCCCTTTTCAACTCTGTGAACGGGACGTCGCGAAGAAGGGCCATCCAGTAGCACT CGGTGATCTCCGTCAAGAGTTCTTCACTATCGATTTTGGGGCAGGCGGCATGGT GACTGCCTGAGCGTCCGGTCCCTCCAGATCGTATGTATTACCAGCTGCCATGGAT TCCCACGCTCTAGTGTGCGCTATGGGATGTCGAGGCCCTCTGAAGCGATGGCG GATATGAAACGGGGGTCTTCATCGATACCTAGGGGGAGACTTGTAAATCTTCTTG AGCGCCTGTTTCGATGGCGCGTACAAAGGCTGCGAAGTGATCTGGAGAGGAGGA GAGGCCGGTATCCCTTTCTGTGTGGAAGACCTTTCTGTAGGAGGCCAGGTGGGTG TCGTGGTAGCGATGCTCATCGCCGTTTGCAAGGTGGGTGGGGAGGGGGCGTGAA GCAGCGAGATCTGCGGCTTCACTACGGAATCTCAAGGCGGATGCATGGCGTTCTT CGGACAT
79	<i>Asparagopsis</i> <i>armata</i> Ireland 3 – Mbb4_like coding sequence	TCAGTTGGAGATCGTAATGCACGTTCCATCAAACCTTGGGGAGGGTCATGGAGAAC TTCTCACCATACGTCAAGCTCTGTTCTTGCAAAATACCGATGGCAACCTCTTCACC CAACCTTGCACCTCTCTTCGTAATCCGAGTAGTAGTGCACACCGGCCAGTTTCTTC CAATACTGATGTTGGCACACAACCTTGTTCAGCTCGTGTTCACCTGTAGCGGTTCA CTGATGTTAACCTTCTCTAGCTTCTGCGCTCTGTGCTGGGTTCAAAGCAGAACCTT TAACTTGATTTGTGATCAAAGAAGGCCTTGAGGATCGTGACACAGGCGCCAGCG ACAGCGGCGTGTCCAGCACCGTAGCTGGGATGCATTGGGCTTCCCTCCGGGAAC GCCATTGGAAGAAGGTAGGTTTCTGCGCTTGCGCCACCCTCGGGGTTGAAATCAT TTCTTCGTGCTTTACCGTTGTGCGAAAACCTCATTCTGCTTGGCGTTGTGACGCGAG ATGCGCGTCATAAGCTCATTGTGCGATCTCGGTAGCGAGCTTCTTAGCGGCTGCGA ATGGCGCTGCGCCGTTCTGCTTTCGGTAGCGCTCGATGAGTCCGCGCAGAGCTT CGGGGCGTAGGCGACGATGCGTACCGAAGCTTCTGGAAGCGCACGCTTAAGTG CTCTGGTTGCAACCTCTGTGACAAGAGAAAGGATGTGAGGCCCGCCAAAGGTGGC AAATCCCTGTTGTTTATCGATGTCGTGCTCCTGCACAAAAGGAAGGCCATGATCGA AGGGAGCCTTTATGTCGAGAAGAATGAGACAGGCATTGAGGTATGCTTGATAGAG GGCGTCGAAATGGACGTAGGTTGCGAGATCGCGCGGGGTGGTAATGAAACGGTA ATCAGTATCTTTGTGCTATGTTTCACGTGAGCGGACGTCCCTGCATTCTGTACGT CGAGCCAGGAGGCCCAAGTAGTCATATAGTCGCGGTTGGAGTGCAGGAGGCATGG CGCGCTGGTCCATTGCGATACCTCCGTATTGAATGAAACCTTCTTCTGCTGGTGC ATTTTCCCGATACCCTGTGTACCGACAAGCAAGAACTGGGAGAGGTAGGGGCCTA CCTGTTACCCAGGCATGTGCGCCGCGGAAGACGTTTGATTTGTTGAAGGGGCCGCG CAGACGTTGGATTTACGATTTGTGAGATCGGATGGGCGCTGGCCGGGCTGCTCC TGAAACTGTACCCAGCGTGTACGACTAATCGATGCGGCTGCGGCAGCAACTGTTT CGTTTCGATGAAATCTGAGAAGGGCACGTGCGCAAGAAGGGCCATCCAATAGCA TTCTGTGATCTCTGTCAAGAGCTCTTCGCTGTCGATTTTAGGTGCAGGAGGCATGG TGAATGCCTGTGCATCAGGCCCTTCGAGATCGAAGGTATTGCCTGCGGCCATGGA TTCCCAGGCGCGAGTGTGAGCGATGGGGAGGTGAGTGCTGGGGATGCGATGCC GGAGATGAAACGAGGTGTTTCATCAATACCTAGGCGGAGGCTCCTGATGTCTTCC TGTGCGCCTGTGTTGATAGCACGCACAAAGGCAGTGAAGTCATCTGTAGATGAGA GAAGGCCTGTCTTTTGTGCTGTGGTAAACCCTTTGTGTAGGATGCGATGTATGAA TCTGAGAAACGGGTCTCATCGCCATTGGGGGTGTGGGTAGGGAGTTTGCGGGAG GCTGCTAGTTTTGCGGCATCTGTGCGTACTTGTAGTGCGGCTGCTTGACGTGTGG TAGACAT
80	<i>Asparagopsis</i> <i>taxiformis</i> Azores – Mbb1_like coding sequence	CTAGATACGGATGGTGAACCGTCAAACCTTGTTCAGCGTCATTGAGAAGTTTTCAC TGAACGTGAGCTTTTGTCTCTGCAGAATACCAATGGCAATCTCCTACCAATGCGA ATACTCTCGATGTAATCAGTGAAGTAATGCACGCCAGCCCAATTGCGACCAATCGA AATATTGGAGCAAATCTTATTCAACTCGCCGTGACGGTCAACGGCTCGTCAATTT CCACTGCCTTAAGACCTGTTCCATTCTCGTCCGTGATGTAGCAGAACGGCAACCT GTAACCACCATCGAAGAAGCGCTTCAACACTGTGACACAAGCGCCTGCAACAGTC GCATGTCCAGCGCCGTACGCGGGATGCATAGGACTTCCCTCTGGGAACGCCATG GGCATCAGCAGATTACCTTTGCTCACATCTCCGTGCGGGTTGAAGTCGTTTGCAC

		GCGGGTTTCCTCGATCGCTCAACAAGTTTTGTTTCTTGTTATGATCGTGACCTTCT GCAACAACCTTCTTGTCAGCGCTTCGGAGAGCTTGGCAGCGCCAGCAAATTCAGG TGCCTTTGTTGCGCAGTATCGATCGACTCGGGACCAATGGCCTCCGGACGCAGA CGACGATGGACGTTGAATTTCTGGAAGCGAACAGCCTTGAGGGCTCGAGTGGCCA CTTCCGGTAAGTAGAGAGAGGATGTGCGGACCGCCGAAAGTGGCAAATCCTTGCTG CTTATCAATGTCGTTATCGAGCTGGAAGGGAATTCAGAGTCGAATGGCGCACCG ATGTCGAGCAAGATGATGCAAGCGTTGAGGTAGGCCTGATACAAGCGCTCGAAAT GCACGTAAGTGGCCAGATCACGAGGAGTGTGAATGAAGCGGAAACGGGTTCCCT CTTCAATTGTACAATTCGCGACCGGAGACGTTGGCGGCATTTTGCACGTCGAGATA GGCGCCGAATGTGGTCATGTAATCAATGTGTGACTTGGCGACACGCACGCGCTGG TCCATACGCATGCCACCGTACTGGATGAATCCGTCGCCAACTTCATTGCCATTGGC AATACCGGTGGTACCGACAAGGAGGAACTGTGACAGATAGGGTCCGACTTCGTCT CCCGGTGTGATACCTCTGAAGACGTTGGCAGTGGTGTGAGGGCCTCTGAGACGG GAACGCTCAGCAGCTGTGAGATGTGCTGGTGGGTTGTTCTTGAATGAAATCCATTG GGTGTTATTGATGGAATCTGCAGCTGACTGAATATGGGCTCAATGTCAATCTCG GGAAGGGAACGTCTCTCAGCAGAGACATCCAGTAGCATTCTGTGACTTCAGTAAC CAATTCATCGCTGTCCAGCTCGGGCGCGGGCGGCATAGTGACAGCCTGAGCATC GGGACCTTCGAGATCGAAGACAAGACCAGCACCGCCACTTTCCAGGCACGGGT CCGACCTCTGGGTCGCTAGCGATACCGGAGGTGAATCTGGGCTCAACGCCCTGC GGACCGAGCGGGAGGTCTGCGAAATCACGAGGATCACCGCTGTCAATTGCGCGA ACAAAGCTATCGTAGTCGATTGCGGACACCACTAGAGCGGTTTCTTGGTATGCG GGAGACCTTGGTGAATTTGGCGAGCAGCAACGGGTACCATCAGGGTTTCTGAA GCGACTCTCCGAGTTGTTGGACAGATGGGTGGGGAGCCACGAGCGCGTGCCAG CTCAGCTGCTGATACGCGGACTTTGAAGGCCACTTCTGCACGATTGGGATTCTGT GTGTCGGTCAT
81	<i>Asparagopsis</i> <i>taxiformis</i> Azores – Mbb2_like coding sequence	ATGGATACCGTTTTCCCCGGAGACTCTCGCCAGAAAGCACAGGGAAAGATGCGCC CCATGCGCTCCTTCGCCATCCTCTCGGCTAATCTCGAAGCTTTCCTCTCTACACAT GCCTTCTCCCTCCTCTTCTCATCTTCTACCTCACCTGTACAGCCCTCATGTTTCGT TGGGGCTTCACCACACAGTGGGAAGAAGACCAGACAACGAACTGATCTATTCA TTTCCATTGCCAGAGGTGCTGGTTACAGTCTCAATCTCAACACAAGCCTCGTCATC CTCATTGCCGCTAGACTCACTTTCACTCTTATCCGCGAAACTCCCTCCAATACATT CTCCCACTCGATAAGATTTTCCGCTTTTCCACATGTTTGTGCGCTACATGATTGCA TTCTCGTTCTCATCCACGGCACTTTCCATATGACATGGATCATCCGCTTCCAAGG ATGGAACCTCGGGTCTCTGGGGTTTCACAATGAGTTTCGTACCCGGTTTCATCATCC TTCCAGTCTTTGTCGTATGCTCATCACTTCCCTTCCCTCACTTCCGCAAGAACAAGT TCCGCTCTTCTACCTCTTCCATCTTTACGGCGCCGCTCTCTTCTTCCATCTCTCA TCTTCCACGGTATGTATTTTGAGAGGCCAGAGACCTACAAATGAGTTACACCTCC CTCATCATCTATCTCCTCGATCGTTTCATCAGACGTATGAAGATCAGCAGTCATGAT CTGGACATTGCCCTGGAAAAATCCATCCTCAAGGACGGTGATATTCTCGAACTCCG TGTTCCCAAACCTTCGACTATCGTCCCGGCCATTATGCAGAGGTTATGGTTCCGT CCATTAACAAGGAATGGCATCCATTCTCCATCGCTAGTGACCCACACGAAGAAACC ATGTGCTTCTACATCAAGGTGCTCGGTGATTGGACCACCGAAGTTCGTAATGCTTT CAAGGCTCGTCTCGATGGTACAATCACTGAACCACTCAAAGTACGTGTTTCGTGGC CCGTACGGAGCTCCATGCCAGGATGTGACGCGTTTCAAGCTGTGCTGCTCGTCT CCGGAGGTGTTGGTGCCACACCAATTTCCGCCATTGTTAAGGAGCTGCACTACCT CAAGACGCAGGCTAAGAACAAGAACGATGGCCCCGGGACGCATTGCCCGCGACAT TGATGTTTCGATTCTGACAGTATCGCTAATCTCTACGATGTGCAAGTGCAGGACA TGGAGAAGGCTACTCACATTGCGCAGCAGAAGAGCATCTACGTTACTGAAATGCTT GAGCTCACCGCCAGGAGGACCTCTTCCCTGCACCGAGTGAGGTCCAGTGTCATG GATCGCATGCATGGATCGTCATCTACAAAGACAGTGCTCAGTACCGATGCTGCTAT TCCCAGCTTGGAGGATGGCCCTGTTGGTGGTGGCCAACCGATGAGCAGGATGCA GCGTTTGTCTCTTCAATTGAGCAAGGCTGGAAACATTGACGAGTGATGAGCACCT TGTCGGAGAACCCGGTTACTTGGGATCAAGTATGTCTGCGCAGAACGATCCATT GACCAACACGACCGATCTTCTGCTCGTACAGTGGCGCGCCTTTACGATAAGAGAGGA ATGCTCTTGGCGTTCATGCACACAGCTCGCTTACCTTTTTCTGCTCCTCACTTT GATTGTACGAATTATTATTATTTCCGTTGCCGCCACTCTGGATTCCGCCCTATTTCCA GCTCAACGATCAATTTGATGGCTACACGCGCTTGTGGCCTGTGCTTGTGACGCGC CTCTTCTCCGTTCCAGTTGCTGCTGCACTGGTGGTCTCCATTACATTTAGTAG TTTTCATGCGCATGCGATACTTTGACACTGCGGCGGAGAACCCTTGACGCTTAGTCC TGATGCCAGCGGCCGTCATCGGCTGTGTGCTTGGCATCCTTACTTGGGCACGACA GGACCCGGAATCTGTTCTTGTCAAGGTTATTGAATATGACTGTTTCATCCCGCTATT GTTCTAGGTCTGAGCTGGCGCTTGTACCGCATCACACGGTCGAGGAGTCTTCTC TCGGATCCGGCATGCCGATGCGATAACTCGGACCACATTCCCGATGTTGACTTTAT CTGGTCGTTCCCTACGAGCAGAGTGATCAATGGTTGCAGGATGAGCTCGGTCCG CTAGCAAAGGTAAGTGAACACTACGACTTCATAGGTATGTGACTAGGGAGAAGGAAC TTGATGTGGAGGCGGCGAAATCATTATTACCAGTGCCAATACTGGACGTCCAAGG

