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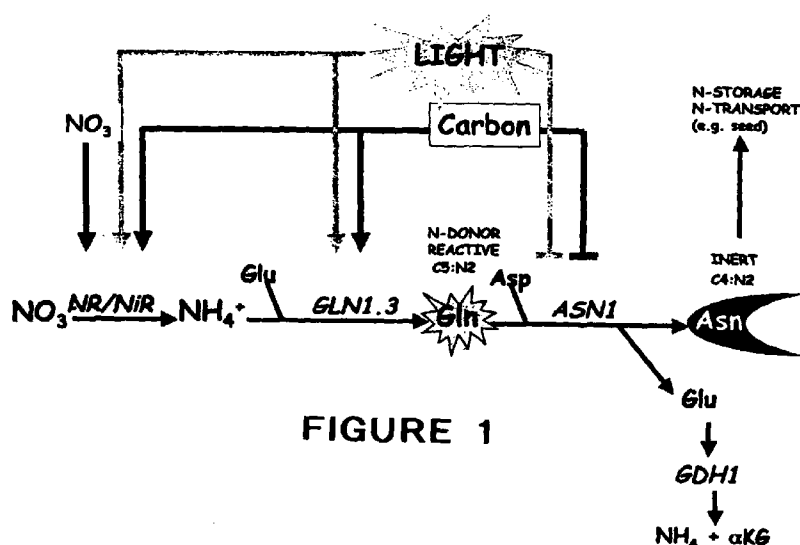


FIGURE 1

(57) Abstract: Provided herein are compositions and methods for producing transgenic plants. In specific embodiments, transgenic plants comprise a construct comprising a polynucleotide encoding CCA1, GLK1 or bZIP1, operably linked to a plant-specific promoter, wherein the CCA1, GLK1 or bZIP1 is ectopically overexpressed in the transgenic plants, and wherein the promoter is optionally a constitutive or inducible promoter. In other embodiments, transgenic plants in which express a lower level of CCA1, GLK1 or bZIP1 are provided. Also provided herein are commercial products {e.g., pulp, paper, paper products, or lumber) derived from the transgenic plants (e.g., transgenic trees) produced using the methods provided herein.

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METHODS OF AFFECTING NITROGEN ASSIMILATION IN PLANTS

The present application claims priority benefits of U.S. Provisional Application No. 60/919,818 filed March 23, 2007, which is incorporated by reference herein in its entirety.

1. INTRODUCTION

[0001] Provided herein are compositions and methods for affecting nitrogen assimilation, usage and storage by overexpressing or underexpressing certain genes in plants. Such genes include nitrogen-responsive master regulatory control genes *CCAI*, *GLK1* and *bZIP1*. In some embodiments, provided herein are compositions and methods for genetically engineering plants to increase *CCAI* or *GLK1* expression or decrease *bZIP1* expression, or any combination thereof. In other embodiments, provided herein are compositions and methods for genetically engineering plants to decrease *CCAI* or *GLK1* expression or increase *bZIP1* expression, or any combination thereof. In certain embodiments, the overexpression or underexpression is in a tissue- or cell-specific manner, *e.g.*, in vegetative tissue or in leaves or in fruit or seeds, or in specific cell types (*e.g.*, mesophyll, phloem, etc. In certain specific embodiments, a plant or tree is genetically engineered to increase or constitutively express *CCAI* and *GLK1* and to decrease expression of *bZIP1* in vegetative (growing) tissues of the plant. Such genetically engineered plants are able to assimilate more nitrogen into Gln, such that more nitrogen is available for biosynthesis, and thereby grow larger, more efficiently or rapidly, and/or have increased biomass. Alternatively, the engineered plants may be used to achieve faster growing or maturing crops or, higher crop yields and/or more nutritious products. In certain embodiments, the engineered plants and methods thereof are used in the production of commercial products. Some non-limiting example include genetically engineered trees for *e.g.*, the production of pulp, paper, paper products or lumber; tobacco, *e.g.*, for the production of cigarettes, cigars, or chewing tobacco; crops, *e.g.*, for the production of fruits, vegetables and other food, including grains, *e.g.*, for the production of wheat, bread, flour, rice, corn; and soybean, canola, *e.g.*, for the production of oils or biofuels. In other specific embodiments, a plant or tree is genetically engineered to increase or constitutively express *bZIP1* and to decrease expression of *CCAI* and *GLK1* in leaves, fruit and/or seed tissues of the plant. This would serve to increase N-assimilation into Asn, an inert N-storage compound used to transport N to seed, for example.

2. BACKGROUND

[0002] Nitrate is a key required nutrient for the synthesis of amino acids, nucleotides and vitamins and is commonly considered to be the most limiting for normal plant growth (Vitousek *et al.*, 2004, Biogeochemistry 13). Nitrogenous fertilizer is usually supplied as ammonium nitrate, potassium nitrate, or urea. Plants are keenly sensitive to nitrogen levels in the soil and, atypically of animal development, adopt their body plan to cope with their environment (Lopez-Bucio *et al.*, 2003, Curr Opin Plant Biol 6:280-287; Malamy *et al.*, 2005, Plant Cell Environ 28:67-77; Walch-Liu *et al.*, 2006, Ann Bot (Lond) 97:875-81). For example, mutants in several general nitrogen (N)-assimilation genes affect root architecture (Little *et al.*, 2005, Proc Natl Acad Sci U S A 102:13693-13698; Remans *et al.*, 2006, Proc Natl Acad Sci U S A 103:19206-19211). Transduction of this nitrogen signal is linked to a massive and concerted gene expression response in the root (Gutierrez *et al.*, 2007, Genome Biol 8:R7; Wang *et al.*, 2003, Plant Physiol 132:556-67).

[0003] Studies on the regulation of genes involved in the N-assimilatory pathway have shown that genes involved in N-assimilation are regulated transcriptionally by both inorganic and organic forms of nitrogen (Figure 1). Genes involved in the uptake and reduction of nitrate (NIA, NIR) are transcriptionally induced by nitrate. By contrast, the glutamine synthetase gene (*GLN1.3*) involved in assimilating inorganic N into organic form (Gln), is transcriptionally repressed by the endproducts of N-assimilation (Glu/Gln) (Figure 1). The repression of *GLN1.3* expression by the product of the GS enzyme reaction serves as a negative feedback loop, that shuts off further assimilation of inorganic N into Gln, when levels of Gln are abundant. As GS is an ATP dependent enzyme, this is likely to be an energy conservation mechanism. By contrast, Gln/Glu levels activate the expression of the *ASN1* gene (asparagine synthetase) which serves to transfer the amide N from Gln onto Asp to make Asn and Glu as a by-product. Asn is an inert amino acid used to store N and used for long distance N-transport (*e.g.*, to seed). The induction of *ASN1* by Glu/Gln is a mechanism that serves to store excess N as Asn, which is used to transport N to seed.

[0004] It would be advantageous to produce plants that would continue to assimilate and utilize N or to store N depending on whether a vegetative plant part or seed is the product, respectively, making N-assimilation independent of the Glu/Gln biofeedback pathway. N-assimilated into Glu/Gln by GS is used in the biosynthesis of all N-containing compounds including essentially all other amino acids, nucleic acids and chlorophyll. By contrast, the conversion of Gln to Asn (an inert N source) is used to transport and store N in seed.

3. SUMMARY

[0005] Master control genes (*CCAI*, *GLK1*, and *bZIP11*) that control N-assimilation in response to Glu sensing have been identified in the present invention. As these genes are transcription factor hubs, they coordinate the N-regulation of the N-assimilatory gene network, with genome-wide responses associated with growth and development in plants. Thus, effecting genome-wide changes in N-assimilation, plant growth and development, by the transgenic manipulation of these master control genes in plants will effect nitrogen use efficiency in vegetative tissues (leaves & roots) and also in seed. Changes in levels of N-assimilated into Gln effect changes in growth of vegetative tissues, while changes in levels of Asn affect seed development and nitrogen content.

[0006] Thus, the present invention relates to the transgenic manipulation of these N-responsive master regulatory genes (*CCAI*, *GLK1*, and *bZIP11*) that control N-assimilation, and other related processes in response to N treatments, so as to increase the overall N-assimilation capacity, whether for increased N usage or N storage. The overexpression of these master control genes (*e.g.*, uncoupled from Glu repression) effectively releases N-assimilation from the feedback repression loop by Glu- leading to increased N-assimilation and usage. As these regulatory genes serve to respond to Glu levels by reciprocally regulating the amount of N-assimilated into Gln versus the amount of Gln metabolized to Asn (for N-storage and transport), the manipulation of these genes in transgenic plants can be used to optimize N-assimilation into Gln versus Asn (Figure 2, Figure 12). Increased N-assimilation is advantageous in all crops. Additionally, in seed crops, the increased synthesis of Asn increases N-transported and stored in seed. The genes, *CCAI*, *GLK1* and/or *bZIP1*, can be expressed using constitutive promoters. Alternately, developmentally regulated promoters can be used to over express *CCAI* and/or *GLK1* that favors Gln production early in the life cycle, while switching to overexpressing *bZIP1* which favors Asn production later in the life cycle (*e.g.*, during seed set). Further, underexpressing *CCAI* and/or *GLK1* favors Asn production and underexpressing *bZIP1* favors Gln production.

[0007] As *CCAI/GLK1* and *bZIP11* are master regulatory genes controlling genes in the N-assimilatory pathway as well as other processes, the manipulation of these genes in transgenic plants can coordinate an increase in N-assimilation and usage (increased Gln synthesis), and/or an increase in stored N (increased Asn synthesis) with genes controlling aspects of growth and development, that are also targets for these master regulatory genes.

[0008] Thus, in one embodiment, the present invention is directed to a method for improving nitrogen assimilation and usage in a plant in which more nitrogen is available for

biosynthesis, said method comprising overexpressing *GLK1* in the plant. In another embodiment, the present invention is directed to a method for improving nitrogen assimilation and usage in a plant in which more nitrogen is available for biosynthesis, said method comprising overexpressing *CCAI* in the plant. In yet another embodiment, the present invention is directed to a method for improving nitrogen assimilation and usage in a plant in which more nitrogen is available for biosynthesis, said method comprising underexpressing *bZIP1* in the plant.

[0009] In another embodiment, the method for improving nitrogen assimilation and usage in a plant in which more nitrogen is available for biosynthesis comprises overexpressing *CCAI* and *GLK1* in the plant. In another embodiment, the method for improving nitrogen assimilation and usage in a plant in which more nitrogen is available for biosynthesis comprises overexpressing *CCAI* and underexpressing *bZIP1* in the plant, or overexpressing *GLK1* and underexpressing *bZIP1* in the plant. In yet another embodiment, the method for improving nitrogen assimilation and usage in a plant in which more nitrogen is available for biosynthesis comprises overexpressing *CCAI*, overexpressing *GLK1* and underexpressing *bZIP1* in the plant.

[0010] The present invention is also directed to methods for altering nitrogen assimilation and storage, *e.g.*, increasing nitrogen storage, in a plant. In one embodiment, the method comprises overexpressing *bZIP1* in the plant. In another embodiment, the method comprises underexpressing *CCAI* in the plant and/or underexpressing *GLK1* in the plant. In another embodiment, the method overexpressing *bZIP1* and underexpressing *CCAI* and/or *GLK1* in the plant. In yet another embodiment, the method comprises overexpressing *bZIP1*, and underexpressing *CCAI* and underexpressing *GLK1* in the plant.

[0011] In certain embodiments, the plant is species of woody, ornamental, decorative, crop, cereal, fruit, or vegetable. In other embodiments, the plant is a species of one of the following genres: *Acorus*, *Aegilops*, *Allium*, *Amborella*, *Antirrhinum*, *Apium*, *Arabidopsis*, *Arachis*, *Beta*, *Betula*, *Brassica*, *Capsicum*, *Ceratopteris*, *Citrus*, *Cryptomeria*, *Cycas*, *Descurainia*, *Eschscholzia*, *Eucalyptus*, *Glycine*, *Gossypium*, *Hedyotis*, *Helianthus*, *Hordeum*, *Ipomoea*, *Lactuca*, *Linum*, *Liriodendron*, *Lotus*, *Lupinus*, *Lycopersicon*, *Medicago*, *Mesembryanthemum*, *Nicotiana*, *Nuphar*, *Pennisetum*, *Persea*, *Phaseolus*, *Physcomitrella*, *Picea*, *Pinus*, *Poncirus*, *Populus*, *Prunus*, *Robinia*, *Rosa*, *Saccharum*, *Schedonorus*, *Secale*, *Sesamum*, *Solanum*, *Sorghum*, *Stevia*, *Thellungiella*, *Theobroma*, *Triphysaria*, *Triticum*, *Vitis*, *Zea*, or *Zinnia*.

[0012] The overexpression of a particular gene can be accomplished by any method known in the art, for example, by transforming a plant cell with a nucleic acid vector comprising the coding sequences of the desired gene operably linked to a promoter active in a plant cell such that the desired gene is expressed at levels higher than normal, *i.e.*, levels found in a control/nontransgenic plant. Such promoters can be constitutively active in all or some plant tissues or can be inducible.

[0013] The underexpression of a desired gene can be accomplished by any method known in the art, such as knocking out the gene or mutating the gene transgenically such that lower than normal levels of the gene product is produced in the transgenic cells or plant. For example, such mutations include frame-shift mutations or mutations resulting in a stop codon in the wild-type coding sequence, thus preventing expression of the gene product. Another exemplary mutation would be the removal of the transcribed sequences from the plant genome, for example, by homologous recombination. Another method for underexpressing a gene is transgenically introducing an insertion or deletion into the transcribed sequence or an insertion or deletion upstream or downstream of the transcribed sequence such that expression of the gene product is decreased as compared to wild-type or appropriate control. Additionally, microRNA can be used to target a particular encoding mRNA for degradation, thus reducing the level of the expressed gene product in the transgenic plant cell.

[0014] The present invention is also directed to a transgenic plant produced by any of the foregoing methods.

[0015] The present invention is also directed to compositions for modulating gene expression in plants. The compositions comprise constructs for the expression of *CCAI*, *GLK1* or *bZIP1*. In certain embodiments, a construct of the invention comprises a promoter, such as a tissue specific promoter, which is expressed in a plant cell, such as a leaf cell, and promotes the expression of *CCAI*, *GLK1* or *bZIP1*.

[0016] Any of a variety of promoters can be utilized in the constructs of the invention depending on the desired outcome. Tissue-specific or tissue-preferred promoters, inducible promoters, developmental promoters, constitutive promoters and/or chimeric promoters can be used to direct expression of the gene product in specific cells or organs the plant, when fused to the appropriate cell or organ specific promoter.

[0017] Chimeric constructs expressing *CCAI*, *GLK1* or *bZIP1* in transgenic plants (using constitutive or inducible promoters) can be used in the compositions and methods provided herein to enhance nitrogen assimilation and usage or increase nitrogen storage.

[0018] The present invention is also directed to a transgenic plant-derived commercial product. In one embodiment, the transgenic plant is a tree, and said commercial product is pulp, paper, a paper product, or lumber. In another embodiment, the transgenic plant is tobacco, and said commercial product is a cigarette, cigar, or chewing tobacco. In yet another embodiment, the transgenic plant is a crop, and said commercial product is a fruit or vegetable. In yet another embodiment, the transgenic plant is a grain, and said commercial product is bread, flour, cereal, oat meal, or rice. In another embodiment, the product is a biofuel or a plant oil.

4. TERMINOLOGY

[0019] Units, prefixes, and symbols may be denoted in their SI accepted form. Unless otherwise indicated, nucleic acids are written left to right in 5' to 3' orientation; amino acid sequences are written left to right in amino to carboxyl orientation, respectively. Numeric ranges recited within the specification are inclusive of the numbers defining the range and include each integer within the defined range. Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes. Unless otherwise provided for, software, electrical, and electronics terms as used herein are as defined in The New IEEE Standard Dictionary of Electrical and Electronics Terms (5th edition, 1993). The terms defined below are more fully defined by reference to the specification as a whole.

[0020] As used herein, the term "agronomic" includes, but is not limited to, changes in root size, vegetative yield, seed yield or overall plant growth. Other agronomic properties include factors desirable to agricultural production and business.

[0021] By "amplified" is meant the construction of multiple copies of a nucleic acid sequence or multiple copies complementary to the nucleic acid sequence using at least one of the nucleic acid sequences as a template. Amplification systems include the polymerase chain reaction (PCR) system, ligase chain reaction (LCR) system, nucleic acid sequence based amplification (NASBA, Cangene, Mississauga, Ontario), Q-Beta Replicase systems, transcription-based amplification system (TAS), and strand displacement amplification (SDA). See, *e.g.*, Diagnostic Molecular Microbiology: Principles and Applications, D. H. Persing *et al.*, Ed., 1993, American Society for Microbiology, Washington, D.C.. The product of amplification is termed an amplicon.

[0022] As used herein, “antisense orientation” includes reference to a duplex polynucleotide sequence that is operably linked to a promoter in an orientation where the antisense strand is transcribed. The antisense strand is sufficiently complementary to an endogenous transcription product such that translation of the endogenous transcription product is often inhibited.

[0023] In its broadest sense, a “delivery system,” as used herein, is any vehicle capable of facilitating delivery of a nucleic acid (or nucleic acid complex) to a cell and/or uptake of the nucleic acid by the cell.

[0024] The term “ectopic” is used herein to mean abnormal subcellular (*e.g.*, switch between organellar and cytosolic localization), cell-type, tissue-type and/or developmental or temporal expression (*e.g.*, light/dark) patterns for the particular gene or enzyme in question. Such ectopic expression does not necessarily exclude expression in tissues or developmental stages normal for said enzyme but rather entails expression in tissues or developmental stages not normal for the said enzyme.

[0025] By “endogenous nucleic acid sequence” and similar terms, it is intended that the sequences are natively present in the recipient plant genome and not substantially modified from its original form.

[0026] The term “exogenous nucleic acid sequence” as used herein refers to a nucleic acid foreign to the recipient plant host or, native to the host if the native nucleic acid is substantially modified from its original form. For example, the term includes a nucleic acid originating in the host species, where such sequence is operably linked to a promoter that differs from the natural or wild-type promoter.

[0027] By “encoding” or “encoded”, with respect to a specified nucleic acid, is meant comprising the information for translation into the specified protein. A nucleic acid encoding a protein may comprise non-translated sequences (*e.g.*, introns) within translated regions of the nucleic acid, or may lack such intervening non-translated sequences (*e.g.*, as in cDNA). The information by which a protein is encoded is specified by the use of codons. Typically, the amino acid sequence is encoded by the nucleic acid using the “universal” genetic code. However, variants of the universal code, such as are present in some plant, animal, and fungal mitochondria, the bacterium *Mycoplasma capricolum*, or the ciliate *Macronucleus*, may be used when the nucleic acid is expressed therein.

[0028] When the nucleic acid is prepared or altered synthetically, advantage can be taken of known codon preferences of the intended host where the nucleic acid is to be expressed. For example, although nucleic acid sequences of the present invention may be expressed in

both monocotyledonous and dicotyledonous plant species, sequences can be modified to account for the specific codon preferences and GC content preferences of monocotyledons or dicotyledons as these preferences have been shown to differ (Murray *et al.*, 1989, Nucl. Acids Res. 17: 477-498). Thus, the maize preferred codon for a particular amino acid may be derived from known gene sequences from maize. Maize codon usage for 28 genes from maize plants is listed in Table 4 of Murray *et al.*, *supra*.

[0029] By “fragment” is intended a portion of the nucleotide sequence. Fragments of the modulator sequence will generally retain the biological activity of the native suppressor protein. Alternatively, fragments of the targeting sequence may or may not retain biological activity. Such targeting sequences may be useful as hybridization probes, as antisense constructs, or as co-suppression sequences. Thus, fragments of a nucleotide sequence may range from at least about 20 nucleotides, about 50 nucleotides, about 100 nucleotides, and up to the full-length nucleotide sequence of the invention.

[0030] As used herein “full-length sequence” in reference to a specified polynucleotide or its encoded protein means having the entire amino acid sequence of, a native (non-synthetic), endogenous, biologically active form of the specified protein. Methods to determine whether a sequence is full-length are well known in the art including such exemplary techniques as northern or western blots, primer extension, S1 protection, and ribonuclease protection. See, *e.g.*, Plant Molecular Biology: A Laboratory Manual, Clark, Ed., 1997, Springer-Verlag, Berlin. Comparison to known full-length homologous (orthologous and/or paralogous) sequences can also be used to identify full-length sequences of the present invention. Additionally, consensus sequences typically present at the 5' and 3' untranslated regions of mRNA aid in the identification of a polynucleotide as full-length. For example, the consensus sequence ANNNNAUGG, where the underlined codon represents the N-terminal methionine, aids in determining whether the polynucleotide has a complete 5' end. Consensus sequences at the 3' end, such as polyadenylation sequences, aid in determining whether the polynucleotide has a complete 3' end.

[0031] The term “gene activity” refers to one or more steps involved in gene expression, including transcription, translation, and the functioning of the protein encoded by the gene.

[0032] The term “genetic modification” as used herein refers to the introduction of one or more exogenous nucleic acid sequences, *e.g.*, *CCAI*, *GLK1* or *bZIP1* encoding sequences, as well as regulatory sequences, into one or more plant cells, which in certain cases can generate whole, sexually competent, viable plants. The term “genetically modified” or “genetically engineered” as used herein refers to a plant which has been generated through the

aforementioned process. Genetically modified plants of the invention are capable of self-pollinating or cross-pollinating with other plants of the same species so that the foreign gene, carried in the germ line, can be inserted into or bred into agriculturally useful plant varieties.

[0033] As used herein, “heterologous” in reference to a nucleic acid is a nucleic acid that originates from a foreign species, or, if from the same species, is substantially modified from its native form in composition and/or genomic locus by deliberate human intervention. For example, a promoter operably linked to a heterologous structural gene is from a species different from that from which the structural gene was derived, or, if from the same species, one or both are substantially modified from their original form. A heterologous protein may originate from a foreign species or, if from the same species, is substantially modified from its original form by deliberate human intervention.

[0034] By “host cell” is meant a cell that contains a vector and supports the replication and/or expression of the vector. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, plant, insect, amphibian, or mammalian cells. Preferably, host cells are monocotyledonous or dicotyledonous plant cells. A particularly preferred monocotyledonous host cell is a maize host cell.

[0035] The term “introduced” in the context of inserting a nucleic acid into a cell, means “transfection” or “transformation” or “transduction” and includes reference to the incorporation of a nucleic acid into a eukaryotic or prokaryotic cell where the nucleic acid may be incorporated into the genome of the cell (*e.g.*, chromosome, plasmid, plastid or mitochondrial DNA), converted into an autonomous replicon, or transiently expressed (*e.g.*, transfected mRNA).

[0036] The term “isolated” refers to material, such as a nucleic acid or a protein, which is: (1) substantially or essentially free from components which normally accompany or interact with it as found in its natural environment. The isolated material optionally comprises material not found with the material in its natural environment; or (2) if the material is in its natural environment, the material has been synthetically altered or synthetically produced by deliberate human intervention and/or placed at a different location within the cell. The synthetic alteration or creation of the material can be performed on the material within or apart from its natural state. For example, a naturally-occurring nucleic acid becomes an isolated nucleic acid if it is altered or produced by non-natural, synthetic methods, or if it is transcribed from DNA which has been altered or produced by non-natural, synthetic methods. See, *e.g.*, Compounds and Methods for Site Directed Mutagenesis in Eukaryotic Cells, Kmiec, U.S. Pat. No. 5,565,350; *In vivo* Homologous Sequence Targeting

in Eukaryotic Cells; Zarling *et al.*, PCT/US93/03868. The isolated nucleic acid may also be produced by the synthetic re-arrangement (“shuffling”) of a part or parts of one or more allelic forms of the gene of interest. Likewise, a naturally-occurring nucleic acid (*e.g.*, a promoter) becomes isolated if it is introduced to a different locus of the genome. Nucleic acids which are “isolated,” as defined herein, are also referred to as “heterologous” nucleic acids.

[0037] As used herein, the term “marker” refers to a gene encoding a trait or a phenotype which permits the selection of, or the screening for, a plant or plant cell containing the marker.

[0038] As used herein, “nucleic acid” includes reference to a deoxyribonucleotide or ribonucleotide polymer, or chimeras thereof, in either single- or double-stranded form, and unless otherwise limited, encompasses known analogues having the essential nature of natural nucleotides in that they hybridize to single-stranded nucleic acids in a manner similar to naturally occurring nucleotides (*e.g.*, peptide nucleic acids).

[0039] By “nucleic acid library” is meant a collection of isolated DNA or RNA molecules which comprise and substantially represent the entire transcribed fraction of a genome of a specified organism or of a tissue from that organism. Construction of exemplary nucleic acid libraries, such as genomic and cDNA libraries, is taught in standard molecular biology references such as Berger and Kimmel, *Guide to Molecular Cloning Techniques*, *Methods in Enzymology*, Vol. 152, Academic Press, Inc., San Diego, Calif. (Berger); Sambrook *et al.*, 1989, *Molecular Cloning--A Laboratory Manual*, 2nd ed., Vol. 1-3; and *Current Protocols in Molecular Biology*, F. M. Ausubel *et al.*, Eds., 1994, *Current Protocols*, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc.

[0040] As used herein “operably linked” includes reference to a functional linkage between a promoter and a second sequence, wherein the promoter sequence initiates and mediates transcription of the DNA sequence corresponding to the second sequence. Generally, operably linked means that the nucleic acid sequences being linked are contiguous and, where necessary to join two protein coding regions, contiguous and in the same reading frame.

[0041] The term “orthologous” as used herein describes a relationship between two or more polynucleotides or proteins. Two polynucleotides or proteins are “orthologous” to one another if they are derived from a common ancestral gene and serve a similar function in different organisms. In general, orthologous polynucleotides or proteins will have similar

catalytic functions (when they encode enzymes) or will serve similar structural functions (when they encode proteins or RNA that form part of the ultrastructure of a cell).

[0042] The term “overexpression” is used herein to mean above the normal expression level in the particular tissue, all and/or developmental or temporal stage for said enzyme/expressed protein product.

[0043] As used herein, the term “plant” is used in its broadest sense, including, but is not limited to, any species of woody, ornamental or decorative, crop or cereal, fruit or vegetable plant, and algae (*e.g.*, *Chlamydomonas reinhardtii*). Non-limiting examples of plants include plants from the genus *Arabidopsis* or the genus *Oryza*. Other examples include plants from the genres *Acorus*, *Aegilops*, *Allium*, *Amborella*, *Antirrhinum*, *Apium*, *Arachis*, *Beta*, *Betula*, *Brassica*, *Capsicum*, *Ceratopteris*, *Citrus*, *Cryptomeria*, *Cycas*, *Descurainia*, *Eschscholzia*, *Eucalyptus*, *Glycine*, *Gossypium*, *Hedyotis*, *Helianthus*, *Hordeum*, *Ipomoea*, *Lactuca*, *Linum*, *Liriodendron*, *Lotus*, *Lupinus*, *Lycopersicon*, *Medicago*, *Mesembryanthemum*, *Nicotiana*, *Nuphar*, *Pennisetum*, *Persea*, *Phaseolus*, *Physcomitrella*, *Picea*, *Pinus*, *Poncirus*, *Populus*, *Prunus*, *Robinia*, *Rosa*, *Saccharum*, *Schedonorus*, *Secale*, *Sesamum*, *Solanum*, *Sorghum*, *Stevia*, *Thellungiella*, *Theobroma*, *Triphysaria*, *Triticum*, *Vitis*, *Zea*, or *Zinnia*.” Plants included in the invention are any plants amenable to transformation techniques, including gymnosperms and angiosperms, both monocotyledons and dicotyledons. Examples of monocotyledonous angiosperms include, but are not limited to, asparagus, field and sweet corn, barley, wheat, rice, sorghum, onion, pearl millet, rye and oats and other cereal grains. Examples of dicotyledonous angiosperms include, but are not limited to tomato, tobacco, cotton, rapeseed, field beans, soybeans, peppers, lettuce, peas, alfalfa, clover, cole crops or *Brassica oleracea* (*e.g.*, cabbage, broccoli, cauliflower, brussel sprouts), radish, carrot, beets, eggplant, spinach, cucumber, squash, melons, cantaloupe, sunflowers and various ornamentals. Examples of woody species include poplar, pine, sequoia, cedar, oak, *etc.* Still other examples of plants include, but are not limited to, wheat, cauliflower, tomato, tobacco, corn, petunia, trees, *etc.* As used herein, the term “cereal crop” is used in its broadest sense. The term includes, but is not limited to, any species of grass, or grain plant (*e.g.*, barley, corn, oats, rice, wild rice, rye, wheat, millet, sorghum, triticale, *etc.*), non-grass plants (*e.g.*, buckwheat flax, legumes or soybeans, *etc.*). As used herein, the term “crop” or “crop plant” is used in its broadest sense. The term includes, but is not limited to, any species of plant or algae edible by humans or used as a feed for animals or used, or consumed by humans, or any plant or algae used in industry or commerce. As used herein, the term “plant” also refers to either a whole plant, a plant part, or organs (*e.g.*, leaves, stems, roots, *etc.*), a plant cell, or a

group of plant cells, such as plant tissue, plant seeds and progeny of same. Plantlets are also included within the meaning of "plant." The class of plants which can be used in the methods of the invention is generally as broad as the class of higher plants amenable to transformation techniques, including both monocotyledonous and dicotyledonous plants.

[0044] The term "plant cell" as used herein refers to protoplasts, gamete producing cells, and cells which regenerate into whole plants. Plant cell, as used herein, further includes, without limitation, cells obtained from or found in: seeds, suspension cultures, embryos, meristematic regions, callus tissue, leaves, roots, shoots, gametophytes, sporophytes, pollen, and microspores. Plant cells can also be understood to include modified cells, such as protoplasts, obtained from the aforementioned tissues.

[0045] As used herein, "polynucleotide" includes reference to a deoxyribopolynucleotide, ribopolynucleotide, or chimeras or analogs thereof that have the essential nature of a natural deoxy- or ribo-nucleotide in that they hybridize, under stringent hybridization conditions, to substantially the same nucleotide sequence as naturally occurring nucleotides and/or allow translation into the same amino acid(s) as the naturally occurring nucleotide(s). A polynucleotide can be full-length or a subsequence of a native or heterologous structural or regulatory gene. Unless otherwise indicated, the term includes reference to the specified sequence as well as the complementary sequence thereof. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "polynucleotides" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritylated bases, to name just two examples, are polynucleotides as the term is used herein. It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful purposes known to those of skill in the art. The term polynucleotide as it is employed herein embraces such chemically-, enzymatically- or metabolically-modified forms of polynucleotides, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including among other things, simple and complex cells.

[0046] The terms "polypeptide", "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical analogue of a corresponding naturally-occurring amino acid, as well as to naturally-occurring amino acid polymers. The essential nature of such analogues of naturally-occurring amino acids is that, when incorporated into a protein, that protein is specifically reactive to antibodies elicited to the same protein but consisting entirely of naturally occurring amino acids. The terms

“polypeptide”, “peptide” and “protein” are also inclusive of modifications including, but not limited to, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation. Further, this invention contemplates the use of both the methionine-containing and the methionine-less amino terminal variants of the protein of the invention.

[0047] As used herein “promoter” includes reference to a region of DNA upstream from the start of transcription and involved in recognition and binding of RNA polymerase and other proteins to initiate transcription. A “plant promoter” is a promoter capable of initiating transcription in plant cells whether or not its origin is a plant cell. Exemplary plant promoters include, but are not limited to, those that are obtained from plants, plant viruses, and bacteria which comprise genes expressed in plant cells such *Agrobacterium* or *Rhizobium*. Examples of promoters under developmental control include promoters that preferentially initiate transcription in certain tissues, such as leaves, roots, or seeds. Such promoters are referred to as “tissue preferred.” Promoters which initiate transcription only in certain tissue are referred to as “tissue specific.” A “cell type” specific promoter primarily drives expression in certain cell types in one or more organs, for example, vascular cells in roots or leaves. An “inducible” or “repressible” promoter is a promoter which is under environmental control. Examples of environmental conditions that may effect transcription by inducible promoters include anaerobic conditions or the presence of light. Tissue specific, tissue preferred, cell type specific, and inducible promoters represent the class of “non-constitutive” promoters. A “constitutive” promoter is a promoter which is active under most environmental conditions.

[0048] As used herein “recombinant” includes reference to a cell or vector that has been modified by the introduction of a heterologous nucleic acid, or to a cell derived from a cell so modified. Thus, for example, recombinant cells express genes that are not found in identical form within the native (non-recombinant) form of the cell, or exhibit altered expression of native genes, as a result of deliberate human intervention. The term “recombinant” as used herein does not encompass the alteration of the cell or vector by events (*e.g.*, spontaneous mutation, natural transformation, transduction, or transposition) occurring without deliberate human intervention.

[0049] As used herein, a “recombinant expression cassette” is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements which permit transcription of a particular nucleic acid in a host cell. The recombinant expression cassette can be incorporated into a plasmid, chromosome, mitochondrial DNA, plastid DNA, virus, or nucleic acid fragment. Typically, the recombinant expression cassette

portion of an expression vector includes, among other sequences, a nucleic acid to be transcribed, and a promoter.

[0050] The term “regulatory sequence” as used herein refers to a nucleic acid sequence capable of controlling the transcription of an operably associated gene. Therefore, placing a gene under the regulatory control of a promoter or a regulatory element means positioning the gene such that the expression of the gene is controlled by the regulatory sequence(s).

Because a microRNA binds to its target, it is a post transcriptional mechanism for regulating levels of mRNA. Thus, an miRNA can also be considered a “regulatory sequence” herein.

Not just transcription factors.

[0051] The term “residue” or “amino acid residue” or “amino acid” are used interchangeably herein to refer to an amino acid that is incorporated into a protein, polypeptide, or peptide (collectively “protein”). The amino acid may be a naturally occurring amino acid and, unless otherwise limited, may encompass non-natural analogs of natural amino acids that can function in a similar manner as naturally occurring amino acids.

[0052] The term “tissue-specific promotor” is a polynucleotide sequence that specifically binds to transcription factors expressed primarily or only in such specific tissue.

[0053] The term “selectively hybridizes” includes reference to hybridization, under stringent hybridization conditions, of a nucleic acid sequence to a specified nucleic acid target sequence to a detectably greater degree (*e.g.*, at least 2-fold over background) than its hybridization to non-target nucleic acid sequences and to the substantial exclusion of non-target nucleic acids. Selectively hybridizing sequences typically have about at least 80% sequence identity, preferably 90% sequence identity, and most preferably 100% sequence identity (*i.e.*, complementary) with each other.

[0054] As used herein, a “stem-loop motif” or a “stem-loop structure,” sometimes also referred to as a “hairpin structure,” is given its ordinary meaning in the art, *i.e.*, in reference to a single nucleic acid molecule having a secondary structure that includes a double-stranded region (a “stem” portion) composed of two regions of nucleotides (of the same molecule) forming either side of the double-stranded portion, and at least one “loop” region, comprising uncomplemented nucleotides (*i.e.*, a single-stranded region).

[0055] The term “stringent conditions” or “stringent hybridization conditions” includes reference to conditions under which a probe will selectively hybridize to its target sequence, to a detectably greater degree than to other sequences (*e.g.*, at least 2-fold over background). Stringent conditions are sequence-dependent and will be different in different circumstances. By controlling the stringency of the hybridization and/or washing conditions, target

sequences can be identified which are 100% complementary to the probe (homologous probing). Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing). Generally, a probe is less than about 1000 nucleotides in length, optionally less than 500 nucleotides in length.

[0056] Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (*e.g.*, 10 to 50 nucleotides) and at least about 60°C for long probes (*e.g.*, greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1x to 2x SSC (20x SSC=3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.5x to 1x SSC at 55 to 60°C Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1x SSC at 60 to 65°C

[0057] Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl, 1984, *Anal. Biochem.*, 138:267-284: $T_m = 81.5^\circ\text{C} + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$; where M is the molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. The T_m is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe. T_m is reduced by about 1°C for each 1% of mismatching; thus, T_m , hybridization and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with $\geq 90\%$ identity are sought, the T_m can be decreased 10°C Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4°C lower than the thermal melting point (T_m); moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10°C lower than the thermal melting point (T_m); low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or

20°C lower than the thermal melting point (T_m). Using the equation, hybridization and wash compositions, and desired T_m , those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a T_m of less than 45°C (aqueous solution) or 32°C (formamide solution) it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen, 1993, *Laboratory Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes*, Part I, Chapter 2 "Overview of principles of hybridization and the strategy of nucleic acid probe assays", Elsevier, New York; and *Current Protocols in Molecular Biology*, Chapter 2, Ausubel *et al.*, Eds., 1995, Greene Publishing and Wiley-Interscience, New York. Hybridization and/or wash conditions can be applied for at least 10, 30, 60, 90, 120, or 240 minutes.

[0058] As used herein, "transcription factor" includes reference to a protein which interacts with a DNA regulatory element to affect expression of a structural gene or expression of a second regulatory gene. "Transcription factor" may also refer to the DNA encoding said transcription factor protein. The function of a transcription factor may include activation or repression of transcription initiation.

[0059] The term "transfection," as used herein, refers to the introduction of a nucleic acid into a cell, for example, a nucleotide sequence able to be transcribed to produce *CCA1*, *GLK1* or *BZIP1* protein.

[0060] As used herein, the term "transformation" means alteration of the genotype of a host plant by the introduction of a *CCA1*, *GLK1* or *BZIP1* nucleic acid sequence.

[0061] As used herein, "transgenic plant" includes reference to a plant which comprises within its genome a heterologous polynucleotide. Generally, the heterologous polynucleotide is stably integrated within the genome such that the polynucleotide is passed on to successive generations. The heterologous polynucleotide may be integrated into the genome alone or as part of a recombinant expression cassette. "Transgenic" is used herein to include any cell, cell line, callus, tissue, plant part or plant, the genotype of which has been altered by the presence of heterologous nucleic acid including those transgenics initially so altered as well as those created by sexual crosses or asexual propagation from the initial transgenic. The term "transgenic" as used herein does not encompass the alteration of the genome (chromosomal or extra-chromosomal) by conventional plant breeding methods or by naturally occurring events such as random cross-fertilization, non-recombinant viral

infection, non-recombinant bacterial transformation, non-recombinant transposition, or spontaneous mutation.

[0062] The term “underexpression” is used herein to mean below the normal expression level in the particular tissue, all and/or developmental or temporal stage for said enzyme/expressed protein product.

[0063] As used herein, “vector” includes reference to a nucleic acid used in introduction of a polynucleotide of the present invention into a host cell. Vectors are often replicons. Expression vectors permit transcription of a nucleic acid inserted therein.

[0064] The following terms are used to describe the sequence relationships between a polynucleotide/polypeptide of the present invention with a reference polynucleotide/polypeptide: (a) “reference sequence”, (b) “comparison window”, (c) “sequence identity”, and (d) “percentage of sequence identity”.

[0065] (a) As used herein, “reference sequence” is a defined sequence used as a basis for sequence comparison with a polynucleotide/polypeptide of the present invention. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full-length cDNA or gene sequence, or the complete cDNA or gene sequence.

[0066] (b) As used herein, “comparison window” includes reference to a contiguous and specified segment of a polynucleotide/polypeptide sequence, wherein the polynucleotide/polypeptide sequence may be compared to a reference sequence and wherein the portion of the polynucleotide/polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Generally, the comparison window is at least 20 contiguous nucleotides/amino acids residues in length, and optionally can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide/polypeptide sequence, a gap penalty is typically introduced and is subtracted from the number of matches.

[0067] Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman, 1981, *Adv. Appl. Math.* 2: 482; by the homology alignment algorithm of Needleman and Wunsch, 1970, *J. Mol. Biol.* 48: 443; by the search for similarity method of Pearson and Lipman, 1988, *Proc. Natl. Acad. Sci.* 85: 2444; by computerized implementations of these algorithms, including, but not limited to: CLUSTAL in the PC/Gene program by Intelligenetics, Mountain View, Calif.; GAP, BESTFIT, BLAST,

FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, Wis., USA; the CLUSTAL program is well described by Higgins and Sharp, 1988, *Gene* 73: 237-244; Higgins and Sharp, 1989, *CABIOS* 5: 151-153; Corpet *et al.*, 1988, *Nucleic Acids Research* 16: 10881-90; Huang *et al.*, 1992, *Computer Applications in the Biosciences* 8: 155-65; and Pearson *et al.*, 1994, *Methods in Molecular Biology* 24: 307-331.

[0068] The BLAST family of programs which can be used for database similarity searches includes: BLASTN for nucleotide query sequences against nucleotide database sequences; BLASTX for nucleotide query sequences against protein database sequences; BLASTP for protein query sequences against protein database sequences; TBLASTN for protein query sequences against nucleotide database sequences; and TBLASTX for nucleotide query sequences against nucleotide database sequences. See, *Current Protocols in Molecular Biology*, Chapter 19, Ausubel *et al.*, Eds., 1995, Greene Publishing and Wiley-Interscience, New York.

[0069] Software for performing BLAST analyses is publicly available, *e.g.*, through the National Center for Biotechnology Information (world-wide web at ncbi.nlm.nih.gov). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold. These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E)

of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, 1989, Proc. Natl. Acad. Sci. USA 89:10915).

[0070] In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, *e.g.*, Karlin & Altschul, 1993, Proc. Natl. Acad. Sci. USA 90:5873-5877). One measure of similarity provided by the BLAST algorithm is the smallest sum probability ($P(N)$), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance.

[0071] BLAST searches assume that proteins can be modeled as random sequences. However, many real proteins comprise regions of nonrandom sequences which may be homopolymeric tracts, short-period repeats, or regions enriched in one or more amino acids. Such low-complexity regions may be aligned between unrelated proteins even though other regions of the protein are entirely dissimilar. A number of low-complexity filter programs can be employed to reduce such low-complexity alignments. For example, the SEG (Wooten and Federhen, 1993, Comput. Chem., 17:149-163) and XNU (Claverie and States, 1993, Comput. Chem., 17:191-201) low-complexity filters can be employed alone or in combination.

[0072] Unless otherwise stated, nucleotide and protein identity/similarity values provided herein are calculated using GAP (GCG Version 10) under default values.

[0073] GAP (Global Alignment Program) can also be used to compare a polynucleotide or polypeptide of the present invention with a reference sequence. GAP uses the algorithm of Needleman and Wunsch (J. Mol. Biol. 48: 443-453, 1970) to find the alignment of two complete sequences that maximizes the number of matches and minimizes the number of gaps. GAP considers all possible alignments and gap positions and creates the alignment with the largest number of matched bases and the fewest gaps. It allows for the provision of a gap creation penalty and a gap extension penalty in units of matched bases. GAP must make a profit of gap creation penalty number of matches for each gap it inserts. If a gap extension penalty greater than zero is chosen, GAP must, in addition, make a profit for each gap inserted of the length of the gap times the gap extension penalty. Default gap creation penalty values and gap extension penalty values in Version 10 of the Wisconsin Genetics Software Package for protein sequences are 8 and 2, respectively. For nucleotide sequences the default gap creation penalty is 50 while the default gap extension penalty is 3. The gap creation and gap extension penalties can be expressed as an integer selected from the group of integers consisting of from 0 to 100. Thus, for example, the gap creation and gap

extension penalties can each independently be: 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30, 40, 50, 60 or greater.

[0074] GAP presents one member of the family of best alignments. There may be many members of this family, but no other member has a better quality. GAP displays four figures of merit for alignments: Quality, Ratio, Identity, and Similarity. The Quality is the metric maximized in order to align the sequences. Ratio is the quality divided by the number of bases in the shorter segment. Percent Identity is the percent of the symbols that actually match. Percent Similarity is the percent of the symbols that are similar. Symbols that are across from gaps are ignored. A similarity is scored when the scoring matrix value for a pair of symbols is greater than or equal to 0.50, the similarity threshold. The scoring matrix used in Version 10 of the Wisconsin Genetics Software Package is BLOSUM62 (see Henikoff & Henikoff, 1989, Proc. Natl. Acad. Sci. USA 89:10915).

[0075] Multiple alignment of the sequences can be performed using the CLUSTAL method of alignment (Higgins and Sharp, 1989, CABIOS. 5:151-153) with the default parameters (GAP PENALTY=10, GAP LENGTH PENALTY=10). Default parameters for pairwise alignments using the CLUSTAL method are KTUPLE 1, GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5.

[0076] (c) As used herein, "sequence identity" or "identity" in the context of two nucleic acid or polypeptide sequences includes reference to the residues in the two sequences which are the same when aligned for maximum correspondence over a specified comparison window. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (*e.g.*, charge or hydrophobicity) and therefore do not change the functional properties of the molecule. Where sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences which differ by such conservative substitutions are said to have "sequence similarity" or "similarity". Means for making this adjustment are well-known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, *e.g.*, according to the algorithm of Meyers and Miller, 1988, Computer Applic.

Biol. Sci., 4:11-17, *e.g.*, as implemented in the program PC/GENE (Intelligenetics, Mountain View, Calif., USA).

[0077] Polynucleotide sequences having “substantial identity” are those sequences having at least about 50%, 60% sequence identity, generally 70% sequence identity, preferably at least 80%, more preferably at least 90%, and most preferably at least 95%, compared to a reference sequence using one of the alignment programs described above. Preferably sequence identity is determined using the default parameters determined by the program. Substantial identity of amino acid sequences generally means sequence identity of at least 50%, more preferably at least 70%, 80%, 90%, and most preferably at least 95%. Nucleotide sequences are generally substantially identical if the two molecules hybridize to each other under stringent conditions.

[0078] (d) As used herein, “percentage of sequence identity” means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity.

[0079] As used herein, the term “transgenic,” when used in reference to a plant (*i.e.*, a “transgenic plant”) refers to a plant that contains at least one heterologous gene in one or more of its cells.

[0080] As used herein, “substantially complementary,” in reference to nucleic acids, refers to sequences of nucleotides (which may be on the same nucleic acid molecule or on different molecules) that are sufficiently complementary to be able to interact with each other in a predictable fashion, for example, producing a generally predictable secondary structure, such as a stem-loop motif. In some cases, two sequences of nucleotides that are substantially complementary may be at least about 75% complementary to each other, and in some cases, are at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, at least about 99.5%, or 100% complementary to each other. In some cases, two molecules that are sufficiently complementary may have a maximum of 40 mismatches (*e.g.*, where one base of the nucleic acid sequence does not have a complementary partner on the other nucleic acid sequence, for

example, due to additions, deletions, substitutions, bulges, *etc.*), and in other cases, the two molecules may have a maximum of 30 mismatches, 20 mismatches, 10 mismatches, or 7 mismatches. In still other cases, the two sufficiently complementary nucleic acid sequences may have a maximum of 0, 1, 2, 3, 4, 5, or 6 mismatches.

[0081] By “variants” is intended substantially similar sequences. For “variant” nucleotide sequences, conservative variants include those sequences that, because of the degeneracy of the genetic code, encode the amino acid sequence of the modulator of the invention. Variant nucleotide sequences include synthetically derived sequences, such as those generated, for example, using site-directed mutagenesis. Generally, variants of a particular nucleotide sequence of the invention will have at least about 40%, 50%, 60%, 65%, 70%, generally at least about 75%, 80%, 85%, preferably at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, and more preferably at least about 98%, 99% or more sequence identity to that particular nucleotide sequence as determined by sequence alignment programs described elsewhere herein using default parameters. By “variant” protein is intended a protein derived from the native protein by deletion or addition of one or more amino acids to the N-terminal and/or C-terminal end of the native protein; deletion or addition of one or more amino acids at one or more sites in the native protein; or substitution of one or more amino acids at one or more sites in the native protein. Such variants may result from, for example, genetic polymorphism or human manipulation. Conservative amino acid substitutions will generally result in variants that retain biological function

[0082] As used herein, the term “yield” or “plant yield” refers to increased plant growth, and/or increased biomass. In one embodiment, increased yield results from increased growth rate and increased root size. In another embodiment, increased yield is derived from shoot growth. In still another embodiment, increased yield is derived from fruit growth.

5. DESCRIPTION OF THE FIGURES

[0083] Figure 1. Schematic diagram of the nitrogen assimilation pathway.

[0084] Figure 2. Schematic diagram of the effects of transgenic overexpression or underexpression of master regulators *CCA1/GLK1/bZIP1* on nitrogen assimilation, usage and storage.

[0085] Figure 3. Network analysis of genes regulated by organic N suggests *CCA1* control N-assimilation in plants. In this Cytoscape-generated network, metabolic genes are drawn as triangles (transcription factors), hexagons (metabolic genes) whereas metabolites are shown as white circles. Arrows, diamonds or lines at the end of an edge indicate

directionality of the interaction. To simplify, some of the genes connecting to *GLK1* and *CCA1* are grouped and summarized based on their associated functions (number in parenthesis indicate the number of genes in the group).

[0086] Figure 4. Altered mRNA levels of target genes and binding of CCA1 protein to target gene promoter regions validate predicted regulation by CCA1. Fig. 4A: RT-qPCR was performed on *CCA1-ox*, *glk1* knockout, and wild-type plants to determine mRNA levels for *ASN1*, *GLN1.3*, and *GDH1*. Three biological and two technical replicates were carried out for each sample. mRNA levels were normalized to clathrin (*At4g24550*). The mean $\pm$ standard error of the mean is shown. Fig. 4B: ChIP assays to show binding of CCA1 to *GLN1.3*, *GDH1* and *bZIP1* gene promoter regions. Control: input DNA control (no IP), -Ab: IP without antibody, CCA1: IP with the CCA1 antibody.

[0087] Figure 5. Exposure of seedlings to pulses of inorganic and organic N shifts the phase of the circadian clock. Figs. 5A-C: Plot of the phase shift of *CCA1::LUC* expression in response to 4-h pulse of inorganic N (20mM KNO_3 /20mM NH_4NO_3), 10mM Glu, or 10 mM Gln against the time at which the pulse was administered to wild-type seedlings. Pulses were administered at 3-hr intervals spanning one complete circadian cycle and data were collected over the next 6 cycles. Phase shifts are double-plotted to emphasize the circadian pattern of the response. Phase advances (the peak in expression occurring earlier) are plotted as positive values and delays are plotted as negative values. Fig. 5D shows the *CCA1::LUC* expression of control (untreated) seedlings. In all panels, the entraining photocycle (16:8) is indicated by the vertical white (light) and gray (dark) bars. The mean $\pm$ standard error of the mean is shown.

[0088] Figure 6. Proposed model of the interaction between the *Arabidopsis* circadian clock and N-assimilatory pathway. Arrows indicate influences that affect the function of the two processes. Black arrow: Clock function would affect N-assimilation. This influence is at least partly due to the direct regulatory role of CCA1 on N-assimilation. Grey arrow: N-assimilation would influence clock function through downstream metabolites such as Glu, Gln and possibly other N-metabolites.

[0089] Figure 7. Signaling by inorganic vs. organic nitrogen can be distinguished by using MSX and Glu treatments. (a) Treatments include $\text{N} \pm \text{MSX} \pm \text{Glu}$. (b) A simplified diagram of the N-metabolic pathway from inorganic nitrate (NO_3) to organic Glu, and the block by MSX. Below this pathway are the predicted effects of the given treatments on nitrogen metabolism. Arrows indicate progression through the pathway. Line breaks, represented with a short perpendicular line, indicate the step in the pathway blocked by MSX.

(c and d). The expected transcript levels for genes induced by inorganic nitrogen (c) vs. genes regulated by Glu or a Glu-derived metabolite (d).

[0090] Figure 8. Analysis of the expression of asparagine synthetase genes. Shown is a comparison of *ASN1* (a) and *ASN2* (b) mRNA levels in control seedlings (transferred to 1 mM NO₃) along with MSX control (treated with NO₃ and 1 mM MSX) compared to seedlings treated with a stepwise combination of Nms, MSX, and Glu/Gln. (a) mRNA levels of *ASN1* are increased in Nms, are sensitive to MSX treatment, and can be recovered with exogenous application of Glu or Gln. (b) mRNA levels of *ASN2* are increased in Nms. However, this expression is insensitive to MSX treatment and is slightly repressed with exogenous application of Glu or Gln. mRNA levels were normalized to *EIF4A* (At3g13920).

[0091] Figure 9. RT-qPCR confirmation of the regulation for two transcription factors TAZ and bZIP1. Shown is confirmation of TAZ (Fig. 9A) and bZIP1 (Fig. 9B) mRNA levels in control seedlings along with the MSX control and compared to seedlings treated with a stepwise combination of Nms, Nms+MSX, and Nms+MSX+Glu (or Gln). In both cases, although increased expression in the presence of N is blocked in the presence of MSX, this suppression can be overcome by exogenous application of Glu or Gln. Plants transferred to control media do not show mRNA levels different from treatments without MSX. Primers used for RT-qPCR are as follows: TAZ forward, 5'-TCCTCGTCTCGGTCTT-3' (SEQ ID NO:1); reverse, 5'-CAACCACCAGGGATTC-3' (SEQ ID NO:2); bZIP forward, 5'-TCAGGTTCCGACATAGATG-3' (SEQ ID NO:3); reverse, 5'-CCACGGTGTACGTCTACA-3' (SEQ ID NO:4).

[0092] Figure 10. Analysis of the expression of *bZIP1* in the *CCA1-ox*. To test some of the predictions of our network *CCA1-ox* and Col-0 plants were collected 3 h after dawn; three biological replicates were taken at each time point. RNA was extracted from whole seedlings (as described in Materials and Methods), and RT-qPCR was performed to measure mRNA levels for *bZIP1* (At5g49450). Two technical replicates were carried out for each sample. mRNA levels were normalized to clathrin (At4g24550).

[0093] Figure 11. Circadian regulation of the response of clock gene (*CCA1*) expression to N-assimilation inhibitors and inorganic and organic N. Mean $\pm$ SEM luciferase activity of *CCA1::LUC* in response to exogenous inorganic N, Glu, or Gln is presented. Seedlings were entrained for 8 days in a 16-h white light/8-h dark photoperiod on MS medium containing 1 mM KNO₃ before being transferred to continuous light and exposed for 4-h pulses of inorganic N (20 mM KNO₃/20 mM NH₄NO₃), 10 mM Glu, or 10 mM Gln presented at 3-h intervals over one circadian cycle before return to MS medium containing 1 mM KNO₃ in

continuous light for luciferase measurements for 6 days. Luciferase activity values were normalized by the mean expression value for the treatment. The entraining photocycle is indicated by the vertical white (light) and gray (dark) bars.

[0094] Figure 12. Schematic diagram of how *CCA1/GLK1/bZIP1* transcription factors coordinate the nitrogen regulation of genes in the nitrogen assimilation pathway.

6. DETAILED DESCRIPTION

[0095] Master control genes (*CCA1*, *GLK1*, and *bZIP11*) that control N-assimilation in response to Glu sensing have been identified in the present invention. As these genes are transcription factor hubs, they coordinate the N-regulation of the N-assimilatory gene network, with genome-wide responses associated with growth and development in plants. Thus, effecting genome-wide changes in N-assimilation, plant growth and development, by the transgenic manipulation of these master control genes in plants effects nitrogen use efficiency in vegetative tissues (leaves & roots) and also in seed. Changes in levels of N-assimilated into Gln effect changes in growth of vegetative tissues, while changes in levels of Asn affect seed development.

[0096] Thus, the present invention relates to the transgenic manipulation of these N-responsive master regulatory genes (*CCA1*, *GLK1*, and *bZIP11*) that control N-assimilation, and other related processes in response to N treatments, so as to increase the overall N-assimilation capacity, whether for increased N usage or N storage. The overexpression of these master control genes (*e.g.*, uncoupled from Glu repression) effectively releases N-assimilation from the feedback repression loop by Glu- leading to increased N-assimilation and usage. As these regulatory genes serve to respond to Glu levels by reciprocally regulating the amount of N-assimilated into Gln versus the amount of Gln metabolized to Asn (for N-storage and transport), the manipulation of these genes in transgenic plants can be used to optimize N-assimilation into Gln versus Asn (Figure 6). Increased N-assimilation is advantageous in all crops. Additionally, in seed crops, the increased synthesis of Asn increases N-transported and stored in seed.

[0097] Thus, in one embodiment, the present invention is directed to a method for improving nitrogen assimilation and usage in a plant in which more nitrogen is available for biosynthesis, said method comprising overexpressing *GLK1* in the plant. In another embodiment, the present invention is directed to a method for improving nitrogen assimilation and usage in a plant in which more nitrogen is available for biosynthesis, said method comprising overexpressing *CCA1* in the plant. In yet another embodiment, the

present invention is directed to a method for improving nitrogen assimilation and usage in a plant in which more nitrogen is available for biosynthesis, said method comprising underexpressing *bZIP1* in the plant.

[0098] In another embodiment, the method for improving nitrogen assimilation and usage in a plant in which more nitrogen is available for biosynthesis comprises overexpressing *CCA1* and *GLK1* in the plant. In another embodiment, the method for improving nitrogen assimilation and usage in a plant in which more nitrogen is available for biosynthesis comprises overexpressing *CCA1* and underexpressing *bZIP1* in the plant, or overexpressing *GLK1* and underexpressing *bZIP1* in the plant. In yet another embodiment, the method for improving nitrogen assimilation and usage in a plant in which more nitrogen is available for biosynthesis comprises overexpressing *CCA1*, overexpressing *GLK1* and underexpressing *bZIP1* in the plant.

[0099] The present invention is also directed to methods for altering nitrogen assimilation and storage, *e.g.*, increasing nitrogen storage, in a plant. In one embodiment, the method comprises overexpressing *bZIP1* in the plant. In another embodiment, the method comprises underexpressing *CCA1* in the plant and/or underexpressing *GLK1* in the plant. In another embodiment, the method overexpressing *bZIP1* and underexpressing *CCA1* and/or *GLK1* in the plant. In yet another embodiment, the method comprises overexpressing *bZIP1*, and underexpressing *CCA1* and underexpressing *GLK1* in the plant.

[00100] In certain embodiments, the plant is species of woody, ornamental, decorative, crop, cereal, fruit, or vegetable. In other embodiments, the plant is a species of one of the following genera: *Acorus*, *Aegilops*, *Allium*, *Amborella*, *Antirrhinum*, *Apium*, *Arabidopsis*, *Arachis*, *Beta*, *Betula*, *Brassica*, *Capsicum*, *Ceratopteris*, *Citrus*, *Cryptomeria*, *Cycas*, *Descurainia*, *Eschscholzia*, *Eucalyptus*, *Glycine*, *Gossypium*, *Hedyotis*, *Helianthus*, *Hordeum*, *Ipomoea*, *Lactuca*, *Linum*, *Liriodendron*, *Lotus*, *Lupinus*, *Lycopersicon*, *Medicago*, *Mesembryanthemum*, *Nicotiana*, *Nuphar*, *Pennisetum*, *Persea*, *Phaseolus*, *Physcomitrella*, *Picea*, *Pinus*, *Poncirus*, *Populus*, *Prunus*, *Robinia*, *Rosa*, *Saccharum*, *Schedonorus*, *Secale*, *Sesamum*, *Solanum*, *Sorghum*, *Stevia*, *Thellungiella*, *Theobroma*, *Triphysaria*, *Triticum*, *Vitis*, *Zea*, or *Zinnia*.

[00101] The overexpression of a particular gene can be accomplished by any method known in the art, for example, by transforming a plant cell with a nucleic acid vector comprising the coding sequences of the desired gene operably linked to a promoter active in a plant cell such that the desired gene is expressed at levels higher than normal, *i.e.*, levels

found in a control/nontransgenic plant. Such promoters can be constitutively active in all or some plant tissues or can be inducible.

[00102] The underexpression of a desired gene can be accomplished by any method known in the art, such as knocking out the gene or mutating the gene transgenically such that lower than normal levels of the gene product is produced in the transgenic cells or plant. For example, such mutations include frame-shift mutations or mutations resulting in a stop codon in the wild-type coding sequence, thus preventing expression of the gene product. Another exemplary mutation would be the removal of the transcribed sequences from the plant genome, for example, by homologous recombination. Another method for underexpressing a gene is transgenically introducing an insertion or deletion into the transcribed sequence or an insertion or deletion upstream or downstream of the transcribed sequence such that expression of the gene product is decreased as compared to wild-type or appropriate control. Additionally, microRNA (native or artificial) can be used to target a particular encoding mRNA for degradation, thus reducing the level of the expressed gene product in the transgenic plant cell.

[00103] The present invention is also directed to a transgenic plant produced by any of the foregoing methods.

[00104] The present invention is also directed to compositions for modulating gene expression in plants. The compositions comprise constructs for the expression of *CCA1*, *GLK1* or *bZIP1*. In certain embodiments, a construct of the invention comprises a promoter, such as a tissue specific promoter, which is expressed in a plant cell, such as a leaf cell, and promotes the expression of *CCA1*, *GLK1* or *bZIP1*.

[00105] Any of a variety of promoters can be utilized in the constructs of the invention depending on the desired outcome. Tissue-specific or tissue-preferred promoters, inducible promoters, developmental promoters, constitutive promoters and/or chimeric promoters can be used to direct expression of the gene product in specific cells or organs the plant, when fused to the appropriate cell or organ specific promoter.

[00106] Chimeric constructs expressing *CCA1*, *GLK1* or *bZIP1* in transgenic plants (using constitutive or inducible promoters) can be used in the compositions and methods provided herein to enhance nitrogen assimilation and usage or increase nitrogen storage.

[00107] The present invention is also directed to a transgenic plant-derived commercial product. In one embodiment, the transgenic plant is a tree, and said commercial product is pulp, paper, a paper product, or lumber. In another embodiment, the transgenic plant is tobacco, and said commercial product is a cigarette, cigar, or chewing tobacco. In yet

another embodiment, the transgenic plant is a crop, and said commercial product is a fruit or vegetable. In yet another embodiment, the transgenic plant is a grain, and said commercial product is bread, flour, cereal, oat meal, or rice. In another embodiment, the product is a biofuel or a plant oil.

6.1 Master Regulators

[00108] CIRCADIAN CLOCK ASSOCIATED 1 (*CCA1*) gene encodes a MYB-related transcription factor involved in the phytochrome induction of a light-harvesting chlorophyll a/b-protein gene. The nucleotide and amino acid sequences of *CCA1* from *Arabidopsis* are known, see Accession No. At2g46830. Further, orthologous *CCA1* genes from other organisms are also known. For example, the *CCA1* gene sequences from poplar can be found under Accession Nos. Poptrl#552368 or Poptrl#731468. The use of *CCA1* in the present invention refers not only to the *Arabidopsis* gene but also the orthologous *CCA1* gene from other species. Thus, in one embodiment, plant species-specific *CCA1* genes can be used in plants of the same species, *e.g.*, tobacco *CCA1* can be overexpressed in tobacco.

Additionally, such orthologous sequences can be identified and isolated using methods known in the art, such as hybridization methods and then testing the isolated sequences for *CCA1* activity, as demonstrated *infra*. Other methods, such as alignment methods described *supra* can also be used to identify and isolate orthologous *CCA1* sequences.

[00109] Golden 2-like genes (*GLK*) are members of the GARP superfamily of transcription factors. *GLK* genes are known to be involved in the regulation of chloroplast development in diverse plant species (Fritter *et al.*, 2002, The Plant Journal 31:713-727). The nucleotide and amino acid sequences of *GLK1* from *Arabidopsis* are known, see Accession No. At2g20570. Further, orthologous *GLK1* genes from other organisms are also known. For example, the *GLK1* gene sequences from poplar and rice can be found under Accession Nos. Poptrl#654401 and Os06g24070, respectively. The use of *GLK1* in the present invention refers not only to the *Arabidopsis* gene but also the orthologous *GLK1* gene from other species. Thus, in one embodiment, plant species-specific *GLK1* genes can be used in plants of the same species, *e.g.*, tobacco *GLK1* can be overexpressed in tobacco.

Additionally, such orthologous sequences can be identified and isolated using methods known in the art, such as hybridization methods and then testing the isolated sequences for *GLK1* activity, such as DNA binding activity. Other methods, such as alignment methods described *supra* can also be used to identify and isolate orthologous *GLK1* sequences.

[00110] *bZIP1* is a transcription factor that belongs to the largest *bZIP* group in *Arabidopsis*, Group S (Jakoby *et al.*, 2002, Trends Plant Sci 7:106-111). It is thought that Group S *bZIP* genes are involved in balancing carbohydrate demand and supply (Rook *et al.*, 1998, Plant J 15:253-263). The nucleotide and amino acid sequences of *bZIP1* from *Arabidopsis* are known, see Accession No. At5g49450. The use of *bZIP1* in the present invention refers not only to the *Arabidopsis* gene but also the orthologous *bZIP1* gene from other species. Thus, in one embodiment, plant species-specific *bZIP1* genes can be used in plants of the same species, *e.g.*, tobacco *bZIP1* can be overexpressed in tobacco. Additionally, such orthologous sequences can be identified and isolated using methods known in the art, such as hybridization methods and then testing the isolated sequences for *bZIP1* activity, such as DNA binding activity. Other methods, such as alignment methods described *supra* can also be used to identify and isolate orthologous *bZIP1* sequences.

6.2 Modulation of Gene Expression

[00111] The methods of the invention involve modulation of the expression of one, two, three or more target nucleotide sequences in a plant, optionally in specific tissues such as vegetative tissues or leaves or seeds. That is, the expression of a target nucleotide sequence of interest may be increased or decreased. In specific embodiments, the target nucleotide sequences are *CCA1*, *GLK1* or *bZIP1*, which can be increased or decreased.

[00112] The target nucleotide sequences may be endogenous or exogenous in origin. By “modulate expression of a target gene” is intended that the expression of the target gene is increased or decreased relative to the expression level in a plant that has not been altered by the methods described herein.

[00113] By “increased or over expression” is intended that expression of the target nucleotide sequence is increased over expression observed in conventional transgenic lines for heterologous genes and over endogenous levels of expression for homologous genes. Heterologous or exogenous genes comprise genes that do not occur in the plant of interest in its native state. Homologous or endogenous genes are those that are natively present in the plant genome. Generally, expression of the target sequence is substantially increased. That is expression is increased at least about 25%-50%, preferably about 50%-100%, more preferably about 100%, 200% and greater.

[00114] By “decreased expression” or “underexpression” it is intended that expression of the target nucleotide sequence is decreased below expression observed in conventional transgenic lines for heterologous genes and below endogenous levels of expression for

homologous genes. Generally, expression of the target nucleotide sequence of interest is substantially decreased. That is expression is decreased at least about 25%-50%, preferably about 50%-100%, more preferably about 100%, 200% and greater.

[00115] Expression levels may be assessed by determining the level of a gene product by any method known in the art including, but not limited to determining the levels of the RNA and protein encoded by a particular target gene. For genes that encode proteins, expression levels may determined, for example, by quantifying the amount of the protein present in plant cells, or in a plant or any portion thereof. Alternatively, if desired target gene encodes a protein that has a known measurable activity, then activity levels may be measured to assess expression levels.

6.3 Transformation / Transfection

[00116] Any method or delivery system may be used for the delivery and/or transfection of the nucleic acid vectors encoding any of the master regulators of the present invention in the cell. The vectors may be delivered to the plant cell either alone, or in combination with other agents.

[00117] Transfection may be accomplished by a wide variety of means, as is known to those of ordinary skill in the art. Such methods include, but are not limited to, *Agrobacterium*-mediated transformation (*e.g.*, Komari *et al.*, 1998, Curr. Opin. Plant Biol., 1:161), particle bombardment mediated transformation (*e.g.*, Finer *et al.*, 1999, Curr. Top. Microbiol. Immunol., 240:59), protoplast electroporation (*e.g.*, Bates, 1999, Methods Mol. Biol., 111:359), viral infection (*e.g.*, Porta and Lomonossoff, 1996, Mol. Biotechnol. 5:209), microinjection, and liposome injection. Other exemplary delivery systems that can be used to facilitate uptake by a cell of the nucleic acid include calcium phosphate and other chemical mediators of intracellular transport, microinjection compositions, and homologous recombination compositions (*e.g.*, for integrating a gene into a preselected location within the chromosome of the cell). Alternative methods may involve, for example, the use of liposomes, electroporation, or chemicals that increase free (or “naked”) DNA uptake, transformation using viruses or pollen and the use of microprojection. Standard molecular biology techniques are common in the art (*e.g.*, Sambrook *et al.*, 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, New York). For example, in one embodiment of the present invention, *Arabidopsis* or another plant species is transformed with a gene encoding *CCA1*, *GLK1* or *bZIP1* using *Agrobacterium*.

[00118] One of skill in the art will be able to select an appropriate vector for introducing the encoding nucleic acid sequence in a relatively intact state. Thus, any vector which will produce a plant carrying the introduced encoding nucleic acid should be sufficient. The selection of the vector, or whether to use a vector, is typically guided by the method of transformation selected.

[00119] The transformation of plants in accordance with the invention may be carried out in essentially any of the various ways known to those skilled in the art of plant molecular biology. (See, for example, *Methods of Enzymology*, Vol. 153, 1987, Wu and Grossman, Eds., Academic Press, incorporated herein by reference).

[00120] Plant cells and plants can comprise two or more nucleotide sequence constructs. Any means for producing a plant comprising the nucleotide sequence constructs described herein are encompassed by the present invention. For example, a nucleotide sequence encoding the modulator can be used to transform a plant at the same time as the nucleotide sequence encoding the precursor RNA. The nucleotide sequence encoding the precursor mRNA can be introduced into a plant that has already been transformed with the modulator nucleotide sequence. Alternatively, transformed plants, one expressing the modulator and one expressing the RNA precursor, can be crossed to bring the genes together in the same plant. Likewise, viral vectors may be used to express gene products by various methods generally known in the art. Suitable plant viral vectors for expressing genes should be self-replicating, capable of systemic infection in a host, and stable. Additionally, the viruses should be capable of containing the nucleic acid sequences that are foreign to the native virus forming the vector. Transient expression systems may also be used.

[00121] *Agrobacterium* transformation is widely used by those skilled in the art to transform dicotyledonous species. Recently, there has been substantial progress towards the routine production of stable, fertile transgenic plants in almost all economically relevant monocot plants (Toriyama *et al.*, 1988, *Bio/Technology* 6:1072-1074; Zhang *et al.*, 1988, *Plant Cell Rep.* 7:379-384; Zhang *et al.*, 1988, *Theor. Appl. Genet.* 76:835-840; Shimamoto *et al.*, 1989, *Nature* 338:274-276; Datta *et al.*, 1990, *Bio/Technology* 8: 736-740; Christou *et al.*, 1991, *Bio/Technology* 9:957-962; Peng *et al.*, 1991, International Rice Research Institute, Manila, Philippines, pp. 563-574; Cao *et al.*, 1992, *Plant Cell Rep.* 11:585-591; Li *et al.*, 1993, *Plant Cell Rep.* 12:250-255; Rathore *et al.*, 1993, *Plant Mol. Biol.* 21:871-884; Fromm *et al.*, 1990, *Bio/Technology* 8:833-839; Tomes *et al.*, 1995, "Direct DNA Transfer into Intact Plant Cells via Microprojectile Bombardment," in *Plant Cell, Tissue, and Organ Culture: Fundamental Methods*, ed. Gamborg and Phillips (Springer-Verlag, Berlin);

D'Halluin *et al.*, 1992, *Plant Cell* 4:1495-1505; Walters *et al.*, 1992, *Plant Mol. Biol.* 18:189-200; Koziel *et al.*, 1993, *Biotechnology* 11: 194-200; Vasil, I. K., 1994, *Plant Mol. Biol.* 25:925-937; Weeks *et al.*, 1993, *Plant Physiol.* 102:1077-1084; Somers *et al.*, 1992, *Bio/Technology* 10: 1589-1594; WO 92/14828). In particular, *Agrobacterium* mediated transformation is now emerging also as an highly efficient transformation method in monocots (Hiei *et al.*, 1994, *The Plant Journal* 6:271-282). See also, Shimamoto, K., 1994, *Current Opinion in Biotechnology* 5:158-162; Vasil *et al.*, 1992, *Bio/Technology* 10:667-674; Vain *et al.*, 1995, *Biotechnology Advances* 13(4):653-671; Vasil *et al.*, 1996, *Nature Biotechnology* 14:702).

[00122] The particular choice of a transformation technology will be determined by its efficiency to transform certain plant species as well as the experience and preference of the person practicing the invention with a particular methodology of choice. It will be apparent to the skilled person that the particular choice of a transformation system to introduce nucleic acid into plant cells is not essential to or a limitation of the invention, nor is the choice of technique for plant regeneration.

6.3.1 *Agrobacterium*

[00123] A *CCA1*, *GLK1* or *bZIP1*-encoding nucleic acid sequences or a nucleic acid designed to disrupt expression of *CCA1*, *GLK1* or *bZIP1* utilized in the present invention can be introduced into plant cells using Ti plasmids of *Agrobacterium tumefaciens* (*A. tumefaciens*), root-inducing (Ri) plasmids of *Agrobacterium rhizogenes* (*A. rhizogenes*), and plant virus vectors. For reviews of such techniques see, for example, Weissbach & Weissbach, 1988, *Methods for Plant Molecular Biology*, Academic Press, NY, Section VIII, pp. 421-463; and Grierson & Corey, 1988, *Plant Molecular Biology*, 2d Ed., Blackie, London, Ch. 7-9, and Horsch *et al.*, 1985, *Science*, 227:1229.

[00124] In using an *A. tumefaciens* culture as a transformation vehicle, it is most advantageous to use a non-oncogenic strain of *Agrobacterium* as the vector carrier so that normal non-oncogenic differentiation of the transformed tissues is possible. It is also preferred that the *Agrobacterium* harbor a binary Ti plasmid system. Such a binary system comprises 1) a first Ti plasmid having a virulence region essential for the introduction of transfer DNA (T-DNA) into plants, and 2) a chimeric plasmid. The chimeric plasmid contains at least one border region of the T-DNA region of a wild-type Ti plasmid flanking the nucleic acid to be transferred. Binary Ti plasmid systems have been shown effective in the transformation of plant cells (De Framond, *Biotechnology*, 1983, 1:262; Hoekema *et al.*,

1983, Nature, 303:179). Such a binary system is preferred because it does not require integration into the Ti plasmid of *A. tumefaciens*, which is an older methodology.

[00125] In some embodiments, a disarmed Ti-plasmid vector carried by *Agrobacterium* exploits its natural gene transferability (EP-A-270355, EP-A-01 16718, Townsend *et al.*, 1984, NAR, 12:8711, U.S. Pat. No. 5,563,055).

[00126] Methods involving the use of *Agrobacterium* in transformation according to the present invention include, but are not limited to: 1) co-cultivation of *Agrobacterium* with cultured isolated protoplasts; 2) transformation of plant cells or tissues with *Agrobacterium*; or 3) transformation of seeds, apices or meristems with *Agrobacterium*.

[00127] In addition, gene transfer can be accomplished by in planta transformation by *Agrobacterium*, as described by Bechtold *et al.*, (C.R. Acad. Sci. Paris, 1993, 316:1194). This approach is based on the vacuum infiltration of a suspension of *Agrobacterium* cells.

[00128] In certain embodiments, a *CCAI*, *GLK1*, *bZIP1*-encoding nucleic acid or mutant thereof is introduced into plant cells by infecting such plant cells, an explant, a meristem or a seed, with transformed *A. tumefaciens* as described above. Under appropriate conditions known in the art, the transformed plant cells are grown to form shoots, roots, and develop further into plants.

[00129] Other methods described herein, such as microprojectile bombardment, electroporation and direct DNA uptake can be used where *Agrobacterium* is inefficient or ineffective. Alternatively, a combination of different techniques may be employed to enhance the efficiency of the transformation process, *e.g.*, bombardment with *Agrobacterium*-coated microparticles (EP-A-486234) or microprojectile bombardment to induce wounding followed by co-cultivation with *Agrobacterium* (EP-A-486233).

6.3.2 CaMV

[00130] In some embodiments, cauliflower mosaic virus (CaMV) is used as a vector for introducing a desired nucleic acid into plant cells (U.S. Pat. No. 4,407,956). CaMV viral DNA genome can be inserted into a parent bacterial plasmid creating a recombinant DNA molecule which can be propagated in bacteria. After cloning, the recombinant plasmid again can be cloned and further modified by introduction of the desired nucleic acid sequence. The modified viral portion of the recombinant plasmid can then be excised from the parent bacterial plasmid, and used to inoculate the plant cells or plants.

6.3.3 Mechanical and Chemical Means

[00131] In some embodiments, a *CCA1*, *GLK1* or *bZIP1*-encoding nucleic acid or a nucleic acid designed to disrupt expression of *CCA1*, *GLK1* or *bZIP1* is introduced into a plant cell using mechanical or chemical means. Exemplary mechanical and chemical means are provided below.

[00132] As used herein, the term “contacting” refers to any means of introducing a *CCA1*, *GLK1* or *bZIP1*-encoding nucleic acid or a nucleic acid designed to disrupt expression of *CCA1*, *GLK1* or *bZIP1* into a plant cell, including chemical and physical means as described above. Preferably, contacting refers to introducing the nucleic acid or vector containing the nucleic acid into plant cells (including an explant, a meristem or a seed), via *A. tumefaciens* transformed with the, e.g., *GLK1*-encoding nucleic acid as described above.

6.3.3.1 Microinjection

[00133] In one embodiment, the *CCA1*, *GLK1* or *bZIP1*-encoding nucleic acid or the nucleic acid designed to disrupt expression of *CCA1*, *GLK1* or *bZIP1* can be mechanically transferred into the plant cell by microinjection using a micropipette. See, e.g., WO 92/09696, WO 94/00583, EP 331083, EP 175966, Green *et al.*, 1987, Plant Tissue and Cell Culture, Academic Press, Crossway *et al.*, 1986, Biotechniques 4:320-334.

6.3.3.2 PEG

[00134] In other embodiment, the nucleic acid can also be transferred into the plant cell by using polyethylene glycol (PEG) which forms a precipitation complex with genetic material that is taken up by the cell.

6.3.3.3 Electroporation

[00135] Electroporation can be used, in another set of embodiments, to deliver a nucleic acid to the cell, e.g., precursor miRNA, or a nucleotide sequence able to be transcribed to produce *CCA1*, *GLK1* or *bZIP1* protein (see, e.g., Fromm *et al.*, 1985, PNA5, 82:5824). “Electroporation,” as used herein, is the application of electricity to a cell, such as a plant protoplast, in such a way as to cause delivery of a nucleic acid into the cell without killing the cell. Typically, electroporation includes the application of one or more electrical voltage “pulses” having relatively short durations (usually less than 1 second, and often on the scale of milliseconds or microseconds) to a media containing the cells. The electrical pulses typically facilitate the non-lethal transport of extracellular nucleic acids into the cells. The exact electroporation protocols (such as the number of pulses, duration of pulses, pulse

waveforms, *etc.*), will depend on factors such as the cell type, the cell media, the number of cells, the substance(s) to be delivered, *etc.*, and can be determined by those of ordinary skill in the art. Electroporation is discussed in greater detail in, *e.g.*, EP 290395, WO 8706614, Riggs *et al.*, 1986, Proc. Natl. Acad. Sci. USA 83:5602-5606; D'Halluin *et al.*, 1992, Plant Cell 4:1495-1505). Other forms of direct DNA uptake can also be used in the methods provided herein, such as those discussed in, *e.g.*, DE 4005152, WO 9012096, U.S. Pat. No. 4,684,611, Paszkowski *et al.*, 1984, EMBO J. 3:2717-2722.

6.3.3.4 Ballistic and Particle Bombardment

[00136] Another method for introducing a *CCA1*, *GLK1* or *bZIP1*-encoding nucleic acid or a nucleic acid designed to disrupt expression of *CCA1*, *GLK1* or *bZIP1* into a plant cell is high velocity ballistic penetration by small particles with the nucleic acid to be introduced contained either within the matrix of such particles, or on the surface thereof (Klein *et al.*, 1987, Nature 327:70). Genetic material can be introduced into a cell using particle gun ("gene gun") technology, also called microprojectile or microparticle bombardment. In this method, small, high-density particles (microprojectiles) are accelerated to high velocity in conjunction with a larger, powder-fired macroprojectile in a particle gun apparatus. The microprojectiles have sufficient momentum to penetrate cell walls and membranes, and can carry RNA or other nucleic acids into the interiors of bombarded cells. It has been demonstrated that such microprojectiles can enter cells without causing death of the cells, and that they can effectively deliver foreign genetic material into intact tissue. Bombardment transformation methods are also described in Sanford *et al.* (Techniques 3:3-16, 1991) and Klein *et al.* (Bio/Techniques 10:286, 1992). Although, typically only a single introduction of a new nucleic acid sequence(s) is required, this method particularly provides for multiple introductions.

[00137] Particle or microprojectile bombardment are discussed in greater detail in, *e.g.*, the following references: U.S. Pat. No. 5,100,792, EP-A-444882, EP-A-434616; Sanford *et al.*, U.S. Pat. No. 4,945,050; Tomes *et al.*, 1995, "Direct DNA Transfer into Intact Plant Cells via Microprojectile Bombardment," in Plant Cell, Tissue, and Organ Culture: Fundamental Methods, ed. Gamborg and Phillips (Springer-Verlag, Berlin); and McCabe *et al.*, 1988, Biotechnology 6:923-926.

6.3.3.5 Colloidal Dispersion

[00138] In other embodiments, a colloidal dispersion system may be used to facilitate delivery of a nucleic acid into the cell, for example, *GLK1*, or a nucleotide sequence able to disrupt expression of *GLK1*. As used herein, a “colloidal dispersion system” refers to a natural or synthetic molecule, other than those derived from bacteriological or viral sources, capable of delivering to and releasing the nucleic acid to the cell. Colloidal dispersion systems include, but are not limited to, macromolecular complexes, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. One example of a colloidal dispersion system is a liposome. Liposomes are artificial membrane vessels. It has been shown that large unilamellar vessels (“LUV”), which range in size from 0.2 to 4.0 microns, can encapsulate large macromolecules within the aqueous interior and these macromolecules can be delivered to cells in a biologically active form (*e.g.*, Fraley *et al.*, 1981, Trends Biochem. Sci., 6:77).

6.3.3.6 Lipids

[00139] Lipid formulations for the transfection and/or intracellular delivery of nucleic acids are commercially available, for instance, from QIAGEN, for example as EFFECTENE® (a non-liposomal lipid with a special DNA condensing enhancer) and SUPER-FECT® (a novel acting dendrimeric technology) as well as Gibco BRL, for example, as LIPOFECTIN® and LIPOFECTACE®, which are formed of cationic lipids such as N-[1-(2,3-dioleoyloxy)-propyl]-N,N,N-trimethylammonium chloride (“DOTMA”) and dimethyl dioctadecylammonium bromide (“DDAB”). Liposomes are well known in the art and have been widely described in the literature, for example, in Gregoriadis, G., 1985, Trends in Biotechnology 3:235-241; Freeman *et al.*, 1984, Plant Cell Physiol. 29:1353).

6.3.3.7 Other Methods

[00140] In addition to the above, other physical methods for the transformation of plant cells are reviewed in the following and can be used in the methods provided herein. Oard, 1991, Biotech. Adv. 9:1-11. See generally, Weissinger *et al.*, 1988, sAnn. Rev. Genet. 22:421-477; Sanford *et al.*, 1987, Particulate Science and Technology 5:27-37; Christou *et al.*, 1988, Plant Physiol. 87:671-674; McCabe *et al.*, 1988, Bio/Technology 6:923-926; Finer and McMullen, 1991, *In vitro* Cell Dev. Biol. 27P:175-182; Singh *et al.*, 1998, Theor. Appl. Genet. 96:319-324; Datta *et al.*, 1990, Biotechnology 8:736-740; Klein *et al.*, 1988, Proc. Natl. Acad. Sci. USA 85:4305-4309; Klein *et al.*, 1988, Biotechnology 6:559-563; Tomes, U.S. Pat. No. 5,240,855; Buising *et al.*, U.S. Pat. Nos. 5,322,783 and 5,324,646; Klein *et al.*,

1988, *Plant Physiol.* 91:440-444; Fromm *et al.*, 1990, *Biotechnology* 8:833-839; Hooykaas-Van Slogteren *et al.*, 1984, *Nature (London)* 311:763-764; Bytebier *et al.*, 1987, *Proc. Natl. Acad. Sci. USA* 84:5345-5349; De Wet *et al.*, 1985, *The Experimental Manipulation of Ovule Tissues*, ed. Chapman *et al.* (Longman, N.Y.), pp. 197-209; Kaeppler *et al.*, 1990, *Plant Cell Reports* 9:415-418 and Kaeppler *et al.*, 1992, *Theor. Appl. Genet.* 84:560-566; Li *et al.*, 1993, *Plant Cell Reports* 12:250-255 and Christou and Ford, 1995, *Annals of Botany* 75:407-413; Osjoda *et al.*, 1996, *Nature Biotechnology* 14:745-750; all of which are herein incorporated by reference.

6.4 Nucleic Acid Constructs

[00141] The *CCAI*, *GLK1*, *bZIP1* sequences of the invention may be provided in nucleotide sequence constructs or expression cassettes for expression in the plant of interest. The cassette will include 5' and 3' regulatory sequences operably linked to an encoding nucleotide sequence of the invention.

[00142] The expression cassette may additionally contain at least one additional gene to be co-transformed into the organism. Alternatively, the additional gene(s) can be provided on multiple expression cassettes.

[00143] In certain embodiments, an expression cassette can be used with a plurality of restriction sites for insertion of the sequences of the invention to be under the transcriptional regulation of the regulatory regions. The expression cassette can additionally contain selectable marker genes (see below).

[00144] The expression cassette will generally include in the 5'-3' direction of transcription, a transcriptional and translational initiation region, a DNA sequence of the invention, *e.g.*, *GLK1* or a sequence designed to disrupt expression of *GLK1*, and a transcriptional and translational termination region functional in plants. The transcriptional initiation region, the promoter, may be native or analogous or foreign or heterologous to the plant host. Additionally, the promoter may be the natural sequence or alternatively a synthetic sequence. By "foreign" is intended that the transcriptional initiation region is not found in the native plant into which the transcriptional initiation region is introduced. As used herein, a chimeric gene comprises a coding sequence operably linked to a transcription initiation region that is heterologous to the coding sequence.

[00145] The termination region may be native with the transcriptional initiation region, may be native with the operably linked DNA sequence of interest, or may be derived from another source. Convenient termination regions are available from the Ti-plasmid of *A.*

tumefaciens, such as the octopine synthase and nopaline synthase termination regions. See also Guerineau *et al.*, 1991, Mol. Gen. Genet. 262:141-144; Proudfoot, 1991, Cell 64:671-674; Sanfacon *et al.*, 1991, Genes Dev. 5:141-149; Mogen *et al.*, 1990, Plant Cell 2:1261-1272; Munroe *et al.*, 1990, Gene 91:151-158; Ballas *et al.*, 1989, Nucleic Acids Res. 17:7891-7903; and Joshi *et al.*, 1987, Nucleic Acid Res. 15:9627-9639.

[00146] In some embodiments, a nucleic acid (*e.g.*, encoding *GLK1* or *bZIP1*) can be delivered to the cell in a vector. As used herein, a “vector” is any vehicle capable of facilitating the transfer of the nucleic acid to the cell such that the nucleic acid can be processed and/or expressed in the cell. The vector may transport the nucleic acid to the cells with reduced degradation, relative to the extent of degradation that would result in the absence of the vector. The vector optionally includes gene expression sequences or other components (such as promoters and other regulatory elements) able to enhance expression of the nucleic acid within the cell. The invention also encompasses the cells transfected with these vectors, including those cells previously described. In certain embodiments, the cells are transfected or transformed with a vector that specifically (or preferably) overexpresses *CCA1* and/or *GLK1* in the vegetative tissues of the plant, but not in the majority of other cell types of the plant.

[00147] To commence a transformation process in certain embodiments, it is first necessary to construct a suitable vector and properly introduce it into the plant cell. Vector(s) employed in the present invention for transformation of a plant cell include an encoding nucleic acid sequence operably associated with a promoter, such as a leaf-specific promoter. Details of the construction of vectors utilized herein are known to those skilled in the art of plant genetic engineering.

[00148] In general, vectors useful in the invention include, but are not limited to, plasmids, phagemids, viruses, other vehicles derived from viral or bacterial sources that have been manipulated by the insertion or incorporation of the nucleotide sequences (or precursor nucleotide sequences) of the invention. Viral vectors useful in certain embodiments include, but are not limited to, nucleic acid sequences from the following viruses: retroviruses; adenovirus, or other adeno-associated viruses; mosaic viruses such as tobamoviruses; potyviruses, nepoviruses, and RNA viruses such as retroviruses. One can readily employ other vectors not named but known to the art. Some viral vectors can be based on non-cytopathic eukaryotic viruses in which non-essential genes have been replaced with the nucleotide sequence of interest. Non-cytopathic viruses include retroviruses, the life cycle of

which involves reverse transcription of genomic viral RNA into DNA with subsequent proviral integration into host cellular DNA.

[00149] Genetically altered retroviral expression vectors can have general utility for the high-efficiency transduction of nucleic acids. Standard protocols for producing replication-deficient retroviruses (including the steps of incorporation of exogenous genetic material into a plasmid, transfection of a packaging cell lined with plasmid, production of recombinant retroviruses by the packaging cell line, collection of viral particles from tissue culture media, and infection of the cells with viral particles) are well known to those of ordinary skill in the art. Examples of standard protocols can be found in Kriegler, M., 1990, *Gene Transfer and Expression, A Laboratory Manual*, W.H. Freeman Co., New York, or Murry, E. J. Ed., 1991, *Methods in Molecular Biology*, Vol. 7, Humana Press, Inc., Clifton, N.J.

[00150] Another-example of a virus for certain applications is the adeno-associated virus, which is a double-stranded DNA virus. The adeno-associated virus can be engineered to be replication-deficient and is capable of infecting a wide range of cell types and species. The adeno-associated virus further has advantages, such as heat and lipid solvent stability; high transduction frequencies in cells of diverse lineages; and/or lack of superinfection inhibition, which may allow multiple series of transductions.

[00151] Another vector suitable for use with the method provided herein is a plasmid vector. Plasmid vectors, have been extensively described in the art and are well-known to those of skill in the art. See, *e.g.*, Sambrook *et al.*, 1989, *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press. These plasmids may have a promoter compatible with the host cell, and the plasmids can express a peptide from a gene operatively encoded within the plasmid. Some commonly used plasmids include pBR322, pUC18, pUC19, pRC/CMV, SV40, and pBlueScript. Other plasmids are well-known to those of ordinary skill in the art. Additionally, plasmids may be custom-designed, for example, using restriction enzymes and ligation reactions, to remove and add specific fragments of DNA or other nucleic acids, as necessary. The present invention also includes vectors for producing nucleic acids or precursor nucleic acids containing a desired nucleotide sequence (which can, for instance, then be cleaved or otherwise processed within the cell to produce a precursor miRNA). These vectors may include a sequence encoding a nucleic acid and an *in vivo* expression element, as further described below. In some cases, the *in vivo* expression element includes at least one promoter.

[00152] Where appropriate, the gene(s) for enhanced expression may be optimized for expression in the transformed plant. That is, the genes can be synthesized using plant-

preferred codons corresponding to the plant of interest. Methods are available in the art for synthesizing plant-preferred genes. See, for example, U.S. Pat. Nos. 5,380,831, and 5,436,391, and Murray *et al.*, 1989, Nucleic Acids Res. 17:477-498.

[00153] Additional sequence modifications are known to enhance gene expression in a cellular host. These include elimination of sequences encoding spurious polyadenylation signals, exon-intron splice site signals, transposon-like repeats, and other such well-characterized sequences that may be deleterious to gene expression. The G-C content of the sequence may be adjusted to levels average for a given cellular host, as calculated by reference to known genes expressed in the host cell. When desired, the sequence is modified to avoid predicted hairpin secondary mRNA structures. However, it is recognized that in the case of nucleotide sequences encoding the miRNA precursors, one or more hairpin and other secondary structures may be desired for proper processing of the precursor into an mature miRNA and/or for the functional activity of the miRNA in gene silencing.

[00154] The expression cassettes can additionally contain 5' leader sequences in the expression cassette construct. Such leader sequences can act to enhance translation. Translation leaders are known in the art and include: picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5' noncoding region) (Elroy-Stein *et al.*, 1989, PNAS USA 86:6126-6130); potyvirus leaders, for example, TEV leader (Tobacco Etch Virus) (Allison *et al.*, 1986); MDMV leader (Maize Dwarf Mosaic Virus); Virology 154:9-20), and human immunoglobulin heavy-chain binding protein (BiP), (Macejak *et al.*, 1991, Nature 353:90-94); untranslated leader from the coat protein miRNA of alfalfa mosaic virus (AMV RNA 4) (Jobling *et al.*, 1987, Nature 325:622-625); tobacco mosaic virus leader (TMV) (Gallie *et al.*, 1989, Molecular Biology of RNA, ed. Cech (Liss, New York), pp. 237-256); and maize chlorotic mottle virus leader (MCMV) (Lommel *et al.*, 1991, Virology 81:382-385). See also, Della-Cioppa *et al.*, 1987, Plant Physiol. 84:965-968.

[00155] In preparing the expression cassette, the various DNA fragments can be manipulated, so as to provide for the DNA sequences in the proper orientation and, as appropriate, in the proper reading frame. Toward this end, adapters or linkers can be employed to join the DNA fragments or other manipulations may be involved to provide for convenient restriction sites, removal of superfluous DNA, removal of restriction sites, or the like. For this purpose, *in vitro* mutagenesis, primer repair, restriction, annealing, resubstitutions, *e.g.*, transitions and transversions, may be involved.

[00156] An illustrative vector encoding *CCAI* for overexpression in plants is described *infra*. Wang *et al.*, 1998, Cell 93:1207-1217 also describes a vector for overexpressing *CCAI*

in plants. An illustrative vector encoding *GLK1* for overexpression in plants is described *infra*. Further, Fitter *et al.*, 2002, The Plant Journal 31:713-727 describe an insertion mutant in the *GLK1* gene such that expression of *GLK1* is disrupted.

6.5 Promoters and Other Regulatory Sequences

[00157] In the broad method of the invention, at least one nucleic acid sequence encoding *CCA1*, *GLK1* or *bZIP1* or a nucleic acid designed to disrupt expression of same is operably linked with a promoter, such as a leaf-preferred or leaf-specific promoter. It may be desirable to introduce more than one copy of a polynucleotide into a plant for enhanced expression. For example, multiple copies of a *GLK1* polynucleotide would have the effect of increasing production of *GLK1* even further in the plant. In specific embodiments, the *GLK1* polynucleotide is expressed primarily or entirely in vegetative cells of the plant.

[00158] In general, promoters are found positioned 5' (upstream) of the genes that they control. Thus, in the construction of promoter gene combinations, the promoter is preferably positioned upstream of the gene and at a distance from the transcription start site that approximates the distance between the promoter and the gene it controls in the natural setting. As is known in the art, some variation in this distance can be tolerated without loss of promoter function. Similarly, the preferred positioning of a regulatory element, such as an enhancer, with respect to a heterologous gene placed under its control reflects its natural position relative to the structural gene it naturally regulates. In certain specific embodiments, *bZIP1* is under the control of a seed-specific promoter, and may optionally comprise other regulatory elements that result in constitutive or inducible expression of *bZIP1*.

[00159] Thus, the nucleic acid, in one embodiment, is operably linked to a gene expression sequence, which directs the expression of the nucleic acid within the cell. A "gene expression sequence," as used herein, is any regulatory nucleotide sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the nucleotide sequence to which it is operably linked. The gene expression sequence may, for example, be a eukaryotic promoter or a viral promoter, such as a constitutive or inducible promoter. Promoters and enhancers consist of short arrays of DNA sequences that interact specifically with cellular proteins involved in transcription, for instance, as discussed in Maniatis *et al.*, 1987, Science 236:1237. Promoter and enhancer elements have been isolated from a variety of eukaryotic sources including genes in plant, yeast, insect and mammalian cells and viruses (analogous control elements, *i.e.*, promoters, are also found in prokaryotes). In some embodiments, the nucleic acid is linked to a gene

expression sequence which permits expression of the nucleic acid in a plant cell. A sequence which permits expression of the nucleic acid in a plant cell is one which is selectively active in the particular plant cell and thereby causes the expression of the nucleic acid in these cells. Those of ordinary skill in the art will be able to easily identify promoters that are capable of expressing a nucleic acid in a cell based on the type of plant cell.

[00160] A number of promoters can be used in the practice of the invention. The promoters can be selected based on the desired outcome. Generally, the nucleotide sequence and the modulator sequences can be combined with promoters of choice to alter gene expression if the target sequences in the tissue or organ of choice. Thus, the nucleotide sequence or modulator nucleotide sequence can be combined with constitutive, tissue-preferred, inducible, developmental, or other promoters for expression in plants depending upon the desired outcome.

[00161] The selection of a particular promoter and enhancer depends on what cell type is to be used and the mode of delivery. For example, a wide variety of promoters have been isolated from plants and animals, which are functional not only in the cellular source of the promoter, but also in numerous other plant species. There are also other promoters (*e.g.*, viral and Ti-plasmid) which can be used. For example, these promoters include promoters from the Ti-plasmid, such as the octopine synthase promoter, the nopaline synthase promoter, the mannopine synthase promoter, and promoters from other open reading frames in the T-DNA, such as ORF7, *etc.* Promoters isolated from plant viruses include the 35S promoter from cauliflower mosaic virus. Promoters that have been isolated and reported for use in plants include ribulose-1,3-biphosphate carboxylase small subunit promoter, phaseolin promoter, *etc.* Thus, a variety of promoters and regulatory elements may be used in the expression vectors of the present invention.

[00162] Promoters useful in the compositions and methods provided herein include both natural constitutive and inducible promoters as well as engineered promoters. The CaMV promoters are examples of constitutive promoters. Other constitutive mammalian promoters include, but are not limited to, polymerase promoters as well as the promoters for the following genes: hypoxanthine phosphoribosyl transferase ("HPTR"), adenosine deaminase, pyruvate kinase, and alpha-actin.

[00163] Promoters useful as expression elements of the invention also include inducible promoters. Inducible promoters are expressed in the presence of an inducing agent. For example, a metallothionein promoter can be induced to promote transcription in the presence of certain metal ions. Other inducible promoters are known to those of ordinary skill in the

art. The *in vivo* expression element can include, as necessary, 5' non-transcribing and 5' non-translating sequences involved with the initiation of transcription, and can optionally include enhancer sequences or upstream activator sequences.

[00164] For example, in some embodiments an inducible promoter is used to allow control of nucleic acid expression through the presentation of external stimuli (*e.g.*, environmentally inducible promoters), as discussed below. Thus, the timing and amount of nucleic acid expression can be controlled in some cases. Non-limiting examples of expression systems, promoters, inducible promoters, environmentally inducible promoters, and enhancers are well known to those of ordinary skill in the art. Examples include those described in International Patent Application Publications WO 00/12714, WO 00/11175, WO 00/12713, WO 00/03012, WO 00/03017, WO 00/01832, WO 99/50428, WO 99/46976 and U.S. Pat. Nos. 6,028,250, 5,959,176, 5,907,086, 5,898,096, 5,824,857, 5,744,334, 5,689,044, and 5,612,472. A general descriptions of plant expression vectors and reporter genes can also be found in Gruber *et al.*, 1993, "Vectors for Plant Transformation," in *Methods in Plant Molecular Biology & Biotechnology*, Glich *et al.*, Eds., p. 89-119, CRC Press.

[00165] For plant expression vectors, viral promoters that can be used in certain embodiments include the 35S RNA and 19S RNA promoters of CaMV (Brisson *et al.*, *Nature*, 1984, 310:511; Odell *et al.*, *Nature*, 1985, 313:810); the full-length transcript promoter from Figwort Mosaic Virus (FMV) (Gowda *et al.*, 1989, *J. Cell Biochem.*, 13D: 301) and the coat protein promoter to TMV (Takamatsu *et al.*, 1987, *EMBO J.* 6:307). Alternatively, plant promoters such as the light-inducible promoter from the small subunit of ribulose bis-phosphate carboxylase (ssRUBISCO) (Coruzzi *et al.*, 1984, *EMBO J.*, 3:1671; Broglie *et al.*, 1984, *Science*, 224:838); mannopine synthase promoter (Velten *et al.*, 1984, *EMBO J.*, 3:2723) nopaline synthase (NOS) and octopine synthase (OCS) promoters (carried on tumor-inducing plasmids of *Agrobacterium tumefaciens*) or heat shock promoters, *e.g.*, soybean hsp17.5-E or hsp17.3-B (Gurley *et al.*, 1986, *Mol. Cell. Biol.*, 6:559; Severin *et al.*, 1990, *Plant Mol. Biol.*, 15:827) may be used. Exemplary viral promoters which function constitutively in eukaryotic cells include, for example, promoters from the simian virus, papilloma virus, adenovirus, human immunodeficiency virus, Rous sarcoma virus, cytomegalovirus, the long terminal repeats of Moloney leukemia virus and other retroviruses, and the thymidine kinase promoter of herpes simplex virus. Other constitutive promoters are known to those of ordinary skill in the art.

[00166] To be most useful, an inducible promoter should 1) provide low expression in the absence of the inducer; 2) provide high expression in the presence of the inducer; 3) use an

induction scheme that does not interfere with the normal physiology of the plant; and 4) have no effect on the expression of other genes. Examples of inducible promoters useful in plants include those induced by chemical means, such as the yeast metallothionein promoter which is activated by copper ions (Mett *et al.*, Proc. Natl. Acad. Sci., U.S.A., 90:4567, 1993); In2-1 and In2-2 regulator sequences which are activated by substituted benzenesulfonamides, *e.g.*, herbicide safeners (Hershey *et al.*, Plant Mol. Biol., 17:679, 1991); and the GRE regulatory sequences which are induced by glucocorticoids (Schena *et al.*, Proc. Natl. Acad. Sci., U.S.A., 88:10421, 1991). Other promoters, both constitutive and inducible will be known to those of skill in the art.

[00167] A number of inducible promoters are known in the art. For resistance genes, a pathogen-inducible promoter can be utilized. Such promoters include those from pathogenesis-related proteins (PR proteins), which are induced following infection by a pathogen; *e.g.*, PR proteins, SAR proteins, beta-1,3-glucanase, chitinase, *etc.* See, for example, Redolfi *et al.*, 1983, Neth. J. Plant Pathol. 89:245-254; Uknes *et al.*, 1992, Plant Cell 4:645-656; and Van Loon, 1985, Plant Mol. Virol. 4:111-116. Of particular interest are promoters that are expressed locally at or near the site of pathogen infection. See, for example, Marineau *et al.*, 1987, Plant Mol. Biol. 9:335-342; Matton *et al.*, 1989, Molecular Plant-Microbe Interactions 2:325-331; Somsisch *et al.*, 1986, Proc. Natl. Acad. Sci. USA 83:2427-2430; Somsisch *et al.*, 1988, Mol. Gen. Genet. 2:93-98; and Yang, 1996, Proc. Natl. Acad. Sci. USA 93:14972-14977. See also, Chen *et al.*, 1996, Plant J. 10:955-966; Zhang *et al.*, 1994, Proc. Natl. Acad. Sci. USA 91:2507-2511; Warner *et al.*, 1993, Plant J. 3:191-201; Siebertz *et al.*, 1989, Plant Cell 1:961-968; U.S. Pat. No. 5,750,386; Cordero *et al.*, 1992, Physiol. Mol. Plant Path. 41:189-200; and the references cited therein.

[00168] Additionally, as pathogens find entry into plants through wounds or insect damage, a wound-inducible promoter may be used in the DNA constructs of the invention. Such wound-inducible promoters include potato proteinase inhibitor (pin II) gene (Ryan, 1990, Ann. Rev. Phytopath. 28:425-449; Duan *et al.*, 1996, Nature Biotechnology 14:494-498); *wun1* and *wun2*, U.S. Pat. No. 5,428,148; *win1* and *win2* (Stanford *et al.*, 1989, Mol. Gen. Genet. 215:200-208); systemin (McGurl *et al.*, 1992, Science 225:1570-1573); WIPI (Rohmeier *et al.*, 1993, Plant Mol. Biol. 22:783-792; Eckelkamp *et al.*, 1993, FEBS Letters 323:73-76); MPI gene (Corderok *et al.*, 1994, Plant J. 6(2):141-150); and the like. Such references are herein incorporated by reference.

[00169] Chemical-regulated promoters can be used to modulate the expression of a gene in a plant through the application of an exogenous chemical regulator. Depending upon the

objective, the promoter may be a chemical-inducible promoter, where application of the chemical induces gene expression, or a chemical-repressible promoter, where application of the chemical represses gene expression. Chemical-inducible promoters are known in the art and include, but are not limited to, the maize In2-2 promoter, which is activated by benzenesulfonamide herbicide safeners, the maize GST promoter, which is activated by hydrophobic electrophilic compounds that are used as pre-emergent herbicides, and the tobacco PR-1 a promoter, which is activated by salicylic acid. Other chemical-regulated promoters of interest include steroid-responsive promoters (see, for example, the glucocorticoid-inducible promoter in Schena *et al.*, 1991, Proc. Natl. Acad. Sci. USA 88:10421-10425 and McNellis *et al.*, 1998, Plant J. 14(2):247-257) and tetramiR167e-inducible and tetramiR167e-repressible promoters (see, for example, Gatz *et al.*, 1991, Mol. Gen. Genet. 227:229-237, and U.S. Pat. Nos. 5,814,618 and 5,789,156), herein incorporated by reference.

[00170] Where enhanced expression in particular tissues is desired, tissue-preferred promoters can be utilized. Tissue-preferred promoters include those described by Yamamoto *et al.*, 1997, Plant J. 12(2):255-265; Kawamata *et al.*, 1997, Plant Cell Physiol. 38(7):792-803; Hansen *et al.*, 1997, Mol. Gen. Genet. 254(3):337-343; Russell *et al.*, 1997, Transgenic Res. 6(2):157-168; Rinehart *et al.*, 1996, Plant Physiol. 112(3):1331-1341; Van Camp *et al.*, 1996, Plant Physiol. 112(2):525-535; Canevascini *et al.*, 1996, Plant Physiol. 12(2):513-524; Yamamoto *et al.*, 1994, Plant Cell Physiol. 35(5):773-778; Lam, 1994, Results Probl. Cell Differ. 20:181-196; Orozco *et al.*, 1993, Plant Mol. Biol. 23(6): 1129-1138; Matsuoka *et al.*, 1993, Proc Natl. Acad. Sci. USA 90(20):9586-9590; and Guevara-Garcia *et al.*, 1993, Plant J 4(3):495-505.

[00171] The particular promoter selected should be capable of causing sufficient expression to result in the production of an effective amount of structural gene product in the transgenic plant, *e.g.*, *GLK1* to cause upregulation of genes such as *GLN1.3* and increased nitrogen assimilation, biomass, overall plant growth or yield, and/or other phenotypes described herein, as compared to wild type. The promoters used in the vector constructs of the present invention may be modified, if desired, to affect their control characteristics. In certain embodiments, chimeric promoters can be used.

[00172] There are promoters known which limit expression to particular plant parts or in response to particular stimuli. One skilled in the art will know of many such plant part-specific promoters which would be useful in the present invention. In certain embodiments, to provide pericycle-specific expression, any of a number of promoters from genes in

Arabidopsis can be used. In some embodiments, the promoter from one (or more) of the following genes may be used: (i) At1g11080, (ii) At3g60160, (iii) At1g24575, (iv) At3g45160, or (v) At1g23130. In specific embodiments, we will also use (vi) promoter elements from the GFP-marker line used in Gifford *et al.* (in preparation) (see also, Bonke *et al.*, 2003, Nature 426, 181-6; Tian *et al.*, 2004, Plant Physiol 135, 25-38). Several of the predicted genes have a number of potential orthologs in rice and poplar and thus are predicted that they will be applicable for use in crop species; (i) Os04g44410, Os10g39560, Os06g51370, Os02g42310, Os01g22980, Os05g06660, and Poptr1#568263, Poptr1#555534, Poptr1#365170; (ii) Os04g49900, Os04g49890, Os01g67580, and Poptr1#87573, Poptr1#80582, Poptr1#565079, Poptr1#99223.

[00173] Promoters used in the nucleic acid constructs of the present invention can be modified, if desired, to affect their control characteristics. For example, the CaMV 35S promoter may be ligated to the portion of the ssRUBISCO gene that represses the expression of ssRUBISCO in the absence of light, to create a promoter which is active in leaves but not in roots. The resulting chimeric promoter may be used as described herein. For purposes of this description, the phrase “CaMV 35S” promoter thus includes variations of CaMV 35S promoter, *e.g.*, promoters derived by means of ligation with operator regions, random or controlled mutagenesis, *etc.* Furthermore, the promoters may be altered to contain multiple “enhancer sequences” to assist in elevating gene expression.

[00174] An efficient plant promoter that may be used in specific embodiments is an “overproducing” or “overexpressing” plant promoter. Overexpressing plant promoters that can be used in the compositions and methods provided herein include the promoter of the small sub-unit (“ss”) of the ribulose-1,5-biphosphate carboxylase from soybean (*e.g.*, Berry-Lowe *et al.*, 1982, J. Molecular & App. Genet., 1:483), and the promoter of the chorophyll a-b binding protein. These two promoters are known to be light-induced in eukaryotic plant cells. For example, see Cashmore, Genetic Engineering of plants: An Agricultural Perspective, p. 29-38; Coruzzi *et al.*, 1983, J. Biol. Chem., 258:1399; and Dunsmuir *et al.*, 1983, J. Molecular & App. Genet., 2:285.

[00175] The promoters and control elements of, *e.g.*, SUCS (root nodules; broadbean; Kuster *et al.*, 1993, Mol Plant Microbe Interact 6:507-14) for roots can be used in compositions and methods provided herein to confer tissue specificity.

[00176] In certain embodiment, two promoter elements can be used in combination, such as, for example, (i) an inducible element responsive to a treatment that can be provided to the

plant prior to N-fertilizer treatment, and (ii) a plant tissue-specific expression element to drive expression in the specific tissue alone.