		TGGGATGATATTTTCCAGACAATCGCCGAGGAAACGCCAAGTAATGGAGCAATTG GTGTGTTCTTCTGTGGACCCACGTGATGGGCAATCAAGTTCGCGATGCCATGCT CAAGGTGCGAGGTGCTGAGCAATTTGCGAGCTGCTTACTTGCGAAATACGCCCGAC GAGGTGTTGATGACCGACTTGAATTTGCCAAATGCTGAAGCAGTGGAGAGGCTGC GATCGTTGGGATGCAGCGTTCAATTCGTCTATAGGGAAGAAAACCTTTGGTTGA
82	<i>Asparagopsis</i> <i>taxiformis</i> Azores – Mbb3_like coding sequence	ATGACGCCGCCAACACGCCGCCAAACAGCGCTCGTCAAGCGCATTGCCGCCGCA GACCTGGCCGCCAATCGTCACCATCCGCATCATGTGCGCAATGCCGACGAATCCA CCTACAAATTGCCAAACCATGTCTGTTCCCTACATATCCGCTTTCACCAAGGGTTTG CCCCATCATCTCGACGGCCGCTCGTTTCCCCACACCACTTTCAACTCTTCGTCCA CGCCGTGCAAACTGGCCATGTCACAGACATTGCCGCCATTCCACTCGGACCCCCA CACTCCTCCTCTTCCGTTCCGGCATCGCCAAGGGCGCCGCCGTGCGCGCATGG GAGTCCATGGCCGCGGGTAACACCTTTGATTTGCAAGGGCCTGATGCACAGGCCG TTACCATGCCCCCTTGTCCGCGTCTCAATTCACACGAGCTCGTCACAGAGATGACA GAGCTTTATTATATGGCACTGTTGCGCGACGTGCCGTTTACGCATTTCAACAAACA TCATCTCGTTCAGTCCGCTGTGCACGACATGAATCATACCCATTGATCAAGCGTCCA ACAGATGCTGTTTACCTCGCCCCGAGCGCCGTGACATCGCTCCAAATTCACCAC TGATAACATCTTCCGCGGTGTAACGCCCGGTGACATAACCGGTCCCTACATTTCCC AGTTTCTCCTTGTGCGGCACAAAGGGTCTCGGCGATGCACACGAAGAAACAGAAGG CTACGTTCAATACGGCGCCACAAGAATCGACCAGCGAGTGCGCACTGTCTGAACCC AAAATTGACTACATGACGACATGGGCCGCTTATCTCGACGTGCAGAATGGTGCCG ACTTACGCCGTCACTCCACCTATGCCAAACCACCGTCTACCCTTCATTAGCACC CCGCGCGACCTCGCAACCTATGTGCATTACGACGCGTTGTATCAAGCGTATCTCA ACGCGTGCATCATCCTGCTCGACATCAACGCGCCATACGATGGCGGACTGCCCTT CACCGCCGACGATGCCGTGACAAAGCAGCAGGGCTTTGCGACATTTGGCGCGCC ACATGTGCTGACACTTGTGACAGAAGTGGCGACACGCGCGCTCAAAGCTGTGCGC TTTCAAAAGTATGCCGTGCATCGGCGTCTGCGGCCGGAAGCTGTGCGCGGTCTAT TGGAGCAGTATAGACGCTACGGTGGTGGACATTCCGATCTGGCATAACATCATTCC TCCGATTCTGTCATCTCGCCGACTCGCTCAGTTCGGATCTGATGTTATGGTCGCCA AGGAGAACGGACGCCAGAATAGCTCGATTACGGATAACGCCCATCCGCGCTCGC ATGACGAAGGTTTCGGATGATACGCATCTGCTTTCCATGGCGTATGCGGAGGGAAG CCCGATGCATCCTAGTTATGGCGCGGGACATGCAACGGTTGCGGGCGCTTGTGTA ACAATCCTGAAAGCGTTCTTCGATCATACGTTCAAACCTGCCGTTTTCGTACGTGTC GTGAGCGATGGGAGGAAATTGAAGACGGTCAAGTTGAGCAGGAAATTGACCGTG GAGGATGAGTTGAACAAGTTGGCAGCGAATATAAGCATTGGACGCAGTTGGGCTG GCGTCCATTACTATTCCGATTATGTTGAGAGCATTCCGTTGGGCGAGGAGGTGGC CATCGGGATGCTCAAGGAGCAGAAGTTAACTTATTCGGAGAAATTCACGATGACAA TACCCAAATTTGACGGCTCCGTCATTGAAATTTAG
83	<i>Asparagopsis</i> <i>taxiformis</i> Azores – Mbb4_like coding sequence	ATGGCAGAGGAACGTGCCCCAAACGCTCTAGACATCCGCATCCAAGCCGCCAGG CTTGCGAAGAAACGTGACCATCCAACCCATGAGGCAAACGGCGATGAGGATCGTT ACCCAGAAACACTCATCGGCTCCTTCACTAAAGGTCTTCCACATGAGAAAGAAACC GGTCTCCTCTCCAACCCCGCCGATTTCCGCCACTTTGTTCCGCGCTATCAACACAG GCGCGATCAAAGACATAAGACGCCTCAAACCTTGAATCGATGAGGATCCTCGCTT CATATCTGGTATTGCCTCCAAGGGCGACAAGCATCCTTTGCCGATACGCGCGCC TGGAATCCATGGCCGCGGCTCTCACGTACGATCTAGAAGCCCTGATGCCCAAG CTGTACCATGCCGCCGGCGCCGAAACTCGACAGTGATGAACTCGTCACAGAGAT TACGGAGAGCTATTGGATGGCTCTTATTCGTGATGTGCCGTTACAGAGTTTGAAC GTGATGGAAATACAGCCGCAGCCGCAGCTTCCATCAGTCGCACTCGTTGGGTACA GTTCAATGAGCAGCCTTCACAGCGTCCGTCAACATTGACCGATGAAGAGATTGCTA GATTGAGGGGTCCGTATACCAAGAAAAATGTATCCGTGGTGTGACGATCCGTGA GAACGTCCGCCCGTATCTGTCTCAGTTCTTACTGGTAGGCACGAAAGGTATCGGC GATGTACAGCAAATTTCCGATGGTTACATTACGTACGGAAGTATGCGAATGGATCA GCGTGTCCGCGTCGCAGCGCCGAAACGCGATTATATGACAACCTTGGGCATCTTGG CTAGATGTGCAGAACGCTGGTGATTTACGTGGACGTGAAATTTACGATGATGATAC ACCGTTCCGCTTCATTACAACCCACGCGACCTTTCGACATGGGTTTCAATTCGACG CGTTATACCAGGCATATTTGAATGCTTGCATCATCCTTCTCGACATCAAGGCGCCG TTCGATCCACACATCCCGTTCCAGGCTGATGACGATGTAGATAAGCAGCAAGGATT TGCAACGTTTGGCGGCCCGCACATCCTATCATTGTGCACGGAAGTGGCTACGAGA GCACTCAAGGCAGTTTCGTTTCCAAAAGTACAACGTGCATCGTCTTCGTCGCGG AGGCTATCGGCGGGCTTGTGGAACGCTTCAAGAAGACAAACGAGATGCCAAGTT TGCCCCAGTGAAGAAGCTGGTGAATGACCTGGACGGCGATATGCTGCGACGCATT GAGCAGCACAACCTGTGAGCAGAATAAGCTTTCAGATGATGGACATGCACGCCGAG ACGACTATTACCGGAGGGTGAGAGTAACCGAGCGTACCTTCTGCCATGGCGTT CCCGGAGGGGAGCCCGATGCACCCGTCAATGTTGTCAGGTACGCCACAGTTGC CGGTGCGTGTGACGGTGCTCAAGGCATTCTTCGACCATGAATACGAGCTGGAC TTCTGCTACGTACCGACACGGATGGCAAGCGTCTGGAGAAGGTAAATATCAATG AAAAATTGACAGTGGAAGGCGAACTGAACAAGCTGTGCGCTAATATCTGTATTGGT