[00177] Any promoter of other expression element described herein or known in the art may be used either alone or in combination with any other promoter or other expression element described herein or known in the art. For example, promoter elements that confer tissue specific expression of a gene can be used with other promoter elements conferring constitutive or inducible expression.

6.6 Isolating Related Promoter Sequences

[00178] Promoter and promoter control elements that are related to those described in herein can also be used in the compositions and methods provided herein. Such related sequence can be isolated utilizing (a) nucleotide sequence identity; (b) coding sequence identity of related, orthologous genes; or (c) common function or gene products.

[00179] Relatives can include both naturally occurring promoters and non-natural promoter sequences. Non-natural related promoters include nucleotide substitutions, insertions or deletions of naturally-occurring promoter sequences that do not substantially affect transcription modulation activity. For example, the binding of relevant DNA binding proteins can still occur with the non-natural promoter sequences and promoter control elements of the present invention.

[00180] According to current knowledge, promoter sequences and promoter control elements exist as functionally important regions, such as protein binding sites, and spacer regions. These spacer regions are apparently required for proper positioning of the protein binding sites. Thus, nucleotide substitutions, insertions and deletions can be tolerated in these spacer regions to a certain degree without loss of function.

[00181] In contrast, less variation is permissible in the functionally important regions, since changes in the sequence can interfere with protein binding. Nonetheless, some variation in the functionally important regions is permissible so long as function is conserved.

[00182] The effects of substitutions, insertions and deletions to the promoter sequences or promoter control elements may be to increase or decrease the binding of relevant DNA binding proteins to modulate transcript levels of a polynucleotide to be transcribed. Effects may include tissue-specific or condition-specific modulation of transcript levels of the polypeptide to be transcribed. Polynucleotides representing changes to the nucleotide sequence of the DNA-protein contact region by insertion of additional nucleotides, changes

to identity of relevant nucleotides, including use of chemically-modified bases, or deletion of one or more nucleotides are considered encompassed by the present invention.

[00183] Typically, related promoters exhibit at least 80% sequence identity, preferably at least 85%, more preferably at least 90%, and most preferably at least 95%, even more preferably, at least 96%, at least 97%, at least 98% or at least 99% sequence identity. Such sequence identity can be calculated by the algorithms and computers programs described above.

[00184] Usually, such sequence identity is exhibited in an alignment region that is at least 75% of the length of a sequence or corresponding full-length sequence of a promoter described herein; more usually at least 80%; more usually, at least 85%, more usually at least 90%, and most usually at least 95%, even more usually, at least 96%, at least 97%, at least 98% or at least 99% of the length of a sequence of a promoter described herein.

[00185] The percentage of the alignment length is calculated by counting the number of residues of the sequence in region of strongest alignment, *e.g.*, a continuous region of the sequence that contains the greatest number of residues that are identical to the residues between two sequences that are being aligned. The number of residues in the region of strongest alignment is divided by the total residue length of a sequence of a promoter described herein. These related promoters may exhibit similar preferential transcription as those promoters described herein.

[00186] In certain embodiments, a promoter, such as a leaf-preferred or leaf-specific promoter, can be identified by sequence homology or sequence identity to any root specific promoter identified herein. In other embodiments, orthologous genes identified herein as leaf-specific genes (*e.g.*, the same gene or different gene that is functionally equivalent) for a given species can be identified and the associated promoter can also be used in the compositions and methods provided herein. For example, using high, medium or low stringency conditions, standard promoter rules can be used to identify other useful promoters from orthologous genes for use in the compositions and methods provided herein. In specific embodiments, the orthologous gene is a gene expressed only or primarily in the root, such as pericycle cells.

[00187] Polynucleotides can be tested for activity by cloning the sequence into an appropriate vector, transforming plants with the construct and assaying for marker gene expression. Recombinant DNA constructs can be prepared, which comprise the polynucleotide sequences of the invention inserted into a vector suitable for transformation of plant cells. The construct can be made using standard recombinant DNA techniques

(Sambrook *et al.*, 1989) and can be introduced to the species of interest by *Agrobacterium*-mediated transformation or by other means of transformation as referenced below.

[00188] The vector backbone can be any of those typical in the art such as plasmids, viruses, artificial chromosomes, BACs, YACs and PACs and vectors of the sort described by (a) BAC: Shizuya *et al.*, 1992, Proc. Natl. Acad. Sci. USA 89: 8794-8797; Hamilton *et al.*, 1996, Proc. Natl. Acad. Sci. USA 93: 9975-9979; (b) YAC: Burke *et al.*, 1987, Science 236:806-812; (c) PAC: Stenberg N. *et al.*, 1990, Proc Natl Acad Sci USA. January; 87(1):103-7; (d) Bacteria-Yeast Shuttle Vectors: Bradshaw *et al.*, 1995, Nucl Acids Res 23: 4850-4856; (e) Lambda Phage Vectors: Replacement Vector, *e.g.*, Frischauf *et al.*, 1983, J. Mol. Biol. 170: 827-842; or Insertion vector, *e.g.*, Huynh *et al.*, 1985, In: Glover N M (ed) DNA Cloning: A practical Approach, Vol. 1 Oxford: IRL Press; T-DNA gene fusion vectors: Walden *et al.*, 1990, Mol Cell Biol 1: 175-194; and (g) Plasmid vectors: Sambrook *et al.*, *infra*.

[00189] Typically, the construct comprises a vector containing a sequence of the present invention operationally linked to any marker gene. The polynucleotide was identified as a promoter by the expression of the marker gene. Although many marker genes can be used, Green Fluorescent Protein (GFP) is preferred. The vector may also comprise a marker gene that confers a selectable phenotype on plant cells. The marker may encode biocide resistance, particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to chlorosulfuron or phosphinotricin (see below). Vectors can also include origins of replication, scaffold attachment regions (SARs), markers, homologous sequences, introns, *etc.*

6.7 Tissue or Cell-Type Preferential Transcription

[00190] The invention also provides a method of providing increased transcription of a nucleic acid sequence in a selected tissue, such as vegetative tissues, leaves, seeds, fruit, *etc.* The method comprises growing a plant having integrated in its genome a nucleic acid construct comprising, an exogeneous gene encoding *CCA1*, *GLK1* or *bZIP1*, said gene operably associated with a tissue specific promoter, whereby transcription of said gene is increased (or decreased) in said selected tissue.

[00191] Specific promoters may be used in the compositions and methods provided herein. As used herein, "specific promoters" refers to a subset of promoters that have a high preference for modulating transcript levels in a specific tissue or organ or cell and/or at a specific time during development of an organism. By "high preference" is meant at least 3-

fold, preferably 5-fold, more preferably at least 10-fold still more preferably at least 20-fold, 50-fold or 100-fold increase in transcript levels under the specific condition over the transcription under any other reference condition considered. Typical examples of temporal and/or tissue or organ specific promoters of plant origin that can be used in the compositions and methods of the present invention, include RCc2 and RCc3, promoters that direct root-specific gene transcription in rice (Xu *et al.*, 1995, Plant Mol. Biol. 27:237 and TobRB27, a root-specific promoter from tobacco (Yamamoto *et al.*, 1991, Plant Cell 3:371). Examples of tissue-specific promoters under developmental control include promoters that initiate transcription only in certain tissues or organs, such as roots

[00192] “Preferential transcription” is defined as transcription that occurs in a particular pattern of cell types or developmental times or in response to specific stimuli or combination thereof. Non-limitative examples of preferential transcription include: high transcript levels of a desired sequence in root tissues; detectable transcript levels of a desired sequence in certain cell types during embryogenesis; and low transcript levels of a desired sequence under drought conditions. Such preferential transcription can be determined by measuring initiation, rate, and/or levels of transcription.

[00193] Promoters and control elements providing preferential transcription in a root can modulate growth, metabolism, development, nutrient uptake, nitrogen fixation, or modulate energy and nutrient utilization in host cells or organisms. In a plant, for example, preferential modulation of genes, transcripts, and/or in a leaf, is useful (1) to modulate root size, shape, and development; (2) to modulate the number of roots, or root hairs; (3) to modulate mineral, fertilizer, or water uptake; (4) to modulate transport of nutrients; or (4) to modulate energy or nutrient usage in relation to other organs and tissues. Up-regulation and transcription down-regulation is useful for these applications. For instance, genes, transcripts, and/or polypeptides that increase growth, for example, may require up-regulation of transcription. In contrast, transcriptional down-regulation may be desired to inhibit nutrient usage in a root to be directed to the leaf instead, for instance.

[00194] Typically, promoter or control elements, which provide preferential transcription in cells, tissues, or organs of a root, produce transcript levels that are statistically significant as compared to other cells, organs or tissues. For preferential up-regulation of transcription, promoter and control elements produce transcript levels that are above background of the assay.

[00195] Root-preferred promoters are known and can be selected from the many available from the literature. See, for example, Hire *et al.*, 1992, Plant Mol. Biol. 20(2): 207-218

(soybean root-preferred glutamine synthetase gene); Keller and Baumgartner, 1991, *Plant Cell* 3(10):1051-1061 (root-preferred control element in the GRP 1.8 gene of French bean); Sanger *et al.*, 1990, *Plant Mol. Biol.* 14(3):433-443 (root-preferred promoter of the mannopine synthase (MAS) gene of *Agrobacterium tumefaciens*); Miao *et al.*, 1991, *Plant Cell* 3(1):11-22 (full-length cDNA clone encoding cytosolic glutamine synthetase (GS), which is expressed in roots and root nodules of soybean). Bogusz *et al.*, 1990, *Plant Cell* 2(7):633-641 (root-preferred promoters from hemoglobin genes from the nitrogen-fixing nonlegume *Parasponia andersonii* and the related non-nitrogen-fixing nonlegume *Trema tomentosa*). Leach and Aoyagi, 1991, *Plant Science (Limerick)* 79(1):69-76 (rolC and rolD root-inducing genes of *Agrobacterium rhizogenes*); Teeri *et al.*, 1989, *EMBO J.* 8(2):343-350 (octopine synthase and TR2' gene); (VfENOD-GRP3 gene promoter); Kuster *et al.*, 1995, *Plant Mol. Biol.* 29(4):759-772 and Capana *et al.*, 1994, *Plant Mol. Biol.* 25(4):681-691 rolB promoter. See also U.S. Pat. Nos. 5,837,876; 5,750,386; 5,633,363; 5,459,252; 5,401,836; 5,110,732; and 5,023,179, root-specific glutamine synthetase (see Tingey *et al.*, 1987, *EMBO J.*, 6:1-9; Edwards *et al.*, 1990, *PNAS*, 87:3439-3463). In addition, promoters of the above-listed orthologous genes in other plant species can be identified and used in the compositions and methods provided herein.

[00196] In specific embodiments, the compositions and methods provided herein use leaf-specific promoters operably associated to a nucleotide encoding *bZIP1*. In certain embodiments, the promoter is a constitutive or inducible promoter. In another specific embodiment, the compositions and methods provided herein use vegetative tissue-specific promoters operably associated to a nucleotide encoding *CCA1* and/or *GLK1*. In certain embodiments, the promoter is a constitutive or inducible promoter.

6.8 Selectable Markers

[00197] Using any gene transfer technique, such as the above-listed techniques, an expression vector harboring the nucleic acid may be transformed into a cell to achieve temporary or prolonged expression. Any suitable expression system may be used, so long as it is capable of undergoing transformation and expressing of the precursor nucleic acid in the cell. In one embodiment, a pET vector (Novagen, Madison, Wis.), or a pBI vector (Clontech, Palo Alto, Calif.) is used as the expression vector. In some embodiments an expression vector further encoding a green fluorescent protein ("GFP") is used to allow simple selection of transfected cells and to monitor expression levels. Non-limiting examples of such vectors include Clontech's "Living Colors Vectors" pEYFP and pEYFP-C.

[00198] The recombinant construct of the present invention may include a selectable marker for propagation of the construct. For example, a construct to be propagated in bacteria preferably contains an antibiotic resistance gene, such as one that confers resistance to kanamycin, tetracycline, streptomycin, or chloramphenicol. Suitable vectors for propagating the construct include plasmids, cosmids, bacteriophages or viruses, to name but a few.

[00199] In addition, the recombinant constructs may include plant-expressible selectable or screenable marker genes for isolating, identifying or tracking of plant cells transformed by these constructs. Selectable markers include, but are not limited to, genes that confer antibiotic resistances (*e.g.*, resistance to kanamycin or hygromycin) or herbicide resistance (*e.g.*, resistance to sulfonylurea, phosphinothricin, or glyphosate). Screenable markers include, but are not limited to, the genes encoding β -glucuronidase (Jefferson, 1987, *Plant Molec Biol. Rep* 5:387-405), luciferase (Ow *et al.*, 1986, *Science* 234:856-859), B and C1 gene products that regulate anthocyanin pigment production (Goff *et al.*, 1990, *EMBO J* 9:2517-2522).

[00200] In some cases, a selectable marker may be included with the nucleic acid being delivered to the cell. As used herein, the term "selectable marker" refers to the use of a gene that encodes an enzymatic or other detectable activity (*e.g.*, luminescence or fluorescence) that confers the ability to grow in medium lacking what would otherwise be an essential nutrient. A selectable marker may also confer resistance to an antibiotic or drug upon the cell in which the selectable marker is expressed. Selectable markers may be "dominant" in some cases; a dominant selectable marker encodes an enzymatic or other activity (*e.g.*, luminescence or fluorescence) that can be detected in any cell or cell line.

[00201] Optionally, a selectable marker may be associated with the *CCA1*-, *GLK1* or *bZIP1*-encoding nucleic acid. Preferably, the marker gene is an antibiotic resistance gene whereby the appropriate antibiotic can be used to select for transformed cells from among cells that are not transformed. Examples of suitable selectable markers include adenosine deaminase, dihydrofolate reductase, hygromycin-B-phosphotransferase, thymidine kinase, xanthine-guanine phospho-ribosyltransferase and amino-glycoside 3'-O-phosphotransferase II. Other suitable markers will be known to those of skill in the art.

6.9 Selection and Identification of Transformed Plants and Plant Cells

[00202] According to the present invention, desired plants may be obtained by engineering the disclosed gene constructs into a variety of plant cell types, including but not limited to,

protoplasts, tissue culture cells, tissue and organ explants, pollens, embryos as well as whole plants. In specific embodiments, the gene constructs are engineered into leaves, preferably with the use of a leaf-specific promoter.

[00203] In an embodiment of the present invention, the engineered plant material is selected or screened for transformants (those that have incorporated or integrated the introduced gene construct(s)) following the approaches and methods described below. An isolated transformant may then be regenerated into a plant. Alternatively, the engineered plant material may be regenerated into a plant or plantlet before subjecting the derived plant or plantlet to selection or screening for the marker gene traits. Procedures for regenerating plants from plant cells, tissues or organs, either before or after selecting or screening for marker gene(s), are well known to those skilled in the art.

[00204] A transformed plant cell, callus, tissue or plant may be identified and isolated by selecting or screening the engineered plant material for traits encoded by the marker genes present on the transforming DNA. For instance, selection may be performed by growing the engineered plant material on media containing inhibitory amount of the antibiotic or herbicide to which the transforming gene construct confers resistance. Further, transformed plants and plant cells may also be identified by screening for the activities of any visible marker genes (*e.g.*, the β -glucuronidase, luciferase, B or C1 genes) that may be present on the recombinant nucleic acid constructs of the present invention. Such selection and screening methodologies are well known to those skilled in the art.

[00205] Physical and biochemical methods also may be also to identify plant or plant cell transformants containing the gene constructs of the present invention. These methods include but are not limited to: 1) Southern analysis or PCR amplification for detecting and determining the structure of the recombinant DNA insert; 2) Northern blot, S1 RNase protection, primer-extension or reverse transcriptase-PCR amplification for detecting and examining RNA transcripts of the gene constructs; 3) enzymatic assays for detecting enzyme or ribozyme activity, where such gene products are encoded by the gene construct; 4) protein gel electrophoresis, Western blot techniques, immunoprecipitation, or enzyme-linked immunoassays, where the gene construct products are proteins. Additional techniques, such as in situ hybridization, enzyme staining, and immunostaining, also may be used to detect the presence or expression of the recombinant construct in specific plant organs and tissues. The methods for doing all these assays are well known to those skilled in the art.

6.10 Screening of Transformed Plants for Those With Improved Agronomic Traits

[00206] According to the present invention, to obtain plants with improved agronomic characteristics, the transformed plants may be screened for those exhibiting the desired physiological alteration. Alternatively, the transformed plants may be directly screened for those exhibiting the desired agronomic changes. A plant with the desired improvement can be isolated by screening the engineered plants for altered expression pattern or level of *CCAI*, *GLK1* and/or *bZIP1*, or downstream gene products such as GLN1.3 or ASN1. A plant can also be screened for nutrient uptake, overall increased plant growth rate, enhanced vegetative yield, improved reproductive yields, increased levels of glutamine or asparagine, or increased nitrogen usage or storage. The screening of the engineered plants can involve Southern analysis to confirm the presence and number of transgene insertions; Northern analysis, RNase protection, primer extension, reverse transcriptase/PCR and the like to measure mRNA levels; measuring the amino acid composition, free amino acid pool or total nitrogen content of various plant tissues; measuring growth rates in terms of fresh weight gains over time; or measuring plant yield in terms of total dry weight and/or total seed weight, or a combination of any of the above methods. The procedures and methods for examining these parameters are well known to those skilled in the art.

[00207] In other embodiments, the screening of the transformed plants may be for improved agronomic characteristics (*e.g.*, faster growth, greater vegetative or reproductive yields, or improved protein contents, *etc.*), as compared to unengineered progenitor plants, when cultivated under growth conditions (*i.e.*, cultivated using soils or media containing or receiving sufficient amounts of nitrogen nutrients to sustain healthy plant growth).

[00208] Plants exhibiting increased growth and/or yield as compared with wild-type plants can be selected by visual observation, methods provided in the Examples, or other methods known in the art.

[00209] A “plant capable of increased yield” refers to a plant that can be induced to express its endogenous *CCAI*, *GLK1* and/or *bZIP1* gene to achieve increased yield. The term “promoter inducing amount” refers to that amount of an agent necessary to elevate such gene expression above such expression in a plant cell not contacted with the agent, by stimulating the endogenous promoter. For example, a transcription factor or a chemical agent may be used to elevate gene expression from native or chimeric *CCAI*, *GLK1* and/or *bZIP1* promoter, thus inducing the promoter and gene expression.

6.11 Cells

[00210] Optionally, germ line cells may be used in the methods described herein rather than, or in addition to, somatic cells. The term “germ line cells” refers to cells in the plant organism which can trace their eventual cell lineage to either the male or female reproductive cell of the plant. Other cells, referred to as “somatic cells” are cells which give rise to leaves, roots and vascular elements which, although important to the plant, do not directly give rise to gamete cells. Somatic cells, however, also may be used. With regard to callus and suspension cells which have somatic embryogenesis, many or most of the cells in the culture have the potential capacity to give rise to an adult plant. If the plant originates from single cells or a small number of cells from the embryogenic callus or suspension culture, the cells in the callus and suspension can therefore be referred to as germ cells. In the case of immature embryos which are prepared for treatment by the methods described herein, certain cells in the apical meristem region of the plant have been shown to produce a cell lineage which eventually gives rise to the female and male reproductive organs. With many or most species, the apical meristem is generally regarded as giving rise to the lineage that eventually will give rise to the gamete cells. An example of a non-gamete cell in an embryo would be the first leaf primordia in corn which is destined to give rise only to the first leaf and none of the reproductive structures.

6.12 Plant Regeneration

[00211] Following transformation, a plant may be regenerated, *e.g.*, from single cells, callus tissue or leaf discs, as is standard in the art. Almost any plant can be entirely regenerated from cells, tissues, and organs of the plant. Available techniques are reviewed in Vasil *et al.*, 1984, in *Cell Culture and Somatic Cell Genetics of Plants*, Vols. I, II, and III, Laboratory Procedures and Their Applications (Academic Press); and Weissbach *et al.*, 1989, *Methods For Plant Mol. Biol.*

[00212] The transformed plants may then be grown, and either pollinated with the same transformed strain or different strains, and the resulting hybrid having expression of the desired phenotypic characteristic identified. Two or more generations may be grown to ensure that expression of the desired phenotypic characteristic is stably maintained and inherited and then seeds harvested to ensure expression of the desired phenotypic characteristic has been achieved.

[00213] Normally, a plant cell is regenerated to obtain a whole plant from the transformation process. The term “growing” or “regeneration” as used herein means growing

a whole plant from a plant cell, a group of plant cells, a plant part (including seeds), or a plant piece (*e.g.*, from a protoplast, callus, or tissue part).

[00214] Regeneration from protoplasts varies from species to species of plants, but generally a suspension of protoplasts is first made. In certain species, embryo formation can then be induced from the protoplast suspension. The culture media will generally contain various amino acids and hormones, necessary for growth and regeneration. Examples of hormones utilized include auxins and cytokinins. Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these variables are controlled, regeneration is reproducible.

[00215] Regeneration also occurs from plant callus, explants, organs or parts. Transformation can be performed in the context of organ or plant part regeneration (see *Methods in Enzymology*, Vol. 118 and Klee *et al.*, *Annual Review of Plant Physiology*, 38:467, 1987). Utilizing the leaf disk-transformation-regeneration method of Horsch *et al.*, *Science*, 227:1229, 1985, disks are cultured on selective media, followed by shoot formation in about 2-4 weeks. Shoots that develop are excised from calli and transplanted to appropriate root-inducing selective medium. Rooted plantlets are transplanted to soil as soon as possible after roots appear. The plantlets can be repotted as required, until reaching maturity.

[00216] In vegetatively propagated crops, the mature transgenic plants are propagated by utilizing cuttings or tissue culture techniques to produce multiple identical plants. Selection of desirable transgenics is made and new varieties are obtained and propagated vegetatively for commercial use.

[00217] In seed propagated crops, mature transgenic plants can be self crossed to produce a homozygous inbred plant. The resulting inbred plant produces seed containing the newly introduced foreign gene(s). These seeds can be grown to produce plants that would produce the selected phenotype, *e.g.*, increased lateral root growth, uptake of nutrients, overall plant growth and/or vegetative or reproductive yields.

[00218] Parts obtained from the regenerated plant, such as flowers, seeds, leaves, branches, fruit, and the like are included in the invention, provided that these parts comprise cells comprising the isolated nucleic acid of the present invention. Progeny and variants, and mutants of the regenerated plants are also included within the scope of the invention, provided that these parts comprise the introduced nucleic acid sequences. Transgenic plants expressing the selectable marker can be screened for transmission of the nucleic acid of the present invention by, for example, standard immunoblot and DNA detection techniques.

Transgenic lines are also typically evaluated on levels of expression of the heterologous nucleic acid. Expression at the RNA level can be determined initially to identify and quantitate expression-positive plants. Standard techniques for RNA analysis can be employed and include PCR amplification assays using oligonucleotide primers designed to amplify only the heterologous RNA templates and solution hybridization assays using heterologous nucleic acid-specific probes. The RNA-positive plants can then analyzed for protein expression by Western immunoblot analysis using the specifically reactive antibodies of the present invention. In addition, in situ hybridization and immunocytochemistry according to standard protocols can be done using heterologous nucleic acid specific polynucleotide probes and antibodies, respectively, to localize sites of expression within transgenic tissue. Generally, a number of transgenic lines are usually screened for the incorporated nucleic acid to identify and select plants with the most appropriate expression profiles.

[00219] A preferred embodiment is a transgenic plant that is homozygous for the added heterologous nucleic acid; *i.e.*, a transgenic plant that contains two added nucleic acid sequences, one gene at the same locus on each chromosome of a chromosome pair. A homozygous transgenic plant can be obtained by sexually mating (selfing) a heterozygous transgenic plant that contains a single added heterologous nucleic acid, germinating some of the seed produced and analyzing the resulting plants produced for altered expression of a polynucleotide of the present invention relative to a control plant (*i.e.*, native, non-transgenic). Back-crossing to a parental plant and out-crossing with a non-transgenic plant are also contemplated.

[00220] Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype. Such regeneration techniques often rely on manipulation of certain phytohormones in a tissue culture growth medium. For transformation and regeneration of maize see, Gordon-Kamm *et al.*, 1990, *The Plant Cell*, 2:603-618.

[00221] Plants cells transformed with a plant expression vector can be regenerated, *e.g.*, from single cells, callus tissue or leaf discs according to standard plant tissue culture techniques. It is well known in the art that various cells, tissues, and organs from almost any plant can be successfully cultured to regenerate an entire plant. Plant regeneration from cultured protoplasts is described in Evans *et al.*, 1983, *Protoplasts Isolation and Culture*, *Handbook of Plant Cell Culture*, Macmillan Publishing Company, New York, pp. 124-176;

and Binding, Regeneration of Plants, Plant Protoplasts, 1985, CRC Press, Boca Raton, pp. 21-73.

[00222] The regeneration of plants containing the foreign gene introduced by *Agrobacterium* from leaf explants can be achieved as described by Horsch *et al.*, 1985, Science, 227:1229-1231. In this procedure, transformants are grown in the presence of a selection agent and in a medium that induces the regeneration of shoots in the plant species being transformed as described by Fraley *et al.*, 1983, Proc. Natl. Acad. Sci. (U.S.A.), 80:4803. This procedure typically produces shoots within two to four weeks and these transformant shoots are then transferred to an appropriate root-inducing medium containing the selective agent and an antibiotic to prevent bacterial growth. Transgenic plants of the present invention may be fertile or sterile.

[00223] The regeneration of plants from either single plant protoplasts or various explants is well known in the art. See, for example, Methods for Plant Molecular Biology, A. Weissbach and H. Weissbach, eds., 1988, Academic Press, Inc., San Diego, Calif.. This regeneration and growth process includes the steps of selection of transformant cells and shoots, rooting the transformant shoots and growth of the plantlets in soil. For maize cell culture and regeneration see generally, The Maize Handbook, Freeling and Walbot, Eds., 1994, Springer, New York 1994; Corn and Corn Improvement, 3rd edition, Sprague and Dudley Eds., 1988, American Society of Agronomy, Madison, Wis.

6.13 Plants and Plant Cells

[00224] Also provided herein are a plant cell having the nucleotide sequence constructs of the invention. A further aspect of the present invention provides a method of making such a plant cell involving introduction of a vector including the construct into a plant cell. For integration of the construct into the plant genome, such introduction will be followed by recombination between the vector and the plant cell genome to introduce the sequence of nucleotides into the genome. RNA encoded by the introduced nucleic acid construct may then be transcribed in the cell and descendants thereof, including cells in plants regenerated from transformed material. A gene stably incorporated into the genome of a plant is passed from generation to generation to descendants of the plant, so such descendants should show the desired phenotype.

[00225] In certain embodiments, a plant cell comprises a *GLK1* nucleotide sequence operably associated with a vegetative tissue specific promoter, which is optionally a constitutive or inducible promoter. In other embodiments, a plant cell comprises multiple

copies of a *GLK1* operably associated with a vegetative tissue specific promoter. In specific embodiments provided herein are plants (and plant cells thereof) that overexpress, constitutively express and/or inducibly express *GLK1* in the vegetative tissues of the plant, as compared to other tissues in the plant and/or as compared to a wild type plant.

[00226] The present invention also provides a plant comprising a plant cell as disclosed. Transformed seeds and plant parts are also encompassed.

[00227] In addition to a plant, the present invention provides any clone of such a plant, seed, selfed or hybrid progeny and descendants, and any part of any of these, such as cuttings, seed. The invention provides any plant propagule, that is any part which may be used in reproduction or propagation, sexual or asexual, including cuttings, seed and so on. Also encompassed by the invention is a plant which is a sexually or asexually propagated off-spring, clone or descendant of such a plant, or any part or propagule of said plant, off-spring, clone or descendant. Plant extracts and derivatives are also provided.

[00228] Any species of woody, ornamental or decorative, crop or cereal, fruit or vegetable plant, and algae (*e.g.*, *Chlamydomonas reinhardtii*) may be used in the compositions and methods provided herein. Non-limiting examples of plants include plants from the genus *Arabidopsis* or the genus *Oryza*. Other examples include plants from the genera *Acorus*, *Aegilops*, *Allium*, *Amborella*, *Antirrhinum*, *Apium*, *Arachis*, *Beta*, *Betula*, *Brassica*, *Capsicum*, *Ceratopteris*, *Citrus*, *Cryptomeria*, *Cycas*, *Descurainia*, *Eschscholzia*, *Eucalyptus*, *Glycine*, *Gossypium*, *Hedyotis*, *Helianthus*, *Hordeum*, *Ipomoea*, *Lactuca*, *Linum*, *Liriodendron*, *Lotus*, *Lupinus*, *Lycopersicon*, *Medicago*, *Mesembryanthemum*, *Nicotiana*, *Nuphar*, *Pennisetum*, *Persea*, *Phaseolus*, *Physcomitrella*, *Picea*, *Pinus*, *Poncirus*, *Populus*, *Prunus*, *Robinia*, *Rosa*, *Saccharum*, *Schedonorus*, *Secale*, *Sesamum*, *Solanum*, *Sorghum*, *Stevia*, *Thellungiella*, *Theobroma*, *Triphysaria*, *Triticum*, *Vitis*, *Zea*, or *Zinnia*.

[00229] Plants included in the invention are any plants amenable to transformation techniques, including gymnosperms and angiosperms, both monocotyledons and dicotyledons.

[00230] Examples of monocotyledonous angiosperms include, but are not limited to, asparagus, field and sweet corn, barley, wheat, rice, sorghum, onion, pearl millet, rye and oats and other cereal grains.

[00231] Examples of dicotyledonous angiosperms include, but are not limited to tomato, tobacco, cotton, rapeseed, field beans, soybeans, peppers, lettuce, peas, alfalfa, clover, cole crops or *Brassica oleracea* (*e.g.*, cabbage, broccoli, cauliflower, brussel sprouts), radish,

carrot, beets, eggplant, spinach, cucumber, squash, melons, cantaloupe, sunflowers and various ornamentals.

[00232] Examples of woody species include poplar, pine, sequoia, cedar, oak, *etc.*

[00233] Still other examples of plants include, but are not limited to, wheat, cauliflower, tomato, tobacco, corn, petunia, trees, *etc.*

[00234] In certain embodiments, plants of the present invention are crop plants (for example, cereals and pulses, maize, wheat, potatoes, tapioca, rice, sorghum, millet, cassaya, barley, pea, and other root, tuber, or seed crops. Exemplary cereal crops used in the compositions and methods of the invention include, but are not limited to, any species of grass, or grain plant (*e.g.*, barley, corn, oats, rice, wild rice, rye, wheat, millet, sorghum, triticale, *etc.*), non-grass plants (*e.g.*, buckwheat flax, legumes or soybeans, *etc.*). Grain plants that provide seeds of interest include oil-seed plants and leguminous plants. Other seeds of interest include grain seeds, such as corn, wheat, barley, rice, sorghum, rye, *etc.* Oil seed plants include cotton, soybean, safflower, sunflower, Brassica, maize, alfalfa, palm, coconut, *etc.* Other important seed crops are oil-seed rape, sugar beet, maize, sunflower, soybean, and sorghum. Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, *etc.*

[00235] Horticultural plants to which the present invention may be applied may include lettuce, endive, and vegetable brassicas including cabbage, broccoli, and cauliflower, and carnations and geraniums. The present invention may also be applied to tobacco, cucurbits, carrot, strawberry, sunflower, tomato, pepper, chrysanthemum, poplar, eucalyptus, and pine.

[00236] The present invention may be used for transformation of other plant species, including, but not limited to, corn (*Zea mays*), canola (*Brassica napus*, *Brassica rapa ssp.*), alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), sunflower (*Helianthus annuus*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*, *Nicotiana benthamiana*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassaya (*Manihot esculenta*), coffee (*Coffea spp.*), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus spp.*), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa spp.*), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond

(*Prunus amygdalus*), sugar beets (*Beta vulgaris*), oats, barley, *Arabidopsis* spp., vegetables, ornamentals, and conifers.

6.14 Cultivation

[00237] Methods of cultivation of plants are well known in the art. For example, for the cultivation of wheat see Alcoz *et al.*, 1993, *Agronomy Journal* 85:1198-1203; Rao and Dao, 1992, *J. Am. Soc. Agronomy* 84:1028-1032; Howard and Lessman, 1991, *Agronomy Journal* 83:208-211; for the cultivation of corn see Tollenaar *et al.*, 1993, *Agronomy Journal* 85:251-255; Straw *et al.*, *Tennessee Farm and Home Science: Progress Report*, Spring 1993, 166:20-24; Miles, S. R., 1934, *J. Am. Soc. Agronomy* 26:129-137; Dara *et al.*, 1992, *J. Am. Soc. Agronomy* 84:1006-1010; Binford *et al.*, 1992, *Agronomy Journal* 84:53-59; for the cultivation of soybean see Chen *et al.*, 1992, *Canadian Journal of Plant Science* 72:1049-1056; Wallace *et al.*, 1990, *Journal of Plant Nutrition* 13:1523-1537; for the cultivation of rice see Oritani and Yoshida, 1984, *Japanese Journal of Crop Science* 53:204-212; for the cultivation of linseed see Diepenbrock and Porksen, 1992, *Industrial Crops and Products* 1:165-173; for the cultivation of tomato see Grubinger *et al.*, 1993, *Journal of the American Society for Horticultural Science* 118:212-216; Cerne, M., 1990, *Acta Horticulture* 277:179-182; for the cultivation of pineapple see Magistad *et al.*, 1932, *J. Am. Soc. Agronomy* 24:610-622; Asoegwu, S. N., 1988, *Fertilizer Research* 15:203-210; Asoegwu, S. N., 1987, *Fruits* 42:505-509; for the cultivation of lettuce see Richardson and Hardgrave, 1992, *Journal of the Science of Food and Agriculture* 59:345-349; for the cultivation of mint see Munsu, P. S., 1992, *Acta Horticulturae* 306:436-443; for the cultivation of camomile see Letchamo, W., 1992, *Acta Horticulturae* 306:375-384; for the cultivation of tobacco see Sisson *et al.*, 1991, *Crop Science* 31:1615-1620; for the cultivation of potato see Porter and Sisson, 1991, *American Potato Journal*, 68:493-505; for the cultivation of brassica crops see Rahn *et al.*, 1992, Conference "Proceedings, second congress of the European Society for Agronomy" Warwick Univ., p.424-425; for the cultivation of banana see Hegde and Srinivas, 1991, *Tropical Agriculture* 68:331-334; Langenegger and Smith, 1988, *Fruits* 43:639-643; for the cultivation of strawberries see Human and Kotze, 1990, *Communications in Soil Science and Plant Analysis* 21:771-782; for the cultivation of songhum see Mahalle and Seth, 1989, *Indian Journal of Agricultural Sciences* 59:395-397; for the cultivation of plantain see Anjorin and Obigbesan, 1985, Conference "International Cooperation for Effective Plantain and Banana Research" Proceedings of the third meeting. Abidjan, Ivory Coast, p. 115-117; for the cultivation of sugar cane see Yadav, R. L., 1986, *Fertiliser News* 31:17-22; Yadav and

Sharma, 1983, Indian Journal of Agricultural Sciences 53:38-43; for the cultivation of sugar beet see Draycott *et al.*, 1983, Conference "Symposium Nitrogen and Sugar Beet" International Institute for Sugar Beet Research--Brussels Belgium, p. 293-303. See also Goh and Haynes, 1986, "Nitrogen and Agronomic Practice" in Mineral Nitrogen in the Plant-Soil System, Academic Press, Inc., Orlando, Fla., p. 379-468; Engelstad, O. P., 1985, Fertilizer Technology and Use, Third Edition, Soil Science Society of America, p.633; Yadav and Sharmna, 1983, Indian Journal of Agricultural Sciences, 53:3-43.

6.15 Products of Transgenic Plants

[00238] Engineered plants exhibiting the desired physiological and/or agronomic changes can be used directly in agricultural production.

[00239] Thus, provided herein are products derived from the transgenic plants or methods of producing transgenic plants provided herein. In certain embodiments, the products are commercial products. Some non-limiting example include genetically engineered trees for *e.g.*, the production of pulp, paper, paper products or lumber; tobacco, *e.g.*, for the production of cigarettes, cigars, or chewing tobacco; crops, *e.g.*, for the production of fruits, vegetables and other food, including grains, *e.g.*, for the production of wheat, bread, flour, rice, corn; and canola, sunflower, *e.g.*, for the production of oils or biofuels.

[00240] In certain embodiments, commercial products are derived from a genetically engineered (*e.g.*, comprising overexpression of *GLK1* in the vegetative tissues of the plant) species of woody, ornamental or decorative, crop or cereal, fruit or vegetable plant, and algae (*e.g.*, *Chlamydomonas reinhardtii*), which may be used in the compositions and methods provided herein. Non-limiting examples of plants include plants from the genus *Arabidopsis* or the genus *Oryza*. Other examples include plants from the genera *Acorus*, *Aegilops*, *Allium*, *Amborella*, *Antirrhinum*, *Apium*, *Arachis*, *Beta*, *Betula*, *Brassica*, *Capsicum*, *Ceratopteris*, *Citrus*, *Cryptomeria*, *Cycas*, *Descurainia*, *Eschscholzia*, *Eucalyptus*, *Glycine*, *Gossypium*, *Hedyotis*, *Helianthus*, *Hordeum*, *Ipomoea*, *Lactuca*, *Linum*, *Liriodendron*, *Lotus*, *Lupinus*, *Lycopersicon*, *Medicago*, *Mesembryanthemum*, *Nicotiana*, *Nuphar*, *Pennisetum*, *Persea*, *Phaseolus*, *Physcomitrella*, *Picea*, *Pinus*, *Poncirus*, *Populus*, *Prunus*, *Robinia*, *Rosa*, *Saccharum*, *Schedonorus*, *Secale*, *Sesamum*, *Solanum*, *Sorghum*, *Stevia*, *Thellungiella*, *Theobroma*, *Triphysaria*, *Triticum*, *Vitis*, *Zea*, or *Zinnia*.

[00241] In some embodiments, commercial products are derived from a genetically engineered gymnosperms and angiosperms, both monocotyledons and dicotyledons. Examples of monocotyledonous angiosperms include, but are not limited to, asparagus, field

and sweet corn, barley, wheat, rice, sorghum, onion, pearl millet, rye and oats and other cereal grains. Examples of dicotyledonous angiosperms include, but are not limited to tomato, tobacco, cotton, rapeseed, field beans, soybeans, peppers, lettuce, peas, alfalfa, clover, cole crops or Brassica oleracea (*e.g.*, cabbage, broccoli, cauliflower, brussel sprouts), radish, carrot, beets, eggplant, spinach, cucumber, squash, melons, cantaloupe, sunflowers and various ornamentals.

[00242] In certain embodiments, commercial products are derived from a genetically engineered (*e.g.*, comprising overexpression of *bZIP1* in the leaves or seeds of the plant) woody species, such as poplar, pine, sequoia, cedar, oak, *etc.*

[00243] In other embodiments, commercial products are derived from a genetically engineered (*e.g.*, comprising overexpression of *CCA1* and *GLK1* in the vegetative tissues of the plant) plant including, but are not limited to, wheat, cauliflower, tomato, tobacco, corn, petunia, trees, *etc.*

[00244] In certain embodiments, commercial products are derived from a genetically engineered crop plants, for example, cereals and pulses, maize, wheat, potatoes, tapioca, rice, sorghum, millet, cassava, barley, pea, and other root, tuber, or seed crops. In one embodiment, commercial products are derived from a genetically engineered (*e.g.*, comprising overexpression of *CCA1* and *GLK1* and underexpression of *bZIP1* in the vegetative tissues of the plant) cereal crops, including, but are not limited to, any species of grass, or grain plant (*e.g.*, barley, corn, oats, rice, wild rice, rye, wheat, millet, sorghum, triticale, *etc.*), non-grass plants (*e.g.*, buckwheat flax, legumes or soybeans, *etc.*). In another embodiment, commercial products are derived from a genetically engineered (*e.g.*, comprising overexpression of *bZIP1* and optionally underexpression of *CCA1* and/or *GLK1* in leaf or seed tissue of the plant) grain plants that provide seeds of interest, oil-seed plants and leguminous plants. In other embodiments, commercial products are derived from a genetically engineered grain seed plants, such as corn, wheat, barley, rice, sorghum, rye, *etc.* In yet other embodiments, commercial products are derived from a genetically engineered (*e.g.*, comprising overexpression of *bZIP1* and optionally underexpression of *CCA1* and/or *GLK1* in leaf or seed tissue of the plant) oil seed plants, such as cotton, soybean, safflower, sunflower, Brassica, maize, alfalfa, palm, coconut, *etc.* In certain embodiments, commercial products are derived from a genetically engineered oil-seed rape, sugar beet, maize, sunflower, soybean, or sorghum. In some embodiments, commercial products are derived from a genetically engineered leguminous plants, such as beans and peas (*e.g.*, guar, locust

bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, *etc.*)

[00245] In certain embodiments, commercial products are derived from a genetically engineered horticultural plant of the present invention, such as lettuce, endive, and vegetable brassicas including cabbage, broccoli, and cauliflower, and carnations and geraniums; tomato, tobacco, cucurbits, carrot, strawberry, sunflower, tomato, pepper, chrysanthemum, poplar, eucalyptus, and pine.

[00246] In still other embodiments, commercial products are derived from a genetically engineered corn (*Zea mays*), canola (*Brassica napus*, *Brassica rapa ssp.*), alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), sunflower (*Helianthus annuus*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*, *Nicotiana benthamiana*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Coffea spp.*), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus spp.*), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa spp.*), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), oats, barley, *Arabidopsis spp.*, vegetables, ornamentals, and conifers.

6.16 Kits

[00247] In one aspect, the present invention provides any of the above-mentioned compositions in kits, optionally including instructions for use of the composition *e.g.*, for the overexpression or underexpression of *CCA1*, *GLK1* or *bZIP1*. The “kit” typically defines a package including one or more compositions of the invention and the instructions, and/or analogs, derivatives, or functionally equivalent compositions thereof. Thus, for example, the kit can include a description of use of the composition for participation in any technique associated in the overexpression or underexpression of genes. The kit can include a description of use of the compositions as discussed herein. Instructions also may be provided for use of the composition in any suitable technique as previously described. The instructions may be of any form provided in connection with the composition.

[00248] The kits described herein may also contain one or more containers, which may contain the inventive composition and other ingredients as previously described. The kits

also may contain instructions for mixing, diluting, and/or administering the compositions in some cases. The kits also can include other containers with one or more solvents, surfactants, preservative and/or diluents (*e.g.*, normal saline (0.9% NaCl), or 5% dextrose) as well as containers for mixing, diluting and/or administering the compositions.

[00249] The compositions of the kit may be provided as any suitable form, for example, as liquid solutions or as dried powders. When the composition provided is a dry powder, the composition may be reconstituted by the addition of a suitable solvent, which may also be provided. In embodiments where liquid forms of the composition are used, the liquid form may be concentrated or ready to use. The solvent will depend on the active compound(s) within the composition. Suitable solvents are well known, for example as previously described, and are available in the literature.

[00250] The invention also involves, in another aspect, promotion of the overexpression of a master regulatory gene of the present invention, *e.g.*, *CCA1/GLK1/bZIP1*, according to any of the systems or methods described herein. As used herein, “promoted” includes all methods of doing business including methods of education, hospital and other clinical instruction, pharmaceutical industry activity including pharmaceutical sales, and any advertising or other promotional activity including written, oral and electronic communication of any form, associated with compositions of the invention. “Instructions” can define a component of promotion, and typically involve written instructions on or associated with packaging of compositions of the invention. Instructions also can include any oral or electronic instructions provided in any manner.

7. EXAMPLE

7.1 Introduction

[00251] Nitrogen (N) is an essential nutrient and a metabolic signal that is sensed and transduced resulting in the control of gene expression in plants. Studies using nitrate reductase (NR) mutant plants, have shown that nitrate can serve as a metabolic signal for inorganic N that regulates gene expression in *Arabidopsis thaliana* and other plant species (Wang *et al.*, 2004, Plant Physiol 136:2512-2522; Wang *et al.*, 2003, Plant Physiol 132:556-567; Forde, 2002, Ann. Rev. Plant Biology 53:203-224; Scheible, *et al.*, 2004, Plant Physiol 136:2483-2499). There is also ample though less direct evidence that the assimilated forms of N such as Glu or Gln may also serve as signals that regulate gene expression in plants (Rawat *et al.*, 1999, Plant J 19:143-152; Oliveira *et al.*, 1999, Plant Physiol 121:301-310).

The ability of plants to sense and respond to levels of inorganic and organic N metabolites provides a mechanism to balance the availability of organic N resources within the plant with the need for N uptake. Because nitrate uptake, reduction and its assimilation into organic form require energy, a mechanism that activates this N assimilatory pathway based on sensing levels of organic N available in the plant is an efficient way to control N-use efficiency (Forde, 2002, *Ann. Rev. Plant Biology* 53:203-224). In plants, the transcription of genes involved in the uptake and assimilation of inorganic N is induced when levels of organic N are low. Conversely, the uptake and reduction of inorganic N are shut off when levels of organic N are high (reviewed in Scheible, *et al.*, 1997, *Plant Cell* 9:783-798).

[00252] Recent microarray studies have shown that nitrate can cause changes in the expression of a large number of genes in *Arabidopsis* (Wang *et al.*, 2004, *Plant Physiol* 136:2512-2522; Wang *et al.*, 2003, *Plant Physiol* 132:556-567). Treatment of *Arabidopsis* seedlings with low levels of nitrate has been shown to increase the levels of mRNA for hundreds of genes within minutes of exposure. The nitrate-responsive genes include nitrate transporters, NR and nitrite reductase, putative transcription factors, stress responses genes, as well as genes whose products play roles in glycolysis, iron metabolism, and sulfate uptake (Wang *et al.*, 2004, *Plant Physiol* 136:2512-2522; Wang *et al.*, 2003, *Plant Physiol* 132:556-567). In a related study, N-starved plants underwent a transcriptome/metabolome analysis 30 min and 3 h after nitrate treatment (Scheible, *et al.*, 2004, *Plant Physiol* 136:2483-2499). The expression of nitrate transporters (at 30 min) preceded the induction of amino acid biosynthetic genes and the repression of amino acid breakdown genes (at 3 h). In addition, increases in amino acid levels were observed, consistent with the changes in expression of the cognate amino acid biosynthesis genes. Putative nitrate-responsive regulatory factors including transcription factors, protein kinases/phosphatases and trehalose and hormone metabolic genes were also identified in that study. Recently, using a NR-null mutant, it was shown that nitrate and not a product of nitrate reduction and assimilation, regulates the expression of genes involved in energy production, metabolism, glycolysis and gluconeogenesis (Wang *et al.*, 2004, *Plant Physiol* 136:2512-2522).

[00253] Nitrogen metabolism genes can be regulated by negative feedback of the products of N assimilation including downstream organic N metabolites such as Glu or Gln. For example, the expression of the ammonium transporter gene ammonium transporter 1 (AMT1.1) is repressed in treatments with high levels of inorganic N. It has been shown that this repression is blocked by methionine sulfoximine (MSX), a non-metabolizable analog of Glu that irreversibly inhibits glutamine synthetase and hence blocks N assimilation into Gln

(Rawat *et al.*, 1999, Plant J 19:143-152). Thus, it appears that organic forms of N may regulate the uptake of N in plants. In addition, the genes encoding asparagine synthetase 1 (*ASN1*) and 2 (*ASN2*), are differentially regulated by organic and inorganic N sources. Organic N treatments were shown to positively regulate levels of *ASN1* mRNA (Oliveira *et al.*, 1999, Plant Physiol 121:301-310), whereas *ASN2* gene expression appears to be responsive to inorganic N sources and not a downstream metabolite (Wang *et al.*, 2004, Plant Physiol 136:2512-2522). Together, these studies prompt a model in which both inorganic as well as organic N sources can each regulate plant gene expression affecting N uptake, reduction and assimilation.

[00254] In study presented below, a genomic approach was used to identify gene networks whose expression is regulated by Glu or Glu-derived metabolites (organic N) in plants. Plants were treated with inorganic nitrogen sources in the presence or absence of MSX, which served to inhibit the assimilation of ammonium into Glu/Gln by blocking glutamine synthetase. The rationale for this approach was that a subset of nitrogen-responsive genes responding specifically to an organic signal (*e.g.* Glu/Gln) would not respond to nitrogen treatment if the synthesis of Glu/Gln was blocked by transient MSX treatments. Network analysis of the genes that responded to organic N revealed that transcription control of gene expression is important for a subnetwork of metabolic genes involved in the synthesis and degradation of asparagine (Asn), an important nitrogen-transport/storage compound synthesized when levels of nitrogen are abundant and degraded when nitrogen reserves are mobilized. The metabolic gene network discovered in this analysis provides molecular evidence for regulation of N-use at the level of gene expression. Moreover, the transcription factors regulated by organic N associated with this network provide a mechanistic link between circadian clock function and N-assimilation in plants.

7.2 Materials and Methods

[00255] Plant growth conditions. Wild type *Arabidopsis thaliana* ecotype Columbia-0 strain was used in all experiments unless indicated otherwise. Seeds were surface sterilized with ethanol and bleach as previously described (Brenner *et al.*, 2000, Plant Physiol. 124:1615-1624) and sowed onto basal MS salts (Sigma, St Louis, MO) with 0.5% (w/v) sucrose, 0.8% BactoAgar, and 1mM KNO₃. After 14 days under long day (16 hours light: 8 hours dark) at 22°C, plants were transiently treated for 2h in the light at the start of their light cycle by transferring them to basal medium with 0.5% sucrose and a combination of inorganic nitrogen sources (20 mM KNO₃ and 20 mM NH₄NO₃) with or without 1mM MSX

(Sigma M-5379), 10 mM glutamate (Sigma G-1501) and/or 10 mM glutamine (Sigma G-3126): N; N+MSX; N+MSX+Glu respectively.

[00256] RNA isolation and quantitative real time PCR. RNA was isolated from whole plants with the TRIzol reagent and according to the instructions of the manufacturer (Invitrogen, Carlsbad, CA). cDNA synthesis from whole mRNA extractions was carried out according to kit manufacturer instructions (Invitrogen, Catalog number 11146-024). Real time quantitative PCR was carried out with a LightCycler (Roche Diagnostics, Mannheim, Germany) as described previously (Thum, K. E., Shasha, D. E., Lejay, L. V. & Coruzzi, G. M. (2003) *Plant Physiol* 132, 440-52).

[00257] Microarray experiments and analysis. cDNA synthesis, array hybridization, and normalization of the signal intensities were performed according to the instructions provided by Affymetrix (Santa Clara, CA). All raw microarray data was processed with MASv5.0 software as follows. Each hybridization was normalized to a median intensity of 150. Each treatment replica was compared with the two baselines to generate 4 comparisons per treatment. Data points with absent/marginal calls (Affymetrix quality control) in both baseline and treatment were removed. Data points with absent call in one hybridization and present call in the other hybridization were eliminated if the probe called present had a signal intensity of <100. The response of each gene was summarized using the Affymetrix change calls "I" for induced, "D" for decreased and "NC" for not changed. Data points were considered only if the change calls were consistent in at least 3 out of the 4 comparisons. This stepwise filtering resulted in a set of 834 genes that were detected and responded consistently in our experiments. We used custom made S-PLUS and PERL functions to analyze and visualize groups of genes with similar expression patterns based on the Affymetrix change calls.

[00258] Network analysis. For network analysis, an existing network model of plant gene interactions was used (Gutierrez, R. A., Lejay, L. V., Dean, A., Chiaromonte, F., Shasha, D. E. & Coruzzi, G. M. (2007) *Genome Biol.* 8(1):R7). In addition, protein:DNA interactions were predicted based as follows: The consensus sequence for transcription binding sites from well curated databases DATF (Guo, A., He, K., Liu, D., Bai, S., Gu, X., Wei, L. & Luo, J. (2005) *Bioinformatics* 21, 2568-2569) and AGRIS (Davuluri, R., Sun, H., Palaniswamy, S., Matthews, N., Molina, C., Kurtz, M. & Grotewold, E. (2003) *BMC Bioinformatics* 4, 25) were searched in 1500 base pairs of upstream sequence using the DNA pattern search tool from the RSA tools server with default parameters (van Helden, J. (2003) *Nucleic Acids Res* 31, 3593 - 3596). The search was performed in both strands of DNA, the upstream region

was not allowed to overlap with the coding region of the upstream gene, motif matches were not allowed to overlap. A motif was considered over-represented if it was present in an upstream sequence more than 3 times the standard deviation above the mean occurrence in all the upstream sequences in the genome. A protein:DNA interaction was predicted when the upstream sequence of the gene contained an over representation of the regulatory motif for that transcription factor and the expression of the transcription factor and putative target gene was highly (≥ 0.7 or ≤ -0.7) and significantly ($p \leq 0.01$) correlated. Similar regulatory predictions for other microarray data sets can be generated with the VirtualPlant system (<http://www.virtualplant.org>) using the "Gene Networks" tool.

[00259] Chromatin immunoprecipitation assays (ChIP): Immunoprecipitations (IP) were performed as previously described (Gendrel, A., Lippman, Z., Martienssen, R. A. & Colot, V. (2005) Profiling histone modification patterns in plants using genomic tiling microarrays Nat Methods 2, 219-224). Briefly, two weeks old wild-type and *CCA1-ox* plants were collected at the beginning of the light cycle and immediately fixed in 1% formaldehyde for 15min in a vacuum at room temperature. Crosslinking was stopped by the addition of glycine to a final concentration of 0.125 M. Nuclei were prepared for chromatin isolation. The isolated chromatin was sonicated ten times for 20s each at 100% power (Diagenode Bioruptor) in an ice water bath. A small aliquot of sheared chromatin was removed to serve as control. The diluted chromatin was used for IP with the CCA1 antibody and one control IP without antibody. The primer sequences used for amplification of the CCA1 binding sites in each of the genes tested are listed in Table 1.

Table 1

Gene	PUB locus	Primer 1	Primer 2
bZIP1	At5g49450	5' -GATCGAAAATAAGGAAAGTGGG-3' (SEQ ID NO:5)	5' -ACTGGTCACCTATTAAGGAAC-3' (SEQ ID NO:6)
TOC1	At5g61380	5' -TGGACGGTGGAGATTAAGTC-3' (SEQ ID NO:7)	5' -ACGAAACGAAGCCGAATCCT-3' (SEQ ID NO:8)
ZTL	At5g57360	5' -AGTCGCCGGAGATTATGAAGACGG-3' (SEQ ID NO:9)	5' -GGTTTTATCTACTTGACCCGACAG-3' (SEQ ID NO:10)
GDH1	At5g18170	5' -TGTTTCAATAGCATTAGCCTCCA-3' (SEQ ID NO:11)	5' -TGGGGAATGTGACACACATAATC-3' (SEQ ID NO:12)
GLN1.3	At3g17820	5' -TTGAATCCGAAGAGGGGAAAA-3' (SEQ ID NO:13)	5' -AACAACTGCTACCAATTTCTTG-3' (SEQ ID NO:14)

[00260] PCR amplifications included 95°C for 2min followed by 36 cycles of 95°C for 15s, 58°C (for bZIP1, TOC1 and GDH1) or 60°C (for ZTL and GLN1.3) for 30s and 72°C for 30s.

[00261] Circadian phase response curves: *CCA1::LUC* seedlings were entrained on MS basal medium plus 0.5% sucrose and 1mM KNO₃ for 8d in 16/8h light/dark (100-150 $\mu\text{mol m}^{-2} \text{s}^{-1}$), after which seedlings were moved into continuous light. At 3-hr intervals, seedlings (n=16 per treatment) were transferred to fresh solid medium plus 2mL liquid Nms or medium containing 10mM Glu or 10mM Gln for 4hr, then rinsed in liquid entrainment medium 3 times for a total of 30 min and transferred individually to the wells of 96-well microtiter plates containing fresh solid media for luciferase activity measurements which were determined with a Packard TopCount scintillation counter as described (Salome, P. A., *et al.* (2002) The out of phase 1 mutant defines a role for PHYB in circadian phase control in *Arabidopsis* Plant Physiol 129, 1674-85). The period and phase of rhythms after the pulses were determined by fast-Fourier transform nonlinear least-square analysis (Plautz, J. D., *et al.* (1997) Quantitative analysis of *Drosophila* period gene transcription in living animals J Biol Rhythms 12, 204-17). The phase shifts were calculated as described (Covington, M. F., *et al.* (2001) ELF3 modulates resetting of the circadian clock in *Arabidopsis* Plant Cell 13, 1305-15).

7.3 Results

[00262] Inorganic versus organic N responses. To uncouple gene responses to inorganic N from those elicited by downstream products of inorganic N assimilation, treatments of *Arabidopsis* seedlings with combinations of inorganic N (nitrate and ammonium), organic forms of N (*e.g.*, Glu, Gln), and MSX, an inhibitor of glutamine synthetase were performed (King *et al.*, 1993, Plant Physiol. 102:1279-1286) (Figure 7). Genes regulated by inorganic N signals should be unaffected by MSX treatment. By contrast, genes responding to a downstream organic N signal should fail to show induction by inorganic N treatments if Glu/Gln synthesis is blocked by MSX. This block of induction by MSX should be relieved by Glu treatment. Following this rationale, two-week-old *Arabidopsis* seedlings grown on low concentrations of N (1mM NO₃⁻) were transferred to media containing 40mM NO₃⁻ and 20mM NH₄⁺ (referred to as "Nms"). Seedlings were then harvested after a 2h treatment time. This treatment was carried out alone (Nms), in the presence of 1mM MSX (Nms+MSX) or 1mM MSX and 10mM Glu (Nms+MSX+Glu). The Nms treatment consists of the same N source found in standard MS salts which is the established standard amount of N for plant growth (Murashige *et al.*, 1962, Plant Physiol. 15:473-497). A concentration of 1mM MSX has previously been established as effective in blocking the N repression of AMT1.1 in *Arabidopsis* seedlings and in decreasing levels of internal organic N (Rawat *et al.*, 1999,

Plant J 19:143-152). A concentration of 10mM for Glu treatments was chosen because this has been shown to be effective in the regulation of N assimilatory genes while not being high enough to be detrimental to plant growth or development (Oliveria *et al.*, 1999, Plant Physiol. 121:301-310). To evaluate the effect of MSX alone, plants were exposed to growth media that contained MSX. To control for the effect of the plant transfer to distinct media, plants were transferred onto media plates without any of the treatment factors. This latter control was used as the base line for the microarray experiments described below.

[00263] To evaluate the experimental design, the mRNA level of genes shown to be responsive to organic N (*ASN1*) or inorganic N (*ASN2*) was determined by reverse transcription followed by real time quantitative PCR (RT-qPCR). This analysis showed that the *ASN1* mRNA level was induced 3.5-fold by the Nms treatment as compared to the control (Figure 8, compare Nms versus the control). This induction of *ASN1* mRNA was blocked when MSX was present (Figure 8A, Nms+MSX versus Nms). Importantly, when exogenous Glu or Gln was added, *ASN1* levels were induced regardless of the presence of MSX (Figure 8A, compare Control to Nms+MSX+Glu and Nms+MSX+Gln). These results indicate that the induction of *ASN1* is due to Glu or a downstream metabolite, as shown previously (Lam *et al.*, 1998, Plant J 16:345-353; Oliveira *et al.*, 2001, Braz J Med Biol Res 34:567-575). In addition, the control treatments showed that MSX alone does not induce expression of *ASN1* or *ASN2* (Figure 8). The addition of Glu or Gln partially blocked the induction of *ASN2* by the Nms treatment (Figure 8B), consistent with the negative regulation by amino acids seen previously (Lam *et al.*, 1998, Plant J 16:345-353). Conversely, the induction of *ASN2* mRNA by Nms was insensitive to MSX addition (Figure 8B), suggesting the induction was mediated by an inorganic N source. This finding was consistent with previous data which indicates that *ASN2* gene expression correlates with ammonium levels (Wong *et al.*, 2004, Plant Physiol 134:332-812).

[00264] **Global genomic responses to organic and inorganic nitrogen signals.** To investigate global gene expression changes that are mediated by Glu or a Glu-derived metabolite, the plant transcriptome was monitored using the ATH1 Affymetrix gene chip. Total RNA was extracted from plants treated with Nms, Nms+MSX or Nms+MSX+Glu as described above; two biological replicates per treatment were performed. The Nms+MSX+Gln treatments were not analyzed using microarrays because Gln and Glu responses were similar in our hands (Figure 8). RNA was labeled and hybridized to the microarrays, the raw intensity values were normalized and the data filtered as described in Materials and Methods. A gene was kept in the data set only if its expression was

reproducible and reliable across the 3 different treatments (Nms, Nms+MSX, Nms+MSX+Glu). A total of 5,904 genes were identified that passed these stringent quality control criteria. In order to verify the microarray results, we analyzed the mRNA levels of selected genes by RT-qPCR including the TAZ zinc binding (At4g37610) and bZIP (At5g49450) transcription factors with results similar to the microarray data (Figure 9). As expected, the genomic experiments verified the previous observation that AMT1.1 and ASN1 are regulated by organic N. In addition, the results identified additional genes regulated by organic N as described below.

[00265] Genes were categorized based on their response to the treatments using the Affymetrix change calls: induced (I), no change (NC) or decreased (D). Each gene was assigned a three-part code (e.g. I- NC- I) which corresponds to the gene expression response in the Nms, Nms+MSX, and Nms+MSX+Glu treatments respectively. 21 unique patterns of response were found (See Annex) and Table 2 (in each column the gene listed on the left is predicted to control the expression of the gene on the right, *i.e.*, At1g74840 is predicted to control the expression of At2g47060, At5g24800 is predicted to control the expression of At5g13930).

Table 2

At1g74840	reg0.9	At2g47060	At5g24800	reg0.7	At5g13930
At5g14540	reg0.9	At5g53370	At5g48655	reg0.8	At5g53370
At3g61150	reg0.7	At4g30810	At1g74840	reg0.8	At5g01820
At2g46830	reg0.8	At5g01820	At5g24800	reg0.8	At2g30040
At5g48655	reg0.7	At2g30040	At2g33710	reg0.8	At2g30040
At4g17490	reg0.8	At2g30040	At2g46830	reg0.7	At2g30040
At5g44190	reg0.8	At2g30040	At1g74840	reg0.7	At4g28100
At2g20570	reg0.8	At4g28100	At1g22070	reg0.7	At4g33300
At2g46830	reg0.7	At1g06000	At5g48655	reg0.9	At5g11790
At1g74840	reg0.8	At4g36640	At1g22070	reg0.8	At4g19810
At5g24800	reg0.9	At4g19810	At5g49450	reg0.9	At2g39980
At3g01560	reg0.7	At2g15970	At1g43160	reg0.9	At2g15970
At1g22070	reg0.7	At2g15970	At2g20570	reg0.7	At2g22240
At5g49450	reg0.8	At1g49500	At2g20570	reg0.8	At1g27730
At2g46830	reg0.9	At1g27730	At4g37260	reg0.7	At3g04070
At5g24800	reg0.8	At2g36290	At5g48655	reg0.7	At5g63790
At5g48655	reg0.7	At4g28250	At2g04880	reg0.9	At5g45340
At2g25000	reg0.7	At5g45340	At2g38470	reg1.0	At5g45340
At5g44190	reg0.8	At1g29670	At5g14540	reg0.7	At1g70330
At1g53910	reg0.7	At1g70330	At5g14540	reg0.8	At3g58560
At2g22430	reg0.8	At2g30870	At5g47230	reg0.7	At2g30870

At5g61890	reg0.7	At2g30870	At2g22430	reg0.8	At2g35930
At2g38470	reg0.7	At1g33590	At3g01560	reg0.7	At5g06320
At5g14540	reg0.7	At5g06320	At3g61150	reg0.7	At2g44210
At5g49450	reg1.0	At2g44080	At3g61890	reg0.7	At5g60850
At1g22070	reg0.7	At3g59220	At2g20570	reg0.7	At1g60780
At1g43160	reg0.7	At1g74840	At5g61890	reg0.8	At1g74840
At5g49450	reg0.9	At4g27410	At5g14540	reg0.8	At2g40270
At4g37260	reg0.7	At1g77510	At5g14540	reg0.8	At4g33400
At1g74840	reg0.7	At4g36250	At3g61890	reg0.9	At5g05600
At1g74840	reg0.9	At1g53310	At2g22430	reg0.7	At4g14960
At1g43160	reg0.9	At5g15960	At5g61890	reg0.9	At5g15960
At2g22430	reg0.8	At3g23750	At1g53910	reg0.8	At3g23750
At5g61890	reg0.8	At3g19680	At3g01560	reg0.8	At2g47180
At1g43160	reg0.7	At2g47180	At5g47230	reg0.8	At2g47180
At5g61890	reg0.7	At2g47180	At2g22430	reg0.7	At5g01540
At5g14540	reg0.7	At2g39530	At5g48655	reg0.8	At2g39530
At2g33710	reg0.8	At2g39530	At1g74840	reg0.9	At1g51680
At1g22070	reg0.8	At4g39330	At5g24800	reg0.7	At4g39330
At1g53910	reg0.9	At4g03260	At5g14540	reg0.8	At1g76670
At2g22430	reg0.7	At1g76670	At3g61150	reg0.7	At1g76670
At5g24800	reg0.9	At5g02270	At2g20570	reg0.8	At5g35735
At5g61890	reg0.8	At3g47960	At1g74840	reg0.8	At3g21230
At2g04880	reg0.8	At4g31500	At4g31800	reg0.7	At4g31500
At3g61150	reg0.8	At5g63850	At3g01560	reg0.7	At2g46600
At4g37260	reg0.9	At1g10760	At1g74840	reg0.8	At3g54640
At5g49450	reg0.7	At1g76590	At1g25560	reg0.7	At1g76590
At1g68840	reg0.8	At1g76590	At5g24800	reg0.7	At5g44190
At1g74840	reg0.9	At5g60920	At5g14540	reg0.8	At5g60920
At1g25560	reg0.8	At4g38470	At1g68840	reg0.7	At4g38470
At2g20570	reg0.8	At2g37430	At2g46830	reg0.9	At2g37430
At2g04880	reg0.8	At2g37430	At2g25000	reg0.8	At2g37430
At2g30250	reg0.7	At2g37430	At2g38470	reg0.9	At2g37430
At4g01250	reg0.7	At2g37430	At2g20570	reg0.9	At1g74460
At2g46830	reg0.8	At1g74460	At1g22070	reg0.7	At4g23630
At3g01560	reg0.9	At3g14280	At5g14540	reg0.7	At3g14280
At3g61150	reg0.7	At3g14280	At2g20570	reg0.7	At3g14280
At2g46830	reg0.8	At3g14280	At2g04880	reg0.8	At5g44070
At2g38470	reg0.9	At5g44070	At4g01250	reg0.7	At5g44070
At5g24800	reg0.7	At1g73080	At2g33710	reg0.9	At3g56710
At4g17490	reg0.9	At3g56710	At2g20570	reg0.8	At3g56710
At2g46830	reg0.8	At3g56710	At1g74840	reg0.8	At2g30490
At3g01560	reg0.7	At2g42540	At1g43160	reg0.9	At2g42540
At5g61890	reg0.8	At2g42540	At1g74840	reg0.7	At1g47128
At2g46830	reg0.7	At1g47128	At5g24800	reg0.7	At4g11280
At2g20570	reg0.7	At3g60030	At4g37260	reg0.7	At3g47620

At5g49450	reg0.8	At3g21870	At5g14540	reg0.8	At4g33050
At5g48655	reg0.7	At4g33050	At3g01560	reg0.7	At5g01600
At1g43160	reg0.8	At5g01600	At1g43160	reg0.8	At3g05890
At1g74840	reg0.7	At2g16630	At4g37260	reg0.9	At2g16630
At2g04880	reg0.9	At5g45340	At2g25000	reg0.7	At5g45340
At2g38470	reg1.0	At5g45340	At3g01560	reg0.7	At2g22880
At5g48655	reg0.7	At2g22880	At2g04880	reg0.8	At3g52400
At1g43160	reg0.9	At1g29395	At5g61890	reg0.7	At1g29395
At1g74840	reg0.8	At2g16430	At1g74840	reg0.8	At4g23210
At1g22070	reg0.7	At4g23210	At5g49450	reg0.8	At4g21150
At1g22070	reg0.9	At3g48610	At5g24800	reg0.7	At3g48610
At5g47230	reg0.7	At2g38700	At1g74840	reg0.7	At4g30280
At5g14540	reg0.7	At1g53500	At5g48655	reg0.8	At1g53500
At3g01560	reg0.7	At2g23120	At5g14540	reg0.8	At5g09440
At2g22430	reg0.8	At5g09440	At1g74840	reg0.8	At5g09440
At5g24800	reg0.7	At2g41630	At2g20570	reg0.8	At1g56150
At2g46830	reg0.8	At1g56150	At5g49450	reg0.7	At1g10070
At2g22430	reg0.8	At3g21240	At3g01560	reg0.8	At5g16010
At4g37260	reg0.9	At5g46710	At1g25560	reg0.7	At5g11420
At1g68840	reg0.7	At5g11420	At5g24800	reg0.7	At4g01250
At5g44190	reg0.7	At3g07790	At2g30250	reg0.7	At1g13110
At2g38470	reg0.8	At1g13110	At4g01250	reg0.9	At1g13110
At1g22070	reg0.8	At2g25000	At2g20570	reg0.9	At2g25000
At2g46830	reg0.8	At2g25000	At2g04880	reg0.8	At2g25000
At2g38470	reg0.7	At2g25000	At4g31800	reg0.8	At2g25000
At5g24800	reg0.7	At1g35780	At3g01560	reg0.8	At5g11110
At1g74840	reg0.9	At5g11110	At1g43160	reg0.8	At5g11110
At5g47230	reg0.7	At5g11110	At5g61890	reg0.7	At5g11110
At3g61890	reg0.8	At4g12490	At1g74840	reg0.7	At1g51700
At1g74840	reg0.8	At3g55970	At4g37260	reg0.7	At3g55970
At4g17500	reg0.8	At5g49910	At1g22070	reg0.7	At4g39800
At1g74840	reg0.8	At4g39800	At2g20570	reg0.7	At4g39800
At2g46830	reg0.8	At4g39800	At2g20570	reg0.8	At2g13790
At2g46830	reg0.8	At2g13790	At3g61890	reg1.0	At1g52400
At2g20570	reg0.8	At5g18470	At2g46830	reg0.7	At5g18470
At2g22430	reg0.9	At1g53910	At5g14540	reg0.9	At2g40140
At5g48655	reg0.9	At2g40140	At2g20570	reg0.8	At2g40890
At2g46830	reg0.8	At2g40890	At1g74840	reg0.7	At3g55070
At4g37260	reg0.7	At1g68520	At1g74840	reg0.9	At1g14780
At1g43160	reg0.8	At1g14780	At5g61890	reg0.9	At1g14780
At2g22430	reg0.9	At2g39210	At2g20570	reg0.9	At1g76600
At2g46830	reg0.9	At1g76600	At2g04880	reg0.9	At1g76600
At2g25000	reg0.8	At1g76600	At2g38470	reg0.8	At1g76600
At5g48655	reg0.8	At5g19240	At2g22430	reg0.7	At3g02910
At2g22430	reg0.9	At3g63010	At3g61890	reg0.9	At3g49120

At1g74840	reg0.7	At3g49120	At4g37260	reg0.8	At3g49120
At5g14540	reg0.7	At3g52450	At2g23320	reg0.7	At3g52450
At4g31800	reg0.9	At3g52450	At1g25560	reg0.7	At5g58710
At1g68840	reg0.7	At5g58710	At5g49450	reg0.7	At5g58710
At3g01560	reg0.8	At4g25650	At1g53910	reg0.7	At4g04020
At4g17490	reg0.7	At4g04020	At5g49450	reg0.9	At3g47340
At5g49450	reg0.8	At1g77120	At5g48655	reg0.7	At2g26190
At4g37260	reg0.7	At5g49450	At1g22070	reg0.9	At1g20440
At1g22070	reg0.7	At5g59820	At5g48655	reg0.8	At1g26250
At1g74840	reg0.8	At5g07010	At4g37260	reg0.7	At5g07010
At1g74840	reg0.7	At3g54690	At2g20570	reg0.7	At3g54690
At2g46830	reg0.8	At3g54690	At2g20570	reg0.8	At5g26920
At2g46830	reg0.7	At5g26920	At3g61890	reg0.8	At2g02990
At1g74840	reg0.8	At5g61890	At5g49450	reg0.7	At2g34500
At1g74840	reg0.8	At4g01700	At2g46830	reg0.7	At4g01700
At2g20570	reg0.9	At5g59730	At2g46830	reg0.9	At5g59730
At3g01560	reg0.8	At3g52470	At5g14540	reg0.8	At3g52470
At5g48655	reg0.7	At3g52470	At2g46830	reg0.8	At3g02800
At5g49450	reg0.8	At4g24800	At4g37260	reg0.7	At4g24800
At2g20570	reg0.8	At5g25630	At2g46830	reg0.7	At5g25630
At5g24800	reg0.7	At5g28900	At2g20570	reg0.7	At4g27280
At2g46830	reg0.8	At4g27280	At5g49450	reg0.9	At3g13450
At5g24800	reg0.9	At1g20510	At2g20570	reg0.7	At1g20510
At2g46830	reg0.8	At1g20510	At5g44190	reg0.7	At1g20510
At2g46830	reg0.7	At1g14730	At5g61890	reg0.7	At1g43160
At3g01560	reg0.8	At5g06700	At5g14540	reg0.8	At5g06700
At1g22070	reg0.7	At5g06700	1g74840	reg0.8	At5g06700
At2g20570	reg0.7	At5g06700	5g24800	reg0.7	At4g34450
At1g43160	reg1.0	At2g28900	At1g74840	reg0.7	At2g28900
At4g37260	reg0.7	At2g28900	2g20570	reg0.7	At5g42310
At3g01560	reg0.8	At5g42310	At5g14540	reg0.8	At5g42310
At3g01560	reg0.7	At2g43620	At3g61890	reg0.8	At2g43620
At1g74840	reg0.7	At3g23810	At2g20570	reg0.8	At3g17820
At2g46830	reg0.7	At3g17820	At3g01560	reg0.8	At3g23820
At5g14540	reg0.7	At3g23820	At1g74840	reg0.8	At3g23820
At1g43160	reg0.7	At3g23820	At5g47230	reg0.8	At3g23820
At5g61890	reg0.8	At3g23820	At5g49450	reg0.9	At3g57520
At3g61890	reg0.9	At4g22212	At2g30250	reg0.7	At2g46225
At4g01250	reg0.7	At2g46225	At4g23810	reg0.8	At2g46225
At5g49450	reg0.7	At4g37260	At5g24800	reg0.7	At2g24940
At1g25560	reg0.9	At3g19390	At1g68840	reg0.9	At3g19390
At3g01560	reg0.8	At1g21790	At1g74840	reg0.8	At1g21790
At4g37260	reg0.8	At1g21790	At4g37260	reg0.7	At1g12780
At2g20570	reg0.7	At5g54490	At2g46830	reg0.9	At5g54490
At1g22070	reg0.9	At3g11670	At5g24800	reg0.7	At3g11670

At5g49450	reg-0.7	At2g30040	At1g25560	reg-0.7	At2g30040
At1g68840	reg-0.7	At2g30040	At2g20570	reg-0.9	At1g80180
At2g46830	reg-0.8	At1g80180	At1g22070	reg-0.7	At1g06760
At5g24800	reg-0.8	At5g61790	At5g48655	reg-0.7	At1g11545
At2g20570	reg-0.8	At1g07040	At2g46830	reg-0.8	At1g07040
At4g17500	reg-0.7	At2g15970	At2g22430	reg-0.9	At1g49500
At5g44190	reg-0.7	At3g04070	At4g37260	reg-0.8	At4g22710
At5g49450	reg-0.8	At5g63790	At5g14540	reg-0.7	At3g60320
At5g48655	reg-0.9	At3g60320	At2g22430	reg-0.7	At3g60320
At3g01560	reg-0.7	At4g37450	At4g37260	reg-0.7	At1g77450
At1g22070	reg-0.7	At1g42480	At2g46830	reg-0.7	At5g64570
At2g20570	reg-0.8	At5g39610	At2g22430	reg-0.8	At5g39610
At3g61890	reg-0.7	At2g34640	At5g24800	reg-0.8	At4g16660
At2g20570	reg-0.7	At5g60680	At2g46830	reg-0.7	At5g60680
At4g17500	reg-0.7	At2g47180	At1g22070	reg-0.9	At1g09210
At2g04880	reg-0.7	At1g68840	At2g38470	reg-0.8	At1g68840
At2g22430	reg-0.7	At1g49860	At5g44190	reg-0.8	At1g09240
At1g74840	reg-0.7	At1g76690	At4g37260	reg-0.9	At1g76690
At1g43160	reg-0.9	At4g31130	At5g61890	reg-0.7	At4g31130
At1g74840	reg-0.7	At4g31130	At4g37260	reg-0.8	At4g31130
At5g49450	reg-0.9	At2g38470	At5g44190	reg-0.7	At4g39980
At5g14540	reg-0.9	At4g12600	At4g37260	reg-0.8	At3g25230
At1g74840	reg-0.8	At1g32170	At2g20570	reg-0.7	At1g32170
At2g46830	reg-0.7	At1g32170	At1g43160	reg-0.7	At2g29490
At5g47230	reg-0.7	At2g29490	At5g61890	reg-0.8	At2g29490
At5g14540	reg-0.8	At5g05440	At5g48655	reg-0.8	At5g05440
At2g33710	reg-0.8	At4g39675	At2g20570	reg-0.7	At2g04280
At2g46830	reg-0.7	At2g04280	At1g74840	reg-0.7	At5g49480
At2g22430	reg-0.7	At5g49480	At3g61150	reg-0.7	At5g49480
At5g48655	reg-0.7	At1g76590	At4g37260	reg-0.7	At1g32920
At2g33710	reg-0.9	At4g38470	At4g17490	reg-0.8	At4g38470
At2g20570	reg-0.7	At4g38470	At2g46830	reg-0.8	At4g38470
At5g44190	reg-0.7	At5g15410	At2g20570	reg-0.7	At1g67910
At2g46830	reg-0.8	At1g67910	At3g01560	reg-0.7	At5g25460
At5g14540	reg-0.9	At5g25460	At5g48655	reg-0.8	At5g25460
At3g61150	reg-0.7	At3g48990	At1g22070	reg-0.8	At3g48990
At5g24800	reg-0.8	At3g48990	At5g49450	reg-0.7	At3g62960
At1g25560	reg-0.8	At3g56710	At1g68840	reg-0.7	At3g56710
At5g44190	reg-0.7	At3g51550	At1g74840	reg-0.8	At3g62120
At4g17500	reg-0.7	At2g42540	At5g49450	reg-0.8	At4g11280
At1g22070	reg-0.8	At3g15950	At3g01560	reg-0.9	At3g19130
At1g74840	reg-0.7	At4g21620	At4g37260	reg-0.8	At4g21620
At5g14540	reg-0.7	At3g21870	At5g48655	reg-0.7	At3g21870
At2g20570	reg-0.8	At3g15450	At2g46830	reg-0.8	At3g15450
At4g17500	reg-0.7	At5g01600	At4g17500	reg-0.7	At3g05890

At2g46830	reg-0.8	At1g22570	At5g48655	reg-0.9	At3g14310
At3g61150	reg-0.8	At5g65390	At2g20570	reg-0.8	At1g76160
At2g46830	reg-0.7	At1g76160	At4g17500	reg-0.7	At1g29395
At5g49450	reg-0.7	At5g66510	At1g74840	reg-0.7	At1g62480
At5g44190	reg-0.8	At3g07390	At2g20570	reg-0.8	At2g33830
At2g46830	reg-0.8	At2g33830	At3g61890	reg-0.7	At3g06680
At4g37260	reg-0.8	At5g23020	At5g24800	reg-0.7	At1g10070
At5g48655	reg-0.8	At4g36670	At2g38470	reg-0.9	At4g36670
At1g22070	reg-0.7	At2g44310	At5g24800	reg-0.7	At2g44310
At2g22430	reg-0.7	At2g44310	At3g61150	reg-0.7	At2g44310
At3g01560	reg-0.7	At4g12880	At5g14540	reg-0.8	At4g12880
At5g48655	reg-0.9	At4g12880	At1g74840	reg-0.8	At4g13770
At4g37260	reg-0.7	At4g13770	At3g61150	reg-0.7	At3g54400
At5g44190	reg-0.7	At5g06530	At5g48655	reg-0.9	At5g11420
At2g33710	reg-0.9	At5g11420	At4g17490	reg-0.8	At5g11420
At1g74840	reg-0.7	At1g19870	At4g37260	reg-0.7	At1g19870
At1g22070	reg-0.8	At1g19870	At4g17500	reg-0.7	At1g35780
At4g17500	reg-0.7	At5g11110	At5g49450	reg-0.9	At1g10960
At5g44190	reg-0.7	At5g06530	At5g44190	reg-0.7	At3g55970
At4g37260	reg-0.8	At3g11700	At3g01560	reg-0.7	At5g49910
At3g61890	reg-0.8	At4g23180	At1g74840	reg-0.9	At4g23180
At4g37260	reg-0.7	At4g23180	At1g74840	reg-0.8	At4g10480
At2g46830	reg-0.7	At4g10480	At2g22430	reg-0.7	At5g43970
At3g61150	reg-0.7	At5g43970	At3g61890	reg-0.7	At5g11670
At1g22070	reg-0.7	At1g56330	At5g48655	reg-0.7	At1g68520
At5g44190	reg-0.7	At1g68520	At3g61150	reg-0.7	At1g31420
At5g44190	reg-1.0	At2g23810	At2g20570	reg-0.9	At3g15630
At2g46830	reg-0.8	At3g15630	At2g20570	reg-0.9	At2g39570
At2g46830	reg-0.8	At2g39570	At5g49450	reg-0.8	At1g76600
At1g74840	reg-0.9	At2g06850	At5g14540	reg-0.7	At2g37640
At5g48655	reg-0.7	At2g37640	At2g20570	reg-0.8	At2g37640
At2g46830	reg-0.9	At2g37640	At1g74840	reg-0.7	At1g02930
At4g37260	reg-0.8	At1g02930	At2g33710	reg-0.8	At5g58710
At3g61890	reg-0.7	At1g64640	At1g74840	reg-0.8	At1g64640
At2g20570	reg-0.8	At3g49780	At2g46830	reg-0.9	At3g49780
At5g24800	reg-0.8	At3g49780	At5g24800	reg-0.7	At3g47340
At5g44190	reg-0.8	At1g09330	At5g48655	reg-0.7	At5g49450
At2g20570	reg-0.8	At5g49450	At2g46830	reg-0.7	At5g49450
At5g44190	reg-0.8	At5g07010	At5g49450	reg-0.7	At2g29550
At1g22070	reg-0.7	At2g34500	At1g74840	reg-0.8	At3g61440
At5g14540	reg-0.8	At2g24500	At5g24800	reg-0.7	At5g11520
At4g37260	reg-0.7	At1g62380	At5g48655	reg-0.7	At1g80070
At2g22430	reg-0.8	At3g13450	At5g14540	reg-0.8	At1g24530
At1g22070	reg-0.7	At1g24530	At5g49450	reg-0.7	At1g20510
At5g14540	reg-0.7	At1g73120	At4g17500	reg-0.7	At1g43160

At1g74840	reg-0.9	At1g53240	At2g20570	reg-0.8	At5g18170
At2g46830	reg-0.8	At5g18170	At3g61890	reg-0.8	At2g30010
At1g74840	reg-0.7	At2g30010	At4g37260	reg-0.9	At2g30010
At5g49450	reg-0.7	At2g30010	At5g24800	reg-0.9	At5g49700
At4g17500	reg-0.8	At2g28900	At5g24800	reg-0.8	At1g15690
At5g44190	reg-0.8	At4g12480	At2g04880	reg-0.9	At5g22920
At2g25000	reg-0.7	At5g22920	At2g38470	reg-1.0	At5g22920
At5g44190	reg-0.8	At3g23810	At5g48655	reg-0.8	At3g57520
At2g20570	reg-0.7	At3g57520	At2g46830	reg-0.8	At3g57520
At5g24800	reg-0.7	At3g57520	At1g53910	reg-0.8	At5g04340
At5g24800	reg-0.8	At2g05380	At2g33710	reg-0.7	At3g19390
At4g17490	reg-0.8	At3g19390	At4g37260	reg-0.8	At3g12740
At2g20570	reg-0.7	At1g12780	At3g61890	reg-0.8	At3g16530

[00266] The largest pattern was NC-NC-NC, representing 5,070 genes not affected by the treatments. The remainder 20 patterns (834 genes) were grouped into six classes that summarize the types of N-responses observed: (A) inorganic N, (B) inorganic N with Glu feedback, (C) organic N with no exogenous Glu rescue, (D) exogenous Glu, (E) exogenous and endogenous Glu and (F) exogenous and endogenous Glu with opposite effects (Table 3).

Table 3

Response	Treatment			Genes	Genes per class
	Nms	Nms+MSX	Nms+MSX+Glu		
A) Inorganic nitrogen	D	D	D	100	159
	I	I	I	59	
B) Inorganic nitrogen and Glu	D	D	NC	30	48
	I	I	NC	15	
	D	D	I	3	
C) Internal Glu	D	NC	NC	194	334
	I	NC	NC	56	
	NC	I	I	49	
	NC	D	D	33	
	D	I	I	2	
D) External Glu	NC	NC	D	89	126
	NC	NC	I	37	
E) Internal/ External Glu	NC	I	NC	55	164
	NC	D	NC	36	
	D	NC	D	47	
	I	NC	I	22	
	I	D	I	3	
	NC	D	I	1	
F) Opposite Internal/External Glu	D	NC	I	2	3
	I	NC	D	1	
					834

Nitrogen responses. Patterns of expression based on their response to the Nms, Nms+MSX and Nms+MSX+Glu treatments. D=decreased; I=increased; NC=not changed. Genes were categorized into six classes based on these patterns.

[00267] The genes regulated in the experiments were compared to published results (Wang *et al.*, 2004, Plant Physiol 136:2512-2522). This previous study identified 595 genes that responded similarly to nitrate treatment in both a NR-null mutant and wild-type plants. Because the mutant plants cannot assimilate nitrate, the responses observed were attributed to the action of nitrate as a signal and not a downstream metabolite. 80 out of these 595 genes showed consistent and reliable responses in the current experiments. Surprisingly, only 17 of these genes were found regulated by inorganic N signals in both studies (Table 4). Among these, we found nitrite reductase and several high affinity nitrate transporters. The majority, 58 of these 80 genes (73%), belonged to the C, D or E classes in the present studies suggesting that many previously described nitrate-responsive genes may respond to organic N signals (Table 4).

Table 4

Regulated by	PUB LOCUS	Gene Name
Inorganic N	At4g19170	9-cis-epoxycarotenoid dioxygenase, putative / neoxanthin cleavage enzyme, putative / carotenoid cleavage dioxygenase, putative similar to 9-cis-epoxycarotenoid dioxygenase [Phaseolus vulgaris][GI:6715257]; neoxanthin cleavage enzyme, Lycopersicon esculentum, PATX:E325797 (68417.m02829)
Inorganic N	At3g61820	aspartyl protease family protein contains Pfam domain, PF00026: eukaryotic aspartyl protease (68416.m06939)
Inorganic N	At4g30190	ATPase 2, plasma membrane-type, putative / proton pump 2, putative / proton-exporting ATPase, putative strong similarity to SP
Inorganic N	At4g31500	cytochrome P450 83B1 (CYP83B1) Identical to Cytochrome P450 (SP:O65782)[Arabidopsis thaliana] (68417.m04474)
Inorganic N	At1g05340	expressed protein (68414.m00541)
Inorganic N	At1g19020	expressed protein (68414.m02367)
Inorganic N	At1g32920	expressed protein (68414.m04055)
Inorganic N	At2g41730	expressed protein (68415.m05158)
		expressed protein similar to PGPS/D12 [Petunia x hybrida] GI:4105794; contains Pfam profile PF04749: Protein of unknown function, DUF614 (68414.m01778)
Inorganic N	At1g14870	F-box family protein contains Pfam PF00646: F-box domain and Pfam PF00560: Leucine Rich Repeat (6 copies); similar to F-box protein
Inorganic N	At5g25350	FBL6 (GI:4432860) [Homo sapiens] (68418.m03007)
		ferredoxin--nitrite reductase, putative strong similarity to ferredoxin--nitrite reductase [Nicotiana tabacum] GI:19893; contains Pfam profiles
Inorganic N	At2g15620	PF03460: Nitrite/Sulfite reductase ferredoxin-like half domain, PF01077: Nitrite and sulphite reductase 4Fe-4S domain (68415.m01789) GDSDL-motif
		lipase/hydrolase family protein similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from
Inorganic N	At5g55050	[Arabidopsis thaliana]; contains Pfam profile PF00657: GDSDL-like
		Lipase/Acylhydrolase (68418.m06861)
Inorganic N	At5g18600	glutaredoxin family protein contains glutaredoxin domain, INTERPRO:IPR002109 (68418.m02201)
Inorganic N	At1g49860	glutathione S-transferase, putative similar to GI:860955 from [Hyoscyamus muticus] (Plant Physiol. 109 (1), 253-260 (1995)) (68414.m05590)
		high-affinity nitrate transporter (ACH1) identical to trans-membrane nitrate transporter protein AtNRT2:1 [Arabidopsis thaliana] GI:3747058,
Inorganic N	At1g08090	high-affinity nitrate transporter ACH1 [Arabidopsis thaliana] GI:3608362 (68414.m00885)
		high-affinity nitrate transporter, putative similar to trans-membrane nitrate transporter protein AtNRT2:1 [Arabidopsis thaliana] GI:3747058,

Inorganic N	At1g12940	high-affinity nitrate transporter ACH1 [Arabidopsis thaliana] GI:3608362 (68414.m01503) nitrate/chlorate transporter (NRT1.1) (CHL1) identical to nitrate/chlorate transporter SP:Q05085 from [Arabidopsis thaliana]; contains Pfam profile: PF00854 POT family (68414.m01402)
Inorganic N	At1g12110	serine O-acetyltransferase, putative identical to GI:608677 from [Arabidopsis thaliana] (68414.m06414)
Organic and Inorganic N	At1g55920	nodulin family protein similar to nodulin-like protein [Arabidopsis thaliana] GI:3329368, nodule-specific protein Nlj70 [Lotus japonicus] GI:3329366 (68415.m01912)
Organic and Inorganic N	At2g16660	
Organic and Inorganic N	At3g45140	lipoxygenase (LOX2) identical to SP
Organic and Inorganic N	At5g64410	oligopeptide transporter OPT family protein similar to SP
Organic and Inorganic N	At5g65010	asparagine synthetase 2 (ASN2) identical to asparagine synthetase (ASN2) [Arabidopsis thaliana] GI:3859536 (68418.m08178)
Organic N	At1g14780	expressed protein (68414.m01767) senescence-associated protein-related similar to senescence-associated protein SAG102 (GI:22331931) [Arabidopsis thaliana] (68414.m02770)
Organic N	At1g22160	ABC transporter family protein contains Pfam profile: PF00005: ABC transporter (68414.m03899)
Organic N	At1g31770	
Organic N	At1g32450	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family (68414.m04005)
Organic N	At1g47128	cysteine proteinase (RD21A) / thiol protease identical to SP
Organic N	At1g49500	expressed protein (68414.m05548)
Organic N	At1g56150	auxin-responsive family protein similar to SP:P33082 Auxin-induced protein X15. [Soybean] {Glycine max} (68414.m06450)
Organic N	At1g67910	expressed protein (68414.m07755)
Organic N	At1g74090	sulfotransferase family protein similar to SP isochorismate synthase 1 (ICS1) / isochorismate mutase identical to GI:17223087 and GB:AF078080; contains Pfam profile PF00425: chorismate binding enzyme; contains TIGRfam profile TIGR00543: isochorismate synthases; identical to cDNA isochorismate synthase 1
Organic N	At1g74710	precursor (ICS1) nuclear gene for plastid product GI:17223086 (68414.m08655)
Organic N	At1g77760	nitrate reductase 1 (NR1) identical to SP sulfate transporter (Sultr1;2) identical to sulfate transporter Sultr1;2 [Arabidopsis thaliana] GI:7768660; contains Pfam profiles PF00916: Sulfate transporter family and PF01740: STAS domain; contains TIGRfam profile TIGR00815: sulfate permease (68414.m09090)
Organic N	At1g78000	
Organic N	At2g15970	cold-acclimation protein, putative (FL3-5A3) similar to cold acclimation WCOR413-like protein gamma form [Hordeum vulgare] gi
Organic N	At2g27830	expressed protein (68415.m03374) AP2 domain-containing transcription factor RAP2.7 (RAP2.7) nearly identical to AP2 domain transcription factor RAP2.7 (GI:2281639) [Arabidopsis thaliana] (68415.m03469)
Organic N	At2g28550	
Organic N	At2g30040	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (68415.m03653) UDP-glucuronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase (68415.m03881)
Organic N	At2g31790	
Organic N	At2g33710	AP2 domain-containing transcription factor family protein similar to RAP2.6 (GI:17065542) {Arabidopsis thaliana} (68415.m04132)
Organic N	At2g33830	dormancy/auxin associated family protein contains Pfam profile: PF05564 dormancy/auxin associated protein (68415.m04151) U-box domain-containing protein similar to immediate-early fungal elicitor protein CMPG1 [Petroselinum crispum] GI:14582200; contains Pfam profile PF04564: U-box domain (68415.m04410)
Organic N	At2g35930	
Organic N	At2g39200	seven transmembrane MLO family protein / MLO-like protein 12 (MLO12) identical to SP
Organic N	At2g39570	ACT domain-containing protein contains Pfam ACT domain PF01842 (68415.m04854) zinc finger (CCCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar) and Pfam domain, PF00023: Ankyrin repeat (68415.m04937)
Organic N	At2g40140	

Organic N	At2g43100	aconitase C-terminal domain-containing protein contains Pfam profile PF00694: Aconitase C-terminal domain (68415.m05350)
Organic N	At3g02910	expressed protein contains Pfam domain PF03674: Uncharacterised protein family (UPF0131) (68416.m00286) zinc finger (C3HC4-type RING finger) family protein (ATL6) contains Pfam profile: PF00097: Zinc finger, C3HC4 type (RING finger) (68416.m00567)
Organic N	At3g05200	non-symbiotic hemoglobin 2 (HB2) (GLB2) identical to SP
Organic N	At3g10520	dihydrolipoamide S-acetyltransferase, putative similar to dihydrolipoamide S-acetyltransferase [Zea mays] GI:5669871; contains Pfam profiles PF00198: 2-oxo acid dehydrogenases acyltransferase (catalytic domain), PF00364: Biotin-requiring enzyme, PF02817: e3 binding domain (68416.m01759)
Organic N	At3g13930	phosphoenolpyruvate carboxylase, putative / PEP carboxylase, putative strong similarity to SP
Organic N	At3g14940	expressed protein (68416.m01982) malate dehydrogenase [NAD], chloroplast (MDH) identical to chloroplast NAD-malate dehydrogenase [Arabidopsis thaliana] GI:3256066; contains InterPro entry IPR001236: Lactate/malate dehydrogenase; contains Pfam profiles PF00056: lactate/malate dehydrogenase, NAD binding domain and PF02866: lactate/malate dehydrogenase, alpha/beta C-terminal domain (68416.m05168)
Organic N	At3g47520	nodulin MtN3 family protein similar to MtN3 GI:1619602 (root nodule development) from [Medicago truncatula] (68416.m05322) AMP-dependent synthetase and ligase family protein similar to peroxisomal-coenzyme A synthetase (FAT2) [gi:586339] from Saccharomyces cerevisiae; contains Pfam AMP-binding enzyme domain PF00501; identical to cDNA; identical to cDNA adenosine monophosphate binding
Organic N	At3g48990	protein 3 AMPBP3 (AMPBP3)GI:20799714 (68416.m05351)
Organic N	At3g49940	LOB domain protein 38 / lateral organ boundaries domain protein 38 (LBD38) identical to SP
Organic N	At3g58990	aconitase C-terminal domain-containing protein contains Pfam profile PF00694: Aconitase C-terminal domain (68416.m06575) transketolase, putative strong similarity to transketolase 1 [Capsicum annuum] GI:3559814; contains Pfam profiles PF02779: Transketolase, pyridine binding domain, PF02780: Transketolase, C-terminal domain, PF00456: Transketolase, thiamine diphosphate binding domain (68416.m06796)
Organic N	At3g60750	BON1-associated protein 1 (BAP1) identical to BON1-associated protein 1 [Arabidopsis thaliana] GI:15487384; contains Pfam profile PF00168: C2 domain; supporting cDNA gi
Organic N	At3g61190	homeobox-leucine zipper protein 12 (HB-12) / HD-ZIP transcription factor 12 identical to homeobox-leucine zipper protein ATHB-12 (GI:6899887) [Arabidopsis thaliana] (68416.m06951)
Organic N	At3g61890	copper amine oxidase family protein contains Pfam domain, PF01179: Copper amine oxidase, enzyme domain (68417.m01946)
Organic N	At4g12280	ammonium transporter 1, member 1 (AMT1.1) identical to SP
Organic N	At4g13510	cytochrome P450 family protein (68417.m02136)
Organic N	At4g13770	glucose-6-phosphate isomerase, putative similar to glucose-6-phosphate isomerase [Spinacia oleracea] GI:3413511; contains Pfam profile PF00342: glucose-6-phosphate isomerase (68417.m03526)
Organic N	At4g24620	cinnamoyl-CoA reductase-related similar to cinnamoyl-CoA reductase from Pinus taeda [GI:17978649], Saccharum officinarum [GI:3341511] (68417.m04326)
Organic N	At4g30470	mannitol transporter, putative similar to mannitol transporter [Apium graveolens var. dulce] GI:12004316; contains Pfam profile PF00083: major facilitator superfamily protein (68417.m05203)
Organic N	At4g36670	LOB domain protein 39 / lateral organ boundaries domain protein 39 (LBD39) identical to SP
Organic N	At4g37540	TAZ zinc finger family protein / BTB/POZ domain-containing protein contains Pfam PF00651 : BTB/POZ domain; contains Pfam PF02135 : TAZ zinc finger; similar to Speckle-type POZ protein (SP:O43791) [Homo sapiens] (68417.m05321)
Organic N	At4g37610	protein kinase family protein similar to protein kinase [gi:170047] from Glycine max; contains Pfam protein kinase domain PF00069 (68417.m05436)
Organic N	At4g38470	

Organic N	At4g39800	inositol-3-phosphate synthase isozyme 1 / myo-inositol-1-phosphate synthase 1 / MI-1-P synthase 1 / IPS 1 identical to SP nicotianamine synthase, putative similar to nicotianamine synthase [Lycopersicon esculentum][GI:4753801], nicotianamine synthase 2
Organic N	At5g04950	[Hordeum vulgare][GI:4894912] (68418.m00524) urophorphyrin III methylase (UPM1) identical to urophorphyrin III methylase (GI:1146165) [Arabidopsis thaliana]; similar to s-adenosyl-L- methionine- dependent uroporphyrinogen III methyltransferase (GI:1490606) [Arabidopsis thaliana]; similar to Diphtine synthase (Diphtamide biosynthesis methyltransferase) (DPH5) (SP:P32469) [Saccharomyces cerevisiae]; contains Pfam PF00590 : Tetrapyrrole (Corrin/Porphyrin)
Organic N	At5g40850	Methylases domain; contains TIGRFAM PF00590: Tetrapyrrole (Corrin/Porphyrin) Methylases (68418.m04960) 6-phosphogluconate dehydrogenase family protein contains Pfam profiles: PF00393 6-phosphogluconate dehydrogenase C-terminal domain, PF03446 NAD binding domain of 6-phosphogluconate (68418.m05063)
Organic N	At5g41670	cytochrome P450 family protein similar to SP
Organic N	At5g45340	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family (68418.m05663)
Organic N	At5g46050	thioesterase family protein similar to SP
Organic N	At5g48370	sodium-inducible calcium-binding protein (ACP1) / sodium-responsive calcium- binding protein (ACP1) identical to NaCl-inducible Ca ²⁺ -binding protein GI:2352828 from [Arabidopsis thaliana] (68418.m06123)
Organic N	At5g49480	pfkB-type carbohydrate kinase family protein contains Pfam profile: PF00294
Organic N	At5g51830	pfkB family carbohydrate kinase (68418.m06426)
Organic N	At5g54170	expressed protein weak similarity to SP protein kinase family protein / non phototropic hypocotyl 1-like protein (NPL1) contains Pfam domains, PF00069: Protein kinase domain and PF00785: PAC motif; similar to SP:O48963 Nonphototropic hypocotyl protein 1 (Phototropin) [Mouse-ear cress] {Arabidopsis thaliana};
Organic N	At5g58140	identical to cDNA non phototropic hypocotyl 1-like (NPL1) GI:5391441 (68418.m07277)

This table contains a list of genes that were previously identified as regulated by inorganic N (Wang *et al.*, 2004 Plant Physiol 136:2512-2522) and that were found regulated in the current study. The first column summarizes the regulatory pattern observed in this study.

[00268] Nitrogen signals control amino acid metabolism in *Arabidopsis* seedlings. To evaluate the biological significance of the observed patterns of response to the treatments, the distribution of functional categories in the six classes defined in Table 3 were analyzed using the BioMaps program (Gutierrez *et al.*, 2007, Genome Biol. 8:R7). To focus on the most prominent biological processes affected, over-represented functional terms ($p \leq 0.01$) with 5 or more genes (Table 5) were analyzed. This analysis indicated that inorganic N represses amino acid biosynthesis, and in particular a subset of genes related to the metabolism of S-containing amino acids. In addition, increased levels of internal Glu appears to induce the expression of genes involved in cell wall biosynthesis, especially genes in the xyloglucan:xyloglucosyl transferase family. Internal Glu also appears to repress genes involved in several aspects of metabolism, most prominently amino acid and carbohydrate metabolism. This analysis also showed that genes involved in secondary metabolism are repressed by both internal and external organic N sources. These results indicate that the balance between organic and inorganic N controls the expression of genes involved in N-

reduction, N-assimilation and amino acid metabolism in Arabidopsis plants and coordinates N-assimilation with cellular processes including for example, cell wall biosynthesis.

Table 5

Response	MIIPS Functional Term	p-value	Genes
Inorganic nitrogen repression (100)	amino acid biosynthesis (12)	0.00322	At3g54640, At4g13890, At3g01120, At5g37600, At3g23810, At2g36880, At4g39980, At4g15560, At5g23020, At3g17390, At5g16570, At3g03780
Internal Glu induction (89)	cell wall (7)	0.00933	At5g64570, At1g03870, At1g32170, At2g01850, At1g11545, At3g23730, At3g14310
Internal Glu repression (246)	METABOLISM (98)	6.95E-05	At3g61190, At5g65620, At5g64440, At5g37990, At3g02360, At1g08920, At5g49720, At1g75680, At2g44160, At2g30490, At5g35170, At1g77760, At4g00370, At1g51680, At1g15130, At3g19420, At4g33580, At1g17840, At3g60750, At2g30870, At3g54690, At1g15950, At2g47180, At5g01820, At5g20070, At4g24620, At2g46830, At5g05730, At4g21850, At1g06640, At5g20980, At5g48370, At4g36640, At4g34050, At2g38010, At4g19810, At3g48690, At2g27860, At5g03555, At1g22610, At2g36690, At3g63010, At3g21240, At4g29900, At2g39210, At1g37130, At4g33680, At1g79380, At4g39800, At4g36250, At5g63850, At1g02400, At1g53500, At1g66900, At5g01800, At4g14440, At1g11840, At3g44720, At2g20360, At2g22240, At5g54960, At4g12280, At5g55910, At1g03590, At2g38700, At5g54160, At1g65960, At2g16430, At5g11110, At2g30040, At4g11570, At3g21230, At5g58140, At4g39640, At5g37510, At4g00360, At3g01560, At4g30440, At2g40890, At2g47880, At3g48560, At5g49630, At1g76670, At5g43370, At4g30470, At4g25300, At2g29450, At2g40140, At4g39330, At1g07890, At4g30280, At1g12000, At2g36290, At5g53370, At1g74710, At3g45640, At3g23820, At3g17820
	amino acid metabolism (28)	0.00017	At3g61190, At5g64440, At5g63850, At4g39640, At5g05730, At4g21850, At1g06640, At5g20980, At1g02400, At2g44160, At3g48560, At5g49630, At2g30490, At1g11840, At1g77760, At3g44720, At1g22610, At4g25300, At5g54960, At3g60750, At2g36690, At1g07890, At3g54690, At1g37130, At1g65960, At1g74710, At4g33680, At3g17820
	complex cofactor binding (13)	0.00235	At4g36250, At3g60750, At5g37510, At4g36640, At1g15950, At2g44160, At3g48560, At1g53500, At2g30490, At2g27860, At4g33680, At5g54960, At4g12280
	C-compound and carbohydrate utilization (36)	0.00673	At4g36250, At3g02360, At5g49720, At1g75680, At2g44160, At1g53500, At1g11840, At2g20360, At2g22240, At5g54960, At4g33580, At3g60750, At3g54690, At1g15950, At5g11110, At2g47180, At4g11570, At4g24620, At3g21230, At5g37510, At5g20980, At4g30440, At3g48560, At3g48690, At2g27860, At1g76670, At4g30470, At4g39330, At4g30280, At3g21240, At3g63010, At2g36290, At1g12000, At5g53370, At3g23820, At4g39800
Internal/External Glu repression (102)	secondary metabolism (19)	0.0036	At3g16150, At1g13110, At4g15390, At3g58990, At1g06000, At4g39950, At4g22710, At4g30210, At1g20510, At2g05710, At5g48010, At5g26030, At1g02500, At5g40850, At1g10360, At1g05010, At2g34460, At5g47990, At5g45340

[00269] Network analysis reveals a metabolic gene network connected to regulatory transcription factors regulated by organic N. To uncover the mechanism underlying gene regulation in response to sensing Glu or a Glu-derived product, network analysis was used to identify the subnetwork of genes regulated by organic N (Figure 3). The subnetwork of N-regulated genes using an Arabidopsis multinet network was generated as described previously (Gutierrez *et al.*, 2007, Genome Biol 8:R7). Cytoscape was used to visualize the resulting subnetworks wherein genes were represented as nodes connected by edges that represented distinct interactions (*e.g.*, metabolic reactions, regulatory interactions). In addition to the

interactions described previously (Gutierrez *et al.*, 2007, Genome Biol 8:R7), regulatory connections were predicted between genes and associated transcription factors (see, Materials and Methods). In order to identify putative “master regulators” that control the expression of genes regulated by organic N, the transcription factors regulated in these experiments were ranked based on the number of regulatory connections in the subnetwork (Table 6). At the top of the list, were a Myb family transcription factor (At1g74840), the central clock gene *CCA1* (At2g46830) and a golden 2-related transcription factor (*GLK1*; At2g20570). Interestingly, both *CCA1* and *GLK1* were predicted to positively affect the expression of a gene for glutamine synthetase (*GLN1.3*) (which uses Glu in a biosynthetic reaction), and to negatively affect the expression of a glutamate dehydrogenase gene (*GDH1*) (which catabolizes Glu) (Figure 3). Moreover, the analysis suggests that both *CCA1* and *GLK1* block the expression of a bZIP transcription factor (*bZIP1*) which is predicted to induce the expression of the Gln-dependent *ASN1* gene. Thus, Glu regulation of the *GLK1* and *CCA1* transcription factors appears to coordinate the expression of genes involved in making Gln (*GLN1.3*) vs. those involved in metabolizing Gln into Glu (*ASN1*, *GDH1*). In addition, another gene in this gene subnetwork encodes a putative asparaginase gene (*ANS*) that controls the degradation of Asn (to Asp and Glu) (Figure 3). The *ASN1* (Asn biosynthesis) and *ANS* (Asn degradation) genes had inverse expression patterns (correlation = -0.51), suggesting that Glu coordinates the reciprocal regulation of Asn synthesis and degradation by coordinating an antiregulation of the cognate.

TABLE 6

Number of connections	PUB LOCUS	Annotation
51	At1g74840	myb family transcription factor.
47	At2g46830	myb-related transcription factor (<i>CCA1</i>)
46	At2g20570	golden2-like transcription factor (<i>GLK1</i>)
31	At4g37260	myb family transcription factor (MYB73)
30	At5g24800	<i>bZIP1</i> transcription factor family protein contains
30	At5g49450	<i>bZIP1</i> family transcription factor
29	At5g14540	proline-rich family protein contains proline rich extensin domains.
29	At5g48655	zinc finger (C3HC4-type RING finger) family protein
24	At1g22070	<i>bZIP1</i> family transcription factor (TGA3)
23	At3g01560	proline-rich family protein contains proline rich extensin

		domains.
20	At2g22430	homeobox-leucine zipper protein 6 (HB-6)
19	At5g44190	myb family transcription factor (GLK2)
16	At1g43160	AP2 domain-containing protein RAP2.6 (RAP2.6)
15	At3g61890	homeobox-leucine zipper protein 12 (HB-12)
14	At5g61890	AP2 domain-containing transcription factor family protein similar to RAP2.6
12	At3g61150	homeobox-leucine zipper family protein
11	At2g38470	WRKY family transcription factor
11	At4g17500	ethylene-responsive element-binding protein 1 (ERF1)
10	At2g25000	WRKY family transcription factor

[00270] Validation of network model predictions highlights the regulatory role of *CCAI* in the N-assimilatory pathway. The model in Figure 3 predicts that *CCAI* and/or *GLK1* genes are important regulators of genes involved in N-assimilation and over-expression of either one of these genes would repress the expression of *ASN1* and *GDH1* and induce the expression of the *GLN1.3* gene. Conversely, a knockout of the *CCAI* or *GLK1* gene should increase *ASN1* and *GDH1* expression levels and diminish *GLN1.3* mRNA levels. To test these hypotheses, we used previously characterized *CCAI* overexpressor (*CCAI-ox*) (Wang *et al.*, 1998, Cell 93:1207-1217) and *GLK1* gene knockout (*glk1*) (Fitter *et al.*, 2002, Plant J 31:713-727) lines. A stronger phenotype for the overexpressor lines was anticipated as compared to the knockout, as the model predicts redundancy in the function of *CCAI* and *GLK1* in regulating *ASN1*, *GDH1* and *GLN1.3* gene expression. *CCAI-ox*, *glk1* and wild-type plants were grown for two weeks as above, and samples were collected in the morning (3 h after dawn). Total RNA was extracted from whole seedlings and RT-qPCR was performed to determine mRNA levels for *ASN1*, *GLN1.3* and *GDH1* in the three genotypes. As shown in Figure 4, all three genes tested showed altered expression patterns in the mutant lines utilized (as determined by analysis of variance, $p \leq 0.05$) which were consistent with the predicted network model shown in Figure 1. In addition, *bZIP1* mRNA level was also repressed in *CCAI-ox* (Figure 10). *ASN1*, *GDH1* and *GLN1.3* mRNA levels were not altered in the *glk1* line, with the exception of a small increase in *GDH1* mRNA levels. This is probably due to the redundant function of *GLK1* and *CCAI* in regulating the expression of the tested genes. In contrast, and as predicted by the model shown in Figure 3, *ASN1* and *GDH1* levels were decreased in the *CCAI-ox* line. Also consistent with the predictions of the model, *GLN1.3* mRNA levels were increased as compared to wild-type in the *CCAI-ox*.