		CGAAACTGGGCTGGCGTGCACTACTACTCGGACTACTTTGAGAGTATCAAAGTTGG TGAGGAGATTGCAATTGGTATTTTGAAGAACAGAAGCTTACGTATGGTGAAGACT TTTTCATGACGCTGTCCAAGTTTGACGGTGAAAAGATCCGTATCTAA
84	<i>Asparagopsis</i> <i>taxiformis</i> Azores – Mbb_like coding sequence	TCAAGCAACAGGATCATCACTTCGCAACACCTCCACAGTGCGCTTGTCAACATTCA GCTCGTGCTTTGGCTGGCTACGAATGACATTAAGGTGGCCATCGAAGCCGACGTA AGTGAAGCTATGTTGCTCCGCGAAGGTGAGCACCTGCTCCTCAAGAATTTCCCTC GCGACTTCCTCTCCGAGGATCAGAGACTCAATGTTGTCGGACGACCAAGTGTACTC CTGCAAGTGATCGACCAAATGCGACATTGTTTGCAATCTTTGTTTCAGCTCACCATCA ACAGTCAGCGTCATACCGTCCGGAAGACACACGGGCTGCAGACATCCATGCGCGT CGGCCCTCAAAGATCTCATTGCGCAAGGGGGTAACTCCACATTAGACGGCTTCGC GTCCTTCACAGCGCACTTTCCGTGCAACTGCACCGTGTTAAAGAATGCCTTCAGAA TAATCGTGCAAGCGCCAGCCACTGTCCCGTGCTGCCCCATACGAGGGATGCAT AGGAGAACCTTCGGGGAACGCCATTGGCAGTAAGTACGACGGAGAAGACGCGCT GCGGTCTTTACACGGTCAGCAAACGTCTGGTTCTGCTGCATGTTCTTGTACAGCAA CAAGGTCGAGGAGACCGCATCCGTGCGAGCCGAGCGACAAGAGCACTTCCT CGCCGAAGTCGCATCGCTCACTCTTCTGCGCGTGGATCAGACCGCCGACTGCTTC AGGCCGGGCCCCGGAGATGAATCTGGAACCTTCTGGTAACGGACTGCCTTGAGAGC CCTGGTCGCAACCTCACAGACAAGGGACAGGATGTGCGGACCGCCGAAAGTCGC GAACGCTGTTTGTGTCGTGCTCGTCGTCATCGCGGAACGGTAAGCCCCGTATCG ACCCCGACACCGTCCGCCAGCAGAGCAAAGCATGCATTCAAGTAGGCTTCGTACA ACGCATCGTAATGGACATATGTCGAAAGGTGCGTCCATCTGCAATAAACCGGAAT ATCGGACTCCCATCAGGAGCACACTTGTAGTCGGGAATTCACCTGCCTGCAT CCGCCCGTCCCTGAACATCGATGAAAGCCTCCACGTTGTATCCAATCTTTTCTT GGCTCAATTGATCTCACTCGCAAGTCAAGCCCCAAGCGAACCGTACATAACCTGTCC TGTTGCAGTACCATCCGTTCCAAGGCCCTGGCTACCGCGGATCAGATATTGTGATA TGACGAGCATCTCGGACCCCAAGCTCCGTAGCCTCTGAAAATATTTCCAGTAGTC AAGTTAAGCTTCCCTCCCGTCTGAACCTCTCCTCATCAGTGAGCCCCCTCCCGAA CTCTTCAGAGACCCACGGCAACGCGCTCAAGGTAGCAATCGCATTATCAAAGAAG GCCTTCGTATCGGGAGAGTCCCAAACTGAAAGGAATATCCCGCGCAAGCGCCA TGAAGTAAAGCTCTGCAATTTCAAACCTCAAGCTCCGCGGACGCGAGCTTCGGCGC GGGCGGCATAGTGACAGCCTGCGCGTGGGTCTTCCAGGTCAAACGCGAGGGCC TGCGCCTGCGCTTTCCACGCGCGCGCCTTGACCTGCGACTCGAACGGCAGGCC GGGCGCGCCGTTTGCAAGCGTGGATTGCCAGCGGCCGGGAGTGTCTTTTGGCAG CTTCGGGCCCCAGCCGATTTTCTTGAAGTCCGCGGGATCGCCCGTGGCCAGCGA CGCGCGGAAGGGGTCGAAAAGATCACGGCTGAAAATCTGACCGGTCTCGGTGTT GTGCCGAGACCCTTCGTGAAAGTGCCGATGAGGGTTTCTTGAATCTGACTCA TCTCCGTTGCTCTTGTGTGGCGAACTCCGCGTTGAATGCCAGTTTGTGCGT TGATCCTGACCTGCTTGGCGTCTTTCGACGCTGCTCCTGGTCGGAGTTGTCTG GGCCATTTTCACGGAGGCGGCGGAAGACTGTCGACGGAAAGCATTGAAAGGGGA ATGCTTCGTGGTGATTGATGCGCCTCTGATACGTGCAACCCCAACTGGCGCAGAG GCTACGAAAGCGTTATGGAACAT
85	cDNA for <i>Asparagopsis</i> <i>taxiformis</i> Mbb1	ATGACCGACACACAGAATCCCAATCGTGCAGAAGTGGCCTTCAAAGTCCGCGTAT CAGCAGCTGAGCTGGCAGCGCTCGTGGCTCCCCAACCCATCTGTCCAACAACTC GGAGAGTCGTTTCAGAAACCCTGATGGTACCCGTTGCTGCTGCCAATTTACCC AAGGGTCTCCCGCATACCAAGGAAACCGCTCTAGTGGTGTCCGCAATCGACTACG ATAGCTTTGTTTCGCGCAATTGACAGCGGTGATCCTCGTGATTTTCGACAGCCTCCCG CTCGGTCCGCAAGGGCGTTGAGCCAGATTACCTCCGGTATCGCTAGCGACCCCA GAGGTCCGAACCCGTGCCTGGGAAAGTGGCGGTGCTGGTCTTGTCTTCGATCTC GAAGGTCCCGATGCTCAGGCTGTCACTATGCCGCCCGCGCCCGAGCTGGACAGC GATGAATTGGTTACTGAAGTCACAGAATGCTACTGGATGTCTCTGCTGAGAGACGT TCCCTTCCCGACATTTGACAGTGATCCCCATATTAGTCAGCTGCAGAGTCCATCA ATAACACCCAATGGATTCAATTCAAGAACAACCCACCAGCACATCTCACAGCTGCT GAGCGTTCCCGTCTCAGAGGCCCATCACCCTGCCAACGTCTTCAGAGGTATCA CACCGGGAGACGAAGTCGGACCCTATCTGTACAGTTCTCCTTGTGCGGTACCAC CGGTATTGCCAATGGCAATGAAGTTGGCGACGGATTATCCAGTACGGTGGCATG CGTATGGACCAAGCGGTGCGTGTGCGCAAGTCACACATTGATTACATGACCACAT TCGGCGCCTATCTCGACGTGCAAAATGCCGCCAACGTCTCCGGTCCGCAATTGTA CAATGAAGAGGAACCCGTTTCCGCTTCATTACACTCCTCGTGTGCTGGCCACTT ACGTGCATTTTCGACGCCCTGTATCAGGCCTACCTCAACGCTTGCATCATCTTGCTC GACATCGGTGCGCCATTGACTCTGGAATTCCCTTCCAGCTCGATAACGACATTGA TAAGCAGCAAGGATTTGCCACTTTTCGGCGGTCCGCACATCCTCTCTAGTTACCG AAGTGGCCACTCGAGCCCTCAAGGCTGTTGCTTCCAGAAATTCACGTCATCG TCGTCTGCGTCCGGAGGCCATTGGTGCCCGAGTCGATCGATACTGCGCAACAAAG GCACCTGAATTTGCTGGCGCTGCCAAGCTCTCCGAAGCGCTGGACAAGAAGTTGT TGCAGAAGGTGCACGATCATAACAAGAAACAAACTTGTGAGCGATCGAGGAAA CCCGCGTGCAAACGACTTCAACCCCGACGGAGATGTGAGCAAAGGTAATCTGCTG

		ATGCCCATGGCGTTCCAGAGGGGAAGTCCTATGCATCCCGCGTACGGCGCTGGA CATGCGACTGTTGCAGGCGCTTGTGTACAGTGTGAAGGCGTTCTTCGATGGTG GTTACAGGTTGCCGTTCTGCTACATCACCGACGAGAATGGAACAGGTCTTAAGGC AGTGGAAATTGACGAGCCGTTGACCGTCGACGGCGAGTTGAATAAGATTGCTCC AATATTTGATTGGTCGCAATTGGGCTGGCGTGCATTACTTCACTGATTACATCGA GAGTATTCGCATTGGTGAGGAGATTGCCATTGGTATTCTGCAGGAGCAAAAGCTG ACGTTTCAGTGAAAACCTCTCAATGACGCTGAACAAGTTTGACGGTTCGACCATCCG TATCTAG
86	cDNA for <i>Asparagopsis armata</i> Mbb4-2	ATGTCCGAAGAACGCCATGCATCCGCCTTGAGAGTCCGTAGTGAAGCCGCAGATC TCGCTGCTTCACGCCCCCTCCCCACCCACCTTGCAAACGGCGATGAGCATCGCTA CCACGACACCCACCTCGCCTCCTACACGAAAAGGTCTTCCACACGAAAAGGATACC GGCCTCTCCTCCTCTCCAGATCACTTCGCAGCCTTTGTACGCGCCATCGAAACAG GCGCTCAAGAAGATATTACAAGTCTCCCCCTAGGTATCGATGAAGACCCCCGTTTC ATATCCGCCATCGCTTCAGAGGGCTCCGACCATCCCATAGCCGACACTAGAGCGT GGGAATCCATGGCAGCTGGTAATACATACGATCTGGAGGGACCGGACGCTCAGG CAGTCACCATGCCGCTGCCCAAAAAATCGATAGTGAAGAAGTCTTGACGGAGAT CACCGAGTGCTACTGGATGGCCCTTCTTCGCGACGTCCCGTTTCACAGAGTTCGAA AGGGATGGCACTACCGCTGCCGCAGCCGCTTCGATCAGCCGAACGCGCTGGGTG CAGTTCCAAGAGCAGCCCCGGCAACGCCCTGCGATCTGTCTGATGCAGAAATTG CACGTTTGCGAGGTCCATTGAGAAAACAAACATCTTCCGCGGCGTGACCCCTGG TGAACAAATCGGTCCCTATCTCTCAGTTCCCTTCTCGTTGGCACAAGGGTATCG CGAACATTGAGGAAATTTGAGATGGATTCAATACGAGGATGCGTATGGAG CAACGTGTTGTTGTTGGCAACCCCAAATAGGGACTACATGACCACCTGGGCATCCT GGCTCGACGTGCAGAACGCAGGTGATGTACGAGGACGTGAAACGTACGACAACG ACACTCCATTCCGTTTCATTACTACACCGCGCGATCTTGCCACCTACGTCCATTT GATGCACTTTACCAGGCATACCTGAACGCATGTCTCATTCTTCTCGACACCAAGGC CCCTTTGATCCAGAAATCCCTTTTGTGGAAGATGATGACATCGATAAACAACAGG GATTGCTACCTTTGGAGGTCCCCATATCCTCTCGCTTGTACAGAGGTGCGCACT AGGGCATTGAAGGCTGTGCGCTTCCAGAAAGTTTGGTACCCACCGCGTCTACGCC CCGAGGCTGTGCGCGGTCTTATCGAGCGATACCGAAAGACGGAGGGAGCAGAGC CCTTTGAGCCCATCCAGAAATCGCCACTGAGATCGACAATGACCTTATGACACGA ATCTCGCAGCACAAACGCCGCGCAGAATGAACCTTCCGACAACGGTGGTGCCCGAA GCGGCGATTATAATCCTGAGGGCTGCGAAAAGCGCAGAAACTTATCTTCTCCCGAT GGCATTCCCGGAGGGTAGCCCAATGCATCCAGCTATGGTGACGGGCATGCTGC TGTGCGGGTGATGTGTGACGATCCTAAAGGCGTTCTTCGACCACACTCACGAG CTTGAATTCGTTATGTGCCAGCAGACGCGCAGAATCTTGAGGAGGTGAAA TCAATGAACCGCTCACAGTGGAGCATGAGCTCAACAAGCTTTGTGCCAACATCAGT ATTGGTAGGAATTGGGCTGGTGTGCACTATTACTCGGATTACATAGAGAGCGCAA GGTTGGGTGAAGAGGTTGCAATTGGTATTCTAGAAGAACAGAGTCTGACGTACGG TGAGGAGTTCTCCATGACTATTCCCAAGTTTGATGGTACGACTATCAAGATTTCAA CTCAAAGTAA
87	cDNA for <i>Chondrus crispus</i> Mbb3 (XM_005719378.1)	ATGGCAACCCCGTGCTTCGCCAGGCGCCGGCCCCCACCCTACGACGATCGCCG CGCCGTCTCCCCCTCACCCCGACCTCCTTCCTGCCGAGGCCGTTCTGCCAAAGC CCTTCCCCCGCTCCCCCGCCACCCCGCATCCGCGCCTCAACGCGCCTCCGCGC GCACCTCCGCGCCCAACCCCCGACCGCGCAGCCACGCGCTGCGCTACCCGC CAGCAGCAAGCGCTGGAGCTGCGCCGCGCGGGCGCAGCTCGCGCACGACCG TGCGCACCCCGCGCACGTGTGAACGGGTGAGGAGCTTACCTGCACCCGAA GACGGGCGCGCGCTGCTGCTGGCCAACCTTACGAAGGGGCTGCCGCACGAGC GCGACACGGGGCTGGCAGCCGACGCCGCGCACTACGACCTCTTCGTGGCGGCG GTCCATTCCGGCTTGCCGACGACATCCGCGCCATCCCGCTCGGCCCGCAGGCC GCGCCCGGCGTCCGCTCCCGCGCTCGCTCCGCTTCCGCTCCGGCATCGCACGC AGCTCGCACCTCTTCCCGCACACTGACGTCCGCGCCTGGGAGAGCATGGCCGCG GGGAACGCGTTTCGACCTGCAGGGGCGGACGCGCAGGCCGTACCATGCCGCC CGCGCCCGCCCTCGCCTCCCCGAGCTCGCGCTGGAGATGACGGAGAACTACTG GATGGCCCTGCTGCGCGACGTCCGCTTCTCGCAGTTTGCCGCGGACCCACCGT CGCCGCCGCCATGGAGAGCATGAACGCTACCGAGTGGGTGCCCCCTCGCGTGCGG CGACGCGTCGGCCGTGCGGAGGAGGAGCGCAAGCGCTGCGCGGGCCGTTTA CCGCGCAGAACGTGTTCCGTGGGAATACGCAAGGCGATTGCAAGGGCCCTATAT CTCCCAATTTCTGCTGTCTGGAAGCGCGGGGCTGGGCCAAGTGAACAGCGCGC GGATGGATACATCCAGTACGGAGCAATGCGTATGGATCAGCGCGTTCTGTGCGC CTCGAGGGGCTTGACTATATGACCACGTGGGAGAGCTGGCTGGATGTGCAGAAC GGGGCCGACTTGCGGGGAAGGGAGTTGTATGAGGACGGCGAACGCTTTAGATTT ATTTGCACCCCGAGGGACTTGGCCACTTATGTCCATTATGATGCCCTGTATCAGGC TTACTTGAACGCGCTGCATTATCATGCTCAACAAGAAGATCCCTTTGACAAGGGCC TGCCGTTCCAGAAGGATGACGACATCGACAAGCAGCAGGGCTTCGCCTTATTCGG CCCGCCGCACATTCTACCCCTGTGCACGGAGGTGCCACCAAGGGCCCTCAAGGG

		CATCCGCTTCCAAAAGTACAACGTCCACCGCCGTCTGCGTCCGGAGGCTGTCGGC GGCCGCGTGGAGCGCTACCACCACAAGTCCGAGGACCCGCTCTTCGCCGACGTC AAGCCGCTGTACGACGCCCTGGATAAGGACATGCTCGAGCGTGTTCGCCGCGCAC AACGCCGAGCAGAACGCCAAGGACGACTTTGGGAACAGCCGCTTCGAAGACTATT CCCCGACGGGTAGCTCCGGCAGGACCTATCTGCTGCCCATGGCGTTTCCGGAGG GCAGCCCCATGCACCCGGCGTACGGCGCAGGGCATGCGGCAGTGGCCGGCGCG TGCACCACTATCCTCAAGGCGTTCTTCGACCACGAGCAGAGCTTGACTTTGCGTA CGTGCCACCGCGGATGGCAGCAAATTGGAGGATGTTGTTGACTCTTTGGGGGAG AAGCTGACCGTCGAGGGAGAGCTCAACAAGGTCTGCTCGAATATCAGCGTCGGG CGCAACTGGGCTGGTGTGCACTACTTTACAGACTATCGCGAGTCCATCATCCTTG GGGAAAAGATTGCCCTCGGCCTGCTGGAGGAGCAGAAAGCTTACGTATGCTGAGG AGTTCTCCATGACGATTCTCTCTTTGATGGTTCCACTGTCACCATTAG
88	Maize RUBS chloroplast signal peptide	ATGGCGCCACCGTGATGATGGCCTCGTCGGCAACCGCCGTCGCCCCGTTCCAG GGTCTCAAGTCCGCCGCCAGCCTCCCCGTGCGCCGCCGAGCACCAGGAGCCTC GGCAACGTCAGCAACGGCGGAAGGATCCGGTGCATG
89	Maize SOD3 mitochondrial signal peptide	ATGGCTCTCCGCACCCTGGCATCGAAGAAGGTCCTATCCTTCCCGTTCCGGCGCG CGGGCCGGCCGTTGGCGGCGGCGGCGTCTGCGAGGGGGGTG
90	Peroxisome signal peptide from Zea mays SK1 gene	CCGCTGGTGGTGCAACTATACAGTGTCTTG
91	Maize Ubi-1 promoter including an intron	CTGCAGTGCAGCGTGACCCGGTCGTGCCCTCTCTAGAGATAATGAGCATTGCAT GTCTAAGTTATAAAAAATTACCACATATTTTTTTTGTACACTTGTGTTGAAGTGCAGT TTATCTATCTTTATACATATATTTAACTTTACTCTACGAATAATATAATCTATAGTAC TACAATAATATCAGTGTTTTAGAGAATCATATAAATGAACAGTTAGACATGGTCTAA AGGACAATTGAGTATTTTGACAACAGGACTCTACAGTTTTATCTTTTAGTGTGCAT GTGTTCTCCTTTTTTTTTGCAAATAGCTTCACCTATATAAATACTTCATCCATTTTATTA GTACATCCATTTAGGGTTTAGGGTTAATGGTTTTATAGACTAATTTTTTTAGTACAT CTATTTTATTCTATTTTAGCCTCTAAATTAAGAAAACTAAAACCTATTTTAGTTTTT TATTTAATAATTTAGATATAAAATAGAATAAAATAAAGTGACTAAAAATTAAACAAATA CCCTTTAAGAAATTAAAAACTAAGGAAACATTTTTCTTGTTTCGAGTAGATAATG CCAGCCTGTTAAACGCCGTGACGAGTCTAACGGACACCAACCAGCGAACCAGCA GCGTCGCGTCGGGCCAAGCGAAGCAGACGGCACGGCATCTCTGTGCTGCCTCT GGACCCCTCTCGAGAGTTCGGCTCCACCGTTGGACTTGCTCCGCTGTCCGGCATCC AGAAATTGCGTGGCGGAGCGGCAGACGTGAGCCGGCACGGCAGGCGGCCTCCT CCTCCTCTCACGGCACCGGCAGCTACGGGGGATTCTTTCCACCGCTCTTCGC TTTCCCTTCTCGCCCGCCGTAATAAATAGACACCCCTCCACACCTCTTTCCCC AACCTCGTGTTGTTGCGGAGCGCACACACACAAACCAGATCTCCCCCAAATCCAC CCGTCGGCACCTCCGCTTCAAGGTACGCCGCTCGTCTCCCCCCCCCCCCCTCTC TACCTTCTCTAGATCGGCGTTCCGGTCCATGGTTAGGGCCCCGGTAGTTCTACTTCT GTTTCATGTTTGTGTTAGATCCGTGTTTGTGTTAGATCCGTGCTGCTAGCGTTCGTA CACGGATGCGACCTGTACGTGACACAGTCTGATTGCTAACTTGCCAGTGTCTCT CTTTGGGAATCCTGGGATGGCTCTAGCCGTTCCGCAGACGGGATCGATTTCATG ATTTTTTTTGTTCGTTGCATAGGGTTTGGTTTGCCCTTTTCTTTATTTCAATATAT GCCGTGCACTTGTTTGTGCGGGTCATCTTTTCATGCTTTTTTTTGTCTTGGTTGTGAT GATGTGGTCTGTTGGGCGGTCGTTCTAGATCGGAGTAGAATTCTGTTTCAAACCTA CCTGGTGGATTTATTAATTTTGGATCTGTATGTGTGTGCCATACATATTCATAGTTA CGAATTGAAGATGATGGATGGAAATATCGATCTAGGATAGGTATACATGTTGATGC GGGTTTTACTGATGCATATACAGAGATGCTTTTTGTTTCGCTTGGTTGTGATGATGTG GTGTGGTTGGGCGGTCGTTTCATTCTGTTCTAGATCGGAGTAGAATACTGTTTCAAAC TACCTGGTGTATTTATTAATTTTGAAGTGTATGTGTGTGCATACATCTTCATAGTT ACGAGTTTAAGATGGATGGAAATATCGATCTAGGATAGGTATACATGTTGATGTGG GTTTTACTGATGCATATACATGATGGCATATGCAGCATCTATTCATATGCTCTAACC TTGAGTACCTATCTATTATAATAACAAGTATGTTTTATAATTATTTGATCTTGATAT ACTTGATGATGGCATATGCAGCAGCTATATGTGGATTTTTTTAGCCCTGCCTTCAT ACGCTATTTATTTGCTTGGTACTGTTTCTTTTGTGATGCTCACCCCTGTTGTTTGGT GTTACTTCTGCAG
92	enhanced 35S promoter	TGAGACTTTTCAACAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCCAG CTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGC CATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTC CCAAAGATGGACCCCCACCCACGAGGAGCATCGTGAAAAAGAAGACGTTCCAAC

		CACGTCTTCAAAGCAAGTGGATTGATGTGAACATGGTGGAGCACGACACTCTCGTCTACTCCAAGAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCTATTGAGACTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTTCAATTGGAGAGGACACGCTGA
93	Linker 1	ATTGCTGCAGCGGCCGAATTC AAG
94	3X (G4S) linker	GGCGGAGGTGGTTCTGGCGGAGGTGGTTCTGGCGGAGGTGGTTCTGGCGGAGGTGGTTCT
95	3x HA	TATCCGTACGACGTGCCAGACTATGCGGGCTATCCCTATGACGTCCCGGACTATGCAGGATACCCTTACGATGTTCTCTGATTACGCT
96	NOS terminator	GATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGATCCGATGATAAGCTGTCAAACATGA
97	eGFP	ATGGTGAGCAAGGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCACCTCGTGACCACCTTCACCTACGGCGTGACGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTTCAGATCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCACCCAGTCGCCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTCTGCTGGAGTTCTGTGACCGCCGCGGGATCACTCACGGCATGGACGAGCTGTACAAGTAA

[0141] Example expressions of the inventive concept are set out in the following clauses.

1. A nucleic acid construct for inducing expression of a polypeptide in a plant cell, the nucleic acid construct comprising a coding sequence encoding a polypeptide comprising a vanadate-dependent haloperoxidase (VHPO), or a functional fragment or homologue thereof;
wherein the coding sequence is operably linked to one or more regulatory elements, suitable to drive expression of the polypeptide in a plant cell.
2. A modified plant cell comprising a nucleic acid coding sequence encoding a polypeptide comprising a vanadate-dependent haloperoxidase (VHPO), or a functional fragment or homologue thereof.
3. The modified plant cell of clause 2, wherein the modified plant cell comprises the construct of clause 1.
4. A plant comprising the modified plant cell of clause 2.

5. The plant of clause 4, wherein the plant expresses VHPO in parts which are edible by livestock, suitably in its leaves or grains.
6. The plant or plant cell of any of clauses 2 to 5, wherein the plant or plant cell produces a brominated hydrocarbon, suitably bromoform.
7. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the VHPO polypeptide is derived from a species selected from *Asparagopsis* spp. (e.g. *A. taxiformis*, *A. armata*), *Acaryochloris marina*, *Alaria esculenta*, *Ascophyllum nodosum*, *Alteromonas naphthalenivorans*; *Caulerpa* spp. (e.g. *Caulerpa taxifolia*); *Chaetomorpha* spp. (e.g. *Chaetomorpha linum*), *Chondrus crispus*, *Colpomenia sinuosa*, *Corallina officinalis*, *Corallina pilulifera*, *Cystoseira trinodis*, *Furcellaria* spp. *Gracilaria* spp. (e.g. *Gracilaria changii*, *Gracilaria vermiculophylla*); *Hormophysa triquetra*, *Hypnea pannosa*, *Laminaria* spp. (e.g. *L. digitata*, *L. saccharina*), *Laurencia filiformis*, *Macrocystis pyrifera*, *Sargassum flavicans*, *Zonaria farlowii*, *Cladophora patentiramea*, *Dictyota bartayresii*, *Gigartina* spp. (e.g. *Gigartina stellata*), *Oedogonium* spp., *Padina* spp. (e.g. *Padina australis*), *Pterocladia capillacea* and *Ulva* spp. (e.g. *U. intestinalis*, *U. linza*, *U. lactuca*).
8. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the VHPO polypeptide is derived from a microalgal or macroalgal species.
9. The nucleic acid construct, plant cell or plant of clause 8, wherein the microalgal species is a member of the genus *Emiliana*, *Calcidiscus* or *Chaetocerus*.
10. The nucleic acid construct, plant cell or plant of clause 8, wherein the macroalgal species is a member of the genus *Asparagopsis* or *Chondrus*.
11. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the VHPO polypeptide is derived from *Asparagopsis armata* or *Asparagopsis taxiformis*.
12. The nucleic acid construct, plant cell or plant of clause 11, wherein the VHPO polypeptide is derived from *Asparagopsis taxiformis* Azores, *Asparagopsis armata* Azores, or *Asparagopsis armata* Ireland.
13. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the VHPO is a vanadate-dependent bromoperoxidase (VBPO).
14. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the VBPO is selected from Mbb1, Mbb3 and Mbb4 of *A. taxiformis*.
15. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the nucleic acid is DNA.
16. The nucleic acid construct, plant cell or plant of clause 15, wherein the DNA is in the form of a plasmid.

17. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the coding sequence comprises a sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of SEQ ID NOS: 47, 49 to 54, 57 to 60, 64 to 67, 71 to 74, 77 to 80, and 82 to 87.
- 17a. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the construct comprises a sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of SEQ ID NOS: 52, 58, or 80.
18. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the coding sequence comprises a sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of SEQ ID NOS: 47, 49 and 50 (Mbb1, Mbb3 or Mbb4 of *A. taxiformis*).
19. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the coding sequence comprises a sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of SEQ ID NOS: 54, 57 to 60, 64 to 67, 71 to 74, and 77 to 79 (VHPO of *A. armata*).
20. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the polypeptide comprising the VHPO comprises an amino acid sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to SEQ ID NOS: 1, 3 to 15, 18 to 21, 25 to 28, 32 to 35, 38 to 41, and 43 to 46.
21. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the polypeptide comprising the VHPO comprises an amino acid sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of Mbb1, Mbb3 and Mbb4 of *A. taxiformis* (SEQ ID NOS: 1, 3 and 4).
22. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the polypeptide comprising the VHPO comprises an amino acid sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of SEQ ID NOS: 15, 18 to 21, 25 to 28, 32 to 35, and 38 to 40 (VHPO of *A. armata*).
23. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the polypeptide comprising the VHPO comprises an amino acid sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of *Chondrus crispus* vBPO (SEQ ID NOS: 5 to 7).
24. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the polypeptide comprising the VHPO comprises an amino acid sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of *Acaryochloris marina* vBPO (SEQ ID NO: 8);

Alteromonas naphthalenivorans vBPO (SEQ ID NO: 9), *Ascophyllum nodosum* vBPO (SEQ ID NO: 10), *Corallina officinalis* vBPO (SEQ ID NO: 11), *Corallina pilulifera* (SEQ ID NO: 12), *Gracilaria changii* vBPO (SEQ ID NO: 13), and *Laminaria digitata* vBPO (SEQ ID NO: 14).

25. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the plant or plant cell is a terrestrial plant.

26a. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the plant or plant cell is a monocotyledon.

26b. The nucleic acid construct, plant cell or plant of clause 26a, wherein the monocotyledon is selected from corn, millet, sorghum or pasture grasses.

27. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the plant or plant cell is a dicotyledon.

28. The nucleic acid construct, plant cell or plant of clause 27, wherein the dicotyledon is alfalfa or clover.

29. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the coding sequence is operably linked to a promoter for driving expression of the polypeptide in a plant cell.

30. The nucleic acid construct, plant cell or plant of clause 29, wherein the promoter is a constitutive or inducible promoter.

31. The nucleic acid construct, plant cell or plant of clause 29 or 30, wherein the promoter is selected from AlcR/AlcA (ethanol inducible); GR fusions, GVG, and pOp/LhGR (dexamethasone inducible); XVE/OlexA (beta-estradiol inducible); and heat shock induction.

32. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the VHPO is monomeric

33. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the coding sequence is operably linked to a nucleic acid sequence encoding a targeting signal.

34. The nucleic acid construct, plant cell or plant of any preceding clause, wherein the polypeptide includes a targeting signal.

35. The nucleic acid construct, plant cell or plant of clause 33 or 34, wherein the targeting signal is a peroxisomal targeting signal, optionally wherein the peroxisomal targeting signal is SEQ ID NO: 90.

36. The nucleic acid construct, plant cell or plant of clause 33 or 34, wherein the targeting signal is a mitochondrial targeting signal, optionally wherein the mitochondrial targeting signal is SEQ ID NO: 89.
37. The nucleic acid construct, plant cell or plant of clause 33 or 34, wherein the targeting signal is a chloroplast targeting signal, optionally wherein the chloroplast targeting signal is SEQ ID NO: 88.
38. An animal feed or animal supplement comprising the modified plant cell or plants of any of clauses 2 to 37.
39. A method for reducing methane production in an animal, comprising growing or culturing the modified plants or plant cells of any of clauses 2 to 37 under conditions suitable for the production of halogenated hydrocarbons, and feeding an effective amount of the modified plants or plant cells to the animal.
- 39b. The method of clause 39, wherein the plant is subjected to stress such as heat shock or drought.
- 39c. The method of clause 39, wherein the growing or culturing of the modified plant or plant cells does not include providing substrates or cofactors relevant to the production of a halogenated hydrocarbon.
- 39d. The method of clause 39, wherein the growing or culturing of the modified plant or plant cells does include providing substrates or cofactors relevant to the production of a halogenated hydrocarbon.
- 39e. The method of clause 39c or clause 39d, wherein the halogenated hydrocarbon is a brominated hydrocarbon.
- 39f. The method of clause 39e, wherein the brominated hydrocarbon is bromoform.
- 39g. The method of any one of clauses 39c, 39d, 39e, or 39f, wherein the substrates or cofactors relevant to the production of a halogenated hydrocarbon include at least one compound selected from the group consisting of KBr, sodium orthovanadate, pentane-2,4-dione, and H₂O₂.
40. A method for reducing methane production in an animal comprising administering to the animal an effective amount of modified plant cells, plants, or animal feed of any of clauses 2 to 37.
41. The method of clause 39 or 40, wherein the animal is a ruminant.
42. The method of any of clauses 39 to 41, wherein the animal is bovine.
43. The method of any of clauses 39 to 42, wherein the animal is a cow, sheep or goat.
44. The method of any of clauses 39 to 43, wherein methane production is reduced.

- 45. The method of any of clauses 39 to 44, wherein feed efficiency is increased.
- 46. A method of preparing a modified plant cell, comprising:
transforming a plant cell with the nucleic acid construct of any of clauses 1 to 37.
- 46b. A method of preparing a modified plant cell comprising:
transfecting a plant cell with a plasmid comprising the nucleic acid construct of any one of clauses 1 to 37.
- 47. The method of clause 46 or 46b, wherein the plant cell is transformed by Agrobacterium-mediated infiltration.
- 48. The method of clause 47, wherein the plant cell is transformed by particle bombardment.
- 48b. The method of clause 46, wherein the plant cell is transformed by using a CRISPR/Cas system, a zinc finger nuclease, a TALEN, a lentivirus, an adenovirus, an AAV, and/or a meganuclease.
- 49. A method of producing an animal feed for reduction of methane production in an animal comprising:
growing the modified plant cell or plant of any of clauses 2 to 37; and
processing the modified plant cell or plant into an animal feed.

CLAIMS

1. A nucleic acid construct for inducing expression of a polypeptide in a plant cell, the nucleic acid construct comprising a coding sequence encoding a polypeptide comprising a vanadate-dependent haloperoxidase (VHPO), or a functional fragment or homologue thereof;
wherein the coding sequence is operably linked to one or more regulatory elements, suitable to drive expression of the polypeptide in a plant cell.
2. A modified plant cell comprising a nucleic acid coding sequence encoding a polypeptide comprising a vanadate-dependent haloperoxidase (VHPO), or a functional fragment or homologue thereof, preferably wherein the modified plant cell comprises the construct of claim 1.
3. A plant comprising the modified plant cell of claim 2.
4. The plant or plant cell of claim 2 or claim 3, wherein the plant or plant cell produces a brominated hydrocarbon, suitably bromoform.
5. The nucleic acid construct, plant cell or plant of any preceding claim, wherein the VHPO polypeptide is derived from a species selected from *Asparagopsis* spp. (e.g. *A. taxiformis*, *A. armata*), *Acaryochloris marina*, *Alaria esculenta*, *Ascophyllum nodosum*, *Alteromonas naphthalenivorans*; *Caulerpa* spp. (e.g. *Caulerpa taxifolia*); *Chaetomorpha* spp. (e.g. *Chaetomorpha linum*), *Chondrus crispus*, *Colpomenia sinuosa*, *Corallina officinalis*, *Corallina pilulifera*, *Cystoseira trinodis*, *Furcellaria* spp. *Gracilaria* spp. (e.g. *Gracilaria changii*, *Gracilaria vermiculophylla*); *Hormophysa triquetra*, *Hypnea pannosa*, *Laminaria* spp. (e.g. *L. digitata*, *L. saccharina*), *Laurencia filiformis*, *Macrocystis pyrifera*, *Sargassum flavicans*, *Zonaria farlowii*, *Cladophora patentiramea*, *Dictyota bartayresii*, *Gigartina* spp. (e.g. *Gigartina stellata*), *Oedogonium* spp., *Padina* spp. (e.g. *Padina australis*), *Pterocladia capillacea* and *Ulva* spp. (e.g. *U. intestinalis*, *U. linza*, *U. lactuca*).
6. The nucleic acid construct, plant cell or plant of any preceding claim, wherein the VHPO polypeptide is derived from a microalgal or macroalgal species.
7. The nucleic acid construct, plant cell or plant of claim 6, wherein the macroalgal species is a member of the genus *Asparagopsis* or *Chondrus*.
8. The nucleic acid construct, plant cell or plant of any preceding claim, wherein the VHPO is a vanadate-dependent bromoperoxidase (VBPO).
9. The nucleic acid construct, plant cell or plant of any preceding claim, wherein the coding sequence comprises a sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of SEQ ID NOS: 47, 49 to 54, 57 to 60, 64 to 67, 71 to 74, 77 to 80, and 82 to 87.

10. The nucleic acid construct, plant cell or plant of any preceding claim, wherein the coding sequence comprises a sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of SEQ ID NOs: 47, 49 and 50 (Mbb1, Mbb3 or Mbb4 of *A. taxiformis*).
11. The nucleic acid construct, plant cell or plant of any preceding claim, wherein the coding sequence comprises a sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of SEQ ID NOs: 54, 57 to 60, 64 to 67, 71 to 74, and 77 to 79 (VHPO of *A. armata*).
12. The nucleic acid construct, plant cell or plant of any preceding claim, wherein the polypeptide comprising the VHPO comprises an amino acid sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to SEQ ID NOs: 1, 3 to 15, 18 to 21, 25 to 28, 32 to 35, 38 to 41, and 43 to 46.
13. The nucleic acid construct, plant cell or plant of any preceding claim, wherein the polypeptide comprising the VHPO comprises an amino acid sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of SEQ ID NOs: 1, 3 and 4 (Mbb1, Mbb3 and Mbb4 of *A. taxiformis*).
14. The nucleic acid construct, plant cell or plant of any preceding claim, wherein the polypeptide comprising the VHPO comprises an amino acid sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of SEQ ID NOs: 15, 18 to 21, 25 to 28, 32 to 35, and 38 to 40 (VHPO of *A. armata*).
15. The nucleic acid construct, plant cell or plant of any preceding claim, wherein the polypeptide comprising the VHPO comprises an amino acid sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of SEQ ID NOs: 5 to 7 (*Chondrus crispus* vBPO).
16. The nucleic acid construct, plant cell or plant of any preceding claim, wherein the polypeptide comprising the VHPO comprises an amino acid sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to any one of *Acaryochloris marina* vBPO (SEQ ID NO: 8); *Alteromonas naphthalenivorans* vBPO (SEQ ID NO: 9), *Ascophyllum nodosum* vBPO (SEQ ID NO: 10), *Corallina officinalis* vBPO (SEQ ID NO: 11), *Corallina pilulifera* (SEQ ID NO: 12), *Gracilaria changii* vBPO (SEQ ID NO: 13), and *Laminaria digitata* vBPO (SEQ ID NO: 14).
17. The nucleic acid construct, plant cell or plant of any preceding claim, wherein the plant or plant cell is a terrestrial plant.
18. The nucleic acid construct, plant cell or plant of any preceding claim, wherein the plant or plant cell is a monocotyledon, preferably wherein the monocotyledon is selected from corn, millet, sorghum or pasture grasses.

19. The nucleic acid construct, plant cell or plant of any preceding claim, wherein the plant or plant cell is a dicotyledon, preferably wherein the dicotyledon is alfalfa or clover.
20. The nucleic acid construct, plant cell or plant of any preceding claim, wherein the coding sequence is operably linked to a promoter for driving expression of the polypeptide in a plant cell.
21. The nucleic acid construct, plant cell or plant of any preceding claim, wherein the coding sequence is operably linked to a nucleic acid sequence encoding a targeting signal and/or wherein the polypeptide includes a targeting signal.
22. The nucleic acid construct, plant cell or plant of claim 21, wherein:
- i) the targeting signal is a peroxisomal targeting signal, optionally wherein the peroxisomal targeting signal is SEQ ID NO: 90;
 - ii) wherein the targeting signal is a mitochondrial targeting signal, optionally wherein the mitochondrial targeting signal is SEQ ID NO: 89; or
 - iii) wherein the targeting signal is a chloroplast targeting signal, optionally wherein the chloroplast targeting signal is SEQ ID NO: 88.
23. An animal feed or animal supplement comprising the modified plant cell or plants of any of claims 2 to 22.
24. A method for reducing methane production in an animal, comprising growing or culturing the modified plants or plant cells of any of claims 2 to 22 under conditions suitable for the production of halogenated hydrocarbons, and feeding an effective amount of the modified plants or plant cells to the animal.
25. A method for reducing methane production in an animal comprising administering to the animal an effective amount of modified plant cells, plants, or animal feed of any of claims 2 to 23.