[00271] The network model predicts that the effect of *CCA1* on the expression of the target genes will be direct. To test this hypothesis, ChIP assays were used using a *CCA1* antibody (Figure 4B). As controls, it was demonstrated that the ChIP assays could detect binding of CCA1 protein to a region of the *TOC1* promoter, a known target of *CCA1*, but was not able to detect the *ZTL* promoter which has no circadian oscillation at the mRNA level. Consistent with the model for CCA1, ChIP assays in both wild-type and *CCA1-ox* lines were able to confirm binding of CCA1 to the promoter regions of *GLN1.3*, *GDH1* and *bZIP1* promoters. These results support the model, and indicate that *CCA1* regulates expression of *bZIP1*, *GDH1* and *GLN1.3* genes directly, and indirectly for *ASN1* through *bZIP1*.

[00272] **N-nutrient signals act as input to the Arabidopsis circadian clock.** *CCA1* is a key component of a negative feedback loop at the center of the *Arabidopsis* circadian clock (McClung, 2006, Plant Cell 18:792-803; Millar, 2004, J. Exp. Bot. 55:277-283). Because the results showed that N-treatments affected *CCA1* expression, it was hypothesized that N might serve as an input capable of affecting the circadian clock function. To test this hypothesis, pulses of inorganic or organic N were provided at intervals spanning a circadian cycle and determined the effects on the phase of the oscillation in *CCA1::LUC* expression. Each treatment resulted in stable phase shifts indicating that N status serves as an input to the circadian clock (Figure 5 and Figure 11). Inorganic N and 10mM Glu treatments conferred slight phase advances whereas 10mM Gln conferred only delays. The Nms and Glu pulses did not affect the period but the Gln pulse shortened the period as determined by one-way analysis of variance and Dunn's multiple comparison tests. Thus, the clock regulates a number of steps in N metabolism, such as NR expression and activity (Pilgrim *et al.*, 1993, Plant Mol Biol 23:349-64) and *ASN1* expression as demonstrated herein (see also Harmer *et al.*, 2000, Science 290:2110-2113). In turn, N status feeds back to the clock, at least in part through its effect on *CCA1* expression.

7.4 Discussion

[00273] In the present study, genomic and pharmacological approaches were used to distinguish organic from inorganic N responses in *Arabidopsis* seedlings. The majority of the genes regulated by the N-treatments used in this study (81%) are responding to organic N signals. Among the genes regulated by organic N, we distinguished two classes of genes: (i) genes that responded only to external Glu application and (ii) genes that responded to internal and external sources of Glu (Table 3). The difference in these two expression patterns raises the possibility that there are different mechanisms for sensing internally produced cellular

Glu vs. extra cellular Glu that is transported between cells. The other possibility is that the differences in internal vs. external Glu responses observed in this study reflect distinct threshold responses to Glu levels. There is precedence for internal and external Glu sensing mechanisms in other organisms. Bacteria regulate ammonium assimilation via a mechanism involving PII, a sensor that measures levels of α -ketoglutarate and Glu (Arcondeguy *et al.*, 2001, Microbiol Mol Biol Rev 65:80-105). Plants contain a PII protein that is localized to chloroplasts (Hsieh *et al.*, 1998, Proc Natl Acad Sci USA 95:13965-13970), a potential sensor of internal levels of Glu. By contrast, extracellular Glu is sensed by Glu receptors in animal brains (Sykova, 2004, Neuroscience 129:861-876). The presence of Glu receptor genes in plants (Lacombe *et al.*, 2001, Science 292:1486-1487) raises the possibility that Glu receptors in plants may serve to sense levels of external apoplastic transported Glu.

[00274] Analysis of the genes regulated by N, identified a gene network with transcription factors that appear to regulate the expression of N-assimilatory genes. New to this study is the finding that the NR genes (*NIA1*, *NIA2*) are repressed by organic N, as is *GLN1.3*, which is involved in Gln biosynthesis. Within this N-regulated network we also found genes involved in N uptake and metabolism including an ammonium transporter (*AMT1.1*), genes involved in assimilating N into and out of Asn (*ASN1*, *ANS*), as well as amino acid transporter genes. Organic N negatively regulated *AMT1.1* and *ANS*, but induced the *ASN1* gene. It was therefore hypothesized that in the presence of Glu, or a Glu-derived metabolite, Asn production is optimized and regulated at the level of transcription by increasing levels of *ASN1* and decreasing levels of *ANS* transcripts. These results are consistent with Asn serving as a major N storage compound (Lam *et al.*, 1994, Plant Physiol 106:1347-1357) controlled by the *ASN1* gene, and suggest a mechanism to maximize Asn production, degradation and distribution depending on levels of internal sources of organic N.

[00275] The network analysis proposed a mechanism for transcriptional regulation of N-assimilation. *ASN1* was a predicted target of the transcription factor bZIP1; *GDH1*, *GLN1.3* and *bZIP1* were predicted targets of GLK1 and CCA1. Because *bZIP1* is also regulated by carbon (Gutierrez *et al.*, 2007, Genome Biol 8:R7), this gene may be an integrator of C and N signaling for regulation of N-assimilation in *Arabidopsis*. This our network model was validated by measuring mRNA levels of the target genes in *CCA1-ox* and *glk1* knockout lines. As predicted, *ASN1* and *GDH1* mRNA levels were down regulated and *GLN1.3* mRNA was elevated in the *CCA1-ox* line. In contrast, mRNA levels for these three genes were not affected in the *glk1* knockout line. The lack of a molecular phenotype in the *glk1* knockout may be explained by the fact that *CCA1* and *GLK1* are predicted to have the same

regulatory function in the subnetwork. The predictions that CCA1 directly targets a number of genes in the network was validated using CCA1 antibodies in ChIP experiments. Because *CCA1* is one of the central components of the circadian clock in *Arabidopsis*, regulation of *CCA1* expression in response to organic N suggests that the circadian clock may receive N nutritional inputs in plants. Thus, in addition to light and temperature (Millar, 2004, J. Exp. Bot. 55:277-283; McClung, 2001, Ann. Rev. Plant Physiol Plant Mol.Biol. 52:139-162), nutrients -such as N- may act as input for the clock. The phase response curve analysis results presented herein are consistent with weak (type 1) resetting similar to those observed in response to light pulses in *Lemna gibba* (Kondo, 1983, Plant Cell Physiol. 24:659-665), KCl or ethanol pulses in *Phaseolus coccineus* (Bunning and Moser, 1973, Proc Natl Acad Sci USA 70:3387-3389) and cAMP or imidazole pulses in *Trifolium repens* (Bollig *et al.*, 1978, Planta 141:225-230), strengthening the hypothesis that N status feeds back to the clock, at least in part through its effect on *CCA1* expression. In *Arabidopsis*, light pulses evoke strong delays (~8 h) in the early night and strong advances (5-10 h) later in the night (Covington *et al.*, 2001, Plant Cell 13:1305-1315). Although the molecular basis of these phase shifts is not definitively established, they may involve induction of *CCA1* by light (Wang *et al.*, 1998, Cell 93:1207-1217). In the above-experiments, N treatment would decrease *CCA1* mRNA abundance. That this elicits only small phase shifts suggests that posttranscriptional regulation buffers against *CCA1* activity changes from reduced mRNA, at least over the time frames tested with our 4-h N pulses. Alternatively, N treatment may also modulate other clock components either at the mRNA, protein abundance or protein activity level in ways that reduce the magnitude of the phase shifts in response to *CCA1* mRNA decrease. The emerging view of the circadian clock is as a key integrator of multiple metabolic and physiologic processes (Lam *et al.*, 1994, Plant Physiol 106:1347-1357; Kondo, 1983, Plant Cell Physiol. 24:659-665). As such it receives input not only from environmental stimuli but also from multiple metabolic pathways, many of which are subject to circadian regulation. Thus, the clock regulates a number of steps in N metabolism, such as NR expression and activity (Bunning and Moser, 1973, Proc Natl Acad Sci USA 70:3387-3389) and *ASN1* expression. In turn, N status feeds back to the clock, at least in part through its effect on *CCA1* expression. This feedback is more subtle than the effects of saturating light pulses and our results are consistent with N status fine tuning clock function rather than conferring large changes such as those observed in response to light (Figure 6).

[00276] Oscillations in the mRNA of genes that code for metabolic enzymes could have an impact on metabolite levels, as recently shown (Gibon *et al.*, 2006, Genome Biology 7:R76).

Predicting time of food availability is key for the survival in most animals (Stephan, 2002, J Biol Rhythms 17:284-292). The data presented herein suggest that this may also be the case in *Arabidopsis*, *e.g.*, anticipating the availability of carbon skeletons produced by photosynthesis to assimilate inorganic N into amino acids. Moreover, this data provides a plausible molecular mechanism for how this could happen in plants via *CCA1*. The present study thus provides evidence that plant nutrition, like in animals, is tightly linked to circadian functions as previously hypothesized (Harmer *et al.*, 2000, Science 290:2110-2113). Recently, it was shown that the central clock gene *Per2* is necessary for food anticipation in mice (Feillet *et al.*, 2006, Curr Biology 16:2016-2022). The present data indicates that the central clock gene *CCA1* plays a role in circadian regulation of N-assimilation in plants (Figure 12). This data is consistent with a model in which the N-assimilatory pathway is a downstream target of the clock with *CCA1* being the direct regulatory factor. Moreover, Glu or other Glu-derived signal act as input to the circadian clock providing a link between plant N-nutrition and circadian rhythms.

8. EQUIVALENTS

[00277] Although the invention is described in detail with reference to specific embodiments thereof, it will be understood that variations which are functionally equivalent are within the scope of this invention. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

[00278] All publications, patents and patent applications mentioned in this specification are herein incorporated by reference into the specification to the same extent as if each individual publication, patent or patent application was specifically and individually indicated to be incorporated herein by reference in their entireties.

Annex: Expression patterns in response to the Nms, Nms MSX, and Nms MSX Glu treatments.

Class and Interpretation	Pattern of response to the treatments	Nms-Nms/MSX	Protein ID	AGI locus	Gene annotation
1 (A) Inorganic Nitrogen induction	I-I	I-I	267293_at	A2g23810	senescence-associated protein similar to senescence-associated protein 5 [Hemerocallis hybrid cultivar]
2 (A) Inorganic Nitrogen induction	I-I	I-I	267028_at	A2g38470	WRKY family transcription factor contains Pf03108 WRKY DNA-binding domain; (88415.m04725)
3 (A) Inorganic Nitrogen induction	I-I	I-I	266800_at	A2g23880	VQ motif-containing protein contains PF05678: VQ motif (88415.m02716)
4 (A) Inorganic Nitrogen induction	I-I	I-I	266097_at	A2g37970	SOL heme-binding family protein weak similarity to SOL protein [Mus musculus] Gi:4686906; contains Pfam profile PF04832: ferredoxin-nitrite reductase, putative strong similarity to ferredoxin-nitrite reductase [Nicotiana tabacum] Gi:19893; contains Pfam profile PF03460: Nitrite/Sulfite reductase ferredoxin-like half domain, PF01077: Nitrite and sulphite reductase 4Fe-4S domain (88415.m01789)
5 (A) Inorganic Nitrogen induction	I-I	I-I	265475_at	A2g15620	alcohol-abundant protein-related similar to embryo-abundant protein Gi:1350531 from [Picea glauca] (88414.m06342)
6 (A) Inorganic Nitrogen induction	I-I	I-I	265075_at	A1g55450	alcohol dehydrogenase (ADH) identical to alcohol dehydrogenase Gi:489467 from [Arabidopsis thaliana] (88414.m06982)
7 (A) Inorganic Nitrogen induction	I-I	I-I	264953_at	A1g77120	expressed protein (88414.m07431)
8 (A) Inorganic Nitrogen induction	I-I	I-I	264636_at	A1g65490	expressed protein (88414.m00541)
9 (A) Inorganic Nitrogen induction	I-I	I-I	264580_at	A1g65340	expressed protein (88415.m03902)
10 (A) Inorganic Nitrogen induction	I-I	I-I	263475_at	A2g31945	expressed protein (88414.m00576)
11 (A) Inorganic Nitrogen induction	I-I	I-I	263182_at	A1g65575	expressed protein similar to PGPSD12 [Petunia x hybrid] Gi:4105794; contains Pfam profile PF04749: Protein of unknown function, DUF814 (88414.m01778)
12 (A) Inorganic Nitrogen induction	I-I	I-I	262832_s_at	A1g14870	expressed protein (88414.m01852)
13 (A) Inorganic Nitrogen induction	I-I	I-I	262571_at	A1g15430	expressed protein (88414.m05395)
14 (A) Inorganic Nitrogen induction	I-I	I-I	262238_at	A1g648300	WRKY family transcription factor similar to WRKY transcription factor GB:BA487058 Gi:8472585 from [Nicotiana tabacum] (88414.m059484)
15 (A) Inorganic Nitrogen induction	I-I	I-I	261892_at	A1g80840	dehydrin (ERD14) identical to SPIPA2763 Dehydrin ERD14 [Arabidopsis thaliana] (88414.m08846)
16 (A) Inorganic Nitrogen induction	I-I	I-I	261749_at	A1g178180	zinc finger (C2H2 type) family protein (ZAT10) / salt-tolerance zinc finger protein (STZ) identical to salt-tolerance zinc finger protein GB:CA464820 Gi:1565227 from [Arabidopsis thaliana]; contains Pfam domain, PF00098: Zinc finger, C2H2 type; identical to cDNA zinc finger protein STZ/ZAT10 (STZ/ZAT10) Gi:9665730 (88414.m03388)
17 (A) Inorganic Nitrogen induction	I-I	I-I	261648_at	A1g27730	expressed protein (88414.m04059)
18 (A) Inorganic Nitrogen induction	I-I	I-I	261193_at	A1g32820	expressed protein (88415.m05158)
19 (A) Inorganic Nitrogen induction	I-I	I-I	260522_x_at	A2g41730	trypsin and protease inhibitor family protein / Kunitz family protein similar to trypsin inhibitor propeptide [Brassica oleracea] Gi:841208; contains Pfam profile PF00197: Trypsin and protease inhibitor (88414.m08478)
20 (A) Inorganic Nitrogen induction	I-I	I-I	260101_at	A1g73260	expressed protein (88414.m08913)
21 (A) Inorganic Nitrogen induction	I-I	I-I	259878_at	A1g76600	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; similar to GRAB1 protein GB:CA405371, a novel member of the NAC domain family (88414.m09019)
22 (A) Inorganic Nitrogen induction	I-I	I-I	259705_at	A1g77450	dehydrin (COR47) identical to dehydrin COR47 (Cold-induced COR47 protein) [Arabidopsis thaliana] SWISS-PROT: P31188 (88414.m02547)
23 (A) Inorganic Nitrogen induction	I-I	I-I	259570_at	A1g20440	expressed protein (88414.m02367)
24 (A) Inorganic Nitrogen induction	I-I	I-I	259479_at	A1g19020	armadillo-beta-catenin repeat family protein contains Pfam profile: PF00514 armadillo-beta-catenin-like repeat (88416.m01109)
25 (A) Inorganic Nitrogen induction	I-I	I-I	259037_at	A3g09350	legume lectin family protein contains Pfam domain, PF00139: Legume lectin beta domain (88416.m02111)
26 (A) Inorganic Nitrogen induction	I-I	I-I	257206_at	A3g16530	expressed protein (88414.m08330)
27 (A) Inorganic Nitrogen induction	I-I	I-I	256337_at	A1g17060	tolB protein-related contains weak similarity to TolB protein precursor (Swiss-Prot P44677) [Haemophilus influenzae] (88417.m00245)
28 (A) Inorganic Nitrogen induction	I-I	I-I	255543_at	A4g01870	1-aminocyclopropane-1-carboxylate synthase 6 / ACC synthase 6 (ACS6) identical to Gi:3746125 (88417.m01824)
29 (A) Inorganic Nitrogen induction	I-I	I-I	254926_at	A4g11280	expressed protein contains Pfam profile: PF03959 domain of unknown function (DUF341) (88417.m03498)
30 (A) Inorganic Nitrogen induction	I-I	I-I	254158_at	A4g24380	calcium-binding EF hand family protein similar to EF-hand Ca ²⁺ -binding protein CCO1 [Triticum aestivum] Gi:9255753; contains no apical meristem (NAM) family protein (RD28) contains Pfam PF02365: No apical meristem (NAM) domain; Arabidopsis thaliana nap gene PID: a1234813; identical to cDNA RD28 mRNA for NAM-like protein Gi:15375403 (88417.m03937)
31 (A) Inorganic Nitrogen induction	I-I	I-I	253915_at	A4g27280	senescence-associated protein (SEN1) identical to senescence-associated protein Gi:1048270 from [Arabidopsis thaliana] (88417.m05078)
32 (A) Inorganic Nitrogen induction	I-I	I-I	253872_at	A4g27410	cytochrome P450, putative similar to Cytochrome P450 91A1 (SP-Q8FG65) [Arabidopsis thaliana], cytochrome P450, Glycymiza echinata, AB001378 (88417.m05292)
33 (A) Inorganic Nitrogen induction	I-I	I-I	253161_at	A4g35770	expressed protein (88417.m05810)
34 (A) Inorganic Nitrogen induction	I-I	I-I	253048_at	A4g37370	pyridine nucleotide-disulphide oxidoreductase family protein low similarity to dihydropyrimidine dehydrogenase from Clostridium magnum [Gi:472330]; contains Pfam profile PF00070 Pyridine nucleotide-disulphide oxidoreductase domain (88416.m04738)
35 (A) Inorganic Nitrogen induction	I-I	I-I	252908_at	A4g39670	phytoalexin 3 (PSK3) identical to phytoalexin 3 (PSK3) SP-Q8M2Y0 from [Arabidopsis thaliana] (88416.m05443)
36 (A) Inorganic Nitrogen induction	I-I	I-I	252671_at	A3g44190	DRE-binding protein (DREB2A) identical to DREB2A Gi:3738230 from [Arabidopsis thaliana]; supported by cDNA, gi. 3738228.dbl, AB007790 (88418.m00583)
37 (A) Inorganic Nitrogen induction	I-I	I-I	252234_at	A3g48780	17.7 kDa class II heat shock protein 17.6A (HSP17.7-C1) identical to heat shock protein 17.6A Gi:3256075 from [Arabidopsis thaliana] (88418.m01406)
38 (A) Inorganic Nitrogen induction	I-I	I-I	250781_at	A5g05410	glutaredoxin family protein contains glutaredoxin domain, INTERPRO:IPR002109 (88418.m02201)
39 (A) Inorganic Nitrogen induction	I-I	I-I	250351_at	A5g12030	glutaredoxin family protein contains glutaredoxin domain, INTERPRO:IPR002109 (88418.m02201)
40 (A) Inorganic Nitrogen induction	I-I	I-I	249996_at	A5g18600	auxin-responsive family protein similar to auxin-induced protein AIR12 Gi:11357180 [Arabidopsis thaliana] (88418.m04278)
41 (A) Inorganic Nitrogen induction	I-I	I-I	249719_at	A5g35735	major intrinsic family protein / MIP family protein contains Pfam profile: MIP PF00230 (88418.m05853)
42 (A) Inorganic Nitrogen induction	I-I	I-I	248790_at	A5g47450	

43	(A) Inorganic Nitrogen induction	I-I-I	248164_at	A15g54490	calcium-binding EF-hand protein, putative similar to EF-hand Ca ²⁺ -binding protein CCD1 (<i>Triticum aestivum</i>) [GI:9255753]; contains INTERPRO:IPR002048 calcium-binding EF-hand domain (88418.m06785)
44	(A) Inorganic Nitrogen induction	I-I-I	248146_at	A15g54940	eukaryotic translation initiation factor SUJ1, putative similar to SPIP32911 Protein translation factor SUJ1 (<i>Saccharomyces cerevisiae</i>); contains Pfam profile PF01253 Translation initiation factor SUJ1 (88418.m06842)
45	(A) Inorganic Nitrogen induction	I-I-I	247855_at	A15g59820	zinc finger (C2H2 type) family protein (ZAT12) identical to zinc finger protein ZAT12 (<i>Arabidopsis thaliana</i>)
46	(A) Inorganic Nitrogen induction	I-I-I	247489_at	A15g61820	gl1418325embICAA67232 (88418.m07500)
47	(A) Inorganic Nitrogen induction	I-I-I	247351_at	A15g63780	expressed protein MIN19, <i>Medicago truncatula</i> , EMBL:MTY15367 (88418.m07757) no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; contains similarity to NAC-domain protein (88418.m08006)
48	(A) Inorganic Nitrogen induction	I-I-I	246744_at	A15g27760	hypoxia-responsive family protein contains Pfam profile: PF04568 hypoxia induced protein conserved region (88418.m03329) sigA-binding protein identical to SigA binding protein (<i>Arabidopsis thaliana</i>) [gi 9860074 gb AAAF34713; contains Pfam PF05678: VQ motif (88418.m08308)
49	(A) Inorganic Nitrogen induction	I-I-I	246283_at	A13g56710	plastocyanin-like domain-containing protein (88418.m02408)
50	(A) Inorganic Nitrogen induction	I-I-I	246099_at	A15g20230	hydrolase, alpha/beta fold family protein low similarity to monoglyceride lipase from <i>Homo sapiens</i> [GI:14594804; Mus musculus]
51	(A) Inorganic Nitrogen induction	I-I-I	245734_at	A11g73480	GI:2832162; contains Pfam profile PF00561: hydrolase, alpha/beta fold family (88414.m08507)
52	(A) Inorganic Nitrogen induction	I-I-I	245711_at	A15g04340	zinc finger (C2H2 type) family protein contains Pfam domain: PF00096: Zinc finger, C2H2 type (88418.m00426)
53	(A) Inorganic Nitrogen induction	I-I-I	245250_at	A14g17490	ethylene-responsive element-binding protein, putative similar to SPI080341 Ethylene responsive element binding factor 5 (AIERF5) (<i>Arabidopsis thaliana</i>) (88417.m02617)
54	(A) Inorganic Nitrogen induction	I-I-I	245026_at	atpH	ATPase III subunit
55	(A) Inorganic Nitrogen induction	I-I-I	245006_at	psaB	PSI P700 apoprotein A2
56	(A) Inorganic Nitrogen induction	I-I-I	245017_at	psaI	PSI I protein
57	(A) Inorganic Nitrogen induction	I-I-I	244981_at	yd5	hypothetical protein
58	(A) Inorganic Nitrogen induction	I-I-I	257536_at	A13g02800	tyrosine specific protein phosphatase family protein contains tyrosine specific protein phosphatases active site, PROSITE:PS00383 (88418.m00272)
59	(A) Inorganic Nitrogen induction	I-I-I	257540_at	A13g21520	expressed protein contains Pfam profile PF05078: Protein of unknown function (DUF878) (88418.m02715)
60	(A) Inorganic Nitrogen induction	D-D-D	267422_at	A12g35050+1	protein kinase family protein contains Pfam profile: PF00069 Eukaryotic protein kinase domain (88415.m04300)
61	(A) Inorganic Nitrogen repression	D-D-D	266586_at	A12g14890	arabinogalactan-protein (AGP) identical to gl1080495 gb AAAG24277 (88415.m01892)
62	(A) Inorganic Nitrogen repression	D-D-D	266022_at	A12g05920	subtilase family protein contains similarity to cucurbit-like serine protease GI:3178874 from (<i>Arabidopsis thaliana</i>) (88415.m00842)
63	(A) Inorganic Nitrogen repression	D-D-D	265733_at	A12g01190	octacosapeptide/Phox/Bem1p (PB1) domain-containing protein Pfam profile PF00564; PB1 domain (88415.m00030)
64	(A) Inorganic Nitrogen repression	D-D-D	265400_at	A12g10940	protease inhibitor/seed storage/seed transfer protein (LTP) family protein similar to proline-rich cell wall protein (<i>Medicago sativa</i>) [GI:3818418; contains Pfam profile PF00234 Protease inhibitor/seed storage/LTP family (88415.m01187)
65	(A) Inorganic Nitrogen repression	D-D-D	265042_at	A11g04040	acid phosphatase class B family protein similar to SPIP15490 STEM 28 kDa glycocyprotein precursor (<i>Vegetative storage protein A</i>) (Glycine max); acid phosphatase [Glycine max] GI:3341443; contains Pfam profile PF03787: HAD superfamily (subfamily IIIB) phosphatase; supporting cDNA gi13926197 gb AF370572.1 AF370572 (88414.m000391)
66	(A) Inorganic Nitrogen repression	D-D-D	265028_at	A11g24530	transducin family protein / WD-40 repeat family protein similar to Vegetalable incompatibility protein HET-E-1 (SP:Q00808) (<i>Podospora anserina</i>); contains 7 WD-40 repeats (PF00400) (88414.m03088)
67	(A) Inorganic Nitrogen repression	D-D-D	264857_at	A11g24170	glycosyl transferase family 8 protein contains Pfam profile: PF01501 glycosyl transferase family 8 (88414.m03049)
68	(A) Inorganic Nitrogen repression	D-D-D	264346_at	A11g12110	nitrate/chlorate transporter (NRT1.1) (CHL1) identical to nitrate/chlorate transporter SP:Q05085 from (<i>Arabidopsis thaliana</i>); contains Pfam profile: PF00654 POT family (88414.m01402)
69	(A) Inorganic Nitrogen repression	D-D-D	264335_s_at	A11g70320	ubiquitin-protein ligase 2 (UPL2) nearly identical to ubiquitin-protein ligase 2 (<i>Arabidopsis thaliana</i>) [GI:7108523; E3, HECT-domain protein family; similar to ubiquitin-protein ligase 2 GI:7108523 from (<i>Arabidopsis thaliana</i>) (88414.m08090)]
70	(A) Inorganic Nitrogen repression	D-D-D	264309_at	A11g62020	customer protein complex, subunit alpha, putative contains Pfam PF00400: WD domain, G-beta repeat; similar to Customer alpha subunit (Alpha-coat protein) (Alpha-COP) (HEP-COP) (SP:P53821) (<i>Homo sapiens</i>) (88414.m06995)
71	(A) Inorganic Nitrogen repression	D-D-D	264260_at	A11g09210	calreticulin 2 (CRT2) identical to SPIQ38858 Calreticulin 2 precursor (<i>Arabidopsis thaliana</i>) (88414.m01028)
72	(A) Inorganic Nitrogen repression	D-D-D	264261_at	A11g08240	nicotianamine synthase, putative similar to nicotianamine synthase (<i>Lycopersicon esculentum</i>) [GI:4753801; nicotianamine synthase 2 (<i>Hordeum vulgare</i>) [GI:4894912] (88414.m01031)]
73	(A) Inorganic Nitrogen repression	D-D-D	263989_at	A12g42880	mitogen-activated protein kinase, putative / MAPK, putative (MPK20) mitogen-activated protein kinase (MAPK)(AMPK20), PMID:12119167 (88415.m05309)
74	(A) Inorganic Nitrogen repression	D-D-D	263836_at	A12g36880	S-adenosylmethionine synthetase, putative similar to S-adenosylmethionine synthetase 3 (Methionine adenosyltransferase 3, AdoMet synthetase 3) (<i>Lycopersicon esculentum</i>) SWISS-PROT:P43282 (88415.m04521)
75	(A) Inorganic Nitrogen repression	D-D-D	263836_at	A12g40230	Bet v 1 allergen family protein contains Pfam profile PF00407: Pathogenesis-related protein Bet v 1 family (88415.m04972)
76	(A) Inorganic Nitrogen repression	D-D-D	263682_at	A11g04430	dehydration-responsive protein-related similar to early-responsive to dehydration stress ERD3 protein (<i>Arabidopsis thaliana</i>) [GI:15320410; contains Pfam profile PF03141: Putative methyltransferase (88414.m00434)]
77	(A) Inorganic Nitrogen repression	D-D-D	263590_at	A12g01820	leucine-rich repeat protein kinase, putative similar to protein kinase TMK1 gi160888 gb AA332876; contains Pfam domains
78	(A) Inorganic Nitrogen repression	D-D-D	263326_at	A12g04280	PF00560: Leucine Rich Repeat and PF00068: Protein kinase domain (88415.m00113)
78	(A) Inorganic Nitrogen repression	D-D-D	263153_s_at	A11g54010	myrosinase-associated protein, putative similar to myrosinase-associated protein GI:1769869 from (<i>Brassica napus</i>); contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif (88414.m06153)
80	(A) Inorganic Nitrogen repression	D-D-D	262504_at	A11g21750	protein disulfide isomerase, putative similar to SPIP29828 Protein disulfide isomerase precursor (PDI) (EC 5.3.4.1) (<i>Medicago sativa</i>); isoform contains non-consensus GA donor splice site at intron 9 (88414.m02722)
81	(A) Inorganic Nitrogen repression	D-D-D	262373_at	A11g73120	expressed protein (88414.m08454)
82	(A) Inorganic Nitrogen repression	D-D-D	261728_at	A11g76180	multi-copper oxidase type I family protein similar to pollen-specific BP10 protein [SPIQ00624] (<i>Brassica napus</i>); contains Pfam profile: PF00394 Multicopper oxidase (88414.m08944)
83	(A) Inorganic Nitrogen repression	D-D-D	261588_at	A11g49750	leucine-rich repeat family protein contains leucine-rich repeats, Pfam:PF00560 (88414.m05578)

84 (A) Inorganic Nitrogen repression	D-D-D	261198_at	A11g12940	high-affinity nitrate transporter, putative similar to trans-membrane nitrate transporter protein ANRT2.1 [Arabidopsis thaliana] GI:3747058, high-affinity nitrate transporter ACH1 [Arabidopsis thaliana] GI:3608362 (88414.m01503) tetrapeptide repeat (TPR)-containing protein low similarity to SPIP46825 Kinesin light chain (KLC) [Loligo pealeii]; contains aspartyl protease family protein contains Pfam domain, PF00026: eukaryotic aspartyl protease (88414.m00046)
85 (A) Inorganic Nitrogen repression	D-D-D	261053_at	A11g01320	high-affinity nitrate transporter (ACH1) identical to trans-membrane nitrate transporter protein ANRT2.1 [Arabidopsis thaliana] GI:3747058, high-affinity nitrate transporter ACH1 [Arabidopsis thaliana] GI:3608362 (88414.m00046)
86 (A) Inorganic Nitrogen repression	D-D-D	261055_at	A11g01300	pyrophosphate-fructose-6-phosphate 1-phosphotransferase alpha subunit, putative / pyrophosphate-dependent 8-phosphofructose-1-kinase, putative strong similarity to SPIQ41140 Pyrophosphate-fructose 6-phosphate 1-phosphotransferase alpha subunit (EC 2.7.1.90) (PFP) (PPI-PFK) [Ricinus communis]; contains Pfam profile PF00365: Phosphofructokinase (88414.m08908)
87 (A) Inorganic Nitrogen repression	D-D-D	260623_at	A11g08090	glutathione S-transferase, putative similar to GI:860955 from [Hyoscyamus muticus] [Plant Physiol. 109 (1), 253-260 (1995)] (88414.m05590)
88 (A) Inorganic Nitrogen repression	D-D-D	259969_at	A11g78550	dehydration-responsive protein-related similar to early-responsive to dehydration stress ERD3 protein [Arabidopsis thaliana] GI:15320410; contains Pfam profile PF03141: Putative methyltransferase (88414.m03605)
89 (A) Inorganic Nitrogen repression	D-D-D	259813_at	A11g49860	GDSL-modif lipase/hydrolase family protein low similarity to family II lipase EXL1 [Arabidopsis thaliana] GI:15054382; contains GDSL-modif lipase/hydrolase family protein low similarity to family II lipase EXL1 [Arabidopsis thaliana] GI:15054382; contains
90 (A) Inorganic Nitrogen repression	D-D-D	259771_at	A11g29470	InterPro Entry IPR01087 Lipolytic enzyme, G-D-S-L family (88414.m03625)
91 (A) Inorganic Nitrogen repression	D-D-D	259786_at	A11g29660	protein disulfide isomerase, putative similar to protein disulfide isomerase precursor GB:P29828 GI:4704766 [Medicago sativa]; Pfam HMM hit: PF00085 Thioredoxins (88414.m09026)
92 (A) Inorganic Nitrogen repression	D-D-D	259757_at	A11g77510	S-methylerythrodiopteroylglutamate-homocysteine methyltransferase, putative / vitamin-B12-independent methionine synthase, putative / cobalamin-independent methionine synthase, putative very strong similarity to SPIQ50008 5-methylerythrodiopteroylglutamate-homocysteine methyltransferase (EC 2.1.1.14) [Vitamin-B12-independent methionine synthase isozyme] [Cobalamin-independent methionine synthase isozyme] (Arabidopsis thaliana); contains Pfam profile PF01717: Methionine synthase, vitamin-B12 independent (88416.m00386)
93 (A) Inorganic Nitrogen repression	D-D-D	259343_s_at	A13g03780	cystathionine gamma-synthase, chloroplast / O-succinylhomoserine (Thiol)-lyase (CGS) (O-succinylhomoserine (Thiol)-lyase) [Arabidopsis thaliana] gamma-synthase, chloroplast precursor (EC 4.2.98.9) (CGS) (O-succinylhomoserine (Thiol)-lyase) [Arabidopsis thaliana] (88416.m00016)
94 (A) Inorganic Nitrogen repression	D-D-D	259279_at	A13g01120	beta-ig-H3 domain-containing protein / fasciclin domain-containing protein contains Pfam profile PF02469: Fasciclin domain (88416.m01434)
95 (A) Inorganic Nitrogen repression	D-D-D	259072_at	A13g11700	auxin-responsive protein / auxin-induced protein (AIR12) identical (with 7 residue gap) to auxin-induced protein AIR12 GI:11357190 [Arabidopsis thaliana] (88416.m00881)
96 (A) Inorganic Nitrogen repression	D-D-D	259018_at	A13g07390	S-adenosylmethionine synthetase, putative similar to S-adenosylmethionine synthetase 2 (Methionine adenosyltransferase 2, AdMet synthetase 2) [Catharanthus roseus] SWISS-PROT:Q86552 (88416.m02222)
97 (A) Inorganic Nitrogen repression	D-D-D	258415_at	A13g17390	adenosylhomocysteine, putative / S-adenosyl-L-homocysteine hydrolase, putative / AdoHcyase, putative strong similarity to SPIP50248[SAAH, TOBAC Adenosylhomocysteine (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase) [Nicotiana glauca]; contains Pfam profile PF00670: S-adenosyl-L-homocysteine hydrolase, NAD binding domain (88416.m02893)
98 (A) Inorganic Nitrogen repression	D-D-D	257173_at	A13g23810	glycosyl transferase family 2 protein similar to beta-(1-3)-glucosyl transferase GB:AA062210 GI:3667658 from [Bradyrhizobium japonicum], cellulose synthase from Agrobacterium tumefaciens [gi:710492] and Agrobacterium radiobacter [gi:710493]; contains Pfam glycosyl transferase, group 2 family protein domain PF00535 (88416.m03521)
99 (A) Inorganic Nitrogen repression	D-D-D	257071_at	A13g28180	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to desactoxylindole 4-hydroxylase [Catharanthus roseus][GI:1916643], flavonol synthase 1 [SPIQ96330]; contains PF03171 2OG-Fe(II) oxygenase superfamily domain (88416.m01713)
100 (A) Inorganic Nitrogen repression	D-D-D	256647_at	A13g13610	leucine-rich repeat transmembrane protein kinase, putative contains Pfam profile: PF00069: Eukaryotic protein kinase domain (88414.m03848)
101 (A) Inorganic Nitrogen repression	D-D-D	256482_at	A11g31420	calreticulin 1 (CRT1) identical to calreticulin (crt1) GI:2052379 [Arabidopsis thaliana] (88414.m06476)
102 (A) Inorganic Nitrogen repression	D-D-D	256218_at	A11g56340	GTP-binding protein (SAR1B) identical to GTP-binding protein (SAR1B) [Arabidopsis thaliana] SP-Q01474 (88414.m06475)
103 (A) Inorganic Nitrogen repression	D-D-D	256224_at	A11g56330	chitinase, putative similar to peanut type II chitinase GI:1237025 from [Arachis hypogaea] (88417.m00221)
104 (A) Inorganic Nitrogen repression	D-D-D	255595_at	A14g01700	tetrapeptide repeat (TPR)-containing protein contains Pfam profile PF00515 TPR Domain (88417.m00363)
105 (A) Inorganic Nitrogen repression	D-D-D	255474_at	A14g02470	cytochrome 1 apoprotein (CRY1) / flavin-type blue-light photoreceptor (HY4) contains Pfam PF03441: FAD binding domain of DNA photolyase, member of Pfam PF00875: deoxyribodipyrimidine photolyase superfamily, 89% identical to Cryptochrome 1 apoprotein (Blue light photoreceptor) [flavin-type blue-light photoreceptor] (SP-Q43125) [Arabidopsis thaliana] (88417.m01489)
106 (A) Inorganic Nitrogen repression	D-D-D	255492_at	A14g02680	beta-adaptin, putative strong similarity to SPIQ10567 Adapter-related protein complex 1 beta 1 subunit (Beta-adaptin 1) [Homo sapiens], beta-adaptin [Drosophila melanogaster] GI:434902; contains Pfam profile: PF01802 Adaptin N terminal region (88417.m01835)
107 (A) Inorganic Nitrogen repression	D-D-D	255068_at	A14g08920	protease inhibitor/seed storage lipid transfer protein (LTP) family protein identical to pEARL1.1 (Accession No. L43080); an Arabidopsis member of a conserved gene family (PGF95-098), Plant Physiol. 109 (4), 1487 (1995); contains Pfam protease inhibitor/seed storage lipid transfer protein (LTP) family domain PF00234 (88417.m01973)
108 (A) Inorganic Nitrogen repression	D-D-D	254925_at	A14g11380	fasciclin-like arabinogalactan-protein (FLA2) identical to gi_1337778, gb_AAK20858 (88417.m01998)
109 (A) Inorganic Nitrogen repression	D-D-D	254805_at	A14g12480	inhibitor/seed storage lipid transfer protein (LTP) family protein identical to gi_1337778, gb_AAK20858 (88417.m01998)
110 (A) Inorganic Nitrogen repression	D-D-D	254785_at	A14g12730	serine hydroxymethyltransferase (FLA2) identical to gi_1337778, gb_AAK20858 (88417.m01998)
111 (A) Inorganic Nitrogen repression	D-D-D	254740_s_at	A14g13890	serine hydroxymethyltransferase (FLA2) identical to gi_1337778, gb_AAK20858 (88417.m01998)
112 (A) Inorganic Nitrogen repression	D-D-D	254564_at	A14g19170	9-cis-epoxycarotenoid dioxygenase, putative / neoxanthin cleavage enzyme, putative / carotenoid cleavage dioxygenase, putative similar to 9-cis-epoxycarotenoid dioxygenase [Phaseolus vulgaris][GI:6715257], neoxanthin cleavage enzyme, Lycopersicon esculentum, PATX:E325787 (88417.m02828)

113	(A) Inorganic Nitrogen repression	D-D-D	254196_at	A14q24190	shepherd protein (SHD) / clavata formation protein, putative nearly identical to SHEPHERD (Arabidopsis thaliana) GI:19570872; contains Pfam profiles PF02518: ATPase, histidine kinase- DNA gyrase B- and HSP90-like domain protein, PF00163: Hsp90 protein (88417.m03472)
114	(A) Inorganic Nitrogen repression	D-D-D	253887_at	A14q27730	oligopeptide transporter OPT family protein similar to SP140900 Sexual differentiation process protein isp4 (Schizosaccharomyces pombe), oligopeptide transporter Opt1p [Candida albicans] GI:2367386; contains Pfam profiles PF03169: OPT oligopeptide transporter protein (88417.m03985)
115	(A) Inorganic Nitrogen repression	D-D-D	253609_at	A14q30190	ATPase 2, plasma membrane-type, putative / proton pump 2, putative / proton-exporting ATPase, putative strong similarity to SPIP19456 ATPase, 2, plasma membrane-type (EC 3.6.3.6) (Proton pump 2) [Arabidopsis thaliana], contains InterPro accession IPR001757: ATPase, E1-E2 type, contains Pfam profile PF00890: Cation transporter/ATPase, N-terminus (88417.m04282)
116	(A) Inorganic Nitrogen repression	D-D-D	253534_at	A14q31500	Cytochrome P450 83B1 (CYP83B1) identical to Cytochrome P450 (SP:Q65782) [Arabidopsis thaliana] (88417.m04474)
117	(A) Inorganic Nitrogen repression	D-D-D	253050_at	A14q37450	arabinogalactan-protein (AGP18) identical to gi_11935088, gb_AA641864 (88417.m05301)
118	(A) Inorganic Nitrogen repression	D-D-D	252971_at	A14q38770	proline-rich family protein (PRP4) similar to proline-rich protein [Arabidopsis thaliana] gi18782442(gb)AAF28388; contains proline-rich extension domains, INTERPRO:IPR002365 (88417.m05490)
119	(A) Inorganic Nitrogen repression	D-D-D	252831_at	A14q39980	2-dehydro-3-deoxyphosphogluconate aldolase 1 / 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 1 / DAHP synthetase 1 (DHS1) nearly identical to SPIP29965 (88417.m05682)
120	(A) Inorganic Nitrogen repression	D-D-D	252255_at	A15q49220	pectinesterase family protein contains Pfam profile, PF01095: pectinesterase (88418.m05378)
121	(A) Inorganic Nitrogen repression	D-D-D	251918_at	A15q54040	photoassimilate-responsive protein-related protein contains weak similarity to mRNA inducible by sucrose and salicylic acid expressed in sugar-accumulating tobacco plants (GI:871487) [Nicotiana tabacum] (88418.m05975)
122	(A) Inorganic Nitrogen repression	D-D-D	251899_at	A15q54400	aspartyl protease family protein contains Pfam profile, PF00028: eukaryotic aspartyl protease (88418.m08015)
123	(A) Inorganic Nitrogen repression	D-D-D	251847_at	A15q54640	tyrosophan synthase, alpha subunit (TSA1) identical to gi:618753 (88418.m06045)
124	(A) Inorganic Nitrogen repression	D-D-D	251413_at	A15q60320	expressed protein contains Pfam profiles: PF04782: protein of unknown function (DUF632), PF04783: protein of unknown function (DUF630) (88418.m06742)
125	(A) Inorganic Nitrogen repression	D-D-D	251287_at	A15q61820	aspartyl protease family protein contains Pfam domain, PF00028: eukaryotic aspartyl protease (88418.m06939)
126	(A) Inorganic Nitrogen repression	D-D-D	251182_at	A15q62600	DNAJ heat shock family protein similar to DNAJ homolog subfamily B member 11 precursor (SP:Q89KV1)[Mus musculus]; contains Pfam PF00226: DNAJ domain; contains PfamPF01556: DNAJ C terminal region (88418.m07032)
127	(A) Inorganic Nitrogen repression	D-D-D	251174_at	A15q63200	patatin-related low similarity to patatin-like latex protein allergen Hev b 7 - Hevea brasiliensis, EMBL:AF113546; contains patatin domain PF01734 (88418.m07100)
128	(A) Inorganic Nitrogen repression	D-D-D	251109_at	A15q61600	ferritin 1 (FER1) identical to ferritin (Arabidopsis thaliana) GI:1246401, GI:8163920 (88418.m00075)
129	(A) Inorganic Nitrogen repression	D-D-D	250437_at	A15q10430	arabinogalactan-protein (AGPA) identical to gi_38831726, gb_AAC77828 (88418.m01209)
130	(A) Inorganic Nitrogen repression	D-D-D	250207_at	A15q13930	chalcone synthase / naringenin-chalcone synthase identical to SPIP13114 (88418.m01629)
131	(A) Inorganic Nitrogen repression	D-D-D	250100_at	A15q16570	glutamine synthetase, putative similar to glutamine synthetase, cytosolic isozyme (glutamate- ammonia ligase) [A.alfafa] SWISS-PROT: P04078 (88418.m01839)
132	(A) Inorganic Nitrogen repression	D-D-D	249887_at	A15q23020	2-isopropylmalate synthase 2 (IMS2) identical to 2-isopropylmalate synthase (IMS2) [Arabidopsis thaliana] GI:12330689 (88418.m02691)
133	(A) Inorganic Nitrogen repression	D-D-D	249812_at	A15q23830	MD-2-related lipid recognition domain-containing protein / ML domain-containing protein contains Pfam profile PF02221: ML domain (88418.m02797)
134	(A) Inorganic Nitrogen repression	D-D-D	249677_at	A15q35970	DNA-binding protein, putative similar to SWISS-PROT: Q80560 DNA-binding protein SMUBP-2 (immunoglobulin MU binding protein domain (88418.m04332)
135	(A) Inorganic Nitrogen repression	D-D-D	249581_at	A15q37600	2, SMUBP-2) [Mesocricetus auratus] (88418.m04332)
136	(A) Inorganic Nitrogen repression	D-D-D	249037_at	A15q44130	glutamine synthetase, putative similar to glutamine synthetase, cytosolic isozyme (Glutamate- ammonia ligase, GS1) [Lotus japonicus] SWISS-PROT: Q42899 (88418.m04529)
137	(A) Inorganic Nitrogen repression	D-D-D	248942_at	A15q45480	fascilin-like arabinogalactan-protein, putative similar to gi_13377784, gb_AAK20881 (88418.m05401)
138	(A) Inorganic Nitrogen repression	D-D-D	248721_at	A15q47780	expressed protein contains Pfam domain, PF04578: Protein of unknown function, DUF594 (88418.m05587)
139	(A) Inorganic Nitrogen repression	D-D-D	248703_at	A15q48430	glycosyl transferase family 8 protein contains Pfam profile: PF01501 glycosyl transferase family 8; strong similarity to unknown protein (embI:CA871043.1) (88418.m05902)
140	(A) Inorganic Nitrogen repression	D-D-D	248252_at	A15q53250	expressed protein low similarity to extracellular dermal glycoprotein EDGP precursor [Daucus carota] GI:285741, SPIP13817 Basic 7S globulin precursor (Glycine max); expression supported by MPSS (88418.m05988)
141	(A) Inorganic Nitrogen repression	D-D-D	248118_at	A15q55050	arabinogalactan-protein, putative (AGP22) similar to arabinogalactan protein [Arabidopsis thaliana] gi10880508(gb)AAG24284 (88418.m06619)
142	(A) Inorganic Nitrogen repression	D-D-D	248037_at	A15q55930	GDSL motif lipase/hydrolase family protein similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from [Arabidopsis thaliana]; contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase (88418.m06881)
143	(A) Inorganic Nitrogen repression	D-D-D	247517_at	A15q61780	oligopeptide transporter OPT family protein similar to SP140900 Sexual differentiation process protein isp4 [Schizosaccharomyces pombe], oligopeptide transporter Opt1p [Candida albicans] GI:2367386; contains Pfam profiles PF03169: OPT oligopeptide transporter protein (88418.m06976)
144	(A) Inorganic Nitrogen repression	D-D-D	247492_at	A15q61890	tudor domain-containing protein / nuclease family protein contains Pfam domains PF00567: Tudor domain and PF00565: Staphylococcal nuclease homologue (88418.m07753)
145	(A) Inorganic Nitrogen repression	D-D-D	247494_at	A15q61790	AP2 domain-containing transcription factor family protein similar to RAP2.6 (GP:17065542) (Arabidopsis thaliana), AP2 domain containing protein, Arabidopsis thaliana, EMBL:AT1AF3099 (88418.m07764)
146	(A) Inorganic Nitrogen repression	D-D-D	247480_at	A15q62390	calnexin 1 (CNX1) identical to calnexin homolog 1, Arabidopsis thaliana, EMBL:AT08315 (SPIP29402) (88418.m07754)
147	(A) Inorganic Nitrogen repression	D-D-D	247189_at	A15q65390	calmodulin-binding family protein contains IQ calmodulin-binding motif, Pfam:PF00612 (88418.m07830)
148	(A) Inorganic Nitrogen repression	D-D-D	246935_at	A15q65550	arabinogalactan-protein (AGP7) (88418.m08224)
149	(A) Inorganic Nitrogen repression	D-D-D	246855_at	A15q68280	F-box family protein contains Pfam PF00646: F-box domain and Pfam PF00560: Leucine Rich Repeat (6 copies); similar to F-box protein FBL8 (GI:4432860) [Homo sapiens] (88418.m03007)
150	(A) Inorganic Nitrogen repression	D-D-D	246510_at	A15q15410	meprin and TRAF homolog domain-containing protein / MATH domain-containing protein low similarity to ubiquitin-specific protease 12 [Arabidopsis thaliana] GI:11993471; contains Pfam profile PF00917: MATH domain (88418.m03137)

151	(A) Inorganic Nitrogen repression	D-D-D	245956_s_at	A15g28540	luminal binding protein 1 (BIP-1) (BIP-1) SWISS-PROT:Q9LKR3 PMID:888624 (68418.m03480) tubulin alpha-3/alpha-5 chain (TUA3) nearly identical to SPIP20363 Tubulin alpha-3/alpha-5 chain (Arabidopsis thaliana) (68418.m02350)
152	(A) Inorganic Nitrogen repression	D-D-D	245915_s_at	A15g19770	proline-rich extensin, putative similar to extensin gji1165322(gbJAA53156; contains proline-rich extensin domains, INTERPRO:IPR002965 (68414.m03202)
153	(A) Inorganic Nitrogen repression	D-D-D	245874_at	A11g26250	pollen Ole e 1 allergen and extensin family protein similar to arabinogalactan protein (Daucus carota) GI:11322245; contains Pfam profile PF01190; Pollen proteins Ole e 1 family (68414.m03472)
154	(A) Inorganic Nitrogen repression	D-D-D	245688_at	A11g28290	1-deoxy-D-xylulose 5-phosphate synthase, putative / 1-deoxyxylulose 5-phosphate synthase, putative / DXP-synthase, putative profile PF01190; 1-deoxy-D-xylulose 5-phosphate synthase, putative / 1-deoxyxylulose 5-phosphate synthase, chloroplast precursor (EC 4.1.3.37) (1-DEF) (CLA1) identical to SPIQ38854 Probable 1-deoxy-D-xylulose 5-phosphate synthase (DXP synthase) (DXPS; [Mouse-sar cres] (Arabidopsis thaliana), DEF (deficient in photosynthesis) protein [Arabidopsis thaliana] GI:1399281 (68417.m02377)
155	(A) Inorganic Nitrogen repression	D-D-D	245281_at	A14g15560	heat shock protein 70, putative / HSP70, putative (68417.m02517)
156	(A) Inorganic Nitrogen repression	D-D-D	245293_at	A14g16660	thioredoxin family protein similar to protein disulfide isomerase [Dictyostelium discoideum] GI:2827440; contains Pfam profile: PF00085 Thioredoxin (68415.m05924)
157	(A) Inorganic Nitrogen repression	D-D-D	245175_at	A2g47470	NADH dehydrogenase D3
158	(A) Inorganic Nitrogen repression	D-D-D	245012_at	ndc	glutathione S-transferase, putative (68415.m03575)
159	(A) Inorganic Nitrogen repression	D-D-D	244984_at	A12g29420	UDP-glucuronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase (68415.m01771)
1	(B) Inorganic Nitrogen induction and external	I-I-NC	268296_at	A12g29420	glycine-rich protein (GRP3S) identical to cDNA glycine-rich protein 3 short isoform (GRP3S) GI:4206766 (68415.m00566)
2	(B) Inorganic Nitrogen induction and external	I-I-NC	265498_at	A2g15480	glutathione S-transferase, putative similar to glutathione S-transferase GI:860955 from [Hoscyamus mucosus] (68414.m00260)
3	(B) Inorganic Nitrogen induction and external	I-I-NC	263046_at	A2g05380	serine O-acetyltransferase, putative identical to GI:608677 from [Arabidopsis thaliana] (68414.m06414)
4	(B) Inorganic Nitrogen induction and external	I-I-NC	262119_s_at	A11g02930	12-oxophylodienoate reductase (OPR2) identical to 12-oxophylodienoate reductase OPR2 GB:AAC78441 [Arabidopsis thaliana] (68414.m08924)
5	(B) Inorganic Nitrogen induction and external	I-I-NC	260602_at	A11g55920	mitogen-activated protein kinase, putative / MAPK, putative (MPK11) similar to MAP kinase 5 GI:4239889 from [Zea mays]; mitogen activated protein kinase (MAPK) (AIMP11), PMID:12119167 (68414.m00073)
6	(B) Inorganic Nitrogen induction and external	I-I-NC	259875_s_at	A11g76680	heat shock protein 70, putative / HSP70, putative strong similarity to heat shock protein GI:425194 [Spinacia oleracea] (68416.m01567)
7	(B) Inorganic Nitrogen induction and external	I-I-NC	259428_at	A11g01560	receptor-like protein kinase 4, putative (RLK4) nearly identical to receptor-like protein kinase 4 [Arabidopsis thaliana] GI:13508745; contains Pfam domain, PF00068: Protein kinase domain; identical to cDNA receptor-like protein kinase 4 (RLK4) GI:13508744
8	(B) Inorganic Nitrogen induction and external	I-I-NC	258245_at	A13g12580	UDP-glucuronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase (68417.m04842)
9	(B) Inorganic Nitrogen induction and external	I-I-NC	254256_at	A14g23180	calmodulin-9 (CAM9) identical to calmodulin 9 GI:5825602 from [Arabidopsis thaliana]; contains Pfam profile PF00036; EF hand
10	(B) Inorganic Nitrogen induction and external	I-I-NC	253288_s_at	A14g34135	(68416.m05695)
11	(B) Inorganic Nitrogen induction and external	I-I-NC	252037_at	A13g51920	peptidyl-prolyl cis-trans isomerase, putative / FK506-binding protein, putative similar to rol1 [Arabidopsis thaliana] GI:1373398 (68418.m06007)
12	(B) Inorganic Nitrogen induction and external	I-I-NC	248857_at	A15g48570	asparagine synthetase 2 (ASN2) identical to asparagine synthetase (ASN2) [Arabidopsis thaliana] GI:3859536 (68418.m08177)
13	(B) Inorganic Nitrogen induction and external	I-I-NC	247218_at	A15g85010	ethylene-responsive element-binding protein 1 (ERF1) / EREBP-2 protein identical to SPIQ80337 Ethylene responsive element binding factor 1 (EREBP-2 protein) [Arabidopsis thaliana]; a false single bp exon was added to circumvent a single basepair insertion in the genomic sequence, supported by cDNA/genome alignment. (68417.m02618)
14	(B) Inorganic Nitrogen induction and external	I-I-NC	245252_at	A14g17500	photosystem II G protein
15	(B) Inorganic Nitrogen induction and external	I-I-NC	245011_at	psbG	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to flavonol synthase [Citrus unshui]gi:4128403; leucoanthocyanidin dioxygenase [Daucus carota]gi:5924383; contains PF03171 2OG-Fe(II) oxygenase superfamily domain (68415.m04698)
16	(B) Inorganic Nitrogen repression and external	D-D-I	267147_at	A12g38240	cold-responsive protein / cold-regulated protein (cor15a) identical to cold-regulated protein cor15a [Arabidopsis thaliana] GI:507149; contains Pfam profile PF02987: Late embryogenesis abundant protein (68415.m05264)
17	(B) Inorganic Nitrogen repression and external	D-D-I	263497_at	A12g42540	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to leucoanthocyanidin dioxygenase, Malus domestica, SPIP51091; contains Pfam profile PF03171: oxidoreductase, 2OG-Fe(II) oxygenase family (68416.m08219)
18	(B) Inorganic Nitrogen repression and external	D-D-I	251770_at	A13g55970	ribonuclease 1 (RNS1) identical to ribonuclease SP-P42813 Ribonuclease 1 precursor (EC 3.1.27.1) [Arabidopsis thaliana], GI:581988 from [Arabidopsis thaliana] (68415.m00251)
19	(B) Inorganic Nitrogen repression and external	D-D-NC	266743_at	A12g02990	mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein contains Pfam PF02468; mitochondrial import inner membrane translocase subunit Tim17 (68415.m03512)
20	(B) Inorganic Nitrogen repression and external	D-D-NC	266225_at	A12g28900	proline-rich family protein contains proline-rich extensin domains, INTERPRO:IPR002965 (68415.m01909)
21	(B) Inorganic Nitrogen repression and external	D-D-NC	265411_at	A12g16630	nodulin family protein similar to nodulin-like protein [Arabidopsis thaliana] GI:3329366, module-specific protein Nlj70 [Lotus japonicus] GI:3329366 (68415.m01912)
22	(B) Inorganic Nitrogen repression and external	D-D-NC	265414_at	A12g16660	pectate lyase family protein similar to pectate lyase GP:14531296 from [Fragaria x ananassa] (68414.m00465)
23	(B) Inorganic Nitrogen repression and external	D-D-NC	264611_at	A11g04680	starch excess protein (SEX1) identical to SEX1 [Arabidopsis thaliana] GI:12044356; supporting cDNA gi12044357(gbJAF312027.1)AF312027 (68414.m01231)
24	(B) Inorganic Nitrogen repression and external	D-D-NC	262784_at	A11g10780	splicing factor, putative strong similarity to splicing factor Prip8 [Homo sapiens] GI:3661610; contains Pfam profile PF01398: Mov34/MNP/PAD-1 family (68414.m09373)
25	(B) Inorganic Nitrogen repression and external	D-D-NC	262068_at	A11g80070	UDP-galactose/UDP-glucose transporter, putative very similar to UDP-galactose/UDP-glucose transporter (GI:22651763) [Arabidopsis thaliana] (68414.m01702)
26	(B) Inorganic Nitrogen repression and external	D-D-NC	261485_at	A11g14360	

27	(B) Inorganic Nitrogen repression and external	D-D-NC	259936_at	A11g71220	UDP-glucose:glycoprotein glucosyltransferase precursor GB 009332 [SPIO09332] from <i>Drosophila melanogaster</i> , [gi:7670746] and [gi:11348464] from <i>Homo sapiens</i> (88414.m08219) stress-responsive protein, putative similar to cold acclimation WCOR413-like protein gamma form [Hordium vulgare] [gi:10449100]gb AA169986; similar to stress-regulated protein SAP1 [Xenophyta viscosa] [gi:21360378]gb AA47505 (88414.m03595)
28	(B) Inorganic Nitrogen repression and external	D-D-NC	259789_at	A11g29395	glycosyl hydrolase family 1 protein / beta-glucosidase, putative (BG1) contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233; 6-phospho-beta-galactosidase; identical to Gi:8651430 from [Arabidopsis thaliana] (88414.m05913)
29	(B) Inorganic Nitrogen repression and external	D-D-NC	259640_at	A11g52400	proline-rich extensin-like family protein contains extensin-like region, Pfam:PF04554 (88414.m02662)
30	(B) Inorganic Nitrogen repression and external	D-D-NC	259553_x_at	A11g21310	expressed protein contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; leucine-rich repeat family protein / protein kinase family protein contains Pfam domains PF00580: Leucine Rich Repeat and beta-fructosidase (BFRUCT1) / beta-fructofuranosidase / cell wall invertase identical to beta-fructofuranosidase Gi:402740 from [Arabidopsis thaliana] (88416.m01742)
31	(B) Inorganic Nitrogen repression and external	D-D-NC	258040_at	A13g21190	UDP-glucuronosyl-UDP-glucosyl transferase family protein contains Pfam profile. PF00201 UDP-glucuronosyl and UDP-glucosyl transferase (88414.m02797)
32	(B) Inorganic Nitrogen repression and external	D-D-NC	257202_at	A13g23750	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to pEARL1 (Accession No. L43080): an Arabidopsis member of a conserved gene family (PGF95-099), Plant Physiol. 109 (4), 1487 (1995); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234 (88417.m01974)
33	(B) Inorganic Nitrogen repression and external	D-D-NC	258787_at	A13g13790	NAD-dependent epimerase/dehydratase family protein similar to UDP-galactase 4-epimerase from <i>Cyanopsis tetragonoloba</i> [gi:3021357] [EMBL:AJ05082]; <i>Bacillus subtilis</i> SPIP55180; contains Pfam profile PF01370 NAD dependent expressed protein (88417.m02985)
34	(B) Inorganic Nitrogen repression and external	D-D-NC	255942_at	A11g22360	epimerase/dehydratase family (88417.m03211)
35	(B) Inorganic Nitrogen repression and external	D-D-NC	254832_at	A14g12490	lipoxigenase (LOX2) identical to SPIP38418 (88416.m04872)
36	(B) Inorganic Nitrogen repression and external	D-D-NC	254468_at	A14g20460	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (88416.m05645)
37	(B) Inorganic Nitrogen repression and external	D-D-NC	254361_at	A14g22212	protein kinase family similar to SPIP00625 Pkin (Homo sapiens); contains Pfam profile PF02678: Pkin (88416.m06602)
38	(B) Inorganic Nitrogen repression and external	D-D-NC	252618_at	A13g45140	guanine nucleotide exchange family protein similar to guanine nucleotide exchange factor, <i>Homo sapiens</i> , Gi:5458754; contains Pfam profile PF01369: Sec7 domain (88416.m08808)
39	(B) Inorganic Nitrogen repression and external	D-D-NC	252066_at	A13g51550	DNAJ heat shock N-terminal domain-containing protein similar to P58 protein, <i>Bos primigenius taurus</i> , PIR:A56534; similar to p58 (Gi:1353270) (<i>Homo sapiens</i>); contains Pfam PF00226: DNAJ domain, contains Pfam PF00515: TPR Domain (88418.m00264)
40	(B) Inorganic Nitrogen repression and external	D-D-NC	251513_at	A13g59220	ABC transporter family protein (88418.m00736)
41	(B) Inorganic Nitrogen repression and external	D-D-NC	251390_at	A13g60860	aspartyl protease family protein contains Pfam profile:PF00026 eukaryotic aspartyl protease (88418.m00796)
42	(B) Inorganic Nitrogen repression and external	D-D-NC	250930_at	A15g03160	sulfotransferase family protein similar to steroid sulfotransferase 3 [Brassica napus] [Gi:3420008, steroid sulfotransferase 1 (Brassica napus) [Gi:3420004; contains Pfam profile PF00885: Sulfotransferase domain (88418.m00794)
43	(B) Inorganic Nitrogen repression and external	D-D-NC	250682_at	A15g07010	phytochelatin synthetase, putative / COBRA cell expansion protein COB, putative similar to phytochelatin synthetase Gi:28570314; similar to GB:AAK56072; identified in Roudier, et al, Plant Phys. (2002) 130:538-548 (PMID:12376623); identical to cDNA putative phytochelatin synthetase Gi:3559804; contains Pfam profile PF04833: Phytochelatin synthetase-like conserved region (88418.m07642)
44	(B) Inorganic Nitrogen repression and external	D-D-NC	247552_at	A15g60920	oligopeptide transporter OPT family protein similar to SPIP40900 Sexual differentiation process protein isp4 (Schizosaccharomyces pombe); contains Pfam profile PF03168: OPT oligopeptide transporter protein (88418.m08091)
45	(B) Inorganic Nitrogen repression and external	D-D-NC	247284_at	A15g64410	cellulose synthase, catalytic subunit, putative similar to gi:2827141 cellulose synthase catalytic subunit (Atb-A), <i>Arabidopsis thaliana</i> (88418.m08141)
46	(B) Inorganic Nitrogen repression and external	D-D-NC	247251_at	A15g64740	calcium-binding EF hand family protein contains INTERPRO:IPR002048 calcium-binding EF-hand domain (88415.m05513)
47	(B) Inorganic Nitrogen repression and external	D-D-NC	267366_at	A12g44310	hydrolase, alpha/beta fold family protein similar to monoglyceride lipase from [Homo sapiens] [Gi:14584804, [Mus musculus] Gi:2632162; contains Pfam profile PF00561: hydrolase, alpha/beta fold family (88415.m04835)
48	(B) Inorganic Nitrogen repression and external	D-D-NC	266983_at	A12g39400	glutathione S-transferase, putative similar to glutathione S-transferase 103-1A [Arabidopsis thaliana] SWISS-PROT:P46421 (88415.m03582)
1	(C) Internal Glu induction	I-NC-NC	266290_at	A12g29490	zinc finger (C2H2 type) family protein contains Pfam profile: PF00098 zinc finger, C2H2 type (88415.m02627)
2	(C) Internal Glu induction	I-NC-NC	265662_at	A12g24500	vacuolar calcium-binding protein-related contains weak similarity to vacuolar calcium binding protein [Raphanus sativus] [gi:9049359]db BAA89394 (88414.m07050)
3	(C) Internal Glu induction	I-NC-NC	265116_at	A11g62480	uracil phosphoribosyltransferase, putative / UMP pyrophosphorylase, putative / UPRTase, putative similar to SPIP05583 Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase) (<i>Arabidopsis thaliana</i>); contains Pfam profile PF00485: Phosphoribosyltransferase / Uridine kinase family (88414.m06394)
4	(C) Internal Glu induction	I-NC-NC	264561_at	A11g55810	curculin-like (mannose-binding) lectin family protein / PAN domain-containing protein similar to S locus glycoprotein [Brassica rapa] [gi:12246840; contains Pfam profile PF01453: Lectin (probable mannose binding) (88414.m09188)
5	(C) Internal Glu induction	I-NC-NC	264279_s_at	A11g78820	heavy-metal-associated domain-containing protein nearly identical to farnesylated protein ATPF2 [Gi:4097545] Pfam profile PF04403: Heavy-metal-associated domain (88415.m04531)
6	(C) Internal Glu induction	I-NC-NC	263866_at	A12g36950	MATE efflux family protein contains Pfam profile: PF01554 uncharacterized membrane protein family (88415.m00385)
7	(C) Internal Glu induction	I-NC-NC	263403_at	A12g04040	methionine-s-adenosyltransferase, putative similar to methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial precursor (MMSDH) [Rattus norvegicus] SWISS-PROT:Q02253 (88415.m01578)
8	(C) Internal Glu induction	I-NC-NC	263275_at	A12g14170	

11	(C)	Internal Glu induction	I-NC-NC	263118_at	A11g03090	methylenetetrahydrofolate synthase, mitochondrial / 3-methylcrotonyl-CoA carboxylase 1 (MCCA) nearly identical to SPIQ42523 Methylenetetrahydrofolate synthase, mitochondrial precursor (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCA alpha subunit) (3-methylcrotonyl-CoA carbon dioxide ligase alpha subunit) (Arabidopsis thaliana) (68414.m02083)
12	(C)	Internal Glu induction	I-NC-NC	262603_at	A11g15380	lactoylglutathione lyase family protein; glyoxalase I family protein contains glyoxalase family protein domain, Pfam:PF00903 (68414.m01841)
13	(C)	Internal Glu induction	I-NC-NC	262517_at	A11g17180	glutathione S-transferase, putative Second of three repeated putative glutathione transferases. 72% identical to glutathione transferase [Arabidopsis thaliana] (gi4006934). Location of ests 191A1017 (gi4006934) and 171N1317 (gi4006934) (68414.m02094)
14	(C)	Internal Glu induction	I-NC-NC	262518_at	A11g17170	glutathione S-transferase [Arabidopsis thaliana] (gi4006934) (68414.m02093)
15	(C)	Internal Glu induction	I-NC-NC	262049_at	A11g00180	expressed protein (68414.m059384)
16	(C)	Internal Glu induction	I-NC-NC	260592_at	A11g55850	cellulose synthase family protein similar to cellulose synthase catalytic subunit [gi:1392588] from Nicotiana glauca, cellulose synthase-5 [gi:9622882] from Zea mays (68414.m06405)
17	(C)	Internal Glu induction	I-NC-NC	259896_at	A11g07910	expressed protein (68414.m07755)
18	(C)	Internal Glu induction	I-NC-NC	259911_at	A11g72680	cinnamyl-alcohol dehydrogenase, putative similar to cinnamyl-alcohol dehydrogenase GB:AAC35846 [Medicago sativa], germin-like protein, putative similar to germin-like protein subfamily T member 1 [SPIP2995]; contains PS00725 germin family signature (68414.m02361)
19	(C)	Internal Glu induction	I-NC-NC	259478_at	A11g18980	60S ribosomal protein L13a (RPL13aA) similar to ribosomal protein L13a GB:O49885 [Lupinus luteus] (68416.m00847)
20	(C)	Internal Glu induction	I-NC-NC	258837_at	A13g07110	signature (68414.m02361)
21	(C)	Internal Glu induction	I-NC-NC	258896_at	A13g09460	signature (68414.m02361)
22	(C)	Internal Glu induction	I-NC-NC	258284_at	A13g16080	60S ribosomal protein L37 (RPL37C) similar to ribosomal protein L37 GB:BA044888 from [Homo sapiens] (68416.m02032)
23	(C)	Internal Glu induction	I-NC-NC	257658_at	A13g13230	expressed protein (68416.m01865)
24	(C)	Internal Glu induction	I-NC-NC	256965_at	A13g13450	2-oxoisovalerate dehydrogenase / 3-methyl-2-oxobutanoate dehydrogenase / branched-chain alpha-keto acid dehydrogenase E1 beta subunit [DINA] identical to branched chain alpha-keto acid dehydrogenase E1 beta subunit [Arabidopsis thaliana] Gi:7021286 (68416.m01692)
25	(C)	Internal Glu induction	I-NC-NC	256453_at	A11g75270	dehydroascorbate reductase, putative similar to Gi:6939839 from [Oryza sativa] (68414.m08744)
26	(C)	Internal Glu induction	I-NC-NC	256385_at	A11g66580	60S ribosomal protein L10 (RPL10C) contains Pfam profile: PF00828: Ribosomal L10 (68414.m07565)
27	(C)	Internal Glu induction	I-NC-NC	256225_at	A11g56220	domancy/auxin associated family protein similar to Auxin-repressed 12.5 kDa protein (Swiss-Prot:Q05349) [Fragaria ananassa]; similar to auxin-repressed protein (Gi:927034) [Fragaria x ananassa]; similar to dormancy-associated protein (Gi:2605887) [Pisum sativum] (68414.m06461)
28	(C)	Internal Glu induction	I-NC-NC	256061_at	A11g07040	expressed protein (68414.m00750)
29	(C)	Internal Glu induction	I-NC-NC	254923_at	A1g011240	serine/threonine protein phosphatase PP1 isozyme 8 (PP1B) identical to SP1p48488 Serine/threonine protein phosphatase PP1 isozyme 8 (EC 3.1.3.16) (Arabidopsis thaliana) (68417.m01820)
30	(C)	Internal Glu induction	I-NC-NC	254831_at	A1g012600	ribosomal protein L7AeL30eS12e/Gadd45 family protein similar to NHP2L7Ae family proteins, see SWISSPROT: P32495 and PMID:2063928. (68417.m01988)
31	(C)	Internal Glu induction	I-NC-NC	254318_at	A1g022530	embryo-abundant protein-related similar to embryo-abundant protein [Picea glauca] Gi:1350531 (68417.m03251)
32	(C)	Internal Glu induction	I-NC-NC	253203_at	A1g034710	arginine decarboxylase 2 (SPE2) identical to SP1Q23141 Arginine decarboxylase 2 (EC 4.1.1.19) (ARGDC 2) (ADC-N) (Arabidopsis thaliana) (68417.m04926)
33	(C)	Internal Glu induction	I-NC-NC	253043_at	A1g037540	LOB domain protein 39 / lateral organ boundaries domain protein 39 (LBD39) identical to SP1Q9SZE8 LOB domain protein 39 (Arabidopsis thaliana) (68417.m05312)
34	(C)	Internal Glu induction	I-NC-NC	252991_at	A1g038470	protein kinase family protein similar to protein kinase [gi:170047] from Glycine max, contains Pfam protein kinase domain PF00089 (68417.m05436)
35	(C)	Internal Glu induction	I-NC-NC	252882_at	A1g039675	expressed protein (68417.m05812)
36	(C)	Internal Glu induction	I-NC-NC	252293_at	A13g48990	AMP-dependent synthetase and ligase family protein similar to peroxisomal-coenzyme A synthetase (FAT2) [gi:586339] from Saccharomyces cerevisiae; contains Pfam AMP-binding enzyme domain PF00501; identical to cDNA; identical to cDNA adenosine monophosphate binding protein 3 AMPBP3 (AMPBP3) [gi:20799714] (68416.m05351)
37	(C)	Internal Glu induction	I-NC-NC	252034_at	A13g52040	expressed protein (68416.m05708)
38	(C)	Internal Glu induction	I-NC-NC	251488_at	A13g59540	60S ribosomal protein L38 (RPL38B) 60S RIBOSOMAL PROTEIN L38 - Lycopersicon esculentum, EMBL:X69879 (68416.m08645)
39	(C)	Internal Glu induction	I-NC-NC	250670_at	A15g06680	polygalacturonase inhibiting protein 1 (PGIP1) identical to polygalacturonase inhibiting protein 1 (PGIP1) [Arabidopsis thaliana] gi17800199 [gi:AAAF69827; contains leucine rich-repeat (LRR) domain Pfam:PF00580, INTERPRO:IPR001611 (68416.m00776)]
40	(C)	Internal Glu induction	I-NC-NC	250385_at	A15g11520	aspartate aminotransferase, chloroplast / transaminase A (ASP3) (YLSA) identical to SP1P48844 Aspartate aminotransferase, aspartate precursor (EC 2.6.1.1) (Transaminase A) (Arabidopsis thaliana); identical to cDNA YLS4 mRNA for aspartate aminotransferase (ASP3), partial cds Gi:13122265 (68416.m01344)
41	(C)	Internal Glu induction	I-NC-NC	250032_at	A15g18170	glutamate dehydrogenase 1 (GDH1) identical to glutamate dehydrogenase 1 (GDH 1) [Arabidopsis thaliana] SWISS-PROT:Q43314 (68416.m02133)
42	(C)	Internal Glu induction	I-NC-NC	249941_at	A15g22270	expressed protein similar to unknown protein (gb AA-F02128.1) (68416.m02595)
43	(C)	Internal Glu induction	I-NC-NC	248752_at	A15g24860	expressed protein (68416.m02914)
44	(C)	Internal Glu induction	I-NC-NC	249487_at	A15g39610	no apical meristem (NAM) family protein contains Pfam PF02385: No apical meristem (NAM) protein; similar to cup-shaped cotyledon CUC2 (Gi:1944132) [Arabidopsis thaliana] (68416.m04797)
45	(C)	Internal Glu induction	I-NC-NC	249125_at	A15g43450	2-oxoglutarate-dependent dioxygenase, putative similar to 2A6 (Gi:596822) and tomato ethylene synthesis regulatory protein E8 (SPIP10987) (68416.m05312)
46	(C)	Internal Glu induction	I-NC-NC	248076_at	A15g43970	expressed protein (68416.m05380)

47	(C) Internal Glu induction	I-NC-NC	248607_at	A15g49480	sodium-inducible calcium-binding protein (ACP1) / sodium-responsive calcium-binding protein (ACP1) identical to NaCl-inducible Ca2+-binding protein Gi:2352828 from [Arabidopsis thaliana] (68418.m08123)
48	(C) Internal Glu induction	I-NC-NC	248381_at	A15g51830	pH8-type carbohydrate kinase family protein contains Pfam profile: PF00294 pH8 family carbohydrate kinase (68418.m08428)
49	(C) Internal Glu induction	I-NC-NC	247283_at	A15g64250	2-nitropropane dioxygenase family / NPD family contains Pfam profile PF03060: oxidoreductase, 2-nitropropane dioxygenase (NPD) family (68418.m08071)
50	(C) Internal Glu induction	I-NC-NC	247009_at	A15g67600	expressed protein (68418.m08524)
51	(C) Internal Glu induction	I-NC-NC	246745_at	A15g27770	60S ribosomal protein L22 (RPL22C) ribosomal protein L22 (cytosolic), PIR:S52084 (68418.m03330) NADP-dependent oxidoreductase, putative (P1) identical to probable NADP-dependent oxidoreductase P1, zein-crystallin homolog (68418.m03957) similar to gi8294355j[BAB02252 [Arabidopsis thaliana] (68414.m01094) similarity to gi8294355j[BAB02252 [Arabidopsis thaliana] (68414.m01094) 60S ribosome subunit biogenesis protein, putative contains similarity to 60S ribosome subunit biogenesis protein NIP7 (Swiss-Prot:Q08962) [Saccharomyces cerevisiae] (68417.m02401) SPIQ39172[gi:886428], Arabidopsis thaliana, similar to allyl alcohol dehydrogenase [Nicotiana tabacum] Gi:6892816; contains (SPIQ39172)[gi:886428], Arabidopsis thaliana, zinc-binding dehydrogenase family (68418.m01988) Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family (68418.m01988)
52	(C) Internal Glu induction	I-NC-NC	246463_at	A15g16870	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative (XTR4) identical to N-terminal partial sequence of xyloglucan endotransglycosylase-related protein XTR4 Gi:1244754 from [Arabidopsis thaliana]; similar to endoxyloglucan transferase [Arabidopsis thaliana] Gi:5533311 (68414.m03957) leucine-rich repeat family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001811; contains similarity to gi8294355j[BAB02252 [Arabidopsis thaliana] (68414.m01094) 60S ribosome subunit biogenesis protein, putative contains similarity to 60S ribosome subunit biogenesis protein NIP7 (Swiss-Prot:Q08962) [Saccharomyces cerevisiae] (68417.m02401) patain, putative similar to patain-like latex allergen [Hevea brasiliensis][PMID:10589016]; contains patain domain PF01734 (68415.m03188) expressed protein (68415.m03771) fasodlin-like arabinogalactan-protein (FLA9) identical to gi_13377784, gb_AAK20881 (68414.m00371) chloroplast nucleoid DNA-binding protein-related contains Pfam profile PF00028: Eukaryotic aspartyl protease;b similar to CND41, chloroplast nucleoid DNA-binding protein (Gi:2541876) [Nicotiana tabacum] (68414.m01094) protease inhibitor/seed storage lipid transfer protein (LTP) family protein similar to 14 kDa polypeptide [Catharanthus roseus] Gi:40741; contains Pfam profile PF00234 (68414.m01359) xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (EXGT-A3) identical to endoxyloglucan transferase [Arabidopsis thaliana] Gi:5533313 (68415.m00118) plastocyanin-like domain-containing protein contains InterPro:IPR003245 plastocyanin-like domain (68414.m07328) xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative similar to endo-xyloglucan transferase Gi:2244732 from [Cosquyllum hirsutum] (68414.m01328) gibberellin-responsive protein, putative similar to SPIP46890 Gibberellin-regulated protein 4 precursor [Arabidopsis thaliana] GUSA4; contains Pfam profile PF02704: Gibberellin regulated protein (68414.m08847) auxin efflux carrier family protein contains auxin efflux carrier domain, Pfam:PF03547 (68414.m08904)
53	(C) Internal Glu induction	I-NC-NC	245784_at	A11g32170	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein similar to SEC14-like protein 2 (Alpha-tocopherol associated protein) (TAP) (bTAP) (Fragment) (SP:P58875) [Bos taurus]; similar to Gi:807958 from [Saccharomyces cerevisiae]; contains Pfam PF00650: CRAL/TRIO domain; contains Pfam PF03765: CRAL/TRIO, N-terminus (68414.m08342) expressed protein contains Pfam profile PF04669: Protein of unknown function (DUF579) (68414.m03422)
54	(C) Internal Glu induction	I-NC-NC	245785_at	A11g33600	60S ribosomal protein L19 (RPL19B) similar to ribosomal protein L19 GB:CAA45090 from [Homo sapiens] (68418.m02142) pectinesterase family protein contains Pfam profiles: PF04043 plant invertase/pectin methyltransferase (68418.m01810) inhibitor, similar to pectin methyltransferase GB:Q42534 from [Arabidopsis thaliana] (68418.m01810)
55	(C) Internal Glu induction	I-NC-NC	245512_at	A14g15770	DNA topoisomerase-related similar to DNA topoisomerase IV subunit A (Gi:26454107) [Mycoplasma penetrans] (68418.m02017) xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative similar to xyloglucan endotransglycosylase-related protein Gi:1244780 from [Arabidopsis thaliana] (68418.m02884) RNA-binding protein, putative similar to RNA Binding Protein 47 [Nicotiana glauca] (68418.m02884) GB:AAAC49850 from [Nicotiana tabacum]; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) (68418.m02429) expressed protein (68414.m04898) protein kinase-related (68414.m07608) plastocyanin-like domain-containing protein (68417.m02016) pinoselinol-laricresinol reductase, putative similar to pinoselinol-laricresinol reductase Th1 [Tsauga heterophylla][Gi:7578915]; contains isoflavone reductase domain PF02716 (68417.m02124) maize dehydrogenase [NAD], chloroplast (MDH) identical to chloroplast NAD-maleate dehydrogenase [Arabidopsis thaliana] Gi:3250066; contains InterPro entry IPR001236: Lactate/maleate dehydrogenase; contains Pfam profiles PF00056: lactate/maleate dehydrogenase, NAD binding domain and PF02866: lactate/maleate dehydrogenase, alpha/beta C-terminal domain (68418.m05168) LOB domain protein 38 / lateral organ boundaries domain protein 38 (LBD38) identical to SPIQ8SN23 LOB domain protein 38 [Arabidopsis thaliana] (68418.m05461) transferase family protein similar to anthranilate N-hydroxycinnamoylbenzoyltransferase, Dianthus caryophyllus [gi:2239089]; contains Pfam transferase family domain PF002458 (68418.m05487)
56	(C) Internal Glu induction	I-NC-NC	245038_at	A2g26560	
57	(C) Internal Glu induction	NC-D-D	267209_at	A12g30930	
58	(C) Internal Glu induction	NC-D-D	265066_at	A12g30870	
59	(C) Internal Glu induction	NC-D-D	264672_at	A11g09750	
60	(C) Internal Glu induction	NC-D-D	264371_at	A11g12090	
61	(C) Internal Glu induction	NC-D-D	263598_at	A2g01850	
62	(C) Internal Glu induction	NC-D-D	261975_at	A11g64640	
63	(C) Internal Glu induction	NC-D-D	261825_at	A11g11545	
64	(C) Internal Glu induction	NC-D-D	260221_at	A11g74870	
65	(C) Internal Glu induction	NC-D-D	259980_at	A11g76520	
66	(C) Internal Glu induction	NC-D-D	259803_at	A11g72150	
67	(C) Internal Glu induction	NC-D-D	259588_at	A11g7930	
68	(C) Internal Glu induction	NC-D-D	258410_at	A13g18780	
69	(C) Internal Glu induction	NC-D-D	258369_at	A13g14310	
70	(C) Internal Glu induction	NC-D-D	257798_at	A13g15950	
71	(C) Internal Glu induction	NC-D-D	257203_at	A13g23730	
72	(C) Internal Glu induction	NC-D-D	257037_at	A13g19130	
73	(C) Internal Glu induction	NC-D-D	256543_at	A11g42480	
74	(C) Internal Glu induction	NC-D-D	255856_at	A11g68940	
75	(C) Internal Glu induction	NC-D-D	254789_at	A14g12880	
76	(C) Internal Glu induction	NC-D-D	254726_at	A14g13660	
77	(C) Internal Glu induction	NC-D-D	252407_at	A13g47520	
78	(C) Internal Glu induction	NC-D-D	252220_at	A13g49940	
79	(C) Internal Glu induction	NC-D-D	252199_at	A13g50270	

80	(C) Internal Glu induction	NC-D-D	251830_at	A1355010	phosphoribosylglycinamide cyclase, chloroplast / phosphoribosyl-aminimidazole synthetase / AIR synthase (PUR5) identical to phosphoribosylglycinamide cyclase, chloroplast precursor SP_Q05728 from [Arabidopsis thaliana]; contains Pfam profiles: PF02769 AIR synthase related protein, C-terminal domain, PF00586 AIR synthase related protein, N-terminal domain (88418.m00108)
81	(C) Internal Glu induction	NC-D-D	251015_at	A1502480	expressed protein p (88418.m00181)
82	(C) Internal Glu induction	NC-D-D	250777_at	A15005440	expressed protein contains Pfam profile PF04882: Protein of unknown function, DUF642 (88418.m01333)
83	(C) Internal Glu induction	NC-D-D	250386_at	A15g11420	DNA-binding protein-related contains Pfam domain PF03478: Domain of unknown function (DUF286), found in AT-hook motifs Pfam:PF02178 (88418.m06153)
84	(C) Internal Glu induction	NC-D-D	248564_at	A15g49700	Yf521-B-like family protein contains Pfam profile PF04146: Yf521-B-like family (88418.m07655)
85	(C) Internal Glu induction	NC-D-D	247555_at	A15g61020	glycosyl hydrolase family 3 protein (88418.m08115)
86	(C) Internal Glu induction	NC-D-D	247286_at	A15g64570	expressed protein contains Pfam profile PF04862: Protein of unknown function, DUF642 (88418.m03028)
87	(C) Internal Glu induction	NC-D-D	246919_at	A15g25460	gibberellin-regulated contains Pfam profile PF03080: Arabidopsis proteins of unknown function 1 precursor (Arabidopsis thaliana); contains Pfam profile PF02704: Gibberellin regulated protein (88418.m01750)
88	(C) Internal Glu induction	NC-D-D	246550_at	A15g14920	chaperonin, putative similar to SWISS-PROT:Q05046- chaperonin CPN60-2, mitochondrial precursor (HSP60-2) [Cucurbita maxima]; contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family (88415.m04069)
89	(C) Internal Glu induction	NC-D-D	245164_at	A2g333210	zinc finger (C3HC4-type RING finger) family protein / ankyrin repeat family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) and Pfam profile: PF00023 ankyrin repeat (88417.m02213)
90	(C) Internal Glu Repression	D-H	264213_at	A11g65400	trans-cinnamate 4-monoxygenase / cinnamic acid 4-hydroxylase (C4H) (CA4H) / cyclochrome P450 73 (CYP73) (CYP73A5) identical to SPIP92994: Trans-cinnamate 4-monoxygenase (EC 1.14.13.11) [Cinnamic acid 4-hydroxylase] (CA4H) (C4H) (P450C4H) (Cyclochrome P450 73); (Arabidopsis thaliana); molecular marker C4H (GB:U71080) (88415.m03714)
91	(C) Internal Glu Repression	D-H	245329_at	A14g14365	expressed protein Pfam profile PF03080: Arabidopsis proteins of unknown function (88415.m05502)
92	(C) Internal Glu Repression	D-NC-NC	267470_at	A2g30490	methyltetrahydrofolate reductase 2 (MTHFR2) identical to SPI08055 Methyltetrahydrofolate reductase (EC 1.5.1.20) (Arabidopsis thaliana) (88415.m05493)
93	(C) Internal Glu Repression	D-NC-NC	267367_at	A2g44210	glutathione S-transferase, putative supported by cDNA GI:443688 GB:D17673 (88415.m03762)
94	(C) Internal Glu Repression	D-NC-NC	267187_s_at	A2g44160	extra-large guanine nucleotide binding protein / G-protein (XLG) identical to extra-large G-protein (XLG) (Arabidopsis thaliana) GI:3201680 (88415.m02801)
95	(C) Internal Glu Repression	D-NC-NC	267154_at	A2g30870	nodulin family protein similar to nodulin-like protein [Arabidopsis thaliana] GI:3329388, nodule-specific protein N170 [Lotus japonicus] GI:3328366 (88415.m04816)
96	(C) Internal Glu Repression	D-NC-NC	267136_at	A2g23460	integral membrane protein, putative contains 3 transmembrane domains, contains Pfam PF04535: Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana) (88415.m04850)
97	(C) Internal Glu Repression	D-NC-NC	266993_at	A2g39210	bile acid:sodium symporter family protein low similarity to SPIQ12908 ileal sodium/bile acid cotransporter (Homo sapiens); contains Pfam profile PF01758: Sodium/Bile acid symporter family (88415.m03227)
98	(C) Internal Glu Repression	D-NC-NC	266987_at	A2g39530	expressed protein (88415.m03649)
99	(C) Internal Glu Repression	D-NC-NC	266857_at	A2g26900	myb-related transcription factor (CCA1) identical to myb-related transcription factor (CCA1) GI:4090569 from [Arabidopsis thaliana] (88415.m05843)
100	(C) Internal Glu Repression	D-NC-NC	266808_at	A2g26995	expressed protein (88415.m05748)
101	(C) Internal Glu Repression	D-NC-NC	266719_at	A2g46830	glutaredoxin family protein contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase) (88415.m05979)
102	(C) Internal Glu Repression	D-NC-NC	266591_at	A2g46225	mevalonate diphosphate decarboxylase (MVD1) identical to mevalonate diphosphate decarboxylase [Arabidopsis thaliana] gi2288887 embCAA74700 (88415.m04753)
103	(C) Internal Glu Repression	D-NC-NC	266516_at	A2g47880	tubulin beta-7 chain (TUB7) identical to GB:M84704 SPIP28515 Tubulin beta-7 chain (Arabidopsis thaliana) (88415.m03588)
104	(C) Internal Glu Repression	D-NC-NC	266414_at	A2g38700	expressed protein (88415.m03377)
105	(C) Internal Glu Repression	D-NC-NC	266295_at	A2g29550	ceramidase family protein contains Pfam domain, PF04734: Neutral/alkaline nonlysosomal ceramidase (88415.m04885)
106	(C) Internal Glu Repression	D-NC-NC	266205_s_at	A2g27860	expressed protein (88415.m02377)
107	(C) Internal Glu Repression	D-NC-NC	266089_at	A2g38010	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to IDS3 [Hordeum vulgare] (GI:4514655), leucoanthocyanidin dioxygenase [SPIP5109] [Malus domestica], contains PF03171: 2OG-Fe(II) oxygenase superfamily domain (88415.m04501)
108	(C) Internal Glu Repression	D-NC-NC	265286_at	A2g20360	clathrin adaptor complex medium subunit family protein contains Pfam profile: PF00828 adaptor complex medium subunit family (88414.m06842)
109	(C) Internal Glu Repression	D-NC-NC	265208_at	A2g36690	protein phosphatase 2C family protein / PP2C family protein similar to protein phosphatase-2C; PP2C (GI:3643088) [Mesembryanthemum crystallinum]; contains Pfam PF00481: Protein phosphatase 2C domain; (88414.m00339)
110	(C) Internal Glu Repression	D-NC-NC	264914_at	A11g60780	ankyrin repeat family protein contains ankyrin repeat domains, Pfam:PF00023 (88414.m01164)
111	(C) Internal Glu Repression	D-NC-NC	264833_at	A11g03590	pyrophosphate-fructose-6-phosphate 1-phosphotransferase beta subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative strong similarity to SPIQ41141 Pyrophosphate-fructose 6-phosphate 1-phosphotransferase beta subunit (EC 2.7.1.90) (PFP) (PPI-PFK) (Ricinua communis); contains Pfam profile PF00365: Phosphofructokinase (88414.m01386)
112	(C) Internal Glu Repression	D-NC-NC	264434_at	A11g10340	lactoylglutathione lyase, putative / glyoxalase I, putative highly similar to putative lactoylglutathione lyase SP_Q39366 from [Brassica oleracea] (88414.m01360)
113	(C) Internal Glu Repression	D-NC-NC	264388_at	A11g12000	equilibrative nucleoside transporter family protein contains similarity to SWISS-PROT:Q14542 equilibrative nucleoside transporter 2 (Equilibrative nitrobenzylmercaptopyrimidine riboside-insensitive nucleoside transporter, Equilibrative NBMPR-insensitive nucleoside transporter, Nucleoside transporter, ei-type, 36 kDa nuclear protein HNP36, Hydrophobic nuclear protein, 36 kDa, Delayed-early response protein 12) [Homo sapiens] (88414.m08091)
114	(C) Internal Glu Repression	D-NC-NC	264372_at	A11g11840	
115	(C) Internal Glu Repression	D-NC-NC	264316_at	A11g70330	

116	(C) Internal Glu Repression	D-NC-NC	264057_at	A12g28550	AP2 domain-containing transcription factor RAP2.7 (RAP2.7) nearly identical to AP2 domain transcription factor RAP2.7 (GI:2281639) [Arabidopsis thaliana] (68415.m03468) arabidogalactan-protein (AGP2) identical to gi 388312 gb AAC77824; supported by cDNA gi 388312 gb AF082299 (68415.m02864)
117	(C) Internal Glu Repression	D-NC-NC	264005_at	A2g222470	homodimeric zipper protein 6 (Hb-6) / HD-ZIP transcription factor 6 identical to homeobox-leucine zipper protein ATH-6 (HD-ZIP protein ATH-6) (SP-P46668) [Arabidopsis thaliana] (68415.m02860)
118	(C) Internal Glu Repression	D-NC-NC	264006_at	A2g22430	U-box domain-containing protein similar to immediate-early fungal effector protein CMPG1 [Petoselinum crispum] GI:14582200; contains Pfam profile PF04564; U-box domain (68415.m04410)
119	(C) Internal Glu Repression	D-NC-NC	263935_at	A12g35930	hydrolase, alpha/beta fold family protein low similarity to 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase [Rhodococcus sp. RHA.1] GI:897831; contains Pfam profile PF00561; hydrolase, alpha/beta fold family (68415.m04453)
120	(C) Internal Glu Repression	D-NC-NC	263900_at	A2g36290	protein kinase family protein contains Pfam domain, PF00069; Protein kinase domain (68415.m04854)
121	(C) Internal Glu Repression	D-NC-NC	263904_at	A2g40270	golden2-like transcription factor (GLK1) identical to golden2-like transcription factor GI:13311003 from [Arabidopsis thaliana]; contains Pfam profile: PF00249 MYB-like DNA-binding domain (68415.m02402)
122	(C) Internal Glu Repression	D-NC-NC	263715_at	A12g20570	WRKY family transcription factor (ZAP1) identical to ZAP1 GI:1064883 from [Arabidopsis thaliana]; contains Pfam profile: PF03106 WRKY DNA-binding domain (68415.m06038)
123	(C) Internal Glu Repression	D-NC-NC	263626_at	A12g04880	purple acid phosphatase (PAP10) identical to purple acid phosphatase (PAP10) GI:20257482 from [Arabidopsis thaliana] (68415.m01881)
124	(C) Internal Glu Repression	D-NC-NC	263553_at	A2g16430	WRKY family transcription factor contains Pfam profile: PF03106 WRKY DNA-binding domain (68415.m02889)
125	(C) Internal Glu Repression	D-NC-NC	263536_at	A12g25000	WRKY family transcription factor contains Pfam profile: PF03106 WRKY DNA-binding domain (68415.m02889)
126	(C) Internal Glu Repression	D-NC-NC	263433_at	A12g22240	inositol-3-phosphate synthase isozyme 2 / myo-inositol-1-phosphate synthase 2 / IPS 2 identical to SPIQ3862 myo-inositol-1-phosphate synthase isozyme 2 (EC 5.5.1.4) (MI-1-P synthase 2) [Arabidopsis thaliana] (68415.m02839)
127	(C) Internal Glu Repression	D-NC-NC	262980_at	A11g75680	glycosyl hydrolase family 9 protein similar to endo-beta-1,4-glucanase GBAAC12685 GI:3025470 from [Pinus radiata] (68414.m08792)
128	(C) Internal Glu Repression	D-NC-NC	262819_at	A11g78390	copine-related low similarity to SPIQ9828 Copine 1 (Homo sapiens) (68414.m09251)
129	(C) Internal Glu Repression	D-NC-NC	262637_at	A11g06640	2-oxoglutarate-dependent dioxygenase, putative similar to 2A8 (GI:599822) and tomato ethylene synthesis regulatory protein EB (SPIP10987); contains Pfam profile: PF00871 Iron/Acscorbate oxidoreductase family (68414.m00701)
130	(C) Internal Glu Repression	D-NC-NC	262588_at	A11g15130	hydroxyproline-rich glycoprotein family protein (68414.m01807)
131	(C) Internal Glu Repression	D-NC-NC	262376_at	A11g72970	glucose-methanol-choline (GMC) oxidoreductase family protein similar to mandelonitrile lyase from Pinus serotina [SPIP52708, SPIP52707]; contains Pfam profile PF00732 GMC oxidoreductase (68414.m08439)
132	(C) Internal Glu Repression	D-NC-NC	262313_at	A11g70900	expressed protein (68414.m08181)
133	(C) Internal Glu Repression	D-NC-NC	262197_at	A11g53910	AP2 domain-containing protein RAP2.12 (RAP2.12) identical to AP2 domain containing protein GI:2281649 from [Arabidopsis thaliana] (68414.m06137)
134	(C) Internal Glu Repression	D-NC-NC	262177_at	A11g74710	isochromate synthase 1 (ICS1) / isochromate mutase identical to GI:1723087 and GB-AF078080; contains Pfam profile PF00425 chromate binding enzyme; contains TIGR00543: isochromate synthase; identical to cDNA isochromate synthase 1 precursor (ICS1) nuclear gene for plastid product GI:1723088 (68414.m08654)
135	(C) Internal Glu Repression	D-NC-NC	262051_at	A11g79890	coatomer protein complex, subunit beta 2 (beta prime), putative contains 7 WD-40 repeats (PF00400) (1 weak); similar to Coatomer beta' subunit (Beta-COP) (p102) (SP-P35006) [Homo sapiens]; similar to Coatomer beta' subunit (Beta-coat protein) (Beta-COP) (p102) (SP-O55028) [Mus musculus] (68414.m08356)
136	(C) Internal Glu Repression	D-NC-NC	262052_at	A11g60020	glutamate decarboxylase 2 (GAD 2) similar to glutamate decarboxylase (gad) GI:294111 from [Petunia hybrida] (68414.m07484)
137	(C) Internal Glu Repression	D-NC-NC	261870_at	A11g2810	C2 domain-containing protein contains INTERPRO:IPR000008 C2 domain (68414.m02823)
138	(C) Internal Glu Repression	D-NC-NC	261835_at	A11g22610	cinnamoyl-CoA reductase, putative nearly identical to CCR1 (GI:12034897), similar to cinnamoyl CoA reductase GI:2058310 from [Eucalyptus gunnii] (68414.m01914)
139	(C) Internal Glu Repression	D-NC-NC	261782_at	A11g15950	leucine-rich repeat family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001811; contains some similarity to receptor-like protein kinases (68414.m03481)
140	(C) Internal Glu Repression	D-NC-NC	261469_at	A11g28340	L-ascorbate peroxidase 1, cytosolic (APX1) identical to SPIQ05431 L-ascorbate peroxidase, cytosolic (EC 1.11.1.11) (AP) [Arabidopsis thaliana]; L-ascorbate peroxidase [Arabidopsis thaliana] gi 16173 emb CAA42168; strong similarity to cytosolic ascorbate peroxidase [Spinacia oleracea] gi 1384110 dbj BAA12890 (68414.m00856)
141	(C) Internal Glu Repression	D-NC-NC	261412_at	A11g07890	expressed protein (68414.m04448)
142	(C) Internal Glu Repression	D-NC-NC	261286_at	A11g35780	NAD-dependent epimerase/dehydratase family protein low similarity to dTDP-D-glucose-4,6-dehydratase from Aneurinibacillus thermoaerophilus GI:16357481; Spingomonas sp. GI:1314581; contains Pfam profile PF01370: NAD dependent epimerase/dehydratase family; putative NDP-rhamnose synthase (rhnd gene) GI:31559256 (68414.m06066)
143	(C) Internal Glu Repression	D-NC-NC	260985_at	A11g53500	VHS domain-containing protein / GAT domain-containing protein weak similarity to Hrs [Rattus norvegicus] GI:8547026; contains VHS domain-containing protein / GAT domain (68414.m02675)
144	(C) Internal Glu Repression	D-NC-NC	260880_at	A11g21380	ubiquitin interaction motif-containing protein contains Pfam profile PF02809: Ubiquitin interaction motif (68414.m05019)
145	(C) Internal Glu Repression	D-NC-NC	260839_at	A11g43690	dehydratase-responsive protein-related similar to early-response to dehydration stress ERD3 protein [Arabidopsis thaliana] GI:15320410; contains Pfam profile PF03141: Putative methyltransferase (68414.m09118)
146	(C) Internal Glu Repression	D-NC-NC	260800_at	A11g78240	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family (68414.m04005)
147	(C) Internal Glu Repression	D-NC-NC	260693_at	A11g32450	TCP family transcription factor 3 (TCP3) identical to transcription factor 3 (TCP3) [Arabidopsis thaliana] (GI:3243274); similar to TCP family transcription factor 3 (TCP3) identical to transcription factor 3 (TCP3) [Arabidopsis thaliana] (68414.m06032)
148	(C) Internal Glu Repression	D-NC-NC	260618_at	A11g53230	flower development protein cyclodase (cyc3) GI:8356811 from [Miscopates orontium] (68414.m06032)
149	(C) Internal Glu Repression	D-NC-NC	260590_at	A11g53310	phosphoenolpyruvate carboxylase, putative / PEP carboxylase, putative (PCC1) strong similarity to SPIP29186 Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCASE) [Solanum tuberosum]; contains Pfam profile PF00311: metal transporter, putative (ZIP11) similar to putative zinc transporter ZIP2 [Arabidopsis thaliana] gi 3252868 gb AAC24186; member of the Zinc (Zn2+)-ion (Fe2+) permease (ZIP) family, PMID:11500563 (68414.m08412)
150	(C) Internal Glu Repression	D-NC-NC	260601_at	A11g55910	

151	(C) Internal Glu Repression	D-NC-NC	260401_at	A11g69840	band 7 family protein strong similarity to hypersensitive-induced response protein [Zea mays] Gi:7718468; contains Pfam profile PF01145: SPFH domain / Band 7 family (68414.m08035)
152	(C) Internal Glu Repression	D-NC-NC	260234_at	A11g74460	GDSL-motif lipase/hydrolase family protein similar to family II lipases EXL3 Gi:15054386, EXL1 Gi:15054382, EXL2 Gi:15054384 from [Arabidopsis thaliana]; contains Pfam profile: PF00657 lipase/acylhydrolase with GDSL-like motif (68414.m08826)
153	(C) Internal Glu Repression	D-NC-NC	260046_at	A11g73800	calmodulin-binding protein similar to calmodulin-binding protein TC860 Gi:1698548 from [Nicotiana tabacum] (68414.m08544) transporter-related low similarity to glucose-6-phosphate/phosphate-translocator precursor [Solanum tuberosum] Gi:2987583, GDP-Mannose transporter [Arabidopsis thaliana] Gi:15487237; contains Pfam profile PF00892: Integral membrane protein (68414.m08921)
154	(C) Internal Glu Repression	D-NC-NC	259882_at	A11g76670	well-associated kinase 1 (WAK1) identical to wall-associated kinase 1 [Arabidopsis thaliana] Gi:3549626; expressed in leaves and stems & induced by pathogen infection (PMID:10308005) (68414.m02656)
155	(C) Internal Glu Repression	D-NC-NC	259561_at	A11g21250	AAA-type ATPase family protein contains Pfam profile: ATPase family PF00004 (68414.m05068)
156	(C) Internal Glu Repression	D-NC-NC	259507_at	A11g43910	jacalin lectin family protein contains Pfam profile: PF01419 jacalin-like lectin domain; similar to myrosinase-binding protein homolog [Arabidopsis thaliana] Gi:2987787 (68416.m02101)
157	(C) Internal Glu Repression	D-NC-NC	259383_at	A13g16470	proline-rich family protein contains proline rich extensin domains, INTERPRO:IPR020865 (68416.m00088)
158	(C) Internal Glu Repression	D-NC-NC	259175_at	A13g01560	digalactosylacylglycerol synthase 1 (DGD1) /MGDG:MGDG galactosyltransferase / galactosylidip galactosyltransferase identical to galactosylidipacylglycerol synthase (DGD1) Gi:5354158 [Arabidopsis thaliana] (68416.m01430)
159	(C) Internal Glu Repression	D-NC-NC	259070_at	A13g11670	sporulation protein-related similar to hypothetical proteins: GB:P51281 [Chloroplast Porphyra purpurea], GB:BAA16982 [Synecochyis sp], GB:P49540 [Odontella sinensis], GB:AA882669 [Chloroplast Cyanidium caldarium]; similar to stage III sporulation protein AA (Gi:18145497) [Clostridium perfringens str. 13]; similar to stage III sporulation protein AA (mutants block sporulation after engulfment) (Gi:22777578) [Oceanobacillus iheyensis] (68416.m01249)
160	(C) Internal Glu Repression	D-NC-NC	258925_at	A13g10420	cell division cycle protein 48 (CDC48) identical to SPIP-54609 Cell division cycle protein 48 homolog (Arabidopsis thaliana) (68416.m01174)
161	(C) Internal Glu Repression	D-NC-NC	258849_at	A13g09840	zinc finger (CCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar) (68416.m00275)
162	(C) Internal Glu Repression	D-NC-NC	258621_at	A13g02830	kinesin motor family protein similar to kinesin heavy chain member 2 GB:NP_032468 from [Mus musculus]; contains Pfam profile PF00225: Kinesin motor domain (68416.m02030)
163	(C) Internal Glu Repression	D-NC-NC	258286_at	A13g18060	glutamine synthetase (GS1) identical to glutamine synthetase, cytosolic isozyme [glutamate- ammonia ligase, GS1] [Arabidopsis thaliana] SWISS-PROT:Q8LV18 (68416.m02272)
164	(C) Internal Glu Repression	D-NC-NC	258160_at	A13g17820	4-coumarate-CoA ligase, putative / 4-coumaroyl-CoA synthase, putative (4CL) similar to 4CL2 [gi:12228665] and 4CL1 [gi:12228648] from [Arabidopsis thaliana], 4CL1 [gi:12228631] from [Nicotiana tabacum] (68416.m02863)
165	(C) Internal Glu Repression	D-NC-NC	258037_at	A13g21230	4-coumarate-CoA ligase 2 / 4-coumaroyl-CoA synthase 2 (4CL2) identical to SPIQ85725 4-coumarate-CoA ligase 2 (EC 6.2.1.12) (4CL2) (4-coumaroyl-CoA synthase 2) [Arabidopsis thaliana] (68416.m02684)
166	(C) Internal Glu Repression	D-NC-NC	258047_at	A13g21240	expressed protein (68416.m02463)
167	(C) Internal Glu Repression	D-NC-NC	258007_at	A13g19420	peroxidase 30 (PER30) (P30) (PRXR8) identical to SPIQ8LSY7 Peroxidase 30 precursor (EC 1.11.1.7) (Aberox P30) (PRXR8) (ATP7a) [Arabidopsis thaliana] (68416.m02746)
168	(C) Internal Glu Repression	D-NC-NC	257852_at	A13g21770	expressed protein contains Pfam profile PF04146: YT521-B-like family (68416.m01827)
169	(C) Internal Glu Repression	D-NC-NC	257849_at	A13g13060	ER lumen protein retaining receptor, putative / HDEL receptor, putative similar to SPIP35402 ER lumen protein retaining receptor (HDEL receptor) [Arabidopsis thaliana]; contains Pfam profile PF00810: ER lumen protein retaining receptor (68416.m03129) expressed protein (68416.m02493)
170	(C) Internal Glu Repression	D-NC-NC	257104_at	A13g25040	NAD-dependent epimerase/dehydratase family protein similar to nucleotide sugar epimerase from Vibrio vulnificus Gi:3093975 (PID.g3093975), WbnF [Escherichia coli] Gi:5739472, CAPI protein [Staphylococcus aureus] SPIP38858; contains Pfam profile: PF01370 NAD dependent epimerase/dehydratase family (68416.m02894)
171	(C) Internal Glu Repression	D-NC-NC	257076_at	A13g19680	6-phosphogluconate dehydrogenase family protein contains Pfam profiles: PF00393 6-phosphogluconate dehydrogenase C-terminal domain, PF03448 NAD binding domain of 6-phosphogluconate ; similar to 6-phosphogluconate dehydrogenase GB:BAA22812 Gi:2529229 [Glycine max] (68416.m00219)
172	(C) Internal Glu Repression	D-NC-NC	256865_at	A13g23820	expressed protein (68414.m06281)
173	(C) Internal Glu Repression	D-NC-NC	256328_at	A13g02360	4-coumarate-CoA ligase 1 / 4-coumaroyl-CoA synthase 1 (4CL1) identical to SPIQ42524 4-coumarate-CoA ligase 1 (EC 6.2.1.12) (4CL1) (4-coumaroyl-CoA synthase 1) [Arabidopsis thaliana] (68414.m05822)
174	(C) Internal Glu Repression	D-NC-NC	256322_at	A11g54980	bZIP family transcription factor (TGA3) identical to transcription factor Gi:304113 from [Arabidopsis thaliana] (68414.m02760)
175	(C) Internal Glu Repression	D-NC-NC	256186_at	A11g51680	ABC transporter family protein similar to ABC transporter Gi:10280532 from [Homo sapiens] (68414.m02208)
176	(C) Internal Glu Repression	D-NC-NC	255953_at	A11g22070	cytochrome P450, putative (68417.m00050)
177	(C) Internal Glu Repression	D-NC-NC	255889_at	A11g17840	sugar transporter family protein contains Pfam profile PF00083: major facilitator superfamily protein (68417.m00051) expressed protein (68417.m00047)
178	(C) Internal Glu Repression	D-NC-NC	255690_at	A14g00360	plastid-associated protein PAP, putative / flutillin, putative strong similarity to plastid-lipid associated proteins PAP1 Gi:14248554, PAP2 Gi:14248556 from [Brassica rapa], flutillin [Brassica napus] Gi:4139097; contains Pfam profile PF04755: PAP_fibritin (68417.m00572)
179	(C) Internal Glu Repression	D-NC-NC	255691_at	A14g00355	early-responsive to dehydration protein-related / ERD protein-related similar to ERD4 protein (early-responsive to dehydration stress) [Arabidopsis thaliana] Gi:15375406; contains Pfam profile PF02714: Domain of unknown function DUF221 (68417.m00619)
180	(C) Internal Glu Repression	D-NC-NC	255671_at	A14g00355	haloacid dehalogenase-like hydrolase family protein similar to genetic modifier [Zea mays] Gi:10444400; contains InterPro accession [PR005834: Haloacid dehalogenase-like hydrolase (68417.m01854)]
181	(C) Internal Glu Repression	D-NC-NC	255364_s_at	A14g04020	copper amine oxidase family protein contains Pfam domain, PF01179: Copper amine oxidase, enzyme domain (68417.m01946)
182	(C) Internal Glu Repression	D-NC-NC	255332_at	A14g04340	
183	(C) Internal Glu Repression	D-NC-NC	254874_at	A14g11570	
184	(C) Internal Glu Repression	D-NC-NC	254833_s_at	A14g12280	