Figure 1A



Figure 1B



Figure 1C



Figure 1D

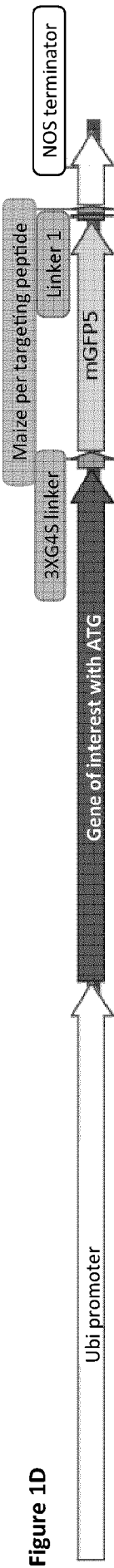


Figure 2A



Figure 2B



Figure 2C

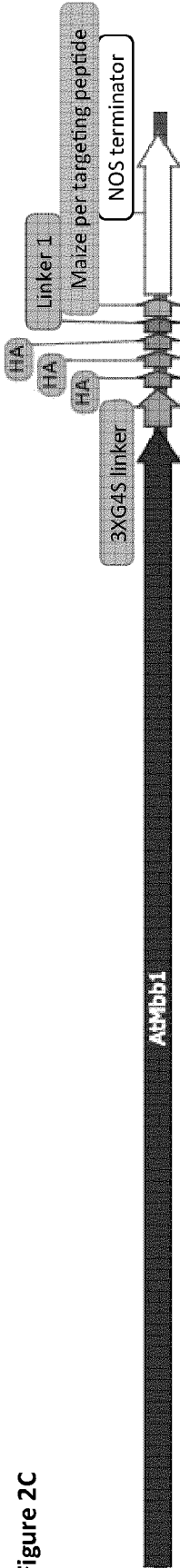


Figure 2D

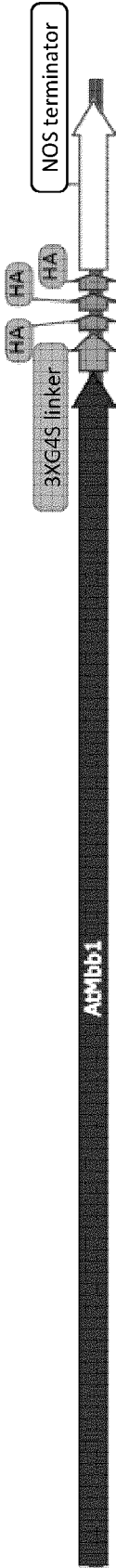


Figure 3B

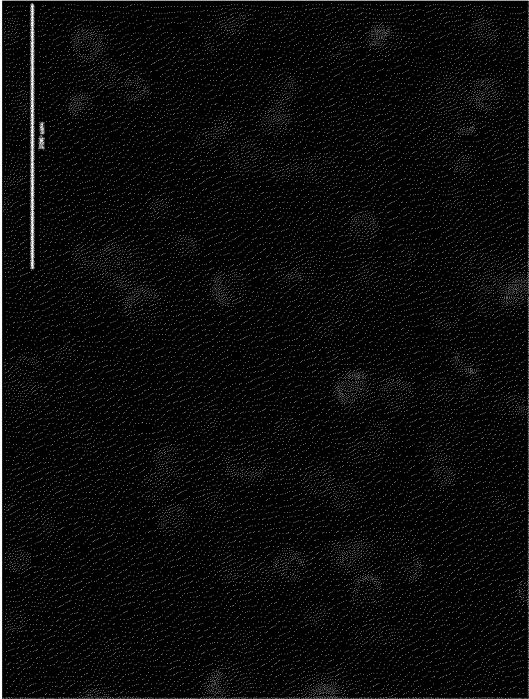


Figure 3D

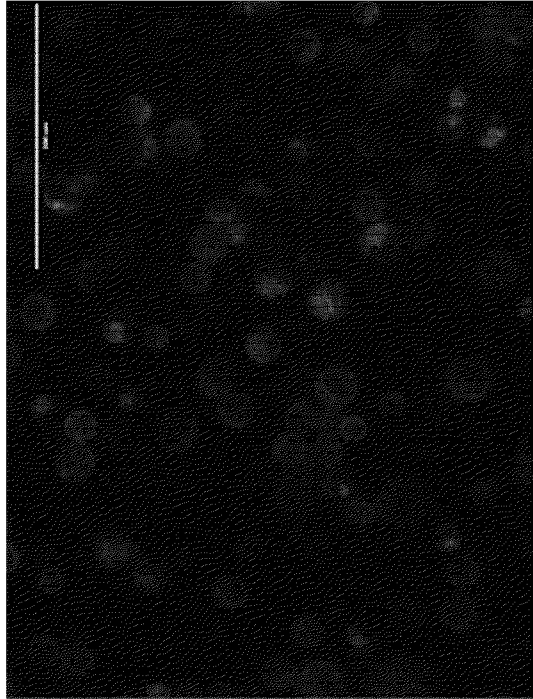


Figure 3A

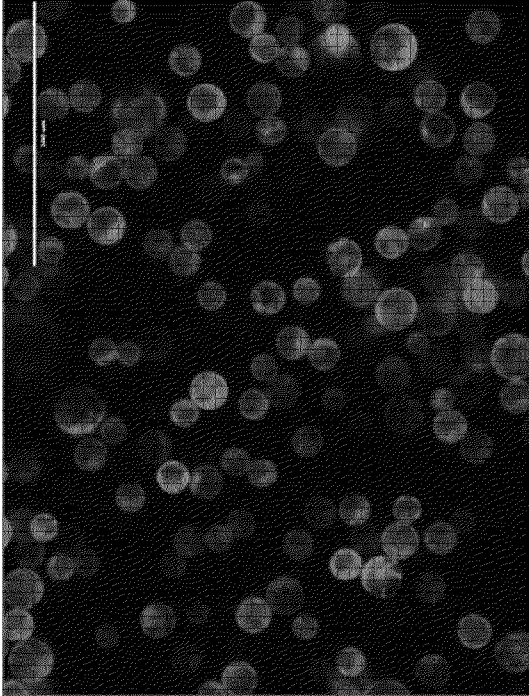


Figure 3C