185 (C) Internal Glu Repression	D-NC-NC	254577_at	A14g19450	nodulin-related weak similarity to module-specific protein Ni70 [Lotus japonicus] GI:3329388 (68417.m02881)
186 (C) Internal Glu Repression	D-NC-NC	254543_at	A14g19810	glycosyl hydrolase family 18 protein similar to chitinase/xylozyme GI:467689 from [Nicotiana tabacum] (68417.m02905)
187 (C) Internal Glu Repression	D-NC-NC	254387_at	A14g21850	methionine sulfoxide reductase domain-containing protein / SellR domain-containing protein low similarity to plin-like transcription factor [Homo sapiens] GI:5059062, SPIP14930 Peptide methionine sulfoxide reductase msa/msrB (EC 1.8.4.6) [Neisseria gonorrhoeae]; contains Pfam profile PF01641; Self domain (68417.m03159)
188 (C) Internal Glu Repression	D-NC-NC	254242_at	A14g23200	protein kinase family protein contains Pfam PF00069; Protein kinase domain (68417.m03346)
189 (C) Internal Glu Repression	D-NC-NC	254243_at	A14g23210	protein kinase family protein contains Pfam domain, PF00069; Protein kinase domain (68417.m03347)
190 (C) Internal Glu Repression	D-NC-NC	254227_at	A14g23630	reticulon family protein (RTNLB1) weak similarity to Nogo-C protein [Rattus norvegicus] GI:6822251; contains Pfam profile PF02453; Reticulon (68417.m03403)
191 (C) Internal Glu Repression	D-NC-NC	254159_at	A14g24240	WRKY family transcription factor contains Pfam profile: PF03108 WRKY DNA-binding domain (68417.m03478)
192 (C) Internal Glu Repression	D-NC-NC	254141_at	A14g24620	glucose-6-phosphate isomerase, putative similar to glucose-6-phosphate isomerase [Spinacia oleracea] GI:3413511; contains Pfam profile PF00342; glucose-6-phosphate isomerase (68417.m03528)
193 (C) Internal Glu Repression	D-NC-NC	254053_s_at	A14g25300	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to flavonol synthase [Petunia x hybrida]GI:311659; anthocyanidin synthase [Torenia toumieri]GI: 12583673; contains PF03171 2OG-Fe(II) oxygenase superfamily domain (68417.m03638)
194 (C) Internal Glu Repression	D-NC-NC	254021_at	A14g25650	Rieske [2Fe-2S] domain-containing protein similar to cell death suppressor protein lls1 from Zea mays [gi:1935909]; Rieske iron-sulfur protein Tc55 from Pisum sativum [gi:2784524]; contains Pfam PF00355 Rieske [2Fe-2S] domain (68417.m03693)
195 (C) Internal Glu Repression	D-NC-NC	253856_at	A14g28100	expressed protein (68417.m04031)
196 (C) Internal Glu Repression	D-NC-NC	253815_at	A14g28250	beta-expansin, putative (EXPB3) similar to soybean pollen allergen (cim1) protein - soybean, PIR2:S48032; beta-expansin gene family, PMID:11841069 (68417.m04047)
197 (C) Internal Glu Repression	D-NC-NC	253702_at	A14g29900	calcium-transporting ATPase, plasma membrane-type, putative / Ca2+-ATPase, putative (ACA10) identical to SPIQ85Z1 similar to SPIQ9LF79 Calcium-transporting ATPase 10, plasma membrane-type (EC 3.6.3.8) [Ca(2+)-ATPase isoform 10] [Arabidopsis thaliana]; (Arabidopsis thaliana) (68417.m04254)
198 (C) Internal Glu Repression	D-NC-NC	253628_at	A14g30280	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative [Arabidopsis thaliana] (68417.m04304)
199 (C) Internal Glu Repression	D-NC-NC	253631_at	A14g30440	similar to xyloglucan endotransglycosylase TCH4 GI:888116 from [Arabidopsis thaliana] (68417.m04304)
200 (C) Internal Glu Repression	D-NC-NC	253600_at	A14g30810	NAD-dependent epimerase/dehydratase family protein similar to nucleotide sugar epimerase from Vibrio vulnificus GI:3093975 [PFD3083975], WbNF [Escherichia coli] GI:5739472, CAPI protein [Staphylococcus aureus] SPIP39856; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family (68417.m04323)
201 (C) Internal Glu Repression	D-NC-NC	253551_at	A14g30998	serine carboxypeptidase S10 family protein similar to serine-type carboxypeptidase (SP-P55748) [Hordeum vulgare] (68417.m04365)
202 (C) Internal Glu Repression	D-NC-NC	253485_at	A14g31800	expressed protein (68417.m04401)
203 (C) Internal Glu Repression	D-NC-NC	253377_at	A14g33300	WRKY family transcription factor (68417.m04517)
204 (C) Internal Glu Repression	D-NC-NC	253357_at	A14g33400	disease resistance protein (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein. (68417.m04737)
205 (C) Internal Glu Repression	D-NC-NC	253351_at	A14g33700	dem protein-related / defective embryo and menisemus protein-related identical to dem GI:2190418 from [Lycopersicon esculentum] (68417.m04747)
206 (C) Internal Glu Repression	D-NC-NC	253300_at	A14g33580	CBS domain-containing protein contains Pfam profiles PF00571: CBS domain, PF01595: Domain of unknown function (68417.m04786)
207 (C) Internal Glu Repression	D-NC-NC	253308_at	A14g33680	carbonic anhydrase family protein / carbonate dehydratase family protein similar to SPIP46512 Carbonic anhydrase 1 (EC 4.2.1.1) [Carbonate dehydratase 1] (Flavaria linearis); contains Pfam profile PF00484: Carbonic anhydrase (68417.m04771)
208 (C) Internal Glu Repression	D-NC-NC	253276_at	A14g34050	aminotransferase class I and II family protein low similarity to Aromatic Aminotransferase from Pyrococcus horikoshii GI:14278621; contains Pfam profile PF00155 aminotransferase, class I and II (68417.m04784)
209 (C) Internal Glu Repression	D-NC-NC	253231_at	A14g34450	caffeoyl-CoA 3-O-methyltransferase, putative nearly identical to GI:2960356 [Populus balsamifera subsp. trichocarpa], GI:684942 [Medicago sativa subsp. sativa] isoform contains a GT-TG intron which removes an internal segment of the protein. (68417.m04831)
210 (C) Internal Glu Repression	D-NC-NC	253083_at	A14g36250	coatomer gamma-2 subunit, putative / gamma-2 coat protein, putative / gamma-2 COP, putative similar to SPIQ9UBF2 Coatomer gamma-2 subunit (Gamma-2 coat protein) (Gamma-2 COP) [Homo sapiens]; contains Pfam profile: PF01602 Adaptin N terminal region (68417.m04896)
211 (C) Internal Glu Repression	D-NC-NC	253024_at	A14g38080	aldehyde dehydrogenase family protein contains aldehyde dehydrogenase (NADP) family protein domain, Pfam:PF00171 (68417.m05156)
212 (C) Internal Glu Repression	D-NC-NC	252921_at	A14g39030	hydroxyproline-rich glycoprotein family protein contains proline-rich extensin domains, INTERPRO:IPR002965; Common family member: A14g22510 [Arabidopsis thaliana] (68417.m05378)
213 (C) Internal Glu Repression	D-NC-NC	252932_at	A14g39080	enhanced disease susceptibility 5 (EDS5) / salicylic acid induction deficient 1 (SID1) identical to SPIQ945F0; contains Pfam profile PF01554: Uncharacterized membrane protein family (68417.m05528)
214 (C) Internal Glu Repression	D-NC-NC	252943_at	A14g39330	vacuolar proton ATPase, putative similar to Swiss-Prot:Q93050 vacuolar proton translocating ATPase 116 kDa subunit A isoform 1 (Clathrin-coated vesicle/synaptic vesicle proton pump 116 kDa subunit, Vacuolar proton pump subunit 1, Vacuolar adenosine triphosphatase subunit Ac116) [Homo sapiens] (68417.m05534)
215 (C) Internal Glu Repression	D-NC-NC	252863_at	A14g39800	mammalian dehydrogenase, putative nearly identical to SPIP42734, probable mannitol dehydrogenase (68417.m05568)
216 (C) Internal Glu Repression	D-NC-NC	252852_at	A13g44720	inositol-3-phosphate synthase isozyme 1 / myo-inositol-1-phosphate synthase 1 / Mli-1-P synthase 1 / IPS 1 identical to SPIP42801 [Arabidopsis thaliana] (68417.m05637)
217 (C) Internal Glu Repression	D-NC-NC	252377_at	A13g47960	prephenate dehydratase family protein similar to bacterial PheA gene products (68416.m04813)

218	(C) Internal Glu Repression	D-NC-NC	252343_at	A13g48810	phosphoesterase family protein low similarity to SPIP85246 Phospholipase C 2 precursor (EC 3.1.4.3) [Mycobacterium tuberculosis]; contains Pfam profile PF04185: Phosphoesterase family (68416.m05307)
219	(C) Internal Glu Repression	D-NC-NC	252325_at	A13g48560	acetylcoA synthase, chloroplast / acetylcoA synthase (ALS) nearly identical to SPIP17597 AcetylcoA synthase, chloroplast precursor (EC 2.2.1.6, formerly EC 4.1.3.18) [Acetohydroxy-acid synthase] (ALS) [Arabidopsis thaliana]
220	(C) Internal Glu Repression	D-NC-NC	252272_at	A13g49670	leucine-rich repeat transmembrane protein kinase, putative CLAVATA1 receptor kinase, Arabidopsis thaliana, EMBL:ATU96879 (68416.m05302)
221	(C) Internal Glu Repression	D-NC-NC	252126_at	A13g50590	leucine-rich repeat transmembrane protein (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein, (68416.m05578)
222	(C) Internal Glu Repression	D-NC-NC	252045_at	A13g52450	U-box domain-containing protein similar to immediate-early fungal elicitor protein CMPG1 [Petrobasidium cispum] Gi:14582200; contains Pfam profile PF04564: U-box domain (68416.m05708)
223	(C) Internal Glu Repression	D-NC-NC	252058_at	A13g52470	harpin-induced family protein / HIN1 family protein / harpin-responsive family protein similar to harpin-induced protein hin1 (Gi:1619321) [Nicotiana tabacum] (68416.m05770)
224	(C) Internal Glu Repression	D-NC-NC	251954_at	A13g53670	expressed protein (68418.m05827)
225	(C) Internal Glu Repression	D-NC-NC	251922_at	A13g54030	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (68418.m05874)
226	(C) Internal Glu Repression	D-NC-NC	251855_at	A13g54690	sugar isomerase (SIS) domain-containing protein / CBS domain-containing protein similar to SPIQ47334 Polysialic acid capsule expression protein kpsF [Escherichia coli]; contains Pfam profiles PF01360: sugar isomerase (SIS) domain, PF00571: CBS domain (68416.m06051)
227	(C) Internal Glu Repression	D-NC-NC	251828_at	A13g55070	expressed protein (68416.m06116)
228	(C) Internal Glu Repression	D-NC-NC	251449_at	A13g59920	Rab GDP dissociation inhibitor (GDI2) identical to Rab GDP dissociation inhibitor AtGDI2 [Arabidopsis thaliana] Gi:2446881 (68416.m06887)
229	(C) Internal Glu Repression	D-NC-NC	251450_at	A13g60030	squamosa promoter-binding protein-like 12 (SPL12) identical to squamosa promoter binding protein-like 12 [Arabidopsis thaliana] Gi:6006395; contains Pfam profiles PF03110: SBP domain, PF00023: Ankyrin repeat (68416.m06704)
230	(C) Internal Glu Repression	D-NC-NC	251398_at	A13g60750	transketolase, putative strong similarity to transketolase 1 [Capsicum annuum] Gi:3559814; contains Pfam profiles PF02779: Transketolase, pyridine binding domain, PF02780: Transketolase, C-terminal domain, PF00456: Transketolase, thiamine diphosphate binding domain (68416.m06796)
231	(C) Internal Glu Repression	D-NC-NC	251310_at	A13g61150	homeobox-leucine zipper family protein / homeobox domain GLABRA2 like protein 1 (HD-GL2-1) similar to Anthocyaninless2 (ANL2) (GP:5702094) Arabidopsis thaliana, EMBL:AF077335 (68418.m06843)
232	(C) Internal Glu Repression	D-NC-NC	251200_at	A13g63010	expressed protein similar to PmC3 [Pinus radiata] Gi:5487873 (68418.m07078)
233	(C) Internal Glu Repression	D-NC-NC	251122_at	A15g01020	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (68418.m00004)
234	(C) Internal Glu Repression	D-NC-NC	251090_at	A15g01820	CBL-interacting protein kinase 14 (CIPK14) identical to CBL-interacting protein kinase 14 [Arabidopsis thaliana]
235	(C) Internal Glu Repression	D-NC-NC	251074_at	A15g01800	gi13249127/gbJAAK16988; contains Pfam profiles PF00069: Protein kinase domain and PF03822: NAF domain, identical to cDNA CBL-interacting protein kinase 14 (CIPK14) Gi:13249128 (68418.m00101)
236	(C) Internal Glu Repression	D-NC-NC	251020_at	A15g02270	saposin B domain-containing protein contains Pfam profiles: PF00028 eukaryotic asparaginyl protease, PF00469 surfactant protein B, PF05184 saposin-like type B, region 1 (68418.m00059)
237	(C) Internal Glu Repression	D-NC-NC	250926_at	A15g03555	ABC transporter family protein NBD-like protein POP, Arabidopsis thaliana, EMBL:AF127684 (68418.m00150)
238	(C) Internal Glu Repression	D-NC-NC	250738_at	A15g05730	permease cytosine/purines, uracil, thiamine, allantoin family (68418.m00313)
239	(C) Internal Glu Repression	D-NC-NC	250645_at	A15g06700	anthranilate synthase, alpha subunit, component 1-1 (ASA1) identical to SPIP32068 (68418.m00630)
240	(C) Internal Glu Repression	D-NC-NC	250183_at	A15g14540	expressed protein strong similarity to unknown protein (emb CA82953.1) (68418.m00757)
241	(C) Internal Glu Repression	D-NC-NC	250054_at	A15g17860	proline-rich family protein contains proline rich extensin domains, INTERPRO:IPR002965 (68418.m01704)
242	(C) Internal Glu Repression	D-NC-NC	249627_at	A15g37510	cation exchanger, putative (CAXT) contains similarity to SWISS-PROT:Q9HC58 NKX3, HUMAN Sodium/potassium/calcium exchanger 3 precursor (Homo sapiens), Cat2-Cation Antiporter (CaCA) Family member PMID:11500563 (68418.m02083)
243	(C) Internal Glu Repression	D-NC-NC	248599_at	A15g37990	NADH-ubiquinone dehydrogenase, mitochondrial, putative similar to NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial from Solanum tuberosum [SPIQ43844] (68418.m04517)
244	(C) Internal Glu Repression	D-NC-NC	249244_at	A15g42270	S-adenosyl-L-methionine:carboxyl methyltransferase family protein similar to defense-related protein cgs1 [Brassica carinata] Gi:14009292; caffeine synthase [Camellia sinensis] Gi:9987143; SAM, jasmonic acid carboxyl methyltransferase
245	(C) Internal Glu Repression	D-NC-NC	249247_at	A15g42310	[Gi:13676829] (68418.m04575)
246	(C) Internal Glu Repression	D-NC-NC	249152_s_at	A15g43370	FlH protease, putative similar to FlH protease Gi:13183728 from [Medicago sativa] (68418.m05145)
247	(C) Internal Glu Repression	D-NC-NC	248968_at	A15g45280	pentapeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat (68418.m05149)
248	(C) Internal Glu Repression	D-NC-NC	248697_at	A15g46370	inorganic phosphate transporter (PHT2) identical to inorganic phosphate transporter [Arabidopsis thaliana] Gi:2780348 (68418.m05301)
249	(C) Internal Glu Repression	D-NC-NC	248619_at	A15g49630	pectinacetylesterase, putative similar to pectinacetylesterase precursor Gi:1431628 from [Vigna radiata] (68418.m05558)
250	(C) Internal Glu Repression	D-NC-NC	248573_at	A15g49720	thioesterase family protein similar to SPIQ9R0X4 48 kDa acyl-CoA thioester hydrolase, mitochondrial precursor (EC 3.1.2.-) [Mus musculus]; contains Pfam profile PF03061: thioesterase family protein (68418.m05976)
251	(C) Internal Glu Repression	D-NC-NC	248263_at	A15g53370	amino acid permease 6 (AAP6) identical to amino acid permease 6 (AAP6) [Arabidopsis thaliana] Gi:1769887 (68418.m06141)
252	(C) Internal Glu Repression	D-NC-NC	248200_at	A15g54180	endo-1,4-beta-glucanase KORRIGAN (KOR) / cellulase (OR16pep) identical to endo-1,4-beta-D-glucanase KORRIGAN [Arabidopsis thaliana] Gi:3978258; similar to endo-1,4-beta-D-glucanase, cellulase Gi:5688613 from [Brassica napus]; identical to cDNA cellulase (OR16pep) Gi:1022806 (68418.m06157)
					pectinesterase family protein (68418.m06632)
					quercetin 3-O-methyltransferase 1 / flavonoid 3-O-methyltransferase 1 [Arabidopsis thaliana] Gi:2781394; SPIQ9FK25 Quercetin 3-O-methyltransferase 1 (EC 2.1.1.78) (AOMT1) (Flavonoid 3-O-methyltransferase 1) (Caffeic acid/5-hydroxyferulic acid O-methyltransferase) [Arabidopsis thaliana] (68418.m06744)

253 (C) Internal Glu Repression	D-NC-NC	248138_at	A15g54960	pyruvate decarboxylase, putative strong similarity to pyruvate decarboxylase 1 [Vitis vinifera] GI:10732844; contains InterPro entry IP000398; Pyruvate decarboxylase (68418.m06845)
254 (C) Internal Glu Repression	D-NC-NC	248034_at	A15g55910	protein kinase, putative contains protein kinase domain, Pfam:PF00069 (68418.m06872)
255 (C) Internal Glu Repression	D-NC-NC	248009_at	A15g56280	COP9 signalosome subunit 6 / CSN subunit 6 (CSN6A) identical to CSN complex subunit 6 [Arabidopsis thaliana] GI:18056665, COP9 complex subunit 6 [Arabidopsis thaliana] GI:18056663; contains Pfam profile PF01398; Mov34/MNP/PAD-1 family; identical to cDNA CSN complex subunit 6A (CSN6A) GI:18056664 (68418.m07024)
256 (C) Internal Glu Repression	D-NC-NC	247653_at	A15g58140	protein kinase family protein / non phototropic hypocotyl 1-like protein (NPL1) contains Pfam domains, PF00089; Protein kinase domain and PF00785; PAC motif; similar to SP-Q48963 Nonphototropic hypocotyl protein 1 (Phototropin) [Mouse-ear cross]
257 (C) Internal Glu Repression	D-NC-NC	247653_at	A15g59950	RNA and export factor-binding protein, putative (68418.m07517)
258 (C) Internal Glu Repression	D-NC-NC	247601_at	A15g60850	Dof-type zinc finger domain-containing protein similar to zinc finger protein OBP4 gi:5059396 from [Arabidopsis thaliana]; EMBL:AF155817 (68418.m07633)
259 (C) Internal Glu Repression	D-NC-NC	247304_at	A15g63850	amino acid transporter 4, putative (AAP4) identical to amino acid transporter Gi:608671 from [Arabidopsis thaliana]; (68418.m08015)
260 (C) Internal Glu Repression	D-NC-NC	247262_at	A15g64440	amidase family protein low similarity to enantiomerase-selective amidase [Rhodococcus sp.] GI:152052; contains Pfam profile PF01425; Amidase (68418.m08095)
261 (C) Internal Glu Repression	D-NC-NC	247152_at	A15g65620	peptidase M3 family protein / thimet oligopeptidase family protein similar to SPp27237 Oligopeptidase A (EC 3.4.24.70) (Salmonella typhimurium); contains Pfam profile PF01432; Peptidase family M3 (68418.m08255)
262 (C) Internal Glu Repression	D-NC-NC	246990_at	A15g67360	cucurbitin-like serine protease (ARA12) Asp48; almost identical to cucurbitin-like serine protease (ARA12) GI:3176874 from [Arabidopsis thaliana] (68418.m08494)
263 (C) Internal Glu Repression	D-NC-NC	246901_at	A15g25630	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535; PPR repeat (68418.m03050)
264 (C) Internal Glu Repression	D-NC-NC	246825_at	A15g26280	meprin and TRAF homology domain-containing protein / MATH domain-containing protein similar to ubiquitin-specific protease 12 [Arabidopsis thaliana] GI:1993471; contains Pfam profile PF00917; MATH domain (68418.m03133)
265 (C) Internal Glu Repression	D-NC-NC	246651_at	A15g35170	adenylate kinase family protein contains Pfam profile: PF00406 adenylate kinase (68418.m04168)
266 (C) Internal Glu Repression	D-NC-NC	246660_at	A15g35180	expressed protein (68418.m04169)
267 (C) Internal Glu Repression	D-NC-NC	246554_at	A15g15450	heat shock protein 100, putative / HSP100; putative / HSP100/CipB, putative similar to HSP100/CipB Gi:9651530 [Phaseolus lunatus] (68418.m01808)
268 (C) Internal Glu Repression	D-NC-NC	246366_at	A11g51850	leucine-rich repeat protein kinase, putative similar to light repressible receptor protein kinase [Arabidopsis thaliana] gi:1321686[emb]CAA66376 (68414.m05845)
269 (C) Internal Glu Repression	D-NC-NC	246228_at	A14g36430	peroxidase, putative identical to peroxidase [Arabidopsis thaliana] gi:6622093[emb]CAB71009; identical to cDNA class III peroxidase ATP31, GI:17530561 (68417.m05175)
270 (C) Internal Glu Repression	D-NC-NC	246247_at	A14g36640	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein similar to polyphosphoinositide binding protein Shp1p (P2739044) (Glycine max, SEC14 cytosolic factor (Phosphatidylinositolphosphatidylcholine transfer protein) (PUPCTP) (SP-P24859) [Kluyveromyces fragilis] and to SEC14 cytosolic factor (SP-P53989) [Candida glabrata] (68417.m05200)
271 (C) Internal Glu Repression	D-NC-NC	246185_at	A15g20980	5-methyltetrahydropteroylglutamate-homocysteine methyltransferase, putative / vitamin-B12-independent methionine synthase, putative / cobalamin-independent methionine synthase, putative strong similarity to SPIQ50008 5-methyltetrahydropteroylglutamate-homocysteine methyltransferase (EC 2.1.1.14) (Vitamin-B12-independent methionine synthase isozyme) (Cobalamin-independent methionine synthase isozyme) [Arabidopsis thaliana]; contains Pfam profile PF01717; Methionine synthase, vitamin-B12 independent (68418.m02494)
272 (C) Internal Glu Repression	D-NC-NC	246126_at	A15g20070	MutT/nudix family protein low similarity to SPIQ19427 NADH pyrophosphatase (EC 3.6.1.-) (Caenorhabditis elegans); contains Pfam profile PF00293; NUDIX domain (68418.m02390)
273 (C) Internal Glu Repression	D-NC-NC	246050_s_at	A15g28900	calcium-binding EF hand family protein contains Pfam profile: PF00036 EF hand (68418.m03562)
274 (C) Internal Glu Repression	D-NC-NC	245971_at	A15g20730	auxin-responsive factor (ARF7) identical to auxin response factor 7 Gi:4104929 from [Arabidopsis thaliana] (68418.m02462)
275 (C) Internal Glu Repression	D-NC-NC	245865_at	A15g09440	phosphate-responsive protein, putative similar to phi-1 (phosphate-induced gene) [Nicotiana tabacum] Gi:3759184; contains Pfam profile PF04874; Phosphate-induced protein 1 conserved region (68418.m01093)
276 (C) Internal Glu Repression	D-NC-NC	245875_at	A11g26240	proline-rich extensin-like family protein similar to hydroxyproline-rich glycoprotein precursor gi:727264[gb]AAA87802; contains proline-rich extensin domains, INTERPRO:IPR002965 (68414.m03201)
277 (C) Internal Glu Repression	D-NC-NC	245803_at	A11g47128	proline-rich extensin domains, INTERPRO:IPR002965 (68414.m03201)
278 (C) Internal Glu Repression	D-NC-NC	245780_at	A11g45688	cytosine proteinase (RD21A) / thiol protease identical to SPIP43297 Cysteine proteinase RD21A precursor (EC 3.4.22.-) (Arabidopsis thaliana), thiol protease RD21A SP-P43297 from [Arabidopsis thaliana] (68414.m05222)
279 (C) Internal Glu Repression	D-NC-NC	245759_at	A11g66900	expressed protein (68414.m07603)
280 (C) Internal Glu Repression	D-NC-NC	245612_at	A14g14440	enoyl-CoA hydratase/isomerase family protein low similarity to PhaB [Pseudomonas putida] GI:3253198; SPIP31551 Camitline racemase (Escherichia coli); contains Pfam profile PF00378 enoyl-CoA hydratase/isomerase family protein (68417.m02227)
281 (C) Internal Glu Repression	D-NC-NC	245270_at	A14g14960	tubulin alpha-6 chain (TUAB) nearly identical to SPIP29511 Tubulin alpha-6 chain (Arabidopsis thaliana) (68417.m02298)
282 (C) Internal Glu Repression	D-NC-NC	245218_s_at	A11g58942	expressed protein (68414.m07603)
283 (C) Internal Glu Repression	D-NC-NC	245201_at	A11g67840	ATP-binding region, ATPase-like domain-containing protein contains Pfam profile PF02518; ATPase, histidine kinase- DNA gyrase B-, and HSP90-like domain protein; similar to ESTs gblA965396.1, dbj AV557055.1, and dbj AV557055.1 (68414.m07743)
284 (C) Internal Glu Repression	D-NC-NC	245211_at	A15g12370	exocyst complex component Sec10-related low similarity to SPIQ00471 Exocyst complex component Sec10 (fSec10) (Homo sapiens) (68418.m01455)
285 (C) Internal Glu Repression	D-NC-NC	245101_at	A12g40890	cytochrome P450 98A3, putative (CYP98A3) identical to Cytochrome P450 98A3 (SPIQ22203) [Arabidopsis thaliana]; similar to gi:17978651 from Pinus taeda (68415.m05046)
286 (C) Internal Glu Repression	NC-H	267451_at	A12g33710	AP2 domain-containing transcription factor family protein similar to RAP2.6 (GI:17065542) [Arabidopsis thaliana] (68415.m04132)

287 (C) Internal Glu Repression	NC-H	267246_at	A12g30250	WRKY family transcription factor (88415.m03682)	WRKY family transcription factor (88415.m03682)
288 (C) Internal Glu Repression	NC-H	267261_at	A12g323120	expressed protein (88415.m02758)	touch-responsive protein / calmodulin-related protein 3, touch-induced (TCH3) identical to calmodulin-related protein 3, touch-induced SP:P25071 from [Arabidopsis thaliana] (88415.m05078)
289 (C) Internal Glu Repression	NC-H	267083_at	A12g41100	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (88415.m03653)	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (88415.m03653)
290 (C) Internal Glu Repression	NC-H	266832_at	A12g30040	serine/threonine protein kinase, putative similar to Pto kinase interact 1 (Pti1)[Lycopersicon esculentum]	serine/threonine protein kinase, putative similar to Pto kinase interact 1 (Pti1)[Lycopersicon esculentum]
291 (C) Internal Glu Repression	NC-H	266749_at	A12g47060	glutathione S-transferase (103-1A) identical to Swiss-Prot:P46421 glutathione S-transferase 103-1A [Arabidopsis thaliana] (88415.m03578)	glutathione S-transferase (103-1A) identical to Swiss-Prot:P46421 glutathione S-transferase 103-1A [Arabidopsis thaliana] (88415.m03578)
292 (C) Internal Glu Repression	NC-H	266299_at	A12g29450	aquaporin, putative similar to plasma membrane aquaporin 2b [Raphanus sativus] (88415.m04796)	aquaporin, putative similar to plasma membrane aquaporin 2b [Raphanus sativus] (88415.m04796)
293 (C) Internal Glu Repression	NC-H	266172_at	A12g39010	zinc finger (C2H2 type) family protein (ZAT1) contains Pfam domain, PF00096; Zinc finger, C2H2 type (88415.m04580)	zinc finger (C2H2 type) family protein (ZAT1) contains Pfam domain, PF00096; Zinc finger, C2H2 type (88415.m04580)
294 (C) Internal Glu Repression	NC-H	266010_at	A12g37430	expressed protein (88415.m03936)	expressed protein (88415.m03936)
295 (C) Internal Glu Repression	NC-H	265670_s_at	A12g32210	cold-acclimation protein, putative (FL3-SA3) similar to cold acclimation WCORA13-like protein gamma form [Hordeum vulgare] gll18449100[gb]AAL69988; similar to stress-regulated protein SAP1 [Xerophyta viscosa] gll2136037[gb]AAM47505; identical to cDNA cold acclimation protein WCORA13-like protein alpha form [G1:10121840, cold acclimation protein homolog [Arabidopsis thaliana] G1:1127595 (88415.m01828)	cold-acclimation protein, putative (FL3-SA3) similar to cold acclimation WCORA13-like protein gamma form [Hordeum vulgare] gll18449100[gb]AAL69988; similar to stress-regulated protein SAP1 [Xerophyta viscosa] gll2136037[gb]AAM47505; identical to cDNA cold acclimation protein WCORA13-like protein alpha form [G1:10121840, cold acclimation protein homolog [Arabidopsis thaliana] G1:1127595 (88415.m01828)
296 (C) Internal Glu Repression	NC-H	265480_at	A12g15970	calcium-binding protein, putative similar to EF-hand Ca2+-binding protein CCD1 [Triticum aestivum] G1:9255753 (88415.m05812)	calcium-binding protein, putative similar to EF-hand Ca2+-binding protein CCD1 [Triticum aestivum] G1:9255753 (88415.m05812)
297 (C) Internal Glu Repression	NC-H	265460_at	A12g46600	sugar transporter, putative similar to ERD8 protein [Arabidopsis thaliana] G1:3123712, sugar-porter family proteins 1 and 2 [Arabidopsis thaliana] G1:14585699, G1:14585701; contains Pfam profile PF00083; major facilitator superfamily protein (88414.m00992)	sugar transporter, putative similar to ERD8 protein [Arabidopsis thaliana] G1:3123712, sugar-porter family proteins 1 and 2 [Arabidopsis thaliana] G1:14585699, G1:14585701; contains Pfam profile PF00083; major facilitator superfamily protein (88414.m00992)
298 (C) Internal Glu Repression	NC-H	264652_at	A11g08920	leucine-rich repeat transmembrane protein kinase, putative (88415.m03895)	leucine-rich repeat transmembrane protein kinase, putative (88415.m03895)
299 (C) Internal Glu Repression	NC-H	263478_at	A12g31880	zinc finger (CCH-type) family protein contains Pfam domain, PF00642; Zinc finger C-x8-C-x5-C-x3-H type (and similar) and Pfam domain, PF00023; Ankyrin repeat (88415.m04837)	zinc finger (CCH-type) family protein contains Pfam domain, PF00642; Zinc finger C-x8-C-x5-C-x3-H type (and similar) and Pfam domain, PF00023; Ankyrin repeat (88415.m04837)
300 (C) Internal Glu Repression	NC-H	263379_at	A12g40140	galactinol synthase, putative similar to galactinol synthase, isoform Gols-1 [G1:5608497 from [Aruca reptans] (88415.m05892)	galactinol synthase, putative similar to galactinol synthase, isoform Gols-1 [G1:5608497 from [Aruca reptans] (88415.m05892)
301 (C) Internal Glu Repression	NC-H	263320_at	A12g47180	leucine-rich repeat transmembrane protein kinase, putative similar to receptor protein kinase G1:1389568 from [Arabidopsis thaliana] (88414.m08450)	leucine-rich repeat transmembrane protein kinase, putative similar to receptor protein kinase G1:1389568 from [Arabidopsis thaliana] (88414.m08450)
302 (C) Internal Glu Repression	NC-H	262360_at	A11g73080	nitrate reductase 2 (NR2) identical to SPLP11035 Nitrate reductase 2 (formerly EC 1.6.6.1) (NR2) [Arabidopsis thaliana] (88414.m04639)	nitrate reductase 2 (NR2) identical to SPLP11035 Nitrate reductase 2 (formerly EC 1.6.6.1) (NR2) [Arabidopsis thaliana] (88414.m04639)
303 (C) Internal Glu Repression	NC-H	261979_at	A11g37130	nitrate reductase 1 (NR1) identical to SPLP11832 Nitrate reductase 1 (formerly EC 1.6.6.1) (NR1)[Arabidopsis thaliana] (88414.m09053)	nitrate reductase 1 (NR1) identical to SPLP11832 Nitrate reductase 1 (formerly EC 1.6.6.1) (NR1)[Arabidopsis thaliana] (88414.m09053)
304 (C) Internal Glu Repression	NC-H	259681_at	A11g77760	gibberellin 2-oxidase, putative / GA2-oxidase, putative similar to GA2ox2 [G1:4878368]; similar to dioxygenase G1:1696096 from [Marah macrocarpa]; contains PF03171 ZOG-Fe(II) oxygenase superfamily protein (88414.m0186)	gibberellin 2-oxidase, putative / GA2-oxidase, putative similar to GA2ox2 [G1:4878368]; similar to dioxygenase G1:1696096 from [Marah macrocarpa]; contains PF03171 ZOG-Fe(II) oxygenase superfamily protein (88414.m0186)
305 (C) Internal Glu Repression	NC-H	259445_at	A11g02400	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097; Zinc finger, C3HC4 type (RING finger) expressed protein (88416.m01807)	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097; Zinc finger, C3HC4 type (RING finger) expressed protein (88416.m01807)
306 (C) Internal Glu Repression	NC-H	258436_at	A13g16720	disease resistance protein (TIR-NBS class), putative domain signature TIR-NBS exists, suggestive of a disease resistance protein, (88414.m07501)	disease resistance protein (TIR-NBS class), putative domain signature TIR-NBS exists, suggestive of a disease resistance protein, (88414.m07501)
307 (C) Internal Glu Repression	NC-H	258362_at	A13g14280	expressed protein (88417.m02387)	expressed protein (88417.m02387)
308 (C) Internal Glu Repression	NC-H	256526_at	A11g60090	WRKY family transcription factor contains Pfam profile: PF03108 WRKY DNA-binding domain (88417.m00184)	WRKY family transcription factor contains Pfam profile: PF03108 WRKY DNA-binding domain (88417.m00184)
309 (C) Internal Glu Repression	NC-H	256017_at	A11g19180	expressed protein (88417.m04241)	expressed protein (88417.m04241)
310 (C) Internal Glu Repression	NC-H	255588_at	A14g01250	cinnamoyl-CoA reductase-related similar to cinnamoyl-CoA reductase from Pinus taeda [G1:17978849], Saccharum officinarum (G1:3341511) (88417.m04326)	cinnamoyl-CoA reductase-related similar to cinnamoyl-CoA reductase from Pinus taeda [G1:17978849], Saccharum officinarum (G1:3341511) (88417.m04326)
311 (C) Internal Glu Repression	NC-H	253643_at	A14g29780	calmodulin-binding family protein contains Pfam profile PF00168; C2 domain (88417.m04846)	calmodulin-binding family protein contains Pfam profile PF00168; C2 domain (88417.m04846)
312 (C) Internal Glu Repression	NC-H	253638_at	A14g30470	gamma-glutamyltranspeptidase family protein similar to SPIP19440 Gamma-glutamyltranspeptidase 1 precursor (EC 2.3.2.2)	gamma-glutamyltranspeptidase family protein similar to SPIP19440 Gamma-glutamyltranspeptidase 1 precursor (EC 2.3.2.2)
313 (C) Internal Glu Repression	NC-H	253414_at	A14g33050	PF00168: C2 domain (88417.m04846)	PF00168: C2 domain (88417.m04846)
314 (C) Internal Glu Repression	NC-H	253284_at	A14g34150	(Gamma-glutamyltransferase 1) (CD224 antigen) (Homo sapiens), contains Pfam profile PF01018: Gamma-glutamyltranspeptidase (88417.m05602)	(Gamma-glutamyltransferase 1) (CD224 antigen) (Homo sapiens), contains Pfam profile PF01018: Gamma-glutamyltranspeptidase (88417.m05602)
315 (C) Internal Glu Repression	NC-H	252906_at	A14g39640	mitogen-activated protein kinase, putative / MAPK, putative (MPK3) identical to mitogen-activated protein kinase homolog (AAMPK3)[Arabidopsis thaliana] SWISS-PROT:Q39023; PMID:12119167 (88416.m04829)	mitogen-activated protein kinase, putative / MAPK, putative (MPK3) identical to mitogen-activated protein kinase homolog (AAMPK3)[Arabidopsis thaliana] SWISS-PROT:Q39023; PMID:12119167 (88416.m04829)
316 (C) Internal Glu Repression	NC-H	252592_at	A13g45640	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097; Zinc finger, C3HC4 type (RING finger) (88416.m05081)	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097; Zinc finger, C3HC4 type (RING finger) (88416.m05081)
317 (C) Internal Glu Repression	NC-H	252474_at	A13g46620	scarecrow transcription factor family protein scarecrow-like 11 - Arabidopsis thaliana, EMBL:AF036307 (88416.m05058)	scarecrow transcription factor family protein scarecrow-like 11 - Arabidopsis thaliana, EMBL:AF036307 (88416.m05058)
318 (C) Internal Glu Repression	NC-H	252463_at	A13g46600	expressed protein similar to PHAC3 [Pinus radiata] G1:5487873 (88416.m05317)	expressed protein similar to PHAC3 [Pinus radiata] G1:5487873 (88416.m05317)
319 (C) Internal Glu Repression	NC-H	252315_at	A13g46890	BON1-associated protein 1 (BAP1) identical to BON1-associated protein 1 [Arabidopsis thaliana] G1:15487384; contains Pfam profile PF00168; C2 domain; supporting cDNA gll15487383[gb]AY045765.1 (88416.m08846)	BON1-associated protein 1 (BAP1) identical to BON1-associated protein 1 [Arabidopsis thaliana] G1:15487384; contains Pfam profile PF00168; C2 domain; supporting cDNA gll15487383[gb]AY045765.1 (88416.m08846)
320 (C) Internal Glu Repression	NC-H	251336_at	A13g61190	homeobox-leucine zipper protein 12 (HB-12) / HD-ZIP transcription factor 12 identical to homeobox-leucine zipper protein ATHB-12 (G1:6899887) [Arabidopsis thaliana] (88416.m08951)	homeobox-leucine zipper protein 12 (HB-12) / HD-ZIP transcription factor 12 identical to homeobox-leucine zipper protein ATHB-12 (G1:6899887) [Arabidopsis thaliana] (88416.m08951)
321 (C) Internal Glu Repression	NC-H	251272_at	A13g61890	lectin protein kinase, putative similar to receptor lectin kinase 3 [Arabidopsis thaliana] gll4100060[gb]AAD00733; contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139 (88418.m00069)	lectin protein kinase, putative similar to receptor lectin kinase 3 [Arabidopsis thaliana] gll4100060[gb]AAD00733; contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139 (88418.m00069)
322 (C) Internal Glu Repression	NC-H	251054_at	A15g01540	harpin-induced family protein / HIN1 family protein / harpin-responsive family protein / NDR1/HIN1-like protein 3 similar to harpin-induced protein hin1 (G1:1819321)[Nicotiana tabacum] (88418.m00708)	harpin-induced family protein / HIN1 family protein / harpin-responsive family protein / NDR1/HIN1-like protein 3 similar to harpin-induced protein hin1 (G1:1819321)[Nicotiana tabacum] (88418.m00708)
323 (C) Internal Glu Repression	NC-H	250876_at	A15g06320	hydroxyproline-rich glycoprotein family protein contains proline-rich extensin domains, INTERPRO:IPR002965 (88418.m01101)	hydroxyproline-rich glycoprotein family protein contains proline-rich extensin domains, INTERPRO:IPR002965 (88418.m01101)
324 (C) Internal Glu Repression	NC-H	250541_at	A15g09520		

325 (C) Internal Glu Repression	NC-H	249818_at	A15g19240	expressed protein (68418.m02291)	expressed protein (68418.m02291)
326 (C) Internal Glu Repression	NC-H	249237_at	A15g20250	expressed protein similar to gda-1 (Plasium sativum) Gi:27654-18 (68418.m05118)	expressed protein similar to gda-1 (Plasium sativum) Gi:27654-18 (68418.m05118)
327 (C) Internal Glu Repression	NC-H	247708_at	A15g59550	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger) (68418.m07482)	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger) (68418.m07482)
328 (C) Internal Glu Repression	NC-H	247279_at	A15g64310	arabinogalactan-type (AGP1) identical to gi:3883120 gb:AAC77823 (68418.m08078)	arabinogalactan-type (AGP1) identical to gi:3883120 gb:AAC77823 (68418.m08078)
329 (C) Internal Glu Repression	NC-H	246982_s_at	A15g24800	bZIP transcription factor family protein contains Pfam profile, PF00170 bZIP transcription factor, identical to cDNA bZIP protein BZO242 Gi:10954098 (68418.m02928)	bZIP transcription factor family protein contains Pfam profile, PF00170 bZIP transcription factor, identical to cDNA bZIP protein BZO242 Gi:10954098 (68418.m02928)
330 (C) Internal Glu Repression	NC-H	246821_at	A15g26920	calmodulin-binding protein similar to calmodulin-binding protein TC800 Gi:1698548 from [Nicotiana tabacum] (68418.m03210)	calmodulin-binding protein similar to calmodulin-binding protein TC800 Gi:1698548 from [Nicotiana tabacum] (68418.m03210)
331 (C) Internal Glu Repression	NC-H	246288_at	A13g56880	VQ motif-containing protein contains PF05678: VQ motif (68416.m06327)	VQ motif-containing protein contains PF05678: VQ motif (68416.m06327)
332 (C) Internal Glu Repression	NC-H	245904_at	A15g11110	sucrose-phosphate synthase, putative similar to sucrose-phosphate synthase isoform 1, Citrus unshiu, PIR:S72648 (68418.m01297)	sucrose-phosphate synthase, putative similar to sucrose-phosphate synthase isoform 1, Citrus unshiu, PIR:S72648 (68418.m01297)
333 (C) Internal Glu Repression	NC-H	245051_at	A12g23320	WRKY family transcription factor identical to WRKY DNA-binding protein 15 Gi:13508742 from [Arabidopsis thaliana] (68415.m02784)	WRKY family transcription factor identical to WRKY DNA-binding protein 15 Gi:13508742 from [Arabidopsis thaliana] (68415.m02784)
334 (C) Internal Glu Repression	NC-H	245041_at	A12g26530	expressed protein (68415.m03183)	expressed protein (68415.m03183)
1 (D) External Glu induction	NC-NC-I	266371_at	A12g41410	calmodulin, putative identical to SPIP30168 Calmodulin-like protein [Arabidopsis thaliana] (68415.m05110)	calmodulin, putative identical to SPIP30168 Calmodulin-like protein [Arabidopsis thaliana] (68415.m05110)
2 (D) External Glu induction	NC-NC-I	266116_at	A12g02180	tobamovirus multiplication protein 3 (TOM3) identical to tobamovirus multiplication protein (TOM3) Gi:15425641 from [Arabidopsis thaliana] (68415.m00154)	tobamovirus multiplication protein 3 (TOM3) identical to tobamovirus multiplication protein (TOM3) Gi:15425641 from [Arabidopsis thaliana] (68415.m00154)
3 (D) External Glu induction	NC-NC-I	264415_at	A11g43160	AP2 domain-containing protein RAP2.6 (RAP2.6) identical to AP2 domain containing protein RAP2.6 Gi:2281637 from [Arabidopsis thaliana] (68414.m04973)	AP2 domain-containing protein RAP2.6 (RAP2.6) identical to AP2 domain containing protein RAP2.6 Gi:2281637 from [Arabidopsis thaliana] (68414.m04973)
4 (D) External Glu induction	NC-NC-I	263901_at	A12g36320	zinc finger (AN1-like) family protein contains Pfam domain, PF01428: AN1-like Zinc finger (68415.m04458)	zinc finger (AN1-like) family protein contains Pfam domain, PF01428: AN1-like Zinc finger (68415.m04458)
5 (D) External Glu induction	NC-NC-I	263228_at	A11g30700	FAD-binding domain-containing protein similar to SPIP30988 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (tetrahydroprotoberberine synthase) [Eschscholzia californica]; contains PF01565 FAD binding domain (68414.m03753)	FAD-binding domain-containing protein similar to SPIP30988 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (tetrahydroprotoberberine synthase) [Eschscholzia californica]; contains PF01565 FAD binding domain (68414.m03753)
6 (D) External Glu induction	NC-NC-I	262901_at	A11g59910	formin homology 2 domain-containing protein / FH2 domain-containing protein contains formin homology 2 domain, Pfam:PF02128 (68414.m06749)	formin homology 2 domain-containing protein / FH2 domain-containing protein contains formin homology 2 domain, Pfam:PF02128 (68414.m06749)
7 (D) External Glu induction	NC-NC-I	262887_at	A11g14780	expressed protein (68414.m01787)	expressed protein (68414.m01787)
8 (D) External Glu induction	NC-NC-I	262677_at	A11g75860	expressed protein (68414.m08811)	expressed protein (68414.m08811)
9 (D) External Glu induction	NC-NC-I	262496_at	A11g21790	expressed protein (68414.m02727)	expressed protein (68414.m02727)
10 (D) External Glu induction	NC-NC-I	262383_at	A11g72940	disease resistance protein (TIR-NBS class), putative domain signature TIR-NBS exists, suggestive of a disease resistance protein. (68414.m08436)	disease resistance protein (TIR-NBS class), putative domain signature TIR-NBS exists, suggestive of a disease resistance protein. (68414.m08436)
11 (D) External Glu induction	NC-NC-I	262166_at	A11g74840	myb family transcription factor similar to myb-related transcription activator Gi:927917 from [Arabidopsis thaliana] (68414.m08672)	myb family transcription factor similar to myb-related transcription activator Gi:927917 from [Arabidopsis thaliana] (68414.m08672)
12 (D) External Glu induction	NC-NC-I	262133_at	A11g78000	sulfate transporter (Sutr1.2) identical to sulfate transporter Sutr1.2 [Arabidopsis thaliana] Gi:7768860, contains Pfam profiles PF00916: Sulfate transporter family and PF01740: STAS domain; contains TIGRfam profile TIGR00815: sulfate permease (68414.m09089)	sulfate transporter (Sutr1.2) identical to sulfate transporter Sutr1.2 [Arabidopsis thaliana] Gi:7768860, contains Pfam profiles PF00916: Sulfate transporter family and PF01740: STAS domain; contains TIGRfam profile TIGR00815: sulfate permease (68414.m09089)
13 (D) External Glu induction	NC-NC-I	261211_at	A11g12780	UDP-glucose 4-epimerase / UDP-glucose 4-epimerase (Galactowaldenase identical to SPIQ42605 [GB:CAA00941] from [Arabidopsis thaliana] (Arch. Biochem. Biophys. 327 (1), 27-34 (1996)) (68414.m01484)	UDP-glucose 4-epimerase / UDP-glucose 4-epimerase (Galactowaldenase identical to SPIQ42605 [GB:CAA00941] from [Arabidopsis thaliana] (Arch. Biochem. Biophys. 327 (1), 27-34 (1996)) (68414.m01484)
14 (D) External Glu induction	NC-NC-I	260556_at	A12g43620	chitinase, putative similar to basic endochitinase CHB4 precursor SP:Q06209 from [Brassica napus] (68415.m05422)	chitinase, putative similar to basic endochitinase CHB4 precursor SP:Q06209 from [Brassica napus] (68415.m05422)
15 (D) External Glu induction	NC-NC-I	259977_at	A11g76590	zinc-binding family protein similar to zinc-binding protein [Plasium sativum] Gi:16117799, contains Pfam profile PF04640: Protein of unknown function, DUF597 (68414.m08912)	zinc-binding family protein similar to zinc-binding protein [Plasium sativum] Gi:16117799, contains Pfam profile PF04640: Protein of unknown function, DUF597 (68414.m08912)
16 (D) External Glu induction	NC-NC-I	258805_at	A13g04010	glycosyl hydrolase family 17 protein similar to beta-1,3-glucanase GB:S12402 [Nicotiana sp], GB:CAA03908 [Citrus sinensis], GB:S44364 [Lycopersicon esculentum] (68418.m00422)	glycosyl hydrolase family 17 protein similar to beta-1,3-glucanase GB:S12402 [Nicotiana sp], GB:CAA03908 [Citrus sinensis], GB:S44364 [Lycopersicon esculentum] (68418.m00422)
17 (D) External Glu induction	NC-NC-I	258751_at	A13g05890	hydrophobic protein (RC12B) / low temperature and salt responsive protein (LTI6B) identical to SPIQ8ZNS8 Hydrophobic protein RC12B (Low temperature and salt responsive protein LTI6B) (Arabidopsis thaliana) (68418.m00682)	hydrophobic protein (RC12B) / low temperature and salt responsive protein (LTI6B) identical to SPIQ8ZNS8 Hydrophobic protein RC12B (Low temperature and salt responsive protein LTI6B) (Arabidopsis thaliana) (68418.m00682)
18 (D) External Glu induction	NC-NC-I	257087_at	A13g20500	calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase (68416.m02598)	calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase (68416.m02598)
19 (D) External Glu induction	NC-NC-I	256417_s_at	A13g11170	omega-3 fatty acid desaturase, chloroplast (FAD7) (FAD7) identical to omega-3 fatty acid desaturase, chloroplast precursor SP:P46310 [Arabidopsis thaliana] (Mouse-ear cross); identical to Pfam profile PF00487: Fatty acid desaturase; identical to cDNA plasid fatty acid desaturase Gi:809491 (68416.m01355)	omega-3 fatty acid desaturase, chloroplast (FAD7) (FAD7) identical to omega-3 fatty acid desaturase, chloroplast precursor SP:P46310 [Arabidopsis thaliana] (Mouse-ear cross); identical to Pfam profile PF00487: Fatty acid desaturase; identical to cDNA plasid fatty acid desaturase Gi:809491 (68416.m01355)
20 (D) External Glu induction	NC-NC-I	256185_at	A11g51700	Ded-type zinc finger domain-containing protein (ADOE1) identical to cDNA adof1 mRNA for ded zinc finger protein, Gi:3608260; contains Pfam profile PF02701: Dof domain, zinc finger (68414.m05626)	Ded-type zinc finger domain-containing protein (ADOE1) identical to cDNA adof1 mRNA for ded zinc finger protein, Gi:3608260; contains Pfam profile PF02701: Dof domain, zinc finger (68414.m05626)
21 (D) External Glu induction	NC-NC-I	254850_at	A14g12000	expressed protein (68417.m01909)	expressed protein (68417.m01909)
22 (D) External Glu induction	NC-NC-I	254667_at	A14g18280	glycine-rich cell wall protein-related glycine-rich protein 1.0 precursor, Phaeodolus vulgaris, PIR1:S01821 (68417.m02713)	glycine-rich cell wall protein-related glycine-rich protein 1.0 precursor, Phaeodolus vulgaris, PIR1:S01821 (68417.m02713)
23 (D) External Glu induction	NC-NC-I	252268_at	A13g48520	Cytochrome P450 family protein similar to Cytochrome P450 94A1 (P450-dependent fatty acid omega-hydroxylase) (SP:Q81117) (Vicia sativa); contains Pfam profile: PF00087 cytochrome P450 (68416.m05298)	Cytochrome P450 family protein similar to Cytochrome P450 94A1 (P450-dependent fatty acid omega-hydroxylase) (SP:Q81117) (Vicia sativa); contains Pfam profile: PF00087 cytochrome P450 (68416.m05298)
24 (D) External Glu induction	NC-NC-I	252291_s_at	A13g49120	peroxidase, putative identical to peroxidase [Arabidopsis thaliana] gi405611 (lembiCAA50877 (68418.m05386)	peroxidase, putative identical to peroxidase [Arabidopsis thaliana] gi405611 (lembiCAA50877 (68418.m05386)
25 (D) External Glu induction	NC-NC-I	252040_at	A13g52060	expressed protein contains Pfam profile PF03287: Arabidopsis protein of unknown function, DUF266 (68416.m05711)	expressed protein contains Pfam profile PF03287: Arabidopsis protein of unknown function, DUF266 (68416.m05711)
26 (D) External Glu induction	NC-NC-I	250793_at	A15g05600	oxido-reductase, 2OG-Fe(II) oxygenase family protein similar to flavonol synthase [Citrus unshiu] gi:4126403, leucoanthocyanidin dioxygenase [Daucus carota] gi:5924383; contains PF03171 2OG-Fe(II) oxygenase superfamily domain (68418.m00609)	oxido-reductase, 2OG-Fe(II) oxygenase family protein similar to flavonol synthase [Citrus unshiu] gi:4126403, leucoanthocyanidin dioxygenase [Daucus carota] gi:5924383; contains PF03171 2OG-Fe(II) oxygenase superfamily domain (68418.m00609)
27 (D) External Glu induction	NC-NC-I	250260_at	A15g13810	glutaredoxin family protein (68418.m01613)	glutaredoxin family protein (68418.m01613)
28 (D) External Glu induction	NC-NC-I	249889_at	A15g22540	expressed protein contains Pfam profile PF03140: Plant protein of unknown function (68418.m02630)	expressed protein contains Pfam profile PF03140: Plant protein of unknown function (68418.m02630)
29 (D) External Glu induction	NC-NC-I	248870_at	A15g48710	zinc-binding family protein similar zinc-binding protein [Plasium sativum] Gi:16117799; contains Pfam profile PF04640: Protein of unknown function, DUF597 (68418.m05755)	zinc-binding family protein similar zinc-binding protein [Plasium sativum] Gi:16117799; contains Pfam profile PF04640: Protein of unknown function, DUF597 (68418.m05755)
30 (D) External Glu induction	NC-NC-I	248189_at	A15g54170	expressed protein weak similarity to SPIQ8UKL8 Phosphatidylcholine transfer protein (PC-TP) [Homo sapiens] (68418.m06745)	expressed protein weak similarity to SPIQ8UKL8 Phosphatidylcholine transfer protein (PC-TP) [Homo sapiens] (68418.m06745)

31 (D) External Gu induction	NC-NC-I	247706_at	A15g59480	haloacid dehalogenase-like hydrolase family protein low similarity to SPIP53078 SSM1 protein (Saccharomyces cerevisiae); contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase (88418, m07454)
32 (D) External Gu induction	NC-NC-I	246481_s_at	A15g15960	stress-responsive protein (KIN1) / stress-induced protein (KIN1) identical to SPIP18812 Stress-induced KIN1 protein (Arabidopsis thaliana) (88418, m01866)
33 (D) External Gu induction	NC-NC-I	246488_at	A15g16010	3-oxo-5-alpha-steroid 4-dehydrogenase family protein / steroid 5-alpha-reductase family protein similar to steroid 5-alpha-reductase . Rattus norvegicus, PIR:A34239 [SPI24008]; contains Pfam 3-oxo-5-alpha-steroid 4-dehydrogenase domain PF02544 (88418, m01872)
34 (D) External Gu induction	NC-NC-I	246253_at	A14g37260	mvp family transcription factor (MYB73) contains Pfam profile: PF00249 mvp-like DNA-binding domain (88417, m05274)
35 (D) External Gu induction	NC-NC-I	246097_at	A15g20270	expressed protein contains Pfam domain, PF03006: Uncharacterised protein family (Hly-III / UPF0073) (88418, m02413)
36 (D) External Gu induction	NC-NC-I	245781_at	A11g45976	expressed protein (88414, m05206)
37 (D) External Gu induction	NC-NC-I	245244_at	A11g44350	IAA-amino acid hydrolase 6, putative (ILL6) / IAA-Ala hydrolase, putative virtually identical to gr1-protein from [Arabidopsis thaliana] GI:3559811; similar to IAA-amino acid hydrolase GI:3421384 from [Arabidopsis thaliana]; contains TIGRfam profile TIGR01891: amidohydrolase; contains Pfam profile PF01546: Peptidase family M20M25M40; identical to cDNA IAA-amino acid conjugate hydrolase-like protein (ILL6), partial cds GI:1797837 (88414, m05110)
38 (D) External Gu repression	NC-NC-D	267130_at	A12g23390	expressed protein (88415, m02793)
39 (D) External Gu repression	NC-NC-D	267050_at	A12g41060	RNA recognition motif (RRM)-containing protein similar to UBP1 interacting protein 1a [Arabidopsis thaliana] GI:19574236; contains InterPro entry IPR005004: RNA-binding region RNP-1 (RNA recognition motif) (RRM) (88415, m05070)
40 (D) External Gu repression	NC-NC-D	266957_at	A12g34840	expressed protein (88415, m04255)
41 (D) External Gu repression	NC-NC-D	266856_at	A12g26910	ABC transporter family protein similar to PDRE-like ABC transporter GI:1514643 from [Spirodela polyrhiza] (88415, m03228)
42 (D) External Gu repression	NC-NC-D	266709_at	A12g03120	signal peptide peptidase family protein contains Pfam domain PF04258: Membrane protein of unknown function (DUF435) (88415, m00265)
43 (D) External Gu repression	NC-NC-D	266395_at	A12g43100	aconitase C-terminal domain-containing protein contains Pfam profile PF00694: Aconitase C-terminal domain (88415, m05350)
44 (D) External Gu repression	NC-NC-D	266215_at	A12g06850	xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (EXT) (EXGT-A1) identical to endo-xyloglucan transferase (ext) GI:469484 and endoxyloglucan transferase (EXGT-A1) GI:5533309 from [Arabidopsis thaliana] (88415, m00767)
45 (D) External Gu repression	NC-NC-D	266093_at	A12g37990	ribosome biogenesis regulatory protein (RRS1) family protein contains Pfam profile PF04839: Ribosome biogenesis regulatory protein (RRS1); similar to Ribosome biogenesis regulatory protein homolog (Swiss-Prot Q15050) [Homo sapiens] (88415, m04663)
46 (D) External Gu repression	NC-NC-D	264738_at	A11g62250	expressed protein (88414, m07022)
47 (D) External Gu repression	NC-NC-D	264360_at	A11g03310	isoamylase, putative / starch debranching enzyme, putative similar to isoamylase isoform 2 [Solanum tuberosum] GI:27728147, isoamylase from [Triticum aestivum] GI:17932898, [Hordeum vulgare] GI:21314275, [Oryza sativa] GI:3252704; contains Pfam profiles PF00128: Alpha amylase catalytic domain, PF02922: isoamylase N-terminal domain, EST's g0H36690, g0AA712462, g0IAA651230 and g0IN95932 come from this gene (88414, m00309)
48 (D) External Gu repression	NC-NC-D	263957_at	A12g35880	expressed protein (88415, m04405)
49 (D) External Gu repression	NC-NC-D	263924_at	A12g36530	enolase identical to SWISS-PROT:P25696 enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase)[C-phospho-D- glycerate hydro lyase] [Arabidopsis thaliana] (88415, m04481)
50 (D) External Gu repression	NC-NC-D	263714_at	A12g20610	aminotransferase, putative similar to nicotianamine aminotransferase from Hordeum vulgare [GI:6498122, GI:6460087]; contains Pfam profile PF00155 aminotransferase, classes I and II (88415, m02411)
51 (D) External Gu repression	NC-NC-D	263477_at	A12g31790	UDP-glucuronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase (88415, m03881)
52 (D) External Gu repression	NC-NC-D	262947_at	A11g75750	gibberellin-regulated protein 1 (GASA1) / gibberellin-responsive protein 1 identical to SPIP46889 Gibberellin-regulated protein 1 precursor (Arabidopsis thaliana); supporting cDNA g0887938[g011766, 1]ATU11766 (88414, m08798)
53 (D) External Gu repression	NC-NC-D	262840_at	A11g14900	high-mobility-group protein / HMG-IY protein nearly identical to high-mobility-group protein HMGI-Y protein (Arabidopsis thaliana) GI:1429211; contains Pfam profiles PF00538: linker histone H1 and H5 family, PF02178: AT hook motif (88414, m01781)
54 (D) External Gu repression	NC-NC-D	262433_s_at	A11g47500	RNA-binding protein 47 (RBP47), putative similar to DNA binding protein GI:1899187 from [Nicotiana tabacum] (88414, m05272)
55 (D) External Gu repression	NC-NC-D	262274_at	A11g68720	cytidine/deoxycytidylate deaminase family protein contains Pfam profile PF00383: Cytidine and deoxycytidylate deaminase zinc-binding region (88414, m07851)
56 (D) External Gu repression	NC-NC-D	262094_at	A11g58110	nucleolar protein Nop56, putative similar to Xnop56 protein [Xenopus laevis] GI:14799394; contains Pfam profile PF01798: Putative snRNA binding domain (88414, m06443)
57 (D) External Gu repression	NC-NC-D	261859_at	A11g50490	ubiquitin-conjugating enzyme 20 (UBC20) nearly identical to ubiquitin-conjugating enzyme UBC20 (Arabidopsis thaliana) GI:22530867; contains Pfam profile PF00178: Ubiquitin-conjugating enzyme (88414, m05662)
58 (D) External Gu repression	NC-NC-D	261603_at	A11g49600	RNA-binding protein 47 (RBP47), putative similar to DNA binding protein ACBF GB:UB0212 GI:1899187 from [Nicotiana tabacum] (88414, m05561)
59 (D) External Gu repression	NC-NC-D	261350_at	A11g79770	expressed protein (88414, m09308)
60 (D) External Gu repression	NC-NC-D	260967_at	A11g12230	transaldolase, putative similar to Swiss-Prot:P30148 transaldolase B (EC 2.2.1.2) [Escherichia coli Q157.H7] (88414, m01415)
61 (D) External Gu repression	NC-NC-D	260830_at	A11g08760	histone H1, putative similar to histone H1-1 GB:CAA44312 GI:16314 from [Arabidopsis thaliana]; identical to cDNA H1-1C mRNA for histone H1-1 (partial) GI:732560 (88414, m00718)
62 (D) External Gu repression	NC-NC-D	260637_at	A11g62380	1-aminocyclopropane-1-carboxylate oxidase, putative / ACC oxidase, putative nearly identical to ACC oxidase (ACC ox1) GI:587086 from [Brassica oleracea] (88414, m07038)
63 (D) External Gu repression	NC-NC-D	260615_at	A11g53240	malate dehydrogenase [NAD], mitochondrial identical to mitochondrial NAD-dependent malate dehydrogenase GI:3928649 SPI082P06 from [Arabidopsis thaliana]; contains InterPro entry IPR001236: Lactate/malate dehydrogenase (88414, m06033)

64 (D) External Glu repression	NC-NC-D	A11g51510	RNA-binding protein, putative similar to RNA-binding protein 8 (Ribbonucleoprotein RBM8) SP-Q9YSS9 from [Homo sapiens], RNA-binding protein Y14 [Xenopus laevis] Gi:11034807, contains InterPro entry IPR00504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) (68414.m05797)
65 (D) External Glu repression	NC-NC-D	A11g74090	sulfotransferase family protein similar to SPIP52837 Flavonol 4'-sulfotransferase (EC 2.8.2.-) (F4-ST) [Flavaria chloraeifolia]; contains Pfam profile PF00685: Sulfotransferase domain (68414.m05811)
66 (D) External Glu repression	NC-NC-D	A11g69420	zinc finger (DHH type) family protein contains Pfam profile: PF01529: DHHC zinc finger domain (68414.m07874)
67 (D) External Glu repression	NC-NC-D	A11g80560	3-isopropylmalate dehydrogenase, chloroplast, putative strong similarity to 3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR GB:P29102 SPIP29102 from [Brassica napus] (68414.m09445)
68 (D) External Glu repression	NC-NC-D	A13g16370	GDSL-motif lipase/hydrolase family protein similar to family II lipases EXL3 Gi:15054388, EXL1 Gi:15054382, EXL2 Gi:15054384 from [Arabidopsis thaliana], contains Pfam profile: PF00657: Lipase Acylhydrolase with GDSL-like motif (68416.m02071)
69 (D) External Glu repression	NC-NC-D	A13g16390	jacalin lectin family protein similar to myosinase-binding protein homolog [Arabidopsis thaliana] Gi:2987787, epithiospecifier [Arabidopsis thaliana] Gi:16118845, contains Pfam profiles PF01418 jacalin-like lectin family, PF01344 Kelch motif (68416.m02075)
70 (D) External Glu repression	NC-NC-D	A13g10520	non-symbiotic hemoglobin 2 (HB2) (GLB2) identical to SPI024521 Non-symbiotic hemoglobin 2 (Hb2) (ARATH GLB2) [Arabidopsis thaliana] (68416.m01262)
71 (D) External Glu repression	NC-NC-D	A13g06680	60S ribosomal protein L29 (RPL29B) similar to 60S ribosomal protein L29 GB:P25868 from [Rattus norvegicus] (68416.m00788)
72 (D) External Glu repression	NC-NC-D	A13g13930	dihydrolipamide S-acyltransferase, putative similar to dihydrolipamide S-acyltransferase [Zea mays] Gi:5669871; contains Pfam profiles PF00198: 2-oxo acid dehydrogenases acyltransferase (catalytic domain), PF00364: Biotin-requiring enzyme, PF02817: e3 binding domain (68416.m01759)
73 (D) External Glu repression	NC-NC-D	A13g25230	peptidyl-prolyl cis-trans isomerase / FK506-binding protein (ROF1) identical to rotamase FKBP (ROF1) GB:U49453 [Arabidopsis thaliana] [Mol. Gen. Genet. 252 (5): 510-517 (1996)] (68416.m03152)
74 (D) External Glu repression	NC-NC-D	A13g29250	short-chain dehydrogenase/reductase (SDR) family protein similar to 3-beta-hydroxysteroiddehydrogenase Gi:15983819 from [Digitalis lanata], contains Pfam profile: PF00108 short chain dehydrogenase (68416.m03670)
75 (D) External Glu repression	NC-NC-D	A13g28570	phosphate transporter family protein contains Pfam profile: PF01384 phosphate transporter family (68416.m03316)
76 (D) External Glu repression	NC-NC-D	A13g27190	uracil phosphoribosyltransferase, putative / UMP pyrophosphorylase, putative / UPR1ase, putative similar to SPI065563 Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase) [Arabidopsis thaliana]; contains Pfam profile PF00485: Phosphoribulokinase / Uridine kinase family (68416.m03400)
77 (D) External Glu repression	NC-NC-D	A13g20050	T-complex protein 1 alpha subunit / TCP-1 alpha / chaperonin (CCT1) identical to SWISS-PROT:P28769: T-complex protein 1, alpha subunit (TCP-1-alpha) [Arabidopsis thaliana] (68416.m02538)
78 (D) External Glu repression	NC-NC-D	A13g20000	porin family protein low similarity to haymaker protein [Mus musculus] Gi:17834088, mitochondrial outer membrane protein MOM35 [Mus musculus] Gi:0650562; contains Pfam profile PF01459: Eukaryotic porin (68416.m02530)
79 (D) External Glu repression	NC-NC-D	A13g14840	leucine-rich repeat family protein / protein kinase family protein contains Pfam domains PF00560: Leucine Rich Repeat and PF00088: Protein kinase domain; contains 2 predicted transmembrane domains (68416.m01874)
80 (D) External Glu repression	NC-NC-D	A11g72040	deoxynucleoside kinase family contains Pfam profile: PF01712 deoxynucleoside kinase (68414.m08327)
81 (D) External Glu repression	NC-NC-D	A11g69530	expansin, putative (EXP1) identical to expansin (At-EXP1) [Arabidopsis thaliana] Gi:1041702; alpha-expansin gene family, PMID:11641069 (68414.m07983)
82 (D) External Glu repression	NC-NC-D	A11g18080	WD-40 repeat family protein / auxin-dependent protein (ARCA) / guanine nucleotide-binding protein beta subunit, putative identical to SPI024456 Guanine nucleotide-binding protein beta subunit-like protein (WD-40 repeat auxin-dependent protein ARCA) [Arabidopsis thaliana]; contains 7 WD-40 repeats (PF00400) (68414.m02238)
83 (D) External Glu repression	NC-NC-D	A11g19870	calmodulin-binding family protein contains Pfam profile: PF00612 IQ calmodulin-binding motif (68414.m02492)
84 (D) External Glu repression	NC-NC-D	A14g02510	chloroplast outer membrane protein, putative similar to chloroplast protein import component Toc159 [Pisum sativum] Gi:8489806, chloroplast outer envelope protein 86 [Pisum sativum] Gi:599958, GTP-binding protein [Pisum sativum] Gi:576509 (68417.m00343)
85 (D) External Glu repression	NC-NC-D	A14g09720	Ras-related GTP-binding protein, putative similar to GTP-binding protein RAB7A from [Lotus japonica] (68417.m01598)
86 (D) External Glu repression	NC-NC-D	A14g10320	isoleucyl-tRNA synthetase, putative / isoleucine-tRNA ligase, putative similar to SPIp41252 isoleucyl-tRNA synthetase, cytoplasmic (EC 6.1.1.5) (isoleucine-tRNA ligase) (IleRS) (IRS) [Homo sapiens]; contains Pfam profile PF00133: tRNA synthetases class I (L, M and V) (68417.m01687)
87 (D) External Glu repression	NC-NC-D	A14g10480	nascent polypeptide associated complex alpha chain protein, putative / alpha-NAC, putative similar to alpha-NAC, non-muscle form [Mus musculus] Gi:1666690; contains Pfam profiles PF01848: NAC domain, PF00627: UBA/TS-N domain (68417.m01720)
88 (D) External Glu repression	NC-NC-D	A14g12230	esterase/lipase/thioesterase family protein low similarity to 2-hydroxy-6-ketono-2,4-dienedioic acid hydrolase, OtpC [Rhodococcus sp.] Gi:8926386; contains InterPro entry IPR000378 (68417.m01940)
89 (D) External Glu repression	NC-NC-D	A14g13770	cytochrome P450 family protein (68417.m02136)
90 (D) External Glu repression	NC-NC-D	A14g18970	GDSL-motif lipase/hydrolase family protein similar to family II lipases EXL3 Gi:15054388, EXL1 Gi:15054382, EXL2 Gi:15054384 from [Arabidopsis thaliana], contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase (68417.m02794)
91 (D) External Glu repression	NC-NC-D	A14g21620	glycine-rich protein (68417.m03134)
92 (D) External Glu repression	NC-NC-D	A14g25630	fibillarin 2 (FIB2) identical to fibillarin 2 Gi:9965655 from [Arabidopsis thaliana] (68417.m03691)
93 (D) External Glu repression	NC-NC-D	A14g28450	transducin family protein / WD-40 repeat family protein, SOF1 involved in RNA processing (68417.m04071)
94 (D) External Glu repression	NC-NC-D	A14g30270	MER1-5 protein (MER1-5) (MER15B) / endo-xyloglucan transferase / xyloglucan endo-1,4-beta-D-glucanase (SEN4) identical to endo-xyloglucan transferase gi:944810, SPIP24806 MER1-5 protein precursor (Endo-xyloglucan transferase) (Xyloglucan endo-1,4-beta-D-glucanase) [Arabidopsis thaliana] (68417.m04303)
95 (D) External Glu repression	NC-NC-D	A14g31130	expressed protein (68417.m04419)
96 (D) External Glu repression	NC-NC-D	A14g34290	SWIB complex BAF60b domain-containing protein contains Pfam profile PF02201: BAF60b domain of the SWIB complex (68417.m04874)

97 (D) External Glu repression	NC-NC-D	253013_at	A14g37910	heat shock protein 70, mitochondrial, putative / HSP70, mitochondrial, putative strong similarity to SP1001898 Heat shock 70 kDa protein, mitochondrial precursor (Phaseolus vulgaris) (68417.m05361)
98 (D) External Glu repression	NC-NC-D	252712_at	A13g43800	glutathione S-transferase, putative glutathione transferase, papaya, PIR:T09781 (68418.m04681)
99 (D) External Glu repression	NC-NC-D	252661_at	A13g44450	expressed protein (68418.m04777)
100 (D) External Glu repression	NC-NC-D	252492_at	A13g46740	chloroplast outer envelope protein, putative similar to chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum] Gi:633607; contains Pfam profile PF01103: outer membrane protein, OMP85 family (68418.m05074)
101 (D) External Glu repression	NC-NC-D	252327_at	A13g48740	nodulin MIN3 family protein similar to MIN3 Gi:1619602 (root nodule development) from [Medicago truncatula] (68418.m05322)
102 (D) External Glu repression	NC-NC-D	252239_at	A13g48990	expressed protein (68418.m05466)
103 (D) External Glu repression	NC-NC-D	252162_at	A13g50670	U1 small nuclear ribonucleoprotein 70 (U1-70k) (68418.m05542)
104 (D) External Glu repression	NC-NC-D	252115_at	A13g51600	nonspecific lipid transfer protein 5 (LTP5) identical to SP1Q9XF52 Nonspecific lipid-transfer protein 5 (LTP 5) [Arabidopsis thaliana] (68418.m05654)
105 (D) External Glu repression	NC-NC-D	251963_at	A13g53570	protein kinase (AFC1) (AMEZ) identical to protein kinase AFC1 (EC 2.7.1.-) [Arabidopsis thaliana] (68418.m05915)
106 (D) External Glu repression	NC-NC-D	251638_at	A13g57490	40S ribosomal protein S2 (RPS2D) 40S ribosomal protein S2 - Arabidopsis thaliana, SWISSPROT:RS2_ARATH (68418.m08400)
107 (D) External Glu repression	NC-NC-D	251322_at	A13g61440	cysteine synthase, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative identical to cysteine synthase (EC 4.2.99.8) [Arabidopsis thaliana] Gi:5624334; contains Pfam profile PF00291: Pyridoxal-phosphate dependent enzyme (68418.m06881)
108 (D) External Glu repression	NC-NC-D	251284_at	A13g62120	RNA synthetase class II (G, H, P and S) family protein similar to SP1Q07814 Bifunctional aminoacyl-tRNA synthetase [includes: Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate-tRNA ligase); Prolyl-tRNA synthetase (EC 6.1.1.15) (Proline-tRNA ligase)] (Homo sapiens), contains Pfam profiles PF00587: RNA synthetase class II core domain (G, H, P, S and T), PF03128: Anticodon binding domain (68418.m06979)
109 (D) External Glu repression	NC-NC-D	250973_at	A15g02870	60S ribosomal protein L4/L1 (RPL4D) 60S ribosomal protein L4, Arabidopsis thaliana, EMBL:CAA78104 (68418.m00230)
110 (D) External Glu repression	NC-NC-D	250936_at	A15g03120	expressed protein (68418.m00260)
111 (D) External Glu repression	NC-NC-D	250918_at	A15g03610	GDSL-motif lipase/hydrolase family protein low similarity to SP1A0602 Anthrac-specific proline-rich protein APG precursor (Arabidopsis thaliana), contains Pfam profile PF00857: GDSL-like Lipase/Acylhydrolase (68418.m00320)
112 (D) External Glu repression	NC-NC-D	250832_at	A15g04950	nicotianamine synthase, putative similar to nicotianamine synthase [Lycopersicon esculentum] (68418.m00524)
113 (D) External Glu repression	NC-NC-D	248797_at	A15g47210	synthase 2 [Hordeum vulgare] (68418.m00524)
114 (D) External Glu repression	NC-NC-D	248582_at	A15g49910	nuclear RNA-binding protein, putative similar to nuclear RNA binding protein Gi:6492264 from [Arabidopsis thaliana] (68418.m05821)
115 (D) External Glu repression	NC-NC-D	247985_at	A15g56540	heat shock protein 70 / HSP70 (HSC70-7) identical to heat shock protein 70 [Arabidopsis thaliana] Gi:6746582 (68418.m06180)
116 (D) External Glu repression	NC-NC-D	247900_at	A15g57290	arabinoxylanase (AGP14) identical to gi10680505/gbAA24282 (68418.m07056)
117 (D) External Glu repression	NC-NC-D	247569_at	A15g61240	60S acidic ribosomal protein P3 (RPP3B) (68418.m07157)
118 (D) External Glu repression	NC-NC-D	247157_at	A15g65770	leucine-rich repeat family protein contains leucine rich-repeat (LRR) domains Pfam:PF00360, INTERPRO:IPR001811; contains similarity to Hcr2-08 [Lycopersicon esculentum] gi13894387/gbAAC78593 (68418.m07681)
119 (D) External Glu repression	NC-NC-D	247076_at	A15g68510	nuclear matrix constituent protein-related low similarity to nuclear matrix constituent protein 1 (NMCP1) [Daucus carota] Gi:2180187 (68418.m08276)
120 (D) External Glu repression	NC-NC-D	246860_at	A15g25840	beta-lactamase hexapeptide repeat-containing protein contains Pfam profile PF00132: Beta-lactamase hexapeptide (four repeats) (68418.m08386)
121 (D) External Glu repression	NC-NC-D	246845_at	A15g26707	expressed protein (68418.m03066)
122 (D) External Glu repression	NC-NC-D	246809_s_at	A15g27140	SAR DNA-binding protein, putative strong similarity to SAR DNA-binding protein-1 [Pisum sativum] Gi:3132896; contains Pfam profile PF01788: Putative snRNA binding domain (68418.m03239)
123 (D) External Glu repression	NC-NC-D	245714_at	A15g04280	glycine-rich RNA-binding protein (68418.m00421)
124 (D) External Glu repression	NC-NC-D	245350_at	A14g16830	nuclear RNA-binding protein (RGG) identical to nuclear RNA binding protein Gi:6492264 from [Arabidopsis thaliana] (68417.m02540)
125 (D) External Glu repression	NC-NC-D	245277_at	A14g15550	UDP-glucose:indole-3-acetate beta-D-glucosyltransferase (IAGLU) identical to UDP-glucose:indole-3-acetate beta-D-glucosyltransferase (IAGLU) Gi:2149126 from [Arabidopsis thaliana] (68417.m02376)
126 (D) External Glu repression	NC-NC-D	244980_at	np36	ribosomal protein L36
1 (E) Internal/External Glu induction	I-D-I	248923_at	A15g19120	expressed protein low similarity to extracellular dermal glycoprotein EDGP precursor [Daucus carota] Gi:285741, SPIP13917 Basic 7S globulin precursor (Glycine max) (68418.m02275)
2 (E) Internal/External Glu induction	I-D-I	249862_at	A15g22620	zinc finger (C3HC4-type RING finger) family protein contains Pfam profiles:PF05495 CHY zinc finger, PF00087 zinc finger, C3HC4 type (RING finger) (68418.m02680)
3 (E) Internal/External Glu induction	I-D-I	248114_at	A15g20250	raffinose synthase family protein / seed inhibition protein, putative (din10) similar to seed inhibition protein GB:AAA32975 Gi:167100 from [Hordeum vulgare]; contains nonconsensus A1 donor splice site at intron 1; contains Pfam profile PF06691: Raffinose synthase or seed inhibition protein Stp1; identical to cDNA seed inhibition protein (din10) partial cds Gi:10834551 (68418.m02410)
4 (E) Internal/External Glu induction	I-NC-I	267461_at	A12g33830	domancy/auxin associated family protein contains Pfam profile: PF05564 domancy/auxin associated protein (68415.m04150)
5 (E) Internal/External Glu induction	I-NC-I	266995_at	A12g34500	cytochrome P450 family protein similar to Cytochrome P450 61 (C-22 steroid desaturase) (SP:P54781) [Saccharomyces cerevisiae] (68415.m04237)
6 (E) Internal/External Glu induction	I-NC-I	266984_at	A12g39570	ACT domain-containing protein contains Pfam ACT domain PF01842 (68415.m04854)
7 (E) Internal/External Glu induction	I-NC-I	266259_at	A12g27830	expressed protein (68415.m03374)
8 (E) Internal/External Glu induction	I-NC-I	265111_at	A11g62510	protease inhibitor/seed storage lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage LTP family domain PF00234 (68414.m07053)

9	(E) Internal/External Glu induction	I-NC-I	264524_at	A11g10070	branched-chain amino acid aminotransferase 2 / branched-chain amino acid transaminase 2 (BCAT2) identical to SPI08M439 Branched-chain amino acid aminotransferase 2, chloroplast precursor (EC 2.6.1.42) (Atbcat-2) (Arabidopsis thaliana); contains Pfam profile: PF01083 aminotransferase class IV (68414.m01136)
10	(E) Internal/External Glu induction	I-NC-I	263157_at	A11g54100	aldehyde dehydrogenase, putative / aniquitin, putative strong similarity to SPI041247 Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3) (Aniquitin 1) (Brassica turgor-responsivedrought-induced gene 26 protein) (Bg-26) (Brassica napus); similar to turgor-responsive protein 26C (aldehyde dehydrogenase family 7 member A1) [Pisum sativum] SWISS-PROT:P25785
11	(E) Internal/External Glu induction	I-NC-I	262399_at	A11g49500	expressed protein (68414.m05548) plant defensin-tusion protein, putative (PDF1.4) plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); similar to SWISS-PROT:P30224, Cysteine-rich antifungal protein 1 precursor (AFP1) (Arabidopsis thaliana) (68414.m02443)
12	(E) Internal/External Glu induction	I-NC-I	261135_at	A11g19810	plasma membrane intrinsic protein 1C (PIP1C) / aquaporin PIP1.3 (PIP1.3) / transmembrane protein B (TMPB) identical to plasma membrane intrinsic protein 1C SP:Q08733 from [Arabidopsis thaliana] (68414.m00079)
13	(E) Internal/External Glu induction	I-NC-I	259431_at	A11g01620	expressed protein (68418.m01202)
14	(E) Internal/External Glu induction	I-NC-I	258939_at	A13g10020	branched chain alpha-keto acid dehydrogenase E2 subunit (din3) identical to branched chain alpha-keto acid dehydrogenase E2 subunit (din3) (Arabidopsis thaliana) GI:7021284 (68416.m00812)
15	(E) Internal/External Glu induction	I-NC-I	258527_at	A13g06850	expressed protein similar to auxin down-regulated protein ARG10 [Vigna radiata] GI:2970051, wall7 (aluminum-induced protein) [Triticum aestivum] GI:451193 (68416.m01980)
16	(E) Internal/External Glu induction	I-NC-I	258402_at	A13g15450	cysteine proteinase, putative / thiol protease, putative contains similarity to cysteine proteinase RD21A (thiol protease) GI:435619, SP:P43257 from [Arabidopsis thaliana] (68416.m02459)
17	(E) Internal/External Glu induction	I-NC-I	258225_at	A13g15630	cyclin family protein similar to cyclin 2 [Trypanosoma brucei] GI:7339572, cyclin 6 [Trypanosoma cruzi] GI:12005317; contains Pfam profile PF00134: Cyclin, N-terminal domain (68416.m02756)
18	(E) Internal/External Glu induction	I-NC-I	258005_at	A13g19390	methylocrotonyl-CoA carboxylase beta chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 2 (MCCB) identical to SPI08LDD8 methylocrotonyl-CoA carboxylase beta chain, mitochondrial precursor (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 2) (MCCase beta subunit) (3-methylcrotonyl-CoA carbon dioxide ligase beta subunit) (Arabidopsis thaliana); contains Pfam profile: PF01039 carboxyl transferase domain (68417.m04829)
19	(E) Internal/External Glu induction	I-NC-I	256894_at	A13g21870	TAZ zinc finger family protein / BTB/POZ domain-containing protein contains Pfam PF00651: BTB/POZ domain; contains Pfam PF02135: TAZ zinc finger; similar to Speckle-type POZ protein (SP:O43791) [Homo sapiens] (68417.m05321)
20	(E) Internal/External Glu induction	I-NC-I	253279_at	A14g34030	asparagine synthetase 1 [glutamine-hydrolyzing] / glutamine-dependent asparagine synthetase 1 (ASN1) identical to SPIP49078 Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4) [Glutamine-dependent asparagine synthetase] (Arabidopsis thaliana) (68416.m05145)
21	(E) Internal/External Glu induction	I-NC-I	253081_at	A14g37610	alkaline alpha galactosidase, putative similar to alkaline alpha galactosidase II [Cucumis melo] GI:29838631; contains Pfam profile PF05691: Raffinose synthase or seed imbibition protein Spt1 (68416.m04003)
22	(E) Internal/External Glu induction	I-NC-I	252415_at	A13g47340	bZIP family transcription factor similar to bZIP transcription factor GI:1789891 from [Arabidopsis thaliana] (68418.m08118)
23	(E) Internal/External Glu induction	I-NC-I	251642_at	A13g57520	expressed protein contains Pfam profile PF04520: Protein of unknown function, DUF584 (68418.m07615)
24	(E) Internal/External Glu induction	I-NC-I	248606_at	A15g06080	AP2 domain-containing transcription factor, putative similar to DNA-binding protein RAV2 GI:3868859 from [Arabidopsis thaliana] (68414.m03173)
25	(E) Internal/External Glu induction	I-NC-I	247565_at	A15g06080	transferrase family protein contains Pfam profile PF02458 transferase family (68415.m04913)
26	(E) Internal/External Glu induction	I-NC-I	255742_at	A11g25560	expressed protein (68415.m05482)
27	(E) Internal/External Glu induction	I-NC-I	267523_at	A12g30610	expansin, putative (EXP3) identical to Alpha-expansin 3 precursor (At-EXP3) [Arabidopsis thaliana] SWISS-PROT:O80932; alpha-expansin gene family, PMID:11841069 (68415.m04617)
28	(E) Internal/External Glu induction	I-NC-I	267337_at	A12g39980	ic20 protein-related similar to Tic20 (GI:3768673) [Pisum sativum] (68415.m05871)
29	(E) Internal/External Glu induction	I-NC-I	267230_at	A12g44080	expressed protein (68415.m02440)
30	(E) Internal/External Glu induction	I-NC-I	267158_at	A12g37640	phytochrome A (PHYA) identical to SPIP14712 Phytochrome A (Arabidopsis thaliana) (68414.m01073)
31	(E) Internal/External Glu induction	I-NC-I	266483_at	A12g47640	histone H2A, putative strong similarity to histone H2A GI:3204128 SPI065759 from Cicer arietinum, Picea abies SPIP35083; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4 (68414.m06235)
32	(E) Internal/External Glu induction	I-NC-I	265384_at	A12g20760	expressed protein contains 3 transmembrane domains; contains Pfam profile PF05832: Eukaryotic protein of unknown function (68414.m01044)
33	(E) Internal/External Glu induction	I-NC-I	264508_at	A11g09570	expressed protein (68415.m00120)
34	(E) Internal/External Glu induction	I-NC-I	264188_at	A11g54690	expressed protein contains similarity to hedgehog-interacting protein GI:4668122 from [Mus musculus] (68414.m08665)
35	(E) Internal/External Glu induction	I-NC-I	263710_at	A11g09330	expressed protein similar to SPIQ43116 Protein disulfide isomerase precursor (PDI) (EC 5.3.4.1) [Ricinus communis]; contains Pfam profile PF00085: Thioredoxin (68414.m04425)
36	(E) Internal/External Glu induction	I-NC-I	263597_at	A12g01870	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family (68414.m02818)
37	(E) Internal/External Glu induction	I-NC-I	262215_at	A11g74790	zinc finger (B-box type) family protein contains Pfam profile: PF00643 B-box zinc finger (68414.m07827)
38	(E) Internal/External Glu induction	I-NC-I	262024_at	A11g35620	DNA-binding protein RAV2 (RAV2) / AP2 domain-containing protein RAP2.8 identical to RAV2 GI:3868859 from [Arabidopsis thaliana], AP2 domain containing protein RAP2.8 (Arabidopsis thaliana) GI:2281641; contains Pfam profile: PF00847 AP2-domain (68414.m07873)
39	(E) Internal/External Glu induction	I-NC-I	261937_at	A11g22570	pyrophosphate-energized vacuolar membrane proton pump / pyrophosphate-energized inorganic pyrophosphatase (AVP-3) identical to pyrophosphate-energized vacuolar membrane proton pump (pyrophosphate-energized inorganic pyrophosphatase) SP:P31414 from [Arabidopsis thaliana] (68414.m01883)
40	(E) Internal/External Glu induction	I-NC-I	260410_at	A11g69670	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAM GB CAA63101 [Petunia x hybrida] (68418.m00430)
41	(E) Internal/External Glu induction	I-NC-I	260266_at	A13g04070	alcohol oxidase-related similar to long chain fatty alcohol oxidase from Candida cloacae [GI:6983581], Candida tropicalis [GI:6983594] (68416.m02951)
42	(E) Internal/External Glu induction	I-NC-I	260037_at	A11g68840	
43	(E) Internal/External Glu induction	I-NC-I	259504_at	A11g15690	
44	(E) Internal/External Glu induction	I-NC-I	259809_at	A13g04070	
45	(E) Internal/External Glu induction	I-NC-I	258299_at	A13g23410	

46	(E) Internal/External	Glu induction	NC-D-NC	257044_at	A0g193720	dynamitin family protein identical to cDNA dynamitin-like protein (ARCS) Gl: 30349145; contains Pfam profile PF003050; Dynamitin family (68416.m02497)
47	(E) Internal/External	Glu induction	NC-D-NC	255540_at	A0g101800	preprotein translocase secA subunit, putative similar to preprotein translocase secA subunit, chloroplast [precursor] SP-Q8S910 from [Arabidopsis thaliana]; non-consensus GA donor splice site at exon 4 (68417.m020237)
48	(E) Internal/External	Glu induction	NC-D-NC	254456_at	A0g21150	ribophorin II (RPN2) family protein contains Pfam profile PF05817; Ribophorin II (RPN2) (68417.m03057)
49	(E) Internal/External	Glu induction	NC-D-NC	254250_at	A0g232290	protein kinase family protein contains Pfam domain PF00069; Protein kinase domain (68417.m03356)
50	(E) Internal/External	Glu induction	NC-D-NC	254089_at	A0g246800	MA3 domain-containing protein similar to programmed cell death 4 protein [Gallus gallus] Gl: 12958564; contains Pfam profile PF02847; MA3 domain (68417.m03552)
51	(E) Internal/External	Glu induction	NC-D-NC	253871_at	A0g27440	protoporphyrinogen oxidoreductase B, chloroplast / PCR B / NADPH-protoporphyrinogen oxidoreductase B (PORB) identical to SP-P21218 protoporphyrinogen oxidoreductase B, chloroplast precursor (EC 1.3.1.33) (PCR B) (NADPH-protoporphyrinogen oxidoreductase B) (POR B) [Arabidopsis thaliana] (68417.m03944)
52	(E) Internal/External	Glu induction	NC-D-NC	253135_at	A0g35830	aconitase hydratase, cytoplasmic / citrate hydro-lyase / aconitase (ACCO) identical to SP-Q42560 Aconitase hydratase, cytoplasmic (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase) [Arabidopsis thaliana]; contains Pfam profiles PF00330; Aconitase family (aconitase hydratase); PF00694; Aconitase C-terminal domain (68417.m05090)
53	(E) Internal/External	Glu induction	NC-D-NC	252425_at	A0g347820	TCP family transcription factor, putative auxin-induced basic helix-loop-helix transcription factor - Gossypium hirsutum, EMBL:AF165924 (68416.m05184)
54	(E) Internal/External	Glu induction	NC-D-NC	252171_at	A0g350600	zinc finger (GATA type) family protein identical to cDNA for GATA transcription factor 4 Gl:2959735 (68416.m08770)
55	(E) Internal/External	Glu induction	NC-D-NC	251373_at	A0g360530	6-phosphogluconate dehydrogenase family protein contains Pfam profiles: PF00393 6-phosphogluconate dehydrogenase C-terminal domain, PF03446 NAD binding domain of 6-phosphogluconate (68416.m05062)
56	(E) Internal/External	Glu induction	NC-D-NC	249268_at	A0g41670	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family (68416.m05663)
57	(E) Internal/External	Glu induction	NC-D-NC	248932_at	A0g46050	heat shock protein-related contains similarity to 101 kDa heat shock protein; HSP101 [Tricium aestivum]
58	(E) Internal/External	Glu induction	NC-D-NC	247874_at	A0g557710	gpi1156180[gpiAAC3689 (68416.m07214)
59	(E) Internal/External	Glu induction	NC-D-NC	247791_at	A0g558710	pepC/poly-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative (RUC7) similar to cyclophilin [Arabidopsis thaliana] gi2443755[gpiAAC871401 (68416.m07355)
60	(E) Internal/External	Glu induction	NC-D-NC	247611_at	A0g60710	zinc finger (C3HC4-type RING finger) family protein low similarity to SPIP97280 Inter-alpha-trypsin inhibitor heavy chain H3 precursor (Mesocricetus auratus); contains Pfam profiles PF00097; Zinc finger, C3HC4 type (RING finger), PF00092; von Willebrand factor type A domain (68416.m07618)
61	(E) Internal/External	Glu induction	NC-D-NC	246580_at	A0g317770	ABC transporter family protein contains Pfam profile: PF00005; ABC transporter (68414.m03899)
62	(E) Internal/External	Glu induction	NC-D-NC	246238_at	A0g36670	mannitol transporter, putative similar to mannitol transporter [Apium graveolens var. dulce] Gl:12004316; contains Pfam profile PF00083; major facilitator superfamily protein (68417.m05203)
63	(E) Internal/External	Glu repression	D-NC-D	266892_at	A0g26080	glycine dehydrogenase [decarboxylating], putative / glycine decarboxylase, putative / glycine cleavage system P-protein, putative strong similarity to SPIP26989 Glycine dehydrogenase [decarboxylating], mitochondrial precursor (EC 1.4.2.4) (Pisum sativum); contains Pfam profile PF02347; Glycine cleavage system P-protein (68415.m03131)
64	(E) Internal/External	Glu repression	D-NC-D	266805_at	A0g30010	expressed protein (68415.m03631)
65	(E) Internal/External	Glu repression	D-NC-D	264956_at	A0g76990	ACT domain containing protein low similarity to undecyltransferase SPIP56884 from Rhizobium meliloti; contains Pfam ACT domain PF01842 (68414.m08964)
66	(E) Internal/External	Glu repression	D-NC-D	264901_at	A0g23090	sulfate transporter, putative similar to sulfate transporter [Arabidopsis thaliana] Gl:2285885; contains Pfam profiles PF00918; Sulfate transporter family, PF01740; STAS domain (68414.m02887)
67	(E) Internal/External	Glu repression	D-NC-D	264903_at	A0g23190	phosphoglucosyltransferase, cytoplasmic, putative / glucose phosphomutase, putative strong similarity to SPIP93805 Phosphoglucosyltransferase, cytoplasmic 2 (EC 5.4.2.2) (Glucose phosphomutase 2) (PGM 2) [Zea mays]; contains InterPro accession IPR008352; Phosphoglucosyltransferase (68414.m02897)
68	(E) Internal/External	Glu repression	D-NC-D	263885_at	A0g36910	multidrug resistance P-glycoprotein (PGP1) identical to P-glycoprotein Gl:3849833 from [Arabidopsis thaliana]; homologous to mammalian mdr gene, contains ATP-binding cassette, related to multi drug resistance proteins (68413.m04527)
69	(E) Internal/External	Glu repression	D-NC-D	263777_at	A0g46450	cyclic nucleotide-regulated ion channel, putative (CNGC12) similar to cyclic nucleotide and calmodulin-regulated ion channel (cngc3) Gl:4581201 from [Arabidopsis thaliana] (68415.m05780)
70	(E) Internal/External	Glu repression	D-NC-D	263348_at	A0g05710	aconitase hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative nearly identical to SPIP49608 Aconitase hydratase, cytoplasmic (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase) [Cucurbita maxima]; contains Pfam profiles PF00330; Aconitase family (aconitase hydratase), PF00694; Aconitase C-terminal domain (68415.m00611)
71	(E) Internal/External	Glu repression	D-NC-D	262793_at	A0g131110	cytochrome P450 71B7 (CYP71B7) identical to (SP-Q96514) cytochrome P450 71B7 [Arabidopsis thaliana]; PF00087 Cytochrome P450 family, ESTs gblT44875, gblT44874, gblT44817, gblT44310 and gblT04541 come from this gene, identical to cDNA cytochrome P450 Gl:1523785, ATCY7187 (68414.m01520)
72	(E) Internal/External	Glu repression	D-NC-D	262374_s_at	A0g72930	Tok-Interleukin-Resistance (TIR) domain-containing protein domain signature TIR exists, suggestive of a disease resistance protein. (68414.m08435)
73	(E) Internal/External	Glu repression	D-NC-D	261569_at	A0g01080	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain; identical to cDNA LATE ELONGATED HYPOCOTYL MYB transcription factor Gl:3261045 (68414.m00006)
74	(E) Internal/External	Glu repression	D-NC-D	260955_at	A0g06000	UDP-glucuronosyl/UDP-glucosyl transferase family protein contains similarity to UDPG glucosyltransferase GB-AA892270 UDP-glucosyltransferase 1 (UGT1A1) from [Solanum berthaultii] (68414.m00628)
75	(E) Internal/External	Glu repression	D-NC-D	260913_at	A0g02500	S-adenosylmethionine synthetase 1 (SAM1) identical to S-adenosylmethionine synthetase 1 (Methionine adenosyltransferase 1, AdoMet synthetase 1) [Arabidopsis thaliana] SWISS-PROT:P23688

79 (E) Internal/External Glu repression	D-NC-D	259788_at	A1g28670	GDSL-motif lipase/hydrolase family protein similar to family II lipase EXL1 Gi:15054382 from [Arabidopsis thaliana]; contains Pfam profile: PF00657 Lipase/Acylhydrolase with GDSL-like motif (68414.m03626)
80 (E) Internal/External Glu repression	D-NC-D	259228_at	A3g07720	kelch repeat-containing protein similar to epithiospecifier (Gi:1618838) [Arabidopsis thaliana]; contains Pfam PF01344: Kelch motif (5 repeats) (68416.m00631)
81 (E) Internal/External Glu repression	D-NC-D	256609_at	A3g02910	expressed protein contains Pfam domain PF03674: Uncharacterised protein family (UPF0131) (68418.m00286)
82 (E) Internal/External Glu repression	D-NC-D	258338_at	A3g16150	L-asparaginase, putative / L-asparagine amidohydrolase, putative similar to Swiss-Prot:P30364 L-asparaginase (EC 3.5.1.1) (L-asparagine amidohydrolase) [Lupinus angustifolius] (68416.m02039)
83 (E) Internal/External Glu repression	D-NC-D	257217_at	A3g14940	phosphoenolpyruvate carboxylase, putative / PEP carboxylase, putative strong similarity to SPIP29196 Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCASE) [Solanum tuberosum]; contains Pfam profile PF00311: phosphoenolpyruvate carboxylase (68418.m01890)
84 (E) Internal/External Glu repression	D-NC-D	257008_at	A3g14210	myrosinase-associated protein, putative similar to GB:CAA71238 from [Brassica napus]; contains Pfam profile:PF00657 Lipase/Acylhydrolase with GDSL-like motif (68416.m01796)
85 (E) Internal/External Glu repression	D-NC-D	256228_at	A1g56190	phosphoglycerate kinase, putative similar to SPIP41758 Phosphoglycerate kinase, chloroplast precursor (EC 2.7.2.3) (Chlamydomonas reinhardtii); contains Pfam profile PF00162: phosphoglycerate kinase (68414.m06458)
86 (E) Internal/External Glu repression	D-NC-D	255957_at	A1g22180	senescence-associated protein-related similar to senescence-associated protein SAG102 (Gi:22331931) [Arabidopsis thaliana] (68414.m02770)
87 (E) Internal/External Glu repression	D-NC-D	255815_at	A4g01290	expressed protein (68417.m00170)
88 (E) Internal/External Glu repression	D-NC-D	255421_at	A4g03260	leucine-rich repeat family protein contains leucine rich repeat (LRR) domains, Pfam:PF00560 (68417.m00445)
89 (E) Internal/External Glu repression	D-NC-D	254723_at	A4g13510	ammonium transporter 1, member 1 (AMT1.1) identical to SPIP54144 High affinity ammonium transporter (AMT1.1) [Arabidopsis thaliana] (68417.m02107)
90 (E) Internal/External Glu repression	D-NC-D	254705_at	A4g17870	expressed protein (68417.m02664)
91 (E) Internal/External Glu repression	D-NC-D	254275_at	A4g22870	tetratricopeptide repeat (TPR)-containing protein similar to Hsc70-interacting protein (Hsp) from [Homo sapiens] SPIP50502, (Rattus norvegicus) SPIP50503; contains Pfam profile PF00515: tetratricopeptide repeat (TPR) domain (68417.m03272)
92 (E) Internal/External Glu repression	D-NC-D	254174_at	A4g24120	transporter, putative similar to iron-phytosiderophore transporter protein yellow stripe 1 [Zea mays] Gi:10770865; contains Pfam profile PF03169: OPT oligopeptide transporter protein (68417.m03482)
93 (E) Internal/External Glu repression	D-NC-D	253521_at	A4g13100	20S proteasome beta subunit A (PBA1) (PRCD) identical to cDNA proteasome subunit prcd Gi:2511593 (68417.m04441)
94 (E) Internal/External Glu repression	D-NC-D	253387_at	A4g33010	glycine dehydrogenase (decarboxylating), putative / glycine decarboxylase, putative / glycine cleavage system P-protein, putative strong similarity to SPIP49361 Glycine dehydrogenase (decarboxylating) A, mitochondrial precursor (EC 1.4.4.2) (Flaveria pringlei); contains Pfam profile PF02347: Glycine cleavage system P-protein (68417.m04695)
95 (E) Internal/External Glu repression	D-NC-D	253205_at	A4g34480	cydase-associated protein (cap1) identical to cydase-associated protein (cap1) Gi:3189136 from [Arabidopsis thaliana] (68417.m04903)
96 (E) Internal/External Glu repression	D-NC-D	252827_at	A4g39950	cytochrome P450 79B2, putative (CYP79B2) identical to cytochrome P450 (79B2) SP:O81348 from [Arabidopsis thaliana] (68417.m05657)
97 (E) Internal/External Glu repression	D-NC-D	251562_at	A3g57890	tubulin-specific chaperone C-related contains weak similarity to Tubulin-specific chaperone C (Tubulin-folding cofactor C) (CFC) (Swiss-Prot:Q15814) [Homo sapiens] (68416.m06453)
98 (E) Internal/External Glu repression	D-NC-D	251581_at	A3g58580	endonuclease/exonuclease/phosphatase family protein similar to SPIP31384 Glucose-repressible alcohol dehydrogenase transcriptional effector (Carbon catabolite repressor protein 4) [Saccharomyces cerevisiae]; contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family (68416.m06527)
99 (E) Internal/External Glu repression	D-NC-D	251524_at	A3g58990	acetyltransferase (phosphatidylcholine-sterol acyltransferase) (68418.m01582)
100 (E) Internal/External Glu repression	D-NC-D	251197_at	A3g62960	malate oxidoreductase, putative similar to NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) (SPIP12828) [Phaseolus vulgaris] (68418.m01364)
101 (E) Internal/External Glu repression	D-NC-D	250337_at	A5g11790	lecithin:cholesterol acyltransferase family protein / LACT family protein similar to SPIP40345 Phospholipid:diacylglycerol acyltransferase (EC 2.3.1.158) (PDAT) [Saccharomyces cerevisiae]; contains Pfam profile PF02450: Lecithin:cholesterol acyltransferase (EC 2.3.1.158) (PDAT) [Saccharomyces cerevisiae]; contains Pfam profile PF03096: Ndr family protein similar to SPIP023969 Pollen specific protein SP21 [Helianthus annuus]; contains Pfam profile PF03096: Ndr family (68418.m01376)
102 (E) Internal/External Glu repression	D-NC-D	250339_at	A5g11670	myb family transcription factor (GLK2) contains Pfam profile: PF00249 myb-like DNA-binding domain (68418.m05407)
103 (E) Internal/External Glu repression	D-NC-D	250253_at	A5g13640	cytochrome P450 family protein similar to Cytochrome P450 83A3 (P450 CYP5) (SP:O81973) [Glycine max] (68418.m05929)
104 (E) Internal/External Glu repression	D-NC-D	249035_at	A5g4190	pentacyclic terpenene synthase, putative similar to pentacyclic terpenene synthase [gi:6650207] [PMID:11247608] Contains Pfam domain PF00432: Prenyltransferase and squalene oxidase repeat (68418.m05833)
105 (E) Internal/External Glu repression	D-NC-D	248727_at	A5g47990	protease inhibitor, putative (DR4) identical to Dr4 Gi:4691114 from [Arabidopsis thaliana]; contains Pfam profile PF00187: Trypsin and protease inhibitor (68414.m08488)
106 (E) Internal/External Glu repression	D-NC-D	248729_at	A5g48010	transferase family protein similar to alcohol acyltransferase [Fragaria x ananassa] [Gi:10121328] [PMID:10810141]
107 (E) Internal/External Glu repression	D-NC-D	245736_at	A1g73330	deacetyl/windoline 4-O-acetyltransferase [Catharanthus roseus] [Gi:4091808] [PMID:9681034] (68417.m02351)
108 (E) Internal/External Glu repression	D-NC-D	245555_at	A4g15390	PSII component
109 (E) Internal/External Glu repression	D-NC-D	245021_at	psbJ	calmodulin-binding family protein contains Pfam profile PF00612: IQ calmodulin-binding motif (68415.m03145)
110 (E) Internal/External Glu Repression	NC+NC	267381_at	A2g26190	flavin reductase-related low similarity to SPIP30043 Flavin reductase (Homo sapiens) (68415.m04228)
111 (E) Internal/External Glu Repression	NC+NC	267005_at	A2g34460	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) zinc finger (C3HC4-type RING finger) (68415.m01764)
112 (E) Internal/External Glu Repression	NC+NC	265472_at	A2g15580	1-aminocyclopropane-1-carboxylate oxidase / ACC oxidase / ethylene-forming enzyme (ACO) (EAT1) identical to 1-aminocyclopropane-1-carboxylate oxidase [gb J66719 (EAT1). ESTs gb J43073, gb J15714, gb P90435, gb R44023, gb AA597826, gb A099876, gb AA650810 and gb 29725 come from this gene (68414.m00502)
113 (E) Internal/External Glu Repression	NC+NC	265194_at	A1g05010	

114 (E) Internal/External Glu Repression	NC+NC	264435_at	A11g10360	glutathione S-transferase, putative similar to glutathione S-transferase (epiQ03666)GTX4_TOBAC; similar to EST gb H36275
115 (E) Internal/External Glu Repression	NC+NC	284107_s_at	A2g13790	gb AB039930 (68414.m01167)
116 (E) Internal/External Glu Repression	NC+NC	263582_at	A2g17120	leucine-rich repeat family protein (68415.m01522)
117 (E) Internal/External Glu Repression	NC+NC	263534_at	A2g24940	peptidoglycan-binding LysM domain-containing protein contains Pfam profile PF01476; LysM domain; supporting cDNA
118 (E) Internal/External Glu Repression	NC+NC	263150_at	A11g54050	gii16226688(gb AF428464.1AF428464 (68415.m01976)
119 (E) Internal/External Glu Repression	NC+NC	262831_at	A11g14730	cytochrome b5 domain-containing protein similar to SPIP70580 Membrane associated progesterone receptor component 1 (Rattus norvegicus); contains Pfam profile PF00173; Heme/Steroid binding domain (68415.m02982)
120 (E) Internal/External Glu Repression	NC+NC	262341_at	A11g64230	17.4 kDa class III heat shock protein (HSP17.4-CII) contains Pfam profile: PF00011 Hsp20/alpha crystallin family; identified as class CIII in Scharf, K.-D., et al.Cel Stress & Chaperones (2001) 6: 225-237. (68414.m08159)
121 (E) Internal/External Glu Repression	NC+NC	262235_at	A11g48350	cytochrome B561 family similar to cytochrome GB:AA011424.GI:4208110 [Mesembryanthemum crystallinum]; contains Pfam domain, PF03188; Cytochrome b561 (68414.m01761)
122 (E) Internal/External Glu Repression	NC+NC	262092_at	A11g56150	ubiquitin-conjugating enzyme, putative identical or nearly so to Ubiquitin-conjugating enzymes SPIP35132, SPIP35131, SPIP35133 from (Arabidopsis thaliana); contains Pfam profile PF00176; Ubiquitin-conjugating enzyme (68414.m07276)
123 (E) Internal/External Glu Repression	NC+NC	261564_at	A11g01720	ribosomal protein L18 family protein similar to ribosomal protein L18.GI:3980238 from [Thermotoga maritima] (68414.m05401)
124 (E) Internal/External Glu Repression	NC+NC	261484_at	A11g14400	auxin-responsive family protein similar to SP-P33032 Auxin-induced protein X15. [Soybean] [Glycine max] (68414.m06450)
125 (E) Internal/External Glu Repression	NC+NC	261445_at	A11g28380	no apical meristem (NAM) family protein contains Pfam PF02365; No apical meristem (NAM) domain; similar to NAC domain protein NAM GB:AA017313.GI:4325282 from [Arabidopsis thaliana] (68414.m00090)
126 (E) Internal/External Glu Repression	NC+NC	261143_at	A11g19770	ubiquitin-conjugating enzyme 1 (UBC1) E2; identical to gi:431259. SP-P25865 (68414.m01707)
127 (E) Internal/External Glu Repression	NC+NC	261081_at	A11g07350	expressed protein (68414.m03487)
128 (E) Internal/External Glu Repression	NC+NC	260831_at	A11g06830	Domain of unknown function, DUJF250 (68414.m02471)
129 (E) Internal/External Glu Repression	NC+NC	260481_at	A11g10960	transformer serine/arginine-rich ribonucleoprotein, putative similar to GB:Y09506 from [Nicotiana tabacum] (Plant Mol. Biol. 35 (3), 281-289 (1997)) (68414.m00783)
130 (E) Internal/External Glu Repression	NC+NC	260180_at	A11g70660	glutaredoxin family protein contains INTERPRO Domain IPR002109; Glutaredoxin (thioltransferase) (68414.m00728)
131 (E) Internal/External Glu Repression	NC+NC	259518_at	A11g20510	ferredoxin, chloroplast, putative strong similarity to FERREDOXIN PRECURSOR GB:P16972 [SPIP16972] from [Arabidopsis thaliana] (68414.m01258)
132 (E) Internal/External Glu Repression	NC+NC	259312_at	A13g05200	ubiquitin-conjugating enzyme family protein similar to TRAF6-regulated IKK activator 1 beta Uev1A [Homo sapiens] GI:10880989; contains Pfam profile PF00179; Ubiquitin-conjugating enzyme (68414.m08146)
133 (E) Internal/External Glu Repression	NC+NC	259249_at	A13g07790	4-coumarate-CoA ligase family protein / 4-coumaroyl-CoA synthase family protein similar to SPIP14912 and SPIP14913 from Petroselinum crispum; contains Pfam AMP-binding enzyme domain PF00501 (68414.m02555)
134 (E) Internal/External Glu Repression	NC+NC	258897_at	A13g05730	zinc finger (C3HC4-type RING finger) family protein (ATL6) contains Pfam profile: PF00097; Zinc finger, C3HC4 type (RING finger) (68418.m00567)
135 (E) Internal/External Glu Repression	NC+NC	258787_at	A13g11840	DGCR14-related similar to DGCR14 protein (DiGeorge syndrome critical region 14) (ES2 protein) (Swiss-Prot:Q80DF8) [Homo sapiens] (68416.m00951)
136 (E) Internal/External Glu Repression	NC+NC	258452_at	A13g22370	expressed protein (68416.m00842)
137 (E) Internal/External Glu Repression	NC+NC	257700_at	A13g12740	U-box domain-containing protein low similarity to immediate-early fungal elicitor protein CMPG1 [Petroselinum crispum] GI:14582200; contains Pfam profile PF04564; U-box domain (68416.m01451)
138 (E) Internal/External Glu Repression	NC+NC	256663_at	A13g12050	alternative oxidase 1a, mitochondrial (AOX1A) identical to GB:Q39219 [SPIQ39219] from [Arabidopsis thaliana] (68416.m02824)
139 (E) Internal/External Glu Repression	NC+NC	256176_s_at	A11g51780	LEM3 (ligand-effector modulator 3) family protein / CDC50 family protein Similar to GI:4565976; GI:4860357; GI:4835763; GI:9757735 from [Arabidopsis thaliana] (68416.m01591)
140 (E) Internal/External Glu Repression	NC+NC	256046_at	A11g07135	Aha1 domain-containing protein contains Pfam PF05146; Aha1 domain; similar to Protein C14orf3 (HSPC322) (Swiss-Prot:Q95433) [Homo sapiens] (68416.m01496)
141 (E) Internal/External Glu Repression	NC+NC	254881_at	A14g12040	IAA-amino acid hydrolase 5 / auxin conjugate hydrolase (ILL5) identical to auxin conjugate hydrolase ILL5 [Arabidopsis thaliana] gi5725649(gb AA048152; contains nonconsensus AT acceptor splice site at exon3 (68414.m05635)
142 (E) Internal/External Glu Repression	NC+NC	254331_s_at	A14g22710	glycine-rich protein (68414.m00759)
143 (E) Internal/External Glu Repression	NC+NC	254231_at	A14g23810	zinc finger (AN1-like) family protein contains Pfam domains, PF01428; AN1-like Zinc finger and PF01754; A2D-like zinc finger (68417.m01915)
144 (E) Internal/External Glu Repression	NC+NC	254120_at	A14g24570	cytochrome P450 family protein contains Pfam profile: PF00067 cytochrome p450 (68417.m03276)
145 (E) Internal/External Glu Repression	NC+NC	253664_at	A14g30210	WRKY family transcription factor AR411 - Arabidopsis thaliana (thale cress), PIDg1669003 (68417.m03423)
146 (E) Internal/External Glu Repression	NC+NC	253482_at	A14g31985	mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein (68417.m03521)
147 (E) Internal/External Glu Repression	NC+NC	253275_at	A14g34180	NADPH-cytochrome p450 reductase, putative / NADPH-ferrihemoprotein reductase, putative similar to NADPH-cytochrome P450 oxidoreductase from [Populus balsamifera subsp. trichocarpa x Populus deltoides] GI:13183564, GI:13183568 (68417.m04296)
148 (E) Internal/External Glu Repression	NC+NC	252422_at	A13g47550	60S ribosomal protein L39 (RPL39C) (68417.m04549)
149 (E) Internal/External Glu Repression	NC+NC	252053_at	A13g52400	cyclase family protein contains Pfam profile: PF04199 putative cyclase (68417.m04850)
150 (E) Internal/External Glu Repression	NC+NC	251727_at	A13g56290	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097; Zinc finger, C3HC4 type (RING finger) (68416.m05763)
151 (E) Internal/External Glu Repression	NC+NC	249983_at	A15g18470	syntaxin, putative (SYP122) similar to SPIQ92SD4 Syntaxin 121 (A1SYP121) (Syntaxin-related protein At-Syr1) [Arabidopsis thaliana] (68416.m026257)
				expressed protein (68416.m06257)
				curculin-like (mannose-binding) lectin family protein contains Pfam profile: PF01453 lectin (probable mannose binding) (68418.m02175)

152	(E) Internal/External Glu Repression	NC-NC	249325_at	A15g40850	uorophyrin III methylase (UPM1) identical to uorophyrin III methylase (GI:146165) [Arabidopsis thaliana], similar to 4-adenosyl-L-methionine-dependent uorophyrinogen III methyltransferase (GI:1490606) [Arabidopsis thaliana]; similar to Diphthine synthase (Diphthamide biosynthesis methyltransferase) (DPH5) (SP:P32469) [Saccharomyces cerevisiae]; contains Pfam PF00590: Tetrapyrrole (Corrin/Protoporphyrin) Methylase domain; contains TIGRFAM PF00590: Tetrapyrrole (Corrin/Protoporphyrin) Methylases
153	(E) Internal/External Glu Repression	NC-NC	249122_at	A15g43850	acredutone dioxygenase (ARDIARD) family protein similar to iron-deficiency induced gene [Hordeum vulgare] GI:14522834, SPL [Homo sapiens] GI:16551383; contains Pfam profile PF03079: ARDIARD family (68418.m05361)
154	(E) Internal/External Glu Repression	NC-NC	249078_at	A15g44070	phytochelatins synthase 1 (PCS1) identical to phytochelatins synthase [Arabidopsis thaliana] gi18254401 gb AA166747; identical to cDNA phytochelatins synthase, GI:18254400 (68418.m05392)
155	(E) Internal/External Glu Repression	NC-NC	248964_at	A15g45340	cytochrome P450 family protein similar to SPI042569 C901_ARATH Cytochrome P450 90A1 (SP:Q42568) [Arabidopsis thaliana]; contains Pfam profile: PF00087: Cytochrome P450 (68418.m05565)
156	(E) Internal/External Glu Repression	NC-NC	248799_at	A15g47220	ethylene-responsive element-binding factor 5 (ERF5) identical to SPJ060341 Ethylene responsive element binding factor 5 (AERF5) [Arabidopsis thaliana] (68418.m05824)
157	(E) Internal/External Glu Repression	NC-NC	248665_at	A15g48655	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (68418.m06017)
158	(E) Internal/External Glu Repression	NC-NC	248327_at	A15g52750	heavy-metal-associated domain-containing protein Pfam profile PF00403: Heavy-metal-associated domain (68418.m06547)
159	(E) Internal/External Glu Repression	NC-NC	247693_at	A15g59730	exocyst subunit EXO70 family protein leucine zipper-containing protein, Lycopersicon esculentum, PIR:S21495 contains Pfam domain PF03081: Exo70 exocyst complex subunit; (68418.m07487)
160	(E) Internal/External Glu Repression	NC-NC	247320_at	A15g64040	photosystem I reaction center subunit PS-I-N, chloroplast, putative / PS-I-N, putative (PSAN) SP:P49107; Plant Physiol. 109 (3), 1126 (1995); similar to SPIP31093 Photosystem I reaction center subunit N, chloroplast precursor (PSI-N) [Hordeum vulgare] (68418.m08040)
161	(E) Internal/External Glu Repression	NC-NC	246970_at	A15g26030	ferrochelatase 1 identical to Swiss-Prot P42043 ferrochelatase 1, chloroplast/mitochondrial precursor (EC 4.99.1.1) (Prothemo ferrolyase) (Heme synthetase) [Arabidopsis thaliana] (68418.m03097)
162	(E) Internal/External Glu Repression	NC-NC	245768_at	A11g33590	disease resistance protein-related / LRR protein-related contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; similar to Hc2-5D [Lycopersicon esculentum] gi3894393 gb AAC78596 (68414.m04158)
163	(E) Internal/External Glu Repression	NC-NC	245247_at	A14g17230	scarce-like transcription factor 13 (SCL13) (68417.m02591)
164	(E) Internal/External Glu Repression	NC-NC	245114_at	A12g41630	transcription initiation factor IIB-1 / general transcription factor TFIIB-1 (TFIIB1) identical to transcription initiation factor IIB-1 (TFIIB1) SP:P48512 from [Arabidopsis thaliana] (68415.m05144)
1	(F) Internal Glu induction / External Glu repress	I-NC	254549_at	A14g19880	glutathione S-transferase-related contains weak hit to Pfam profile PF00043: Glutathione S-transferase, C-terminal domain (68417.m02914)
2	(F) Internal Glu repression / External Glu ind.	D-NC-I	266992_at	A12g39200	seven transmembrane MLO family protein / MLO-like protein 12 (MLO12) identical to SPI080961 MLO-like protein 12 (AtMLO12) [Arabidopsis thaliana], membrane protein MLO12 [Arabidopsis thaliana] gi14091594 gb AAK53805; similar to MLO protein SWISS-PROT:P93766, NCBI_gi:1877221 [Hordeum vulgare] [Barley] (68415.m04815)
3	(F) Internal Glu repression / External Glu ind.	D-NC-I	253277_at	A14g34230	cinnamyl-alcohol dehydrogenase, putative similar to cinnamyl alcohol dehydrogenase, Nicotiana tabacum [SP:P30359], Populus deltoides, PATCHX-G288753 (68417.m04864)
1	Not regulated	NC-NC-NC	267630_at	A12g42130	expressed protein contains weak hit to Pfam PF04755: PAP_fibrillin (68415.m05211)
2	Not regulated	NC-NC-NC	267638_at	A12g42210	mitochondrial import inner membrane translocase subunit Tim17 (Tim22) family protein weak similarity to SPIP25710 NADH-ubiquinone oxidoreductase 2.1.3 kDa subunit (EC 1.6.5.3) (EC 1.6.99.3) [Neurospora crassa], SPIQ12328 Mitochondrial import inner membrane translocase subunit Tim17 (68415.m05224)
3	Not regulated	NC-NC-NC	267640_at	A12g32850	COP1 regulatory protein photomorphogenesis repressor, identical to COP1 regulatory protein/FUSCA protein FUS1 GI:402685 SP:P43254 (68415.m04039)
4	Not regulated	NC-NC-NC	267596_s_at	A12g33050	leucine-rich repeat family protein contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; similar to Hc2-08 [Lycopersicon esculentum] gi3894387 gb AAC78593 (68415.m04053)
5	Not regulated	NC-NC-NC	267601_at	A12g32960	expressed protein (68415.m04042)
6	Not regulated	NC-NC-NC	267607_s_at	A12g28740	epoxide hydrolase, soluble (sEH) identical to ATsEH [Arabidopsis thaliana] GI:1109600 (68415.m03207)
7	Not regulated	NC-NC-NC	267608_at	A12g28770	plectin-related contains weak similarity to Swiss-Prot Q9J55 plectin 1 (PLTN, PCN, 300-kDa intermediate filament-associated protein, IFAP300) [Cricetus griseus] (68415.m03210)
8	Not regulated	NC-NC-NC	267609_at	A12g28780	expressed protein contains Pfam profile TBP (TATA-binding protein) -interacting protein 120 (TIP120); contains TIGRFAM profile TIGR01612: reticulocyte binding protein (68415.m03212)
9	Not regulated	NC-NC-NC	267610_at	A12g26650	potassium channel protein 1 (AKT1) identical to AKT1 [Arabidopsis thaliana] gi583112 gb AA468810; member of the 1 pore, 6 transmembrane (1P6TM, Shaker-type) K+ channel family, PMID:11500563 (68415.m03197)
10	Not regulated	NC-NC-NC	267617_at	A12g26670	heme oxygenase 1 (HO1) (HY1) identical to plasmid heme oxygenase (HY1) [Arabidopsis thaliana] GI:4877362, heme oxygenase 1 [Arabidopsis thaliana] GI:4530591 GB:AF132475; annotation updated per Seth J. Davis at University of Wisconsin-Madison (68415.m03199)
11	Not regulated	NC-NC-NC	267619_at	A12g26730	leucine-rich repeat transmembrane protein kinase, putative (68415.m03208)
12	Not regulated	NC-NC-NC	267624_at	A12g39660	protein kinase, putative similar to protein kinase gi166809 gb AA18853 (68415.m04864)
13	Not regulated	NC-NC-NC	267591_at	A12g39705	expressed protein (68415.m04871)
14	Not regulated	NC-NC-NC	267562_at	A12g39870	radical SAM domain-containing protein similar to hypotheical protein PIR[S76698]S76698 contains Pfam profile PF04055: radical SAM domain protein (68415.m04966)
15	Not regulated	NC-NC-NC	267577_at	A12g30710	RabGAP/TBC domain-containing protein similar to SPJ08484 GTPase-activating protein GYP1 [Saccharomyces cerevisiae]; contains Pfam profile PF00566: TBC domain (68415.m03746)
16	Not regulated	NC-NC-NC	267580_at	A12g41890	expressed protein (68415.m05194)
17	Not regulated	NC-NC-NC	267583_at	A12g41960	expressed protein (68415.m05191)
18	Not regulated	NC-NC-NC	267586_at	A12g41950	expressed protein (68415.m05190)

19	Not regulated	267533_at	NC-NC-NC	A2g42070	MutT/nudix family protein similar to SP Q58549 ADP-ribase pyrophosphatase (EC 3.6.1.13) [Methanococcus jannaschii]; contains Pfam profile PF00293: NUDIX domain (68415.m05520)
20	Not regulated	267535_at	NC-NC-NC	A2g41940	zinc finger (C2H2 type) domain contains Pfam domain, PF00096: Zinc finger, C2H2 type (68415.m05188)
21	Not regulated	267539_at	NC-NC-NC	A2g42030	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (68415.m05198)
22	Not regulated	267544_at	NC-NC-NC	A2g32720	cytochrome b5, putative similar to Cytochrome B5 SP:P49098 from [Nicotiana tabacum] (68415.m04004)
23	Not regulated	267553_s_at	NC-NC-NC	A2g32850	expressed protein contains Pfam PF05895: Protein of unknown function (DUF-661) (68415.m03388)
24	Not regulated	267561_at	NC-NC-NC	A2g45590	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (68415.m05669)
25	Not regulated	267498_at	NC-NC-NC	A2g45720	armadillo/beta-catenin repeat family protein contains Pfam profile PF00514: Armadillo/beta-catenin-like repeat (68415.m05686)
26	Not regulated	267504_at	NC-NC-NC	A2g45530	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00087 zinc finger, C3HC4 type (RING finger) (68415.m05682)
27	Not regulated	267506_at	NC-NC-NC	A2g45520	expressed protein (68415.m05661)
28	Not regulated	267507_at	NC-NC-NC	A2g45710	40S ribosomal protein S27 (RPS27A) (68415.m05685)
29	Not regulated	267510_at	NC-NC-NC	A2g45640	sin3 associated polypeptide p18 family protein similar to Sin3 associated polypeptide p18 (2H0R0202) (Swiss-Prot:O00422) [Homo sapiens] (68415.m05675)
30	Not regulated	267511_at	NC-NC-NC	A2g45670	calchectin B subunit-related contains Pfam PF00038: EF hand domain and Prosite PS00018: EF-hand calcium-binding domain; contains Pfam profile PF01553: Acyltransferase, weak similarity to Calchectin B subunit isoform 2 (Protein phosphatase 2B regulatory subunit 2) (Protein phosphatase 3 regulatory subunit B alpha isoform 2) (Swiss-Prot:O63811) [Mus musculus] (68415.m05678)
31	Not regulated	267513_at	NC-NC-NC	A2g45620	nucleotidyltransferase family protein low similarity to SP Q13833: Caffeine-induced death protein 1 (Schizosaccharomyces pombe); contains Pfam profiles PF03828: PAP25A associated domain, PF01809: Nucleotidyltransferase domain (68415.m05672)
32	Not regulated	267515_at	NC-NC-NC	A2g45680	TCP family transcription factor, putative similar to PCF2 (G1250440) [Oryza sativa] (68415.m05680)
33	Not regulated	267517_at	NC-NC-NC	A2g30510	expressed protein contains 4 predicted transmembrane domains; similar to c_p0040404298r (G1:14597780) [Physcomitrella patens] (68415.m03710)
34	Not regulated	267520_at	NC-NC-NC	A2g30460	photosystem II reaction center W (PsbW) protein-related similar to photosystem II reaction center W protein SP:Q41387 from [Spinacia oleracea] (68415.m03723)
35	Not regulated	267526_at	NC-NC-NC	A2g30570	plastocyanin-like domain-containing protein / plantacyanin, putative similar to plantacyanin G1:3395754 from [Spinacia oleracea] (68415.m00234)
36	Not regulated	267472_at	NC-NC-NC	A2g02850	protein kinase (APK2b) identical to protein kinase APK2b [Arabidopsis thaliana] g12852449dbj BAA24695 (68415.m00224)
37	Not regulated	267486_at	NC-NC-NC	A2g02800	S-louc lectin protein kinase family protein contains Pfam domain PF00954: S-louc glycoprotein family, PF00068: Protein kinase domain and PF01453: Lectin (probable mannose binding) (68415.m02233)
38	Not regulated	267490_at	NC-NC-NC	A2g19130	domain and PF01453: Lectin (probable mannose binding) (68415.m02233)
39	Not regulated	267442_at	NC-NC-NC	A2g19080	melaxin-related contains 1 transmembrane domain; similar to Melaxin 1 (component of a preprotein import complex) (Swiss-Prot:P47802) [Mus musculus]; (68415.m02228)
40	Not regulated	267446_s_at	NC-NC-NC	A2g33840	tRNA synthetase class I (W and Y) family protein similar to SP P54577 Tyrosyl-tRNA synthetase (EC 6.1.1.1) (Tyrosyl-tRNA ligase) (TyRS) (Homo sapiens); contains Pfam profile PF00578: tRNA synthetases class I (W and Y) (68415.m04153)
41	Not regulated	267448_at	NC-NC-NC	A2g33700	protein phosphatase 2C, putative / PP2C, putative contains PF00481: Protein phosphatase 2C domain; similar to protein phosphatase-2C (PP2C) (G1:3643085) [Mesembryanthemum crystallinum] (68415.m04130)
42	Not regulated	267459_at	NC-NC-NC	A2g33850	expressed protein contains 1 transmembrane domain; similar to Protein E8 (Swiss-Prot:Q01187) [Gossypium hirsutum] (68415.m04155)
43	Not regulated	267463_at	NC-NC-NC	A2g33845	DNA-binding protein-related contains weak similarity to G-quartet DNA binding protein 3 [Tetrahymena thermophila] (68415.m04155)
44	Not regulated	267435_at	NC-NC-NC	A2g33800	ribosomal protein S5 family protein contains Pfam profiles PF03719: Ribosomal protein S5, C-terminal domain, PF00333: Ribosomal protein S5, N-terminal domain (68415.m04147)
45	Not regulated	267405_at	NC-NC-NC	A2g33740	copper-binding protein (CUTA) identical to copper-binding protein CUTA G1:12963361 from [Arabidopsis thaliana]; contains Pfam profile: PF03061 CuA1 divalent ion tolerance protein (68415.m04136)
46	Not regulated	267413_at	NC-NC-NC	A2g34960	amino acid permease family protein similar to cationic amino acid transporter 3 [Rattus norvegicus] G1:2116552; contains Pfam profile PF00324: Amino acid permease (68415.m04290)
47	Not regulated	267419_at	NC-NC-NC	A2g335010	thioredoxin family protein similar to SP Q42443 Thioredoxin H-type (TRX-H) (Oryza sativa); contains Pfam profile: PF00085 Thioredoxin (68415.m04295)
48	Not regulated	267421_at	NC-NC-NC	A2g335040	AICARFT/IMPCHase bienzyme family protein similar to SP P12048 Bifunctional purine biosynthesis protein purH [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) (AICAR transformylase); IMP cyclohydrolase (EC 3.5.4.10) (inosinicase) (IMP synthetase) (ATIC)] [Bacillus subtilis]; contains Pfam profiles PF01808: AICARFT/IMPCHase bienzyme, PF02142: MGS-like domain (68415.m04296)
49	Not regulated	267423_at	NC-NC-NC	A2g335060	potassium transporter family protein similar to HAK2 [Hordeum vulgare] G1:708599; potassium transporter HAK2p [Mesembryanthemum crystallinum] g11409147 lg BAAK53759; KUP/HAK/KT Transporter family member, PMID:11500583; contains Pfam profile PF02705: K+ potassium transporter (68415.m04301)
50	Not regulated	267430_at	NC-NC-NC	A2g34860	chaperone protein dnaJ-related contains Pfam PF00684: DnaJ central domain (4 repeats); similar to Chaperone protein dnaJ [Heat shock protein 40] (SP:Q9U9R9) [Methanoscintia thermophila] (68415.m04260)
51	Not regulated	267432_at	NC-NC-NC	A2g335020	UTP--glucose-1-phosphate undiyltransferase family protein similar to SP Q18222 UDP-N-acetylhexosamine pyrophosphorylase (Anigen X) (Homo sapiens); contains Pfam profile PF01704: UTP--glucose-1-phosphatase undiyltransferase (68415.m04296)
52	Not regulated	267401_at	NC-NC-NC	A2g28210	ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023 (68415.m03147)
53	Not regulated	267374_at	NC-NC-NC	A2g28230	uncase / urate oxidase / nodulin 35

54	Not regulated	NC-NC-NC	267375_at	guanine nucleotide binding protein (G-protein) alpha-1 subunit / GP-alpha-1 (GPA1) identical to SPp18064 Guanine nucleotide-binding protein alpha-1 subunit (Arabidopsis thaliana) (88415.m03156)
55	Not regulated	NC-NC-NC	267377_at	beta-ketacyl-CoA synthase family (FIDDLEHEAD) (FHD) identical to GB.AJ010713 (fiddlehead protein) (88415.m03151)
56	Not regulated	NC-NC-NC	267385_at	DC1 domain-containing protein highly similar to GP2435515(AF024504; contains Pfam profile PF03107: DC1 domain (88415.m05520)
57	Not regulated	NC-NC-NC	267393_at	expressed protein contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as 'axi 1 protein from Nicotiana tabacum -related' based on similarity to axi 1 protein (GB:X80301) (GI:558920) from [Nicotiana tabacum], which, due to scientific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497. (88415.m05532)
58	Not regulated	NC-NC-NC	267385_at	ribose-phosphate pyrophosphokinase, putative / phosphonbonyl diphosphate synthetase, putative very strong similarity to phosphonbonyl pyrophosphatase [Spiraea olaracea] (GI:4802848; contains Pfam profile PF00156: Phosphonbonyl transferase domain (88415.m05539))
59	Not regulated	NC-NC-NC	267342_at	UbaA prenyltransferase family protein similar to SP(Q12887) Protoheme IX larnesyltransferase, mitochondrial precursor (EC 2.5.1.-) (Heme O synthase) (Homo sapiens), SP(P21592) COX10 (Saccharomyces cerevisiae) (88415.m05535)
60	Not regulated	NC-NC-NC	267346_at	coronatin-insensitive 1 / COI1 (FBL2) E3 ubiquitin ligase SCF complex F-box subunit; identical to LRR-containing F-box protein (88415.m04808)
61	Not regulated	NC-NC-NC	267348_at	GI:3158394 from [Arabidopsis thaliana] (88415.m04808)
62	Not regulated	NC-NC-NC	267358_at	microsomal signal peptidase 25 kDa subunit, putative (SPC25) identical to Probable microsomal signal peptidase 25 kDa subunit (EC 3.4.-.-) (SPase 25 kDa subunit) (SPC25) (Swiss-Prot:P58684) [Arabidopsis thaliana]; contains non-consensus AT-AC splice sites; contains 1 transmembrane domain; (88415.m04810)
63	Not regulated	NC-NC-NC	267360_at	proline transporter 1 (ProT1) identical to proline transporter 1 GI:1769901 from [Arabidopsis thaliana] (88415.m04903)
64	Not regulated	NC-NC-NC	267363_at	expressed protein (88415.m04822)
65	Not regulated	NC-NC-NC	267338_at	peroxisomal membrane protein (PMP36) identical to 38kDa-peroxisomal membrane protein (PMP36) GI:15146342 from [Arabidopsis thaliana] (88415.m04911)
66	Not regulated	NC-NC-NC	267312_at	eukaryotic translation initiation factor 3 subunit 5 (eIF-3 epsilon) / eIF3i (TIF3F1) identical to SPIO04202 Eukaryotic translation initiation factor 3 subunit 5 (eIF-3 epsilon) (eIF3 p32 subunit) (eIF3i) [Arabidopsis thaliana]; contains Pfam profile PF01398: RNA polymerase I specific transcription initiation factor RRN3 (GI:7670100) [Homo sapiens] similar to RNA polymerase I specific transcription initiation factor RRN3 (Swiss-Prot:P36070) [Saccharomyces cerevisiae] (88415.m04287)
67	Not regulated	NC-NC-NC	267315_at	CCAAT-binding transcription factor (CBF-BNF-YA) family protein contains Pfam profile: PF02045 CCAAT-binding transcription factor (CBF-BNF-YA) subunit B (88415.m04284)
68	Not regulated	NC-NC-NC	267323_at	membrane protein, putative contains 3 transmembrane domains; (88415.m08034)
69	Not regulated	NC-NC-NC	267330_at	expressed protein (88415.m02248)
70	Not regulated	NC-NC-NC	267309_at	expressed protein weak similarity to Cell growth regulating nucleolar protein (Swiss-Prot:Q08288) [Mus musculus] (88415.m02261)
71	Not regulated	NC-NC-NC	267278_at	expressed protein (88415.m02258)
72	Not regulated	NC-NC-NC	267280_at	diacylglycerol O-acyltransferase / acyl CoA diacylglycerol acyltransferase (DGAT) identical to gi:5050613. gi:5825553 (88415.m02272)
73	Not regulated	NC-NC-NC	267290_at	SET domain-containing protein similar to SP(Q60018) Cryptic loci regulator 4 (Histone-lysine N-methyltransferase) (Schizosaccharomyces pombe); contains Pfam profile PF00856: SET domain (88415.m02835)
74	Not regulated	NC-NC-NC	267297_at	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (88415.m02840)
75	Not regulated	NC-NC-NC	267302_at	ubiquitin family protein low similarity to SP(Q9UQ13) Leucine-rich repeat protein SHOC-2 (Ras-binding protein Sur-8) (Homo sapiens); contains Pfam profiles PF00240: Ubiquitin family, PF01535: PPR repeat, PF00560: Leucine Rich Repeat (88415.m03683)
76	Not regulated	NC-NC-NC	267306_at	Ran-binding protein 1b (RanBP1b) nearly identical to atranbp1b [Arabidopsis thaliana] GI:2058284 (88415.m03656)
77	Not regulated	NC-NC-NC	267307_at	laccase, putative / diphenol oxidase, putative similar to laccase [Populus balsamifera subsp. trichocarpa] (GI:3805960) (88415.m03874)
78	Not regulated	NC-NC-NC	267277_at	transducin family protein / WD-40 repeat family protein similar to SEC13-related protein (SP:P55735) [Homo sapiens] (88415.m03654)
79	Not regulated	NC-NC-NC	267247_at	expressed protein (88415.m03871)
80	Not regulated	NC-NC-NC	267251_at	casein kinase II alpha chain, putative similar to casein kinase II, alpha chain (CK II) [Zea mays] SWISS-PROT:P28523; contains protein kinase domain, Pfam:PF00069 (88415.m02750)
81	Not regulated	NC-NC-NC	267257_at	casein kinase II alpha chain, putative identical to probable casein kinase II, alpha chain [Arabidopsis thaliana] SWISS-PROT:Q08487 (88415.m02751)
82	Not regulated	NC-NC-NC	267258_at	PROT:Q04817; similar to casein kinase II, alpha chain II, alpha chain domain-containing protein contains Pfam domain, PF00514: Armadillo/beta-actinin-like repeats and Pfam, PF04584: U-box domain (88415.m02763)
83	Not regulated	NC-NC-NC	267260_at	cattenin-like repeats and Pfam, PF04584: U-box domain (88415.m02759)
84	Not regulated	NC-NC-NC	267262_at	arabinogalactan-protein (AGP17) identical to gi.11935086_gb_AAG41863 (88415.m02759)
85	Not regulated	NC-NC-NC	267265_at	sinapoylglucose:malate sinapoyltransferase (SNG1) similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza sativa]; contains Pfam profile PF00450: Serine carboxypeptidase; identical to cDNA sinapoylglucose:malate sinapoyltransferase (SNG1) (88415.m02733)
86	Not regulated	NC-NC-NC	267268_at	GI:8698618 (88415.m02733)
87	Not regulated	NC-NC-NC	267226_at	serine carboxypeptidase S10 family protein similar to serine carboxypeptidase I precursor (SP:P37890) from [Oryza sativa] (88415.m02731)
88	Not regulated	NC-NC-NC	267266_at	NRAMP metal ion transporter 3 (NRAMP3) identical to metal transporter Nramp3 [Arabidopsis thaliana] gi 6488012 p AAAF13278; member of the natural resistance-associated macrophage protein (NRAMP) metal transporter family, PMID:11500563 (88415.m02765)
89	Not regulated	NC-NC-NC	267226_at	expressed protein (88415.m05472)

88	Not regulated	NC-NC-NC	267233_s_at	A12g43920	thiol methyltransferase, putative similar to thiol methyltransferase 1 [Gi:14583119 from <i>Brassica oleracea</i>] (68415.m05459)
89	Not regulated	NC-NC-NC	267236_at	A12g44100	Rab GDP dissociation inhibitor (GDI1) identical to GDP dissociation inhibitor [Arabidopsis thaliana] Gi:1655424 (68415.m05464)
90	Not regulated	NC-NC-NC	267211_at	A12g44065	ribosomal protein L2 family protein similar to ribosomal protein L2 [Gossypium arboreum] Gi:17644114; contains Pfam profile PF03947; Ribosomal Proteins L2, C-terminal domain (68415.m05476)
91	Not regulated	NC-NC-NC	267212_at	A12g44060	late embryogenesis abundant family protein / LEA family protein similar to ethylene-responsive late embryogenesis-like protein [Lycopersicon esculentum] Gi:1684830; contains Pfam profile PF03166; Late embryogenesis abundant protein (68415.m05477)
92	Not regulated	NC-NC-NC	267185_at	A12g43950	expressed protein (68415.m05463)
93	Not regulated	NC-NC-NC	267188_at	A12g44050	6,7-dimethyl-8-ribityllumazine synthase / DMRL synthase / lumazine synthase / riboflavin synthase identical to 6,7-dimethyl-8-ribityllumazine synthase, chloroplast [precursor] SP_O80575 from [Arabidopsis thaliana] (68415.m05478)
94	Not regulated	NC-NC-NC	267189_at	A12g44180	methionyl aminopeptidase, putative / methionine aminopeptidase, putative / peptidase M, putative similar to SPIP50579 Methionine aminopeptidase 2 (EC 3.4.11.19) [MeAP 2] (Homo sapiens); contains Pfam profile PF00557; metalloprotease family M24 (68415.m05496)
95	Not regulated	NC-NC-NC	267186_at	A12g30950	FtsH protease (VAR2) identical to zinc dependent protease VAR2 Gi:7650138 from [Arabidopsis thaliana] (68415.m03775)
96	Not regulated	NC-NC-NC	267208_at	A12g30980	shaggy-related protein kinase delta / ASK-delta / ASK4 identical to shaggy-related protein kinase delta (ASK-delta) (ASK-delta) [Arabidopsis thaliana] SWISS-PROT:Q39010 (68415.m03778)
97	Not regulated	NC-NC-NC	267151_at	A12g30970	aspartate aminotransferase, mitochondrial / transaminase A (ASP1) identical to SPIP46643 Aspartate aminotransferase, mitochondrial precursor (EC 2.8.1.1) [Transaminase A] [Arabidopsis thaliana] (68415.m03777)
98	Not regulated	NC-NC-NC	267152_at	A12g31040	ATP synthase protein I -related contains weak similarity to Swiss-Prot:P08443 ATP synthase protein I [Synechococcus sp.] (68415.m03786)
99	Not regulated	NC-NC-NC	267153_at	A12g30860	glutathione S-transferase, putative identical to GB-Y12295 (68415.m03761)
100	Not regulated	NC-NC-NC	267161_at	A12g37680	phytochrome A specific signal transduction component (PAT3) / far-red elongated hypocotyl protein 1 (FHY1) identical to phytochrome A specific signal transduction component PAT3 [Arabidopsis thaliana] gi19421968[gb AA187850; identical to far-red elongated hypocotyl protein 1 [Arabidopsis thaliana] gi17148773[gb AA135819 (68415.m04621)
101	Not regulated	NC-NC-NC	267171_at	A12g37590	Dof-type zinc finger domain-containing protein (68415.m04612)
102	Not regulated	NC-NC-NC	267175_s_at	A12g37620	actin 1 (ACT1) identical to SPIP10871 Actin 1 (Actin 3) [Arabidopsis thaliana] (68415.m04615)
103	Not regulated	NC-NC-NC	267179_at	A12g37550	arabidopsis pde1 suppressor 1 protein (ASP1) identical to arabidopsis pde1 suppressor 1 (Asp1) from Gi:4519782 [Arabidopsis thaliana]; contains InterPro accession IPR001164; Human Rev interacting-like protein (hRIP) (68415.m04605)
104	Not regulated	NC-NC-NC	267180_at	A12g37570	expressed protein (68415.m04608)
105	Not regulated	NC-NC-NC	267181_at	A12g37760	aldo-keto reductase family protein similar to chalcone reductase [Sesbania rostrata][Gi:2792155], and aldose reductase ALDRXV4 [Xerophyta viscosa][Gi:4539644], [Hordium vulgare][Gi:729592] (68415.m04633)
106	Not regulated	NC-NC-NC	267121_at	A12g23540	GDSL-motif lipase/hydrolase family protein similar to family II lipase EXL1 Gi:15054382 from [Arabidopsis thaliana]; contains Pfam profile PF00657; GDSL-like Lipase/Acylhydrolase (68415.m02809)
107	Not regulated	NC-NC-NC	267127_at	A12g23610	esterase, putative similar to ethylene-induced esterase [Citrus sinensis] Gi:14279437; polynuclear aldehyde esterase [Rauvolfia serpentina] Gi:8651393; contains Pfam profile PF00561; hydrolase, alpha/beta fold family (68415.m02817)
108	Not regulated	NC-NC-NC	267128_at	A12g23620	esterase, putative similar to ethylene-induced esterase [Citrus sinensis] Gi:14279437; polynuclear aldehyde esterase [Rauvolfia serpentina] Gi:8651393; contains Pfam profile PF00561; hydrolase, alpha/beta fold family (68415.m02818)
109	Not regulated	NC-NC-NC	267132_at	A12g23420	nicotinate phosphoribosyltransferase (NAPRTase) (68415.m02796)
110	Not regulated	NC-NC-NC	267134_at	A12g23450	phosphoribosyltransferase family protein contains protein kinase domain, Pfam:PF00069 (68415.m02798)
111	Not regulated	NC-NC-NC	267142_at	A12g38290	ammonium transporter 2 (AMT2) identical to SPIQBM6N7 Ammonium transporter 2 (AMT2) [Arabidopsis thaliana] (68415.m04703)
112	Not regulated	NC-NC-NC	267145_at	A12g38130	GCN5-related N-acetyltransferase, putative similar to SPIQ3503 L-A virus GAG protein N-acetyltransferase (EC 2.3.1.-) (68415.m04680)
113	Not regulated	NC-NC-NC	267098_at	A12g38140	(Saccharomyces cerevisiae); contains Pfam profile PF00583; acetyltransferase, GNAT family (68415.m04682)
114	Not regulated	NC-NC-NC	267090_at	A12g38270	chloroplast 30S ribosomal protein S31 (PSRP4) (68415.m04682)
115	Not regulated	NC-NC-NC	267092_at	A12g38120	CAX-interacting protein, putative identical to cDNA CAXIP1-like protein Gi:27752306; contains Pfam profile PF00462; Glutaredoxin; contains TIGRfam profile TIGR00365; glutaredoxin-related protein (68415.m04700)
116	Not regulated	NC-NC-NC	267093_at	A12g38170	amino acid permease, putative (AUX1) identical to AUX1 Gi:1531758 from [Arabidopsis thaliana] (68415.m04678)
117	Not regulated	NC-NC-NC	267094_at	A12g38080	calcium exchanger (CAX1) identical to high affinity calcium antiporter CAX1 [Arabidopsis thaliana] gi9256741[gb AA805913, except a possible frameshift at base 58008. Sequence has been confirmed with 5 sequencing reads.; Cax2-Cation Antiporter (CaCA) Family member PMID:11500563 (68415.m04685)
118	Not regulated	NC-NC-NC	267095_at	A12g38280	laccase, putative / diphenol oxidase, putative similar to diphenol oxidase [Nicotiana tabacum][Gi:1685087] (68415.m04674)
119	Not regulated	NC-NC-NC	267096_at	A12g38180	AMP deaminase, putative / myoadenylate deaminase, putative similar to SPIP15274 AMP deaminase (EC 3.5.4.6) [Myoadenylate deaminase] [Saccharomyces cerevisiae]; contains Pfam profile PF00982; Adenosine/AMP deaminase (68415.m04701)
120	Not regulated	NC-NC-NC	267102_at	A12g41500	GDSL-motif lipase/hydrolase family protein similar to SPIP41734 Icanmyl acetate-hydrolyzing esterase (EC 3.1.-) [Saccharomyces cerevisiae]; contains Pfam profile PF00657; Lipase/Acylhydrolase with GDSL-like motif (68415.m04688)
121	Not regulated	NC-NC-NC	267106_s_at	A12g14740	WD-40 repeat family protein / small nuclear ribonucleoprotein Prp4-related similar to U4/U6 small nuclear ribonucleoprotein hPrp4 (GP-2708305) (Homo sapiens); contains Pfam PF00400; WD domain, G-beta repeat (7
122	Not regulated	NC-NC-NC	267057_at	A12g32500	copies)[19877698][gb AU238529.1AU238529 (68415.m05127)
123	Not regulated	NC-NC-NC	267059_at	A12g32520	vacuolar sorting receptor, putative nearly identical to vacuolar sorting receptor homolog [Arabidopsis thaliana] Gi:1737220; contains a calcium-binding EGF-like domain signature (68415.m01662)
124	Not regulated	NC-NC-NC	267062_at	A12g32600	expressed protein (68415.m03971)
					dieneolase hydrolase family protein low similarity to dieneolase hydrolase [Pseudomonas resinovorans] Gi:13094163; contains Pfam profile PF01738; Dieneolase hydrolase family (68415.m03973)
					hydroxyproline-rich glycoprotein family protein similar to SWISS-PROT:Q15428 (68415.m03980)

125	Not regulated	NC-NC-NC	267063_at	A12g41120	expressed protein (68415.m05079)
126	Not regulated	NC-NC-NC	267064_at	A12g41110	calmodulin-2/3/5 (CAM2) (CAL1) almost identical to Calmodulin-2/2/5 SP:P25069 from [Arabidopsis thaliana] (68415.m05078)
127	Not regulated	NC-NC-NC	267069_at	A12g41010	VQ motif-containing protein contains PF05878; VQ motif (68415.m05065)
128	Not regulated	NC-NC-NC	267073_at	A12g41160	ubiquitin-associated (UBA)/ITS-N domain-containing protein contains Pfam profile PF00627; UBA/ITS-N domain (68415.m05084)
129	Not regulated	NC-NC-NC	267077_at	A12g40970	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain (68415.m05060)
130	Not regulated	NC-NC-NC	267080_at	A12g41190	amino acid transporter family protein low similarity to vesicular GABA transporter [Rattus norvegicus] Gi:2587081; belongs to INTERPRO:IPR002422 amino acid/polyamine transporter, family II (68415.m05087)
131	Not regulated	NC-NC-NC	267084_at	A12g41180	sigA-binding protein-related low similarity to SigA binding protein [Arabidopsis thaliana] Gi:6980074; contains Pfam domain PF05878; VQ motif (68415.m05086)
132	Not regulated	NC-NC-NC	267052_at	A12g38410	VHS domain-containing protein / GAT domain-containing protein weak similarity to hepatocyte growth factor-regulated tyrosine kinase substrate HRS isoform 2 [Homo sapiens] Gi:9022389; contains Pfam profiles PF00780; VHS domain, PF03127; GAT domain (68415.m04718)
133	Not regulated	NC-NC-NC	267027_at	A12g38330	MATE efflux family protein low similarity to enhanced disease susceptibility 5 [Arabidopsis thaliana] Gi:16589070; contains Pfam profile PF01554; Uncharacterized membrane protein family (68415.m04709)
134	Not regulated	NC-NC-NC	267033_at	A12g38450	expressed protein (68415.m04722)
135	Not regulated	NC-NC-NC	266996_at	A12g34490	cytochrome P450 family similar to Cytochrome P450 81 (C-22 sterol desaturase) (SP:P54781) [Saccharomyces cerevisiae]; contains Pfam profile: PF00067 cytochrome P450; supported by full-length cDNA: Ceres:158108. (68415.m04235)
136	Not regulated	NC-NC-NC	267000_at	A12g34310	expressed protein (68415.m04197)
137	Not regulated	NC-NC-NC	267002_s_at	A12g34430	chlorophyll A-B binding protein / LHClI type I (LHB1B1) identical to photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] Gi:16368 (68415.m04223)
138	Not regulated	NC-NC-NC	267004_at	A12g34260	transducin family protein / WD-40 repeat family protein similar to Vegetalite incompatibility protein HET-E-1 (SP:Q00808) [Podospira anserina] (68415.m04191)
139	Not regulated	NC-NC-NC	266998_at	A12g39310	jacalin lectin family protein similar to myrosinase-binding protein homolog [Arabidopsis thaliana] Gi:2987787; contains Pfam profile PF01419 jacalin-like lectin domain (68415.m04826)
140	Not regulated	NC-NC-NC	266991_at	A12g39290	phosphatidyglycerolphosphate synthase (PGS1) identical to phosphatidyglycerolphosphate synthase Gi:13365518 from [Arabidopsis thaliana] (68415.m04824)
141	Not regulated	NC-NC-NC	266963_at	A12g39450	cation efflux family protein contains cation efflux family protein domain, Pfam:PF01545 (68415.m04842)
142	Not regulated	NC-NC-NC	266975_at	A12g39380	exocyst subunit EXO70 family protein contains Pfam domain PF03081; Exo70 exocyst complex subunit; (68415.m04833)
143	Not regulated	NC-NC-NC	266977_at	A12g39420	esterase/lipase/cholesterase family protein similar to monoglyceride lipase from [Homo sapiens] Gi:14594904, [Mus musculus] Gi:2632162; contains Interpro entry IPR000379 (68415.m04833)
144	Not regulated	NC-NC-NC	266978_at	A12g39430	disease resistance protein-related / divergent protein-related contains similarity to disease resistance response protein 206-d [Pisum sativum] gi:508844(gb AAAB18669; contains similarity to divergent protein [Thuja plicata] gi:6894705(gb AAAF25365 (68415.m04840)
145	Not regulated	NC-NC-NC	266979_at	A12g39470	photosystem II reaction center PsaP family protein (68415.m04844)
146	Not regulated	NC-NC-NC	266938_at	A12g18950	homogenisate phytyltransferase family protein (HPT1) / tocopherol phytyltransferase family protein (TPT1) identical to gi:17104828; contains Pfam profile PF01040; Uba1 prenyltransferase family; identical to cDNA tocopherol polyphenyltransferase (TPT1) Gi:17104827 (68415.m02212)
147	Not regulated	NC-NC-NC	266948_at	A12g18850	SET domain-containing protein low similarity to ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I [Spinacia oleracea] Gi:3403236; contains Pfam profile PF00856; SET domain (68415.m02196)
148	Not regulated	NC-NC-NC	266950_at	A12g18910	hydroxyproline-rich glycoprotein family protein (68415.m02208)
149	Not regulated	NC-NC-NC	266955_at	A12g34520	ribosomal protein S14 mitochondrial family protein identical to ribosomal protein S14 (Arabidopsis thaliana) NCBI_gi:4583554 (68415.m04240)
150	Not regulated	NC-NC-NC	266956_at	A12g34510	expressed protein contains Pfam profile PF04882; Protein of unknown function, DUFB42 (68415.m04239)
151	Not regulated	NC-NC-NC	266958_at	A12g34630	geranyl diphosphate synthase, putative / GPPS; putative / dimethylallyltransferase, putative / prenyl transferase, putative identical to Gi:11322985 A. thaliana geranyl diphosphate synthase (68415.m04254)
152	Not regulated	NC-NC-NC	266899_at	A12g34620	mitochondrial transcription termination factor-related / mTERF-related contains Pfam profile PF02536; mTERF (68415.m04253)
153	Not regulated	NC-NC-NC	266904_at	A12g34590	transketolase family protein similar to SPO66113 Pyruvate dehydrogenase E1 component, beta subunit (EC 1.2.4.1). [Zymomonas mobilis]; contains Pfam profiles PF02779; Transketolase, pyridine binding domain, PF02780; Transketolase, C-terminal domain (68415.m04250)
154	Not regulated	NC-NC-NC	266911_at	A12g45910	protein kinase family protein / U-box domain-containing protein contains Pfam profiles PF00069 Eukaryotic protein kinase domain, PF04584; U-box domain, supported by tandem duplication of (Gi:3388604) (TIGR_Ath1:A2g45920) [Arabidopsis thaliana]
155	Not regulated	NC-NC-NC	266924_at	A12g45730	eukaryotic initiation factor 3 gamma subunit family protein contains Pfam profile PF04189; Eukaryotic initiation factor 3, gamma subunit (68415.m05688)
156	Not regulated	NC-NC-NC	266896_at	A12g45810	DEAD/DEAH box helicase, putative (68415.m05687)
157	Not regulated	NC-NC-NC	266898_at	A12g45990	expressed protein (68415.m05718)
158	Not regulated	NC-NC-NC	266876_at	A12g44820	expressed protein (68415.m05578)
159	Not regulated	NC-NC-NC	266885_at	A12g44610	Ras-related GTP-binding protein, putative similar to GTP-binding protein Gi:623588 from [Nicotiana tabacum] ; contains an ADP-ribosylation factors family signature for proteins involved in protein trafficking (68415.m05553)
160	Not regulated	NC-NC-NC	266887_at	A12g44650	chloroplast chaperonin 10 (cpn10) identical to chloroplast chaperonin 10 Gi:14041813 from [Arabidopsis thaliana] (68415.m05557)
161	Not regulated	NC-NC-NC	266889_at	A12g44640	expressed protein (68415.m05556)

162	Not regulated	A2g44620	266890_at	NC-NC-NC	acyl carrier protein, mitochondrial / ACP / NADH-ubiquinone oxidoreductase 9.8 kDa subunit identical to SPIP53665 Acyl carrier protein, mitochondrial precursor (ACP) (NADH-ubiquinone oxidoreductase 9.8 kDa subunit) (MIACP-1) [Arabidopsis thaliana]; identical to cDNA acyl carrier protein precursor GI:468265 (88415.m05554)
163	Not regulated	A2g25980	266898_at	NC-NC-NC	jacalin lectin family protein similar to myrosinase-binding protein homolog [Arabidopsis thaliana] GI:2987787; contains Pfam profile PF01419 jacalin-like lectin domain (88415.m03120)
164	Not regulated	A2g28110	266945_at	NC-NC-NC	expressed protein (88415.m03133)
165	Not regulated	A2g25970	266846_at	NC-NC-NC	KH domain-containing protein (88415.m03117)
166	Not regulated	A2g26060	266847_at	NC-NC-NC	transducin family protein / WD-40 repeat family protein contains 7 WD-40 repeats (PF00400); similar to WD40-repeat containing protein Cio 1 (SP.076071) [Homo sapiens] (88415.m03129)
167	Not regulated	A2g25950	266848_at	NC-NC-NC	expressed protein (88415.m03115)
168	Not regulated	A2g26920	266855_at	NC-NC-NC	ubiquitin-associated (UBA)/TS-N domain-containing protein contains Pfam profile PF00627: UBA/TS-N domain (88415.m03229)
169	Not regulated	A2g26830	266861_at	NC-NC-NC	cholesterolamine kinase family protein similar to SPIQ9HBU8 Ethanolamine kinase (EC 2.7.1.82) (EKI)(Homo sapiens), GmCK3p (Glycine max) GI:1438883; contains Pfam profile PF01633: Choline/ethanolamine kinase (88415.m03219)
170	Not regulated	A2g28930	266863_at	NC-NC-NC	4-diphosphocytidylyl-2-C-methyl-D-erythritol kinase (CMK) (CDPMEK) identical to 4-diphosphocytidylyl-2-C-methyl-D-erythritol kinase, chloroplast precursor (CMK) (4-cytidine-5'-diphospho)-2-C-methyl-D-erythritol kinase (CDPMEK) [Arabidopsis thaliana] SWISS-PROT:Q61014 (88415.m03230)
171	Not regulated	A2g29980	266865_at	NC-NC-NC	omega-3 fatty acid desaturase, endoplasmic reticulum (FAD3) identical to SP_46823 (88415.m03646)
172	Not regulated	A2g29960	266835_at	NC-NC-NC	pyridine nucleotide-disulphide oxidoreductase family protein similar to SPIP23240 Rotenone-insensitive NADH-ubiquinone oxidoreductase, mitochondrial precursor (EC 1.8.5.3) (Internal NADH dehydrogenase) [Saccharomyces cerevisiae]; contains Pfam profile PF00070: Pyridine nucleotide-disulphide oxidoreductase (88415.m03646)
173	Not regulated	A2g30000	266806_at	NC-NC-NC	expressed protein contains Pfam domain PF03660: Uncharacterized protein family (UPF0123) (88415.m03650)
174	Not regulated	A2g44920	266813_at	NC-NC-NC	thylakoid lumenal 15 kDa protein, chloroplast identical to SPIQ22160 Thylakoid lumenal 15 kDa protein, chloroplast precursor (p15) [Arabidopsis thaliana]; contains 8 pentapeptide repeats (88415.m05591)
175	Not regulated	A2g44900	266815_at	NC-NC-NC	armadillo-beta-catenin repeat family protein / F-box family protein contains similarity to F-box protein FBL2 GI:6010699 from [Rattus norvegicus]; contains Pfam profiles PF00514: Armadillo-beta-catenin-like repeat, PF00646: F-box domain (88415.m05598)
176	Not regulated	A2g44870	266819_at	NC-NC-NC	expressed protein (88415.m05598)
177	Not regulated	A2g22860	266799_at	NC-NC-NC	phytoalexin 2 (PSK2) identical to phytoalexins 2 (PSK2) from [Arabidopsis thaliana] (88415.m02714)
178	Not regulated	A2g28950	266790_at	NC-NC-NC	expansin, putative (EXPA) similar to expansin GI:2828241 from [Brassica napus]; contains Pfam profile PF01357: Pollen allergen (88415.m03521)
179	Not regulated	A2g02860	266791_at	NC-NC-NC	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger); contains PROSITE PS00190: Cytochrome c family heme-binding site signature (88415.m00244)
180	Not regulated	A2g02860	266792_at	NC-NC-NC	sucrose transporter / sucrose-proton symporter (SUC3) identical to sucrose transporter [Arabidopsis thaliana] GI:8052190; similar to sucrose transporters from [Oryza sativa] (apoptical cultivar-group) GI:2723471, [Zea mays] GI:5771354, [Triticum aestivum] GI:19548165; contains Pfam profile PF00083: major facilitator superfamily protein (88415.m00235)
181	Not regulated	A2g02860	266796_at	NC-NC-NC	mucin-related similar to putative mucin GI:18071389 [Oryza sativa] (88415.m00238)
182	Not regulated	A2g03090	266770_at	NC-NC-NC	expansin, putative (EXP15) identical to SWISS-PROT:O60622 alpha-expansin 15 precursor (At-EXP15)[Arabidopsis thaliana]; alpha-expansin gene family, PMID:11641069 (88415.m00262)
183	Not regulated	A2g02970	266744_at	NC-NC-NC	nucleoside triphosphatase family protein / GDA/CD39 family protein low similarity to SPIP55772 Ectonucleoside triphosphatase diphosphohydrolase 1 (EC 3.6.1.5) (Ecto-apyrase) [Mus musculus]; contains Pfam profile PF01150: GDA/CD39 (nucleoside triphosphatase) family (88415.m00249)
184	Not regulated	A2g02850	266745_at	NC-NC-NC	phytochrome kinase substrate 1 (PKS1) identical to Swiss-Prot:Q8SW11 phytochrome kinase substrate 1 [Arabidopsis thaliana] (88415.m00242)
185	Not regulated	A2g02870	266747_at	NC-NC-NC	kelch repeat-containing F-box family protein weak similarity to Kelch-like protein 5 (Swiss-Prot:Q86PQ7) [Homo sapiens]; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain (88415.m00237)
186	Not regulated	A2g46920	266758_at	NC-NC-NC	protein phosphatase 2C family protein / PP2C family protein similar to protein phosphatase-2c (GI:3608412) [Mesembryanthemum crystallinum]; contains Pfam PF00481: Protein phosphatase 2C domain (88415.m05860)
187	Not regulated	A2g47130	266761_at	NC-NC-NC	short-chain dehydrogenase/reductase (SOR) family protein similar to 3-beta-hydroxysteroid dehydrogenase GI:15983819 from [Digitalis lanata] (88415.m05886)
188	Not regulated	A2g46910	266767_at	NC-NC-NC	plastid-lipid associated protein PAP / fibrillin family protein contains Pfam profile PF04755: PAP_fibrillin (88415.m05858)
189	Not regulated	A2g47110	266768_s_at	NC-NC-NC	ubiquitin extension protein 6 (UBO6) / 40S ribosomal protein S27A (RPS27AB) identical to GI:168939 (88415.m05883)
190	Not regulated	A2g46930	266735_at	NC-NC-NC	pedicellate esterase, putative similar to pedicellate esterase precursor GI:1431629 from [Nippon radialis] (88415.m05862)
191	Not regulated	A2g46750	266712_at	NC-NC-NC	FAD-binding domain-containing protein low similarity to SPIP58710 L-glutamate oxidase (EC 1.1.3.8) [Mus musculus]; contains Pfam profile PF01585: FAD binding domain (88415.m05842)
192	Not regulated	A2g46820	266716_at	NC-NC-NC	expressed protein (88415.m05842)
193	Not regulated	A2g46790	266720_s_at	NC-NC-NC	pseudo-response regulator 9 (APRR9) / timing of CAB expression 1-like protein (TL1) identical to pseudo-response regulator 9 (APRR9) from [Arabidopsis thaliana]; timing of CAB expression 1-like protein [Arabidopsis thaliana] GI:9247022; contains Pfam profile PF00072: Response regulator receiver domain; identical to cDNA timing of CAB expression 1-like protein GI:8247021 (88415.m05837)
194	Not regulated	A2g03270	266679_at	NC-NC-NC	DNA-binding protein, putative similar to Swiss-Prot:Q60560 DNA-binding protein SMUBP-2 (Immunoglobulin MU binding protein 2) (SMUBP-2) (Insulin II gene enhancer-binding protein) (RIPE3B-binding complex 3B2 P110 subunit) (RIP-1)(Mesocricetus auratus); identical to putative helicase (apoc-2 gene) (NCBI gi:11191230) (88415.m00280)
195	Not regulated	A2g19950	266683_at	NC-NC-NC	expressed protein contains 2 transmembrane domains; weak similarity to HPSR2 - heavy chain potential motor protein (GI:871048)
196	Not regulated	A2g19710	266685_at	NC-NC-NC	[Giardia intestinalis] (88415.m02332)
197	Not regulated				expressed protein contains Pfam profile: PF03388 eukaryotic protein of unknown function, DUF282 (88415.m02303)

197	Not regulated	NC-NC-NC	266687_at	Al2g19870	protein arginine N-methyltransferase, putative similar to protein arginine N-methyltransferase 1-variant 1 [Homo sapiens] Gi:7453577 (88415.m02298)
198	Not regulated	NC-NC-NC	266694_at	Al2g19790	clathrin adaptor complex small chain family protein contains Pfam profile: PF01217 clathrin adaptor complex small chain (88415.m02312)
199	Not regulated	NC-NC-NC	266695_at	Al2g19810	zinc finger (CCCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-xC-x5-C-x3-H type (and similar) (88415.m02316)
200	Not regulated	NC-NC-NC	266696_at	Al2g19680	mitochondrial ATP synthase g subunit family protein contains Pfam profile: PF04718 mitochondrial ATP synthase g subunit (88415.m02300)
201	Not regulated	NC-NC-NC	266698_at	Al2g19830	SNF7 family protein contains Pfam domain, PF03357: SNF7 family (88415.m02319)
202	Not regulated	NC-NC-NC	266699_at	Al2g19730	60S ribosomal protein L28 (RPL28A) (88415.m02305)
203	Not regulated	NC-NC-NC	266700_at	Al2g19740	60S ribosomal protein L31 (RPL31A) (88415.m02306)
204	Not regulated	NC-NC-NC	266701_at	Al2g19760	profilin 1 (PRO1) (PFN1) (PRF1) / allergen Ara t8 identical to profilin 1 (Allergen Ara t8) SP:Q4249 Gi:1353770 from [Arabidopsis thaliana] (88415.m02309)
205	Not regulated	NC-NC-NC	266702_at	Al2g19860	hexokinase 2 (HXK2) identical to hexokinase 2 [Arabidopsis thaliana] Swiss-Prot:P93634 (88415.m02322)
206	Not regulated	NC-NC-NC	266704_at	Al2g19940	semialdehyde dehydrogenase family protein similar to N-acetyl-glutaryl-phosphate reductase [Campylobacter jejuni] Gi:8650382; contains Pfam profiles PF02774: Semialdehyde dehydrogenase dimerisation domain, PF01118: Semialdehyde dehydrogenase
207	Not regulated	NC-NC-NC	266705_at	Al2g19750	NAD binding domain (88415.m02330)
208	Not regulated	NC-NC-NC	266678_at	Al2g25870	40S ribosomal protein S30 (RPS30A) (88415.m02307)
209	Not regulated	NC-NC-NC	266648_at	Al2g25840	haloacid dehalogenase-like hydrolase family protein contains Pfam profiles PF00702: haloacid dehalogenase-like hydrolase, PF02130: Uncharacterized protein family UPF0054 (88415.m03105)
210	Not regulated	NC-NC-NC	266649_at	Al2g25810	RNA synthetase class I (W and Y) family protein contains Pfam profile: PF00579 RNA synthetases class I (W and Y) (88415.m03100)
211	Not regulated	NC-NC-NC	266652_at	Al2g25750	tonoplast intrinsic protein, putative similar to tonoplast intrinsic protein Gi:4594429 from [Nicotiana tabacum] (88415.m03087)
212	Not regulated	NC-NC-NC	266657_at	Al2g25910	3'-5' exonuclease domain-containing protein / K homology domain-containing protein / KH domain (88415.m03109)
213	Not regulated	NC-NC-NC	266690_at	Al2g25920	profiles PF01612: 3'-5' exonuclease, PF00013: KH domain (88415.m03110)
214	Not regulated	NC-NC-NC	266672_at	Al2g25950	expressed protein (88415.m03110)
215	Not regulated	NC-NC-NC	266673_at	Al2g25930	inorganic phosphate transporter, putative similar to brain specific Na ⁺ -dependent inorganic phosphate cotransporter [Rattus norvegicus] Gi:507415; contains Pfam profile PF00083: major facilitator superfamily protein (88415.m03602)
216	Not regulated	NC-NC-NC	266646_at	Al2g29700	thiamine biosynthesis family protein / thC family protein contains Pfam profile: PF01964 ThC family (88415.m03589)
217	Not regulated	NC-NC-NC	266624_s_at	Al2g35390	pleckstrin homology (PH) domain-containing protein (PH1) identical to ALPH1 [Arabidopsis thaliana] Gi:5926716; contains Pfam profile PF00169: PH domain (88415.m03610)
218	Not regulated	NC-NC-NC	266635_at	Al2g35470	ribose-phosphate pyrophosphokinase 1 / phosphoribosyl diphosphate synthetase 1 (PRS1) identical to phosphoribosyl diphosphate synthetase 1 (ribiose-phosphate pyrophosphokinase 1 (PRS1) [Arabidopsis thaliana] Gi:633140, SPIQ42581 (88415.m04338)
219	Not regulated	NC-NC-NC	266639_at	Al2g35520	expressed protein (88415.m04345)
220	Not regulated	NC-NC-NC	266641_at	Al2g35605	defender against cell death 2 (DAD2) identical to defender against cell death 2 (DAD-2, AIDAD2) [Arabidopsis thaliana] SWISS-PROT:Q22622 (88415.m04350)
221	Not regulated	NC-NC-NC	266642_at	Al2g35410	SWIB complex BAF80b domain-containing protein contains Pfam profile PF02201: BAF80b domain of the SWIB complex (88415.m04363)
222	Not regulated	NC-NC-NC	266608_at	Al2g35500	33 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp33, putative similar to SPIP19684 33 kDa ribonucleoprotein, chloroplast precursor (Nicotiana sylvestris); contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) (88415.m04340)
223	Not regulated	NC-NC-NC	266613_at	Al2g14900	shikimate kinase-related low similarity to shikimate kinase precursor from Lycopersicon esculentum [SPIQ00487] (88415.m04348)
224	Not regulated	NC-NC-NC	266587_at	Al2g14880	gibberellin-regulated family protein similar to SPIP46690 Gibberellin-regulated protein 4 precursor [Arabidopsis thaliana] GASA4; contains Pfam profile PF02704: Gibberellin regulated protein (88415.m01694)
225	Not regulated	NC-NC-NC	266605_at	Al2g46020	SWIB complex BAF80b domain-containing protein contains Pfam profile PF02201: BAF80b domain of the SWIB complex (88415.m01691)
226	Not regulated	NC-NC-NC	266581_at	Al2g46140	transcription regulatory protein SNF2, putative similar to SPIP22082 Transcription regulatory protein SNF2 (SWI/SNF complex component SNF2) [Saccharomyces cerevisiae]; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain (88415.m05724)
227	Not regulated	NC-NC-NC	266582_at	Al2g46090	late embryogenesis abundant protein, putative / LEA protein, putative similar to SPIP46518 Late embryogenesis abundant protein Lea14-A [Gossypium hirsutum]; contains Pfam profile PF03168: Late embryogenesis abundant protein (88415.m05738)
228	Not regulated	NC-NC-NC	266553_at	Al2g46170	diacylglycerol kinase family protein contains INTERPRO domain, IPR001206, DAG-kinase catalytic domain (88415.m05733)
229	Not regulated	NC-NC-NC	266554_s_at	Al2g46280	reticulon family protein (RTNLB5) weak similarity to Nogo-C protein [Rattus norvegicus] Gi:6822251; contains Pfam profile PF02453: Reticulon (88415.m05741)
230	Not regulated	NC-NC-NC	266557_at	Al2g46080	eukaryotic translation initiation factor 3 subunit 2 / TGF-beta receptor interacting protein 1 / eIF-3 beta / TRIP-1 (TIF31) identical to eukaryotic translation initiation factor 3 subunit 2 (SP-Q38894) [Arabidopsis thaliana]; contains Pfam PF00400: WD domain, G-beta repeat (5 copies) (88415.m05755)
231	Not regulated	NC-NC-NC	266586_at	Al2g24040	expressed protein (88415.m05732)
					hydrophobic protein, putative / low temperature and salt responsive protein, putative similar to SPIQ32NO7 Hydrophobic protein RC12A [Low temperature and salt responsive protein LT16A] [Arabidopsis thaliana]; contains Pfam profile PF01679: Uncharacterized protein family (88415.m02872)

232	Not regulated	NC-NC-NC	266572_at	A12g23840	HNH endonuclease domain-containing protein contains Pfam profile PF01844: HNH endonuclease (88415.m02848) translation initiation factor 3 (IF-3) family protein similar to SPIP233319 Translation initiation factor IF-3 (Proteus vulgaris); contains Pfam profiles PF00707: Translation initiation factor IF-3, C-terminal domain, PF05198: Translation initiation factor IF-3, N-terminal domain (88415.m02874)
233	Not regulated	NC-NC-NC	266575_at	A12g24060	expressed protein contains 2 transmembrane domains; contains Pfam profile PF05620: Protein of unknown function (DUF788) domain (88415.m02858)
234	Not regulated	NC-NC-NC	266576_at	A12g23940	cyclic nucleotide-regulated ion channel / cyclic nucleotide-gated channel (CNGC8) identical to cyclic nucleotide and calmodulin-regulated ion channel (cngc8) GI:4581207 from [Arabidopsis thaliana] (88415.m02863)
235	Not regulated	NC-NC-NC	266520_at	A12g23980	expressed protein contains Pfam domain PF02575: Uncharacterized BCR, YaaB family COG0718 (88415.m02869)
236	Not regulated	NC-NC-NC	266521_at	A12g24020	RNA recognition motif (RRM)-containing protein (88415.m01952)
237	Not regulated	NC-NC-NC	266534_at	A12g16940	expressed protein (88415.m01948)
238	Not regulated	NC-NC-NC	266536_at	A12g16900	GCIP-interacting family protein similar to GCIP-interacting protein mp28 (GI:27372822) [Mus musculus]; similar to GCIP-interacting protein P28 (GI:11987378) [Homo sapiens] (88415.m01939)
239	Not regulated	NC-NC-NC	266537_at	A12g16860	HEM protein-related weak similarity to Membrane-associated protein Hem (Hem-2) (Swiss-Prot:P55162) [Drosophila melanogaster]; weak similarity to Nck-associated protein 1 (NAP-1) (p125Nap1) (Membrane-associated protein HEM-2) (Swiss-Prot:P55161) [Rattus norvegicus] (88415.m04307)
240	Not regulated	NC-NC-NC	266541_at	A12g35110	DNA-binding protein-related contains Pfam domain PF03479: Domain of unknown function (DUF298), found in AT-hook motifs Pfam:PF02178 (88415.m04326)
241	Not regulated	NC-NC-NC	266546_at	A12g35270	expressed protein (88415.m04331)
242	Not regulated	NC-NC-NC	266547_at	A12g35320	expressed protein (88415.m04325)
243	Not regulated	NC-NC-NC	266551_at	A12g35280	glycine cleavage system H protein, mitochondrial, putative similar to SPIQ39732 Glycine cleavage system H protein, mitochondrial precursor (Flavinea anomala); contains Pfam profile PF01597: Glycine cleavage H-protein (88415.m04308)
244	Not regulated	NC-NC-NC	266517_at	A12g35120	precursor (88415.m04312)
245	Not regulated	NC-NC-NC	266519_at	A12g35155	expressed protein (88415.m05987)
246	Not regulated	NC-NC-NC	266509_at	A12g47940	DegP2 protease (DEGP2) identical to DegP2 protease GI:13172275 from [Arabidopsis thaliana]; identical to cDNA DegP2 protease (DEGP2) nuclear gene for chloroplast product GI:13172274 (88415.m05985)
247	Not regulated	NC-NC-NC	266510_at	A12g47990	transducin family protein / WD-40 repeat family protein similar to Vegetalable incompatibility protein HET-E-1 (SP:Q00808) (Podospira arsenaria); contains 5 WD-40 repeats (PF00400); similar to beta transducin-like protein HET-E2C*4 (GP:17225206)Podospira arsenaria (88415.m06006)
248	Not regulated	NC-NC-NC	266512_at	A12g47690	NADH-ubiquinone oxidoreductase-related contains weak similarity to NADH-ubiquinone oxidoreductase 15 kDa subunit (EC 1.6.5.3) (EC 1.6.98.3) (Complex I:15 kDa) (Swiss-Prot:O43920) [Homo sapiens] (88415.m05956)
249	Not regulated	NC-NC-NC	266513_at	A12g47700	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type(RING finger) (88415.m05957)
250	Not regulated	NC-NC-NC	266514_at	A12g47890	zinc finger (B-box type) family protein (88415.m05981)
251	Not regulated	NC-NC-NC	266482_at	A12g47640	small nuclear ribonucleoprotein D2, putative / snRNP core protein D2, putative / Sm protein D2, putative similar to small nuclear ribonucleoprotein Sm D2 (snRNP core protein D2) (Sm-D2) [Mus musculus] SWISS-PROT:P43330 (88415.m05944)
252	Not regulated	NC-NC-NC	266483_at	A12g47610	expressed protein (88415.m05987)
253	Not regulated	NC-NC-NC	266485_at	A12g47630	esterase/lipase/cholesterase family protein similar to monoglyceride lipase from [Homo sapiens] GI:14594904, [Mus musculus] GI:2632182; contains Interpro entry IPR000378 (88415.m05942)
254	Not regulated	NC-NC-NC	266459_at	A12g47970	NPL4 family protein contains Pfam domain, PF05021: NPL4 family (88415.m06001)
255	Not regulated	NC-NC-NC	266460_at	A12g47930	hydroxyproline-rich glycoprotein family protein contains proline-rich extensin domains, INTERPRO:IPR002965 (88415.m05993)
256	Not regulated	NC-NC-NC	266468_at	A12g47960	expressed protein (88415.m05999)
257	Not regulated	NC-NC-NC	266474_at	A12g31110	expressed protein (88415.m03798)
258	Not regulated	NC-NC-NC	266476_at	A12g31090	expressed protein (88415.m03797)
259	Not regulated	NC-NC-NC	266478_at	A12g31170	IRNA synthetase class I (C) family protein similar to cysteine-IRNA ligase [Escherichia coli] GI:41203; contains Pfam profile PF01406: tRNA synthetase class I (C) (88415.m03805)
260	Not regulated	NC-NC-NC	266481_at	A12g31070	TCP family transcription factor, putative similar to TCP1 protein (GI:20269127) (Lupinus albus) and cycloidea (GI:12002867) [Lycopersicon esculentum] (88415.m03781)
261	Not regulated	NC-NC-NC	266445_at	A12g43105	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to prolyl 4-hydroxylase, alpha subunit, from Homo sapiens [GI:18073925]; contains PF03171 2OG-Fe(II) oxygenase superfamily domain (88415.m05346)
262	Not regulated	NC-NC-NC	266448_at	A12g43080	aconitase C-terminal domain-containing protein contains Pfam profile PF00694: Aconitase C-terminal domain (88415.m05348)
263	Not regulated	NC-NC-NC	266451_at	A12g43090	Ras-related protein (ARA-4) / small GTP-binding protein, putative identical to SP:P28187 Ras-related protein ARA-4 (Arabidopsis thaliana) (88415.m05356)
264	Not regulated	NC-NC-NC	266394_at	A12g43130	transcription factor S-II (TFIIS) domain-containing protein similar to SPIP49373 Transcription elongation factor S-II (TFIIS) (Schizosaccharomyces pombe); contains Pfam profile PF01098: Transcription factor S-II (TFIIS) (88415.m04737)
265	Not regulated	NC-NC-NC	266407_at	A12g38560	expressed protein (88415.m04760)
266	Not regulated	NC-NC-NC	266410_at	A12g38770	haloacid dehalogenase-like hydrolase family protein similar to SPIP71447 Beta-phosphoglucomutase (EC 5.4.2.8) (Lactobacillus lactis); contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase (88415.m04757)
267	Not regulated	NC-NC-NC	266413_at	A12g38740	expressed protein contains Pfam profile PF03647: Uncharacterized protein family (UPF0136) (88415.m04738)
268	Not regulated	NC-NC-NC	266417_at	A12g38550	annexin 4 (ANNA4) nearly identical to annexin [Arabidopsis thaliana] GI:6503084; contains Pfam profile PF00191: Annexin (88415.m04758)
269	Not regulated	NC-NC-NC	266418_at	A12g38750	nonspecific lipid transfer protein 1 (LTP1) identical to SPIQ42588 (88415.m04735)
270	Not regulated	NC-NC-NC	266421_at	A12g38540	

271	Not regulated	266363_at	NC-NC-NC	haloacid dehalogenase-like hydrolase family protein low similarity to SPQ04915 Rhythmically expressed gene 2 protein (DREG-2) (Drosophila melanogaster); contains InterPro accession PR005834; Haloacid dehalogenase-like hydrolase (88415.m05094)
272	Not regulated	266370_at	NC-NC-NC	expressed protein (88415.m05104)
273	Not regulated	266356_at	NC-NC-NC	udcayarin1 identical to udcayarin1 (G1:3399767 from [Arabidopsis thaliana]; contains Pfam profile PF02238; Plastocyanin-like domain; identical to cDNA udcayarin1 (G1:3399766 (88415.m03949)
274	Not regulated	266359_at	NC-NC-NC	cholinephosphate cytidylyltransferase, putative / phosphorylcholine transferase, putative / CTP-phosphocholine cytidylyltransferase, putative strong similarity to CTP-phosphocholine cytidylyltransferase [Brassica napus] (G1:1418125; contains Pfam profile PF01487; Cytidylyltransferase (88415.m03943)
275	Not regulated	266334_at	NC-NC-NC	expressed protein (88415.m03957)
276	Not regulated	266342_at	NC-NC-NC	C2 domain-containing protein similar to zinc finger and C2 domain protein G1:9857238 from [Arabidopsis thaliana] (88415.m00078)
277	Not regulated	266345_at	NC-NC-NC	hypothetical protein (88415.m00060)
278	Not regulated	266328_at	NC-NC-NC	epsin N-terminal homology (ENTH) domain-containing protein contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain; similar to clathrin assembly protein AP-180 (G1:6492344) [Xenopus laevis] (88415.m00084)
279	Not regulated	266329_at	NC-NC-NC	expressed protein (88415.m00083)
280	Not regulated	266331_at	NC-NC-NC	gibberellin response modulator (RGA1) / gibberellin-responsive modulator identical to GB-Y11338, member of SCARECROW family (88415.m00081)
281	Not regulated	266300_at	NC-NC-NC	auxin transport protein, putative similar to auxin transport protein PIN7 [Arabidopsis thaliana] (G1:5817305) [AAD52897 (88415.m00082)
282	Not regulated	266303_at	NC-NC-NC	leucine-rich repeat transmembrane protein kinase, putative (88415.m03251)
283	Not regulated	266306_at	NC-NC-NC	exonuclease family protein contains exonuclease domain, Pfam-PF00928 (88415.m03235)
284	Not regulated	266310_at	NC-NC-NC	COP9 signalosome complex subunit 2 / CSN complex subunit 2 (CSN2) proteasome, COP9-complex and eIF3-domain protein; identical to CSN complex subunit 2 [Arabidopsis thaliana] (G1:18056655; identical to cDNA CSN complex subunit 2 (CSN2) (G1:18056654 (88415.m03241)
285	Not regulated	266314_at	NC-NC-NC	PAZ domain-containing protein / piwi domain-containing protein similar to SPI090281 Eukaryotic translation initiation factor 2C 2 (Rattus norvegicus); contains Pfam profiles PF02171: Pwi domain, PF02170: PAZ domain (88415.m03249)
286	Not regulated	266315_at	NC-NC-NC	C2H2 zinc-finger protein SERRATE (SE) identical to C2H2 zinc-finger protein SERRATE (G1:14486602 from [Arabidopsis thaliana] (88415.m03256)
287	Not regulated	266317_at	NC-NC-NC	calmodulin-2/3/5 (CAM5) (TCH1) identical to calmodulin G1:474183 from [Arabidopsis thaliana]; SPIP25089 Calmodulin-2/3/5 (Arabidopsis thaliana) (88415.m03245)
288	Not regulated	266319_s_at	NC-NC-NC	fatty acid elongase 3-oxoacyl-CoA synthase, putative similar to G1:4091810; contains Pfam profile PF02787: Chalcone and stilbene synthases, C-terminal domain (88415.m05828)
289	Not regulated	266322_at	NC-NC-NC	auxin-responsive family protein similar to indole-3-acetic acid induced protein ARG7 (SP:P32295) [Phaseolus aureus] (88415.m05826)
290	Not regulated	266271_at	NC-NC-NC	glutathione S-transferase, putative (88415.m03577)
291	Not regulated	266275_at	NC-NC-NC	troponin reductase, putative / troponin dehydrogenase, putative similar to SPIP50162 Troponin reductase-1 (EC 1.1.2.09) (TfR-1) (Troponin dehydrogenase) [Datura stramonium] (88415.m03568)
292	Not regulated	266277_at	NC-NC-NC	troponin reductase, putative / troponin dehydrogenase, putative similar to troponin reductase SP:P50165 from [Datura stramonium] (88415.m03560)
293	Not regulated	266279_at	NC-NC-NC	troponin reductase, putative / troponin dehydrogenase, putative similar to troponin reductase SP:P50165 from [Datura stramonium] (88415.m03558)
294	Not regulated	266285_at	NC-NC-NC	expressed protein (88415.m03547)
295	Not regulated	266289_at	NC-NC-NC	steroid 4-alpha-methyl-oxidase 1 (SMO1) nearly identical to steroid 4-alpha-methyl-oxidase G1:16973469 from [Arabidopsis thaliana]; identical to cDNA steroid 4-alpha-methyl-oxidase (SMO) partial cds, G1:16973431 (88415.m03570)
296	Not regulated	266291_at	NC-NC-NC	troponin reductase, putative / troponin dehydrogenase, putative similar to troponin reductase SP:P50165 from [Datura stramonium] (88415.m03561)
297	Not regulated	266293_at	NC-NC-NC	troponin reductase, putative / troponin dehydrogenase, putative similar to troponin reductase SP:P50165 from [Datura stramonium] (88415.m03567)
298	Not regulated	266237_at	NC-NC-NC	DNA-directed RNA polymerase (A) and III(C) 14 kDa subunit (RPAC14) identical to RNA polymerase (A) and III(C) 14 kDa subunit (AIRPAC14) [Arabidopsis thaliana] (G1:1184066 (88415.m03588)
299	Not regulated	266238_at	NC-NC-NC	serine/threonine protein phosphatase PP1 isozyme 1 (TOPP1) / phosphoprotein phosphatase 1 identical to SPIP30368] Serine/threonine protein phosphatase PP1 isozyme 1 (EC 3.1.3.16) [Arabidopsis thaliana], phosphoprotein phosphatase 1 (G1:166572 [Arabidopsis thaliana] (88415.m03573)
300	Not regulated	266239_at	NC-NC-NC	mitochondrial import inner membrane translocase (TIM10) identical to mitochondrial import inner membrane translocase subunit Tim10 [Arabidopsis thaliana] Swiss-Prot:Q9ZV33; contains Pfam domain, PF02953: Tim10/ODDP family zinc finger (88415.m03587)
301	Not regulated	266247_at	NC-NC-NC	DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain (88415.m03352)
302	Not regulated	266253_at	NC-NC-NC	histone deacetylase-related / HD-related similar to nuclear histone deacetylase HD2-p39 [Zea mays] (G1:2257756; contains non-consensus donor splice site AT at exon2 and acceptor splice site AC at exon3, (88415.m03375)
303	Not regulated	266257_at	NC-NC-NC	prephenate dehydratase family protein (88415.m03373)
304	Not regulated	266280_at	NC-NC-NC	AAA-type ATPase family protein / vacuolar sorting protein-related similar to SPIP46467 SKD1 protein (Vacuolar sorting protein 4b) [Mus musculus]; contains Pfam profiles PF00004: ATPase AAA family, PF04212: MIT domain (88415.m03346)
305	Not regulated	266261_at	NC-NC-NC	zinc finger (AN1-like) family protein contains Pfam domains, PFO 428: AN1-like Zinc finger and PF01754: AZD-like zinc finger (88415.m03342)
306	Not regulated	266206_at	NC-NC-NC	expressed protein contains 1 transmembrane domain; similar to Unknown mitochondrial protein A12g27730 (Swiss-Prot:Q9ZUX4) [Arabidopsis thaliana] similar to F1FO-ATPase inhibitor protein (G1:5821432) [Oryza sativa] (88415.m03381)

307	Not regulated	NC-NC-NC	266216_at	A12g28810	Dof-type zinc finger domain-containing protein similar to zinc finger protein OBP22 GI:5059394 from [Arabidopsis thaliana] (68415.m03503)
308	Not regulated	NC-NC-NC	266221_at	A12g28780	NAD-dependent epimerase/dehydratase family protein similar to UDP-glucuronic acid decarboxylase Uxa1p from <i>Filobasidiella neofornis</i> GI:14318327; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family (68415.m03487)
309	Not regulated	NC-NC-NC	266223_at	A12g28790	osmotin-like protein, putative similar to SPIQ41350 Osmotin-like protein precursor (Lycopodium obscurum); contains Pfam profile PF00314; Thaumatin family (68415.m03500)
310	Not regulated	NC-NC-NC	266224_at	A12g28800	chloroplast membrane protein (ALBINO3) Oxa1p homolog (PMID:11148275); identical to chloroplast membrane protein ALBINO3 [Arabidopsis thaliana] GI:2206332 (68415.m03501)
311	Not regulated	NC-NC-NC	266228_at	A12g28910	CAX-interacting protein 4 (CAXIP4) contains Pfam domain PF00098; Zinc knuckle; identical to cDNA CAX-interacting protein 4 GI:27651998 (68415.m03513)
312	Not regulated	NC-NC-NC	266229_at	A12g28840	ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023 (68415.m03508)
313	Not regulated	NC-NC-NC	266202_at	A12g02400	cinnamoyl-CoA reductase family similar to cinnamoyl-CoA reductase from <i>Pinus taeda</i> (GI:17978649), <i>Eucalyptus gunnii</i> (GI:2058311) (68415.m00180)
314	Not regulated	NC-NC-NC	266180_at	A12g02470	PHD finger family protein contains Pfam domain, PF00628: PHD-finger (68415.m00188)
315	Not regulated	NC-NC-NC	266181_at	A12g02390	glutathione S-transferase zeta 1 (GSTZ1) (GSTZ1) identical to SPIQ2V03/GT21_ARATH:Glutathione S-transferase zeta-class 1 (EC 2.5.1.18) (AIGSTZ1) (Maleylacetone isomerase) (EC 5.2.1.-) (MAI) [Arabidopsis thaliana]; contains Pfam profiles PF02788; Glutathione S-transferase, N-terminal domain and PF00043:Glutathione S-transferase, C-terminal domain (68415.m00177)
316	Not regulated	NC-NC-NC	266188_at	A12g39000	GCN5-related N-acetyltransferase (GNAT) family protein contains Pfam profile PF00583: acetyltransferase, GNAT family (68415.m04793)
317	Not regulated	NC-NC-NC	266189_at	A12g39020	GCN5-related N-acetyltransferase (GNAT) family protein similar to SPIQ8SMB8 Tyramine N-fenolyltransferase 4/11 (EC 2.3.1.110) (Hydroxycinnamoyl-CoA: tyramine N-hydroxycinnamoyltransferase) [Nicotiana glauca]; contains Pfam profile PF00583: acetyltransferase, GNAT family (68415.m04797)
318	Not regulated	NC-NC-NC	266192_at	A12g39070	expressed protein (68415.m04802)
319	Not regulated	NC-NC-NC	266193_at	A12g39080	protease inhibitor, putative similar to SPIP24076 Glu S-griseus protease inhibitor (BGIA) [Monarda charentais]; contains Pfam profile PF00280: Potato inhibitor I family (68415.m04776)
320	Not regulated	NC-NC-NC	266168_at	A12g38870	ABC transporter family protein (68415.m03408)
321	Not regulated	NC-NC-NC	266158_at	A12g28070	superoxide dismutase [Cu-Zn], chloroplast (SODCP) / copper/zinc superoxide dismutase (CSD2) identical to GP:3273753:AF081518 (68415.m03423)
322	Not regulated	NC-NC-NC	266165_at	A12g28190	protein kinase-related similar to GAL83 protein [Solanum tuberosum] GI:5702015; contains Pfam profile PF04739: 5'-AMP-activated protein kinase, beta subunit, complex-interacting region; supporting cDNA g122652763/bb1A4/61295.1 (68415.m03408)
323	Not regulated	NC-NC-NC	266138_at	A12g28060	remorin family protein contains Pfam domain, PF03763: Remorin, C-terminal region (68415.m00153)
324	Not regulated	NC-NC-NC	266117_at	A12g02170	plant defensin-fusion protein, putative (PDF2.3) plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be) (68415.m00149)
325	Not regulated	NC-NC-NC	266118_at	A12g02130	plant defensin-fusion protein, putative (PDF2.2) plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); similar to SWISS-PROT:O65740 (68415.m00146)
326	Not regulated	NC-NC-NC	266119_at	A12g02100	zinc finger (C2H2 type) family protein contains Pfam domain, PF00096: Zinc finger, C2H2 type (68415.m00143)
327	Not regulated	NC-NC-NC	266120_at	A12g02070	zinc finger (CCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar) (68415.m00152)
328	Not regulated	NC-NC-NC	266121_at	A12g02160	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to 14 kDa polypeptide [Catharanthus roseus] GI:407410; contains Pfam profile PF00234: LTP family domain PF00234 (68415.m05825)
329	Not regulated	NC-NC-NC	266123_at	A12g45180	expressed protein weak similarity to PGPS/D12 [Petunia x hybrida] GI:4105794; contains Pfam profile PF04748: Protein of unknown function, DUF614 (68415.m05604)
330	Not regulated	NC-NC-NC	266137_at	A12g45010	vesicle-associated membrane protein, putative / VAMP, putative similar to VAP27 GI:6688926 [Nicotiana glauca] (68415.m05818)
331	Not regulated	NC-NC-NC	266103_at	A12g45140	expressed protein (68415.m04647)
332	Not regulated	NC-NC-NC	266079_at	A12g37860	chaperone protein dnaJ-related weak similarity to Chaperone protein dnaJ (Swiss-Prot:O8ZFC5) [Methylobacterium sp.] (68415.m04664)
333	Not regulated	NC-NC-NC	266090_at	A12g38000	expressed protein (68415.m04661)
334	Not regulated	NC-NC-NC	266094_at	A12g37975	3-oxo-5-alpha-steroid 4-dehydrogenase, putative / steroid 5-alpha-reductase, putative identical to gi:1280811; contains a steroid 5-alpha reductase, C-terminal domain (68415.m04671)
335	Not regulated	NC-NC-NC	266095_at	A12g38050	vacuoleless1 (VCL1) contains Pfam profiles: PF04841 Vps18, N-terminal region, PF04840: Vps18, C-terminal region; identical to cDNA VCL1 (VCL1) GI:13877132 (68415.m04667)
336	Not regulated	NC-NC-NC	266096_at	A12g38020	expressed protein (68415.m04657)
337	Not regulated	NC-NC-NC	266101_at	A12g37940	Endothelial-monocyte activating polypeptide II (EMAP-II) (Small inducible cytokine subfamily E member 1) [Homo sapiens]; contains Pfam profile PF01588: Putative IRNA binding domain (68415.m05017)
338	Not regulated	NC-NC-NC	266057_at	A12g40690	expressed protein (68415.m05029)
339	Not regulated	NC-NC-NC	266059_at	A12g40765	diacylglycerol kinase, putative contains INTERPRO domain, IPR001208, DAG-kinase catalytic domain (68415.m02181)
340	Not regulated	NC-NC-NC	266062_at	A12g18730	expressed protein (68415.m02185)
341	Not regulated	NC-NC-NC	266073_at	A12g18770	small nuclear ribonucleoprotein E, putative / snRNP-E, putative / Sm protein E, putative similar to SWISS-PROT:P08578 small nuclear ribonucleoprotein E (snRNP-E) (Sm protein E, Sm-E, Sme) (68415.m02182)
342	Not regulated	NC-NC-NC	266074_at	A12g18740	expressed protein (68415.m02177)
343	Not regulated	NC-NC-NC	266017_at	A12g18690	

344	Not regulated	NC-NC-NC	266018_at	A12g181710	preprotein translocase secY subunit, chloroplast precursor (CpSecY) [Arabidopsis thaliana] (68415.m02179)
345	Not regulated	NC-NC-NC	266035_at	A12g05990	enoyl-[acyl-carrier protein] reductase [NADH], chloroplast, putative / NADH-dependent enoyl-ACP reductase, putative strong similarity to enoyl-[acyl-carrier protein] reductase [NADH] SP-P80030 from [Brassica napus] (68415.m00651)
346	Not regulated	NC-NC-NC	266036_s_at	A12g05840	20S proteasome alpha subunit A2 (PAA2) identical to GB-AF043519 (68415.m00832)
347	Not regulated	NC-NC-NC	266037_at	A12g05940	protein kinase, putative similar to auxin-regulated dual specificity cytosolic kinase [Lycopersicon esculentum] gll14484938lghAAK62821 (68415.m00645)
348	Not regulated	NC-NC-NC	266015_at	A12g24190	short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family IPR002198 short-chain dehydrogenase/reductase (SDR) superfamily (68415.m02890)
349	Not regulated	NC-NC-NC	265990_at	A12g24280	serine carboxypeptidase S28 family protein contains Pfam profile: PF05577 Serine carboxypeptidase S28 (68415.m02801)
350	Not regulated	NC-NC-NC	265998_at	A12g24270	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase, putative similar to NADP-dependent glyceraldehyde-3-phosphate dehydrogenase (NON-phosphorylating glyceraldehyde 3-phosphate, glyceraldehyde-3-phosphate dehydrogenase [NADP-]) [Nicotiana glauca] (68415.m02899)
351	Not regulated	NC-NC-NC	265999_at	A12g24100	expressed protein (68415.m02879)
352	Not regulated	NC-NC-NC	266000_at	A12g24180	cytochrome P450 family protein (68415.m02889)
353	Not regulated	NC-NC-NC	266001_at	A12g24150	expressed protein contains Pfam profile PF03008: Uncharacterised protein family (Hly-Ili / UPF0073) (68415.m02885)
354	Not regulated	NC-NC-NC	265953_at	A12g37490	adenylylate kinase family protein contains Pfam profile: PF00408 adenylylate kinase (68415.m04570)
355	Not regulated	NC-NC-NC	265958_at	A12g37250	expressed protein weak similarity to tmHP (G1:22902096) [Takifugu rubripes] (68415.m04569)
356	Not regulated	NC-NC-NC	265959_at	A12g37240	histone H2B, putative strong similarity to histone H2B from Lycopersicon esculentum G1:3021483, G1:3021485, Capsicum annuum SPI049118; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4 (68415.m04596)
357	Not regulated	NC-NC-NC	265960_at	A12g37470	nodulin MIN21 family protein similar to MIN21 G1:2598575 (root nodule development) from [Medicago truncatula] (68415.m04595)
358	Not regulated	NC-NC-NC	265962_at	A12g37460	40S ribosomal protein S5 (RPSSA) identical to GP-3043428 (68415.m04572)
359	Not regulated	NC-NC-NC	265963_s_at	A12g37270	arginine biosynthesis protein ArgJ family contains Pfam profile: PF01960 ArgJ family (68415.m04599)
360	Not regulated	NC-NC-NC	265965_at	A12g37500	29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative similar to SPIQ43348 29 kDa
361	Not regulated	NC-NC-NC	265966_at	A12g37220	ribonucleoprotein, chloroplast precursor (RNA-binding protein cp29) [Arabidopsis thaliana] (68415.m04566)
362	Not regulated	NC-NC-NC	265968_at	A12g37410	mitochondrial import inner membrane translocase (TIM17) nearly identical to SPIQSP35 Mitochondrial import inner membrane translocase subunit TIM17 [Arabidopsis thaliana] (68415.m04567)
363	Not regulated	NC-NC-NC	265930_at	A12g18510	pre-mRNA splicing factor, putative similar to SPIQ15427 Splicing factor 3B subunit 4 (Spliceosome associated protein 49) (SAP 49) (SF3b50) (Pre-mRNA splicing factor SF3b 49 kDa subunit) (Homo sapiens); contains Pfam profile PF00078: RNA recognition motif.
364	Not regulated	NC-NC-NC	265940_at	A12g19480	(a.k.a. RRM, RBD, or RNP domain) (68415.m02157)
365	Not regulated	NC-NC-NC	265943_at	A12g19570	nucleosome assembly protein (NAP), putative similar to nucleosome assembly protein 1 [Glycine max] G1:161252; contains Pfam profile PF00956: Nucleosome assembly protein (NAP) (68415.m02277)
366	Not regulated	NC-NC-NC	265947_at	A12g19540	cytidine deaminase (CDD) / cytidine aminohydrolyase identical to cytidine deaminase (CDD) [Arabidopsis thaliana] G1:3048700 (68415.m02286)
367	Not regulated	NC-NC-NC	265918_at	A12g19500	transducin family protein / WD-40 repeat family protein contains WD-40 repeats (PF00400); similar to Glutamate-rich WD repeat protein (GRWD) (SP-C9B087) [Homo sapiens] (68415.m02283)
368	Not regulated	NC-NC-NC	265920_s_at	A12g15120	fatty acid elongase, putative similar to fatty acid elongase 1 [G1:881615] (68415.m01720)
369	Not regulated	NC-NC-NC	265894_at	A12g15050	lipid transfer protein, putative similar to SPIQ42841 nonspecific lipid-transfer protein A precursor (LTP A) (Wax-associated protein 9A) [Brassica oleracea]; contains Pfam Protease inhibitor/seed storage/LTP family domain PF00234 (68415.m01714)
370	Not regulated	NC-NC-NC	265895_at	A12g15000	expressed protein (68415.m01707)
371	Not regulated	NC-NC-NC	265909_at	A12g25720	expressed protein (68415.m03083)
372	Not regulated	NC-NC-NC	265911_at	A12g25670	expressed protein (68415.m03076)
373	Not regulated	NC-NC-NC	265887_at	A12g25710	holocarboxylase synthetase 1 (HCS1) identical to holocarboxylase synthetase 1 (hcs1) [Arabidopsis thaliana] G1:1889365 (68415.m03081)
374	Not regulated	NC-NC-NC	265858_at	A12g01720	riboflavin I family protein similar to SPIQ4843 Dolichyl-diphosphoglycerate-protein glycosyltransferase 67 kDa subunit precursor (EC 2.4.1.119) (Ribophorin I) (Homo sapiens); contains Pfam profile PF04597: Ribophorin I (68415.m00100)
375	Not regulated	NC-NC-NC	265866_at	A12g01710	DNAJ heat shock N-terminal domain-containing protein similar to AHM1 [Triticum aestivum] G1:6891487; contains Pfam profile PF00228: DnaJ domain (68415.m00099)
376	Not regulated	NC-NC-NC	265867_at	A12g01620	expressed protein (68415.m00098)
377	Not regulated	NC-NC-NC	265868_at	A12g01650	zinc finger (C2H2 type) family protein contains Pfam domain, PF00098: Zinc finger, C2H2 type (68415.m00091)
378	Not regulated	NC-NC-NC	265874_at	A12g01640	expressed protein (68415.m00090)
379	Not regulated	NC-NC-NC	265883_at	A12g42310	expressed protein (68415.m05237)
380	Not regulated	NC-NC-NC	265852_at	A12g42350	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger) protein kinase C substrate, heavy chain-related similar to Protein kinase C substrate, 80 kDa protein, heavy chain (PKCSH) (80K-H protein) (Swiss-Prot:P14314) [Homo sapiens]; contains 1 transmembrane domain; (68415.m05246)
381	Not regulated	NC-NC-NC	265855_at	A12g42390	serine/threonine protein phosphatase PP2A-3 catalytic subunit (PP2A3) identical to SPIQ07100 Serine/threonine protein phosphatase PP2A-3 catalytic subunit (EC 3.1.3.16) [Arabidopsis thaliana]; contains Pfam profile PF00149: Ser/Thr protein phosphatase (68415.m05258)
382	Not regulated	NC-NC-NC	265857_s_at	A12g42500	leucine-rich repeat transmembrane protein kinase, putative similar to somatic embryogenesis receptor-like kinase 1 (SERK1) [Zea mays] gll13887318lmbICAC37840; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069 (68415.m04368)
383	Not regulated	NC-NC-NC	265844_at	A12g35620	

384	Not regulated	NC-NC-NC	265825_at	A12g35635	ubiquitin family protein contains INTERPRO:IPR000628 ubiquitin domain (68415.m04370)
385	Not regulated	NC-NC-NC	265826_at	A12g35795	DNAJ heat shock N-terminal domain-containing protein contains Pfam profile PF00228 DNAJ domain (68415.m04384)
386	Not regulated	NC-NC-NC	265795_at	A2g35780	serine carboxypeptidase S10 family protein similar to Serine carboxypeptidase II chains A and B (SP-P08819) (EC 3.4.16.6)
387	Not regulated	NC-NC-NC	265798_at	A2g35780	[Triticum aestivum (Wheat)]: (68415.m04390)
388	Not regulated	NC-NC-NC	265800_at	A12g35630	expressed protein (68415.m04392)
389	Not regulated	NC-NC-NC	265805_s_at	A12g18020	microtubule organization 1 protein (MOR1) identical to microtubule organization 1 protein GI:14317953 from [Arabidopsis thaliana] (68415.m04369)
390	Not regulated	NC-NC-NC	265810_at	A2g18090	60S ribosomal protein L8 (RPL8A) (68415.m02094)
391	Not regulated	NC-NC-NC	265816_s_at	A12g18110	PHD finger family protein / SWIB complex BAF80b domain-containing protein / GYF domain-containing protein contains Pfam profiles PF02201: BAF80b domain of the SWIB complex, PF02213: GYF domain, PF06828: PHD-finger (68415.m02103)
392	Not regulated	NC-NC-NC	265818_at	A2g18040	elongation factor 1-beta, putative / EF-1-beta, putative nearly identical to eEF-1beta [Arabidopsis thaliana] GI:396606 (68415.m02105)
393	Not regulated	NC-NC-NC	265819_at	A2g17972	peptidyl-prolyl cis-trans isomerase (PIN1) / cyclophilin / rotamase identical to Chain A, Solution Structure Of Pin1 at From Arabidopsis Thaliana GI:22218833; contains Pfam profile PF06839: PPC-type PPIASE domain (68415.m02097)
394	Not regulated	NC-NC-NC	265768_at	A12g48020	expressed protein (68415.m02086)
395	Not regulated	NC-NC-NC	265770_at	A12g48100	sugar transporter, putative similar to ERD6 protein [Arabidopsis thaliana] GI:3123712, sugar-porter family proteins 1 and 2 [Arabidopsis thaliana] GI:14585699, GI:14585701; contains Pfam profile PF00083: major facilitator superfamily protein (68415.m06010)
396	Not regulated	NC-NC-NC	265773_at	A12g48070	exonuclease family protein contains Pfam domain PF00829: exonuclease (68415.m06020)
397	Not regulated	NC-NC-NC	265776_at	A12g07340	expressed protein (68415.m06016)
398	Not regulated	NC-NC-NC	265777_at	A12g07350	prefoldin-related KE2 family protein contains similarity to Swiss-Prot O60925 prefoldin subunit 1 [Homo sapiens]; contains Pfam domain, PF01920: KE2 family protein (68415.m00841)
399	Not regulated	NC-NC-NC	265790_at	A12g01170	amino acid permease family protein weak similarity to GABA permease [Emenella nidulans] GI:4972245; contains Pfam profile PF00324: Amino acid permease (68415.m00025)
400	Not regulated	NC-NC-NC	265796_at	A12g01250	60S ribosomal protein L7 (RPL7B) (68415.m00037)
401	Not regulated	NC-NC-NC	265739_at	A12g01270	thioredoxin family protein low similarity to quiescin [Homo sapiens] GI:13257405; contains Pfam profiles PF00085: Thioredoxin, PF04777: Ery1 / Air family (68415.m00040)
402	Not regulated	NC-NC-NC	265740_at	A12g01150	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (68415.m00024)
403	Not regulated	NC-NC-NC	265741_at	A12g01320	ABC transporter family protein (68415.m00046)
404	Not regulated	NC-NC-NC	265742_s_at	A12g01290	expressed protein (68415.m00043)
405	Not regulated	NC-NC-NC	265759_at	A12g13100	glycerol-3-phosphate transporter, putative / glycerol 3-phosphate permease, putative similar to glycerol-3-phosphate transporter [glycerol 3-phosphate permease] [Homo sapiens] GI:7543982; contains Pfam profile PF00083: major facilitator superfamily protein (68415.m01436)
406	Not regulated	NC-NC-NC	265703_at	A12g03430	ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023 (68415.m00301)
407	Not regulated	NC-NC-NC	265704_at	A12g03420	expressed protein (68415.m00300)
408	Not regulated	NC-NC-NC	265707_at	A12g03390	uvrBuvrC motif-containing protein contains Pfam profile PF02151: UvrBuvrC motif (68415.m00298)
409	Not regulated	NC-NC-NC	265712_s_at	A12g03330	expressed protein (68415.m00292)
410	Not regulated	NC-NC-NC	265716_at	A12g03350	expressed protein contains Pfam profile PF04398: Protein of unknown function, DUF538 (68415.m00294)
411	Not regulated	NC-NC-NC	265720_at	A12g40110	Yippee family protein similar to mdg-1 [Mus musculus] GI:10441848, Yippee protein [Drosophila melanogaster] GI:5713278; contains Pfam profile PF03226: Yippee putative zinc-binding protein (68415.m04930)
412	Not regulated	NC-NC-NC	265722_at	A12g40100	chlorophyll A-B binding protein (LHC8A-3) identical to Lhc8A-3 protein [Arabidopsis thaliana] GI:4741956; contains Pfam profile: PF00504 chlorophyll A-B binding protein (68415.m04929)
413	Not regulated	NC-NC-NC	265697_at	A12g32170	expressed protein -supported by cDNA GI:20259498 (68415.m03932)
414	Not regulated	NC-NC-NC	265669_at	A12g32040	integral membrane transporter family protein contains 9 transmembrane domains; contains Pfam PF03092: BT1 family; contains TIGRFAMS TIGR00788: folate/biotin transporter, similar to high affinity folic acid/methotrexate transporter 5 (GI:21898554)
415	Not regulated	NC-NC-NC	265671_at	A12g32060	40S ribosomal protein S12 (RPS12C) (68415.m03914)
416	Not regulated	NC-NC-NC	265673_at	A12g32090	[Leishmania tarentolae] (68415.m03914)
417	Not regulated	NC-NC-NC	265676_at	A12g32070	lactoylglutathione lyase family protein / glyoxalase 1 family protein contains glyoxalase family protein domain, Pfam:PF00903 (68415.m03922)
418	Not regulated	NC-NC-NC	265677_at	A12g32080	CCR4-NOT transcription complex protein, putative similar to SWISS-PROT:Q60809 CCR4-NOT transcription complex, subunit 7 (CCR4-associated factor 1, (CAF1) [Mus musculus] (68415.m03919)
419	Not regulated	NC-NC-NC	265679_at	A12g32240	PUR alpha-1 protein identical to PUR alpha-1 GI:5081612 from [Arabidopsis thaliana]; contains Pfam profile: PF04845 PUA ssDNA and RNA-binding protein (68415.m03920)
420	Not regulated	NC-NC-NC	265685_at	A12g24430	expressed protein contains Pfam profile: PF04508 viral A-type inclusion protein repeat (68415.m03940)
421	Not regulated	NC-NC-NC	265691_at	A12g24330	no apical menstem (NAM) family protein contains Pfam PF02365: No apical menstem (NAM) domain; (68415.m02919)
422	Not regulated	NC-NC-NC	265683_at	A12g24290	expressed protein (68415.m02908)
423	Not regulated	NC-NC-NC	265684_at	A12g24420	expressed protein (68415.m02903)
424	Not regulated	NC-NC-NC	265697_at	A12g27490	DNA repair ATPase-related contains 2 transmembrane domains; similar to DNA double-strand break repair rad50 ATPase, (Swiss-Prot:O33600) [Sulfolobus acidocaldarius] (68415.m02917)
425	Not regulated	NC-NC-NC	265642_at	A12g27450	dephospho-CoA kinase family similar to Dephospho-CoA kinase (EC 2.7.1.24) (Dephospho-CoA kinase) (Swiss-Prot:Q92BF2) [Listeria innocua]; contains Pfam profile PF01121: Dephospho-CoA kinase (68415.m03322)
					carbon-nitrogen hydrolase family protein low similarity to beta-alanine synthase [Drosophila melanogaster] GI:14334083; contains carbon-nitrogen hydrolase family protein (68415.m03317)