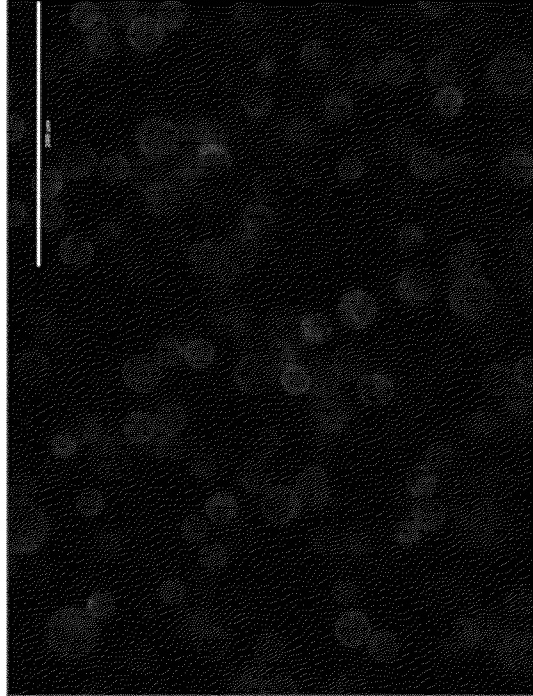


Figure 4B

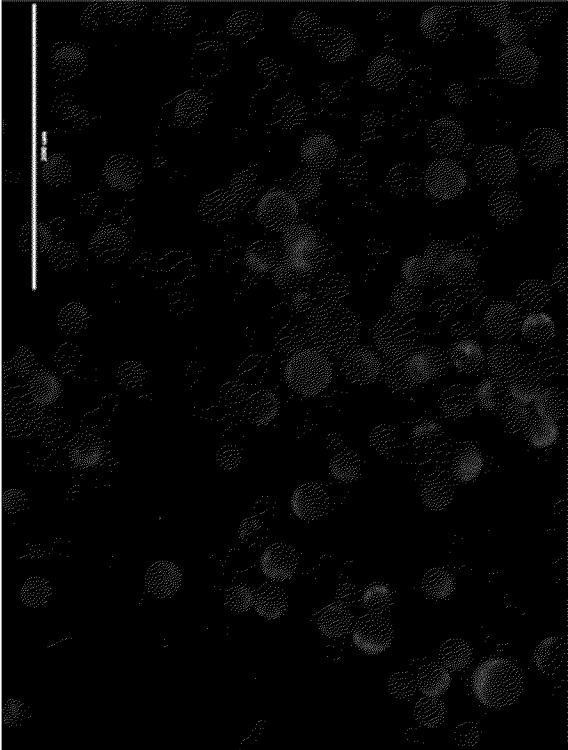


Figure 4D

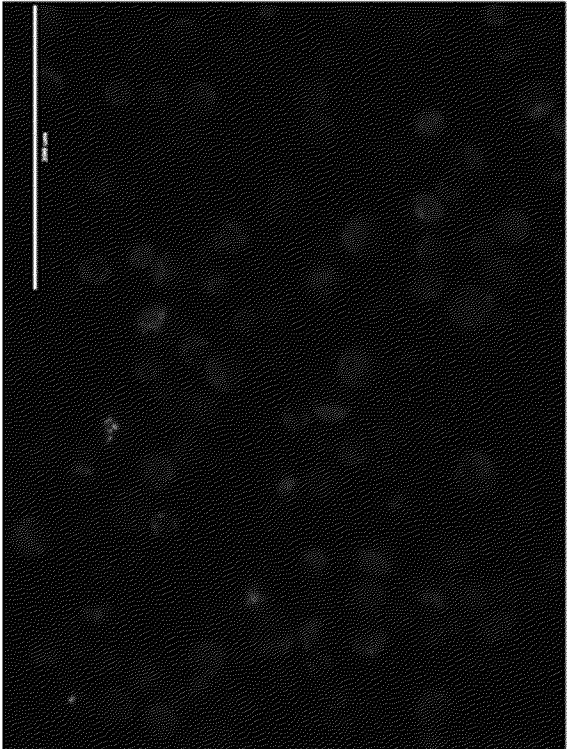


Figure 4A

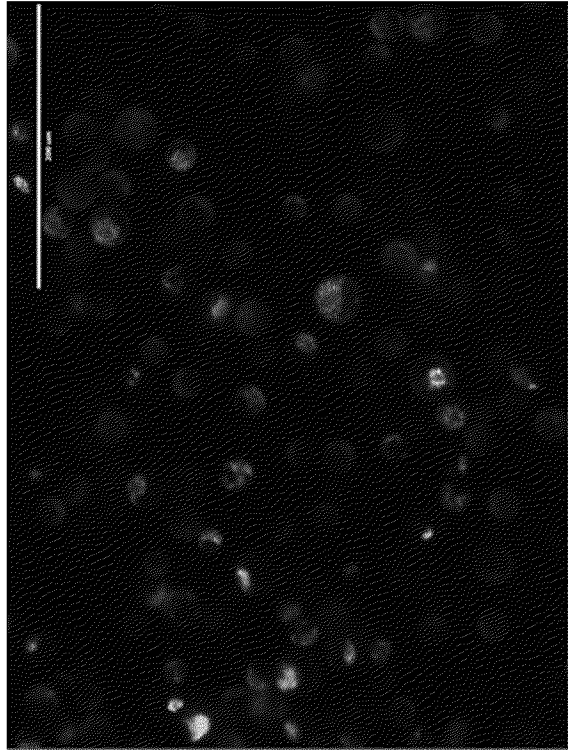


Figure 4C

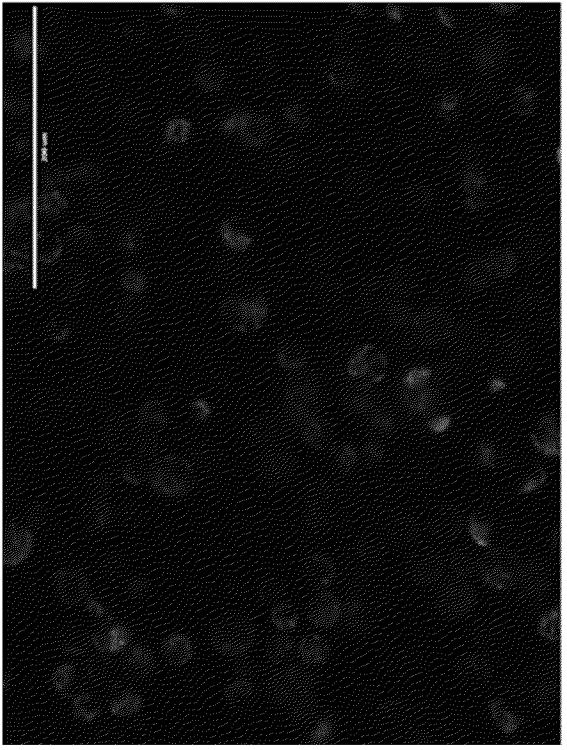


Figure 5



Figure 6A

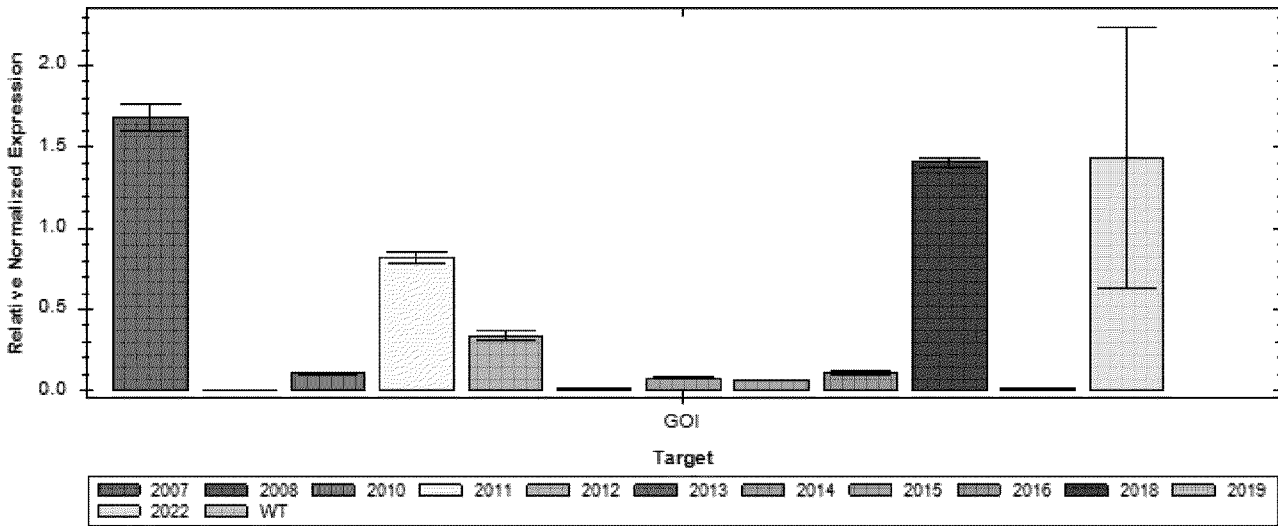


Figure 6B

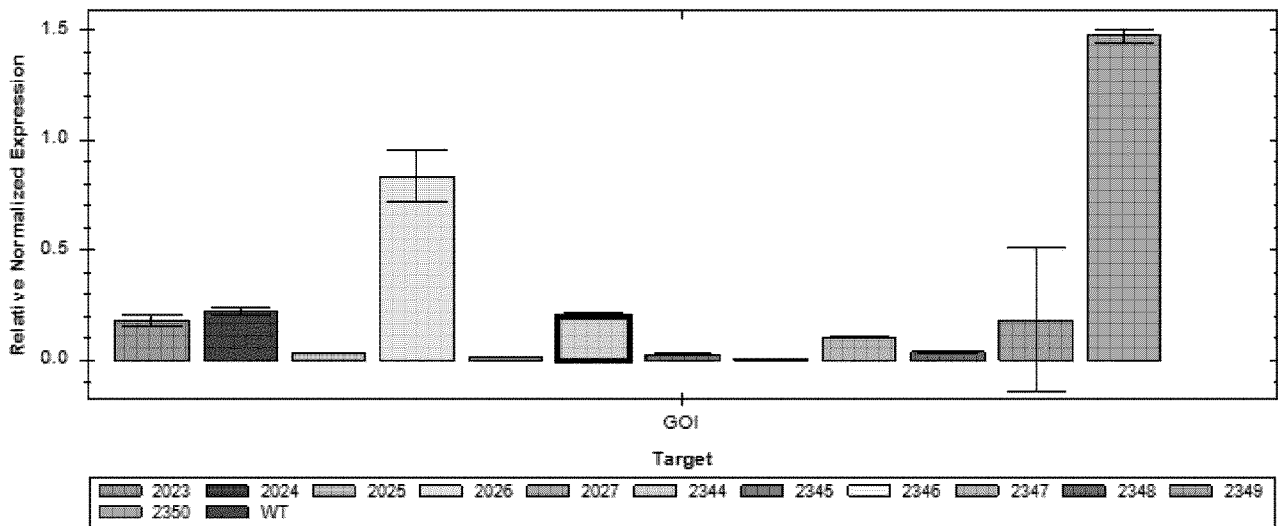
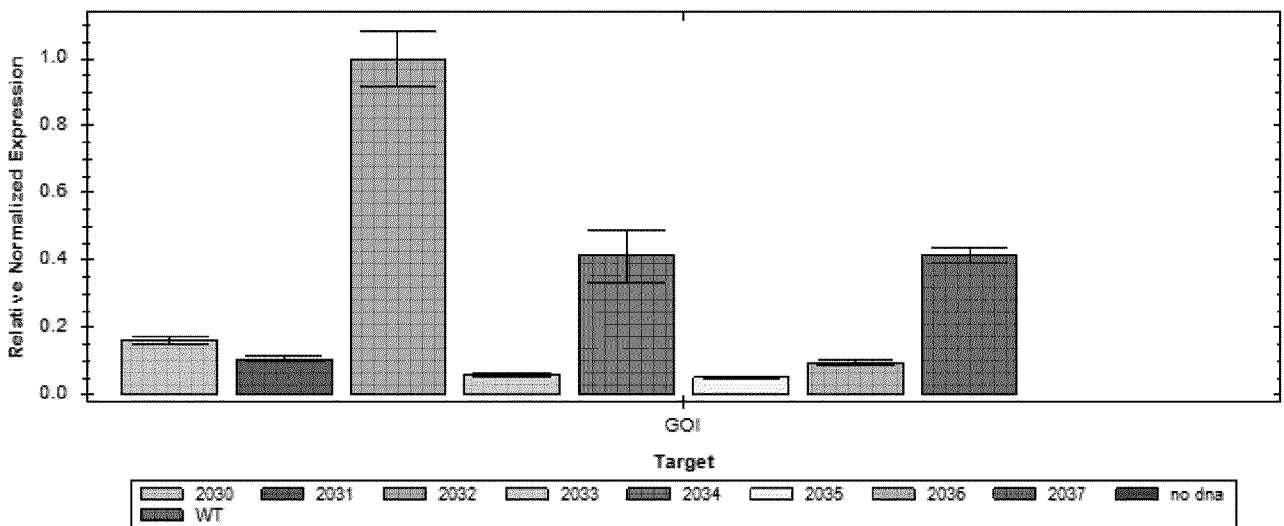


Figure 6C



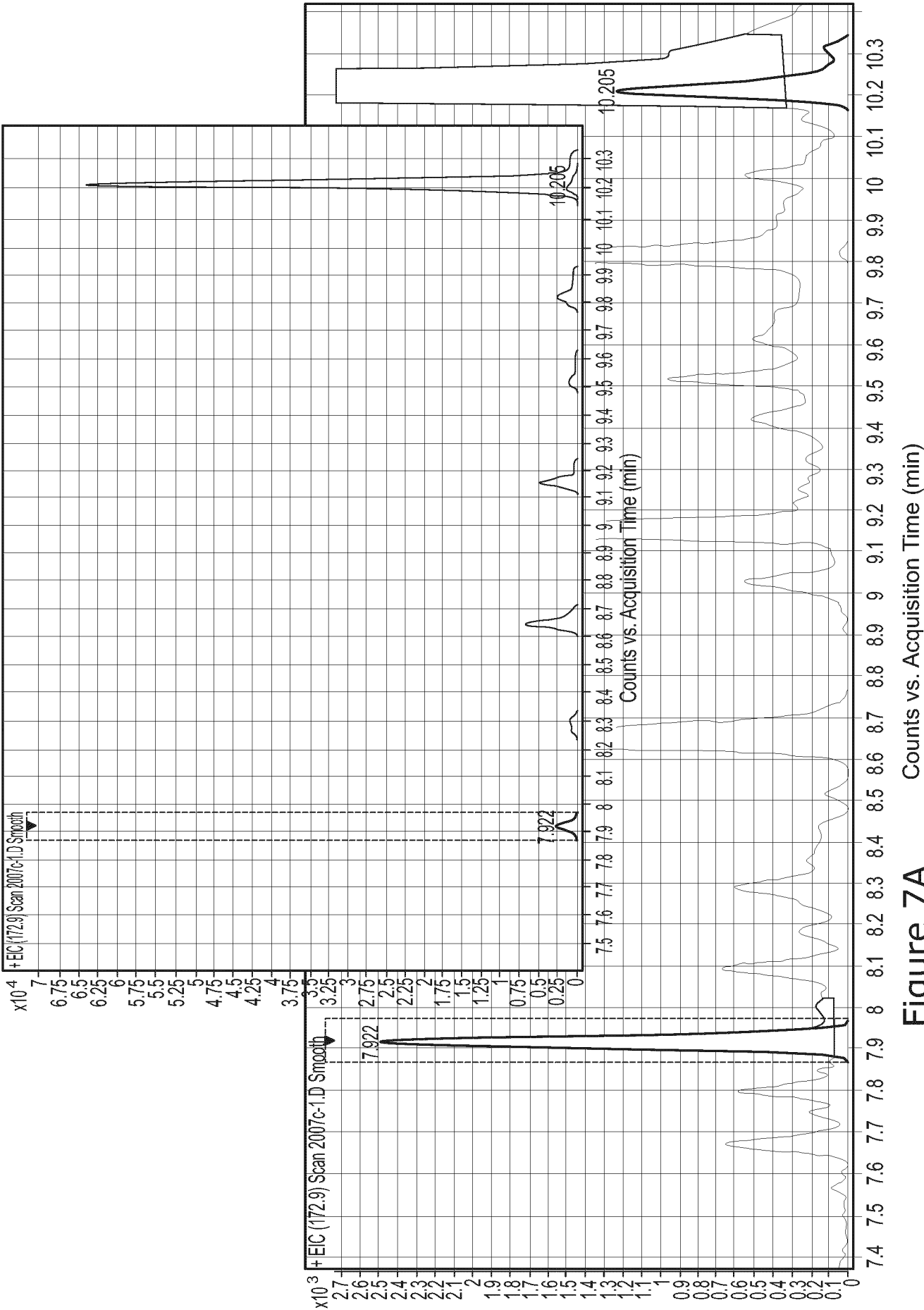


Figure 7A

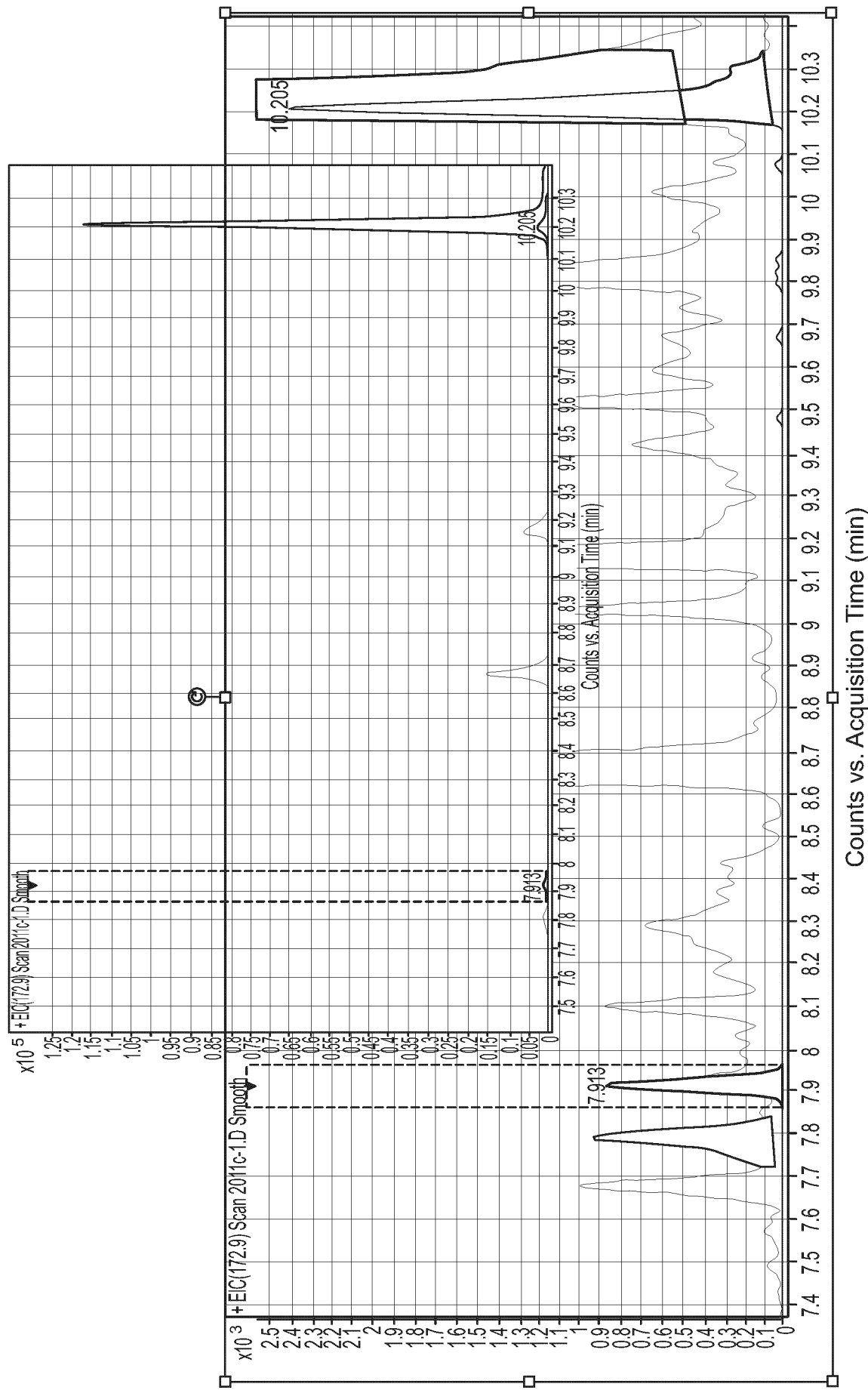


Figure 7B

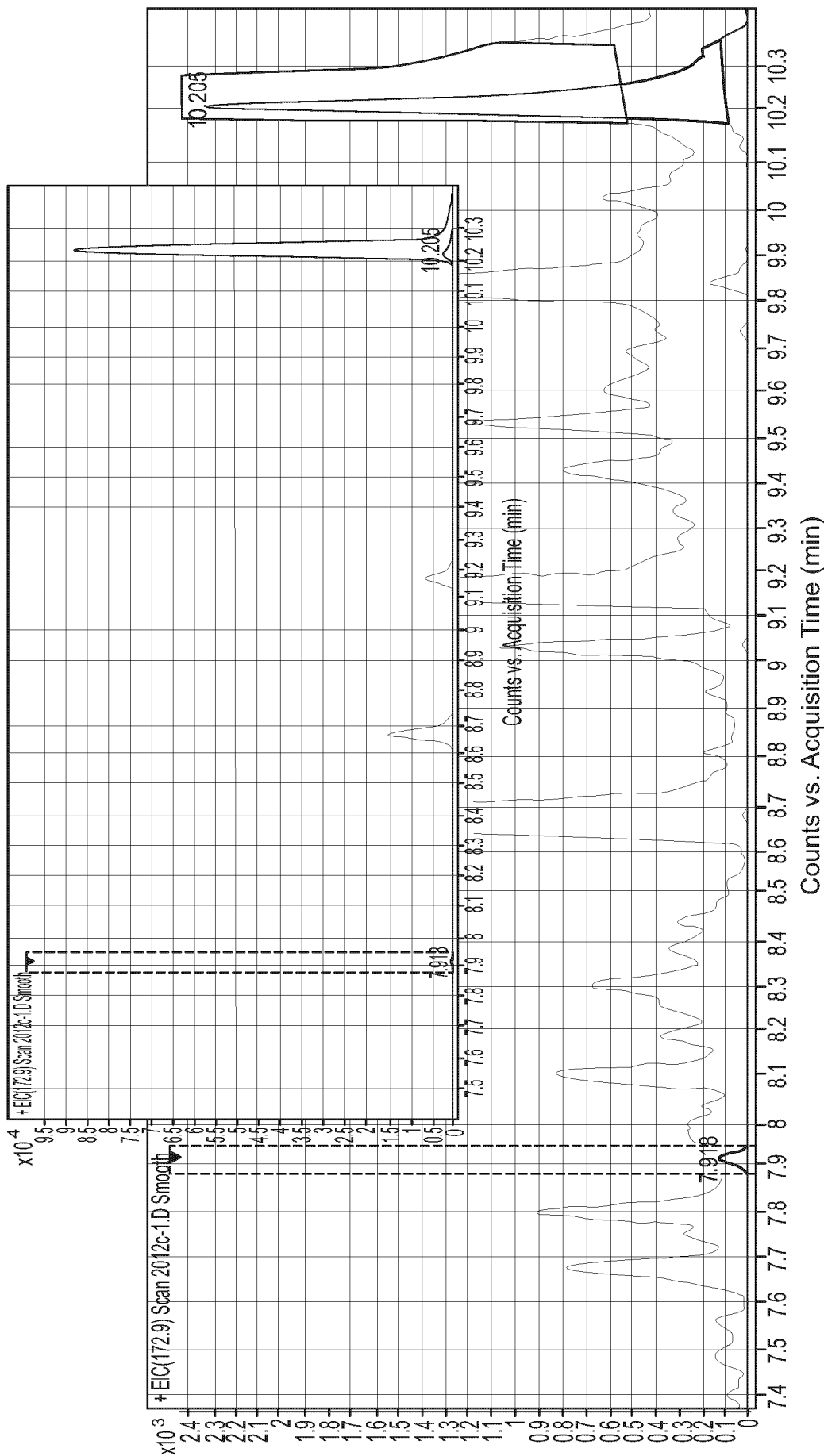


Figure 7C

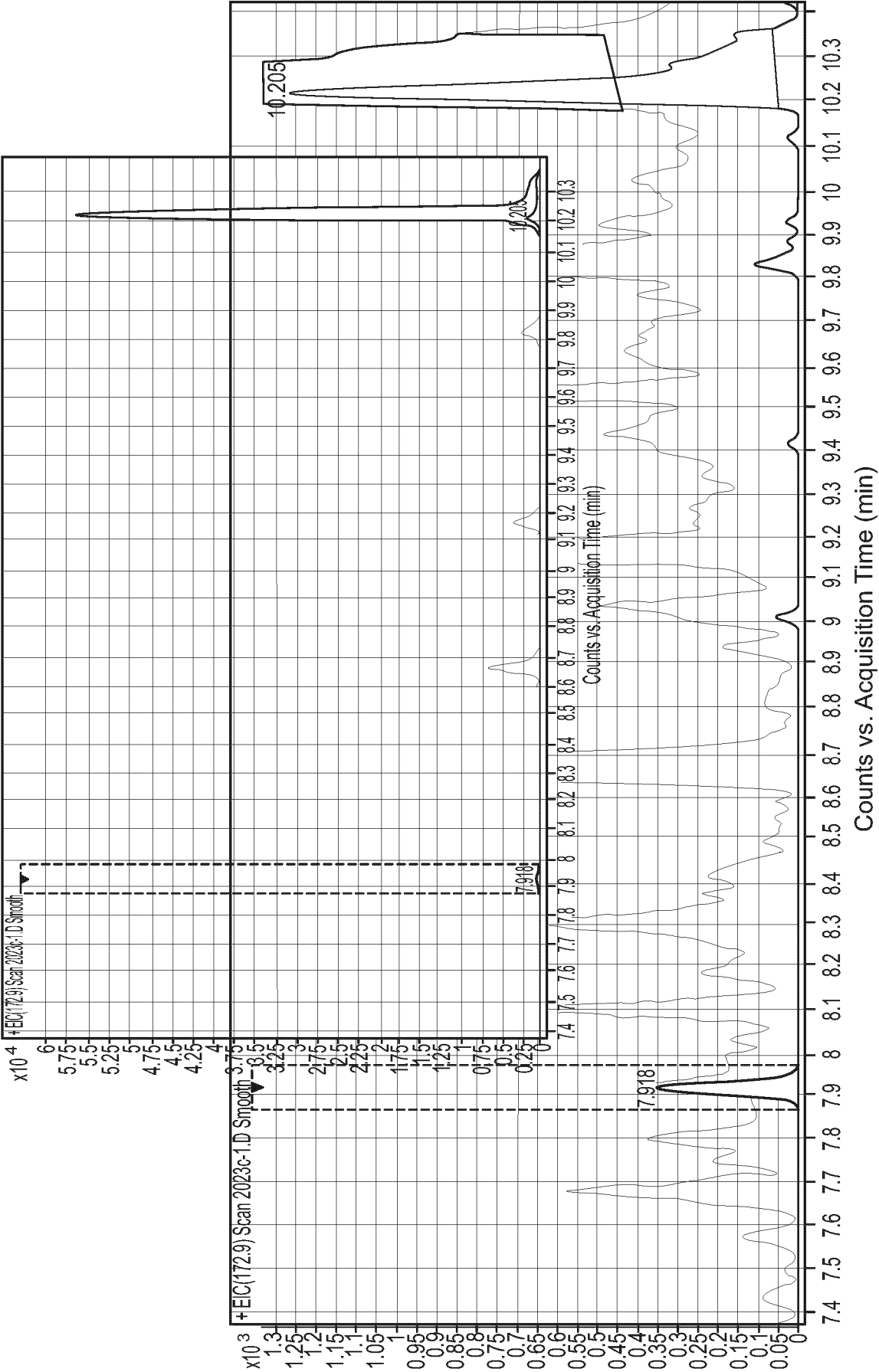


Figure 7D

Figure 7E

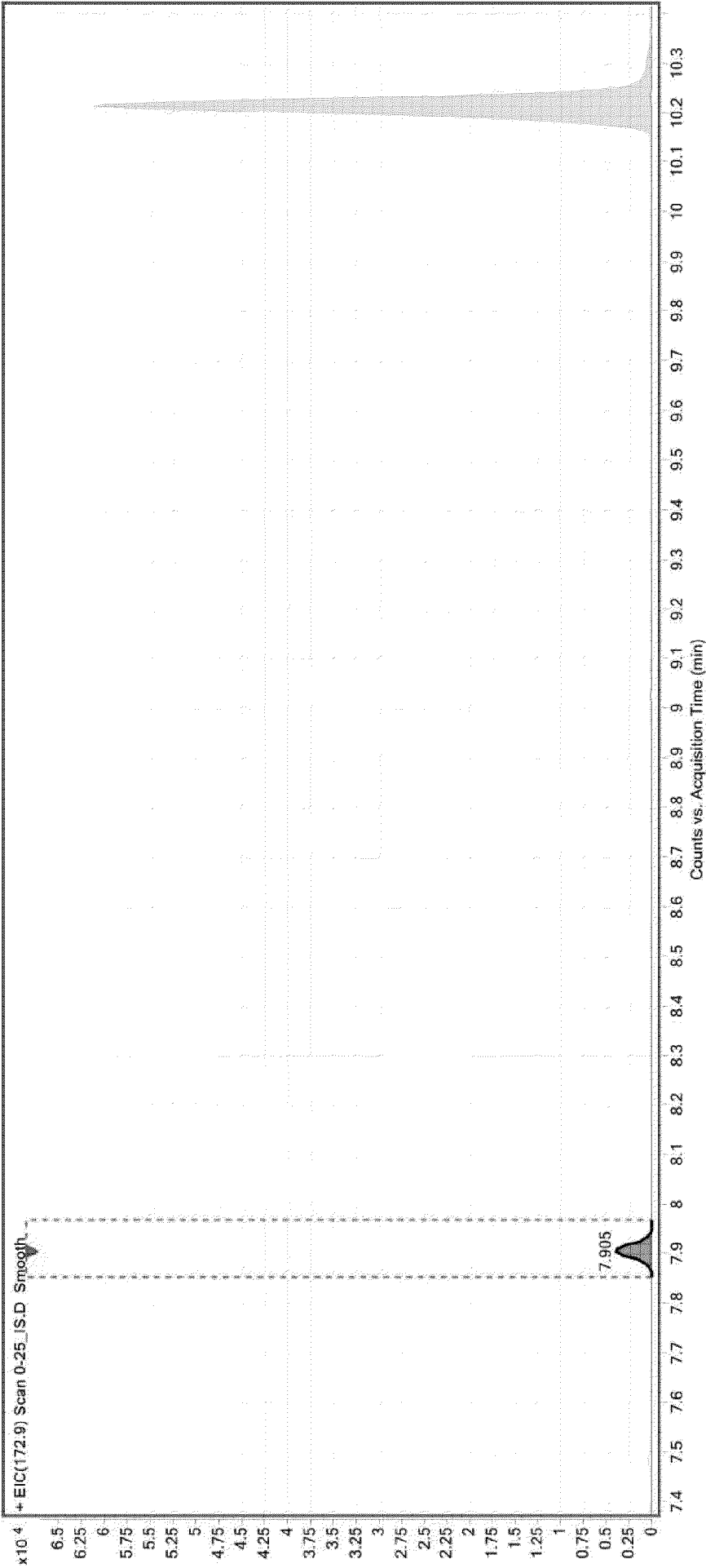


Figure 8