426	Not regulated	NC-NC-NC	265646_at	lipase, putative similar to lipase [Arabidopsis thaliana] GI:1145927; contains Pfam profile PF00657; Lipase/Acylhydrolase with GDSL-like motif (88415.m03296)
427	Not regulated	NC-NC-NC	265648_at	glycosyl hydrolase family 17 protein similar to glucan endo-1,3-beta-glucosidase precursor SP-P52409 from [Triticum aestivum] (88415.m03324)
428	Not regulated	NC-NC-NC	265649_at	ferredoxin, putative similar to non-photosynthetic ferredoxin from Citrus sinensis (GI:1360725); Ferredoxin, root R-B2 from Raphanus sativus [SP P14937]; contains Pfam profile PF00111 2Fe-2S iron-sulfur cluster binding domain (88415.m03327) phosphate translocator-related low similarity to SP P52178 Triose phosphate/phosphate translocator, non-green plastid, chloroplast precursor (CTPT) [Brassica oleracea], phosphoenolpyruvate/phosphate translocator precursor [Mesembryanthemum crystallinum]
429	Not regulated	NC-NC-NC	265617_at	GI:9285275 (88415.m03055)
430	Not regulated	NC-NC-NC	265626_at	expressed protein (88415.m03276)
431	Not regulated	NC-NC-NC	265628_at	expressed protein (88415.m03280)
432	Not regulated	NC-NC-NC	265630_at	OTU-like cysteine protease family protein contains Pfam profile PF02338: OTU-like cysteine protease (88415.m03291)
433	Not regulated	NC-NC-NC	265570_at	proline iminopeptidase identical to GP-1710151/U72711 (88415.m01594)
434	Not regulated	NC-NC-NC	265575_at	expressed protein contains Pfam domain, PF04367: Protein of unknown function (DUF502) (88415.m02352)
435	Not regulated	NC-NC-NC	265593_s_at	ribosomal protein L4 family protein contains Pfam profile PF00573: ribosomal protein L4/L1 family (88415.m02344)
436	Not regulated	NC-NC-NC	265594_at	26S protease regulatory complex subunit 4, putative similar to Swiss-Prot:P46801 26S protease regulatory subunit 4 (P26S4)
437	Not regulated	NC-NC-NC	265595_at	[Drosophila melanogaster] (88415.m02353)
438	Not regulated	NC-NC-NC	265571_s_at	expressed protein (88415.m03427)
439	Not regulated	NC-NC-NC	265573_at	zinc finger (C2H2 type) family protein contains Pfam domain, PF00096: Zinc finger, C2H2 type (88415.m03424)
440	Not regulated	NC-NC-NC	265569_at	expressed protein (88415.m00598)
441	Not regulated	NC-NC-NC	265510_at	autophagy 8d (APG8d) identical to autophagy 8d [Arabidopsis thaliana] GI:19812157; contains Pfam profile PF02891: Microtubule associated protein 1A/1B, light chain 3 (88415.m00599)
442	Not regulated	NC-NC-NC	265538_at	expressed protein and gene finder (88415.m01818)
443	Not regulated	NC-NC-NC	265495_at	expressed protein contains Pfam PF05705: Eukaryotic protein of unknown function (DUF829) (88415.m01787)
444	Not regulated	NC-NC-NC	265474_at	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat (88415.m01786)
445	Not regulated	NC-NC-NC	265476_at	thioredoxin M-type 3, chloroplast (TRX-M3) identical to SP Q8SEU7 Thioredoxin M-type 3, chloroplast precursor (TRX-M3) [Arabidopsis thaliana] (88415.m01783)
446	Not regulated	NC-NC-NC	265450_at	AAA-type ATPase family protein contains Pfam profile: ATPase family PF00004 (88415.m05815)
447	Not regulated	NC-NC-NC	265456_at	expressed protein (88415.m05784)
448	Not regulated	NC-NC-NC	265457_at	expressed protein (88415.m05807)
449	Not regulated	NC-NC-NC	265458_at	pyridoxamine 5'-phosphate oxidase (GI:22294052) [Thermosynechococcus elongatus BP-1] (88415.m05810)
450	Not regulated	NC-NC-NC	265461_at	phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein contains INTERPRO:IPR000828 ubiquitin domain (88415.m05790)
451	Not regulated	NC-NC-NC	265471_at	peroxidase 21 (PER21) (P21) (PRXR5) identical to SP Q42580 Peroxidase 21 precursor (EC 1.11.1.7) (Atperox P21) (PRXR5) (ATP2aATP2b) [Arabidopsis thaliana] (88415.m04555)
452	Not regulated	NC-NC-NC	265417_at	DNA-binding S1FA family protein contains Pfam profile: PF04689 DNA binding protein S1FA (88415.m04554)
453	Not regulated	NC-NC-NC	265419_at	secretory carrier membrane protein (SCAMP) family protein contains Pfam domain, PF04144: SCAMP family (88415.m02456)
454	Not regulated	NC-NC-NC	265426_at	expressed protein (88415.m02436)
455	Not regulated	NC-NC-NC	265442_at	expressed protein (88415.m02469)
456	Not regulated	NC-NC-NC	265415_at	expressed protein (88415.m02482)
457	Not regulated	NC-NC-NC	265385_at	diacylglycerol kinase, putative contains INTERPRO domain, IPR001206, DAG-kinase catalytic domain (88415.m02463)
458	Not regulated	NC-NC-NC	265386_at	expressed protein (88415.m02466)
459	Not regulated	NC-NC-NC	265390_at	expressed protein . (88415.m02450)
460	Not regulated	NC-NC-NC	265391_at	glycosyl transferase family 8 protein contains Pfam profile: PF01501 glycosyl transferase family 8 (88415.m02448)
461	Not regulated	NC-NC-NC	265392_at	lipic acid synthase (LIP1) identical to gi:3928758 contains Pfam profile PF04055: radical SAM domain protein (88415.m02458)
462	Not regulated	NC-NC-NC	265393_at	expressed protein weak similarity to formiminotransferase cycloaminase (GI:3380084) [Gallus gallus] (88415.m02453)
463	Not regulated	NC-NC-NC	265394_at	CAAX amino terminal protease family protein contains Pfam profile PF02517 CAAX amino terminal protease family protein (88415.m02435)
464	Not regulated	NC-NC-NC	265402_at	BSD domain-containing protein contains Pfam profile PF03909: BSD domain (88415.m01169)
465	Not regulated	NC-NC-NC	265382_at	shikimate kinase family protein similar to thermosensitive glucokinase from Escherichia coli [SP P39208] [SP P46859]; contains Pfam profile PF01202: shikimate kinase (88415.m01925)
466	Not regulated	NC-NC-NC	265352_at	peptidyl-prolyl cis-trans isomerase, cytosolic / cyclophilin / rotamase (ROC3) identical to cytosolic cyclophilin [Arabidopsis thaliana] (GI:1305455 (88415.m01906)
467	Not regulated	NC-NC-NC	265354_at	actin-depolymerizing factor 5 (ADF5) identical to SP Q92NT3 Actin-depolymerizing factor 5 (ADF-5) (AAADF5) [Arabidopsis thaliana] (88415.m01916)
468	Not regulated	NC-NC-NC	265356_at	translocon-associated protein (TRAP), putative similar to Swiss-Prot:P45434 translocon-associated protein, alpha subunit precursor (TFAP-alpha. Signal sequence receptor alpha subunit, SSR-alpha) [Arabidopsis thaliana] (88415.m01904)
469	Not regulated	NC-NC-NC	265357_at	ubiquitin-conjugating enzyme, putative strong similarity to SP P35133 Ubiquitin-conjugating enzyme E2:17 kDa 10 (EC 6.3.2.18) (Ubiquitin-protein ligase 10) [Arabidopsis thaliana]; contains Pfam profile PF00179: Ubiquitin-
470	Not regulated	NC-NC-NC	265374_at	membrane protein, putative contains 2 transmembrane domains; (88415.m00723)
471	Not regulated	NC-NC-NC	265375_at	SNF7 family protein contains Pfam domain, PF03357: SNF7 family (88415.m00724)

472	Not regulated	NC-NC-NC	265334_at	Al2g18370	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to lipid-transfer protein [Nicotiana glauca]
473	Not regulated	NC-NC-NC	265338_at	Al2g18400	Gi:6782438; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234 (88415.m02140)
474	Not regulated	NC-NC-NC	265340_at	Al2g18330	ribosomal protein L8 family protein (88415.m02143)
475	Not regulated	NC-NC-NC	265319_at	Al2g22870	AAA-type ATPase family protein contains Pfam profile PF00004 ATPase family associated with various cellular activities (AAA) (88415.m02136)
476	Not regulated	NC-NC-NC	265289_at	Al2g22890	auxin-responsive protein / indoleacetic acid-induced protein 8 (IAA8) identical to SPIQ38828 Auxin-responsive protein IAA8 (Arabidopsis thaliana) (88415.m02888)
477	Not regulated	NC-NC-NC	265291_at	Al2g22720	(Indoleacetic acid-induced protein 8) (Arabidopsis thaliana) (88415.m02889)
478	Not regulated	NC-NC-NC	265307_at	Al2g20310	expressed protein (88415.m02891)
479	Not regulated	NC-NC-NC	265284_at	Al2g20230	expressed protein (88415.m02372)
480	Not regulated	NC-NC-NC	265288_at	Al2g20270	expressed protein (88415.m02384)
481	Not regulated	NC-NC-NC	265258_at	Al2g20390	glutaredoxin family protein contains glutaredoxin domain, Pfam:PF00462 (88415.m02368)
482	Not regulated	NC-NC-NC	265259_at	Al2g20330	transducin family protein / WD-40 repeat family protein similar to Transcriptional repressor rco-1 (SP:P78706) [Neurospora crassa]; similar to TUP1 (GB:AF079369); contains 6 WD-40 repeats (PF00400) (88415.m02374)
483	Not regulated	NC-NC-NC	265265_at	Al2g22900	expressed protein (88415.m05314)
484	Not regulated	NC-NC-NC	265266_at	Al2g42890	RNA recognition motif (RRM)-containing protein (88415.m05311)
485	Not regulated	NC-NC-NC	265270_at	Al2g42910	ribose-phosphate pyrophosphokinase 4 / phosphotriphosphate synthetase 4 (PRSA) identical to phosphotriphosphate pyrophosphokinase 4 (pr-s4) [Arabidopsis thaliana] GI:4902472 (88415.m05316)
486	Not regulated	NC-NC-NC	265274_at	Al2g28450	zinc finger (CCHH-type) family protein contains Pfam domain, PF00642; Zinc finger C-x8-C-x5-C-x3-H type (and similar) (88415.m03456)
487	Not regulated	NC-NC-NC	265281_at	Al2g28370	expressed protein contains Pfam PF04535; Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) [Arabidopsis thaliana] (88415.m03448)
488	Not regulated	NC-NC-NC	265256_at	Al2g28390	SAND family protein similar to Sand (GI:3928166) [Tadugu rubripes]; contains Pfam PF03104; SAND family protein (88415.m03450)
489	Not regulated	NC-NC-NC	265226_at	Al2g28430	expressed protein (88415.m03454)
490	Not regulated	NC-NC-NC	265228_s_at	Al2g07698	ATP synthase alpha chain, mitochondrial, putative very strong similarity to SPIP23413 ATP synthase alpha chain, mitochondrial (EC 3.6.3.14) [Brassica campestris]; contains Pfam profiles PF00066: ATP synthase alpha/beta family nucleotide-binding domain, PF00306: ATP synthase ab C terminal, PF02874: ATP synthase alpha/beta family beta-barrel domain (88415.m00948)
491	Not regulated	NC-NC-NC	265230_s_at	Al2g07707	hypothetical protein L3 family protein contains Pfam profile PF02326: YMF19 hypothetical plant mitochondrial protein (88415.m00957)
492	Not regulated	NC-NC-NC	265247_at	Al2g43030	ribosomal protein L3 family protein contains Pfam profile PF00297; ribosomal protein L3 (88415.m05340)
493	Not regulated	NC-NC-NC	265248_at	Al2g43010	phytochrome-interacting factor 4 (PIF4) / basic helix-loop-helix protein 9 (bHLH9) / short under red-light 2 (SRL2) identical to SPIQ8W2F3 Phytochrome-interacting factor 4 (Basic helix-loop-helix protein 9) (bHLH9) (Short under red-light 2) (Arabidopsis thaliana); supporting cDNA gi18028965 (AF251694.1) (AF251694.1) (88415.m05337)
494	Not regulated	NC-NC-NC	265252_at	Al2g01980	sodium proton exchanger, putative (NHX7) (SOS1) identical to putative Na ⁺ /H ⁺ antiporter SOS1 [Arabidopsis thaliana] gi1851571 (gbAAAF76139; Member of The Monovalent Cation-Proton Antiporter (CPA1) Family, PMID:11500563 (88415.m00133) NADH-ubiquinone oxidoreductase B18 subunit, putative contains Pfam PF05678; NADH-ubiquinone oxidoreductase B18 subunit (NDUFB7); similar to NADH-ubiquinone oxidoreductase B18 subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-B18) (CI-B18) [Call adhesion protein SQM1] (Swiss-Prot:P17568) [Homo sapiens]; similar to NADH-ubiquinone oxidoreductase NDUFB7 subunit (GI:9651635) [Homo sapiens] (88415.m00140)
495	Not regulated	NC-NC-NC	265219_at	Al2g02050	peptide transporter (PTR2-B) / oligopeptide transporter 1-1, putative (OPT1-1) identical to peptide transporter PTR2-B SP-P46032 from [Arabidopsis thaliana]; contains Pfam profile PF00854 POT family; identical to cDNA NT1 GI:510237 (88415.m00139)
496	Not regulated	NC-NC-NC	265220_at	Al2g02040	expressed protein contains Pfam profile: PF01925 domain of unknown function DUF81 (88415.m04482)
497	Not regulated	NC-NC-NC	265203_at	Al2g36630	60S ribosomal protein L24 (RPL24A) (88415.m04490)
498	Not regulated	NC-NC-NC	265210_at	Al2g36620	hexose transporter, putative similar to hexose transporters from Nicotiana tabacum (GI:8347244), Solanum tuberosum (GI:8347248), Arabidopsis thaliana (GI:8347250), contains Pfam profile PF00083; major facilitator superfamily protein (88414.m00504)
499	Not regulated	NC-NC-NC	265212_at	Al1g05030	tyrosine specific protein phosphatase family protein contains tyrosine specific protein phosphatases active site, PROSITE:PS00383 (88414.m00501)
500	Not regulated	NC-NC-NC	265214_at	Al1g05000	expressed protein (88414.m00507)
501	Not regulated	NC-NC-NC	265218_at	Al1g05050	expressed protein (88414.m00509)
502	Not regulated	NC-NC-NC	265192_at	Al1g05060	spermidine synthase 1 (SPDSYN1) putrescine aminopropyltransferase 1 identical to SPIQ8ZUB3 Spermidine synthase 1 (EC 2.5.1.16) [Putrescine aminopropyltransferase 1] (SPDSY 1) (Arabidopsis thaliana) (88414.m03004)
503	Not regulated	NC-NC-NC	265193_at	Al1g05070	DNA-binding protein-related contains weak similarity to G-quartet DNA binding protein 3 [Tetrahymena thermophila]
504	Not regulated	NC-NC-NC	265172_at	Al1g23820	gi14583503 (gbAAAD25098 (88414.m02897)
505	Not regulated	NC-NC-NC	265183_at	Al1g23750	expressed protein (88414.m02893)
506	Not regulated	NC-NC-NC	265184_at	Al1g23710	ADP-ribosylation factor identical to SP-QBSRC3 ADP-ribosylation factor 1-like [Arabidopsis thaliana], ADP-ribosylation factor Gi:166598 [Arabidopsis thaliana] (88414.m02946)
507	Not regulated	NC-NC-NC	265187_at	Al1g23490	aldehyde dehydrogenase, mitochondrial (ALDH3) nearly identical to mitochondrial aldehyde dehydrogenase ALDH3 [Arabidopsis thaliana] gi118950248 (gbAAL99612; contains Pfam profile PF00171; aldehyde dehydrogenase (NAD) family protein (88414.m03002)
508	Not regulated	NC-NC-NC	265188_at	Al1g23800	F-box family protein contains Pfam PF00646; F-box domain; similar to SP-Q9Y311 F-box only protein 7 [Homo sapiens]; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1.A15g67250 (88414.m03000)
509	Not regulated	NC-NC-NC	265190_at	Al1g23780	

510 Not regulated	NC-NC-NC	285132_at	A11g23830	expressed protein (68414.m03006)
511 Not regulated	NC-NC-NC	285148_at	A11g51160	synbindin, putative similar to Swiss-Prot:Q9ES56 synbindin (TRS23 homolog) [Mus musculus] (68414.m05752)
512 Not regulated	NC-NC-NC	285150_at	A11g51200	zinc finger (AN1-like) family protein contains Pfam domains, PF01428: AN1-like Zinc finger and PF01754: A20-like zinc finger (68414.m05759)
513 Not regulated	NC-NC-NC	285162_at	A11g30910	molybdenum cofactor sulfatase family protein weak similarity to molybdenum cofactor sulfatase (LOS5/ABA3) [Arabidopsis thaliana] Gi:3407282; contains Pfam profiles PF03476: MOSC N-terminal beta barrel domain, PF03473: MOSC domain (68414.m03781)
514 Not regulated	NC-NC-NC	285129_at	A11g30970	zinc finger (C2H2 type) family protein contains Pfam domain PF00096: Zinc finger, C2H2 type (68414.m03792)
515 Not regulated	NC-NC-NC	285130_at	A11g30890	integral membrane HRF1 family protein contains Pfam domain PF03878: Hrf1 family (68414.m03779)
516 Not regulated	NC-NC-NC	285101_at	A11g30880	expressed protein similar to ESTs gbIR30049 and gbIT46176 (68414.m03778)
517 Not regulated	NC-NC-NC	285102_at	A11g30870	cationic peroxidase, putative similar to cationic peroxidase (gil1232068), similar to EST gbIA100412 (68414.m03776)
518 Not regulated	NC-NC-NC	285113_at	A11g62460	
519 Not regulated	NC-NC-NC	285117_at	A11g62500	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to auxin down regulated GB:X69640 Gi:298442 from [Glycine max]; contains Pfam profile PF00234: Protease inhibitor/seed storage/LTP family (68414.m07052)
520 Not regulated	NC-NC-NC	285121_at	A11g62560	flavin-containing monooxygenase family protein / FMO family protein similar to flavin-containing monooxygenase GB:AAA21178 Gi:349534 SPIP32417 from [Oryctolagus cuniculus]; contains Pfam profile PF00743 Flavin-binding monooxygenase-like (68414.m07056)
521 Not regulated	NC-NC-NC	285071_at	A11g55520	transcription initiation factor IID-2 (TFIID-2) / TATA-box factor 2 (TBP2) identical to Swiss-Prot:P28148TF22_ARATH Transcription initiation factor TFIID-2 (TATA-box factor 2) (TATA sequence-binding protein 2) (TBP-2) [Arabidopsis thaliana] (68414.m06351)
522 Not regulated	NC-NC-NC	285073_at	A11g55480	expressed protein (68414.m06346)
523 Not regulated	NC-NC-NC	285082_at	A11g03910	expressed protein low similarity to cactin [Drosophila melanogaster] Gi:7673875; expression supported by MPSS (68414.m00376)
524 Not regulated	NC-NC-NC	285036_at	A11g04080	hydroxyproline-rich glycoprotein family protein Contains similarity to pre-mRNA processing protein PRP39 gb L29224 from S. cerevisiae. ESTs gbIR64908 and gbIT88158, gbIN38703 and gbIAA651043 come from this gene (68414.m00396)
525 Not regulated	NC-NC-NC	285037_at	A11g03860	prohibitin, putative similar to SPIP24142 Prohibitin (B-cell receptor associated protein 32) (BAP 32) [Rattus norvegicus]; contains Pfam profile PF01145: SPFH domain / Band 7 family (68414.m00388)
526 Not regulated	NC-NC-NC	285043_at	A11g03900	expressed protein (68414.m00374)
527 Not regulated	NC-NC-NC	285048_at	A11g52050	jacalin lectin family protein similar to myrosinase-binding protein homolog [Arabidopsis thaliana] Gi:2997767; contains Pfam profile PF01419 jacalin-like lectin domain (68414.m05872)
528 Not regulated	NC-NC-NC	285057_at	A11g52140	expressed protein (68414.m05883)
529 Not regulated	NC-NC-NC	285032_at	A11g61580	60S ribosomal protein L3 (rplL3B) identical to ribosomal protein Gi:806278 from [Arabidopsis thaliana] (68414.m06939)
530 Not regulated	NC-NC-NC	285033_at	A11g61520	chlorophyll A-B binding protein / LHCl type III (LHCA3.1) nearly identical to PSI type III chlorophyll a/b-binding protein Gi:430947; contains Pfam profile: PF00504 chlorophyll A-B binding protein; similar to PSI type III chlorophyll a/b-binding protein Gi:430947 from [Arabidopsis thaliana] (68414.m06931)
531 Not regulated	NC-NC-NC	285035_at	A11g61820	expressed protein contains Pfam profile: PF01363 FYVE zinc finger (68414.m06943)
532 Not regulated	NC-NC-NC	285005_at	A11g61667	expressed protein contains Pfam profile PF04398: Protein of unknown function, DUF538 (68414.m06953)
533 Not regulated	NC-NC-NC	285006_at	A11g61570	mitochondrial import inner membrane translocase (TIM13) identical to mitochondrial import inner membrane translocase subunit Tim13 [Arabidopsis thaliana] Swiss-Prot:Q9XK48; contains Pfam domain, PF02953: Tim10/ODP family zinc finger (68414.m06938)
534 Not regulated	NC-NC-NC	285013_at	A11g24460	myosin-related contains TIGRFAM TIGR01612: reticulocyte binding protein; similar to Myosin heavy chain, non-muscle (Zipper protein) (Myosin II) (SP:Q99323) [Drosophila melanogaster] similar to EST gbIT78116 (68414.m03081)
535 Not regulated	NC-NC-NC	285014_at	A11g24430	transferase family protein similar to decacetylindole 4-O-acetyltransferase from Catharanthus roseus Gi:4091808 GB:AAAC98311; acetyl CoA: benzylalcohol acetyltransferase Clarkia breweri Gi:3170250, acetyl-CoA:benzylalcohol acetyltransferase Clarkia
536 Not regulated	NC-NC-NC	285021_at	A11g24610	SET domain-containing protein low similarity to SPIQ43088 Ribulose-1,5 biphosphate carboxylase/oxygenase large subunit N-methyltransferase, chloroplast precursor (EC 2.1.1.127) [Pisum sativum]; contains Pfam profile PF00856: SET domain (68414.m03096)
537 Not regulated	NC-NC-NC	285025_at	A11g24575	expressed protein (68414.m03093)
538 Not regulated	NC-NC-NC	285027_at	A11g24450	ribonuclease III family protein contains similarity to Swiss-Prot:P51837 ribonuclease III (EC 3.1.26.3) (RNase III) [Coxiella burnetii] (68414.m03080)
539 Not regulated	NC-NC-NC	284977_at	A11g27090	glycine-rich repeat transmembrane protein kinase, putative similar to CLV1 receptor kinase GB:AA58929 Gi:2160756 from leucine-rich repeat transmembrane protein (68414.m03302)
540 Not regulated	NC-NC-NC	284980_at	A11g27190	[Arabidopsis thaliana] (68414.m03312)
541 Not regulated	NC-NC-NC	284984_at	A11g27000	bZIP family transcription factor (68414.m03292)
542 Not regulated	NC-NC-NC	284990_at	A11g27210	expressed protein (68414.m07052)
543 Not regulated	NC-NC-NC	284996_at	A11g67230	expressed protein contains Pfam profile PF04669: Protein of unknown function (DUF579) (68414.m07684)
544 Not regulated	NC-NC-NC	284998_at	A11g67330	expressed protein contains similarity to MHC class II antigen Gi:9502037 from [Aotus nancymae] (68414.m07668)
545 Not regulated	NC-NC-NC	285001_at	A11g67350	lactoyglutathione lyase, putative / glyoxalase I, putative similar to putative lactoyglutathione lyase SP:Q39368, Gi:2494843 from [Brassica oleracea] (68414.m07657)
546 Not regulated	NC-NC-NC	284970_at	A11g67280	zinc finger (MYND type) family protein / F-box family protein (68414.m07665)
547 Not regulated	NC-NC-NC	284942_at	A11g67340	RNA recognition motif (RRM)-containing protein contains Pfam PF00076: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain); similar to RNA-binding protein with multiple splicing homolog (RBP-MS) (HEAT, RRM Expressed Sequence) (Hemes) (Swiss-Prot:Q9YGI5) [Xenopus laevis]; similar to RNA-binding protein with multiple splicing (RBP-MS) (Swiss-Prot:Q93062) [Homo sapiens] (68414.m08957)
548 Not regulated	NC-NC-NC	284944_at	A11g76940	

549	Not regulated	NC-NC-NC	264952_at	At1g76900	F-box family protein / tubby family protein similar to Tubby protein (SP:P50586) (Mus musculus); similar to Chain A, C-Terminal Domain Of Mouse Brain Tubby Protein (GI:6730156) [Mus musculus]; similar to Tubby related protein 1 (Tubby-like protein 1) (Swiss-Prot:Q00294) [Homo sapiens]; similar to phosphodiesterase (GI:487578) [Mus musculus]; contains Pfam profile: PF01187; Tub family, contains Pfam PF00648; F-box domain (68414, m08948)
550	Not regulated	NC-NC-NC	264954_at	At1g77080	mutase family protein similar to carboxyvinyl-carboxyphosphonate phosphorinase GB:O48290 from [Arabidopsis thaliana]; similar to carboxyphosphonate pyruvate mutase (GI:47149) [Streptomyces hygroscopicus]; contains Pfam PF00161; Isocitrate lyase signature (68414, m08972)
551	Not regulated	NC-NC-NC	264955_at	At1g76920	F-box family protein (FBX3) contains similarity to staminal pistillidia GI:4101570, the pea ortholog of Fim and UFO from [Pisum sativum] (68414, m08954)
552	Not regulated	NC-NC-NC	264959_at	At1g77090	thylakoid luminal 29.8 kDa protein identical to SPIQ4282[TL30, ARATH (Arabidopsis thaliana); contains a PaBP domain AF370571; SIMILAR TO GI:13926195-F2K20.16 (68414, m08978)
553	Not regulated	NC-NC-NC	264916_at	At1g60810	ATP citrate-lyase-related similar to ATP citrate-lyase GI:949889 from [Rattus norvegicus] (68414, m08645)
554	Not regulated	NC-NC-NC	264922_s_at	At1g60830	U2 snRNP auxiliary factor large subunit, putative similar to GI:3650823 from [Nicotiana glauca] (J. Biol. Chem. 273 (51), 34603-34610 (1998)) (68414, m08946)
555	Not regulated	NC-NC-NC	264928_at	At1g60710	aldoketo reductase family protein contains Pfam profile PF00248; oxidoreductase, aldoketo reductase family (68414, m08834)
556	Not regulated	NC-NC-NC	264935_at	At1g61150	expressed protein similar to Protein C20orf11 (Swiss-Prot:Q9NWU2) [Homo sapiens] (68414, m08889)
557	Not regulated	NC-NC-NC	264936_at	At1g61140	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related similar to ATPase [Homo sapiens] GI:531196; contains Pfam profiles PF00271; Helicase conserved C-terminal domain, PF00178; SNF2 family N-terminal domain, PF00097; Zinc finger, C3HC4 type (RING finger) (68414, m08888)
558	Not regulated	NC-NC-NC	264883_s_at	At1g61250	secretory carrier membrane protein (SCAMP) family protein (SC3) contains Pfam domain, PF04144; SCAMP family (68414, m08902)
559	Not regulated	NC-NC-NC	264894_at	At1g623040	hydroxyproline-rich glycoprotein family protein contains proline-rich domains, INTERPRO:IPR000694 (68414, m02878)
560	Not regulated	NC-NC-NC	264897_at	At1g23220	dynein light chain type 1 family protein similar to SPIQ02414 Dynein light chain LC8, flagellar outer arm (Anthriscus crassispina); contains Pfam profile PF01221; Dynein light chain type 1 (68414, m02904)
561	Not regulated	NC-NC-NC	264904_s_at	At2g17420	thioredoxin reductase 2 / NADPH-dependent thioredoxin reductase 2 (NTR2) identical to SPIQ39242 (68415, m02010)
562	Not regulated	NC-NC-NC	264908_at	At2g17440	leucine-rich repeat family protein contains Pfam PF00560; Leucine Rich Repeats (68415, m02012)
563	Not regulated	NC-NC-NC	264875_at	At2g17390	ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023 (68415, m02008)
564	Not regulated	NC-NC-NC	264847_at	At2g17380	clathrin assembly protein AP19 identical to clathrin assembly protein AP19 GI:2231698 from [Arabidopsis thaliana] (68415, m02007)
565	Not regulated	NC-NC-NC	264848_at	At2g17350	expressed protein (68415, m02004)
566	Not regulated	NC-NC-NC	264850_at	At2g17340	pantothenate kinase-related contains Pfam domain, PF01837; Protein of unknown function; supported by tandem duplication of pantothenate kinase-related protein (TIGR, At1-A2017320) [Arabidopsis thaliana] (68415, m02003)
567	Not regulated	NC-NC-NC	264854_at	At2g17450	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097; Zinc finger, C3HC4 type (RING finger) (68415, m02014)
568	Not regulated	NC-NC-NC	264862_at	At1g24330	armadillo/beta-catenin repeat family protein / U-box domain-containing family protein contains Pfam domain, PF00514; Armadillo/beta-catenin-like repeats and Pfam, PF04564; U-box domain (68414, m03069)
569	Not regulated	NC-NC-NC	264865_at	At1g24120	DNAJ heat shock protein, putative similar to Altered Response to Gravity [Arabidopsis thaliana] GI:424962; contains Pfam profile PF00228 DnaJ domain (68414, m03043)
570	Not regulated	NC-NC-NC	264869_at	At1g24350	expressed protein contains Pfam domain, PF02681; Uncharacterized BCR, COG1963 (68414, m03071)
571	Not regulated	NC-NC-NC	264871_at	At1g24180	pyruvate dehydrogenase E1 component alpha subunit, mitochondrial, putative similar to SPIP52901 Pyruvate dehydrogenase E1 component alpha subunit, mitochondrial precursor (EC 1.2.4.1) (PDHE1-A) [Arabidopsis thaliana]; contains Pfam profile PF00678; component alpha subunit, mitochondrial (68414, m03050)
572	Not regulated	NC-NC-NC	264816_at	At1g03530	Dehydrogenase E1 component (68414, m03050)
573	Not regulated	NC-NC-NC	264820_at	At1g03475	expressed protein similar to hypothetical protein GB:O14360 (68414, m00334)
574	Not regulated	NC-NC-NC	264824_at	At1g03420	coproporphyrinogen III oxidase, putative / coproporphyrinogenase, putative / coproporphyrinogenase, putative similar to vulgare [SPIQ42840]; ESTs gblAA586260 and dbjD48620; contains Pfam domain coproporphyrinogen III oxidase, aerobic [PF01218] (68414, m00328)
575	Not regulated	NC-NC-NC	264828_at	At1g03380	expressed protein similar to gblT45484, embjZ30724, and embjZ30531 (68414, m00322)
576	Not regulated	NC-NC-NC	264834_at	At1g03730	expressed protein (68414, m00317)
577	Not regulated	NC-NC-NC	264836_at	At1g03610	expressed protein similar to ESTs gblAA605440 and gblH37232 (68414, m00353)
578	Not regulated	NC-NC-NC	264837_at	At1g03600	photosystem II family protein similar to SP:P74367 (Synechococcus sp.); similar to ESTs embjZ27038, gblAA451546, embjZ29876, gblT45359 and gblR90316 (68414, m00340)
579	Not regulated	NC-NC-NC	264838_at	At1g03430	two-component phosphorelay mediator, putative strong similarity to ATP1 [Arabidopsis thaliana] GI:4158241 (68414, m00323)
580	Not regulated	NC-NC-NC	264840_at	At1g03440	leucine-rich repeat family protein contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001811 (68414, m00324)
581	Not regulated	NC-NC-NC	264843_at	At1g03400	2-oxoglutarate-dependent dioxygenase, putative similar to 2A6 (GI:599622) and tomato ethylene synthesis regulatory protein E8 (SPIP10987); similar to ESTs embjZ34690, gblT04168, gblH37738, gblT76913, gblT43801, amd gblT21984 (68414, m00320)
582	Not regulated	NC-NC-NC	264845_at	At1g03675	cold-shock DNA-binding family protein contains Pfam domains, PF00313; 'Cold-shock' DNA-binding domain and PF00098; Zinc knuckle (68415, m02070)
583	Not regulated	NC-NC-NC	264789_at	At2g17870	violaxanthin de-epoxidase precursor, putative (AVDE1) similar to EST gblN37812 (68414, m00948)
584	Not regulated	NC-NC-NC	264796_at	At1g08890	
585	Not regulated	NC-NC-NC	264799_at	At1g08550	

586 Not regulated	264802_at	NC-NC-NC	syntaxin-related protein KNOLLE (KN) / syntaxin 111 (SYP111) identical to SPIQ42374 Syntaxin-related protein KNOLLE (Syntaxin 111) (AISYP111) (Arabidopsis thaliana); BAC F22013 has a deletion of a cytosine at position 7887 (88414.m00948)
587 Not regulated	264803_at	NC-NC-NC	expressed protein (88414.m00951)
588 Not regulated	264807_at	NC-NC-NC	Presenilin family protein similar to SPIP52166 Presenilin sel-12 (Caenorhabditis elegans); contains Pfam profile PF01080; Presenilin (88414.m00966)
589 Not regulated	264808_at	NC-NC-NC	prenylated rab acceptor (PRA1) family protein weak similarity to prenylated Rab acceptor 1 (PRA1) (Homo sapiens) Gi:4877285; contains Pfam profile PF03208: Prenylated rab acceptor (PRA1) (88414.m00976)
590 Not regulated	264809_at	NC-NC-NC	superoxide dismutase [Cu-Zn] (SODCC) / copper/zinc superoxide dismutase (CSD1) identical to SWISS-PROT: P24704 (88414.m00983)
591 Not regulated	264810_at	NC-NC-NC	GPI-anchor transamidase, putative similar to SPIP49018 GPI-anchor transamidase (EC 3.-.-.-) (GPI transamidase) (Saccharomyces cerevisiae); contains Pfam profile PF01650: Peptidase C13 family (88414.m00972)
592 Not regulated	264811_at	NC-NC-NC	expressed protein (88414.m00959)
593 Not regulated	264778_at	NC-NC-NC	prefoldin, putative similar to Swiss-Prot:Q9NQ44 prefoldin subunit 4 (Protein C-1) (Homo sapiens) (88414.m00977)
594 Not regulated	264782_at	NC-NC-NC	myb family transcription factor (MYB60) (88414.m00980)
595 Not regulated	264787_at	NC-NC-NC	S-locus protein kinase, putative similar to KI domain interacting kinase 1 [Zea mays] gi2735017[gp/AB83634; contains S-locus glycoprotein family domain, Pfam:PF00954 (88414.m00917)
596 Not regulated	264772_at	NC-NC-NC	T-complex protein 11 contains Pfam PF05784; T-complex protein 11 (88414.m02868)
597 Not regulated	264724_at	NC-NC-NC	COP9 signalosome subunit 5B / CSN subunit 5B (CSN5B) / c-JUN coactivator protein AJH1, putative (AJH1) COP9 complex subunit CSN5-1; identical to Arabidopsis homologs of a c-Jun coactivator AJH1 Gi:3641314 from [Arabidopsis thaliana]; identical to cDNA CSN complex subunit 5B (CSN5B) Gi:1805682; contains Pfam profile PF01398: Mov34/MNPAD-1 family (88414.m02864)
598 Not regulated	264725_at	NC-NC-NC	expressed protein (88414.m02858)
599 Not regulated	264727_at	NC-NC-NC	cytochrome c, putative similar to cytochrome c [Pumpkin, Winter squash] SWISS-PROT:P00051 (88414.m02852)
600 Not regulated	264728_at	NC-NC-NC	expressed protein (88414.m02853)
601 Not regulated	264736_at	NC-NC-NC	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family; contains non-consensus CA donor site at intron 4 (88414.m07016)
602 Not regulated	264716_at	NC-NC-NC	matrxin family protein similar to SPIP29136 Metalloendoproteinase 1 precursor (EC 3.4.24.-) (SMEP1) (Glycine max); contains InterPro accession IPR001818: Matrxin (88414.m08074)
603 Not regulated	264692_at	NC-NC-NC	DNA-binding family protein contains Pfam domains, PF00249: Myb-like DNA-binding domain and PF00098: Zinc knuckle (88414.m08056)
604 Not regulated	264699_at	NC-NC-NC	expressed protein (88414.m08054)
605 Not regulated	264700_at	NC-NC-NC	expressed protein (88414.m08065)
606 Not regulated	264701_at	NC-NC-NC	expressed protein similar to hypothetical protein Gi:4455225 from [Arabidopsis thaliana] (88414.m08073)
607 Not regulated	264703_at	NC-NC-NC	serine/threonine protein phosphatase PP2A-5 catalytic subunit (PP2A5) identical to SPI00495 [PP2A5, ARATH Serine/threonine protein phosphatase PP2A-5 catalytic subunit (EC 3.1.3.16) (Arabidopsis thaliana); contains Pfam profile PF00148: Ser/Thr protein phosphatase (88414.m08051)
608 Not regulated	264705_at	NC-NC-NC	IRNA synthetase class I (L, L, M and V) family protein similar to cytosolic leucyl-tRNA synthetase [Candida albicans] Gi:9858190; contains Pfam profile PF00133: RNA synthetases class I (L, L, M and V) (88414.m01079)
609 Not regulated	264708_at	NC-NC-NC	ethylene-responsive protein, putative similar to ERO protein [Lycopersicon esculentum] Gi:5669654; contains Pfam profile PF00582: universal stress protein family (88414.m01093)
610 Not regulated	264709_at	NC-NC-NC	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain (88414.m01096)
611 Not regulated	264687_at	NC-NC-NC	cysteine protease, papain-like (XBCP3) identical to papain-like cysteine peptidase XBCP3 Gi:14600257 from [Arabidopsis thaliana]; contains Pfam profiles PF00112: Papain family cysteine protease and PF00398: Granulin (88414.m01108)
612 Not regulated	264684_at	NC-NC-NC	KH domain-containing quaking protein, putative similar to GB-AAC67357 (88414.m01084)
613 Not regulated	264688_at	NC-NC-NC	2,3-bisphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative strong similarity to SPIQ42808 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1) (Phosphoglyceromutase) (Mesembryanthemum crystallinum); contains Pfam profile PF01676: Metalloenzyme superfamily (88414.m01087)
614 Not regulated	264689_at	NC-NC-NC	Ras-related GTP-binding protein, putative similar to GTP-binding protein Gi:1370148 from [Lotus japonicus] (88414.m01080)
615 Not regulated	264670_s_at	NC-NC-NC	elongation factor 1B-gamma, putative / eEF-1B gamma, putative Similar to elongation factor 1-gamma (gblEF1G_XENLA). ESTs gblT20564, gblT45940, gblT04527 come from this gene (88414.m01081)
616 Not regulated	264676_at	NC-NC-NC	histidine acid phosphatase family protein contains Pfam profile PF00328: Histidine acid phosphatase; similar to multiple inositol polyphosphate phosphatase (Gi:4105496) [Mus musculus]; EST gblR64758 comes from this gene (88414.m01111)
617 Not regulated	264679_s_at	NC-NC-NC	60S ribosomal protein L21 (RPL21C) Similar to ribosomal protein L21 (gblL38826). ESTs gblAA395597, gblATT55187 come from this gene (88414.m01086)
618 Not regulated	264685_at	NC-NC-NC	endo-1,4-beta-glucanase, putative / cellulase, putative similar to endo-1,4-beta-glucanase Gi:2065530 from [Lycopersicon esculentum] (88414.m07442)
619 Not regulated	264627_at	NC-NC-NC	enoyl-CoA hydratase/isomerase family protein low similarity to enoyl-CoA hydratase [Escherichia coli] Gi:2764828, carnitine racemase SPIP31551 [Escherichia coli]; contains Pfam profile PF00378 enoyl-CoA hydratase/isomerase family protein (88414.m07434)
620 Not regulated	264639_at	NC-NC-NC	ubiquitin carboxyl-terminal hydrolase family 1 protein similar to 26S proteasome regulatory complex subunit p37A [Drosophila melanogaster] Gi:6434982; contains Pfam profile PF01088: Ubiquitin carboxyl-terminal hydrolase, family 1 (88414.m07448)
621 Not regulated	264641_at	NC-NC-NC	ATP-dependent Clp protease proteolytic subunit, putative similar to nClpP5 Gi:5360595 from [Arabidopsis thaliana] (88414.m01017)

622	Not regulated	NC-NC-NC	264644_at	A11g08960	cation exchanger, putative (CAX11) similar to sodium/calcium exchanger protein [Mus musculus] gi 13925661 gb AAK49407.2 ; Cation Antiporter (CaCA) Family member PMID:11500583 (68414.m00986)
623	Not regulated	NC-NC-NC	264645_at	A11g08940	phosphoglycerate/bisphosphoglycerate mutase family protein contains Pfam profile PF00300; phosphoglycerate mutase family (68414.m00985)
624	Not regulated	NC-NC-NC	264649_at	A11g09060	transcription factor lumorji (lmC) domain-containing protein contains Pfam domain, PF02373; imC domain (68414.m01010)
625	Not regulated	NC-NC-NC	264651_at	A11g08880	histone H2A, putative Strong similarity to histone H2A Cicer arietinum SP085759; Picea abies SP1P35063; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4; ESTs gb ATTS3874, gb T48627, gb T14194 come from this gene (68414.m00888)
626	Not regulated	NC-NC-NC	264653_at	A11g08980	amidase family protein similar to component of chloroplast outer membrane translocan Toc64 [Pium salivum] GI:7453538; contains Pfam profile PF01425; Amidase; supporting cDNA gi 11493701 gb AF202077.1 AF202077 (68414.m01001)
627	Not regulated	NC-NC-NC	264656_at	A11g09010	glycoside hydrolase family 2 protein low similarity to mannosidase [gi:5359712] from Cellulomonas fimi (68414.m01005)
628	Not regulated	NC-NC-NC	264657_at	A11g09100	26S protease regulatory subunit 6A, putative identical to SP:O04018 from [Arabidopsis thaliana] (68414.m01016)
629	Not regulated	NC-NC-NC	264595_at	A11g04750	synaptobrevin family protein similar to Vesicle-associated membrane protein 222 (AIVAMP722) Synaptobrevin-related protein 1 (SP:PA7182) [Arabidopsis thaliana]; (68414.m00470)
630	Not regulated	NC-NC-NC	264609_at	A11g04530	expressed protein (68414.m00445)
631	Not regulated	NC-NC-NC	264613_at	A11g04640	biotin/ipoate A/B protein ligase family protein similar to lipoyltransferase (LIP2p) [Arabidopsis thaliana] GI:15887052; contains Pfam profile PF03099; Biotin/ipoate A/B protein ligase family (68414.m00460)
632	Not regulated	NC-NC-NC	264615_at	A11g04590	expressed protein isoform contains GG acceptor splice site at intron 7 (68414.m00452)
633	Not regulated	NC-NC-NC	264619_at	A2g17760	aspartyl protease family protein contains Eukaryotic and viral aspartyl proteases active site, PROSITE:PS00141 (68415.m02057)
634	Not regulated	NC-NC-NC	264622_at	A2g17790	vacuolar protein sorting-associated protein 35 family protein / VPS35 family protein similar to vacuolar protein sorting 35 [Mus musculus] GI:11875394; contains Pfam profile PF03635; Vacuolar protein sorting-associated protein 35 (68415.m02062)
635	Not regulated	NC-NC-NC	264591_at	A2g17670	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535; PPR repeat (68415.m02045)
636	Not regulated	NC-NC-NC	264594_at	A2g17640	serine O-acetyltransferase, putative (SAT-108) similar to Arabidopsis thaliana serine acetyltransferase GI:905391 (68415.m02040)
637	Not regulated	NC-NC-NC	264570_at	A11g05350	thfF family protein low similarity to SP:30138 Adenylyltransferase thfF (EC 2.7.7.-) [Escherichia coli]; contains Pfam profile PF00899; ThfF family (68414.m00542)
638	Not regulated	NC-NC-NC	264575_at	A11g05190	ribosomal protein L8 family protein Similar to Mycobacterium RlpF (gb Z84385). ESTs gb T57585, gb R30580, gb T04698 come from this gene (68414.m00523)
639	Not regulated	NC-NC-NC	264576_at	A11g05360	expressed protein Similar to Arabidopsis hypothetical protein PID:6326839 (gb Z97337) contains transmembrane domains (68414.m00543)
640	Not regulated	NC-NC-NC	264579_at	A11g05205	expressed protein (68414.m00525)
641	Not regulated	NC-NC-NC	264584_at	A11g05140	membrane-associated zinc metalloprotease, putative similar to Hypothetical zinc metalloprotease A13971 (SP:QB084) [strain PCC 7120] [Arabidopsis sp.]; Similar to Synchocystis hypothetical protein (gb D90808); contains Pfam PF00595; PDZ domain (Also known as DHR or GLGF); contains TIGRFAM TIGR00054; membrane-associated zinc metalloprotease, putative (68414.m00517)
642	Not regulated	NC-NC-NC	264585_at	A11g05180	auxin-resistance protein AXR1 (AXR1) identical to SP:IP42744 Auxin-resistance protein AXR1 [Arabidopsis thaliana]; contains Pfam profile PF00898; Thif family; identical to cDNA ubiquitin activating enzyme E1-related protein (AXR1) GI:304103 (68414.m00521)
643	Not regulated	NC-NC-NC	264545_at	A11g55670	photosystem I reaction center subunit V, chloroplast, putative / PSI-LG, putative (PSAG) identical to SP:Q857N7; similar to SP:Q00327 Photosystem I reaction center subunit V, chloroplast precursor (PSI-LG) (Photosystem I 9 kDa protein) [Hordeum vulgare]; contains Pfam profile PF01241; Photosystem I psaG / psaK (68414.m06372)
644	Not regulated	NC-NC-NC	264504_at	A11g09430	ATP-citrate synthase (ATP-citrate (pro-S)-lyase/citrate cleavage enzyme), putative similar to ATP-citrate-lyase (GI:16848642) [Arabidopsis thaliana]; similar to ATP-citrate (pro-S)-lyase (EC 4.1.3.8) (Citrate cleavage enzyme)(SP:Q91V92) [Mus musculus]; Location of EST gb Z34587 (68414.m01055)
645	Not regulated	NC-NC-NC	264510_at	A11g09530	phytochrome interacting factor 3 (PIF3) identical to phytochrome interacting factor 3 (PIF3) GI:3928585 from [Arabidopsis thaliana] (68414.m01068)
646	Not regulated	NC-NC-NC	264515_at	A11g10080	integral membrane family protein contains Pfam PF00894; Erp28 like protein (68414.m01131)
647	Not regulated	NC-NC-NC	264523_at	A11g10030	CTP synthase, putative / UTP--ammonia ligase, putative similar to SP:IP7812 CTP synthase (EC 6.3.4.2) (UTP--ammonia ligase) (Homo sapiens); contains Pfam profile PF00117; glutamine amidotransferase class-I; similar to ESTs gb AA660762, gb AA220982, gb AA008137, gb A054783, and gb AA100804 (68414.m03768)
648	Not regulated	NC-NC-NC	264529_at	A11g30820	ribulose biphosphate carboxylase small chain 1A / RuBisCO small subunit 1A (RBCS-1A) (AT5A1) identical to SP:IP10785 [Arabidopsis thaliana] (68414.m07629)
649	Not regulated	NC-NC-NC	264474_s_at	A11g67090	Ribulose biphosphate carboxylase small chain 1A, chloroplast precursor (EC 4.1.1.39) (RuBisCO small subunit 1A) [Arabidopsis thaliana] (68414.m07629)
650	Not regulated	NC-NC-NC	264476_at	A11g77130	glycogenin glucosyltransferase (glycogenin)-related contains similarity to glycogenin-1 from Mus musculus (SP:Q8R082). Rattus norvegicus [SP:Q08720], Homo sapiens (SP:IP46976) (68414.m08985)
651	Not regulated	NC-NC-NC	264484_at	A11g77260	dehydration-responsive protein-related similar to early-responsive to dehydration stress ERD3 protein [Arabidopsis thaliana] GI:15320410; contains Pfam profile PF03141; Putative methyltransferase (68414.m08988)
652	Not regulated	NC-NC-NC	264438_at	A11g27400	60S ribosomal protein L17 (RPL17A) similar to GB:PS1413 from [Arabidopsis thaliana]; similar to ESTs gb L33542 and gb AA660016 (68414.m03340)
653	Not regulated	NC-NC-NC	264439_at	A11g27450	adenine phosphoribosyltransferase 1 (APT1) nearly identical to SP:IP31166 Adenine phosphoribosyltransferase 1 (EC 2.4.2.7) (APRT) [Arabidopsis thaliana] (68414.m03346)

654	Not regulated	NC-NC-NC	264440_at	A11g27340	F-box family protein contains Pf00846; F-box domain; similar to fim protein; similar to ESTs gb T42445, gb T78780, gb AA650733, and emb Z17748 (88414.m03330) lechitin:cholesterol acyltransferase family protein / LACT family protein similar to LCAT-like lysophospholipase (LLPL) [Homo sapiens] Gi:4589720; contains Pfam profile PF02450; Lecithin:cholesterol acyltransferase (phosphatidylcholine-sterol acyltransferase) (88414.m03350) expressed protein (88414.m03338) nuclear transport factor 2 (NTF2); putative similar to Swiss-Prot P33331 nuclear transport factor 2 (NTF-2) (Nuclear transport factor P10) (Saccharomyces cerevisiae) (88414.m03327) expressed protein similar to ESTs gb T20511, gb T45308, gb H36493, and gb AA651176 (88414.m01144) expressed protein similar to EST gb AA598098 (88414.m01143) short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family PR002188 short-chain dehydrogenase/reductase (SDR) superfamily (88414.m01161) expressed protein (88414.m01148) 60S ribosomal protein L3 (RPL3A) identical to ribosomal protein Gi:166858 from [Arabidopsis thaliana] (88414.m04974) expressed protein contains Pfam domain, PF04367; Protein of unknown function (DUF502) (88414.m04968) expressed protein contains Pfam profile: PF01925 domain of unknown function DUF81; identical to cDNA hypothetical protein, partial Gi:4079631 (88414.m06963) DNAJ heat shock N-terminal domain-containing protein similar to SP Q8UBS4 DnaJ homolog subfamily B member 11 precursor Homo sapiens; contains Pfam profile PF00226 DnaJ domain (88414.m06968) expressed protein similar to membrane protein PTM1 precursor isoform Gi:1931644 from [Arabidopsis thaliana] (88414.m06956) postsynaptic protein-related similar to postsynaptic protein CRIP1 Gi:3098551 from [Rattus norvegicus] (88414.m06967) two-component responsive regulator family protein / response regulator family protein contains Pfam profile: PF00072 response regulator receiver domain (88415.m03011) protein phosphatase 2C, putative / PP2C; putative (88415.m02999) ribonuclease H1 family protein contains Pfam profile: PF01351 ribonuclease H1 (88415.m03003) fumarylacetoacetase, putative similar to fumarylacetoacetate hydrolase, Beta-diketonase, FAA[Rattus norvegicus] SWISS-PROT:P25093 (88414.m01391) glycosyl hydrolase family 17 protein similar to elicitor inducible chitinase Nt-SuE76 Gi:11071974 from [Nicotiana tabacum] (88414.m01358)
655	Not regulated	NC-NC-NC	264442_at	A11g27480	vesicle transport protein SEC22; putative identified as SEC22 by Raikhel, NV, et al. in Plant Physiol. 124: 1558-88 (2000); similar to vesicle trafficking protein gb U91538 from Mus musculus; ESTs gb F15494 and gb F14097 come from this gene (88414.m01371)
656	Not regulated	NC-NC-NC	264443_at	A11g27385	alanine racemase family protein contains Pfam domain, PF01168; Alanine racemase, N-terminal domain (88414.m01378) seryl-RNA synthetase, putative / serine-RNA ligase, putative similar to PR T03949 serine-RNA ligase (EC 6.1.1.1) serS (Zea mays); contains Pfam profiles PF00587: tRNA synthetase class II core domain (G, H, P, S and T), PF02403: Seryl-RNA synthetase N-terminal domain (88414.m01367) C2 domain-containing protein / GRAM domain-containing protein contains Pfam profiles PF00168: C2 domain, contains PF02893: GRAM domain; similar to Chain A, Crystal Structure Of Synaptotagmin III C2aC2B Length(Gi:6890525); similar to Synaptotagmin III phenazine biosynthesis PhnC/PhzF family protein contains Pfam profile: PF02567 phenazine biosynthesis-like protein exonuclease family protein similar to Exosome complex exonuclease RRP4 (Ribosomal RNA processing protein 4)(SP:P38792) (88414.m00299) (Saccharomyces cerevisiae) (88414.m00315) expressed protein ESTs gb H36966, gb R65511, gb T42324 and gb T20569 come from this gene (88414.m00307) expressed protein (88414.m00303) BSD domain-containing protein contains Pfam profile PF03909: BSD domain (88414.m00314) expressed protein (88414.m08093) NHL repeat-containing protein contains Pfam profile PF01436: NHL repeat (88414.m08085) carbonic anhydrase, putative / carbonic dehydratase, putative similar to SP P42737 Carbonic anhydrase 2 (EC 4.2.1.1) (Saccharomyces cerevisiae) (88414.m08085) spermidine synthase 2 (SPDSYN2) / putrescine aminopropyltransferase 2 identical to SP O48861 Spermidine synthase 2 (EC 2.5.1.16) (Putrescine aminopropyltransferase 2) (SPDSY 2) (Arabidopsis thaliana) (88414.m08088) tetraicopeptide repeat (TPR)-containing protein low similarity to protein antigen LmST11 [Leishmania major] Gi:1698880; contains Pfam profile PF00515 TPR Domain; EST gb Z47802 and gb Z48402 come from this gene (88414.m00409) expressed protein (88414.m00413) ABC transporter family protein Strong similarity to MRP-like ABC transporter gb U92650 from A. thaliana and canalicular multi-drug resistance protein gb L49379 from Rattus norvegicus (88414.m00401) expressed protein contains similarity to glutamic acid/alanine-rich protein Gi:6707830 from [Trypanosoma congolense] (88414.m06983) MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopodium esculentum] Gi:12231298; contains Pfam profile PF01554: Uncharacterized membrane protein family (88414.m06982) gamma-glutamyl hydrolase, putative / gamma-Glu-X carboxypeptidase, putative / conjugase, putative similar to gamma glutamyl hydrolase Gi:1679658 SP P53164 from [Glycine max] (88414.m09170) ubiquitin-conjugating enzyme, putative nearly identical to ubiquitin-conjugating enzyme E2 [Catharanthus roseus] Gi:5381319; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme (88414.m09193) expressed protein (88414.m08196)
657	Not regulated	NC-NC-NC	264446_at	A11g27310	
658	Not regulated	NC-NC-NC	264463_at	A11g10150	
659	Not regulated	NC-NC-NC	264467_at	A11g10140	
660	Not regulated	NC-NC-NC	264468_at	A11g10310	
661	Not regulated	NC-NC-NC	264407_at	A11g10180	
662	Not regulated	NC-NC-NC	264471_at	A11g43170	
663	Not regulated	NC-NC-NC	264472_at	A11g43130	
664	Not regulated	NC-NC-NC	264474_at	A11g61740	
665	Not regulated	NC-NC-NC	264477_at	A11g61770	
666	Not regulated	NC-NC-NC	264479_at	A11g61670	
667	Not regulated	NC-NC-NC	264399_at	A11g61780	
668	Not regulated	NC-NC-NC	264374_at	A12g25180	
669	Not regulated	NC-NC-NC	264376_at	A12g25070	
670	Not regulated	NC-NC-NC	264381_at	A12g25100	
671	Not regulated	NC-NC-NC	264396_at	A11g12050	
672	Not regulated	NC-NC-NC	264397_at	A11g11820	
673	Not regulated	NC-NC-NC	264373_at	A11g11890	
674	Not regulated	NC-NC-NC	264349_at	A11g11930	
675	Not regulated	NC-NC-NC	264350_at	A11g11870	
676	Not regulated	NC-NC-NC	264351_at	A11g03370	
677	Not regulated	NC-NC-NC	264355_at	A11g03210	
678	Not regulated	NC-NC-NC	264357_at	A11g03360	
679	Not regulated	NC-NC-NC	264362_at	A11g03290	
680	Not regulated	NC-NC-NC	264366_at	A11g03250	
681	Not regulated	NC-NC-NC	264367_at	A11g03350	
682	Not regulated	NC-NC-NC	264337_at	A11g07030	
683	Not regulated	NC-NC-NC	264340_at	A11g70280	
684	Not regulated	NC-NC-NC	264313_at	A11g70410	
685	Not regulated	NC-NC-NC	264317_at	A11g70310	
686	Not regulated	NC-NC-NC	264322_at	A11g04190	
687	Not regulated	NC-NC-NC	264326_at	A11g04230	
688	Not regulated	NC-NC-NC	264330_at	A11g04120	
689	Not regulated	NC-NC-NC	264307_at	A11g61900	
690	Not regulated	NC-NC-NC	264289_at	A11g61890	
691	Not regulated	NC-NC-NC	264300_at	A11g78670	
692	Not regulated	NC-NC-NC	264303_s_at	A11g78870	
693	Not regulated	NC-NC-NC	264306_at	A11g78890	

694	Not regulated	264248_at	NC-NC-NC	At1g78700	brassinosteroid signalling positive regulator-related contains similarity to BZR1 protein [Arabidopsis thaliana] gi 20270971 gb AAAM18490 (68414.m09173)
695	Not regulated	264250_at	NC-NC-NC	At1g78680	gamma-glutamyl hydrolase (GGH1) / gamma-Glu-X carboxypeptidase / conjugase identical to SP/O65355 Gamma-glutamyl hydrolase precursor (EC 3.4.19.9) (Gamma-Glu-X carboxypeptidase) (Conjugase) (GH) [Arabidopsis thaliana] (68414.m08171)
696	Not regulated	264255_at	NC-NC-NC	At1g09140	SF2/ASF-like splicing modulator (SRP50) nearly identical to SF2/ASF-like splicing modulator Sp30 [Arabidopsis thaliana] gi 4775270 (68414.m01018)
697	Not regulated	264256_at	NC-NC-NC	At1g09270	importin alpha-1 subunit, putative (IMPAA4) similar to importin alpha-1 subunit [Karyopherin alpha-1 subunit, KAP alpha] [Arabidopsis thaliana] SWISS-PROT:Q96321 (68414.m01035)
698	Not regulated	264244_at	NC-NC-NC	At1g60440	eukaryotic pantothenate kinase family protein similar to pantothenate kinase Gi:4181500 from [Aspergillus nidulans], contains Pfam profile PF03630; Fumibile (68414.m08004)
699	Not regulated	264246_at	NC-NC-NC	At1g60140	glycosyl transferase family 20 protein / trehalase-phosphatase family protein contains Pfam profile: PF02356 trehalase-phosphatase (68414.m06775)
700	Not regulated	264219_at	NC-NC-NC	At1g60420	DC1 domain-containing protein contains Pfam domain PF03107; DC1 domain (68414.m06802)
701	Not regulated	264221_s_at	NC-NC-NC	At1g60170	pre-mRNA processing ribonucleoprotein binding region-containing protein similar to U4/U6 snRNP-associated 61 kDa protein [Homo sapiens] Gi:18249847; contains Pfam profile PF01798; Putative snRNA binding domain (68414.m06778)
702	Not regulated	264229_at	NC-NC-NC	At1g67480	Kelch repeat-containing F-box family protein similar to SKP1 interacting partner 6 [Arabidopsis thaliana] Gi:10716957; contains Pfam profiles PF01344; Kelch motif, PF00646; F-box domain (68414.m07685)
703	Not regulated	264233_at	NC-NC-NC	At1g67430	60S ribosomal protein L17 (RPL17B) similar to ribosomal protein Gi:19101 from [Hordeum vulgare] (68414.m07875)
704	Not regulated	264236_at	NC-NC-NC	At1g54680	expressed protein (68414.m06234)
705	Not regulated	264239_at	NC-NC-NC	At1g54770	expressed protein (68414.m06245)
706	Not regulated	264189_s_at	NC-NC-NC	At1g54630	acyl carrier protein 3, chloroplast (ACP-3) nearly identical to SP/P25702 Acyl carrier protein 3, chloroplast precursor (ACP) [Arabidopsis thaliana] (68414.m06230)
707	Not regulated	264190_at	NC-NC-NC	At1g54630	CCAAT-box binding transcription factor Hap5a, putative similar to heme activated protein Gi:8289037 from [Arabidopsis thaliana] Gi:14577940 CCAAT-binding protein subunit HAP5 (Hypocrea jecorina) similar to Transcription factor GB:CAA74053 Gi:2398533 from [Arabidopsis thaliana] similarity to transcription factor Hap5a similar to transcription factor Hap5a [Arabidopsis thaliana] (68414.m06230)
708	Not regulated	264192_at	NC-NC-NC	At1g54710	expressed protein (68414.m06251)
709	Not regulated	264193_at	NC-NC-NC	At1g54610	protein kinase family protein contains Pfam domain, PF00069; Protein kinase domain (68414.m06228)
710	Not regulated	264195_at	NC-NC-NC	At1g22690	Gibberellin-responsive protein, putative similar to SP/P46688 Gibberellin-regulated protein 2 precursor [Arabidopsis thaliana]; contains Pfam profile PF02704; Gibberellin regulated protein (68414.m02835)
711	Not regulated	264205_at	NC-NC-NC	At1g22790	expressed protein (68414.m07398)
712	Not regulated	264207_at	NC-NC-NC	At1g22750	expressed protein (68414.m02842)
713	Not regulated	264210_at	NC-NC-NC	At1g22640	myb family transcription factor (MYB4) similar to myb-related protein Gi:1020155 from [Arabidopsis thaliana] (68414.m02828)
714	Not regulated	264211_at	NC-NC-NC	At1g22770	giantsea protein (Gi) identical to giantsea protein SP:Q9SQI2 from [Arabidopsis thaliana] (68414.m02845)
715	Not regulated	264156_at	NC-NC-NC	At1g65280	DNAJ heat shock N-terminal domain-containing protein contains Pfam profile PF00228 DnaJ domain (68414.m07402)
716	Not regulated	264158_at	NC-NC-NC	At1g65260	PspA/IM30 family protein contains Pfam PF04012; PspA/IM30 family profile; similar to Membrane-associated 30 kDa protein, chloroplast precursor (M30) (Swiss-Prot:Q93943) [Pisum sativum]; similar to Phage shock protein A (Gi:28806161) [Vibrio parahaemolyticus]; similar to Phage shock protein A, (Swiss-Prot:P23853) [Shigella flexneri] (68414.m07398)
717	Not regulated	264159_at	NC-NC-NC	At1g65270	expressed protein (68414.m07404)
718	Not regulated	264164_at	NC-NC-NC	At1g65295	expressed protein (68414.m07404)
719	Not regulated	264165_at	NC-NC-NC	At1g65410	ABC transporter family protein contains similarity to toluene tolerance protein Tlg2A Gi:4336798 from [Pseudomonas putida] (68414.m07421)
720	Not regulated	264168_at	NC-NC-NC	At1g02080	transcriptional regulator-related contains Pfam PF04054; CCR4-Not complex component, Not1; contains TIGRFAM TIGR01612; reticulocyte binding protein; similar to General negative regulator of transcription subunit 1 (SP:P25955) [Saccharomyces cerevisiae]; Location of ESTs gb T44328 and gb AA395265 (68414.m00130)
721	Not regulated	264170_at	NC-NC-NC	At1g02260	transmembrane protein, putative similar to P protein (Melanocyte-specific transporter protein) (SP:Q04871) (Homo sapiens); contains 8 transmembrane domains (68414.m00165)
722	Not regulated	264172_at	NC-NC-NC	At1g02120	GRAM domain-containing protein-related contains low similarity to PF02893; GRAM domain (68414.m00138)
723	Not regulated	264173_at	NC-NC-NC	At1g02160	expressed protein (68414.m00143)
724	Not regulated	264177_at	NC-NC-NC	At1g02150	pentatricopeptide (PPR) repeat-containing protein low similarity to DNA-binding protein [Triticum aestivum] Gi:8958202; contains Pfam profile: PF01535 PPR repeat (68414.m00141)
725	Not regulated	264178_at	NC-NC-NC	At1g02170	latex-abundant family protein (AMC1) / caspase family protein contains similarity to latex-abundant protein [Hevea brasiliensis] gi:AA13218; contains Pfam profile PF00856; ICE-like protease (caspase) p20 domain (68414.m00145)
726	Not regulated	264152_at	NC-NC-NC	At1g02140	mago nashi family protein similar to Mago Nashi, Genbank Accession Number U03559; contains Pfam PF02792; Mago nashi protein domain (68414.m00140)
727	Not regulated	264121_at	NC-NC-NC	At1g02280	GTP-binding protein (Toc33) identical to atToc33 protein (Gi:1155793) [Arabidopsis thaliana]; Carboxyl-terminal end highly similar to GTP-binding protein SP:U43377, location of EST gb AA394770 and gb K30089; identical to cDNA for chloroplast atToc33 protein Gi:1155792 (68414.m00169)
728	Not regulated	264122_at	NC-NC-NC	At1g02130	Ras-related protein (ARA-5) / small GTP-binding protein, putative identical to Ras-related protein ARA-5 SP:P28188 from [Arabidopsis thaliana] (68414.m00139)
729	Not regulated	264123_at	NC-NC-NC	At1g02270	endonuclease/exonuclease/phosphatase family, PF00036 EF hand family protein contains Pfam profiles: PF03372 endonuclease/exonuclease/phosphatase family, PF00036 EF hand (68414.m00167)
730	Not regulated	264130_at	NC-NC-NC	At1g79160	expressed protein (68414.m09230)
731	Not regulated	264140_at	NC-NC-NC	At1g79210	20S proteasome alpha subunit B, putative nearly identical to SP/O23708 Proteasome subunit alpha type 2 (EC 3.4.25.1) (20S proteasome alpha subunit B) [Arabidopsis thaliana] and to At1g16470 (68414.m08235)

732	Not regulated	NC-NC-NC	264120_at	A1g78340	latex-abundant protein, putative (AMC7) / caspase family protein similar to latex-abundant protein [Hevea brasiliensis] gb AAD13216; contains Pfam domain, PF00658: ICE-like protease (caspase) p20 domain (68414.m09246)
733	Not regulated	NC-NC-NC	264092_at	A1g78040	phosphatase II 10 kDa polypeptide identical to photosystem II 10 kDa polypeptide, chloroplast [precursor] SP:P27202 from [Arabidopsis thaliana]; contains Pfam profile: PF04725 photosystem II 10 kDa polypeptide PabR (68414.m09216)
734	Not regulated	NC-NC-NC	264097_s_at	A1g78010	NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial (TYKY) identical to SPIQ42598 NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (Complex 1-23KD) (C1-23KD) (C1-28.5KD)
735	Not regulated	NC-NC-NC	264098_at	A1g78260	expressed protein (68414.m09213)
736	Not regulated	NC-NC-NC	264099_at	A1g78050	DNA repair protein recA, identical to DNA repair protein recA, chloroplast [Precursor] SP:Q39198 from [Arabidopsis thaliana]
737	Not regulated	NC-NC-NC	264102_at	A1g78270	: contains Pfam profile: PF00154 recA bacterial DNA recombination protein (68414.m09217)
738	Not regulated	NC-NC-NC	264084_at	A2g31240	expressed protein contains Pfam profile PF04148: Y752-B-like family (68414.m09241)
739	Not regulated	NC-NC-NC	264089_at	A2g31200	tetratricopeptide repeat (TPR)-containing protein contains Pfam profile PF00515: TPR Domain (68415.m03815)
740	Not regulated	NC-NC-NC	264059_at	A2g31305	actin-depolymerizing factor 6 (ADF6) identical to SPIQ9ZSK2 Actin-depolymerizing factor 6 (ADF-6) (AADF6) [Arabidopsis thaliana] (68415.m03810)
741	Not regulated	NC-NC-NC	264061_at	A2g27970	expressed protein (68415.m03822)
742	Not regulated	NC-NC-NC	264069_at	A2g28000	cyclin-dependent kinase, putative / CDK, putative similar to Cks1 protein [Arabidopsis thaliana] g 2274859 emb CAAQ3859 (68415.m03390)
743	Not regulated	NC-NC-NC	264070_at	A2g27960	Rubisco subunit binding-protein alpha subunit, chloroplast / 60 kDa chaperonin alpha subunit / CPN-60 alpha identical to SWISS-PROT:P21238: Rubisco subunit binding-protein alpha subunit, chloroplast precursor (60 kDa chaperonin alpha subunit, CPN-60 alpha) [Arabidopsis thaliana] (68415.m03393)
744	Not regulated	NC-NC-NC	264076_at	A2g28540	cyclin-dependent kinase / CDK (CKS1) identical to Cks1 protein [Arabidopsis thaliana] g 2274859 emb CAAQ3859 (68415.m03389)
745	Not regulated	NC-NC-NC	264078_at	A2g28470	expressed protein (68415.m03467)
746	Not regulated	NC-NC-NC	264080_at	A2g28520	beta-galactosidase, putative / lactase, putative similar to Beta-galactosidase precursor SP:P48980 from [Lycopersicon esculentum]
747	Not regulated	NC-NC-NC	264056_at	A2g28510	vacuolar proton ATPase, putative similar to Swiss-Prot:Q93050 vacuolar proton translocating ATPase 118 kDa subunit A isoform 1 (Clathrin-coated vesicle/synaptic vesicle proton pump 118 kDa subunit, Vacuolar proton pump subunit 1, Vacuolar adenosine triphosphatase subunit Acl18) (Homo sapiens) (68415.m03465)
748	Not regulated	NC-NC-NC	264028_at	A2g03660	Dof-type zinc finger domain-containing protein similar to elicitor-responsive Dof protein ERDP G1:6092016 from [Plum sativum] (68415.m03464)
749	Not regulated	NC-NC-NC	264037_at	A2g03750	expressed protein Alternative splicing exists based on EST evidence (68415.m00327)
750	Not regulated	NC-NC-NC	264038_at	A2g03690	sulfotransferase family protein similar to similar to steroid sulfotransferase 3 [Brassica napus] G1:3420008, steroid sulfotransferase 1 [Brassica napus] G1:3420004, contains Pfam profile PF00685: Sulfotransferase domain (68415.m00335)
751	Not regulated	NC-NC-NC	264040_at	A2g03730	coenzyme Q biosynthesis Coq4 family protein / ubiquinone biosynthesis Coq4 family protein contains Pfam profile PF05019: Coenzyme Q (ubiquinone) biosynthesis protein Coq4 (68415.m00328)
752	Not regulated	NC-NC-NC	264048_at	A2g22400	ACT domain-containing protein (ACRS) contains Pfam ACT domain PF01842 (68415.m00333)
753	Not regulated	NC-NC-NC	263995_at	A2g22540	NOL1/NOP2/sun family protein contains Pfam profile PF01189: NOL1/NOP2/sun family (68415.m02656)
754	Not regulated	NC-NC-NC	263998_at	A2g22510	short vegetative phase protein (SVP) identical to cDNA short vegetative phase protein (SVP) G1:10944318; (68415.m02673)
755	Not regulated	NC-NC-NC	264003_at	A2g22475	hydroxyproline-rich glycoprotein family protein similar to proline-rich cell wall protein [Gossypium barbadense]
756	Not regulated	NC-NC-NC	264008_at	A2g21120	g 451544 gb AAAT7384; contains proline-rich extensin domains, INTERPRO:IPR002865 (68415.m02670)
757	Not regulated	NC-NC-NC	264012_at	A2g21080	GRAM domain-containing protein / ABA-responsive protein-related similar to ABA-responsive protein [Hordeum vulgare] expressed protein (68415.m02506)
758	Not regulated	NC-NC-NC	264018_at	A2g21170	expressed protein (68415.m02502)
759	Not regulated	NC-NC-NC	264019_at	A2g21130	triosephosphate isomerase, chloroplast, putative similar to Triosephosphate isomerase, chloroplast precursor: SPIP-48498 from Spinacia oleracea, SPIP48225 from Secale cereale (68415.m02511)
760	Not regulated	NC-NC-NC	264020_at	A2g21160	peptidyl-prolyl cis-trans isomerase / cyclophilin (CYP2) / rotamase identical to cyclophilin [Arabidopsis thaliana]
761	Not regulated	NC-NC-NC	264022_at	A2g21185	g 2443757 gb AA871402; similar to peptidyl-prolyl cis-trans isomerase, PPIase (cyclophilin, cyclosporin A-binding protein)
762	Not regulated	NC-NC-NC	264024_at	A2g21180	[Arabidopsis thaliana] SWISS-PROT:P34780 (68415.m02507)
763	Not regulated	NC-NC-NC	263978_at	A2g42680	translocin-associated protein alpha (TRAP alpha) family protein contains Pfam profile: PF03898 translocin-associated protein (TRAP), alpha subunit (68415.m02510)
764	Not regulated	NC-NC-NC	263980_at	A2g42770	expressed protein (68415.m02513)
765	Not regulated	NC-NC-NC	263986_at	A2g42780	expressed protein (68415.m02512)
766	Not regulated	NC-NC-NC	263987_at	A2g42690	ethylene-responsive transcriptional coactivator, putative similar to ethylene-responsive transcriptional coactivator [Lycopersicon esculentum] g 596963 gb AA040402; (68415.m05283)
767	Not regulated	NC-NC-NC	263990_at	A2g42810	peroxisomal membrane 22 kDa family protein contains Mpv17 / PMP22 family domain, Pfam:PF04117 (68415.m05298)
768	Not regulated	NC-NC-NC	263938_at	A2g35800	citrate synthase, glyoxysomal, putative strong similarity to SPIP49299 Citrate synthase, glyoxysomal precursor (Cucurbita maxima); contains Pfam profile PF00285: Citrate synthase (68415.m05298)

769	Not regulated	NC-NC-NC	263939_at	A12g36070	mitochondrial import inner membrane translocase subunit TIM44, putative contains similarity to Swiss-Prot:O35857 import inner membrane translocase subunit TIM44, mitochondrial precursor [Mus musculus]; contains Pfam domain PF04280: Mitochondrial import inner membrane translocase subunit TIM44 (88415.m04428)
770	Not regulated	NC-NC-NC	263949_at	A12g36080	ubiquitin-conjugating enzyme family protein similar to DNA-binding protein CROC-1B [Homo sapiens] GI:1069082; contains Pfam profile PF00178: Ubiquitin-conjugating enzyme (88415.m04427)
771	Not regulated	NC-NC-NC	263951_at	A12g35960	harpin-induced family protein / HIN1 family protein / harpin-responsive family protein similar to harpin-induced protein hin1 (GI:1618321) [Nicotiana tabacum] (88415.m04414)
772	Not regulated	NC-NC-NC	263954_at	A12g35840	sucrose-phosphatase 1 (SPP1) identical to sucrose-phosphatase (SPP1) [Arabidopsis thaliana] GI:1112757 (88415.m04400)
773	Not regulated	NC-NC-NC	263958_at	A12g35940	homeodomain-containing protein contains 'Homeobox' domain signature, Prosite:PS00027 (88415.m04411)
774	Not regulated	NC-NC-NC	263958_at	A12g36240	peritrapezoid (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat (88415.m04448)
775	Not regulated	NC-NC-NC	263928_at	A12g36330	integral membrane protein, putative contains 4 transmembrane domains; contains Pfam PF04535: Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135856) [Arabidopsis thaliana] (88415.m04459)
776	Not regulated	NC-NC-NC	263929_at	A12g36310	inosine-uridine preferring nucleoside hydrolase family protein similar to Chain A, Crystal Structure Of Nucleoside Hydrolase From Leishmania Major GI:8569431; contains Pfam profile PF01156: Inosine-uridine preferring nucleoside hydrolase (88415.m04457)
777	Not regulated	NC-NC-NC	263930_at	A12g36300	integral membrane Yip1 family protein contains Pfam domain, PF04693: Yip1 domain (88415.m04455)
778	Not regulated	NC-NC-NC	263904_at	A12g36380	ABC transporter family protein related to multi drug resistance proteins and P-glycoproteins (88415.m04464)
779	Not regulated	NC-NC-NC	263908_at	A12g36250	chloroplast division protein FtsZ (FtsZ2-1) identical to chloroplast division protein AFB22-1 [Arabidopsis thaliana] (GI:15636809)
780	Not regulated	NC-NC-NC	263920_at	A12g36410	plastid division protein FtsZ [Arabidopsis thaliana] GI:14195704 (88415.m04449)
781	Not regulated	NC-NC-NC	263921_at	A12g36460	expressed protein contains Pfam profile PF04948: Family of unknown function (DUF682) (88415.m04469)
782	Not regulated	NC-NC-NC	263922_s_at	A12g36580	fructose-bisphosphate aldolase, putative similar to PIR[S63073 fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic [Oryza sativa]; contains Pfam profile PF00274 Fructose-bisphosphate aldolase class-1 (88415.m04475)
783	Not regulated	NC-NC-NC	263888_at	A12g21950	pyruvate kinase, putative similar to pyruvate kinase, cytosolic isozyme [Glycine max] SWISS-PROT:Q42806 (88415.m04486)
784	Not regulated	NC-NC-NC	263873_at	A12g21860	SKP1 interacting partner 6 (SKIP6) identical to SKP1 interacting partner 6 GI:10716957 from [Arabidopsis thaliana]
785	Not regulated	NC-NC-NC	263874_at	A12g21870	volaxanthin de-epoxidase-related contains weak similarity to volaxanthin de-epoxidase precursor gi1438875 [Ipomoea batatas]
786	Not regulated	NC-NC-NC	263880_at	A12g21960	expressed protein (88415.m02598)
787	Not regulated	NC-NC-NC	263886_at	A12g36980	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain (88415.m04532)
788	Not regulated	NC-NC-NC	263887_at	A12g36880	major intrinsic family protein / MIP family protein contains Pfam profile: MIP PF00230 (88415.m04516)
789	Not regulated	NC-NC-NC	263840_at	A12g36885	expressed protein (88415.m04522)
790	Not regulated	NC-NC-NC	263842_at	A12g36935	expressed protein (88415.m04517)
791	Not regulated	NC-NC-NC	263856_at	A12g04410	expressed protein (88415.m04445)
792	Not regulated	NC-NC-NC	263859_at	A12g04360	expressed protein (88415.m04037)
793	Not regulated	NC-NC-NC	263862_at	A12g04550	dual specificity protein phosphatase family protein contains Pfam profile: PF00782 dual specificity phosphatase, catalytic domain (88415.m00481)
794	Not regulated	NC-NC-NC	263808_at	A12g04340	expressed protein (88415.m00431)
795	Not regulated	NC-NC-NC	263809_at	A12g04570	GDSL-motif lipase/hydrolase family protein similar to family II lipase EXL3 (GI:15054386), EXL1 (GI:15054382), EXL2 (GI:15054384) [Arabidopsis thaliana]; contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif (88415.m00485)
796	Not regulated	NC-NC-NC	263810_at	A12g04520	eukaryotic translation initiation factor 1A, putative / eIF-1A, putative / eIF-4C, putative strong similarity to translation initiation factor (eIF-1A) [Beta vulgaris] GI:17979795; contains Pfam profile PF01176: Eukaryotic translation factor 1A (88415.m00458)
797	Not regulated	NC-NC-NC	263811_at	A12g04350	long-chain-fatty-acid-CoA ligase family protein / long-chain acyl-CoA synthetase family protein (LACS8) similar to LACS 4 [SPI035547] from Rattus norvegicus, LACS 4 [SPI060488] from Homo sapiens; contains Pfam HMM hit: AMP-binding enzymes PF00501 (88415.m00433)
798	Not regulated	NC-NC-NC	263821_s_at	A12g09990	40S ribosomal protein S16 (RPS16A) Same as GB-Q42340 (88415.m01037)
799	Not regulated	NC-NC-NC	263824_at	A12g04390	transducin family protein / WD-40 repeat family protein contains 4 WD-40 repeats (PF00400); similar to block of proliferation protein Bop1 (GI:1679772) [Mus musculus] (88415.m04977)
800	Not regulated	NC-NC-NC	263826_at	A12g04010	Ca(2+)-dependent nuclease, putative similar to Ca(2+)-dependent nuclease [Arabidopsis thaliana] (GI:7684292 (88415.m04983)
801	Not regulated	NC-NC-NC	263831_at	A12g040300	ferritin, putative similar to ferritin subunit comp2 precursor [Vigna unguiculata] GI:2970654; contains Pfam profile PF00210: Eukaryotic translation initiation factor 2 subunit 1 (Eukaryotic translation initiation factor 2 alpha subunit) (eIF-2-alpha) (EIF-2alpha)
802	Not regulated	NC-NC-NC	263835_at	A12g040280	eukaryotic translation initiation factor 2 subunit 1, putative / eIF-2A, putative / eIF-2-alpha, putative similar to Swiss-Prot:P05198 eukaryotic translation initiation factor 2 subunit 1 (Eukaryotic translation initiation factor 2 alpha subunit) (eIF-2-alpha) (EIF-2alpha)
803	Not regulated	NC-NC-NC	263802_at	A12g04030	expressed protein identical to Protein A12g04030 (Swiss-Prot:Q22882) [Arabidopsis thaliana]; similar to Glioma tumor suppressor candidate region gene 2 protein (p60) (Swiss-Prot:Q22882) [Homo sapiens] (88415.m04986)
804	Not regulated	NC-NC-NC	263805_at	A12g04040	expressed protein similar to GI:7572912 (A12g04040) [Arabidopsis thaliana] (88415.m04981)
805	Not regulated	NC-NC-NC	263774_at	A12g040280	dehydration-responsive family protein similar to early-responsive to dehydration stress ERD3 protein [Arabidopsis thaliana] (GI:15320410; contains Pfam profile PF03141: Putative methyltransferase (88415.m04858)
806	Not regulated	NC-NC-NC	263776_s_at	A12g46440	cyclic nucleotide-regulated ion channel, putative (CNGC11) similar to cyclic nucleotide and calmodulin-regulated ion channel (CNGC1) GI:4581201 from [Arabidopsis thaliana] (88415.m05779)
807	Not regulated	NC-NC-NC	263778_at	A12g46470	OXA1 protein, putative similar to Oxa1 protein [Arabidopsis thaliana] (GI:10176922 (88415.m05783)

808	Not regulated	263785_at	NC-NC-NC	expressed protein (68415.m05774) auxin-responsive GH3 family protein similar to auxin-responsive GH3 product [Glycine max] Gi:18591; contains Pfam profile PF03321; GH3 auxin-responsive promotor (68415.m05770)
809	Not regulated	263786_at	NC-NC-NC	expressed protein (68415.m05777)
810	Not regulated	263787_at	NC-NC-NC	kelch repeat-containing F-box family protein similar to SKP1 interacting partner 4 [Arabidopsis thaliana] Gi:10716953; contains Pfam profiles PF01344; Kelch motif; PF00646; F-box domain (68415.m02931)
811	Not regulated	263788_at	NC-NC-NC	WRKY family transcription factor identical to WRKY transcription factor 17 Gi:15991743 from [Arabidopsis thaliana] (68415.m02934)
812	Not regulated	263789_at	NC-NC-NC	expressed protein weak similarity to MTD1 [Medicago truncatula] Gi:9294810 (68415.m02932)
813	Not regulated	263790_at	NC-NC-NC	expressed protein weak similarity to MTD1 [Medicago truncatula] Gi:9294810 (68415.m02932)
814	Not regulated	263791_at	NC-NC-NC	forkhead-associated domain-containing protein / FHA domain-containing protein (68415.m02562)
815	Not regulated	263792_at	NC-NC-NC	ubiquitin fusion degradation UFD1 family protein similar to SPIP70362 Ubiquitin fusion degradation protein 1 homolog (UB fusion protein 1) [Mus musculus]; contains Pfam profile PF03152; Ubiquitin fusion degradation protein UFD1 (68415.m02532)
816	Not regulated	263793_at	NC-NC-NC	expressed protein (68415.m02534)
817	Not regulated	263794_at	NC-NC-NC	expressed protein similar to YNF (Gi:2804536) [Bacillus subtilis] (68415.m02533)
818	Not regulated	263795_at	NC-NC-NC	fructose-bisphosphate aldolase, putative strong similarity to plastidic fructose-bisphosphate aldolase (EC 4.1.2.13) from Nicotiana glauca (NPALDP1) [Gi:4827251]; Onyza sativa; PIR2:102057 [SPIQ40877] (68415.m02538)
819	Not regulated	263796_at	NC-NC-NC	vacuolar protein ATPase, putative similar to vacuolar protein ATPase 100-kDa subunit from Dictyostelium discoideum P1384136 [gi AA849621] (68415.m02548)
820	Not regulated	263797_at	NC-NC-NC	RNA recognition motif (RRM)-containing protein contains InterPro entry IPR000504; RNA-binding region RNP-1 (RNA recognition motif) (RRM) (68415.m02551)
821	Not regulated	263798_at	NC-NC-NC	expressed protein (68415.m02405)
822	Not regulated	263799_at	NC-NC-NC	malate oxidoreductase, putative similar to NAD-dependent malic enzyme 82 kDa isoform, mitochondrial precursor (EC 1.1.1.39) (NAD-ME) (SP:P37221) [Solanum tuberosum] (68415.m01495)
823	Not regulated	263800_at	NC-NC-NC	GDP-mannose transporter (GONST1) identical to GDP-mannose transporter SP:Q941R4 from [Arabidopsis thaliana] (68415.m01504)
824	Not regulated	263801_at	NC-NC-NC	ABC transporter family protein (68415.m01500)
825	Not regulated	263802_at	NC-NC-NC	mRNA cap-binding protein (ABH1) identical to mRNA cap binding protein [Arabidopsis thaliana] Gi:15192738; contains Pfam profile PF02854; MIF4G domain; identical to cDNA nuclear cap-binding protein CBP90 Gi:8515770 (68415.m01493)
826	Not regulated	263803_at	NC-NC-NC	expressed protein (68414.m08781)
827	Not regulated	263804_at	NC-NC-NC	culin, putative similar to Culin homolog 3 (CUL-3) SP:Q13618, Gi:3639052 from [Homo sapiens]; contains Pfam profile PF00888; Culin family (68414.m03270)
828	Not regulated	263805_at	NC-NC-NC	60S ribosomal protein L10 (RPL10B) Nearly identical to ribosomal protein L10, e. Weim's tumor suppressor homologue, gi 17882 (Z15157), however differences in sequence indicate this is a different member of the L10 family (68414.m03281)
829	Not regulated	263806_at	NC-NC-NC	expressed protein Location of EST Z2841817A, gi 856686 (68414.m03282)
830	Not regulated	263807_at	NC-NC-NC	60S ribosomal protein L34 (RPL34A) identical to GB:Q42351, location of EST 105E277, gi 22624 (68414.m03278)
831	Not regulated	263808_at	NC-NC-NC	expressed protein (68414.m03819)
832	Not regulated	263809_at	NC-NC-NC	zinc-binding protein, putative / protein kinase C inhibitor, putative similar to 14 kDa zinc-binding protein (Protein kinase C inhibitor, PKC) [Zea mays] Swiss-Prot:P42856 (68414.m03812)
833	Not regulated	263810_at	NC-NC-NC	parB-like nuclease domain-containing protein contains Pfam profile PF02195; ParB-like nuclease domain (68414.m03815)
834	Not regulated	263811_at	NC-NC-NC	expressed protein (68414.m03809)
835	Not regulated	263812_at	NC-NC-NC	inositol monophosphatase family protein similar to SPIP29218 Myo-inositol-1(or 4)-monophosphatase (EC 3.1.3.25) (inositol monophosphatase) [Homo sapiens]; contains Pfam profile PF00458; inositol monophosphatase family; EST gi AA597395 comes from this gene (68414.m03818)
836	Not regulated	263813_at	NC-NC-NC	expressed protein contains Pfam profile PF04398; Protein of unknown function, DUF538 (68414.m01042)
837	Not regulated	263814_at	NC-NC-NC	aldo/keto reductase family protein similar to SPIQ46933 Tas protein [Escherichia coli]; Babesia aldo-keto reductase SPIP40690; contains Pfam profile PF00248; oxidoreductase, aldo/keto reductase family (68414.m00433)
838	Not regulated	263815_at	NC-NC-NC	lesion inducing protein-related similar to ORF, able to induce HR-like lesions [Nicotiana tabacum] (68414.m00424)
839	Not regulated	263816_at	NC-NC-NC	maprin and TRAF homology domain-containing protein / MATH domain-containing protein / MATH domain (MATH) domain protease 12 [Arabidopsis thaliana] Gi:1199347; contains Pfam PF00817; Maprin And TRAF-Homology (MATH) domain (68414.m00421)
840	Not regulated	263817_at	NC-NC-NC	prenylated rab acceptor (PRA1) family protein weak similarity to prenylated Rab acceptor [Mus musculus] Gi:7716652; contains Pfam profile PF03208; Prenylated rab acceptor (PRA1) (68414.m00417)
841	Not regulated	263818_at	NC-NC-NC	thioesterase family protein contains Pfam profile PF03061; thioesterase family protein; EST gi 45093 comes from this gene (68414.m00420)
842	Not regulated	263819_at	NC-NC-NC	malate dehydrogenase, cytosolic, putative strong similarity to malate dehydrogenase from Mesembryanthemum crystallinum [SPIQ24047], Medicago sativa [SPIQ48905], Prunus persica [Gi:15982946]; contains InterPro entry IPR001236; Lactate/malate dehydrogenase (68414.m00432)
843	Not regulated	263820_at	NC-NC-NC	transducin family protein / WD-40 repeat family protein contains 6 WD-40 repeats (PF00400); similar to cell cycle control protein cwl8 (SP:O14011) [Schizosaccharomyces pombe (Fission yeast)] (68414.m00442)
844	Not regulated	263821_at	NC-NC-NC	40S ribosomal protein S15 (RPS15A) Strong similarity to Onyza 40S ribosomal protein S15. ESTs gi 292788, gi ATTS0365 come from this gene (68414.m00416)
845	Not regulated	263822_at	NC-NC-NC	2-oxoglutarate-dependent dioxygenase, putative Similar to Arabidopsis 2A8 (gi X83098) and to tomato ethylene synthesis regulatory protein E8 (SPIP10967); EST gi 176913 comes from this gene (68414.m00425)

846	Not regulated	NC-NC-NC	263669_at	A11g04400	cryptochrome 2 apoprotein (CRY2) / blue light photoreceptor (PHH1) 97% identical to photolyase (PHH1) (SP:Q86524) and cryptochrome 2 apoprotein (CRY2) (SP:U43397). ESTs gb W42681 and gb Z25638 come from this gene; contains Pfam profiles PF03441: FAD binding domain of DNA photolyase and PF00875: deoxyribodipyrimidine photolyase; identical to cDNA Cvi
847	Not regulated	NC-NC-NC	263673_at	A12g04800	cryptochrome 2 (CRY2) GI:18026375 (88414.m00430) expressed protein (88415.m00493) cellular repressor of E1A-stimulated genes (CREG) family contains 1 transmembrane domain; similar to CREG2 (GI:24371079) [Homo sapiens] and (GI:24371081) [Mus musculus]; similar to cellular repressor of E1A-stimulated genes CREG (GI:3550343) [Homo sapiens] (88415.m00479) DNA-directed RNA polymerase II, putative similar to SPIQ24320 DNA-directed RNA polymerase II 14.4 kDa polypeptide (EC 2.7.7.6) (RPB6) [Drosophila melanogaster]; contains Pfam profile PF01192: RNA polymerases K / 14 to 18 kDa subunit (88415.m00473)
848	Not regulated	NC-NC-NC	263647_at	A12g04690	ferredoxin thioreductase catalytic beta chain family protein contains Pfam profile: PF02943 ferredoxin thioreductase catalytic beta (88415.m00480) expressed protein (88415.m00509) expressed protein (88415.m00492) expressed protein (88415.m01277) expressed protein (88415.m01276) expressed protein (88415.m03024)
849	Not regulated	NC-NC-NC	263621_at	A12g04630	microtubule associated protein (MAP65/ASE1) family protein low similarity to protein regulating cytokinesis 1 (PRC1) [Homo sapiens] GI:2865521; contains Pfam profile PF03999: Microtubule associated protein (MAP65/ASE1 family) (88415.m00125) purple acid phosphatase, putative contains Pfam profile: PF00149 calcheurin-like phosphatase; identical to purple acid phosphatase (GI:20257479) [Arabidopsis thaliana]; (88415.m00122) homeodomain-containing protein (88415.m01877) pentatricopeptide (PTP) repeat-containing protein contains Pfam profile PF01535: PPR repeat (88415.m01864) proline-rich extensin-like family protein contains proline-rich extensin domains, INTERPRO:IPR002965 (88415.m02987) ADP-ribosylation factor 3 (ARF3) identical to GP-453191 ADP-ribosylation factor 3 [Arabidopsis thaliana]; contains domain PF00025: ADP-ribosylation factor family (88415.m02959) RHO1 family protein similar to extragenic suppressor of the bimD6 mutation (SUDD) [Emmentella nidulans] GI:2338556, RHO1 [Saccharomyces cerevisiae] GI:1359602; contains Pfam profile PF01163: RHO1 family (88418.m04486) Rieske [2Fe-2S] domain-containing protein similar to Rieske iron-sulfur protein Tc55 from Pisum sativum [gi:2764524]; contains zinc finger (B-box type) family protein (88415.m02968) chaperone protein dnaJ-related similar to Tst1-interacting protein TSIP1 (GI:4337001) [Nicotiana tabacum] (88415.m02973) myb family transcription factor contains PFAM profile: PF00249 myb-like DNA-binding domain (88415.m02575) RER1B protein identical to SPIQ048671 RER1B protein (AIREB1) [Arabidopsis thaliana] (88415.m02569) universal stress protein (USP) family protein / responsive to desiccation protein (RD2) strong similarity to RD2 protein [Arabidopsis thaliana] GI:15320408; contains Pfam profile PF00562: universal stress protein family; identical to cDNA RD2 GI:15320407 (88415.m02571) 40S ribosomal protein S25 (RPS25B) (88415.m02567)
850	Not regulated	NC-NC-NC	263591_at	A12g01910	phosphoenolpyruvate carboxylase, putative / PEP carboxylase, putative (PPC2) strong similarity to phosphoenolpyruvate carboxylase [Brassica napus] GI:507808; contains Pfam profile PF00311: phosphoenolpyruvate carboxylase (88415.m05271) DEAD box RNA helicase, putative similar to SPIQ00571 DEAD-box protein 3 [Helicase-like protein 2] [Homo sapiens], DEAD box RNA helicase DDX3 [Homo sapiens] GI:3523150; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain (88415.m05262)
851	Not regulated	NC-NC-NC	263595_at	A12g01890	14-3-3 protein GF14 mu (GRF9) identical to GF14 mu, GI:3551052, SP:Q86299 from [Arabidopsis thaliana] (88415.m05270) cold-responsive protein / cold-regulated protein (cor15b) nearly identical to cold-regulated gene cor15b [Arabidopsis thaliana] GI:456016; contains Pfam profile PF02987: Late embryogenesis abundant protein (88415.m05263) expressed protein (88415.m05268) expressed protein (88415.m01339) expressed protein (88415.m03888) ankyrin repeat family protein contains ankyrin repeat domains, Pfam:PF00023 (88415.m03886)
852	Not regulated	NC-NC-NC	263557_at	A12g04700	ankyrin protein kinase, putative similar to ankyrin-kinase [Medicago truncatula] gi1870070 [gb AAL78674; contains Pfam profile PF00023: Ankyrin repeat; identical to cDNA calcineurin B-like protein 10 (CBL10) GI:29150247; blast match of 87% identity and 1.9e-200 P-value to GPI1870070 [gb AAL78674; 1AFA58699_1AFA58699 ankyrin-kinase (Medicago truncatula) (88415.m03882) expressed protein (88415.m03876)
853	Not regulated	NC-NC-NC	263532_at	A12g04795	UDP-glucuronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase (88415.m03877)
854	Not regulated	NC-NC-NC	263536_at	A12g11910	GDSL-motif lipase/hydrolase family protein similar to Anther-specific proline-rich protein APC from Brassica napus (SPIP40603), Arabidopsis thaliana (GI:22559); contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif (88415.m03065)
855	Not regulated	NC-NC-NC	263537_at	A12g11890	
856	Not regulated	NC-NC-NC	263589_at	A12g25280	
857	Not regulated	NC-NC-NC	263591_at	A12g01910	
858	Not regulated	NC-NC-NC	263595_at	A12g01890	
859	Not regulated	NC-NC-NC	263557_at	A12g04700	
860	Not regulated	NC-NC-NC	263552_x_at	A12g17033	
861	Not regulated	NC-NC-NC	263529_at	A12g24765	
862	Not regulated	NC-NC-NC	263532_s_at	A15g37350	
863	Not regulated	NC-NC-NC	263533_at	A12g24820	
864	Not regulated	NC-NC-NC	263537_at	A12g24790	
865	Not regulated	NC-NC-NC	263541_at	A12g24890	
866	Not regulated	NC-NC-NC	263549_at	A12g21650	
867	Not regulated	NC-NC-NC	263516_at	A12g21600	
868	Not regulated	NC-NC-NC	263517_at	A12g21820	
869	Not regulated	NC-NC-NC	263519_at	A12g21580	
870	Not regulated	NC-NC-NC	263491_at	A12g42600	
871	Not regulated	NC-NC-NC	263493_at	A12g42520	
872	Not regulated	NC-NC-NC	263494_at	A12g42590	
873	Not regulated	NC-NC-NC	263495_at	A12g42530	
874	Not regulated	NC-NC-NC	263496_at	A12g42570	
875	Not regulated	NC-NC-NC	263513_at	A12g12400	
876	Not regulated	NC-NC-NC	263498_at	A12g31840	
877	Not regulated	NC-NC-NC	263459_at	A12g31820	
878	Not regulated	NC-NC-NC	263461_at	A12g31800	
879	Not regulated	NC-NC-NC	263466_at	A12g31740	
880	Not regulated	NC-NC-NC	263472_at	A12g31950	
881	Not regulated	NC-NC-NC	263473_at	A12g31750	
882	Not regulated	NC-NC-NC	263482_at	A12g03980	

883	Not regulated						heat shock protein, putative strong similarity to heat shock protein [Arabidopsis thaliana] Gi:1908930; contains Pfam profiles PF02518: ATPase, histidine kinase, DNA gyrase B, and HSP90-like domain protein, PF00183: Hsp90 protein (88415.m00371)
884	Not regulated						ubiquitin-specific protease 4 (UBP4) identical to Gi:2347100 (88415.m02847)
885	Not regulated						aminotransferase class I and II family protein similar to aspartate aminotransferase from <i>Bacillus stearothermophilus</i> SP[Q59228, Thermus aquaticus SP[Q33822]; contains Pfam profile PF00155: aminotransferase, classes I and II (88415.m02841)
886	Not regulated						expressed protein (88415.m03477)
887	Not regulated						[IR] domain-containing protein / ARIADNE-like protein AR17 (AR17) identical to ARIADNE-like protein AR17 [Arabidopsis thaliana] Gi:29125028; contains similarity to Swiss-Prot Q94981: aradine-1 protein (Ar-1) [Drosophila melanogaster]; contains Pfam profile PF01485: IIR domain (88415.m03850)
888	Not regulated						secY family protein low similarity to SP[Q31159] Preprotein translocase secY subunit (Synechococcus sp); contains Pfam profile PF00344: eubacterial secY protein (88415.m03852)
889	Not regulated						expressed protein (88415.m03870)
890	Not regulated						Ras-related GTP-binding protein, putative similar to GTP-binding protein Gi:289370 from [Brassica napus] (88415.m03867)
891	Not regulated						expressed protein (88415.m03846)
892	Not regulated						40S ribosomal protein S3 (RPS3A) (88415.m03862)
893	Not regulated						subtilisin-like protease (AIR3) almost identical to subtilisin-like protease AIR3 Gi:4218991 from [Arabidopsis thaliana], missing 200 aa at N-terminus (88415.m00400)
894	Not regulated						expressed protein (88415.m00383)
895	Not regulated						zinc finger (C2H2 type) family protein contains Pfam domain, PF00096: Zinc finger, C2H2 type (88415.m03490)
896	Not regulated						expressed protein (88415.m02524)
897	Not regulated						bZIP family transcription factor contains a bZIP transcription factor basic domain signature (PDOC00036) (88415.m02520)
898	Not regulated						expressed protein weak similarity to Ribosome biogenesis protein MAK21 (Swiss-Prot Q12176) [Saccharomyces cerevisiae] (88415.m01992)
899	Not regulated						protein kinase, putative similar to protein kinase APK1A [Arabidopsis thaliana] Swiss-Prot Q06548 (88415.m01888)
900	Not regulated						expressed protein (88415.m01991)
901	Not regulated						ubiquitin family protein weak similarity to PLIC-2 (ubiquitin-like type II) [Homo sapiens] Gi:9937505; contains Pfam profiles PF00240: Ubiquitin family, PF06627: UBA/ITS-N domain (88415.m01986)
902	Not regulated						nucleolar RNA-binding Nop10p family protein similar to Nop10p (GI:8096250) [Homo sapiens] (88415.m02392)
903	Not regulated						nonsense-mediated mRNA decay NMD3 family protein contains Pfam profile, PF04981: NMD3 family protein (88415.m00343)
904	Not regulated						scramblase-related weak similarity to Phospholipid scramblase 1 (PL scramblase 1) (Ca2)-dependent phospholipid scramblase 1) (Transplasmalase associated protein 1) (TRA1) (NOR1) (Swiss-Prot Q8UJ00) [Mus musculus]; weak similarity to Phospholipid scramblase 4 (PL scramblase 4) (Ca2)-dependent phospholipid scramblase 4) (Swiss-Prot Q8NRQ2) [Homo sapiens] (88415.m00516)
905	Not regulated						chlorophyll A-B binding protein / LHClI type II (LHCb2.2) identical to Lhc2 protein [Arabidopsis thaliana] Gi:4741948; contains Pfam profile PF00504: Chlorophyll A-B binding protein (88415.m00528)
906	Not regulated						serine-glyoxylate aminotransferase-related similar to serine-glyoxylate aminotransferase (Gi:21535798) [Methylobacterium dichloromethanicum]; contains TIGRFAM TIGR01364: phosphoserine aminotransferase; contains Pfam PF00286: aminotransferase, class VI (88415.m01474)
907	Not regulated						zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097: zinc finger, C3HC4 type (RING finger) (88415.m02626)
908	Not regulated						UBP1 interacting protein 1a (UBA1a) nearly identical to UB1P1 interacting protein 1a [Arabidopsis thaliana] Gi:19574236; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM); based on cDNA of partial mRNA for UB1P1 interacting protein 1a (uba1a) Gi:19574235 (88415.m02623)
909	Not regulated						lipase family protein similar to SP[Q7098] Triacylglycerol lipase, gastric precursor (EC 3.1.1.3) [Homo sapiens]; contains Pfam profile PF04083: ab-hydrolase associated lipase region (88415.m01737)
910	Not regulated						UNC-50 family protein contains Pfam profile PF05216: UNC-50 family; contains 5 transmembrane domains; similar to inner nuclear membrane RNA-binding protein unc-50 related protein (Gi:2735550) [Rattus norvegicus] (88415.m01738)
911	Not regulated						ADP-ribosylation factor 1 (ARF1) identical to ADP-ribosylation factor ARF1 ([Arabidopsis thaliana] (SP-P36397) (GP:166586) (88415.m05890)
912	Not regulated						zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097: zinc finger, C3HC4 type (RING finger) (88415.m00412)
913	Not regulated						leucine-rich repeat family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001811 (88415.m01747)
914	Not regulated						expressed protein (88415.m01741)
915	Not regulated						protein kinase family protein contains protein kinase domain, Pfam:PF00069 (88415.m01242)
916	Not regulated						40S ribosomal protein S14 (RPS14A) (88415.m04438)
917	Not regulated						peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative contains Pfam domain, PF00160: peptidyl-prolyl cis-trans isomerase, cyclophilin-type (88415.m04436)
918	Not regulated						calmodulin-binding protein-related contains similarity to potato calmodulin-binding protein PCBP Gi:17633110 from [Solanum tuberosum] (88415.m04764)
919	Not regulated						vacuolar ATP synthase 16 kDa proteolipid subunit 5 / V-ATPase 16 kDa proteolipid subunit 5 (AVAP5) identical to SP[Q59227 Vacuolar ATP synthase 16 kDa proteolipid subunit 13/5 (EC 3.6.3.14) (V-ATPase 16 kDa proteolipid subunit 13/5) (Arabidopsis thaliana) Gi:926929; contains Pfam profile PF00137: ATP synthase subunit C (88415.m01893)
920	Not regulated						hydroxyacylglutathione hydrolase, putative / glyoxalase II, putative similar to glyoxalase II isozyme [Arabidopsis thaliana] gi:2570338[gi:AAAC49865 (88415.m03829)

921 Not regulated	NC-NC-NC	263253_at	A12g31370	bZIP transcription factor (POSF21) identical to GB-004088 (88415.m03832)
922 Not regulated	NC-NC-NC	263255_at	A11g10490	expressed protein contains Pfam profile PF05127: Putative ATPase (DUF699) (88414.m01181)
923 Not regulated	NC-NC-NC	263256_at	A11g10500	hesB-like domain-containing protein similar to IscA (putative iron-sulfur cluster assembly protein) (Azotobacter vinelandii) Gi:2271523; contains Pfam profile PF01521: HesB-like domain (88414.m01182)
924 Not regulated	NC-NC-NC	263235_at	A11g10430	serine/threonine protein phosphatase PP2A-1 catalytic subunit (EC 3.1.3.16) (Arabidopsis thaliana); contains Pfam profile PF00149: Ser/Thr protein phosphatase (88414.m01175)
925 Not regulated	NC-NC-NC	263206_at	A11g10590	DNA-binding protein-related contains weak similarity to G-quartet DNA binding protein 3 (Tetrahymena thermophila) (88414.m01180)
926 Not regulated	NC-NC-NC	263208_at	A11g10480	zinc finger (C2H2 type) family protein contains Pfam profile: PF00098 zinc finger, C2H2 type (88414.m01180)
927 Not regulated	NC-NC-NC	263209_at	A11g10522	expressed protein (88414.m01185)
928 Not regulated	NC-NC-NC	263222_at	A11g30840	protein kinase, putative contains protein kinase domain, Pfam:PF00069 (88414.m03747)
929 Not regulated	NC-NC-NC	263224_at	A11g30580	expressed protein (88414.m03741)
930 Not regulated	NC-NC-NC	263226_at	A11g30890	SEC14 cytosolic factor family protein / phosphoglycerate transfer family protein contains Pfam PF00650: CRAL/TRIO domain; contains Pfam PF03765: CRAL/TRIO, N-terminus; similar to cytosolic factor (Phosphatidylinositol(4-phosphatidylcholine) transfer protein) (PI3PCTP) (SP: P24280) (Saccharomyces cerevisiae); ESTs gb176582, gb176582, gb176582 come from this gene (88414.m03752)
931 Not regulated	NC-NC-NC	263227_at	A11g30750	expressed protein (88414.m03758)
932 Not regulated	NC-NC-NC	263205_at	A11g05500	C2 domain-containing protein similar to Ca ²⁺ -dependent lipid-binding protein (CLB1) Gi:2789434 from [Lycopersicon esculentum] (88414.m00561)
933 Not regulated	NC-NC-NC	263179_at	A11g05710	ethylene-responsive protein, putative similar to ethylene-inducible ER33 protein [Lycopersicon esculentum] (88414.m00561)
934 Not regulated	NC-NC-NC	263180_at	A11g05620	glucanase-like protein (88414.m04479)
935 Not regulated	NC-NC-NC	263181_at	A11g05720	inosine-uridine preferring nucleoside hydrolase family protein similar to Chain A, Crystall Structure Of Nucleoside Hydrolase From Leishmania MajorGi:859431; contains Pfam profile PF01156: Inosine-uridine preferring nucleoside hydrolase (88414.m00583)
936 Not regulated	NC-NC-NC	263183_at	A11g05570	selenoprotein family protein contains Prosite PS00190: Cytochrome c family heme-binding site signature; similar to 15 kDa selenoprotein (Gi:12314088) (Homo sapiens) (88414.m00586)
937 Not regulated	NC-NC-NC	263185_at	A11g05520	callose synthase 1 (CALST1)/1,3-beta-glucan synthase 1 nearly identical to callose synthase 1 catalytic subunit [Arabidopsis thaliana] Gi:13849388 (88414.m00575)
938 Not regulated	NC-NC-NC	263193_at	A11g36050	transport protein, putative similar to Swiss-Prot:Q15438 protein transport protein Sec23A [Homo sapiens] (88414.m00585)
939 Not regulated	NC-NC-NC	263172_at	A11g54170	expressed protein (88414.m04479)
940 Not regulated	NC-NC-NC	263145_at	A11g54090	ataxin-2-related similar to SCA2 (Gi:1770390) [Homo sapiens]; similar to ataxin-2 (Gi:3005020) [Mus musculus] (88414.m08175)
941 Not regulated	NC-NC-NC	263152_at	A11g54060	exocyst subunit EXO70 family protein contains Pfam domain PF03081: Exo70 exocyst complex subunit (88414.m08164)
942 Not regulated	NC-NC-NC	263154_at	A11g54110	expressed protein similar to 80-interacting protein 1 (NSIP1) (Nicotiana tabacum) Gi:18149189 (88414.m08160)
943 Not regulated	NC-NC-NC	263156_at	A11g54030	calion exchanger, putative (CAX10) Ca ²⁺ -Calion Antipporter (CaCA) Family member PMID:11500563 (88414.m08168)
944 Not regulated	NC-NC-NC	263162_at	A11g54150	GDSL-motif lipase, putative similar to myrosinase-associated proteins Gi:1789968, Gi:1789970, Gi:1216391, Gi:1216389 from [Brassica napus]; contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase (88414.m08156)
945 Not regulated	NC-NC-NC	263170_at	A11g03000	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00087 zinc finger, C3HC4 type (RING finger) (88414.m08173)
946 Not regulated	NC-NC-NC	263113_at	A11g03150	AAA-type ATPase family protein contains Pfam domain, PF00004: ATPase, AAA family (ATPases 'A' associated with diverse cellular 'A' activities) (88414.m00271)
947 Not regulated	NC-NC-NC	263120_at	A11g78490	GCN5-related N-acetyltransferase (GNAT) family protein similar to SPIP07347 N-terminal acetyltransferase complex ARD1 subunit (Arabidopsis thaliana) (88414.m00292)
948 Not regulated	NC-NC-NC	263122_at	A11g78510	cytochrome P450 family protein similar to Cytochrome P450 90A1 (SP:Q42569) [Arabidopsis thaliana] (88414.m09149)
949 Not regulated	NC-NC-NC	263126_at	A11g78460	solaneyl diphosphate synthase (SPS) identical to solanelyl diphosphate synthase [Arabidopsis thaliana] Gi:19811233; contains Pfam profile PF00348: Polyphenyl synthetase (88414.m09151)
950 Not regulated	NC-NC-NC	263128_at	A11g78600	SQUL heme-binding family protein weak similarity to SOUL protein [Mus musculus] Gi:4886908; contains Pfam profile PF04832: SOUL heme-binding protein (88414.m09143)
951 Not regulated	NC-NC-NC	263129_at	A11g78620	zinc finger (B-box type) family protein similar to zinc finger protein Gi:3618316 from [Oryza sativa] (88414.m09160)
952 Not regulated	NC-NC-NC	263132_at	A11g78560	integral membrane family protein contains Pfam domain PF01940: Integral membrane protein (88414.m09162)
953 Not regulated	NC-NC-NC	263136_at	A11g78580	bile acid sodium symporter family protein low similarity to SPIQ12908 ileal sodium/bile acid cotransporter (Homo sapiens); contains Pfam profile PF01758: Sodium Bile acid symporter family (88414.m09156)
954 Not regulated	NC-NC-NC	263137_at	A11g78660	alpha, alpha-trehalose-phosphatase synthase, UDP-forming, putative / trehalose-6-phosphate synthase, putative / UDP-glucose-glucosephosphate glucosyltransferase, putative similar to trehalose-6-phosphate synthase SL-TPSP (Selaginella lepidophylla) Gi:4100325; contains Pfam profile PF00982: Glycosyltransferase family 20, PF02358: Trehalose-phosphatase (88414.m09158)
955 Not regulated	NC-NC-NC	263111_s_at	A11g65190	gamma-glutamyl hydrolase, putative / gamma-Glu-X carboxypeptidase, putative / conjugase, putative similar to SPO85355 Gamma-glutamyl hydrolase precursor (EC 3.4.19.9) (Gamma-Glu-X carboxypeptidase) (Conjugase) (GH) [Arabidopsis thaliana] (88414.m09167)
956 Not regulated	NC-NC-NC	263096_at	A2g16060	protein kinase family protein contains similarity to protein kinases (88414.m07391)
957 Not regulated	NC-NC-NC	263097_at	A2g16070	non-symbiotic hemoglobin 1 (HB1) (GLB1) identical to SPIQ24520 Non-symbiotic hemoglobin 1 (Hb1) (ARATH GLB1) (Arabidopsis thaliana) (88415.m01842)
958 Not regulated	NC-NC-NC	263074_at	A2g17560	expressed protein (88415.m01842)
				high mobility group protein gamma (HMGgamma) / HMG protein gamma nearly identical to HMG protein (HMGgamma) (Arabidopsis thaliana) Gi:2632355 (88415.m02032)

959	Not regulated	NC-NC-NC	263076_at	A12g17520	protein kinase family protein / Ire1 homolog-2 (IRE1-2) contains protein kinase domain, Pfam:PF00068; identical to Ire1 homolog-2 [Arabidopsis thaliana] GI:1527139; cDNA Ire1 homolog-2 GI:1527139 (68414.m02026)
960	Not regulated	NC-NC-NC	263077_at	A12g17510	ribonuclease II family protein similar to SPIP37202 Mitotic control protein dis3 (Schizosaccharomyces pombe); contains Pfam PF00773; RNB-like protein (68415.m02025)
961	Not regulated	NC-NC-NC	263047_at	A12g17630	phosphoserine aminotransferase, putative similar to Phosphoserine aminotransferase, chloroplast precursor (PSAT) (SP:Q86255) [Arabidopsis thaliana]; contains TIGRFAM TIGR01364; phosphoserine aminotransferase, contains Pfam PF00268; aminotransferase, class V (68415.m02039)
962	Not regulated	NC-NC-NC	263019_at	A11g23870	glycosyl transferase family 20 protein / trehalose-phosphatase family protein contains Pfam profile: PF02358 trehalose-phosphatase (68414.m03011)
963	Not regulated	NC-NC-NC	263023_at	A11g23960	expressed protein contains Pfam profile PF04776; Protein of unknown function (DUF626) (68414.m03025)
964	Not regulated	NC-NC-NC	263035_at	A11g23960	splicing factor RSZp21 (RSZP21) / 9C8-like SR protein (SRZ21) nearly identical to 9C8-like splicing factor SRZ21 [Arabidopsis thaliana] GI:3435096; RSZp21 protein [Arabidopsis thaliana] GI:2582843 (68414.m03009)
965	Not regulated	NC-NC-NC	263036_at	A11g23880	NHL repeat-containing protein contains Pfam profile PF01436; NHL repeat (68414.m03013)
966	Not regulated	NC-NC-NC	263037_at	A11g23230	expressed protein (68414.m02806)
967	Not regulated	NC-NC-NC	263044_at	A11g23360	UblE/COQ5 methyltransferase family protein similar to 2-hexaprenyl-1,4-naphthoquinone methyltransferase GB:BA25287
968	Not regulated	NC-NC-NC	263010_at	A11g23330	Gi:2982680 from Micrococcus luteus; contains Pfam profile PF01208; methyltransferase, UblE/COQ5 family (68414.m02821)
969	Not regulated	NC-NC-NC	263014_at	A11g23400	expressed protein (68414.m02917)
970	Not regulated	NC-NC-NC	263015_at	A11g23430	expressed protein (68414.m02830)
971	Not regulated	NC-NC-NC	262985_s_at	A11g23280	60S ribosomal protein L27A (RPL27AB) similar to 60S RIBOSOMAL PROTEIN L27A GB:P48637 GI:1710530 from [Arabidopsis thaliana] (68414.m02913)
972	Not regulated	NC-NC-NC	263000_at	A11g54350	ABC transporter family protein similar to hypothetical ABC transporter ATP-binding protein GI:9955395 from [Micrococcus aeruginosa] (68414.m06196)
973	Not regulated	NC-NC-NC	263001_at	A11g54360	expressed protein (68414.m06197)
974	Not regulated	NC-NC-NC	262954_at	A11g54500	rubredoxin family protein similar to SPIP00270 Rubredoxin (Rd) [Desulfovibrio gigas]; contains Pfam profile PF00301; Rubredoxin (68414.m06216)
975	Not regulated	NC-NC-NC	262955_at	A11g54520	expressed protein (68414.m06218)
976	Not regulated	NC-NC-NC	262956_at	A11g54270	eukaryotic translation initiation factor 4A-2 / eIF-4A-2 similar to eukaryotic translation initiation factor 4A GI:16086 from [Nicotiana glauca] (68414.m06187)
977	Not regulated	NC-NC-NC	262957_s_at	A11g54250	DNA-directed RNA polymerase I, II, and III, putative similar to SPIP52434 DNA-directed RNA polymerases I, II, and III 17.1 kDa polypeptide (EC 2.7.7.6) (RPB1) (RPB8) (Homo sapiens); contains Pfam profile PF03870; RNA polymerase Rpb8 (68414.m06185)
978	Not regulated	NC-NC-NC	262958_at	A11g54410	dehydrin family protein contains Pfam domain, PF00257; Dehydrin (68414.m06207)
979	Not regulated	NC-NC-NC	262959_at	A11g54290	eukaryotic translation initiation factor SU11, putative similar to PIP32911 Protein translation factor SU11 [Saccharomyces cerevisiae]; contains Pfam profile PF01253; Translation initiation factor SU11 (68414.m06189)
980	Not regulated	NC-NC-NC	262960_at	A11g54320	LEM3 (ligand-effect modulator 3) family protein / CDC50 family protein Similar to GI:11994416; GI:4866337; GI:4835783; GI:8757735 from [Arabidopsis thaliana] (68414.m06193)
981	Not regulated	NC-NC-NC	262964_at	A11g54380	spliceosome protein-related contains Pfam domain, PF04938; Survival motor neuron (SMN) interacting protein 1 (SIP1) (68414.m06200)
982	Not regulated	NC-NC-NC	262966_at	A11g75760	ER lumen protein retaining receptor family protein similar to SPIP33946 ER lumen protein retaining receptor 1 (KDEL receptor 1) (Bos taurus); contains Pfam profile PF00810; ER lumen protein retaining receptor (68414.m08799)
983	Not regulated	NC-NC-NC	262975_at	A11g75540	zinc finger (B-box type) family protein similar to zinc finger protein GB:BA33202 GI:3618312 from [Oryza sativa] (68414.m08779)
984	Not regulated	NC-NC-NC	262978_at	A11g75780	tubulin beta-1 chain (TUBB1) nearly identical to SPIP12411 Tubulin beta-1 chain (Arabidopsis thaliana) (68414.m08801)
985	Not regulated	NC-NC-NC	262948_at	A11g75560	zinc knuckle (CCHC-type) family protein contains Pfam domain, PF00068; Zinc knuckle (68414.m08781)
986	Not regulated	NC-NC-NC	262928_at	A11g65720	expressed protein (68414.m07459)
987	Not regulated	NC-NC-NC	262930_at	A11g65690	harpin-induced protein-related / HIN1-related / harpin-responsive protein-related similar to hin1 homolog (GI:13122296) [Arabidopsis thaliana]; similar to hin1 (GI:22830759) [Nicotiana glauca]; contains 1 transmembrane domain; (68414.m07456)
988	Not regulated	NC-NC-NC	262931_at	A11g65700	small nuclear ribonucleoprotein, putative / snRNP, putative / Sn protein, putative similar to U6 snRNA-associated Sm-like protein LSm8 (Homo sapiens) SWISS-PROT:O85777 (68414.m07457)
989	Not regulated	NC-NC-NC	262932_at	A11g65820	microsomal glutathione S-transferase, putative similar to MGST3_HUMAN SP:O14860 (68414.m07469)
990	Not regulated	NC-NC-NC	262937_at	A11g79560	FtsH protease, putative contains similarity to chloroplast FtsH protease GI:5804762 from [Nicotiana glauca] (68414.m09275)
991	Not regulated	NC-NC-NC	262944_at	A11g79550	phosphoglycerate kinase, putative similar to SPIP41759 Phosphoglycerate kinase, chloroplast precursor (EC 2.7.2.3) [Chlamydomonas reinhardtii]; contains Pfam profile PF00162; phosphoglycerate kinase (68414.m09273)
992	Not regulated	NC-NC-NC	262945_at	A11g79510	expressed protein (68414.m09268)
993	Not regulated	NC-NC-NC	262946_at	A11g79390	2-dehydro-3-deoxyphosphogluconate aldolase / phospho-2-dehydro-3-deoxyphosphogluconate aldolase / 3-deoxy-D-manno-octulosonic acid synthetase (KDSA) (KDSA) identical to Swiss-Prot:Q9AV97 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.18) (Phospho-2-dehydro-3-deoxyphosphogluconate aldolase) (3-deoxy-D-manno-octulosonic acid 8-phosphate synthetase) (KDO 8-P synthase) [Arabidopsis thaliana] (68414.m09268)
994	Not regulated	NC-NC-NC	262920_at	A11g79500	ABC transporter family protein similar to PDR5-like ABC transporter GI:1514643 from [Spiridella polytriza] (68414.m08745)
995	Not regulated	NC-NC-NC	262899_at	A11g59870	

996	Not regulated	262906_at	NC-NC-NC	ATP-dependent RNA helicase, putative similar to SPIP47047 ATP-dependent RNA helicase DOB1 (Saccharomyces cerevisiae), HUA enhancer 2 [Arabidopsis thaliana] GI:16024836; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain (68414.m07629)
997	Not regulated	262909_at	NC-NC-NC	serine/threonine protein phosphatase PP2A-2 catalytic subunit (PP2A2) identical to SPIQ07099 Serine/threonine protein phosphatase PP2A-2 catalytic subunit (68414.m07629)
998	Not regulated	262910_at	NC-NC-NC	phosphatase (68414.m07356)
999	Not regulated	262913_at	NC-NC-NC	expressed protein contains Pfam profile: PF04801 protein of unknown function (DUF569 (68414.m0718)
1000	Not regulated	262859_at	NC-NC-NC	aldo/keto reductase, putative similar to NADPH-dependent cytochrome P450 4A3240 from (Solanum melongena) (68414.m07357)
1001	Not regulated	262860_at	NC-NC-NC	dependent 6'-deoxychalcone synthase (Glycine max)[GI:18728] (68414.m0754)
1002	Not regulated	262860_at	NC-NC-NC	translational activator family protein similar to HSCCN1 (Homo sapiens) GI:2282578 (68414.m07348)
1003	Not regulated	262875_at	NC-NC-NC	expressed protein contains Pfam PF05634: Arabidopsis thaliana protein of unknown function (DUF794) (68414.m07348)
1004	Not regulated	262876_at	NC-NC-NC	expressed protein (68414.m07384)
1005	Not regulated	262878_at	NC-NC-NC	DSS1/SEM1 family protein contains Pfam profile PF05160: DSS1/SEM1 family (68414.m07341)
1006	Not regulated	262880_at	NC-NC-NC	expressed protein (68414.m07344)
1007	Not regulated	262881_at	NC-NC-NC	ribosomal protein S5 family protein contains similarity to 30S ribosomal protein S5 GI:6969105 from (Campylobacter jejuni) (68414.m07355)
1008	Not regulated	262882_at	NC-NC-NC	integral membrane transporter family protein contains 11 transmembrane domains; contains Pfam PF03092: BT1 family; contains TIGRFAMS TIGR00788: folate/biotin transporter (68414.m07356)
1009	Not regulated	262885_at	NC-NC-NC	cytochrome P450, putative similar to cytochrome P450 GI:438240 from (Solanum melongena) (68414.m07357)
1010	Not regulated	262830_at	NC-NC-NC	tubulin alpha-1 chain (TUA1) nearly identical to SPIP11139 Tubulin alpha-1 chain (Arabidopsis thaliana) (68414.m07340)
1011	Not regulated	262837_at	NC-NC-NC	purple acid phosphatase, putative contains Pfam profile: PF00149 calcineurin-like phosphoesterase; similar to purple acid phosphatase (GI:20257479) [Arabidopsis thaliana] (68414.m01757)
1012	Not regulated	262841_at	NC-NC-NC	dynamitin-like protein C (DLTC) nearly identical to dynamitin-like protein C (Arabidopsis thaliana) GI:19569772 (68414.m01774)
1013	Not regulated	262842_at	NC-NC-NC	semialdehyde dehydrogenase family protein similar to SP-Q31219 Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) (ASA dehydrogenase) (ASADH) (Legionella pneumophila); contains Pfam profiles PF02774: Semialdehyde dehydrogenase dimerisation domain, PF01118: Semialdehyde dehydrogenase NAD binding domain (68414.m01770)
1014	Not regulated	262844_at	NC-NC-NC	xyloglucan-xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (XTR2) identical to endoxyloglucan transferase (Arabidopsis thaliana) GI:5533311 (68414.m01780)
1015	Not regulated	262845_at	NC-NC-NC	invertase/pectin methyltransferase inhibitor family protein similar to pectinesterase GB-X85218 GI:732912 SPIQ43111 (Phaseolus vulgaris), SPIQ42534 from Arabidopsis thaliana; contains Pfam profile PF04043: Plant invertase/pectin methyltransferase inhibitor (68414.m01780)
1016	Not regulated	262796_at	NC-NC-NC	expressed protein (68414.m01782)
1017	Not regulated	262797_at	NC-NC-NC	expressed protein (68414.m01748)
1018	Not regulated	262801_at	NC-NC-NC	cysteine endopeptidase, papain-type (XCP2) identical to papain-type cysteine endopeptidase XCP2 GI:6708183 from (Arabidopsis thaliana) (68414.m02612)
1019	Not regulated	262805_at	NC-NC-NC	transporter-related low similarity to D-xylose proton-symporter [Lactobacillus brevis] GI:2895856; contains Pfam profile PF00083: major facilitator superfamily protein (68414.m02611)
1020	Not regulated	262813_at	NC-NC-NC	expressed protein (68414.m02629)
1021	Not regulated	262814_at	NC-NC-NC	DNA-binding protein-related contains Pfam domain PF03479: Domain of unknown function (DUF298), found in AT-hook motifs Pfam:PF02178 (68414.m02617)
1022	Not regulated	262823_at	NC-NC-NC	MATE efflux family protein similar to opening regulated protein DDTFR18 [Lycopersicon esculentum] GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family, EST gb W43487 comes from this gene (68414.m01340)
1023	Not regulated	262826_at	NC-NC-NC	heat shock protein, putative strong similarity to gb Z70314 heat-shock protein from Arabidopsis thaliana and is a member of the PF100012 Hsp70 protein family (68414.m01339)
1024	Not regulated	262790_at	NC-NC-NC	ATP-dependent Clp protease proteolytic subunit (ClpP) identical to ATP-dependent Clp protease proteolytic subunit GI:2827888 from (Arabidopsis thaliana); contains Pfam profile PF00574: Clp protease; contains TIGRfam profile TIGR00483: ATP-dependent Clp protease, proteolytic subunit ClpP (68414.m01348)
1025	Not regulated	262781_s_at	NC-NC-NC	cytochrome P450 family protein identical to gb D78605 cytochrome P450 monooxygenase from Arabidopsis thaliana and is a member of the PF100087 Cytochrome P450 family, ESTs gb Z18072, gb Z5218 and gb T43468 come from this gene (68414.m01516)
1026	Not regulated	262782_at	NC-NC-NC	cytochrome P450 71B28, putative (CYP71B28) identical to Cytochrome P450 (SP-Q9SAE3) [Arabidopsis thaliana]; strong similarity to gb X97884 cytochrome P450 from Arabidopsis thaliana and is a member of the PF100087 Cytochrome P450 family, ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb A1100027 come from this gene (68414.m01518)
1027	Not regulated	262796_at	NC-NC-NC	20S proteasome beta subunit E1 (PBE1) (PRCE) identical to GB:023717; identical to cDNA proteasome subunit prca GI:2511595 (68414.m01514)
1028	Not regulated	262790_at	NC-NC-NC	zinc finger (C3HC4-type RING finger) family protein similar to MTD2 [Medicago truncatula] GI:9294812; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger) (68414.m01225)
1029	Not regulated	262791_at	NC-NC-NC	expressed protein (68414.m01225)
1030	Not regulated	262796_at	NC-NC-NC	eukaryotic translation initiation factor 3 subunit 3 / eIF-3 gamma (eIF3h) (Arabidopsis thaliana); contains Pfam profile PF01398: initiation factor 3 subunit 3 (eIF-3 gamma) (eIF3 p38 subunit) (eIF3h) (Arabidopsis thaliana); contains Pfam profile PF01398: Mov34/IMP/PAAD-1 family (68414.m01245)
1031	Not regulated	262790_at	NC-NC-NC	sodium symporter-related contains five transmembrane domains; Interpro IPR001991 Sodium:dicarboxylate symporter, EST gb F13926 comes from this gene (68414.m01244)
1032	Not regulated	262796_at	NC-NC-NC	GDSL-motif lipase, putative similar to lipase [Arabidopsis thaliana] GI:1145627; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family (68414.m03517)

1031	Not regulated	NC-NC-NC	262745_at	A11g28600	lipase, putative similar to lipase [Arabidopsis thaliana] (G1:145627; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family (68414.m03522)
1032	Not regulated	NC-NC-NC	262749_at	A11g28580	GDSL-motif lipase, putative similar to lipase [Arabidopsis thaliana] (G1:145627; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family (68414.m03519)
1033	Not regulated	NC-NC-NC	262750_at	A11g28710	expressed protein similar to G1:2827651, G1:7527728, G1:4406788, G1:6063544, G1:10764853 from [Arabidopsis thaliana] (68414.m03536)
1034	Not regulated	NC-NC-NC	262754_at	A11g16350	inosine 5'-monophosphate dehydrogenase, putative strong similarity to SP1P47996 gbl[34684 inosine monophosphate dehydrogenase (IMPDH) from Arabidopsis thaliana; member of the PF00478 IMP dehydrogenase family (68414.m01958)
1035	Not regulated	NC-NC-NC	262705_at	A11g16260	protein kinase family protein contains Pfam domain, PF00069; protein kinase domain (68414.m01947)
1036	Not regulated	NC-NC-NC	262708_at	A11g16280	DEAD/DEAH box helicase, putative similar to gbl13612 DEAD-box protein (dbp45A) from Drosophila melanogaster and is a member of PF00270 DEAD/DEAH box helicase family (68414.m01949)
1037	Not regulated	NC-NC-NC	262707_at	A11g16290	expressed protein (68414.m01950)
1038	Not regulated	NC-NC-NC	262708_at	A11g16190	DNA repair protein RAD23, putative similar to DNA repair by nucleotide excision (NER) RAD23 protein, isoform II G1:1914885 from [Daucus carota] (68414.m01939)
1039	Not regulated	NC-NC-NC	262710_at	A11g16210	expressed protein ESTs gb T04357 and gb AA595092 come from this gene (68414.m01941)
1040	Not regulated	NC-NC-NC	262712_at	A11g16460	mercaptopyruvate sulfurtransferase (MST2) (R0H2) identical to mercaptopyruvate sulfurtransferase G1:6009863 and thiosulfate sulfurtransferase G1:5817004 from [Arabidopsis thaliana]; contains PF00381 Rhodanese-like domain (68414.m01968)
1041	Not regulated	NC-NC-NC	262721_at	A11g43560	thioredoxin family protein contains Pfam profile: PF00085 Thioredoxin; similar to thioredoxin G1:142153 from [Synechococcus PCC6301] (68414.m05000)
1042	Not regulated	NC-NC-NC	262725_at	A11g43580	expressed protein (68414.m05003)
1043	Not regulated	NC-NC-NC	262727_at	A11g75900	pathogenesis-related thaumatin family protein similar to receptor serine/threonine kinase PR5K [Arabidopsis thaliana] (G1:1235680; contains Pfam profile: PF00314 Thaumatin family (68414.m08805)
1044	Not regulated	NC-NC-NC	262700_at	A11g76020	expressed protein (68414.m08826)
1045	Not regulated	NC-NC-NC	262876_at	A11g75950	E3 ubiquitin ligase SCF complex subunit SKP1/YASK1 (A11) E3 ubiquitin ligase; skp1a; identical to Skp1a G1:3068807, Skp1p G1:1432083 and Ulp1 G1:3719209 from [Arabidopsis thaliana]; contains Pfam profiles PF01486; Skp1 family, dimension domain and PF03931; Skp1 family, tetramerization domain; (68414.m08821)
1046	Not regulated	NC-NC-NC	262878_at	A11g75810	expressed protein (68414.m08806)
1047	Not regulated	NC-NC-NC	262682_at	A11g75900	family II extracellular lipase 3 (EXL3) EXL3 (PMID:11431568); similar to enter-specific proline-rich protein (APC) SP:P40802 [Arabidopsis thaliana] (68414.m08816)
1048	Not regulated	NC-NC-NC	262684_s_at	A11g76030	vacuolar ATP synthase subunit B / V-ATPase B subunit / vacuolar proton pump B subunit / V-ATPase 57 kDa subunit identical to SPIP11574 Vacuolar ATP synthase subunit B (EC 3.6.3.14) (V-ATPase B subunit) (Vacuolar proton pump B subunit) (V-ATPase 57 kDa subunit) (Arabidopsis thaliana) (68414.m08827)
1049	Not regulated	NC-NC-NC	262686_at	A11g75990	26S proteasome regulatory subunit S3, putative (RPN3) similar to 26S proteasome regulatory subunit S3 SP:P83768 [Nicotiana glauca] (68414.m08824)
1050	Not regulated	NC-NC-NC	262691_at	A11g62740	tabacum (Common tobacco) (68414.m08824)
1051	Not regulated	NC-NC-NC	262693_at	A11g62780	stress-inducible protein, putative similar to stl (stress inducible protein) (Glycine max) G1:872116; contains Pfam profile PF00515 TPR Domain (68414.m07081)
1052	Not regulated	NC-NC-NC	262667_at	A11g62810	expressed protein (68414.m07088)
1053	Not regulated	NC-NC-NC	262639_at	A11g62820	copper amine oxidase, putative similar to copper amine oxidase [Cicer arretinum] gbl381909[emb]CAA08855 (68414.m07091)
1054	Not regulated	NC-NC-NC	262645_at	A11g62750	calmodulin, putative similar to calmodulin SP:PQ4465 from [Trypanosoma brucei gambiense]; contains INTERPRO:IPR002048 calcium-binding EF-hand domain (68414.m07092)
1055	Not regulated	NC-NC-NC	262660_at	A11g14000	elongation factor Tu family protein similar to elongation factor G SP:P34811 [Glycine max (Soybean)] (68414.m07082)
1056	Not regulated	NC-NC-NC	262607_at	A11g13990	protein kinase family protein / ankyrin repeat family protein contains Pfam profiles: PF00089 protein kinase domain, PF00023 ankyrin repeat (68414.m01852)
1057	Not regulated	NC-NC-NC	262609_at	A11g13930	expressed protein (68414.m01850)
1058	Not regulated	NC-NC-NC	262612_at	A11g14150	expressed protein weakly similar to drought-induced protein SD-6 (PIR:S71562) common sunflower (fragment) (68414.m01635)
1059	Not regulated	NC-NC-NC	262618_at	A11g06560	oxygen evolving enhancer 3 (PsbO) family protein extrinsic pII protein; contains Pfam profile PF05757: Oxygen evolving enhancer protein 3 (PsbO) (68414.m01672)
1060	Not regulated	NC-NC-NC	262621_at	A11g06530	NOL1/NOP2/sun family protein contains Pfam profile PF01189; NOL1/NOP2/sun family (68414.m00695)
1061	Not regulated	NC-NC-NC	262624_at	A11g06450	myosin heavy chain-related similar to myosin heavy chain (G1:1408194) [Placopsecten magellanicus]; similar to Myosin heavy chain, clone 203 (Fragment) (SP:P39922) [Hydra attenuata]; contains one transmembrane domain (68414.m00692)
1062	Not regulated	NC-NC-NC	262626_at	A11g06430	CCR4-NOT transcription complex protein, putative similar to SWISS-PROT:Q8UFF9 CCR4-NOT transcription complex, subunit 8 (CAF1-like protein, CALIF) [Homo sapiens] (68414.m00683)
1063	Not regulated	NC-NC-NC	262629_at	A11g06460	FtsH protease, putative similar to zinc dependent protease G1:7650138 from [Arabidopsis thaliana] (68414.m00680)
1064	Not regulated	NC-NC-NC	262632_at	A11g06680	31.2 kDa small heat shock family protein / hsp20 family protein contains Pfam profile: PF00011 Hsp20/alpha crystallin family (68414.m00684)
1065	Not regulated	NC-NC-NC	262634_at	A11g06690	photosystem II oxygen-evolving complex 23 (OEC23) JBC 14:211-238 (2002); identical to 23 kDa polypeptide of oxygen-evolving complex (OEC) GB:CAA68785 G1:1769805 [Arabidopsis thaliana] (68414.m00708)
1066	Not regulated	NC-NC-NC	262638_at	A11g06650	aldo/keto reductase family protein contains Pfam profile PF00248; oxidoreductase, aldo/keto reductase family (68414.m00710)
1067	Not regulated	NC-NC-NC	262581_at	A11g15370	2-oxoglutarate-dependent dioxygenase, putative similar to 2A6 (G1:598622) and tomato ethylene synthesis regulatory protein E8 (SPIP10987); contains Pfam profile: PF00871 Iron/Ascorbate oxidoreductase family (68414.m00704)
1068	Not regulated	NC-NC-NC	262583_at	A11g15110	expressed protein (68414.m01840)
					phosphatidyl serine synthase family protein contains Pfam profile: PF03034 phosphatidyl serine synthase (68414.m01804)

1069	Not regulated	NC-NC-NC	262584_at	A11g15440	transducin family protein / WD-40 repeat family protein Strong similarity to gb_X95263 Periodic tryptophan protein 2 gene (PWP2) from Homo sapiens and contains 6 WD40, G-beta repeat domains (68414.m01855) zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (68414.m01803) expressed protein ESTs gblH37295 and gblR84895 come from this gene (68414.m01844) ubiquinol-cytochrome C reductase complex 7.8 kDa protein, putative / mitochondrial hinge protein, putative similar to SPIP48504 (68414.m01803) Ubiquinol-cytochrome C reductase complex 7.8 kDa protein (EC 1.10.2.2) (Mitochondrial hinge protein) (CR7) (Solanum tuberosum); contains Pfam profile PF02320: Ubiquinol-cytochrome C reductase hinge protein (68414.m01805) 60S ribosomal protein L37 (RPL37A) almost identical to GB_Q43292 (68414.m01825) expressed protein EST gblN65487 comes from this gene (68414.m01828) expressed protein (68414.m01836)
1070	Not regulated	NC-NC-NC	262590_at	A11g15100	
1071	Not regulated	NC-NC-NC	262592_at	A11g15400	
1072	Not regulated	NC-NC-NC	262593_at	A11g15120	
1073	Not regulated	NC-NC-NC	262594_at	A11g15250	
1074	Not regulated	NC-NC-NC	262598_at	A11g15260	
1075	Not regulated	NC-NC-NC	262599_at	A11g15350	
1076	Not regulated	NC-NC-NC	262600_at	A11g15340	
1077	Not regulated	NC-NC-NC	262602_at	A11g15270	methyl-CpG-binding domain-containing protein contains Pfam profile PF01428: Methyl-CpG binding domain (68414.m01835) expressed protein ESTs gblAA650895, gblAA720043 and gblR28777 come from this gene (68414.m01827) oxidoreductase NAD-binding domain-containing protein Contains Pfam profile PF00175: Oxidoreductase NAD-binding domain; ESTs gblH78345 and gblAA651465 come from this gene (68414.m01808) peptide deformylase, mitochondrial / polypeptide deformylase 1A (PDF1A) nearly identical to SPIQ9FV53 Peptide deformylase, mitochondrial precursor (EC 3.5.1.88) (PDF) (Polypeptide deformylase) (Arabidopsis thaliana); contains Pfam profile PF01327: polypeptide deformylase; supporting cDNA gbl11320951gblAF250959:1AF250959 (68414.m01843) expressed protein ESTs gblR30528, gblZ48463, gblZ48467, gblAA597369 and gblAA394772 come from this gene (68414.m01823)
1078	Not regulated	NC-NC-NC	262572_at	A11g15140	
1079	Not regulated	NC-NC-NC	262573_at	A11g15390	ubiquitin family protein contains INTERPRO:IPR000626 ubiquitin domain (68414.m03835) phosphorylation reaction center subunit III family protein contains Pfam profile: PF02507: photosystem I reaction center subunit III (68414.m03833) expressed protein contains Pfam profile: PF03398 eukaryotic protein of unknown function, DUF292 (68414.m04246) somatic embryogenesis receptor-like kinase 2 (SERK2) nearly identical to somatic embryogenesis receptor-like kinase 2 [Arabidopsis thaliana] GI:14573457; contains Pfam domains PF00560: Leucine Rich Repeat and PF00089: Protein kinase domain; identical to cDNA somatic embryogenesis receptor-like kinase 2 (SERK2) GI:14573458 (68414.m04245) transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related contains Pfam profile: PF02308 AUX/IAA family (68414.m04257) lectin protein kinase family protein contains Pfam domains, PF01453: Lectin (probable mannose binding) and PF00069: Protein kinase domain (68414.m04256) no apical meristem (NAM) family protein contains Pfam PF02385: No apical meristem (NAM) protein; similar to NAM protein GI:6069595 [Petunia hybrida]; nam-like protein 9 (GI:21105746) [Petunia x hybrida]; NAC1 GI:7716952 [Medicago truncatula] (68414.m04241)
1080	Not regulated	NC-NC-NC	262574_at	A11g15230	
1081	Not regulated	NC-NC-NC	262544_at	A11g15425	
1082	Not regulated	NC-NC-NC	262551_at	A11g13340	
1083	Not regulated	NC-NC-NC	262557_at	A11g13130	
1084	Not regulated	NC-NC-NC	262562_at	A11g34220	
1085	Not regulated	NC-NC-NC	262563_at	A11g34210	
1086	Not regulated	NC-NC-NC	262566_at	A11g34310	
1087	Not regulated	NC-NC-NC	262567_at	A11g34300	
1088	Not regulated	NC-NC-NC	262514_at	A11g34190	
1089	Not regulated	NC-NC-NC	262519_at	A11g17160	pfkB-type carbohydrate kinase family protein contains Pfam profile: PF00294 pfkB family carbohydrate kinase (68414.m02092) cell cycle control protein-related contains similarity to Swiss-Prot:Q9P7C5 cell cycle control protein cwf18 [Schizosaccharomyces pombe] (68414.m02087) ubiquitin-specific protease 15 (UBP15) almost identical to ubiquitin-specific protease 15 GI:11993475 [Arabidopsis thaliana], 7 amino acid difference (68414.m02085) D111/G-patch domain-containing protein Similar to SPIQ8EA8 Tuftein-interacting protein 11 [Mus musculus]; contains Pfam profile PF01585: G-patch domain (68414.m02077) geranyl diphosphate synthase, putative / GPPS, putative / dimethylallyltransferase, putative / prenyl transferase, putative similar to GI:11322965; Except for first 55 amino acids, 52% identical to Prenyl transferase (Cyanophora paradoxa) (gi 99282); Location of est 120E9T7 (gblT43950) (68414.m02073) expressed protein distantly related to dentin phosphoryn [Homo sapiens] (GI:4322870) (68414.m02097) ubiquitin-conjugating enzyme, putative similar to ubiquitin conjugating enzyme 6 from [Homo sapiens] GI:14029287, [Mus musculus] GI:14029283, contains Pfam profile PF00179: Ubiquitin-conjugating enzyme (68414.m02105) integral membrane family protein Location of est 138A23177 (gblT45563); contains TIGRFAM TIGR01589 : plant integral membrane protein TIGR01589; contains Pfam PF04535 : Domain of unknown function (DUF588) (68414.m02096) oxidoreductase, ZOG-Fe(II) oxygenase family protein similar to flavin monooxygenase [Petunia x hybrida]GI:311658], leucoanthracidin dioxygenase [Malus domestica]SPIP51091; contains PF03171 ZOG-Fe(II) oxygenase superfamily domain (68414.m02087) wound-responsive family protein similar to wound-responsive protein 14.05 (GI:16506938) [Castanea sativa]; ESTs gb 142839 and gblAA395192 come from this gene (68414.m02702)
1093	Not regulated	NC-NC-NC	262526_at	A11g17050	
1094	Not regulated	NC-NC-NC	262532_at	A11g17210	expressed protein EST gblT21171 comes from this gene (68414.m02731) 20S proteasome beta subunit C1 (PBC1) (PRCT) almost identical to GB:AA32069 from [Arabidopsis thaliana], EST gblT78747 comes from this gene; identical to cDNA proteasome subunit prct GI:2511567 (68414.m02719) expressed protein (68414.m02725)
1095	Not regulated	NC-NC-NC	262537_s_at	A11g17280	F-box family protein Contains PF00846 F-box domain. ESTs gblJ90412, gblJ237268 and gblT68189 come from this gene similar to SKP1 interacting partner 2 (SKIP2) TIGR_Art1A5697250 (68414.m02724) replication factor C 37 kDa, putative Similar to SWISS-PROT:P35249 activator 1 37 kDa subunit (Replication factor C 37 kDa subunit, A1 37 kDa subunit, RF-C 37 kDa subunit, RFC37) [Homo sapiens]; contains Pfam domain, PF00004: ATPase, AAA family (68414.m02714)
1096	Not regulated	NC-NC-NC	262539_at	A11g17200	
1097	Not regulated	NC-NC-NC	262482_at	A11g17020	
1098	Not regulated	NC-NC-NC	262487_at	A11g21610	
1099	Not regulated	NC-NC-NC	262488_at	A11g21820	
1100	Not regulated	NC-NC-NC	262489_at	A11g21830	
1101	Not regulated	NC-NC-NC	262497_at	A11g21720	
1102	Not regulated	NC-NC-NC	262499_at	A11g21770	
1103	Not regulated	NC-NC-NC	262500_at	A11g21760	
1104	Not regulated	NC-NC-NC	262501_at	A11g21690	

1105	Not regulated	NC-NC-NC	A11g21670	expressed protein similar to TolB protein precursor (SP:P50601) (Pseudomonas aeruginosa) (68414.m02712)
1106	Not regulated	NC-NC-NC	A11g11140	expressed protein (68414.m01287)
1107	Not regulated	NC-NC-NC	A11g11240	seven transmembrane MLO family protein / MLO-like protein 2 (MLO2) identical to membrane protein Mlo2 [Arabidopsis thaliana] gi14091574(gb AAK53795; similar to Mlo [Hordeum vulgare subsp. vulgare] gi187722[emb CA806083 SWISS-PROT:P83766] (68414.m01299)
1108	Not regulated	NC-NC-NC	A11g11310	expressed protein contains Pfam profile PF03618: Domain of unknown function (68414.m01283)
1109	Not regulated	NC-NC-NC	A11g11200	S-locus protein kinase, putative similar to receptor protein kinase [Ipomoea trifida] gi833954(gb AAC23542; contains protein kinase domain, Pfam:PF00069; contains S-locus glycoprotein family domain, Pfam:PF00954 (68414.m01284)
1110	Not regulated	NC-NC-NC	A11g11280	cell division protein fish homolog 1, chloroplast (FTSH1) (FTSH) identical to SP:Q38102 Cell division protein fish homolog 1, chloroplast precursor (EC 3.4.24.-) [Arabidopsis thaliana] (68414.m05834)
1111	Not regulated	NC-NC-NC	A11g50250	serine/threonine protein phosphatase, putative nearly identical to serine/threonine protein phosphatase [Arabidopsis thaliana] Gi:14582208 (68414.m05648)
1112	Not regulated	NC-NC-NC	A11g50370	expressed protein similar to Cbl protein (Gi:3724039) [Bacillus megaterium]; similar to YlnE protein (Gi:2482861) [Bacillus subtilis]; similar to NirR (Gi:4433637) [Staphylococcus carnosus] (68414.m05628)
1113	Not regulated	NC-NC-NC	A11g50170	thioredoxin x nearly identical to thioredoxin x GB:AAF15952 Gi:6539618 from [Arabidopsis thaliana] (68414.m05641)
1114	Not regulated	NC-NC-NC	A11g50320	pyridoxine-carboxylate peptidase family protein similar to Pyridoxine-carboxylate peptidase (Swiss-Prot:O58321) [Pyrococcus horikoshii]; contains Prosite PS00141: Eukaryotic and viral aspartyl proteases active site (68414.m02936)
1115	Not regulated	NC-NC-NC	A11g23440	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to thiogalactosidase (Gi:871992) [Arabidopsis thaliana] (68414.m05285)
1116	Not regulated	NC-NC-NC	A11g2426_s_at	contains Pfam profile PF01554: Uncharacterized membrane protein family (68414.m05275)
1117	Not regulated	NC-NC-NC	A11g47600	amino acid transporter family protein similar to lysine and histidine specific transporter Gi:2576361 from [Arabidopsis thaliana]; contains Pfam profile PF01490: Transmembrane amino acid transporter protein (68414.m05296)
1118	Not regulated	NC-NC-NC	A11g47530	expressed protein identical to hypotheical protein GB:AAD46040 Gi:5698814 from [Arabidopsis thaliana] (68414.m05252)
1119	Not regulated	NC-NC-NC	A11g47670	long-chain-fatty-acid-CoA ligase / long-chain acyl-CoA synthetase nearly identical to acyl CoA synthetase (MF45P) Gi:1617268 from [Brassica napus] (68414.m05541)
1120	Not regulated	NC-NC-NC	A11g47420	ribosomal protein S17 family protein similar to 40S ribosomal protein S17 Gi:1620985 from [Nicotiana glauca] (68414.m05537)
1121	Not regulated	NC-NC-NC	A11g49430	expressed protein S17 family protein similar to 40S ribosomal protein S17 Gi:1620985 from [Nicotiana glauca] (68414.m05537)
1122	Not regulated	NC-NC-NC	A11g49400	BURP domain-containing protein similar to SPIQ08298 Dehydration-responsive protein RD22 precursor [Arabidopsis thaliana]; contains Pfam profile PF03181: BURP domain (68414.m05528)
1123	Not regulated	NC-NC-NC	A11g49320	expressed protein (68414.m05548)
1124	Not regulated	NC-NC-NC	A11g49510	expressed protein contains Pfam profile PF04819: Family of unknown function (DUF716) (Plant viral-response family) (68414.m05544)
1125	Not regulated	NC-NC-NC	A11g49470	cytochrome c biogenesis protein family contains Pfam PF05140: ResB-like family; similar to CCS1 (Gi:2749939) [Chlamydomonas reinhardtii]; similar to Ccs1 (Gi:8137102) [Synecococcus sp. PCC 6301] (68414.m05535)
1126	Not regulated	NC-NC-NC	A11g49360	transcriptional factor B3 family protein contains Pfam profile PF02362: B3 DNA binding domain (68414.m05546)
1127	Not regulated	NC-NC-NC	A11g49480	Ras-related GTP-binding protein, putative contains Pfam profile: PF00071 Ras family (68414.m05526)
1128	Not regulated	NC-NC-NC	A11g49300	expressed protein (68414.m04305)
1129	Not regulated	NC-NC-NC	A11g34630	protein phosphatase 2C: putative / PP2C, putative similar to GB:AAD17805 from [Lotus japonicus] (Proc. Natl. Acad. Sci. U.S.A. 96 (4), 1738-1743 (1999)) (68414.m04321)
1130	Not regulated	NC-NC-NC	A11g34750	protein disulfide isomerase-related contains weak similarity to Pfam:PF08003 protein disulfide isomerase A4 precursor (Protein ERp-72, ERp72) [Mus musculus] (68414.m04329)
1131	Not regulated	NC-NC-NC	A11g34780	mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein (68414.m08418)
1132	Not regulated	NC-NC-NC	A11g72820	SNF7 family protein contains Pfam domain, PF03357: SNF7 family (68414.m08445)
1133	Not regulated	NC-NC-NC	A11g73030	expressed protein (68414.m08448)
1134	Not regulated	NC-NC-NC	A11g73060	vacuolar ATP synthase subunit E, putative / V-ATPase E subunit, putative / vacuolar proton pump E subunit, putative similar to SPIQ39258 Vacuolar ATP synthase subunit E (EC 3.6.3.14) (V-ATPase E subunit) [Vacuolar proton pump E subunit] (Arabidopsis thaliana); contains Pfam profile PF01991: ATP synthase (E31 kDa) subunit (68414.m07273)
1135	Not regulated	NC-NC-NC	A11g64200	reticulon family protein (RTNLB3) weak similarity to SPIQ95197 Reticulon protein 3 (Neuroendocrine-specific protein-like) [Homo sapiens]; contains Pfam profile PF02453: Reticulon (68414.m07260)
1136	Not regulated	NC-NC-NC	A11g64090	no apical menistem (NAM) family protein contains Pfam PF02365: No apical menistem (NAM) domain (68414.m07262)
1137	Not regulated	NC-NC-NC	A11g64105	serine/threonine protein phosphatase PP1 isozyme 3 (EC 3.1.3.16) (Arabidopsis thaliana), phosphoprotein phosphatase 1 Serine/threonine protein phosphatase PP1 isozyme 3 (EC 3.1.3.16) (68414.m07254)
1138	Not regulated	NC-NC-NC	A11g64040	GB:AAA32838 Gi:166799 from [Arabidopsis thaliana] (68414.m07254)
1139	Not regulated	NC-NC-NC	A11g63980	D1111C-patch domain-containing protein contains Pfam profile PF01585: G-patch domain (68414.m07247)
1140	Not regulated	NC-NC-NC	A12g48130	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage/LTP family domain PF00234 (68415.m06025)
1141	Not regulated	NC-NC-NC	A11g27540	F-box family protein similar to F-box protein family, AFBX7 (Gi:20197899) [Arabidopsis thaliana]; confirmed by FLDNA Gi:16604421; contains uncharacterized Arabidopsis domain shared by 33 Arabidopsis proteins (68414.m03357)
1142	Not regulated	NC-NC-NC	A11g27600	glycosyl transferase family 43 protein similar to Galactosylglucosyltransferase 3-beta-glucuronosyltransferase 1, Rattus norvegicus [SPIQ35789]; Homo sapiens [SPIQ927W7]; contains Pfam domain Glycosyltransferase family 43 [PF03360] (68414.m03367)
1143	Not regulated	NC-NC-NC	A11g27530	expressed protein Similar to gb AF151884 CGI-126 protein from Homo sapiens. EST gb 218048 comes from this gene (68414.m03358)

1144	Not regulated	NC-NC-NC	262304_at	A11g70890	major latex protein-related / MLP-related low similarity to major latex protein [Papaver somniferum][GI:294062]; contains Pfam profile PF00407; Pathogenesis-related protein Bet v 1 family (88414.m08178)
1145	Not regulated	NC-NC-NC	262306_s_at	A11g70890	asparaginyl-IRNA synthetase, cytoplasmic, putative / asparagine-IRNA ligase, putative similar to SYNC1 protein GI:5670315 [SPO35W96] from [Arabidopsis thaliana] (88414.m08188)
1146	Not regulated	NC-NC-NC	262308_at	A11g71010	phosphatidylinositol-4-phosphate 5-kinase family protein low similarity to phosphatidylinositol 3,5-kinase [Candida albicans] GI:14571648; contains Pfam profile PF01504; Phosphatidylinositol-4-phosphate 5-Kinase (88414.m08182)
1147	Not regulated	NC-NC-NC	262312_at	A11g70830	Bet v 1 allergen family protein similar to Cst-2 [Cucumis sativus][GI:5762258][J Am Soc Hort Sci 124, 136-139 (1998)]; contains Pfam profile PF00407; Pathogenesis-related protein Bet v 1 family (88414.m08170)
1148	Not regulated	NC-NC-NC	262288_at	A11g70780	inorganic carbon transport protein-related contains weak similarity to Swiss-Prot:P27372 inorganic carbon transport protein [Synechocystis sp.] (88414.m08158)
1149	Not regulated	NC-NC-NC	262289_at	A11g70770	expressed protein (88414.m08158)
1150	Not regulated	NC-NC-NC	262280_at	A11g70850	Bet v 1 allergen family protein similar to Cst-2 [Cucumis sativus][GI:5762258][J Am Soc Hort Sci 124, 136-139 (1998)] contains Pfam profile PF00407; Pathogenesis-related protein Bet v 1 family (88414.m08173)
1151	Not regulated	NC-NC-NC	262280_at	A11g68580	agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein contains Pfam profile PF01426; BAH domain and PF05641; Agenet domain (88414.m07835)
1152	Not regulated	NC-NC-NC	262281_at	A11g68570	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family (88414.m07834)
1153	Not regulated	NC-NC-NC	262283_at	A11g68590	plastid-specific 30S ribosomal protein 3, putative / PSRP-3, putative similar to SPIP82412 Plastid-specific 30S ribosomal protein 3, chloroplast precursor (PSRP-3) [Spinacia oleracea]; contains Pfam profile PF04839; Plastid and cyanobacterial ribosomal protein expressed protein (88414.m07837)
1154	Not regulated	NC-NC-NC	262286_at	A11g68585	thioesterase family protein similar to CornAB [Bacillus licheniformis] GI:1834379; contains Pfam profile PF03061; thioesterase expressed protein (88414.m05397)
1155	Not regulated	NC-NC-NC	262237_at	A11g48320	family protein (88414.m05397)
1156	Not regulated	NC-NC-NC	262251_at	A11g53760	expressed protein (88414.m06117)
1157	Not regulated	NC-NC-NC	262253_s_at	A11g53880	eukaryotic translation initiation factor 2B family protein / eIF-2B family protein similar to SPIQ64270 Translation initiation factor eIF-2B alpha subunit [Rattus norvegicus]; contains Pfam profiles PF04525; Protein of unknown function (DUF567), PF01008; Initiation factor 2 subunit family (88414.m06133)
1158	Not regulated	NC-NC-NC	262254_at	A11g53920	GDSL-motif lipase/hydrolase family protein similar to Anther-specific proline-rich proteins SPIP40803 SPIP40802 from [Arabidopsis thaliana]; contains Pfam profile PF00657; GDSL-like Lipase/Acylhydrolase (88414.m06138)
1159	Not regulated	NC-NC-NC	262258_at	A11g53850	20S proteasome alpha subunit E1 (PAE1) identical to 20S proteasome subunit PAE1 GI:3421087 from [Arabidopsis thaliana] (88414.m06129)
1160	Not regulated	NC-NC-NC	262225_at	A11g53840	pectinesterase family protein contains Pfam profile: PF01095 pectinesterase (88414.m06128)
1161	Not regulated	NC-NC-NC	262203_at	A12g01080	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain (88415.m00011)
1162	Not regulated	NC-NC-NC	262204_at	A12g01100	expressed protein (88415.m00016)
1163	Not regulated	NC-NC-NC	262168_at	A11g74730	expressed protein (88414.m06059)
1164	Not regulated	NC-NC-NC	262172_at	A11g74870	ribosomal protein S9 (RPS9) identical to ribosomal protein S9 [Arabidopsis thaliana] GI:5456946 (88414.m08703)
1165	Not regulated	NC-NC-NC	262173_at	A11g74920	betaine-aldehyde dehydrogenase, putative identical to betaine-aldehyde dehydrogenase, chloroplast precursor (BADH) [Arabidopsis thaliana] SWISS-PROT:Q8S795; strong similarity to betaine aldehyde dehydrogenase [Amaranthus hypochondriacus] GI:2388710 (88414.m08691)
1166	Not regulated	NC-NC-NC	262174_at	A11g74910	ADP-glucose pyrophosphorylase family protein contains Pfam profile PF00483; Nucleoside transferase, low similarity to mannose-1-phosphate guanylyltransferase [Hypocrea jecorina] GI:3323397 (88414.m08685)
1167	Not regulated	NC-NC-NC	262175_at	A11g74880	expressed protein (88414.m08679)
1168	Not regulated	NC-NC-NC	262176_at	A11g74860	3-ketoacyl-ACP synthase, putative similar to 3-ketoacyl-ACP synthase [Cupressus pulcherrima] gi3800747[gb AA-C08860; identical to cDNA beta-ketoacyl-ACP synthetase 2, nuclear gene for plastid product GI:14582700 (88414.m08689)
1169	Not regulated	NC-NC-NC	262180_at	A11g78050	phosphoglycerate/bisphosphoglycerate mutase family protein similar to SPIP31217 Phosphoglycerate mutase 1 (EC 5.4.2.1) [Escherichia coli O157:H7]; contains Pfam profile PF00300; phosphoglycerate mutase family (88414.m08095)
1170	Not regulated	NC-NC-NC	262181_at	A11g78060	glycosyl hydrolase family 3 protein similar to xylosidase GI:2102635 from [Aspergillus niger] (88414.m08098)
1171	Not regulated	NC-NC-NC	262195_at	A11g78040	pollen Ole a 1 allergen and extensin family protein contains Pfam domain, PF01190; Pollen proteins Ole a 1 family (88414.m08094)
1172	Not regulated	NC-NC-NC	262137_at	A11g77920	bZIP family transcription factor contains Pfam profile: PF00170 bZIP transcription factor (88414.m09080)
1173	Not regulated	NC-NC-NC	262145_at	A11g52730	transducin family protein / WD-40 repeat family protein contains 7 WD-40 repeats (PF00400), similar to UNR-interacting protein (WD-40 repeat protein PT-WD) (SP-Q8Y3F4) [Homo sapiens] (88414.m05958)
1174	Not regulated	NC-NC-NC	262157_at	A11g52670	biotin/lysoyl attachment domain-containing protein similar to SPIQ06881 Biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP) [Arabidopsis sp.]; contains Pfam profile PF00384; Biotin-requiring enzyme (88414.m05956)
1175	Not regulated	NC-NC-NC	262159_at	A11g52720	expressed protein (88414.m05956)
1176	Not regulated	NC-NC-NC	262160_at	A11g52590	expressed protein (88414.m05937)
1177	Not regulated	NC-NC-NC	262161_at	A11g52600	signal peptidase, putative similar to SPIP13679 Microsomal signal peptidase 21 kDa subunit (EC 3.4.-.-) [Canis familiaris]; contains Pfam profile PF00461; Signal peptidase (88414.m05938)
1178	Not regulated	NC-NC-NC	262107_at	A11g02750	drought-responsive family protein contains similarity to drought-induced mRNA, D19 [Arabidopsis thaliana] gi469110[emb CAA55321 (88414.m00228)
1179	Not regulated	NC-NC-NC	262109_at	A11g02730	cellulose synthase family protein similar to cellulose synthase catalytic subunit [gi:13925881] from Nicotiana glauca, cellulose synthase-4 [gi:9622880] from Zea mays (88414.m00226)
1180	Not regulated	NC-NC-NC	262110_at	A11g02840	pre-mRNA splicing factor SF2 (SF2) / SR1 protein identical to SPIQ22315 Pre-mRNA splicing factor SF2 (SR1 protein) [Arabidopsis thaliana] (88414.m00244)
1181	Not regulated	NC-NC-NC	262112_at	A11g02870	expressed protein (88414.m00252)
1182	Not regulated	NC-NC-NC	262113_at	A11g02820	late embryogenesis abundant 3 family protein / LEA3 family protein similar to late embryogenesis abundant protein 5 GI:2981187 from [Nicotiana glauca]; contains Pfam profile PF03242; Late embryogenesis abundant protein (88414.m00242)

1183	Not regulated	NC-NC-NC	262114_at	At1g02860	SPX (SYG1/Pho81/XPR1) domain-containing protein / zinc finger (C3HC4-type RING finger) protein-related weak similarity to tripartite motif protein TRIM13 [Mus musculus] GI:12407427, gpSurf50 (Homo sapiens) GI:899300; contains Pfam profiles PF03105; SPX domain, PF00097; Zinc finger, C3HC4 type (RING finger) (68414.m00251)
1184	Not regulated	NC-NC-NC	262116_at	At1g02816	expressed protein contains Pfam profile PF04398; Protein of unknown function, DUF538 (68414.m00241)
1185	Not regulated	NC-NC-NC	262117_at	At1g02780	60S ribosomal protein L19 (RPL19A) similar to ribosomal protein L19 GI:38127 from [Homo sapiens] (68414.m00233)
1186	Not regulated	NC-NC-NC	262118_at	At1g02850	glycosyl hydrolase family 1 protein contains Pfam PF00232; Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233; 6-phospho-beta-galactosidase; similar to hydroxyisourate hydrolase (GI:19569603) [Glycine max] (68414.m00247)
1187	Not regulated	NC-NC-NC	262077_at	At1g59810	dynamitin-like protein, putative (ADL3) strong similarity to dynamitin-like protein 6 (ADL6) [Arabidopsis thaliana] GI:6651399; contains Pfam profiles PF01031; Dynamitin central region, PF00350; Dynamitin family, PF02212; Dynamitin GTPase effector domain, PF00169; PH domain; identical to cDNA dynamitin-like protein ADL3, GI:4803835 (68414.m06704)
1188	Not regulated	NC-NC-NC	262078_at	At1g59520	expressed protein (CW7) (68414.m06684)
1189	Not regulated	NC-NC-NC	262086_at	At1g56010	transcription activator NAC1 (NAC1) contains Pfam PF02365; No apical meristem (NAM) domain; identical to NAC1 GB-AAF21437 GI:6649236 from [Arabidopsis thaliana] (68414.m08427)
1190	Not regulated	NC-NC-NC	262064_at	At1g56075	adenine phosphoribosyltransferase 2 (APT2) identical to SPIQ42563 Adenine phosphoribosyltransferase 2 (EC 2.4.2.7) (APRT) (Arabidopsis thaliana) (68414.m09371)
1191	Not regulated	NC-NC-NC	262039_at	At1g80050	expressed protein (68414.m09387)
1192	Not regulated	NC-NC-NC	262044_s_at	At1g80210	cytochrome c oxidase family protein contains Pfam domain, PF01215; Cytochrome c oxidase subunit Vb (68414.m08389)
1193	Not regulated	NC-NC-NC	262048_at	At1g80230	DNAJ heat shock N-terminal domain-containing protein / sec3 domain-containing protein similar to SPIQ8UGP8 Translocation protein SEC33 homolog (Homo sapiens); contains Pfam profiles PF00226 DNAJ domain, PF02889 Sec3 domain (68414.m08342)
1194	Not regulated	NC-NC-NC	262053_at	At1g79940	expressed protein (68414.m09348)
1195	Not regulated	NC-NC-NC	262055_at	At1g79970	expressed protein (68414.m09389)
1196	Not regulated	NC-NC-NC	262057_at	At1g80040	expressed protein (68414.m09352)
1197	Not regulated	NC-NC-NC	262058_at	At1g79975	DNAJ heat shock protein, putative similar to SPIQ05646 Chaperone protein dnaJ (Eryipelothrix muscipathiae); contains Pfam profiles PF00226; DNAJ domain, PF01556; DNAJ C-terminal region, PF00684; DNAJ central domain (4 repeats) (68414.m08366)
1198	Not regulated	NC-NC-NC	262059_at	At1g80030	beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative similar to neutral invertase [Daucus carota] GI:4200165; contains Pfam profile PF04853; Plant neutral invertase (68414.m04417)
1199	Not regulated	NC-NC-NC	262038_at	At1g35580	calcium-dependent protein kinase 2 (CDPK2) identical to calcium-dependent protein kinase [Arabidopsis thaliana] gi 804881 db BA04830; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00038; INTERPRO:IPR002048 (68414.m04435)
1200	Not regulated	NC-NC-NC	262026_at	At1g35670	50S ribosomal protein L21, chloroplast / CL21 (RPL21) identical to 50S ribosomal protein L21, chloroplast precursor (CL21) [Arabidopsis thaliana] SWISS-PROT:P51412 (68414.m04436)
1201	Not regulated	NC-NC-NC	262029_at	At1g35680	GDSL-motif lipase/hydrolase family protein similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from [Arabidopsis thaliana]; contains Pfam profile PF00657; GDSL-like Lipase/Acylhydrolase (68414.m04180)
1202	Not regulated	NC-NC-NC	261981_at	At1g33811	expressed protein similar to A13g29240 [Arabidopsis thaliana]; contains Pfam profile PF02622; Uncharacterized ACR, COG1878 (68414.m04175)
1203	Not regulated	NC-NC-NC	261982_at	At1g33780	expressed protein contains Pfam profile PF04669; Protein of unknown function (DUF579) (68414.m04178)
1204	Not regulated	NC-NC-NC	261989_at	At1g33800	ABC transporter family protein similar to ABC transporter protein GB-AAF31030 GI:8699653 from [Leishmania major] (68414.m07317)
1205	Not regulated	NC-NC-NC	262005_at	At1g64550	expressed protein similar to Hypothetical 72.2 kDa protein in RPS27A-GPM1 intergenic region (Swiss-Prot:P36056)
1206	Not regulated	NC-NC-NC	261972_at	At1g64600	RWP-RK domain-containing protein similar to nodule inception protein [Lotus japonicus] GI:6448578; contains Pfam profile: RWP-2042 RWP-RK domain (68414.m07315)
1207	Not regulated	NC-NC-NC	261945_at	At1g64530	hydrolase, alpha/beta fold family protein low similarity to 2-hydroxy-6-oxo-7-methyl-2,4-dienoate hydrolase [Pseudomonas putida] GI:282275; contains Pfam profile PF00561; hydrolase, alpha/beta fold family (68414.m07331)
1208	Not regulated	NC-NC-NC	261948_at	At1g64680	ribosomal protein S6 family protein similar to plastid ribosomal protein S6 precursor GB-AAF64311 GI:7582401 from [Spinacia oleracea] (68414.m07313)
1209	Not regulated	NC-NC-NC	261949_at	At1g64670	26S proteasome regulatory subunit, putative (RPN12) similar to 26S proteasome regulatory complex subunit p30 GB-AAF08395 GI:6434966 from [Drosophila melanogaster] (68414.m07314)
1210	Not regulated	NC-NC-NC	261954_at	At1g64510	short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family (IPR002188 short-chain dehydrogenase/reductase (SDR) superfamily (68414.m07321)
1211	Not regulated	NC-NC-NC	261955_at	At1g64520	glutaredoxin family protein (68414.m07312)
1212	Not regulated	NC-NC-NC	261956_at	At1g64590	peroxiredoxin type 2, putative strong similarity to type 2 peroxiredoxin [Brassica rapa subsp. pekinensis] GI:4928472; contains Pfam profile: PF00578 AhpC/TSA [alkyl hydroperoxide reductase and thiol-specific antioxidant] family (68414.m07486)
1213	Not regulated	NC-NC-NC	261958_at	At1g64500	isocitrate dehydrogenase, putative / NAADP+ isocitrate dehydrogenase, putative strong similarity to isocitrate dehydrogenase SPIQ40345 from [Medicago sativa] (68414.m07481)
1214	Not regulated	NC-NC-NC	261919_at	At1g65980	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family (68414.m02816)
1215	Not regulated	NC-NC-NC	261920_at	At1g65930	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family (68414.m02815)
1216	Not regulated	NC-NC-NC	261924_at	At1g22550	alcohol dehydrogenase, putative similar to alcohol dehydrogenase ADH GI:7705214 from [Lycopersicon esculentum]; contains Pfam zinc-binding dehydrogenase domain PF00107 (68414.m02805)
1217	Not regulated	NC-NC-NC	261925_at	At1g22540	cytochrome c oxidase subunit 6b, putative (COX6b) nearly identical to subunit 6b of cytochrome c oxidase [Arabidopsis thaliana] GI:6518353 (68414.m02806)
1218	Not regulated	NC-NC-NC	261930_at	At1g22440	expressed protein contains Pfam PF04418; Domain of unknown function (DUF543) (68414.m02813)
1219	Not regulated	NC-NC-NC	261939_at	At1g22450	
1220	Not regulated	NC-NC-NC	261940_at	At1g22520	

1221	Not regulated	NC-NC-NC	261892_at	A11g080770	expressed protein (68414.m09476) MIF4G domain-containing protein / MA3 domain-containing protein similar to SPIQ9PER9 Cell cycle control protein cwf22 (Schizosaccharomyces pombe); contains Pf02854; MIF4G domain, PF02847; MA3 domain (68414.m09485) expressed protein (68414.m09469) CCR4-NOT transcription complex protein, putative similar to SWISS-PROT:Q60808 CCR4-NOT transcription complex, subunit 7 (CCR4-associated factor 1, [CAF-1] [Mus musculus]) (68414.m09477) XH/XS domain-containing protein / XS zinc finger domain-containing protein contains Pfam domains PF03468; XH domain, PF03468; XS domain and PF03470; XS zinc finger domain (68414.m09478)
1222	Not regulated	NC-NC-NC	261895_at	A11g080930	NRAMP metal ion transporter 1 (NRAMP1) identical to NRAMP1 protein [Arabidopsis thaliana] [gi:108911]gb AAAF36535; member of the natural resistance-associated macrophage protein (NRAMP) metal transporter family; PMID:11500563 (68414.m09483) transducin family protein / WD-40 repeat family protein contains 5 WD-40 repeats (PF00400) (1 weak); similar to Hypothetical RAE1-like protein (SP-Q38942) [Arabidopsis thaliana]; similar to mRNA-associated protein mmp 41 (mRNA export protein) (GB:AAAC28126) (GI:1903456) [RAE1] (MRNP41) (SP:P78406) [Homo sapiens] (68414.m09466) phospholipidglycerol acyltransferase family protein low similarity to SPIQ59601 1'-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) (Neisseria gonorrhoeae); contains Pfam profile PF01553; Acyltransferase (68414.m09488)
1223	Not regulated	NC-NC-NC	261896_s_at	A11g080700	expressed protein (68414.m09496) expressed protein (68414.m09486) zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (68414.m07372) zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (68414.m05653)
1224	Not regulated	NC-NC-NC	261897_at	A11g080950	OTU-like cysteine protease family protein contains Pfam profile PF02338; OTU-like cysteine protease (68414.m05688) indigoidine synthase A like protein similar to IndA protein (GI:7576263) [Erwinia chrysanthemi]; contains Pfam profile PF04227; indigoidine synthase A like protein (68414.m05665)
1225	Not regulated	NC-NC-NC	261902_at	A11g080860	C2 domain-containing protein low similarity to cold-regulated gene SRC2 [Glycine max] (GI:2055230; contains Pfam profile PF00188; C2 domain (68414.m05675) scarecrow-like transcription factor 5 (SCL5) similar to SCARECROW GB:AA806318 GI:1497987 from [Arabidopsis thaliana] (68414.m05683)
1226	Not regulated	NC-NC-NC	261904_at	A11g080500	expressed protein (68414.m05655) formate-tetrahydrofolate ligase / 10-formyltetrahydrofolate synthetase (THFS) identical to 10-formyltetrahydrofolate synthetase (Arabidopsis thaliana) GI:5821663 (68414.m05660)
1227	Not regulated	NC-NC-NC	261898_at	A11g080670	7-dehydrocholesterol reductase / 7-DHC reductase / sterol delta-7-reductase (ST7R) / dwarf5 protein (DWF5) identical to SPIQBLDUE 7-dehydrocholesterol reductase (EC 1.3.1.21) (7-DHC reductase) (Sterol delta-7-reductase) (Dwarf5 protein) (Arabidopsis thaliana) (68414.m05652) scarecrow-like transcription factor 3 (SCL3) identical to GB:AA224404 GI:4580515 from [Arabidopsis thaliana] (Plant J. 18 (1), 111-119 (1988)) (68414.m05651)
1228	Not regulated	NC-NC-NC	261899_at	A11g080540	lysine decarboxylase family protein contains Pfam profile PF03841; lysine decarboxylase family (68414.m05677) expressed protein (68414.m01314) thioredoxin family protein similar to thioredoxin H-type from Arabidopsis thaliana SPIP29448, Nicotiana tabacum SPIQ07090; contains Pfam profile: PF00085 Thioredoxin (68414.m01324)
1229	Not regulated	NC-NC-NC	261882_at	A11g11530	expressed protein contains Pfam profile PF04748; Protein of unknown function, DUF814 (68414.m01307) expressed protein (68414.m01309) plastid developmental protein DAG, putative similar to DAG protein, chloroplast precursor [Garden snapdragon] SWISS-PROT:Q38732 (68414.m01313) eukaryotic translation initiation factor-related contains weak similarity to Swiss-Prot:P23588 eukaryotic translation initiation factor 4B (eIF-4B) [Homo sapiens] (68414.m01319)
1230	Not regulated	NC-NC-NC	261883_at	A11g11480	universal stress protein (USP) family protein contains Pfam PF00582; universal stress protein family domain; similar to ethylene-responsive ER6 protein (GI:5669654) [Lycopersicon esculentum] (68414.m01304)
1231	Not regulated	NC-NC-NC	261887_at	A11g11380	ADP-ribosylation factor, putative similar to ADP-ribosylation factor GI:166586 from [Arabidopsis thaliana] (68414.m01205) expressed protein (68414.m01207) heat shock protein 70, putative / HSP70, putative similar to heat shock protein hsp70 GI:1771478 from [Pisum sativum] (68414.m01924)
1232	Not regulated	NC-NC-NC	261888_at	A11g10630	TMS membrane family protein / tumour differentially expressed (TDE) family protein contains Pfam domain, PF03348; TMS membrane protein/tumour differentially expressed protein (TDE) (68414.m01838) expressed protein (68414.m01921) expressed protein (68414.m01917)
1233	Not regulated	NC-NC-NC	261788_at	A11g15980	expressed protein (68414.m01919) expressed protein (68414.m01937) expressed protein (68414.m01929) ovule development protein, putative similar to ovule development protein AINTEGUMENTA (GI:1208099)[Arabidopsis thaliana] (68414.m01926)
1234	Not regulated	NC-NC-NC	261790_at	A11g16000	magnesium transporter CorA-like family protein (MRS2-1) low similarity to SPIQ01926 RNA splicing protein MRS2, mitochondrial precursor (Saccharomyces cerevisiae); contains Pfam profile PF01544; CorA-like Mg2+ transporter protein (68414.m01820)
1235	Not regulated	NC-NC-NC	261791_at	A11g16170	
1236	Not regulated	NC-NC-NC	261793_at	A11g16080	
1237	Not regulated	NC-NC-NC	261794_at	A11g16060	
1238	Not regulated	NC-NC-NC	261795_at	A11g16010	
1239	Not regulated	NC-NC-NC			
1240	Not regulated	NC-NC-NC			
1241	Not regulated	NC-NC-NC			
1242	Not regulated	NC-NC-NC			
1243	Not regulated	NC-NC-NC			
1244	Not regulated	NC-NC-NC			
1245	Not regulated	NC-NC-NC			
1246	Not regulated	NC-NC-NC			
1247	Not regulated	NC-NC-NC			
1248	Not regulated	NC-NC-NC			
1249	Not regulated	NC-NC-NC			
1250	Not regulated	NC-NC-NC			
1251	Not regulated	NC-NC-NC			
1252	Not regulated	NC-NC-NC			
1253	Not regulated	NC-NC-NC			
1254	Not regulated	NC-NC-NC			
1255	Not regulated	NC-NC-NC			
1256	Not regulated	NC-NC-NC			
1257	Not regulated	NC-NC-NC			
1258	Not regulated	NC-NC-NC			
1259	Not regulated	NC-NC-NC			

1260	Not regulated	NC-NC-NC	261801_at	A11g30520	acyl-activating enzyme 14 (AAE14) identical to acyl-activating enzyme 14 [Arabidopsis thaliana]; similar to SPIQ42524 4-coumarate-CoA ligase 1 (EC 6.2.1.12) (4-coumaroyl-CoA synthase 1) [Arabidopsis thaliana]; contains Pfam profile PF00501: AMP-binding enzyme; identical to cDNA acyl-activating enzyme 14 (A11g30520) GI:29893263 (68414.m03734)
1261	Not regulated	NC-NC-NC	261808_at	A11g30510	ferredoxin-NADP(+) reductase, putative / adrenodoxin reductase, putative strong similarity to SPIP41345 Ferredoxin-NADP reductase, root isozyme, chloroplast precursor (EC 1.18.1.2) (FNR) (Oryza sativa); ferredoxin-NADP reductase precursor [Zea mays] GI:500751 (68414.m03730)
1262	Not regulated	NC-NC-NC	261808_at	A11g30460	DNA-damage-repair/replication protein, chloroplast (DRT111) nearly identical to SPIP42688 DNA-damage-repair/replication protein DRT111, chloroplast precursor [Arabidopsis thaliana]; contains Pfam profiles PF01585: G-patch domain, PF00078: RNA recognition motif, (a.k.a. RRM, RBD, or RNP domain) (68414.m03726)
1263	Not regulated	NC-NC-NC	261810_at	A11g08130	DNA ligase / polydeoxyribonucleotide synthase [ATP] identical to SPIQ42572 DNA ligase (EC 6.5.1.1) (Polydeoxyribonucleotide synthase [ATP]) [Arabidopsis thaliana]; contains Pfam profiles: PF01068 ATP dependent DNA ligase domain, PF04679 ATP dependent DNA ligase C terminal region, PF04675 DNA ligase N terminus (68414.m00892)
1264	Not regulated	NC-NC-NC	261815_at	A11g08325	bZIP family transcription factor contains Pfam profile: PF00170 bZIP transcription factor (68414.m00920)
1265	Not regulated	NC-NC-NC	261756_at	A11g08320	aspartyl protease family protein contains Pfam profile: PF00026: Eukaryotic aspartyl protease; similar to CND41, chloroplast nucleoid DNA binding protein (GI:2541876) (Nicotiana tabacum) (68414.m00907)
1266	Not regulated	NC-NC-NC	261757_at	A11g08210	prephenate dehydratase family protein contains similarity to prephenate dehydratase GI:1008717 from [Amycolatopsis methanolica] (68414.m00910)
1267	Not regulated	NC-NC-NC	261758_at	A11g08250	plastocyanin identical to plastocyanin GI:1865683 from [Arabidopsis thaliana] (68414.m08837)
1268	Not regulated	NC-NC-NC	261769_at	A11g76100	prolyl oligopeptidase, putative / prolyl endopeptidase, putative / post-proline cleaving enzyme, putative similar to SPIQ6QUR8 Prolyl oligopeptidase (EC 3.4.21.26) (Post-proline cleaving enzyme) [Mus musculus]; contains Pfam profiles PF00326: prolyl oligopeptidase family, PF02897: Prolyl oligopeptidase, N-terminal beta-propeller domain (68414.m08842)
1269	Not regulated	NC-NC-NC	261770_at	A11g76140	maoC-like dehydratase domain-containing protein contains similarity to Swiss-Prot:P51659 estradiol 17 beta-dehydrogenase 4 (17-beta-HSD 4) (17-beta-hydroxysteroid dehydrogenase 4) [Homo sapiens]; contains Pfam profile PF01575: MaoC like domain (68414.m08843)
1270	Not regulated	NC-NC-NC	261771_at	A11g76150	expressed protein (68414.m08834)
1271	Not regulated	NC-NC-NC	261748_at	A11g76070	thioredoxin family protein low similarity to thioredoxin (TRX) [Fasciola hepatica] GI:6887568; contains Pfam profile PF00085: Thioredoxin (68414.m08835)
1272	Not regulated	NC-NC-NC	261751_at	A11g76080	alpha-amylase, putative / 1,4-alpha-D-glucan glucanohydrolase, putative strong similarity to alpha-amylase GI:7532788 from [Malus x domestica] contains Pfam profile PF00128: Alpha amylase, catalytic domain (68414.m08841)
1273	Not regulated	NC-NC-NC	261754_at	A11g76130	expressed protein (68414.m08849)
1274	Not regulated	NC-NC-NC	261723_at	A11g76200	small nuclear ribonucleoprotein D3, putative / snRNP core protein D3, putative / Sm protein D3, putative similar to SWISS-PROT:P43331 small nuclear ribonucleoprotein Sm D3 (snRNP core protein D3, Sm-D3) [Musae] (68414.m08862)
1275	Not regulated	NC-NC-NC	261725_at	A11g76300	clathrin coat assembly protein, putative similar to clathrin coat assembly protein AP17 GB:CA65533 GI:2695958 from [Zea mays]; contains Pfam profile: PF01217 clathrin adaptor complex small chain (68414.m05324)
1276	Not regulated	NC-NC-NC	261733_at	A11g47830	peroxisomal biogenesis factor 11 family protein / PEX11 family protein contains Pfam PF05648: Peroxisomal biogenesis factor 11 (PEX11) (68414.m05310)
1277	Not regulated	NC-NC-NC	261739_at	A11g47750	expressed protein (68414.m05308)
1278	Not regulated	NC-NC-NC	261740_at	A11g47740	cysteine desulfurase, putative similar to nitrogen fixation protein (nifS) GB:D64004 GI:1001701 from [Synecococcus sp.]; contains TIGRFAM TIGR01384: phosphoserine aminotransferase, contains Pfam PF00268: aminotransferase, class V (68414.m00940)
1279	Not regulated	NC-NC-NC	261744_at	A11g08490	expressed protein (68414.m00927)
1280	Not regulated	NC-NC-NC	261746_at	A11g08380	histone deacetylase family protein (HDA8) identical to HDA8 [Arabidopsis thaliana] GI:21360988low similarity to SPIQ922V5 family, supporting cDNA GI:21360987 [IpilAF510187.1] (68414.m00938)
1281	Not regulated	NC-NC-NC	261720_at	A11g08460	histone deacetylase 6 (HD6) (Histone deacetylase nHDA2) [Mus musculus]; contains Pfam profile PF00850: Histone deacetylase family, supporting cDNA GI:21360987 [IpilAF510187.1] (68414.m00938)
1282	Not regulated	NC-NC-NC	261721_at	A11g08480	expressed protein (68414.m00939)
1283	Not regulated	NC-NC-NC	261692_at	A11g08450	calreticulin 3 (CRT3) identical to similar to SPIQ04153 Calreticulin 3 precursor [Arabidopsis thaliana] (68414.m00934)
1284	Not regulated	NC-NC-NC	261693_at	A11g08370	hydroxyproline-rich glycoprotein family protein contains proline-rich extensin domains, INTERPRO:IPRO02865; contains some similarity to transcription factor [Danio rerio] gi15617376 [embICAC69871] (68414.m00926)
1285	Not regulated	NC-NC-NC	261694_at	A11g08360	60S ribosomal protein L10A (RPL10A) similar to 60S ribosomal protein L10A GB:AACT3045 GI:3860277 from [Arabidopsis thaliana] (68414.m00925)
1286	Not regulated	NC-NC-NC	261695_at	A11g08520	magnesium-chelatase subunit CHL1, chloroplast, putative / Mg-protoporphyrin IX chelatase, putative (CHL1) similar to Mg-chelatase SPIQ24133 from [Nicotiana tabacum] GB:AF014399 GI:2318118 from [Pisum sativum] (68414.m00943)
1287	Not regulated	NC-NC-NC	261696_at	A11g08470	sirtocidine synthase family protein similar to sirtocidine synthase [Rauvolfia serpentina] [SPIP15324] (68414.m00938)
1288	Not regulated	NC-NC-NC	261709_at	A11g32790	RNA-binding protein, putative similar to RNA-binding protein GB:CA840027 GI:4539439 from [Arabidopsis thaliana] (68414.m04042)
1289	Not regulated	NC-NC-NC	261711_at	A11g32700	zinc-binding family protein similar to zinc-binding protein [Pisum sativum] GI:16117799; contains Pfam profile PF04640: Protein of unknown function, DUF597 (68414.m04032)
1290	Not regulated	NC-NC-NC	261718_at	A11g18350	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (68414.m02297)
1291	Not regulated	NC-NC-NC	261661_at	A11g18380	hydrolase, alpha/beta fold family protein similar to monoglyceride lipase from [Homo sapiens] GI:14594804, [Mus musculus] GI:2632162, [Rattus norvegicus] GI:19697888; contains Pfam profile PF00561: hydrolase, alpha/beta fold family (68414.m02294)
1292	Not regulated	NC-NC-NC	261666_at	A11g18440	peptidyl-RNA hydrolase family protein contains Pfam profile PF01185: peptidyl-RNA hydrolase (68414.m02301)
1293	Not regulated	NC-NC-NC	261667_at	A11g18460	lipase family protein similar to triacylglycerol lipase, gastric precursor (EC 3.1.1.3) [Canis familiaris] [SPIP80035] (68414.m02303)
1294	Not regulated	NC-NC-NC	261672_at	A11g18450	actin-related protein 4 (ARP4) nearly identical to actin-related protein 4 (ARP4) [Arabidopsis thaliana] [SPIP15324] (68414.m02302)

1295	Not regulated	1295	NC-NC-NC	261674_at	A11g18270	ketose-bisphosphate aldolase class-II family protein low similarity to KuaY (tagatose-1,6-bisphosphate aldolase) [Escherichia coli] Gi:8895753; contains Pfam profile PF01116; Fructose-bisphosphate aldolase class-II (68414.m02280)
1296	Not regulated	1296	NC-NC-NC	261677_at	A11g18470	zinc finger (C3HC4-type RING finger) protein contains Pfam profile: PF00097 zinc finger (68414.m02304)
1297	Not regulated	1297	NC-NC-NC	261682_at	A11g47330	expressed protein contains Pfam profile PF01595; Domain of unknown function (68414.m05240)
1298	Not regulated	1298	NC-NC-NC	261689_at	A11g50030	target of rapamycin protein (TOR) identical to pTOR [Arabidopsis thaliana] Gi:12002902; contains Pfam profiles PF00454
1299	Not regulated	1299	NC-NC-NC	261634_at	A11g49970	Phosphatidylinositol 3'- and 4'-kinase, PF02259 FAT domain, PF02260 FATC domain (68414.m05614)
1300	Not regulated	1300	NC-NC-NC	261635_at	A11g50020	ATP-dependent Clp protease proteolytic subunit (ClpP1) (nClpP5) identical to nClpP5 GB:BAAB2069 Gi:5360595 from [Arabidopsis thaliana]; identical to cDNA nClpP5 (nuclear encoded ClpP5) Gi:5360594 (68414.m05607)
1301	Not regulated	1301	NC-NC-NC	261637_at	A11g49950	expressed protein (68414.m05613)
1302	Not regulated	1302	NC-NC-NC	261638_at	A11g49975	DNA-binding protein, putative contains similarity to DNA-binding protein PcdMYB1 (Petroselinum crispum) gi 2224898 gb AA81689 (68414.m05602)
1303	Not regulated	1303	NC-NC-NC	261642_at	A11g27680	expressed protein (68414.m05608)
1304	Not regulated	1304	NC-NC-NC	261644_s_at	A11g27830	glucose-1-phosphate adenylyltransferase large subunit 2 (APL2) / ADP-glucose pyrophosphorylase identical to SPIP55230 (68414.m03383)
1305	Not regulated	1305	NC-NC-NC	261655_at	A11g01940	peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein contains Pfam domain, PF00160; peptidyl-prolyl cis-trans isomerase, cyclophilin-type (68414.m00112)
1306	Not regulated	1306	NC-NC-NC	261622_at	A11g01970	pentatricopeptide (PPR) repeat-containing protein low similarity to 67 kD chloroplastic RNA-binding protein RSP67.2 [Raphanus sativus] Gi:9755886; contains Pfam profile PF01535; PPR repeat (68414.m00115)
1307	Not regulated	1307	NC-NC-NC	261626_at	A11g01990	expressed protein (68414.m00117)
1308	Not regulated	1308	NC-NC-NC	261627_at	A11g01910	anion-transporting ATPase, putative similar to SPI043681 Arsenical pump-driving ATPase (EC 3.6.3.16) [Arsenite-translocating ATPase] (Arsenical resistance ATPase) [Arsenite-transporting ATPase] (ARSA) [ASNA-L] (Homo sapiens); contains Pfam profile PF02374; Anion-transporting ATPase (68414.m00106)
1309	Not regulated	1309	NC-NC-NC	261606_at	A11g49570	peroxidase, putative identical to peroxidase ATP5a [Arabidopsis thaliana] gi 1546702 emb CAA67341; similar to peroxidase SWISS PROT:P80679 from [Armoiracia rusticana] (68414.m05558)
1310	Not regulated	1310	NC-NC-NC	261607_at	A11g49660	expressed protein (68414.m05558)
1311	Not regulated	1311	NC-NC-NC	261612_at	A11g49710	lucosyltransferase-like protein, putative / FucT2, putative / FucTB, putative (FUT12) identical to Putative fucosyltransferase-like protein (FucT2) (AFU0112) (Swiss-Prot:Q8FX97) [Arabidopsis thaliana]; similar to glycoprotein 3-alpha-L-fucosyltransferase A (SP-Q8LJK1) [Arabidopsis thaliana]; contains Pfam profile PF00852; Fucosyl transferase (68414.m05573)
1312	Not regulated	1312	NC-NC-NC	261620_s_at	A11g33140	60S ribosomal protein L9 (RPL90A/C) similar to RIBOSOMAL PROTEIN L9 GB:P49209 from [Arabidopsis thaliana] (68414.m04093)
1313	Not regulated	1313	NC-NC-NC	261566_at	A11g33230	expressed protein (68414.m04106)
1314	Not regulated	1314	NC-NC-NC	261570_at	A11g01120	fatty acid elongase 3-ketoacyl-CoA synthase 1 (KCS1) nearly identical to GB:AAC99312 Gi:4091810 from [Arabidopsis thaliana] (68414.m00015)
1315	Not regulated	1315	NC-NC-NC	261577_at	A11g01080	33 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp33, putative similar to 33 kDa RIBONUCLEOPROTEIN GB:P19884 from [Nicotiana sylvestris] (68414.m00010)
1316	Not regulated	1316	NC-NC-NC	261582_at	A11g01160	SSXT protein-related / transcription co-activator-related similar to SVT/SSX4 fusion protein (Gi:1127695) [Homo sapiens]; supporting cDNA gi2153969 gb AY102640.1; contains Pfam profile PF05030; SSXT protein (N-terminal region) (68414.m00026)
1317	Not regulated	1317	NC-NC-NC	261583_at	A11g01090	pyruvate dehydrogenase E1 component alpha subunit, chloroplast identical to pyruvate dehydrogenase E1 alpha subunit GB:AA886803 Gi:2454182 from [Arabidopsis thaliana]; identical to cDNA pyruvate dehydrogenase E1 alpha subunit mRNA, nuclear gene encoding plastid protein Gi:2454181 (68414.m00011)
1318	Not regulated	1318	NC-NC-NC	261591_at	A11g01740	protein kinase family protein low similarity to protein kinase [Arabidopsis thaliana] Gi:2852449; contains Pfam profile: PF00069
1319	Not regulated	1319	NC-NC-NC	261563_at	A11g01630	Protein kinase domain (68414.m00093)
1320	Not regulated	1320	NC-NC-NC	261534_at	A11g01820	SEC14 cytosolic factor, putative / phosphoglycerate transfer protein, putative contains Pfam PF00850 : CRALTRIO domain and PF03785 : CRALTRIO, N-terminus; similar to polyphosphonitride binding protein Sht2p GB:AA894599 Gi:2739046 from [Glycine max] (68414.m00080)
1321	Not regulated	1321	NC-NC-NC	261535_at	A11g01725	peroxisomal biogenesis factor 11 family protein / PEX11 family protein contains Pfam PF05648; Peroxisomal biogenesis factor 11 (PEX11) (68414.m00101)
1322	Not regulated	1322	NC-NC-NC	261536_at	A11g01790	K+ efflux antiporter, putative (KEA1) identical to GB:AA001191 Gi:4101473 from [Arabidopsis thaliana]; Monovalent cation:proton antiporter family 2 (CPA2 family) member, PMID:11500563 (68414.m00098)
1323	Not regulated	1323	NC-NC-NC	261537_at	A11g01800	short-chain dehydrogenase/reductase (SDR) family protein similar to carbonyl reductase Gi:1049108 from [Mus musculus] (68414.m00098)
1324	Not regulated	1324	NC-NC-NC	261540_at	A11g63810	expressed protein (68414.m07191)
1325	Not regulated	1325	NC-NC-NC	261530_at	A11g63460	glutathione peroxidase, putative contains Pfam profile: PF00255 glutathione peroxidases (68414.m07176)
1326	Not regulated	1326	NC-NC-NC	261509_at	A11g71740	hypothetical protein (68414.m08292)
1327	Not regulated	1327	NC-NC-NC	261513_at	A11g71840	transducin family protein / WD-40 repeat family protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pfam profile:PF00400 WD domain, G-beta repeat (7 copies) (68414.m08302)
1328	Not regulated	1328	NC-NC-NC	261515_at	A11g71800	cleavage stimulation factor, putative similar to cleavage stimulation factor 64 kilodalton subunit GB:AA047839 Gi:5713194 from [Drosophila melanogaster]; SPIP33240 Cleavage stimulation factor, 64 kDa subunit (Homo sapiens); contains InterPro entry IPR000504; RNA-binding region RNP-1 (RNA recognition motif) (RRM) (68414.m08298)
1329	Not regulated	1329	NC-NC-NC	261517_at	A11g71780	expressed protein (68414.m08298)
1330	Not regulated	1330	NC-NC-NC	261519_at	A11g71810	ABC1 family protein contains Pfam domain, PF03109; ABC1 family (68414.m08299)

1331	Not regulated	NC-NC-NC	261522_at	At1g17170	inositol polyphosphate 5-phosphatase, putative similar to inositol polyphosphate 5-phosphatase I [Arabidopsis thaliana] Gi:10444261 (68414.m08289)
1332	Not regulated	NC-NC-NC	261523_at	At1g17860	protein tyrosine phosphatase 1 (PTP1) identical to protein tyrosine phosphatase 1 Gi:3170531 from [Arabidopsis thaliana], contains Pfam profile: PF00102 protein-tyrosine phosphatase (68414.m08304)
1333	Not regulated	NC-NC-NC	261524_at	At1g14300	expressed protein contains Pfam PF04063: Domain of unknown function (DUF384) (68414.m01695)
1334	Not regulated	NC-NC-NC	261526_at	At1g14370	protein kinase (APK2a) identical to protein kinase APK2a Gi:2852447 from [Arabidopsis thaliana] (68414.m01703)
1335	Not regulated	NC-NC-NC	261461_at	At1g14260	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger) (68414.m01889)
1336	Not regulated	NC-NC-NC	261483_at	At1g14270	CAAX amino terminal protease family protein contains Pfam profile PF02517: CAA-X amino terminal protease family (68414.m01691)
1337	Not regulated	NC-NC-NC	261486_at	At1g14510	PHD finger family protein contains Pfam domain, PF00828: PHD-finger (68414.m01720)
1338	Not regulated	NC-NC-NC	261487_at	At1g14340	RNA recognition motif (RRM)-containing protein (68414.m01899)
1339	Not regulated	NC-NC-NC	261489_at	At1g14450	expressed protein contains similarity to cytochrome c oxidase subunit I Gi:5678701 from [Loligo pealeii] (68414.m01714)
1340	Not regulated	NC-NC-NC	261490_at	At1g14320	60S ribosomal protein L10 (RPL10A) / Wilm's tumor suppressor protein-related similar to tumor suppressor Gi:575354 from [Oryza sativa] (68414.m01897)
1341	Not regulated	NC-NC-NC	261492_at	At1g14280	acid phosphatase, putative similar to acid phosphatase [Lupinus albus] Gi:5360721; contains Pfam profile PF01598 steroid desaturase (68414.m01694)
1342	Not regulated	NC-NC-NC	261493_at	At1g14410	DNA-binding protein-related similar to DNA-binding protein p24 Gi:9651810 from [Solanum tuberosum] (68414.m01709)
1343	Not regulated	NC-NC-NC	261495_at	At1g28410	expressed protein (68414.m03493)
1344	Not regulated	NC-NC-NC	261439_at	At1g28395	expressed protein (68414.m03489)
1345	Not regulated	NC-NC-NC	261440_at	At1g28510	expressed protein (68414.m03505)
1346	Not regulated	NC-NC-NC	261408_s_at	At1g07820	histone H4 identical to histone H4 from Lycopersicon esculentum Gi:297150, Lolium temulentum SPIP02308, Acropora formosa Gi:455652, Citrus jambhiri Gi:1679787 (68414.m00847)
1347	Not regulated	NC-NC-NC	261409_at	At1g07640	Dot-type zinc finger domain-containing protein identical to zinc finger protein OBP2 Gi:5059394 from [Arabidopsis thaliana] (68414.m00819)
1348	Not regulated	NC-NC-NC	261411_at	At1g07790	histone H2B, putative strong similarity to histone H2B Arabidopsis thaliana Gi:2407802, Gossypium hirsutum SPI022582, Lycopersicon esculentum Gi:3021489, Capsicum annuum SPO49118; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4 (68414.m00843)
1349	Not regulated	NC-NC-NC	261413_at	At1g07630	protein phosphatase 2C family protein / PP2C family protein similar to protein phosphatase-2c Gi:3608412 [Mesembryanthemum crystallinum]; contains Pfam PF00481: Protein phosphatase 2C domain (68414.m00818)
1350	Not regulated	NC-NC-NC	261415_at	At1g07750	cucurbit family protein similar to legumin (11S-globulin) from Ginkgo biloba [Gi:949886], 11S globulin from Avena sativa [Gi:472867] (68414.m00837)
1351	Not regulated	NC-NC-NC	261417_at	At1g07700	thioredoxin family protein low similarity to thioredoxin [Gallus gallus] Gi:212766; contains Pfam profile: PF00085 Thioredoxin (68414.m00827)
1352	Not regulated	NC-NC-NC	261418_at	At1g07830	ribosomal protein L28 family protein similar to GB:CAA83057 from [Saccharomyces cerevisiae] (68414.m00848)
1353	Not regulated	NC-NC-NC	261420_at	At1g07720	beta-ketoacyl-CoA synthase family protein similar to GB:AAC99312 from [Arabidopsis thaliana] (Plant J. (1998) in press)
1354	Not regulated	NC-NC-NC	261422_at	At1g18730	expressed protein (68414.m02336)
1355	Not regulated	NC-NC-NC	261424_at	At1g18700	DNAJ heat shock N-terminal domain-containing protein low similarity to SPI09QV8 DnaJ homolog subfamily B member 7 Mus musculus; contains Pfam profile PF00226 DnaJ domain (68414.m02333)
1356	Not regulated	NC-NC-NC	261425_at	At1g18880	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family (68414.m02350)
1357	Not regulated	NC-NC-NC	261405_at	At1g18740	expressed protein (68414.m02337)
1358	Not regulated	NC-NC-NC	261406_at	At1g18800	nucleosome assembly protein (NAP) family protein similar to SPI001105SET protein (HLA-DR associated protein II) (PHAPlI) (Phosphatase 2A inhibitor 2PP2A) (Homo sapiens); contains Pfam profile PF00956: Nucleosome assembly protein (NAP) (68414.m02343)
1359	Not regulated	NC-NC-NC	261376_at	At1g18660	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00087 zinc finger, C3HC4 type (68414.m02326)
1360	Not regulated	NC-NC-NC	261377_at	At1g18850	expressed protein (68414.m02347)
1361	Not regulated	NC-NC-NC	261378_at	At1g18890	calcium-dependent protein kinase 1 (CDPK1) identical to calcium-dependent protein kinase [Arabidopsis thaliana] gi1804880djlBAA04829; contains protein kinase domain, Pfam:PF00036, INTERPRO:IPR002048 (68414.m02351)
1362	Not regulated	NC-NC-NC	261379_at	At1g18720	expressed protein similar to YGL010w-like protein Gi:2982301 from [Picea mariana] (68414.m02335)
1363	Not regulated	NC-NC-NC	261386_at	At1g05430	expressed protein (68414.m00551)
1364	Not regulated	NC-NC-NC	261397_at	At1g79920	hexose transporter, putative similar to hexose transporter Gi:8347246 from [Solanum tuberosum]; contains Pfam profile PF00083: major facilitator superfamily protein (68414.m09322)
1365	Not regulated	NC-NC-NC	261403_at	At1g79590	syntaxin 52 (SYPS2) identical to Swiss-Prot:Q9AKK7 syntaxin 52 A2 (A1SYPS2) [Arabidopsis thaliana] (68414.m09280)
1366	Not regulated	NC-NC-NC	261344_at	At1g79710	integral membrane transporter family protein similar to high affinity folic acid/methotrexate transporter 5 (Gi:21888554) [Leishmania tarentolae]; InterPro:IPR001991/PRO0173 Sodium/dicarboxylate symporter family (68414.m09286)
1367	Not regulated	NC-NC-NC	261346_at	At1g79720	aspartyl protease family protein contains Pfam domain, PF00026: eukaryotic aspartyl protease (68414.m09298)
1368	Not regulated	NC-NC-NC	261348_at	At1g79810	PeaZ/Pex12 N-terminal domain-containing protein / zinc finger (C3HC4-type RING finger) family protein contains Pfam profiles PF00097: zinc finger C3HC4 type (RING finger), PF04757: PexZ/Pex12 amino terminal region (68414.m09318)
1369	Not regulated	NC-NC-NC	261351_at	At1g79790	haloacid dehalogenase-like hydrolase family protein contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase (68414.m09312)
1370	Not regulated	NC-NC-NC	261352_at	At1g79650	DNA repair protein RAD23, putative similar to DNA repair by nucleotide excision (NER) RAD23 protein, isoform II Gi:1914685 from [Daucus carota]; contains Pfam profiles PF00240: Ubiquitin family, PF00827: UBA-TS-N domain (68414.m09287)

1371	Not regulated	NC-NC-NC	261354_at	MutT/nudix family protein contains Pfam NUDIX domain (PF00293); very low similarity to Chain A and Chain B of Escherichia coli isopentenyl diphosphate:dimethylallyl diphosphate isomerase [gi:15826361] [gi:15826360] (88414.m05294)
1372	Not regulated	NC-NC-NC	261362_s_at	60S ribosomal protein L35a (RPL35aB) identical to GB:CA881600 from [Arabidopsis thaliana] (88414.m04838)
1373	Not regulated	NC-NC-NC	261373_at	Cydylyltransferase family contains Pfam profile: PF02348 cydylyltransferase (88414.m05998)
1374	Not regulated	NC-NC-NC	261314_at	GTP-binding family protein contains Pfam domain, PF01926: GTPase of unknown function (88414.m05995)
1375	Not regulated	NC-NC-NC	261315_at	ethylene-responsive element-binding factor 8 / ERF transcription factor 8 (ERF8) identical to ERF transcription factor 8 (88414.m06025)
1376	Not regulated	NC-NC-NC	261320_at	RNA-binding S4 domain-containing protein (88414.m06015)
1377	Not regulated	NC-NC-NC	261322_at	purine permease family protein similar to purine permease [Arabidopsis thaliana] GI:7620007; contains Pfam profile PF03151: Domain of unknown function, DUF250 (88414.m05126)
1378	Not regulated	NC-NC-NC	261323_at	universal stress protein (USP) family protein contains Pfam profile PF00582: universal stress protein family (88414.m05128)
1379	Not regulated	NC-NC-NC	261324_at	expressed protein (88414.m05129)
1380	Not regulated	NC-NC-NC	261326_s_at	aminoacylase, putative / N-acyl-L-amino-acid amidohydrolase, putative similar to aminoacylase-1 (N-acyl-L-amino-acid amidohydrolase, ACY-1) [Homo sapiens] SWISS-PROT:Q03154 (88414.m05103)
1381	Not regulated	NC-NC-NC	261328_at	Ybak/prolyl-RNA synthetase family protein contains Pfam PF04073: Ybak / prolyl-RNA synthetases associated domain; similar to 25.7 kDa protein (GI:7271117) [Cicer arietinum] (88414.m05136)
1382	Not regulated	NC-NC-NC	261334_at	expressed protein (88414.m05153)
1383	Not regulated	NC-NC-NC	261338_at	expressed protein (88414.m05147)
1384	Not regulated	NC-NC-NC	261293_at	expressed protein (88414.m04610)
1385	Not regulated	NC-NC-NC	261294_at	dihydroxyacetone kinase family protein similar to dihydroxyacetone kinases; contains Pfam profiles PF02733: DAK1 domain, PF02734: DAK2 domain (88414.m05414)
1386	Not regulated	NC-NC-NC	261295_at	expressed protein (88414.m05416)
1387	Not regulated	NC-NC-NC	261299_at	vacuolar protein sorting-associated protein 26 (88414.m05429)
1388	Not regulated	NC-NC-NC	261301_at	protein sorting-associated protein 26 (88414.m05429)
1389	Not regulated	NC-NC-NC	261304_at	zinc finger (Ran-binding) family protein contains Pfam domain, PF00841: Zn-finger in Ran binding protein and others (88414.m05431)
1390	Not regulated	NC-NC-NC	261308_at	expressed protein (88414.m05415)
1391	Not regulated	NC-NC-NC	261309_at	leucine-rich repeat transmembrane protein kinase, putative contains similarity to many predicted protein kinases (88414.m05418)
1392	Not regulated	NC-NC-NC	261279_at	phosphoethanolamine N-methyltransferase 2, putative (NMT2) very similar to PEM2_ARATH Putative phosphoethanolamine N-methyltransferase 2 (EC 2.1.1.103) (SP:O844H0)[Arabidopsis thaliana]; very similar to Halotolerance protein Hal3b (SP:P84063)[Arabidopsis thaliana]; to similar to GB:AAF61950 from [Spinacia oleracea] (88414.m05434)
1393	Not regulated	NC-NC-NC	261252_at	chitinase-like protein 1 (CTL1) similar to class I chitinase GI:7798856 from [Haliobolobos perplexa var. perplexa]; contains Pfam profile PF00182: Chitinase class I; identical to cDNA chitinase-like protein 1 (CTL1) CTL1-ELP1 allele GI:17226328 (88414.m00612)
1394	Not regulated	NC-NC-NC	261253_at	Ras-related protein (ARA-1) (ARA) / small GTP-binding protein, putative nearly identical to SP:P19892 Ras-related protein ARA-1 [Arabidopsis thaliana] (Gene 76-313-319(1989)) (88414.m00608)
1395	Not regulated	NC-NC-NC	261254_at	aspartyl protease family protein contains Pfam PF00026: Eukaryotic aspartyl protease (88414.m00611)
1396	Not regulated	NC-NC-NC	261267_at	basic helix-loop-helix (bHLH) family protein (88414.m00607)
1397	Not regulated	NC-NC-NC	261270_at	expressed protein (88414.m03257)
1398	Not regulated	NC-NC-NC	261220_at	eukaryotic translation initiation factor 5A, putative / eIF-5A, putative strong similarity to SPI09AXQ6 Eukaryotic translation initiation factor 5A-1 (eIF-5A 1) (Lycopodium obscurum) (88414.m03243)
1399	Not regulated	NC-NC-NC	261225_at	ER lumen protein retaining receptor family protein similar to SPIP23848 ER lumen protein retaining receptor 1 (KDEL receptor 1) (Bos taurus); contains Pfam profile PF00810: ER lumen protein retaining receptor (88414.m02502)
1400	Not regulated	NC-NC-NC	261227_at	expressed protein (88414.m02515)
1401	Not regulated	NC-NC-NC	261238_at	26S proteasome regulatory subunit S3, putative (RPN3) similar to SP:Q06384 from [Daucus carota] (88414.m02524)
1402	Not regulated	NC-NC-NC	261190_at	expressed protein (88414.m04044)
1403	Not regulated	NC-NC-NC	261198_at	ribosomal protein L11 family protein similar to chloroplast ribosomal protein L11 GI:21312 from [Spinacia oleracea] (88414.m04053)
1404	Not regulated	NC-NC-NC	261197_at	basic helix-loop-helix (bHLH) family protein / F-box family protein contains Pfam profiles: PF00846 F-box domain, PF00010 helix-loop-helix DNA-binding domain (88414.m01494)
1405	Not regulated	NC-NC-NC	261202_at	glyceraldehyde 3-phosphate dehydrogenase, chloroplast, putative / NADP-dependent glyceraldehyde phosphate dehydrogenase, putative similar to SPIP25856 Glyceraldehyde 3-phosphate dehydrogenase A, chloroplast precursor (EC 1.2.1.13) (NADP-dependent glyceraldehyde phosphate dehydrogenase subunit A) [Arabidopsis thaliana]; contains Pfam profiles PF02800: Glyceraldehyde 3-phosphate dehydrogenase C-terminal domain, PF00044: Glyceraldehyde 3-phosphate dehydrogenase NAD binding domain (88414.m01498)
1406	Not regulated	NC-NC-NC	261203_at	flower pigmentation protein (AN11) contains 3 WD-40 repeats (PF00400); identical to GB:AAC18912 from [Arabidopsis thaliana] (Genes Dev. 11 (11): 1422-1434 (1997)) (88414.m01499)
1407	Not regulated	NC-NC-NC	261204_s_at	expressed protein (88414.m01492)
1408	Not regulated	NC-NC-NC	261206_at	eukaryotic release factor 1 family protein / eRF1 family protein contains Pfam profiles: PF03463 eRF1 domain 1, PF03464 eRF1 domain 2, PF03465 eRF1 domain 3 (88416.m03325)
1409	Not regulated	NC-NC-NC	261207_at	S1 RNA-binding domain-containing protein contains Pfam domain, PF00575: S1 RNA binding domain (88414.m01486)
1410	Not regulated	NC-NC-NC	261209_at	expressed protein (88414.m01490)
				proline-rich family protein contains proline rich extensin domains, INTERPRO:IPR002965 (88414.m01489)

1411	Not regulated	NC-NC-NC	261210_at	At1g12840	vacuolar ATP synthase subunit C (VATC) / V-ATPase C subunit / vacuolar proton pump C subunit (DET3) identical to vacuolar ATP synthase subunit C SP-Q9SDS7 from [Arabidopsis thaliana] (68414.m01491)
1412	Not regulated	NC-NC-NC	261183_at	At1g34550	expressed protein contains Pfam profile PF04765: Protein of unknown function (DUF616); expression supported by MPSS (68414.m04294)
1413	Not regulated	NC-NC-NC	261165_at	At1g34430	dihydropyrimidine S-acetyltransferase, putative similar to dihydropyrimidine S-acetyltransferase (LTA2) [Arabidopsis thaliana] Gi:5881963; contains Pfam profiles PF00198: 2-oxo acid dehydrogenases acyltransferase (catalytic domain), PF00364: Biotin-requiring enzyme, PF02817: e3 binding domain (68414.m04277)
1414	Not regulated	NC-NC-NC	261173_at	At1g04830	RabGAP/TBC domain-containing protein low similarity to SP1Q08484 GTPase-activating protein GYP1 [Saccharomyces cerevisiae]; contains Pfam profile PF00566: TBC domain (68414.m00479)
1415	Not regulated	NC-NC-NC	261176_at	At1g04780	ankyrin repeat family protein contains Pfam PF00023: Ankyrin repeat (68414.m00474)
1416	Not regulated	NC-NC-NC	261177_at	At1g04770	male sterility MS5 family protein similar to male sterility MS5 [Arabidopsis thaliana] Gi:3859112; contains Pfam profile PF00515 TPR Domain (68414.m00473)
1417	Not regulated	NC-NC-NC	261153_at	At1g04850	ubiquitin-associated (UBA)/UBT-N domain-containing protein weak similarity to SPIP45974 Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.1.2.15) (Homo sapiens); contains Pfam profile PF00627: UBA/UBT-N domain (68414.m00481)
1418	Not regulated	NC-NC-NC	261154_at	At1g04970	lipid-binding serum glycoprotein family protein low similarity to SPIP17213 Bactericidal permeability-increasing protein precursor (BPI) (Homo sapiens); contains Pfam profile PF02866: LBP / BPI / CETP family, C-terminal domain (68414.m00485)
1419	Not regulated	NC-NC-NC	261155_at	At1g04960	expressed protein (68414.m00494)
1420	Not regulated	NC-NC-NC	261128_at	At1g04950	TATA box-binding protein-associated factor (TAF) family protein contains Pfam profile: PF02969 TATA box binding protein associated factor (68414.m00492)
1421	Not regulated	NC-NC-NC	261128_at	At1g04860	ubiquitin-specific protease 2 (UBP2) identical to Gi:11993463 (68414.m00482)
1422	Not regulated	NC-NC-NC	261130_at	At1g04870	protein arginine N-methyltransferase family protein similar to SP1Q06LA8 Protein arginine N-methyltransferase 6 (EC 2.1.1.-) (Homo sapiens) (68414.m00483)
1423	Not regulated	NC-NC-NC	261132_at	At1g18800	expressed protein contains Pfam PF02405: Domain of unknown function DUF140; similar to TOLUENE TOLERANCE PROTEIN TTG2B (Brucella melitensis 16M) (Gi:17862923) (68414.m02477)
1424	Not regulated	NC-NC-NC	261138_at	At1g18600	pH-B-type carbohydrate kinase family protein contains Pfam profile: PF00294 pH-B family carbohydrate kinase (68414.m02441)
1425	Not regulated	NC-NC-NC	261149_s_at	At1g19570	dehydroascorbate reductase, putative similar to GB-BAA49072 from (Oryza sativa) (68414.m02437)
1426	Not regulated	NC-NC-NC	261105_at	At1g63300	expressed protein (68414.m07114)
1427	Not regulated	NC-NC-NC	261107_at	At1g63010	SPX (SYG1/Pho81/XPR1) domain-containing protein contains Pfam profile PF03105: SPX domain (68414.m07115)
1428	Not regulated	NC-NC-NC	261110_at	At1g75440	ubiquitin-conjugating enzyme 16 (UBC16) E2; identical to gi:2801444, GB-AAC39325 from [Arabidopsis thaliana] (Plant Mol. Biol. 23 (2), 387-398 (1993)) (68414.m08763)
1429	Not regulated	NC-NC-NC	261119_at	At1g75350	ribosomal protein L31 family protein similar to SP-O46917 from (Guillardia theta) (68414.m08752)
1430	Not regulated	NC-NC-NC	261120_at	At1g75410	BEL1-like homeodomain 3 protein (BLH3) identical to BEL1-like homeodomain 3 (Gi:13877515) [Arabidopsis thaliana] (68414.m08760)
1431	Not regulated	NC-NC-NC	261122_at	At1g75330	ornithine carbamoyltransferase, chloroplast / ornithine transcarbamylase / OTCase (OTC) identical to SPI050039 Ornithine carbamoyltransferase, chloroplast precursor (EC 2.1.3.3) (OTCase) (Ornithine transcarbamylase) [Arabidopsis thaliana] (68414.m08750)
1432	Not regulated	NC-NC-NC	261089_at	At1g07570	protein kinase (APK1a) identical to Protein kinase APK1A from [Arabidopsis thaliana] SWISS-PROT:Q08548 (68414.m00810)
1433	Not regulated	NC-NC-NC	261064_at	At1g07510	FtsH protease, putative similar to AAA-metalloprotease FtsH (Pisum sativum) Gi:15021781; contains Pfam profiles PF01434: Peptidase family M41, PF00004: ATPase AAA family (68414.m00804)
1434	Not regulated	NC-NC-NC	261070_at	At1g07390	leucine-rich repeat family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to Hc2-SD (Lycopodium obscurum) gi3694393/gpAAC76596 (68414.m00788)
1435	Not regulated	NC-NC-NC	261075_at	At1g07280	expressed protein (68414.m00774)
1436	Not regulated	NC-NC-NC	261078_at	At1g07320	50S ribosomal protein L4, chloroplast (CL4) identical to SP-O50061 from [Arabidopsis thaliana] (68414.m00779)
1437	Not regulated	NC-NC-NC	261079_s_at	At1g07470	transcription factor IIA large subunit, putative / TFIIA large subunit, putative nearly identical to transcription factor IIA large subunit Gi:2826884 from [Arabidopsis thaliana]; contains Pfam profile: PF03153 transcription factor IIA, alpha/beta subunit (68414.m00797)
1438	Not regulated	NC-NC-NC	261083_at	At1g07310	C2 domain-containing protein contains similarity to shock protein SRC2 [Glycine max] gi2055230/dbjBAA19769 : contains Pfam profile PF00168: C2 domain (68414.m00778)
1439	Not regulated	NC-NC-NC	261084_at	At1g07440	tropinone reductase, putative / tropine dehydrogenase, putative similar to tropinone reductase SP-P50165 from [Datura stramonium] (68414.m00794)
1440	Not regulated	NC-NC-NC	261060_at	At1g17340	phosphoinositide phosphatase family protein contains similarity to phosphoinositide phosphatase SAC1 [Rattus norvegicus] gi11095248/gpAAC29810; contains Pfam domain, PF02363: Sac1 homology domain; identical to cDNA SAC domain protein 5 (SACS) Gi:31415728 (68414.m02113)
1441	Not regulated	NC-NC-NC	261031_at	At1g17360	COP1-interacting protein-related similar to COP1-interacting Protein 7 (CIP7) (Gi:3327870) [Arabidopsis thaliana] (68414.m02116)
1442	Not regulated	NC-NC-NC	261036_at	At1g17470	developmentally regulated GTP-binding protein (DRG1) identical to developmentally regulated GTP binding protein (DRG1) [Arabidopsis thaliana] Gi:2345150 (68414.m02143)
1443	Not regulated	NC-NC-NC	261038_at	At1g17490	expressed protein (68414.m02147)
1444	Not regulated	NC-NC-NC	261040_at	At1g17370	oligonucleotide-binding protein, putative similar to oligonucleotide binding protein [Nicotiana glauca] Gi:6996560; contains InterPro entry IPR005004: RNA-binding region RNP-1 (RNA recognition motif) (RRM) (68414.m02118)
1445	Not regulated	NC-NC-NC	261048_at	At1g01420	UDP-glucuronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase (68414.m00057)
1446	Not regulated	NC-NC-NC	261026_at	At1g01240	expressed protein (68414.m00039)

1447	Not regulated	NC-NC-NC	261027_at	A11g01340	cyclic nucleotide-regulated ion channel (CNGC10) [ACBK1] almost identical to CaM-regulated potassium ion channel (ACBK1) Gi:8515883 from [Arabidopsis thaliana], contains Pfam domain, PF00520: Ion transport protein (88414.m00049)
1448	Not regulated	NC-NC-NC	261017_at	A11g26570	UDP-glucose 6-dehydrogenase, putative strong similarity to SPIQ96558 UDP-glucose 6-dehydrogenase (EC 1.1.1.22) [UDP-Glc dehydrogenase] (UDP-GlcDH) (UDP-GDH) (Glycine max); contains Pfam profiles PF03721: UDP-glucose/GDP-mannose dehydrogenase family NAD binding domain, PF00984: UDP-glucose/GDP-mannose dehydrogenase family central domain, PF03720: UDP-glucose/GDP-mannose dehydrogenase family UDP binding domain (88414.m03237)
1449	Not regulated	NC-NC-NC	261018_at	A11g26550	peptidyl-prolyl cis-trans isomerase PPIC-type family protein similar to SPIQ97237 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 (EC 5.2.1.8) (Rolamase Pin4) (PPIase Pin4) (Homo sapiens); contains Pfam profile PF00638: PPIC-type PPIase domain (88414.m03235)
1450	Not regulated	NC-NC-NC	261023_at	A11g12200	flavin-containing monooxygenase family protein / FMO family protein low similarity to FMO2 from Homo sapiens (SPIQ89518); contains Pfam profile: PF00743 Flavin-binding monooxygenase-like (88414.m01412)
1451	Not regulated	NC-NC-NC	260993_at	A11g12140	flavin-containing monooxygenase family protein / FMO family protein similar to flavin-containing monooxygenase [Cavia porcellus] Gi:191259; contains Pfam profile PF00743: Flavin-binding monooxygenase-like (88414.m01406)
1452	Not regulated	NC-NC-NC	260968_at	A11g12250	thylakoid lumenal protein-related weak similarity to SPIQ22160 Thylakoid lumenal 15 kDa protein, chloroplast precursor (p15) [Arabidopsis thaliana]; contains Pfam profile PF00805: Pentapeptide repeats (8 copies) (88414.m01417)
1453	Not regulated	NC-NC-NC	260975_at	A11g53430	leucine-rich repeat family protein / protein kinase family protein contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain (88414.m06056)
1454	Not regulated	NC-NC-NC	260979_at	A11g53510	mitogen-activated protein kinase, putative / MAPK, putative (MPK18) mitogen-activated protein kinase (MAPK)(AMPK18), PMID:12119167 (88414.m06068)
1455	Not regulated	NC-NC-NC	260981_at	A11g53460	expressed protein (88414.m06060)
1456	Not regulated	NC-NC-NC	260982_at	A11g53520	chalcone-flavanone isomerase-related low similarity to Gi:499036 (Vitis vinifera) (88414.m06070)
1457	Not regulated	NC-NC-NC	260988_at	A11g53570	mitogen-activated protein kinase kinase kinase (MAPKKK), putative (MAP3Ka) identical to MEK kinase (MAP3Ka)[Arabidopsis thaliana] gi4204912/gbIAAD10948 (88414.m06080)
1458	Not regulated	NC-NC-NC	260964_at	A11g45050	ubiquitin-conjugating enzyme 15 (UBC15) E2; identical to ubiquitin-conjugating enzyme 15 Gi:2801442 from [Arabidopsis thaliana] (88414.m05165)
1459	Not regulated	NC-NC-NC	260938_at	A11g45170	expressed protein contains similarity to vacuolating cytotoxin (vacA) Gi:8634155 from [Helicobacter pylori] (88414.m05170)
1460	Not regulated	NC-NC-NC	260940_at	A11g45000	26S proteasome regulatory complex subunit p42D, putative similar to 26S proteasome regulatory complex subunit p42D [Drosophila melanogaster] gi8434958/gbIAAF08391 (88414.m05158)
1461	Not regulated	NC-NC-NC	260944_at	A11g45130	beta-galactosidase, putative / lactase, putative similar to beta-galactosidase [Lycopersicon esculentum] Gi:7939619, beta-galactosidase BG1 Gi:15081596 from [Vitis vinifera]; contains Pfam profile PF01301: Glycosyl hydrolases family 35 (88414.m05173)
1462	Not regulated	NC-NC-NC	260946_at	A11g06010	expressed protein (88414.m00629)
1463	Not regulated	NC-NC-NC	260949_at	A11g08110	F-box family protein contains similarity to F-box protein FBX3 Gi:6103843 from [Homo sapiens]; similar to SKP1 interacting partner 2 (SKP2) TIGR_Ah1A15g67250 (88414.m00640)
1464	Not regulated	NC-NC-NC	260953_at	A11g06070	bZIP transcription factor, putative (bZIP69) similar to transcriptional activator RF2a GB:AF005482 Gi:2253277 from [Oryza sativa]; contains Pfam profile PF00170: bZIP transcription factor (88414.m00636)
1465	Not regulated	NC-NC-NC	260956_at	A11g06040	zinc finger (B-box type) family protein / salt-tolerance protein (STO) identical to SPIQ98288 Salt-tolerance protein [Arabidopsis thaliana]; contains Pfam profile PF00843: B-box zinc finger (88414.m00632)
1466	Not regulated	NC-NC-NC	260958_at	A11g06060	RanBP-related similar to RANBP4 (Gi:13194576)[Homo sapiens] (88414.m00635)
1467	Not regulated	NC-NC-NC	260959_at	A11g06050	expressed protein (88414.m00634)
1468	Not regulated	NC-NC-NC	260927_at	A11g05940	amino acid permease family protein low similarity to SPIP30823 High-affinity cationic amino acid transporter-1 (CAT-1) (Rattus norvegicus); contains Pfam profile PF00324: Amino acid permease (88414.m00623)
1469	Not regulated	NC-NC-NC	260912_at	A11g07560	ATP-dependent Clp protease proteolytic subunit (ClpP1) identical to nClpP1 GB:BAAB2065 Gi:5360579 from [Arabidopsis thaliana]; contains Pfam profile PF00574: Clp protease, contains TIGRfam profile TIGR00493: ATP-dependent Clp protease, proteolytic subunit ClpP (88414.m00207)
1470	Not regulated	NC-NC-NC	260914_at	A11g02640	glycosyl hydrolase family 3 protein similar to beta-xylosidase GB:Z84377 Gi:2102655 from [Aspergillus niger] (88414.m00214)
1471	Not regulated	NC-NC-NC	260915_at	A11g02660	lipase class 3 family protein contains Pfam profile PF01764: Lipase (88414.m00216)
1472	Not regulated	NC-NC-NC	260916_at	A11g02475	expressed protein (88414.m00198)
1473	Not regulated	NC-NC-NC	260919_at	A11g21520	expressed protein (88414.m02691)
1474	Not regulated	NC-NC-NC	260923_at	A11g21570	zinc finger (CCHH-type) family protein contains Pfam domain, PF00842: Zinc finger C-x-C-x-C-x3-H type (and similar) (88414.m02697)
1475	Not regulated	NC-NC-NC	260924_at	A11g21590	protein kinase family protein contains Pfam domain, PF00069: Protein kinase domain (88414.m02699)
1476	Not regulated	NC-NC-NC	260899_at	A11g21370	expressed protein (88414.m02673)
1477	Not regulated	NC-NC-NC	260902_at	A11g21440	mutase family protein similar to carboxyvinyl-carboxyphosphonate phosphorylmutase GB:O49290 from [Arabidopsis thaliana]; similar to carboxyphosphoenolpyruvate mutase (Gi:47148) [Streptomyces hygroscopicus]; contains Prosite PS00161: Isocitrate lyase signature (88414.m02681)
1478	Not regulated	NC-NC-NC	260872_at	A11g21350	expressed protein (88414.m02669)
1479	Not regulated	NC-NC-NC	260877_at	A11g21500	expressed protein (88414.m02689)
1480	Not regulated	NC-NC-NC	260878_at	A11g21450	scarecrow-like transcription factor 1 (SCL1) identical to scarecrow-like 1 GB:AAF21043 Gi:6644390 from [Arabidopsis thaliana] (88414.m02682)
1481	Not regulated	NC-NC-NC	260889_at	A11g29130	transcriptional regulator family protein similar to Transcriptional regulator protein HCNPG (Swiss-Prot:Q02614) [Mus musculus] (88414.m03574)
1482	Not regulated	NC-NC-NC	260894_at	A11g29220	ER lumen protein retaining receptor (ERD2) / HDEL receptor identical to SP:P43502 ER lumen protein retaining receptor (HDEL receptor) [Arabidopsis thaliana] (88414.m03585)
1483	Not regulated	NC-NC-NC	260897_at	A11g29330	

1484	Not regulated	NC-NC-NC	260898_at	ribosomal protein L34 family protein similar to plastid ribosomal protein L34 precursor GB:AAF64157.GI:7578860 from [Spinacia oleracea] (68414.m03558)
1485	Not regulated	NC-NC-NC	260871_at	expressed protein (68414.m03554)
1486	Not regulated	NC-NC-NC	260840_at	expressed protein similar to hypothetical protein GB:AA887625.GI:2342727 from [Arabidopsis thaliana] (68414.m03556)
1487	Not regulated	NC-NC-NC	260842_at	26S proteasome regulatory subunit, putative (RPN6) similar to 19S proteasome subunit 9 GB:AAAC34120.GI:3450888 from [Arabidopsis thaliana] (68414.m03567)
1488	Not regulated	NC-NC-NC	260843_at	expressed protein (68414.m03557)
1489	Not regulated	NC-NC-NC	260844_at	peroxisomal targeting signal type 2 receptor (PEX7) identical to peroxisomal targeting signal type 2 receptor (Pex7p) (GI:9502414) [Arabidopsis thaliana]; WD-40 repeat protein family member, contains 6 WD-40 repeats (PF00400); similar to peroxisomal targeting signal 2 receptor (PTS2R) (Peroxin-7) (PEX7) (SP:O06828) [Homo sapiens] (68414.m03578)
1490	Not regulated	NC-NC-NC	260855_at	MORN (Membrane Occupation and Recognition Nexus) repeat-containing protein / phosphatidylinositol-4-phosphate 5-kinase-related similar to phosphatidylinositol-4-phosphate 5-kinase AIP1P5K1 [Arabidopsis thaliana] GI:3702691; contains Pfam profile PF02483; MORN repeat (68414.m02743)
1491	Not regulated	NC-NC-NC	260856_at	AP2 domain-containing transcription factor family protein similar to TINY GB:CAA64359.GI:1246403 from [Arabidopsis thaliana] (68414.m02742)
1492	Not regulated	NC-NC-NC	260868_at	expressed protein (68414.m05053)
1493	Not regulated	NC-NC-NC	260813_at	Vire2-interacting protein (VIP1) identical to Vire2-interacting protein VIP1 GB:AAAF37279.GI:7258340 from [Arabidopsis thaliana] (68414.m05020)
1494	Not regulated	NC-NC-NC	260814_at	serine decarboxylase identical to serine decarboxylase [Arabidopsis thaliana] GI:15011302; contains Pfam profile PF00282; Pyridoxal-dependent decarboxylase conserved domain (68414.m05021)
1495	Not regulated	NC-NC-NC	260817_at	peptidase M16 family protein / insulinase family protein contains Pfam domain, PF05183; Peptidase M16 inactive domain; similar to insulin-degrading enzyme (Insulysin, Insulinase, Insulin protease) [Mouse] SWISS-PROT:O8JHR7 (68414.m00733)
1496	Not regulated	NC-NC-NC	260818_at	transporter-related low similarity to SP:Q8NTN3 UDP-glucuronidase/UDP-N-acetylglucosamine transporter (Homo sapiens), SP:Q85Y15 UDP-sugar transporter UST74c (Drosophila melanogaster), SP:Q18778 UDP-sugar transporter sqv-7 (Caenorhabditis elegans); contains 8 predicted transmembrane domains (68414.m00732)
1497	Not regulated	NC-NC-NC	260822_at	RNA polymerase Rpb7 N-terminal domain-containing protein similar to SP:IP35718 DNA-directed RNA polymerase III 25 kDa polypeptide (EC 2.7.7.6) [Saccharomyces cerevisiae]; contains Pfam profile PF03876; RNA polymerase Rpb7, N-terminal domain (68414.m00722)
1498	Not regulated	NC-NC-NC	260832_at	glycosyl transferase family 8 protein contains Pfam profile: PF01501 glycosyl transferase family 8 (68414.m00721)
1499	Not regulated	NC-NC-NC	260835_at	serine/threonine protein kinase, putative similar to Pto kinase interact 1 (Pti1)[Lycopodium obscurum]
1500	Not regulated	NC-NC-NC	260780_at	glycyl-RNA synthetase / valine-RNA ligase (VALRS) nearly identical to SP:IP93736 Valyl-RNA synthetase (EC 6.1.1.9) (Valine-IRNA ligase) (ValRS) (Arabidopsis thaliana) (68414.m01737)
1501	Not regulated	NC-NC-NC	260781_at	expressed protein (68414.m01738)
1502	Not regulated	NC-NC-NC	260782_at	UBX domain-containing protein contains Pfam profiles PF00788; UBX domain, PF02808; Ubiquitin interaction motif (68414.m01732)
1503	Not regulated	NC-NC-NC	260784_at	myb family transcription factor identical to GB:CAA90748.GI:1263093 from [Arabidopsis thaliana]; contains PFAM profile:PF00249 (68414.m00650)
1504	Not regulated	NC-NC-NC	260785_at	expressed protein (68414.m00652)
1505	Not regulated	NC-NC-NC	260793_at	expressed protein (68414.m00651)
1506	Not regulated	NC-NC-NC	260794_at	VHS domain-containing protein / GAT domain-containing protein weak similarity to SP:Q8UJY5 ADP-ribosylation factor binding protein GGA1 [Homo sapiens]; contains Pfam profiles PF00780; VHS domain, PF03127; GAT domain (68414.m00653)
1507	Not regulated	NC-NC-NC	260803_at	glutathione S-transferase, putative similar to glutathione transferase GI:2853219 from [Carica papaya] (68414.m09129)
1508	Not regulated	NC-NC-NC	260807_at	VQ motif-containing protein contains PF05678; VQ motif (68414.m09128)
1509	Not regulated	NC-NC-NC	260775_at	14-3-3 protein GF14 omega (GRF2) identical to GF14omega isoform GI:487781 from [Arabidopsis thaliana] (68414.m09125)
1510	Not regulated	NC-NC-NC	260747_at	expressed protein (68414.m09138)
1511	Not regulated	NC-NC-NC	260751_at	stomatal cytokinesis defective / SCD1 protein (SCD1) contains Pfam PF02141; DENN (AEX-3) domain; contains Pfam PF00400; WD domain, G-beta repeat (8 copies); identical to stomatal cytokinesis defective [Arabidopsis thaliana] GI:19743728; supporting cDNA, gi19743727 gb AY062605.1; PMID 12874123 (68414.m05498)
1512	Not regulated	NC-NC-NC	260756_at	eukaryotic translation initiation factor 2B family protein / eIF-2B family protein similar to guanine nucleotide exchange factor, eIF-2B, delta subunit [Mus musculus] GI:529428; contains Pfam profile PF01008; Initiation factor 2 subunit family (68414.m05489)
1513	Not regulated	NC-NC-NC	260766_at	universal stress protein (USP) family protein contains Pfam PF00582; universal stress protein family; similar to hypothetical protein GI:7770340 from [Arabidopsis thaliana] (68414.m05487)
1514	Not regulated	NC-NC-NC	260787_s_at	NADH-ubiquinone oxidoreductase-related similar to NADH-ubiquinone oxidoreductase 12 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-12KD) (CI-12KD) [Swiss-Prot:Q03015] [Neurospora crassa] (68414.m05509)
1515	Not regulated	NC-NC-NC	260769_at	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain (68414.m05485)
1516	Not regulated	NC-NC-NC	260772_at	aspartyl protease family protein contains Pfam PF00026; Eukaryotic aspartyl protease, contains similarity to nucellin GI:2280203 from [Hordeum vulgare] (68414.m05500)
1517	Not regulated	NC-NC-NC	260714_at	10 kDa chaperonin (CPN10) identical to SP:P34893 from [Arabidopsis thaliana] (68414.m01790)
1518	Not regulated	NC-NC-NC	260718_at	expressed protein contains Pfam profile PF04146; Y1521-B-like family (68414.m05369)

5119	Not regulated	NC-NC-NC	A11g48140	dihydroipoamide dehydrogenase 1, mitochondrial / lipamide dehydrogenase 1 (MTLPD1) identical to GB-AAF34795 sapiens (68414.m05372)
520	Not regulated	NC-NC-NC	A11g48030	[gi:12704698] from [Arabidopsis thaliana] (68414.m05350)
521	Not regulated	NC-NC-NC	A11g17580	myosin, putative similar to myosin GI:433663 from [Arabidopsis thaliana] (68414.m02185)
522	Not regulated	NC-NC-NC	A11g17510	expressed protein (68414.m02151)
523	Not regulated	NC-NC-NC	A11g32520	expressed protein (68414.m04013)
524	Not regulated	NC-NC-NC	A11g32260	expressed protein identical to hypothetical protein GB-AAF81322 GI:8920600 from [Arabidopsis thaliana] (68414.m03969)
525	Not regulated	NC-NC-NC	A11g32470	glycine cleavage system H protein, mitochondrial, putative similar to SPIP25855 Glycine cleavage system H protein 1, mitochondrial precursor [Arabidopsis thaliana], contains Pfam profile PF01697: Glycine cleavage H-protein (68414.m04007)
526	Not regulated	NC-NC-NC	A11g32400	senescence-associated family protein contains Pfam profile PF00335: Tetraspanin family (68414.m03987)
527	Not regulated	NC-NC-NC	A11g32410	vacuolar protein sorting 55 family protein / VP555 family protein contains Pfam domain PF04133: Vacuolar protein sorting 55 (68414.m03989)
528	Not regulated	NC-NC-NC	A11g32500	ATP-binding-cassette transporter, putative similar to ATP-binding-cassette transporter (ABC1) described in PMID:11156608 (68414.m04010)
529	Not regulated	NC-NC-NC	A11g32360	zinc finger (CCHC-type) family protein contains Pfam domain, PF00842: Zinc finger C-x8-C-x5-C-x3-H type (and similar) (68414.m03988)
530	Not regulated	NC-NC-NC	A11g32440	pyruvate kinase, putative similar to pyruvate kinase isozyme G, chloroplast precursor [Nicotiana tabacum] SWISS-PROT:Q40546 (68414.m04004)
531	Not regulated	NC-NC-NC	A11g19380	expressed protein (68414.m02409)
532	Not regulated	NC-NC-NC	A11g19440	very-long-chain fatty acid condensing enzyme, putative similar to GB-AAD37122 from [Arabidopsis thaliana] (68414.m02422)
533	Not regulated	NC-NC-NC	A11g19310	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (68414.m02401)
534	Not regulated	NC-NC-NC	A11g19450	integral membrane protein, putative / sugar transporter family protein similar to GB:UA3928 GI:1209756 integral membrane protein from [Beta vulgaris], contains Pfam profile PF00083: major facilitator superfamily protein; contains TIGRfam TIGR00878: Sugar transporter (68414.m02423)
535	Not regulated	NC-NC-NC	A11g08110	lactoylglutathione lyase, putative / glyoxalase I, putative similar to lactoylglutathione lyase SP:O04885 from [Brassica juncea] (68414.m00888)
536	Not regulated	NC-NC-NC	A11g08040	expressed protein contains Pfam profile PF05212: Protein of unknown function (DUF707) (68414.m00878)
537	Not regulated	NC-NC-NC	A11g62420	expressed protein contains Pfam profile PF04720: Protein of unknown function (DUF506) (68414.m07042)
538	Not regulated	NC-NC-NC	A11g62390	octoapeptide/Phox/Bem1p (PB1) domain-containing protein / tetraoctapeptide repeat (TPR)-containing protein contains Pfam profiles PF00564: PB1 domain, PF00515: TPR Domain (68414.m07038)
539	Not regulated	NC-NC-NC	A11g53290	galactosyltransferase family protein contains Pfam profile: PF01762: galactosyltransferase, contains similarity to Avr9 elicitor response protein GI:4138265 from [Nicotiana tabacum] (68414.m060040)
540	Not regulated	NC-NC-NC	A11g53280	DJ-1 family protein similar to DJ-1 protein [Homo sapiens] GI:1780755; similar to DJ-1 beta (GI:18642508) [Drosophila melanogaster], contains Pfam profile: PF01965 ThiUPiP1 family: TIGRFAM TIGR01383: DJ-1 family protein (68414.m06038)
541	Not regulated	NC-NC-NC	A11g53310	sodium/calcium exchanger family protein / calcium-binding EF hand family protein contains Pfam profiles: PF01699 sodium/calcium exchanger protein, PF00036 EF hand (68414.m06031)
542	Not regulated	NC-NC-NC	A11g53320	F-box family protein / tubby family protein (TULP7) similar to Tubby related protein 2 (Tubby-like protein 2) (P4-6 protein) (Fragment) (SP:P46698) [Mus musculus]; similar to phosphodiesterase (GI:467578) [Mus musculus]; similar to Tubby protein homolog 1 (Swiss-Prot:Q09306) [Caenorhabditis elegans] contains Pfam profile: PF01187: Tub family, contains Pfam PF00848: F-box domain (68414.m06043)
543	Not regulated	NC-NC-NC	A11g55890	penicillipeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat (68414.m06410)
544	Not regulated	NC-NC-NC	A11g55860	expressed protein weak similarity to SPIP53808 Phosphatidylcholine transfer protein (PC-TP) [Mus musculus] (68414.m06418)
545	Not regulated	NC-NC-NC	A11g55840	SEC14 cytosolic factor (SEC14) / phosphoglyceride transfer protein similar to polyphosphoinositide binding protein SEC14 homolog Sh1p (GB:AA894598) [Glycine max]; identified in Eur J Biochem 1988 Dec 1;254(2):402-10 as AISEC14, characterized by functional complementation in S. cerevisiae, (68414.m06404)
546	Not regulated	NC-NC-NC	A12g43780	expressed protein (68415.m05442)
547	Not regulated	NC-NC-NC	A12g43770	transducin family protein / WD-40 repeats (repeat family protein contains 7 WD-40 repeats (PF00400); similar to U5 snRNP-specific 40 Lda protein (GI:3820594) [Homo sapiens] (68415.m05441)
548	Not regulated	NC-NC-NC	A12g43630	expressed protein (68415.m05423)
549	Not regulated	NC-NC-NC	A12g43850	ankyrin protein kinase, putative (APK1) similar to ankyrin-kinase [Medicago truncatula] gi 18700701 gb AA178674; contains Pfam profile PF00089: Protein kinase domain, contains Pfam profile PF00023: Ankyrin repeat (68415.m05451)
550	Not regulated	NC-NC-NC	A12g43750	cysteine synthase, chloroplast / O-acetylserine (thiol)-lyase / O-acetylserine sulfhydrylase / cysACS1 (OASB) identical to SPIP47899 (Arabidopsis thaliana); identical to cDNA O-acetylserine lyase (AI:OAS.7-4) GI:69833575 (68415.m05439)
551	Not regulated	NC-NC-NC	A12g43780	mitogen-activated protein kinase, putative / MAPK, putative (MAPK) identical to mitogen-activated protein kinase homolog 8 (AIMPX8) [Arabidopsis thaliana] SWISS-PROT:Q39026; PMID:12119167 (68415.m05443)
552	Not regulated	NC-NC-NC	A12g43760	molybdopterin biosynthesis MoaE family protein contains Pfam profile: PF02391 molybdopterin converting factor, subunit 2 (68415.m05440)

1553	Not regulated	NC-NC-NC	280578_at	A2g47350	PAPA-1-like family protein / zinc finger (HIT type) family protein contains Pfam domains, PF04795: PAPA-1-like conserved region and PF04438: HIT zinc finger (88415.m05910)
1554	Not regulated	NC-NC-NC	280579_at	A2g47380	cytochrome c oxidase subunit Vc family protein / COX5C family protein contains Pfam profile: PF05789 cytochrome c oxidase subunit Vc (COX5C) (88415.m05914)
1555	Not regulated	NC-NC-NC	280525_at	A2g47250	RNA helicase, putative similar to SPIP53131 Pre-mRNA splicing factor RNA helicase PRP43 (Helicase JA1) (Saccharomyces cerevisiae); contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain (88415.m05900)
1556	Not regulated	NC-NC-NC	280529_at	A2g47400	CP12 domain-containing protein contains Pfam profile: PF02872 CP12 domain (88415.m05918)
1557	Not regulated	NC-NC-NC	280532_at	A2g47330	DEAD/DEAH box helicase, putative similar to RNA helicase [Rattus norvegicus] GI:897915; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain (88415.m05908)
1558	Not regulated	NC-NC-NC	280538_at	A2g43460	60S ribosomal protein L38 (RPL38A) (88415.m05401)
1559	Not regulated	NC-NC-NC	280542_at	A2g43560	immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein identical to Probable FKBP-type peptidyl-prolyl cis-trans isomerase 2, chloroplast precursor (Piase) (Rotamase) (SP:022870)[Arabidopsis thaliana]; contains Pfam PF00254: peptidyl-prolyl cis-trans isomerase, FKBP-type (88415.m05412)
1560	Not regulated	NC-NC-NC	280543_at	A2g43330	sugar transporter family protein similar to SPIQ96QE2 Proton myo-inositol co-transporter (Hmit) [Homo sapiens], SPIQ01440 Membrane transporter D1 (Leishmania donovani); contains Pfam profile PF00083: major facilitator superfamily protein (88415.m05388)
1561	Not regulated	NC-NC-NC	280544_at	A2g43350	expressed protein (88415.m05410)
1562	Not regulated	NC-NC-NC	280545_at	A2g43320	glutathione peroxidase, putative (88415.m05380)
1563	Not regulated	NC-NC-NC	280546_at	A2g43550	trypsin inhibitor, putative similar to SPIP26780 Trypsin inhibitor 2 precursor (MTI-2) (Sinapis alba) (88415.m05407)
1564	Not regulated	NC-NC-NC	280547_at	A2g43380	trypsin inhibitor, putative similar to SPIP26780 Trypsin inhibitor 2 precursor (MTI-2) (Sinapis alba) (88415.m05411)
1565	Not regulated	NC-NC-NC	280548_at	A2g43535	biotin synthase (BioB) (BioD) identical to SPIP54987 Pfam profile PF04055: radical SAM domain protein (88415.m05391)
1566	Not regulated	NC-NC-NC	280549_at	A2g43335	trypsin inhibitor, putative similar to SPIP26780 Trypsin inhibitor 2 precursor (MTI-2) (Sinapis alba) (88415.m05409)
1567	Not regulated	NC-NC-NC	280550_at	A2g43420	3-beta hydroxysteroid dehydrogenase/isomerase family protein contains Pfam profile PF01073 3-beta hydroxysteroid dehydrogenase/isomerase domain; similar to NAD(P)-dependent steroid dehydrogenase from Homo sapiens [SPIQ15738], Mus musculus [SPIQ9R1J0] (88415.m05396)
1568	Not regulated	NC-NC-NC	280552_at	A2g43430	hydroxyacylglutathione hydrolase, mitochondrial / glyoxalase II (GLX2-1) identical to SPIQ24485 Hydroxyacylglutathione hydrolase, mitochondrial precursor (EC 3.1.2.6) (Glyoxalase II) (88415.m05397)
1569	Not regulated	NC-NC-NC	280553_at	A2g41800	expressed protein contains Pfam profile PF04862: Protein of unknown function, DUF842 (88415.m05166)
1570	Not regulated	NC-NC-NC	280554_at	A2g41790	peptidase M16 family protein / insulinase family protein contains Pfam domain, PF05193: Peptidase M16 inactive domain; similar to insulin-degrading enzyme (insulinasin, insulin protease) [Muscle] SWISS-PROT:Q8JHR7 (88415.m05165)
1571	Not regulated	NC-NC-NC	280523_at	A2g41720	penetratocopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat (88415.m05156)
1572	Not regulated	NC-NC-NC	280497_at	A2g41840	40S ribosomal protein S2 (RPS2C) (88415.m05171)
1573	Not regulated	NC-NC-NC	280498_at	A2g41710	ovule development protein, putative similar to ovule development protein AINTEGUMENTA (GI:1209099) [Arabidopsis thaliana]; Pfam domain (PF00847) (88415.m05154)
1574	Not regulated	NC-NC-NC	280499_at	A2g41760	expressed protein (88415.m05162)
1575	Not regulated	NC-NC-NC	280502_at	A11g47270	F-box family protein / lubby family protein contains Pfam profiles: PF00846 F-box domain, PF01167 Tub family; similar to Chain A, C-Terminal Domain Of Mouse Brain Tubby Protein Lengp(GI:6730158) [Mus musculus]; similar to phosphodiesterase (GI:467578) [Mus musculus]; similar to Tubby protein homolog (Swiss-Prot:Q88808) [Rattus norvegicus] (88414.m05233)
1576	Not regulated	NC-NC-NC	280503_at	A11g47250	20S proteasome alpha subunit F2 (PAF2) (PRC2B) (PRS1) identical to GB:AA32063 from [Arabidopsis thaliana] (Genetics 149 (2), 677-692 (1998)); identical to cDNA proteasome subunit prc2b GI:2511565 (88414.m05231)
1577	Not regulated	NC-NC-NC	280507_at	A11g47200	MFP1 attachment factor, putative contains similarity to MFP1 attachment factor 1 GI:7546725 from [Lycopersicon esculentum] similar to MFP1 attachment factor 1 [Glycine max] pI7546729/pI7546725 (88414.m05223)
1578	Not regulated	NC-NC-NC	280508_at	A11g47260	bacterial transferase hexapeptide repeat-containing protein contains Pfam profile PF00132: Bacterial transferase hexapeptide (four repeats) (88414.m05232)
1579	Not regulated	NC-NC-NC	280509_at	A11g47240	NRAMP metal ion transporter 2, putative (NRAMP2) similar to metal transporter Nramp3 [Arabidopsis thaliana]
1580	Not regulated	NC-NC-NC	280511_at	A11g51570	gi1648012/pI7AAAF13278: member of the natural resistance-associated macrophage protein (NRAMP) metal transporter family, PMID:11500563 (88414.m05230)
1581	Not regulated	NC-NC-NC	280517_at	A11g51420	C2 domain-containing protein contains INTERPRO:IPRO000008 C2 domain (88414.m05804)
1582	Not regulated	NC-NC-NC	280518_at	A11g51540	sucrose-phosphatase, putative similar to sucrose-phosphatase (SPP1) [Arabidopsis thaliana] GI:11127757; contains Pfam profile PF05116: Sucrose-6P-phosphate phosphohydrolase (88414.m05788)
1583	Not regulated	NC-NC-NC	280465_at	A11g10910	kelch repeat-containing protein contains Pfam profile PF01344: Kelch motif (88414.m05801)
1584	Not regulated	NC-NC-NC	280486_at	A11g10900	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat (88414.m01253)
1585	Not regulated	NC-NC-NC	280476_at	A11g11060	phosphatidylinositol-4-phosphate 5-kinase family protein similar to phosphatidylinositol-4-phosphate 5-kinase AtPIP5K1 [Arabidopsis thaliana] GI:3702691; contains Pfam profiles PF01504: Phosphatidylinositol-4-phosphate 5-Kinase, PF02493: MORN repeat (88414.m01252)
1586	Not regulated	NC-NC-NC	280482_at	A11g10950	expressed protein (88414.m01267)
1587	Not regulated	NC-NC-NC	280442_at	A11g68220	endomembrane protein 70, putative (88414.m01257)
1588	Not regulated	NC-NC-NC	280443_at	A11g68185	expressed protein (88414.m07793)
1589	Not regulated	NC-NC-NC	280444_at	A11g68300	ubiquitin-related similar to ubiquitin-like protein sm3/pmt3 SP:O13351 from [Fission yeast] (88414.m07789)
1590	Not regulated	NC-NC-NC	280426_at	A11g72370	universal stress protein (USP) family protein similar to ER6 protein [Lycopersicon esculentum] GI:5669654; contains Pfam profile PF00582: universal stress protein family (88414.m07802)
					40S ribosomal protein SA (RPSa) identical to laminin receptor-like protein GB:U01955 [Arabidopsis thaliana]; identical to cDNA laminin receptor homologue GI:16378 (88414.m08371)

1591	Not regulated	NC-NC-NC	260428_at	A11g72340	eukaryotic translation initiation factor 2B family protein / eIF-2B family protein similar to SPIQ64270 Translation initiation factor eIF-2B alpha subunit (Rattus norvegicus); contains Pfam profile PF01008: initiation factor 2 subunit family (88414.m08366)
1592	Not regulated	NC-NC-NC	260403_at	A11g69810	WRKY family transcription factor (88414.m08032)
1593	Not regulated	NC-NC-NC	260409_at	A11g69835	expressed protein (88414.m08048)
1594	Not regulated	NC-NC-NC	260413_at	A11g69800	CBS domain-containing protein low similarity to SPIQUG19 5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain) (AMPK gamma3) (Homo sapiens); contains Pfam profile PF00571: CBS domain (88414.m08031)
1595	Not regulated	NC-NC-NC	260418_s_at	A11g69750	cox19 family protein contains Pfam profile PF05490: Cox19 protein (88414.m08026)
1596	Not regulated	NC-NC-NC	260419_at	A11g69730	protein kinase family protein contains Pfam profile: PF00069 Eukaryotic protein kinase domain (88414.m08024)
1597	Not regulated	NC-NC-NC	260421_at	A11g69640	acid phosphatase, putative similar to Gi:5360721 from [Lusinus albus] (88414.m08012)
1598	Not regulated	NC-NC-NC	260395_at	A11g69780	homodimer-leucine zipper protein 13 (HB-13) / HD-ZIP transcription factor 13 identical to homeobox gene 13 protein (GP:12325190) [Arabidopsis thaliana] (88414.m08029)
1599	Not regulated	NC-NC-NC	260398_at	A11g69700	ABA-responsive protein (HVA22C) identical to AHVA22c [Arabidopsis thaliana] Gi:4884938 (88414.m08021)
1600	Not regulated	NC-NC-NC	260399_at	A11g69820	60S ribosomal protein L34 (RPL34B) similar to SP:Q42351 from [Arabidopsis thaliana] (88414.m08008)
1601	Not regulated	NC-NC-NC	260370_at	A11g69740	porphobilinogen synthase, putative / delta-aminolevulinic acid dehydratase, putative similar to delta-aminolevulinic acid dehydratase (Alad) Gi:493019 [SP:IP43210] from Glycine max, SP:IP24493 from Spinacia oleracea, SP:IP20124 from Pisum sativum (88414.m08025)
1602	Not regulated	NC-NC-NC	260371_at	A11g69690	TCP family transcription factor, putative similar to PCF1 (Gi:2580438) and PCF2 [Gi:2580440] Oryza sativa] (88414.m08020)
1603	Not regulated	NC-NC-NC	260374_at	A11g73960	expressed protein similar to TATA binding protein associated factor (Gi:2827282) [Homo sapiens], similar to Transcription initiation factor TFIIID 150 kDa subunit (TAFII150) (TAFII150) [Swiss-Prot:Q24325] [Drosophila melanogaster] (88414.m08565)
1604	Not regulated	NC-NC-NC	260379_at	A11g73880	UDP-glucuronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201: UDP-glucuronosyl and UDP-glucosyl transferase (88414.m08556)
1605	Not regulated	NC-NC-NC	260383_s_at	A11g74060	60S ribosomal protein L8 (RPL8B) similar to 60S ribosomal protein L8 (YL 18 like) GB:CA857309 from [Cyanophora paradoxa]
1606	Not regulated	NC-NC-NC	260390_at	A11g73940	expressed protein (88414.m08578)
1607	Not regulated	NC-NC-NC	260391_at	A11g74020	stricoidine synthase family protein similar to stricoidine synthase [Rauvolfia serpentina][SP:IP15324]; contains stricoidine synthase domain PF03088 (88414.m08572)
1608	Not regulated	NC-NC-NC	260393_at	A11g73920	lipase family protein similar to lipase GB:CAA74737 [SPIO46108] from [Drosophila melanogaster] (88414.m08560)
1609	Not regulated	NC-NC-NC	260396_at	A11g73990	peptidase U7 family protein similar to protease IV GB:AAA57008 from [Escherichia coli]; contains Pfam profile PF01343: Peptidase family U7 (88414.m08569)
1610	Not regulated	NC-NC-NC	260398_at	A11g69250	nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein contains Pfam profiles PF02138: Nuclear transport factor 2 (NTF2) domain, PF00076: RNA recognition motif (a.k.a. RRM, RBD, or RNP domain) (88414.m07935) serine/threonine protein kinase, putative identical to serine/threonine kinase [Arabidopsis thaliana] [gi2352084]gb AA888776 (88414.m07925)
1611	Not regulated	NC-NC-NC	260339_at	A11g69220	leucine-rich repeat family protein / protein kinase family protein contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain (88414.m07941)
1612	Not regulated	NC-NC-NC	260345_at	A11g69270	eukaryotic translation initiation factor 5A, putative / eIF-5A, putative strong similarity to eukaryotic initiation factor 5A (2) (Nicotiana glauca) [gi19702, SP:GBAXQ8] Eukaryotic translation initiation factor 5A-1 (eIF-5A 1) [Lycopersicon esculentum] (88414.m07872)
1613	Not regulated	NC-NC-NC	260350_at	A11g69410	beta-1,3-glucanase-related low similarity to elicitor inducible beta-1,3-glucanase NIEG-E76 [Nicotiana tabacum] Gi:11071874 (88414.m07847)
1614	Not regulated	NC-NC-NC	260352_at	A11g69295	chloroplast division protein, putative (MinE1) identical to chloroplast division protein homolog MinE1 Gi:17511220 from [Arabidopsis thaliana] (88414.m07866)
1615	Not regulated	NC-NC-NC	260356_at	A11g69390	appr-1-p processing enzyme family protein contains Pfam domain PF01661: Appr-1-p processing enzyme family (88414.m07856) chorismate mutase, putative similar to gi:5732018 and SP:IP42736; contains Pfam profile: PF01817: Chorismate mutase (88414.m07962)
1616	Not regulated	NC-NC-NC	260358_at	A11g69340	protein kinase family protein contains Pfam domain: PF00069: Protein kinase domain (88414.m08117)
1617	Not regulated	NC-NC-NC	260360_at	A11g69370	protein kinase family protein contains Pfam domain: PF00069: Protein kinase domain (88414.m08118)
1618	Not regulated	NC-NC-NC	260362_at	A11g70530	expressed protein contains Pfam profile PF02713: Domain of unknown function DUF220 (88414.m08109)
1619	Not regulated	NC-NC-NC	260303_at	A11g70520	ADP-ribosylation factor, putative nearly identical to ADP-ribosylation factor 1 GB:P36397 [Arabidopsis thaliana]; ADP-ribosylation factor Gi:1665588 [Arabidopsis thaliana] (88414.m08110)
1620	Not regulated	NC-NC-NC	260304_at	A11g70460	ABC transporter (TAP1) contains Pfam profile: PF00005 ABC transporters; similar to TAP1 protein (transporter of processed antigen) GB:AA05033 [Chromomycium mylium]; identical to cDNA transporter associated with antigen processing-like protein (TAP1) Gi:19335721 (88414.m08135)
1621	Not regulated	NC-NC-NC	260305_at	A11g70610	glutamate:glyoxylate aminotransferase 2 (GGT2) identical to glutamate:glyoxylate aminotransferase 2 [Arabidopsis thaliana] Gi:24461829; similar to alanine aminotransferase from Penicillium melleum [SP:IP34106]; Gi:4730884 from Oryza sativa; contains Pfam profile PF00155: aminotransferase, classes I and II (88414.m08127)
1622	Not regulated	NC-NC-NC	260308_at	A11g70580	F-box family protein contains Pfam PF00646: F-box domain; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1A5g67250 (88414.m08131)
1623	Not regulated	NC-NC-NC	260309_at	A11g70590	proline-rich family protein contains proline-rich extensin domains, INTERPRO:IPR002965; contains 1 predicted transmembrane domain (88414.m07223)
1624	Not regulated	NC-NC-NC	260310_at	A11g70590	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (88414.m07235)
1625	Not regulated	NC-NC-NC	260314_at	A11g63830	
1626	Not regulated	NC-NC-NC	260321_at	A11g63900	

1627	Not regulated	NC-NC-NC	A11g63780	bix domain-containing protein contains Pfam domain, PF04427; Bix domain (88414.m07218) 2C-methyl-D-erythritol 2,4-cyodiphosphate synthase, putative similar to 2C-methyl-D-erythritol 2,4-cyodiphosphate synthase (88414.m07245)
1628	Not regulated	NC-NC-NC	A11g63970	zinc finger (C3HC4-type RING finger) family protein low similarity to SPQ90972 RING finger protein 13 (Gallus gallus); contains Pfam profile: PF00087 zinc finger, C3HC4 type (RING finger) (88414.m09412)
1629	Not regulated	NC-NC-NC	A11g60400	DNA-binding protein, putative similar to DNA-binding protein (Triticum aestivum) GI:6958202; contains Pfam profile: PF01535 PPR repeat (88414.m09397)
1630	Not regulated	NC-NC-NC	A11g60270	glycerol kinase, putative similar to glycerol kinase (ATP: glycerol 3-phosphotransferase, Glycerokinase, GK)[Mycobacterium tuberculosis] Swiss-Prot: O69684 (88414.m09423)
1631	Not regulated	NC-NC-NC	A11g60460	VO motif-containing protein contains PF05678; VO motif (88414.m09421)
1632	Not regulated	NC-NC-NC	A11g60450	expressed protein similar to Sedlin (Swiss-Prot: O14582) [Homo sapiens]; similar to MBP-1 interacting protein-2A; MIP-2A (GI:9937493) [Homo sapiens] (88414.m09433)
1633	Not regulated	NC-NC-NC	A11g60500	acetylornithine aminotransferase, mitochondrial, putative / acetylornithine transaminase, putative / AOT, putative / ACOAT, putative similar to SPI004866 Acetylornithine aminotransferase, mitochondrial precursor (EC 2.6.1.11) (ACOAT) (Acetylornithine transaminase) (AOT) (Alnus glutinosa); contains Pfam profile PF00202; aminotransferase, class III (88414.m09457)
1634	Not regulated	NC-NC-NC	A11g60600	nodulin family protein similar to nodulin-like protein [Arabidopsis thaliana] GI:3329368, node-specific protein Nt70 [Lotus japonicus] GI:3329366 (88414.m09439)
1635	Not regulated	NC-NC-NC	A11g60530	GMP synthase [glutamine-hydrolyzing], putative / glutamine amidotransferase, putative similar to SPIP38825 GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (Glutamine amidotransferase) (GMP synthase) (Saccharomyces cerevisiae); contains Pfam profile PF00117; glutamine amidotransferase class-I (88414.m07203)
1636	Not regulated	NC-NC-NC	A11g63660	peptidase M1 family protein similar to SPIP04825 Aminopeptidase N (EC 3.4.11.2) (Alpha-aminoacylpeptide hydrolase)
1637	Not regulated	NC-NC-NC	A11g63770	[Escherichia coli]; contains Pfam profile PF01433; Peptidase family M1 (88414.m07216)
1638	Not regulated	NC-NC-NC	A11g63690	protease-associated (PA) domain-containing protein contains protease associated (PA) domain, Pfam: PF02225 (88414.m07207)
1639	Not regulated	NC-NC-NC	A11g74210	glycophosphoryl diester phosphodiesterase family protein low similarity to glycophosphodiester phosphodiesterase [Borrelia hermslii] GI:1398038; contains Pfam profile PF03009; Glycophosphoryl diester phosphodiesterase family (88414.m08585)
1640	Not regulated	NC-NC-NC	A11g74340	dolichol phosphate-mannose biosynthesis regulatory protein-related similar to dolichol phosphate-mannose biosynthesis regulatory protein SP-082324 from [Mus musculus] (88414.m08611)
1641	Not regulated	NC-NC-NC	A11g68530	very-long-chain fatty acid condensing enzyme (CUT1) identical to very-long-chain fatty acid condensing enzyme (CUT1) GB:AF129511 (required for cuticular wax biosynthesis and pollen fertility; Millar A.A., et al. Plant Cell (1998)) (88414.m07828)
1642	Not regulated	NC-NC-NC	A11g74440	expressed protein similar to YGL010w-like protein GB:AA332136 [Picea mariana] (88414.m08624)
1643	Not regulated	NC-NC-NC	A11g74530	expressed protein (88414.m08634)
1644	Not regulated	NC-NC-NC	A11g74370	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (88414.m08618)
1645	Not regulated	NC-NC-NC	A11g74410	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (88414.m08620)
1646	Not regulated	NC-NC-NC	A11g74640	expressed protein contains Pfam profile: PF00561 alpha-beta hydrolase fold (88414.m08644)
1647	Not regulated	NC-NC-NC	A11g74560	nucleosome assembly protein (NAP) family protein similar to SPI001105 SET protein (HLA-DR associated protein II) (PHAPII) (Phosphatase 2A inhibitor 12PP2A) [Homo sapiens]; contains Pfam profile: PF00958 nucleosome assembly protein (NAP) (88414.m08638)
1648	Not regulated	NC-NC-NC	A11g74470	geranylgeranyl reductase identical to geranylgeranyl reductase GB:Y14044 [Arabidopsis thaliana] (involvement: chlorophyll, the tocopherol and the phytylquinone pathways Eur. J Biochem 1998, Jan 15;251(1-2):413-7) (88414.m08627)
1649	Not regulated	NC-NC-NC	A11g74520	ABA-responsive protein (HVA22a) identical to A1HVA22a [Arabidopsis thaliana] GI:4884932 (88414.m08633)
1650	Not regulated	NC-NC-NC	A11g74360	leucine-rich repeat transmembrane protein kinase, putative similar to brassinosteroid insensitive 1 GB:AA49810 (putative receptor protein kinase); contains Pfam profiles: PF00560 Leucine Rich Repeat (17 repeats), PF00069 Eukaryotic protein kinase domain (88414.m08615)
1651	Not regulated	NC-NC-NC	A11g74360	phosphoglucosyltransferase, cytoplasmic, putative / glucose phosphomutase, putative strong similarity to SPIP93804 Phosphoglucosyltransferase, cytoplasmic 1 (EC 5.4.2.2) (Glucose phosphomutase 1) (PGM 1) [Zea mays]; contains InterPro accession IPR006352; Phosphoglucosyltransferase mutase (88414.m08153)
1652	Not regulated	NC-NC-NC	A11g67560	lipoygenase family protein similar to 13-lipoxygenase GB:CAA65269 [Solanum tuberosum], gi:1654140 [Lycopersicon esculentum] (88414.m07897)
1653	Not regulated	NC-NC-NC	A11g52910	expressed protein (88414.m05983)
1654	Not regulated	NC-NC-NC	A11g52880	no apical meristem (NAM) family protein contains Pfam PF02365; No apical meristem (NAM) domain; similar to NAM (no apical meristem) GB:CAA63101 from [Pelutia x hybrida]; identical to cDNA NAC domain protein GI:4325285 (88414.m05979)
1655	Not regulated	NC-NC-NC	A11g52930	bix domain-containing protein contains Pfam domain, PF04427; Bix domain (88414.m05985)
1656	Not regulated	NC-NC-NC	A11g79850	30S ribosomal protein S17, chloroplast / CS17 (RPS17) identical to 30S ribosomal protein S17, chloroplast precursor GB:P16180 [Arabidopsis thaliana] (88414.m09328)
1657	Not regulated	NC-NC-NC	A11g36390	co-chaperone GrpE family protein similar to co-chaperone CCE1 precursor isoform b [Chlamydomonas reinhardtii] GI:15384278; contains Pfam profile PF01025; co-chaperone GrpE (88414.m04520)
1658	Not regulated	NC-NC-NC	A11g36320	expressed protein similar to hypothetical protein GB:CA837532 from [Arabidopsis thaliana], (88414.m04514)
1659	Not regulated	NC-NC-NC	A11g36310	expressed protein (88414.m04513)
1660	Not regulated	NC-NC-NC	A11g66330	senescence-associated family protein similar to senescence-associated protein (GI:12836895) [Ipomoea batatas] (88414.m07532)

1661	Not regulated	NC-NC-NC	260107_at	A11g66430	pKb-type carbohydrate kinase family protein contains Pfam profile: PF00294 pKb family carbohydrate kinase (88414.m07548)
1662	Not regulated	NC-NC-NC	260083_at	A11g63220	C2 domain-containing protein similar to phloem protein RPP19 [Oryza sativa (japonica cultivar-group)] (GI:2198839; contains Pfam profile PF00188; C2 domain (88414.m07146))
1663	Not regulated	NC-NC-NC	260087_at	A11g73200	expressed protein (88414.m08471)
1664	Not regulated	NC-NC-NC	260089_at	A11g73170	expressed protein (88414.m08468)
1665	Not regulated	NC-NC-NC	260094_at	A11g73250	GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase (GER1) identical to GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4 reductase (GER1)GI:6018479 from [Arabidopsis thaliana] (88414.m08477)
1666	Not regulated	NC-NC-NC	260095_at	A11g73230	nucleosome-associated complex (NAC) domain-containing protein similar to SPIP20290 Transcription factor BTf3 (RNA polymerase B transcription factor 3) (Homo sapiens); contains Pfam profile PF01849; NAC domain (88414.m08475)
1667	Not regulated	NC-NC-NC	260099_at	A11g73180	eukaryotic translation initiation factor-related similar to eukaryotic translation initiation factor 2A (GI:21956484) [Homo sapiens]; similar to Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p16) (eIF3 p10) (eIF3b) (Swiss-Prot:P55884) [Homo sapiens] (88414.m08469)
1668	Not regulated	NC-NC-NC	260102_at	A11g35470	SPR1/RYanodine receptor (SPRY) domain-containing protein similar to RanBPM [Homo sapiens] (GI:15080874; contains Pfam profile PF00622; SPRY domain (88414.m04400))
1669	Not regulated	NC-NC-NC	260108_at	A11g35420	dienelectone hydrolase family protein low similarity to dienelectone hydrolase [Rhodococcus opacus] (GI:23094407; contains Pfam profile PF01738; Dienelectone hydrolase family (88414.m04394))
1670	Not regulated	NC-NC-NC	260079_s_at	A11g35460	basic helix-loop-helix (bHLH) family protein similar to GI:6166283 from Pinus taeda (88414.m04398)
1671	Not regulated	NC-NC-NC	260082_at	A11g78180	mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein (88414.m09110)
1672	Not regulated	NC-NC-NC	260051_at	A11g78210	hydrolase, alpha/beta fold family protein low similarity to hydrolases from Rhodococcus sp. EtbD2 (GI:3273241; EtbD1 (GI:3273239; contains Pfam profile PF00561; hydrolase, alpha/beta fold family (88414.m09114))
1673	Not regulated	NC-NC-NC	260055_at	A11g78150	expressed protein (88414.m09107)
1674	Not regulated	NC-NC-NC	260056_at	A11g78140	methyltransferase-related similar to Probable delta(24)-sterol C-methyltransferase (Swiss-Prot:O14321) [Schizosaccharomyces pombe]; similar to C5-O-methyltransferase (GI:5921167) [Streptomyces avermitilis]; similar to S-adenosyl-methionine-sterol-C-methyltransferase (GI:3560474) [Nicotiana tabacum] (88414.m09106)
1675	Not regulated	NC-NC-NC	260057_at	A11g78200	protein phosphatase 2C, putative / PP2C, putative similar to protein phosphatase 2C (Medicago sativa); contains Pfam profile: PF00481 Protein phosphatase 2C (88414.m09112)
1676	Not regulated	NC-NC-NC	260060_at	A11g73680	pathogen-responsive alpha-dioxygenase, putative similar to pathogen-inducible alpha-dioxygenase [Nicotiana attenuata] (GI:12539609; contains Pfam profile PF03098; Animal haem peroxidase (88414.m08532)
1677	Not regulated	NC-NC-NC	260063_at	A11g73720	transducin family protein / WD-40 repeat family protein contains 5 WD-40 repeats (PF00400); similar to Wll die slowly protein (SP-Q9V3J8)[Drosophila melanogaster] (88414.m08536)
1678	Not regulated	NC-NC-NC	260070_at	A11g73830	basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain (88414.m08548)
1679	Not regulated	NC-NC-NC	260071_at	A11g73840	hydroxyproline-rich glycoprotein family protein similar to proline-rich protein precursor GB/AAC34889 [Glycine max] (88414.m08549)
1680	Not regulated	NC-NC-NC	260073_at	A11g73660	protein kinase family protein contains Pfam profile: PF00069 eukaryotic protein kinase domain (88414.m08530)
1681	Not regulated	NC-NC-NC	260076_at	A11g73630	calcium-binding protein, putative similar to calcium binding protein GI:14589311 from [Sesbania rostrata]; contains Pfam profile: PF00038 EF hand (4 copies) (88414.m08524)
1682	Not regulated	NC-NC-NC	260078_at	A11g73790	expressed protein (88414.m08543)
1683	Not regulated	NC-NC-NC	260044_at	A11g73655	immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein similar to (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (SP-Q26468) [Spodoptera frugiperda]; contains Pfam PF00254; peptidyl-prolyl cis-trans isomerase, FKBP-type (88414.m08529)
1684	Not regulated	NC-NC-NC	260048_at	A11g73750	expressed protein contains Pfam profile: PF00561 alpha/beta hydrolase fold (88414.m08539)
1685	Not regulated	NC-NC-NC	260049_at	A11g29940	DNA-directed RNA polymerase family protein similar to SPIP22138 DNA-directed RNA polymerase I 135 kDa polypeptide (EC 2.7.7.6) (RNA polymerase I subunit 2) [Saccharomyces cerevisiae]; contains Pfam profiles PF04563; RNA polymerase beta subunit, PF04560; RNA polymerase Rpb2 domain 7, PF04561; RNA polymerase Rpb2 domain 2, PF04565; RNA polymerase Rpb2 domain 3, PF00562; RNA polymerase Rpb2 domain 6 (88414.m03658)
1686	Not regulated	NC-NC-NC	260020_at	A11g29990	prefoldin, putative similar to Swiss-Prot:O15212 prefoldin subunit 6 (Protein Ke2) [Homo sapiens] (88414.m03668)
1687	Not regulated	NC-NC-NC	260028_at	A11g29980	expressed protein contains Pfam profile PF04882; Protein of unknown function, DUF942 (88414.m03666)
1688	Not regulated	NC-NC-NC	260042_at	A11g68820	membrane protein, putative contains 7 transmembrane domains; similar to inhibitor of apoptosis-2 IAP-2 (GI:20043383) [Mamestra configurata nucleopolyhedrovirus] (88414.m07868)
1689	Not regulated	NC-NC-NC	259990_s_at	A11g68050	F-box family protein (FKF1) / adagio 3 (ADO3) E3 ubiquitin ligase SCF complex F-box subunit; identical to FKF1 (GI:6960305 and Adagio 3 (GI:13487072 from [Arabidopsis thaliana]; contains Pfam profile PF01334; Kelch motif, PF00785; PAC motif and PF00646; F-box domain; contains TIGRfam profile TIGR00228; PAS domain S-box identical to cDNA Adagio 3 (ADO3) (GI:13487071 (88414.m07774))
1690	Not regulated	NC-NC-NC	259995_at	A11g67930	Golgi transport complex protein-related similar to golgi transport complex protein (GTC90) (GI:5453870 [Homo sapiens] (stimulates in vitro Golgi transport J. Biol. Chem. 273 (45), 26565-26576 (1998)) (88414.m07757)
1691	Not regulated	NC-NC-NC	260002_at	A11g67940	ABC transporter family protein similar to ABC transporters: GB/BAAT7878 [Escherichia coli]; GB/P07655 [Escherichia coli]; contains Pfam profile: PF00005 ABC transporter (88414.m07758)
1692	Not regulated	NC-NC-NC	260003_at	A11g68100	IAA-alanine resistance protein 1, putative similar to IAA-alanine resistance protein 1 [Arabidopsis thaliana] SWISS-PROT:Q8ME47; contains ZIP Zinc transporter domain, Pfam:PF02535; identical to cDNA IAA-alanine resistance protein 1 mRNA (GI:6942042 (88414.m07779))
1693	Not regulated	NC-NC-NC	260005_at	A11g67920	expressed protein (88414.m07756)
1694	Not regulated	NC-NC-NC	260006_at	A11g68000	CDP-diacylglycerol--inositol 3-phosphatidylinositol synthase (PIS1) GB/AJ000539 (gi:3387632) (88414.m07768)
1695	Not regulated	NC-NC-NC	260008_at	A11g68070	zinc finger (C3HC4-type RING finger) family protein very low similarity to RING-H2 finger protein RHG1a [Arabidopsis thaliana] (GI:3822225; contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (88414.m07778)

1696	Not regulated	NC-NC-NC	260009_at	A11g67950	RNA recognition motif (RRM)-containing protein (68414.m07759)
1697	Not regulated	NC-NC-NC	260012_at	A11g67885	expressed protein (68414.m07749)
1698	Not regulated	NC-NC-NC	259984_at	A11g53680	glutathione S-transferase, putative similar to GI:2853219 from [Canica papaya] (68414.m06108)
1699	Not regulated	NC-NC-NC	259985_at	A11g53670	transcription factor-related similar to p11n-like transcription factor [Homo sapiens] GI:5059062; contains Pfam profile PF01641: SelfR domain (68414.m06107)
1700	Not regulated	NC-NC-NC	259978_at	A11g76540	cell division control protein, putative similar to SWISS-PROT:Q38775, cell division control protein 2 homolog D [Antirrhinum majus]; contains protein kinase domain, Pfam:PF00069 (68414.m08907)
1701	Not regulated	NC-NC-NC	259981_at	A11g76450	oxygen-evolving complex-related SP:Q85720; contains a PabP domain (68414.m08891)
1702	Not regulated	NC-NC-NC	259983_at	A11g76490	3-hydroxy-3-methylglutaryl-CoA reductase 1 / HMG-CoA reductase 1 (HMG1) identical to HMG-CoA reductase 1 [SP:PF14891] (68414.m08899)
1703	Not regulated	NC-NC-NC	259984_at	A11g76460	RNA recognition motif (RRM)-containing protein low similarity to RRM-containing protein SEB-4 [Xenopus laevis] GI:8895688; contains Pfam profile: PF00078 RNA recognition motif (a.k.a. RRM, RBD, or RNP domain) (68414.m08893)
1704	Not regulated	NC-NC-NC	259955_s_at	A11g75080	brassinosteroid signalling positive regulator (BZR1) identical to BZR1 protein [Arabidopsis thaliana] gi 20270871 gb AAAM18490 (68414.m08719)
1705	Not regulated	NC-NC-NC	259927_at	A11g75100	expressed protein low similarity to SPIO14976 Cyclin G-associated kinase (EC 2.7.1.-) (Homo sapiens) (68414.m08722)
1706	Not regulated	NC-NC-NC	259933_at	A11g34350	expressed protein (68414.m04264)
1707	Not regulated	NC-NC-NC	259942_at	A11g71280	nuclear transport factor 2 (NTF2) family protein contains Pfam domain, PF02136: Nuclear transport factor 2 (NTF2) domain (68414.m08261)
1708	Not regulated	NC-NC-NC	259943_at	A11g71480	eukaryotic translation initiation factor SU11 family protein weak similarity to SPIP41214 Ligatin (Hepatocellular carcinoma-associated antigen 56) (Homo sapiens); contains Pfam profile PF01253: Translation initiation factor SU11 (68414.m08235)
1709	Not regulated	NC-NC-NC	259948_at	A11g71350	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (68414.m08247)
1710	Not regulated	NC-NC-NC	259950_at	A11g71410	disease resistance family protein / LRR family protein contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; similar to HcZ2-5D [Lycopersicon esculentum] gi 3984393 gb AAC78596 (68414.m08248)
1711	Not regulated	NC-NC-NC	259952_at	A11g71400	expressed protein (68414.m08251)
1712	Not regulated	NC-NC-NC	259984_at	A11g71430	expressed protein (68414.m08482)
1713	Not regulated	NC-NC-NC	259909_at	A11g60870	haloacid dehalogenase-like hydrolase family protein similar to Potential phospholipid-transporting ATPase (EC 3.6.3.1) from Homo sapiens [SP:Q9Y2C0, SPIO43520]; contains InterPro accession IPR005834; Haloacid dehalogenase-like hydrolase (68414.m08407)
1714	Not regulated	NC-NC-NC	259910_at	A11g72700	RNA synthetase beta subunit family protein contains Pfam profiles: PF03484 phenylalanine-tRNA synthetase, B5 domain, PF03483 B3/4 domain; an isoform contains a non-consensus TG acceptor splice site at a terminal exon. (68414.m08338)
1715	Not regulated	NC-NC-NC	259920_at	A11g72550	protein phosphatase 2C P2C-HA / PP2C P2C-HA (PP2C-HA) identical to protein phosphatase 2C (AP2C-HA) GB:AAJ003119 [Arabidopsis thaliana] Plant Mol. Biol. 38 (5), 879-883 (1998) (68414.m08414)
1716	Not regulated	NC-NC-NC	259922_at	A11g72770	DNA-binding family protein / histone H1/H5 family protein similar to DNA-binding protein PcdYB1 [Petroselinum crispum] GI:2224897; contains Pfam profiles PF00538: linker histone H1 and H5 family, PF00248: Myb-like DNA-binding domain (68414.m08411)
1717	Not regulated	NC-NC-NC	259924_at	A11g72740	expressed protein (68414.m08398)
1718	Not regulated	NC-NC-NC	259983_at	A11g72630	thioredoxin family protein similar to thioredoxin CH2, M-type, chloroplast precursor GB:P23400 SPIP23400 [Chlamydomonas reinhardtii]; contains Pfam profile: PF00085 Thioredoxin (68414.m08933)
1719	Not regulated	NC-NC-NC	259868_at	A11g78760	5-formyltetrahydrofolate cyclo-ligase family protein contains Pfam profile PF01812 5-formyltetrahydrofolate cyclo-ligase (68414.m08830)
1720	Not regulated	NC-NC-NC	259880_at	A11g78730	protein kinase, putative similar to protein kinase APK1B, SWISS-PROT:P46573; contains protein kinase domain, Pfam:PF00069 (68414.m08872)
1721	Not regulated	NC-NC-NC	259887_at	A11g76360	expressed protein (68414.m07818)
1722	Not regulated	NC-NC-NC	259856_at	A11g68440	expressed protein (68414.m07818)
1723	Not regulated	NC-NC-NC	259860_at	A11g68040	protein kinase family protein contains protein kinase domain, Pfam:PF00089 (68414.m09483)
1724	Not regulated	NC-NC-NC	259881_at	A11g60615	expressed protein (68414.m05892)
1725	Not regulated	NC-NC-NC	259838_at	A11g52220	photosystem I reaction center subunit VI, chloroplast, putative / PSI-H, putative (PSAH2) identical to SPIQ85U8; similar to PSI-H precursor [Nicotiana sylvestris] GI:407355; contains Pfam profile PF03244: Photosystem I reaction centre subunit VI (68414.m05893)
1726	Not regulated	NC-NC-NC	259840_at	A11g52230	expressed protein similar to PGPS/D12 [Pelutia x hybrida] GI:4105794; contains Pfam profile PF04748: Protein of unknown function, DUF6114 (68414.m05890)
1727	Not regulated	NC-NC-NC	259841_at	A11g52200	expressed protein contains Pfam PF04418: Domain of unknown function (DUF543) (68414.m08344)
1728	Not regulated	NC-NC-NC	259847_at	A11g72170	leucine-rich repeat transmembrane protein kinase, putative similar to GI:3641252 from [Malus x domestica] (Plant Mol. Biol. 40 (6), 945-957 (1999)) (68414.m08346)
1729	Not regulated	NC-NC-NC	259848_at	A11g72180	oxidoreductase family protein similar to D-3-phosphoglycerate dehydrogenase from Arabidopsis thaliana [SP:Q04130], glyoxylate reductase from Homo sapiens (gi:6002730); contains Pfam D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain PF02826 (68414.m08347)
1730	Not regulated	NC-NC-NC	259849_at	A11g72190	leucine-rich repeat transmembrane protein kinase, putative similar to GI:3641252 from [Malus x domestica] (Plant Mol. Biol. 40 (6), 945-957 (1999)) (68414.m08358)
1731	Not regulated	NC-NC-NC	259853_at	A11g72300	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein similar to GI:807956 from [Saccharomyces cerevisiae] similar to polyphosphonitride binding protein Seh2p (GI:2739048) (Glycine max); contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CHAULTRIO, N-terminus (68414.m08343)
1732	Not regulated	NC-NC-NC	259804_at	A11g72160	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00087 zinc finger, C3HC4 type (RING finger) (68414.m05589)
1733	Not regulated	NC-NC-NC	259816_at	A11g48850	5-methylthioribose kinase (family contains TIGRfam TIGR01767; 5-methylthioribose kinase profile (68414.m05586)
1734	Not regulated	NC-NC-NC	259819_at	A11g48820	

1735	Not regulated	NC-NC-NC	259824_at	A11g66240	copper homeostasis factor, putative / copper chaperone, putative (CCH) similar to gi:3168940 contains Pfam profile PF004003: Heavy-metal-associated domain (68414.m07519)
1736	Not regulated	NC-NC-NC	259825_at	A11g66260	RNA and export factor-binding protein, putative similar to Gi:7159843 from [Mus musculus] (RNA 6 (4), 639-650 (2000)) (68414.m07522)
1737	Not regulated	NC-NC-NC	259826_at	A11g29340	arnidilobeta-catenin repeat family protein / U-box domain-containing protein contains Pfam domain, PF00514: Arnidilobeta-catenin-like repeats and Pfam, PF04564: U-box domain (68414.m03587)
1738	Not regulated	NC-NC-NC	259827_s_at	A11g29350	expressed protein (68414.m03588)
1739	Not regulated	NC-NC-NC	259769_at	A11g29400	RNA recognition motif (RRM)-containing protein similar to Gi:6650523 from [Arabidopsis thaliana] (68414.m03596)
1740	Not regulated	NC-NC-NC	259770_s_at	A11g29410	phosphoribosylanthranilate isomerase, putative strong similarity to Gi:819749 from [Arabidopsis thaliana] (Plant Cell 7 (4), 447-461 (1995)) (68414.m03598)
1741	Not regulated	NC-NC-NC	259775_s_at	A11g29630	expressed protein (68414.m03612)
1742	Not regulated	NC-NC-NC	259781_s_at	A11g29700	expressed protein (68414.m03629)
1743	Not regulated	NC-NC-NC	259792_at	A11g29690	expressed protein (68414.m03628)
1744	Not regulated	NC-NC-NC	259765_at	A11g64370	expressed protein (68414.m07295)
1745	Not regulated	NC-NC-NC	259737_at	A11g64400	long-chain-fatty-acid-CoA ligase, putative / long-chain acyl-CoA synthetase, putative similar to Gi:1617270 (MF7P) from [Brassica napus] (68414.m07299)
1746	Not regulated	NC-NC-NC	259738_at	A11g64355	expressed protein (68414.m07293)
1747	Not regulated	NC-NC-NC	259741_at	A11g71020	arnidilobeta-catenin repeat family protein / U-box domain-containing protein contains Pfam domain, PF00514: Arnidilobeta-catenin-like repeats and Pfam, PF04564: U-box domain (68414.m08187)
1748	Not regulated	NC-NC-NC	259745_at	A11g71190	expressed protein (68414.m08214)
1749	Not regulated	NC-NC-NC	259752_at	A11g71040	multi-copper oxidase type I family protein similar to SP107788 Spore coat protein A (Bacillus subtilis); contains Pfam profile PF00394: Multicopper oxidase (68414.m08199)
1750	Not regulated	NC-NC-NC	259754_at	A11g71090	auxin efflux carrier family protein contains auxin efflux carrier domain, Pfam:PF03547 (68414.m08204)
1751	Not regulated	NC-NC-NC	259756_at	A11g71080	expressed protein (68414.m08203)
1752	Not regulated	NC-NC-NC	259761_at	A11g77590	long-chain-fatty-acid-CoA ligase family protein / long-chain acyl-CoA synthetase family protein (LACS9) similar to LACS 3 (SP1095573) from Homo Sapiens, LACS 3 (SP1063151) from Rattus norvegicus; contains Pfam HMM hit: AMP-binding enzymes PF00501 (68414.m09034)
1753	Not regulated	NC-NC-NC	259732_at	A11g77470	replication factor C 36 kDa, putative similar to SWISS-PROT:PA0937 activator 1 36 kDa subunit (Replication factor C 36 kDa subunit, A1 36 kDa subunit, RF-C 36 kDa subunit, RFC36) [Homo sapiens] (68414.m09021)
1754	Not regulated	NC-NC-NC	259707_at	A11g77490	L-ascorbate peroxidase, thylakoid-bound (APX) identical to thylakoid-bound ascorbate peroxidase GB:CAA67428 [Arabidopsis thaliana] (68414.m09024)
1755	Not regulated	NC-NC-NC	259710_at	A11g77670	aminotransferase class I and II family protein similar to kynurenine aminotransferase / glutamine transaminase K Gi:1030068 [Rattus norvegicus] (68414.m09043)
1756	Not regulated	NC-NC-NC	259712_at	A11g77440	20S proteasome beta subunit C (PBC2) identical to residues 14-204 of 20S proteasome beta subunit PBC2 GB:AAAC32089 [Arabidopsis thaliana] (68414.m09018)
1757	Not regulated	NC-NC-NC	259717_at	A11g61010	cleavage and polyadenylation specificity factor, putative similar to cleavage and polyadenylation specificity factor 73 kDa subunit [Homo sapiens] SWISS-PROT:Q9UKF6 (68414.m08869)
1758	Not regulated	NC-NC-NC	259723_at	A11g60960	metal transporter, putative (RT3) identical to putative metal transporter IRT3 [Arabidopsis thaliana] gi17365789 [gbAA138438]; similar to iron-regulated transporter 1 [Lycopersicon esculentum] gi8716481 [gb AA197509; member of the Zinc (Zn2+)-Iron (Fe2+) permease (ZIP) family, PMID:11500563 (68414.m06662)
1759	Not regulated	NC-NC-NC	259724_at	A11g60940	serine/threonine protein kinase, putative similar to serine/threonine-protein kinase ASK1 from [Arabidopsis thaliana], SWISS-PROT:PA43291 (68414.m06859)
1760	Not regulated	NC-NC-NC	259727_at	A11g60950	ferredoxin, chloroplast (PETF) identical to FERREDOXIN PRECURSOR GB:P16972 (SP16972) from [Arabidopsis thaliana] (68414.m06981)
1761	Not regulated	NC-NC-NC	259678_at	A11g77750	30S ribosomal protein S13, chloroplast, putative similar to putative 30S ribosomal protein S13, chloroplast precursor GB:P42732 [Arabidopsis thaliana] (68414.m09052)
1762	Not regulated	NC-NC-NC	259685_at	A11g63090	F-box family protein / SKP1 interacting partner 3-related contains Pfam profile PF00646: F-box domain (68414.m07127)
1763	Not regulated	NC-NC-NC	259687_at	A11g63110	cell division cycle protein-related contains 9 transmembrane domains; similar to PIG-U (Gi:27372215) [Rattus norvegicus]; similar to Cell division cycle protein 91-like 1 (CDC91-like 1 protein) (PIG-U) (Swiss-Prot:Q9H490) [Homo sapiens] (68414.m07130)
1764	Not regulated	NC-NC-NC	259688_at	A11g63120	rhomboid family protein contains PFAM domain PF01684, Rhomboid family (68414.m07133)
1765	Not regulated	NC-NC-NC	259695_at	A11g63170	zinc finger (C3HC4-type RING finger) family protein low similarity to SP106003 Goliath protein (G1 protein) [Drosophila melanogaster]; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger) (68414.m07139)
1766	Not regulated	NC-NC-NC	259697_at	A11g69320	basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain (68414.m07887)
1767	Not regulated	NC-NC-NC	259642_at	A11g69030	BSD domain-containing protein contains Pfam profile PF03908: BSD domain (68414.m07888)
1768	Not regulated	NC-NC-NC	259645_at	A11g69010	basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain (68414.m07888)
1769	Not regulated	NC-NC-NC	259653_at	A11g55240	expressed protein contains Pfam profile PF04819: Family of unknown function (DUF716) (Plant viral-response family)
1770	Not regulated	NC-NC-NC	259660_at	A11g55260	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage/LTP family domain PF00234 (68414.m06312)
1771	Not regulated	NC-NC-NC	259661_at	A11g55265	expressed protein contains Pfam profile PF04398: Protein of unknown function, DUF538 (68414.m06313)
1772	Not regulated	NC-NC-NC	259663_at	A11g55190	prenylated rab acceptor (PRA1) family protein contains Pfam profile PF03208: Prenylated rab acceptor (PRA1) (68414.m06304)
1773	Not regulated	NC-NC-NC	259665_at	A11g55180	expressed protein (68414.m06298)

1774 Not regulated	NC-NC-NC	259666_at	SC35-like splicing factor, 33 kD (SCL33) nearly identical to SC35-like splicing factor SCL33, 33 kD [Arabidopsis thaliana] GI:9843659 (68414.m03318)
1775 Not regulated	NC-NC-NC	259671_at	protein kinase family protein contains Pfam PF00069: Protein kinase domain (68414.m05900)
1776 Not regulated	NC-NC-NC	259638_at	coatomer protein complex, subunit beta 2 (beta prime), putative contains 7 WD-40 repeats (PF00400) (1 weak); similar to (SP-O55029) Coatomer beta subunit (Beta-COP) (p102) (SP-O55028) [Mus musculus]; similar to GI:238098 Ran-binding protein 1 domain-containing protein / RanBP1 domain-binding protein weak similarity to SPQ08717 Ran-specific GTPase-activating protein 1 (Ran binding protein 1) (RANBP1) (Sp1-binding protein) (Schizosaccharomyces pombe); contains Pfam profile PF00638: RanBP1 domain (68414.m05911)
1777 Not regulated	NC-NC-NC	259639_at	expressed protein contains Pfam profile PF04782: protein of unknown function (DUF632) (68414.m05904)
1778 Not regulated	NC-NC-NC	259626_at	bZIP transcription factor family protein contains Pfam profile PF00170: bZIP transcription factor (68414.m04949)
1779 Not regulated	NC-NC-NC	259627_at	expressed protein (68414.m04946)
1780 Not regulated	NC-NC-NC	259633_at	haloacid dehalogenase-like hydrolase family protein low similarity to SPIP5649 CbpY protein (Rhodobacter sphaeroides); contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase (68414.m06497)
1781 Not regulated	NC-NC-NC	259603_at	ZDS proteasome beta subunit G1 (PBG1) (PRCH) identical to ZDS proteasome beta subunit (PBG1) GI:3421123 [Arabidopsis thaliana]; identical to cDNA proteasome subunit pch GI:2511597 (68414.m06492)
1782 Not regulated	NC-NC-NC	259604_at	small nuclear ribonucleoprotein family protein / snRNP family protein contains similarity to U4/U6 small nuclear ribonucleoprotein hPrp3 [Homo sapiens] gi2708307/gbAAC51926 (68414.m03435)
1783 Not regulated	NC-NC-NC	259582_at	expressed protein (68414.m03440)
1784 Not regulated	NC-NC-NC	259586_at	lipid transfer protein-related low similarity to lipid transfer protein Picea abies GI:2627141; contains Pfam profile: PF00234: Protease inhibitor/seed storage/TP family (68414.m03424)
1785 Not regulated	NC-NC-NC	259587_at	nuclear transport factor 2 (NTF2), putative similar to Swiss-Prot:P33331 nuclear transport factor 2 (NTF-2) [Nuclear transport factor P10] [Saccharomyces cerevisiae] (68414.m03426)
1786 Not regulated	NC-NC-NC	259592_at	expressed protein contains similarity to cytochrome oxidase I GI:128267 from (Xantholinus sp.) (68414.m03452)
1787 Not regulated	NC-NC-NC	259593_at	auxin-responsive GH3 family protein similar to auxin-responsive GH3 product [Glycine max] GI:16591; contains Pfam profile PF03321: GH3 auxin-responsive promoter (68414.m03446)
1788 Not regulated	NC-NC-NC	259594_at	pyridoxal-dependent decarboxylase family protein similar to sphingosine-1-phosphate lyase [Homo sapiens] GI:10129683; contains Pfam profile PF00282: Pyridoxal-dependent decarboxylase conserved domain (68414.m03427)
1789 Not regulated	NC-NC-NC	259596_at	EXS family protein / ERD1XPR1SYG1 family protein similar to PHO1 protein [Arabidopsis thaliana] GI:20069032; contains Pfam profiles PF03105: SPX domain, PF03124: EXS family (68414.m04383)
1790 Not regulated	NC-NC-NC	259598_at	Bet v 1 allergen family protein similar to Cst-2 [Cucumis sativus] GI:5782258 [J Am Soc Hort Sci 124, 138-139 (1999)] contains Pfam profile PF00407: Pathogenesis-related protein Bet v 1 family (68414.m04372)
1791 Not regulated	NC-NC-NC	259599_at	transducin family protein / WD-40 repeat family protein contains 6 WD-40 repeats (PF00400); similar to Rbap-46 polypeptide (GI:9454362) [Gallus gallus] (68414.m02559)
1792 Not regulated	NC-NC-NC	259548_at	expressed protein (68414.m02545)
1793 Not regulated	NC-NC-NC	259548_at	protein kinase family protein contains Pfam domain PF00068: Protein kinase domain (68414.m02587)
1794 Not regulated	NC-NC-NC	259564_at	dolichyl-phosphate beta-D-mannosyltransferase, putative / dolichyl-phosphate mannosyltransferase, putative / mannose-P-dolichol synthase, putative similar to DPM1 from Homo sapiens [SPQ08762]; member of glycosyltransferase family 2 (68414.m02567)
1795 Not regulated	NC-NC-NC	259571_at	small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative similar to small nuclear ribonucleoprotein Sm D3 (snRNP core protein D3, Sm-D3) [Mus musculus] SWISS-PROT:P43331 (68414.m02569)
1796 Not regulated	NC-NC-NC	259541_at	catalase 3 (SEN2) almost identical to catalase 3 SP-Q42547, GI:3123188 from [Arabidopsis thaliana]; identical to catalase 3 (SEN2) mRNA, partial cds GI:3156369 (68414.m02577)
1797 Not regulated	NC-NC-NC	259542_at	stress-inducible protein, putative similar to stl (stress inducible protein) [Glycine max] GI:872118; contains Pfam profile PF00515 ATP-dependent Clp protease proteolytic subunit (ClpP2) identical to nClpP2 GI:5360589 from [Arabidopsis thaliana]
1798 Not regulated	NC-NC-NC	259543_at	TPR Domain (68414.m01419)
1799 Not regulated	NC-NC-NC	259544_at	(68414.m01434)
1800 Not regulated	NC-NC-NC	259515_at	Pep3Vps18/deep orange family protein contains Pfam profile PF05131: Pep3Vps18/deep orange family, similar to Vacuolar protein sorting 18 (VPS18) (SP-Q8P253) [Homo sapiens] (68414.m01441)
1801 Not regulated	NC-NC-NC	259519_at	hypothetical protein: expression supported by MPSS (68414.m01451)
1802 Not regulated	NC-NC-NC	259521_at	calmodulin, putative similar to calmodulin SP-P04465 from [Trypanosoma brucei gambiense] (68414.m01423)
1803 Not regulated	NC-NC-NC	259532_at	superoxide dismutase copper chaperone, putative similar to copper chaperone for superoxide dismutase [Homo sapiens] gi2431868/gbAAC51764 (68414.m01449)
1804 Not regulated	NC-NC-NC	259533_at	armadillo/beta-catenin repeat family protein / kinesin motor family protein (68414.m01436)
1805 Not regulated	NC-NC-NC	259538_at	protein kinase family protein contains protein kinase domain, Pfam:PF00068; contains similarity to calcium-dependent protein kinase GI:5162877 from [Marchantia polymorpha] (68414.m01461)
1806 Not regulated	NC-NC-NC	259511_at	kinase GI:5162877 from [Marchantia polymorpha] (68414.m01461)
1807 Not regulated	NC-NC-NC	259513_at	expressed protein (68414.m01903)
1808 Not regulated	NC-NC-NC	259484_at	Golgi SNARE 11 protein identical to Golgi SNARE 11 protein (GI:13898993) [Arabidopsis thaliana]; similar to putative cis-Golgi SNARE protein GI:2583133 from [Arabidopsis thaliana]; similar to SPQ08549 28 kDa Golgi SNARE protein (28 kDa cis-Golgi SNARE p28) (GOS-28) [Homo sapiens]; similar to Golgi SNARE protein (Golgi SNAP receptor complex member 1) (28 kDa cis-Golgi SNARE p28) (GOS-28) (SP-Q82831) [Rattus norvegicus] (68414.m01905)
1809 Not regulated	NC-NC-NC	259497_at	PRL1-interacting factor L, putative strong similarity to PRL1-interacting factor L GI:1139268 from [Arabidopsis thaliana]; contains Pfam profile PF02492: Cobalamin synthesis protein/P47K (68414.m01887)
1810 Not regulated	NC-NC-NC	259498_at	leucine-rich repeat family protein (68414.m01888)
1811 Not regulated	NC-NC-NC	259499_at	
1812 Not regulated	NC-NC-NC	259500_at	

1813	Not regulated	259501_at	NC-NC-NC	WD-40 repeat family protein contains 10 WD-40 repeats (PF00400) (1 weak) (68414.m01869) kelch repeat-containing F-box family protein similar to SPIQ0ER30 Kelch-related protein 1 (Sarcosin) (Rattus norvegicus); contains Pfam profiles PF01344; Kelch motif, PF00646; F-box domain (68414.m01881)
1814	Not regulated	259502_at	NC-NC-NC	ribosomal protein S15 family protein contains similarity to ribosomal protein S15 (68414.m01897)
1815	Not regulated	259505_at	NC-NC-NC	protein phosphatase 2C, putative / PP2C, putative similar to protein phosphatase type 2C (Gi:4336438 from [Lotus japonicus] (68414.m05065))
1816	Not regulated	259506_at	NC-NC-NC	expressed protein (68414.m05076)
1817	Not regulated	259468_at	NC-NC-NC	expressed protein (68414.m02374)
1818	Not regulated	259468_at	NC-NC-NC	inter-alpha-trypsin inhibitor heavy chain-related similar to SPIQ081704 Inter-alpha-trypsin inhibitor heavy chain H3 precursor (Mus musculus); contains Pfam profile PF00092; von Willebrand factor type A domain (68414.m02377)
1819	Not regulated	259470_at	NC-NC-NC	expressed protein (68414.m02378)
1820	Not regulated	259474_at	NC-NC-NC	expressed protein (68414.m02380)
1821	Not regulated	259475_at	NC-NC-NC	myo family transcription factor similar to Myo511 Gi:7705208 from [Solanum tuberosum] (68414.m02363)
1822	Not regulated	259476_at	NC-NC-NC	small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative similar to U6 snRNA-associated Sm-like protein LSM1 (Small nuclear ribonucleic acid Sm, Cancer-associated Sm-like) [Homo sapiens] SWISS-PROT.O15116 (68414.m02378)
1823	Not regulated	259477_at	NC-NC-NC	expressed protein (68414.m02385)
1824	Not regulated	259480_at	NC-NC-NC	expressed protein similar to KTI12 protein (SP:P34253) (Saccharomyces cerevisiae); contains Prosite PS00070; Aldehyde dehydrogenases cysteine active site (68414.m01628)
1825	Not regulated	259450_at	NC-NC-NC	calcineurin-like phosphoesterase family protein contains Pfam profile: PF00148 calcineurin-like phosphoesterase (68414.m01631)
1826	Not regulated	259420_at	NC-NC-NC	ELM2 domain-containing protein contains Pfam profile: PF01448 ELM2 domain (68414.m01629)
1827	Not regulated	259423_at	NC-NC-NC	beta-1,3-glucanase-related similar to beta-1,3-glucanase-like protein (Gi:14279169) [Olea europaea] similar to Glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) ((1-3)-beta-glucan endohydrolase) ((1-3)-beta-glucanase) (Beta-1,3- endoglucanase) (Swiss-Prot:P52408) [Triticum aestivum] (68414.m01623)
1828	Not regulated	259424_at	NC-NC-NC	expressed protein identical to cDNA unknown protein Gi:1922247 emb110087.1 (68414.m00066)
1829	Not regulated	259436_at	NC-NC-NC	protein kinase family protein contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002250 (68414.m00070)
1830	Not regulated	259437_at	NC-NC-NC	expressed protein (68414.m00072)
1831	Not regulated	259440_at	NC-NC-NC	chitinase, putative similar to chitinase precursor Gi:5880845 from [Petroselinum crispum] (68414.m00182)
1832	Not regulated	259443_at	NC-NC-NC	cytochrome c oxidase assembly protein CtaG / Cox11 family similar to cytochrome c oxidase assembly protein cox11 Gi:1244782 from [Saccharomyces cerevisiae]; similar to Cytochrome c oxidase assembly protein COX11, mitochondrial precursor (SP:Q9Y6N1)[Homo sapiens]; contains Pfam PF04442; Cytochrome c oxidase assembly protein CtaG / Cox11 (68414.m00188)
1833	Not regulated	259446_at	NC-NC-NC	expressed protein contains similarity to hepatocellular carcinoma-associated antigen 59 Gi:7156847 from [Homo sapiens] (68414.m00178)
1834	Not regulated	259415_at	NC-NC-NC	cathepsin B-like cysteine protease, putative similar to cathepsin B-like cysteine proteinase [Nicotiana rustica] Gi:809175; contains Pfam profile PF00112; Papain family cysteine protease (68414.m00175)
1835	Not regulated	259416_at	NC-NC-NC	glycosyl transferase family 20 protein / trehalose-phosphatase family protein contains Pfam profile: PF02358 trehalose-phosphatase (68414.m00076)
1836	Not regulated	259393_at	NC-NC-NC	Ras-related GTP-binding protein (ARA-2) identical to Ras-related protein ARA-2 SP:P28185 from [Arabidopsis thaliana] (68414.m00677)
1837	Not regulated	259395_at	NC-NC-NC	shaggy-related protein kinase iota / ASK-icta (ASK9) (GSK1) identical to shaggy-related protein kinase iota (ASK-icta) [Arabidopsis thaliana] SWISS-PROT.Q33012 (68414.m00675)
1838	Not regulated	259396_at	NC-NC-NC	D-3-phosphoglycerate dehydrogenase / 3-PGDH identical to SPIO04130 (68414.m02196)
1839	Not regulated	259403_at	NC-NC-NC	expressed protein (68414.m02190)
1840	Not regulated	259406_at	NC-NC-NC	serine/threonine protein phosphatase 2A (PP2A) 65 kDa regulatory subunit, putative similar to protein phosphatase 2A 65 kDa regulatory subunit Gi:683502 from [Arabidopsis thaliana] (68414.m01546)
1841	Not regulated	259407_at	NC-NC-NC	serine/threonine protein phosphatase 2A (PP2A) 65 kDa regulatory subunit A identical to protein phosphatase 2A 65 kDa regulatory subunit (pDf1) Gi:683502 from [Arabidopsis thaliana] (68414.m03211)
1842	Not regulated	259408_at	NC-NC-NC	expressed protein (68414.m01556)
1843	Not regulated	259357_at	NC-NC-NC	glyceraldehyde 3-phosphate dehydrogenase, cytosolic, putative / NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, putative very strong similarity to SPIP25858 Glyceraldehyde 3-phosphate dehydrogenase, cytosolic (EC 1.2.1.12) [Arabidopsis thaliana]; contains Pfam profiles PF02800; Glyceraldehyde 3-phosphate dehydrogenase C-terminal domain, PF00044; Glyceraldehyde 3-phosphate dehydrogenase NAD binding domain (68414.m01570)
1844	Not regulated	259361_at	NC-NC-NC	metallopeptidase M24 family protein similar to SPIQ01662 Methionine aminopeptidase 1 precursor (EC 3.4.11.18) [Saccharomyces cerevisiae]; contains Pfam profile PF00557; metallopeptidase family M24 (68414.m01540)
1845	Not regulated	259363_at	NC-NC-NC	DNA-binding protein RAV1 (RAV1) identical to SPIQ92ZWM9 DNA-binding protein RAV1 (Arabidopsis thaliana), RAV1 Gi:3688857 from [Arabidopsis thaliana] (68414.m01539)
1846	Not regulated	259364_at	NC-NC-NC	expressed protein (68414.m07803)
1847	Not regulated	259367_at	NC-NC-NC	expressed protein (68414.m07803)
1848	Not regulated	259373_at	NC-NC-NC	expressed protein (68414.m07812)
1849	Not regulated	259378_at	NC-NC-NC	mitotic phosphoprotein N' end (MPPN) family protein contains Pfam profile PF05172; MPPN (Mitotic Phosphoprotein N' end) (mmlc) domain (68416.m02059)
1850	Not regulated	259380_at	NC-NC-NC	ABC transporter family protein similar to PDR5-like ABC transporter Gi:1514643 from [Spiroplasma polymyza]; contains Pfam profile: PF00005 ABC transporter (68416.m02066)
1851	Not regulated	259384_at	NC-NC-NC	jacalin lectin family protein similar to SPIQ9SAV1 Myrosinase binding protein-like A1g52030 [Arabidopsis thaliana]; contains Pfam profile: PF01419 jacalin-like lectin domain (68416.m02063)

1852	Not regulated	NC-NC-NC	A13g16480	mitochondrial processing peptidase alpha subunit, putative similar to mitochondrial processing peptidase alpha subunit, mitochondrial precursor, Alpha-MPP (Ubiquinol-cytochrome C reductase subunit II) [Potato] SWISS-PROT:P26877 (68416.m02103)
1853	Not regulated	NC-NC-NC	A13g16270	amino acid permease family protein similar to calionic amino acid transporter-1 [Rattus norvegicus] GI:1589917; contains Pfam profile PF00324; Amino acid permease (68416.m00377)
1854	Not regulated	NC-NC-NC	A13g03720	adenylylsulfate kinase, putative similar to adenylylsulfate kinase 1, chloroplast precursor (APS kinase, Adenosine-5-phosphosulfate kinase, ATP adenosine-5-, phosphosulfate 3'-phosphotransferase) [Arabidopsis thaliana] SWISS-PROT:Q43295 (68416.m00404)
1855	Not regulated	NC-NC-NC	A13g03900	expressed protein (68416.m00402)
1856	Not regulated	NC-NC-NC	A13g03890	expressed protein (68416.m00398)
1857	Not regulated	NC-NC-NC	A13g03880	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00087 zinc finger, C3HC4 type (RING finger) (68416.m00573)
1858	Not regulated	NC-NC-NC	A13g05250	integral membrane Yip1 family protein contains Pfam domain, PF04683: Yip1 domain (68416.m00576)
1859	Not regulated	NC-NC-NC	A13g05280	aminopeptidase P, cytosolic, putative similar to cytosolic aminopeptidase P from [Homo sapiens] [Rattus norvegicus] GI:2760920; contains Pfam profile PF00557: metalloproteinase family M24 (68416.m00583)
1860	Not regulated	NC-NC-NC	A13g05350	nucleotide repair protein, putative similar to nucleotide repair protein [Lilium longiflorum] GI:3287891, SP107982 DNA excision repair protein ERCC-1 (Homo sapiens); contains Pfam profile PF00633: Helix-hairpin-helix motif (68416.m00568)
1861	Not regulated	NC-NC-NC	A13g05210	expressed protein (68416.m00556)
1862	Not regulated	NC-NC-NC	A13g05070	signal peptidase subunit family protein contains Pfam profile: PF04573 signal peptidase subunit (68416.m00571)
1863	Not regulated	NC-NC-NC	A13g05230	GDSL-motif lipase/hydrolase family protein similar to early nodulin ENOD8 [Medicago sativa] GI:304037, elicitor-induced glycoprotein IEP4 [Daucus carota] GI:1911765, lanatostide 15'-O-acetyltransferase [Digitalis lanata] GI:3688284; contains InterPro Entry IPRO01087 Lipolytic enzyme, G-D-S-L family (68416.m00565)
1864	Not regulated	NC-NC-NC	A13g05180	protein kinase family protein contains Pfam domain, PF00069: Protein kinase domain (68416.m00548)
1865	Not regulated	NC-NC-NC	A13g05050	sugar transporter, putative similar to sugar-portal family proteins 1 and 2 [Arabidopsis thaliana] GI:14585701; contains Pfam profile PF00083: major facilitator superfamily protein (68416.m00562)
1866	Not regulated	NC-NC-NC	A13g05165	SAR DNA-binding protein, putative strong similarity to SAR DNA-binding protein (68416.m00562)
1867	Not regulated	NC-NC-NC	A13g05080	profile PF01798: Putative snRNA binding domain (68416.m00546)
1868	Not regulated	NC-NC-NC	A13g05090	transducin family protein / WD-40 repeat family protein contains seven G-protein beta WD-40 repeats; similar to uncharacterized KIAA1449 protein (gi:7958157) [Homo sapiens] (68416.m00552)
1869	Not regulated	NC-NC-NC	A13g01200	expressed protein contains Pfam domain PF03818: Domain of unknown function (DUF298) (68416.m00026)
1870	Not regulated	NC-NC-NC	A13g01090	Srr1-related protein kinase (KIN10) (SKIN10) identical to Srr1-related protein kinase, KIN10 SP:Q36987 from [Arabidopsis thaliana] (68416.m00013)
1871	Not regulated	NC-NC-NC	A13g01130	expressed protein (68416.m00017)
1872	Not regulated	NC-NC-NC	A13g01280	porin, putative similar to SPIP42055 34 kDa outer mitochondrial membrane protein porin (Voltage-dependent anion-selective channel protein) (VDAC) (Solanum tuberosum); contains Pfam profile PF01459: Eukaryotic porin (68416.m00035)
1873	Not regulated	NC-NC-NC	A13g01060	expressed protein (68416.m00007)
1874	Not regulated	NC-NC-NC	A13g01150	polypyrimidine tract-binding protein, putative / heterogeneous nuclear ribonucleoprotein, putative similar to Polypyrimidine tract-binding protein 1 (PTB) (Heterogeneous nuclear ribonucleoprotein 1) (hnRNP 1) from [Sus scrofa] SPIQ29098, [Mus musculus] SPIP17225; contains InterPro entry IPRO00504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) (68416.m00019)
1875	Not regulated	NC-NC-NC	A13g11450	DNAJ heat shock N-terminal domain-containing protein / cell division protein-related similar to GSA [Yohor carteri f. nagaiensis] GI:4633129; contains Pfam profiles PF00228 DnaJ domain, PF00248 Myb-like DNA-binding domain (68416.m01368)
1876	Not regulated	NC-NC-NC	A13g11500	small nuclear ribonucleoprotein G, putative / snRNP-G, putative / Sm protein / Sm protein G, putative similar to SWISS-PROT:Q15357 small nuclear ribonucleoprotein G (snRNP-G, Sm protein G, Sm-G, SmG) [Homo sapiens] (68416.m01402)
1877	Not regulated	NC-NC-NC	A13g11550	integral membrane family protein similar to unknown protein GB:AAD26967 [Arabidopsis thaliana]; contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam GB:AAD535 : Domain of unknown function (DUF588) (68416.m01408)
1878	Not regulated	NC-NC-NC	A13g11560	expressed protein (68416.m01410)
1879	Not regulated	NC-NC-NC	A13g11410	protein phosphatase 2C, putative / PP2C, putative identical to protein phosphatase 2C (PP2C) GB:P49598 [Arabidopsis thaliana]; contains Pfam profile PF00481: Protein phosphatase 2C; identical to cDNA protein phosphatase 2C GI:833027 (68416.m01392)
1880	Not regulated	NC-NC-NC	A13g11600	expressed protein weak similarity to B-type cyclin (GI:849074) [Nicotiana tabacum] (68416.m01418)
1881	Not regulated	NC-NC-NC	A13g11530	vacuolar protein sorting 55 family protein / VPS55 family protein contains Pfam domain PF04133: Vacuolar protein sorting 55 (68416.m01405)
1882	Not regulated	NC-NC-NC	A13g11630	2-cys peroxiredoxin, chloroplast (BAS1) identical to SPIQ86291 2-cys peroxiredoxin BAS1, chloroplast precursor [Arabidopsis thaliana]; contains Pfam profile: PF00578 AhpC/TSA (alkyl hydroperoxide reductase and thiol-specific antioxidant) family (68416.m01425)
1883	Not regulated	NC-NC-NC	A13g11400	eukaryotic translation initiation factor 3G / eIF3g nearly identical to eukaryotic translation initiation factor 3g [Arabidopsis thaliana] GI:12407751 (68416.m01390)
1884	Not regulated	NC-NC-NC	A13g11510	40S ribosomal protein S14 (RPS14B) similar to 40S ribosomal protein S14 GB:P19950 [Zae mays] (68416.m01403)
1885	Not regulated	NC-NC-NC	A13g11590	expressed protein (68416.m00946)
1886	Not regulated	NC-NC-NC	A13g07565	expressed protein (68416.m00948)
1887	Not regulated	NC-NC-NC	A13g07660	expressed protein (68416.m00918)
1888	Not regulated	NC-NC-NC	A13g07570	membrane protein, putative similar to membrane protein SDR2 (GI:1747306) [Mus musculus] (68416.m00907)

1889	Not regulated	NC-NC-NC	259248_at	A13g07770	heat shock protein-related strong similarity to heat-shock protein [Secale cereale] GI:556673; contains Pfam profiles PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein, PF00183: Hsp90 protein (68416.m00947)
1890	Not regulated	NC-NC-NC	259253_at	A13g07640	expressed protein (68416.m00815)
1891	Not regulated	NC-NC-NC	259254_at	A13g07630	prephenate dehydratase family protein similar to P-protein: chorismate mutase, prephenate dehydratase GB:P43900 [Haemophilus influenzae] (68416.m00913)
1892	Not regulated	NC-NC-NC	259257_at	A13g07760	expressed protein (68416.m00943)
1893	Not regulated	NC-NC-NC	259258_at	A13g07670	SET domain-containing protein similar to ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I [Spinacia oleracea] GI:3403236; contains Pfam profile PF00856: SET domain (68416.m00819)
1894	Not regulated	NC-NC-NC	259224_at	A13g07800	thymidine kinase, putative similar to thymidine kinase [Oryza sativa] SWISS-PROT:Q81263 (68416.m00953)
1895	Not regulated	NC-NC-NC	259226_at	A13g07700	ABC1 family protein contains Pfam domain, PF03109: ABC1 family (68416.m00925)
1896	Not regulated	NC-NC-NC	259227_at	A13g07750	3' exonuclease family domain 1-containing protein similar to SPIQ15024 Exosome complex exonuclease RRP42 (EC 3.1.13.-) (Ribosomal RNA processing protein 42) [Homo sapiens]; contains Pfam profile PF01138: 3' exonuclease family, domain 1 expressed protein (68416.m00939)
1897	Not regulated	NC-NC-NC	259207_at	A13g09050	expressed protein (68416.m01064)
1898	Not regulated	NC-NC-NC	259215_at	A13g09090	gill113868989ip/AAG31444; contains Pfam domain PF01639: FG-GAP repeat (68416.m01069)
1899	Not regulated	NC-NC-NC	259196_at	A13g03600	ribosomal protein S2, mitochondrial (RPS2) identical to SPIQ9CBB Mitochondrial ribosomal protein S2 (Arabidopsis thaliana); contains Pfam profile PF00318: ribosomal protein S2 (68416.m00363)
1900	Not regulated	NC-NC-NC	259198_at	A13g03610	phagocytosis and cell motility protein ELMO1-related contains weak similarity to ELMO1 [Mus musculus] gi 16118551 gb AAL14464 (68416.m00364)
1901	Not regulated	NC-NC-NC	259178_at	A13g01650	copine-related low similarity to SPIQ99829 Copine I (Homo sapiens) (68416.m00098)
1902	Not regulated	NC-NC-NC	259184_at	A13g01520	universal stress protein (USP) family protein similar to ERB protein (GI:5669634) [Lycopodium obscurum]; contains Pfam profile PF00582: universal stress protein family (68416.m00080)
1903	Not regulated	NC-NC-NC	259185_at	A13g01550	triose phosphate/phosphate translocator, putative similar to SWISS-PROT:P52178 triose phosphate/phosphate translocator [Cauliflower][Brassica oleracea] (68416.m00085)
1904	Not regulated	NC-NC-NC	259190_at	A13g01780	expressed protein est hit, (68416.m00118)
1905	Not regulated	NC-NC-NC	259192_at	A13g01740	expressed protein (68416.m00111)
1906	Not regulated	NC-NC-NC	259194_at	A13g01540	DEAD box RNA helicase (DRH1) identical to RNA helicase DRH1 GB:BAA28347 GI:3149952 [Arabidopsis thaliana]; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain (68416.m00082)
1907	Not regulated	NC-NC-NC	259164_at	A13g01770	DNA-binding bromodomain-containing protein contains bromodomain, INTERPRO:IPR001467 (68416.m00116)
1908	Not regulated	NC-NC-NC	259137_at	A13g10300	calcium-binding EF hand family protein low similarity to SPIP12815 Programmed cell death protein 6 (Probable calcium-binding protein ALG-2) [Mus musculus]; contains INTERPRO:IPR002048 calcium-binding EF-hand domain (68416.m01234)
1909	Not regulated	NC-NC-NC	259138_s_at	A13g10270	DNA topoisomerase, ATP-hydrolyzing, putative / DNA topoisomerase II, putative / DNA gyrase, putative similar to SPIQ50827 DNA gyrase subunit B (EC 5.99.1.3) [Bacillus halodurans]; contains Pfam profiles PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein, PF02004: DNA topoisomerase II (N-terminal region), PF00986: DNA gyrase, B subunit, carboxyl terminus, PF01751: Toprim domain (68416.m01231)
1910	Not regulated	NC-NC-NC	259141_at	A13g10220	tubulin folding cofactor B identical to tubulin folding cofactor B GI:20514259 from [Arabidopsis thaliana], identical to cDNA tubulin folding cofactor B GI:20514258 (68416.m01223)
1911	Not regulated	NC-NC-NC	259148_at	A13g10350	anion-transporting ATPase family protein similar to SPIQ43681 Arsenical pump-driving ATPase (EC 3.6.3.16) [Arsentia-translocating ATPase] (Arsenical resistance ATPase) (Arsentia-transporting ATPase) (ARSA) (ASNA-1) [Homo sapiens]; contains Pfam profile PF02374: Anion-transporting ATPase; contains non-consensus GA donor splice site at intron 5 (68416.m01241)
1912	Not regulated	NC-NC-NC	259152_at	A13g10210	expressed protein similar to putative protein GB:CAA20045 [Arabidopsis thaliana] (68416.m01222)
1913	Not regulated	NC-NC-NC	259153_at	A13g10250	expressed protein (68416.m01226)
1914	Not regulated	NC-NC-NC	259154_at	A13g10260	reticulum family protein weak similarity to Nogo-C protein [Rattus norvegicus] GI:6822251; contains Pfam profile PF02453: Reticulon; identical to cDNA GI:32331854 (68416.m01228)
1915	Not regulated	NC-NC-NC	259155_at	A13g10330	transcription initiation factor IIB-2 / general transcription factor TFIIB-2 (TFIIB2) identical to SPIQ8SS44 Transcription initiation factor IIB-2 (General transcription factor TFIIB-2) (ATFIIB2) (Arabidopsis thaliana) (68416.m01239)
1916	Not regulated	NC-NC-NC	259111_at	A13g05520	F-actin capping protein alpha subunit family protein contains Pfam profile: PF01287 F-actin capping protein alpha subunit (68416.m00605)
1917	Not regulated	NC-NC-NC	259112_at	A13g05560	60S ribosomal protein L22-2 (RPL22B) identical to 60S ribosomal protein L22-2 SP:Q8M9W1 from [Arabidopsis thaliana] (68416.m00813)
1918	Not regulated	NC-NC-NC	259115_at	A13g01360	expressed protein contains Pfam profile PF04819: Family of unknown function (DUF716) (Plant viral-response family) (68416.m00057)
1919	Not regulated	NC-NC-NC	259118_at	A13g01310	unknown protein similar to unknown protein GB:BAA24863 [Homo sapiens], unknown protein GB:BAA20831 [Homo sapiens], unknown protein GB:AAB42264 [Caenorhabditis elegans] (68416.m00042)
1920	Not regulated	NC-NC-NC	259119_at	A13g01340	protein transport protein SEC13 family protein / WD-40 repeat family protein similar to Protein transport protein SEC13 SPIQ04491 [Saccharomyces cerevisiae] and SEC13 (SP:P53024) [Pichia pastoris] (68416.m00051)
1921	Not regulated	NC-NC-NC	259121_at	A13g02220	expressed protein (68416.m00203)
1922	Not regulated	NC-NC-NC	259123_at	A13g02200	proteasome family protein contains Pfam domain, PF01399: PCI domain (68416.m00198)
1923	Not regulated	NC-NC-NC	259125_at	A13g02300	regulator of chromosome condensation (RCC1) family protein weak similarity to UVB-resistance protein UVR8 [Arabidopsis thaliana] GI:5476530; contains Pfam profile PF00415: Regulator of chromosome condensation (RCC1) (68416.m00212)
1924	Not regulated	NC-NC-NC	259131_at	A13g02180	expressed protein (68416.m00192)

1925	Not regulated	NC-NC-NC	259085_at	Al3g05000	transport protein particle (TRAPP) component Bet3 family protein similar to Transport protein particle 33 kDa subunit (TRAPP 33 kDa subunit) (Swiss-Prot:Q98394) [Saccharomyces cerevisiae]; contains Pfam profile PF04051: Transport protein particle (TRAPP) component, Bet3 (88416.m00543)
1926	Not regulated	NC-NC-NC	259086_at	Al3g04920	40S ribosomal protein S24 (RPS24A) similar to ribosomal protein S19 GB:445612 [Solanum tuberosum] and similar to ribosomal protein S24 GB:4508703 [Homo sapiens] (88416.m00534)
1927	Not regulated	NC-NC-NC	259092_at	Al3g04870	zeta-carotene desaturase (ZDS1) carotene 7,8-desaturase identical to SPIQ38893 Zeta-carotene desaturase, chloroplast precursor (EC 1.14.99.30) [Carotene 7,8-desaturase] (Arabidopsis thaliana) (88416.m00528)
1928	Not regulated	NC-NC-NC	259095_at	Al3g05020	acyl carrier protein 1, chloroplast (ACP-1) identical to SPIP11829 Acyl carrier protein 1, chloroplast precursor (ACP) (Arabidopsis thaliana) (88416.m00545)
1929	Not regulated	NC-NC-NC	259098_at	Al3g04840	40S ribosomal protein S3A (RPS3A) similar to 40S ribosomal protein S3A (S phase specific protein GBIS289) GB:P48398 [Brassica rapa] (88416.m00525)
1930	Not regulated	NC-NC-NC	259097_at	Al3g04830	expressed protein (88416.m00523)
1931	Not regulated	NC-NC-NC	259098_at	Al3g04790	ribose 5-phosphate isomerase-related similar to ribose-5-phosphate isomerase GI:18654317 from [Spinacia oleracea] (88416.m00518)
1932	Not regulated	NC-NC-NC	259099_at	Al3g05010	transmembrane protein, putative similar to GB:AA681078; contains weak similarity to the SAPB protein (TR:E236624) [Arabidopsis thaliana]; similar to seven transmembrane domain orphan receptor (GI:4321619) [Mus musculus] contains 7 transmembrane domains; (88416.m00544)
1933	Not regulated	NC-NC-NC	259100_at	Al3g04880	DNA-damage-repair/tolerance protein (DRT102) identical to DNA-damage-tolerance protein DRT102 SP:Q05212 from [Arabidopsis thaliana]; contains Pfam profile: PF02502 ribose/galactose isomerase (88416.m00530)
1934	Not regulated	NC-NC-NC	259102_at	Al3g11860	harpin-induced family protein / HIN1 family protein / harpin-responsive family protein similar to harpin-induced protein hin1 (GI:1619321) [Nicotiana tabacum] (88416.m01428)
1935	Not regulated	NC-NC-NC	259103_at	Al3g11890	expressed protein (88416.m01433)
1936	Not regulated	NC-NC-NC	259069_at	Al3g11710	lysyl-IRNA synthetase, putative / lysine-IRNA ligase, putative similar to SPIQ43776 Lysyl-IRNA synthetase (EC 6.1.1.6) (Lysine-IRNA ligase) (Lycopodium esculentum); contains Pfam profile PF00152: IRNA synthetases class II (D, K and N) (88416.m01435)
1937	Not regulated	NC-NC-NC	259047_at	Al3g03390	short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily (88416.m00331)
1938	Not regulated	NC-NC-NC	259051_at	Al3g03330	Ku70-binding family protein similar to Ku70-binding protein GB:AA031085 Gi:4867999 [Homo sapiens]; contains Prosite PS00142: Neutral zinc metalloproteinases, zinc-binding region signature (88416.m00340)
1939	Not regulated	NC-NC-NC	259056_at	Al3g03420	eukaryotic translation initiation factor 2B family protein / eIF-2B family protein similar to SPIP49770 Translation initiation factor eIF-2B beta subunit (eIF-2B GDP-GTP exchange factor) (Homo sapiens); contains Pfam profile PF01008: initiation factor 2 subunit family (88416.m00869)
1940	Not regulated	NC-NC-NC	259059_at	Al3g07300	lipase class 3 family protein contains Pfam profile PF01764: Lipase (88416.m00882)
1941	Not regulated	NC-NC-NC	259060_at	Al3g07400	glycine-rich protein (88416.m00903)
1942	Not regulated	NC-NC-NC	259068_at	Al3g07560	armadillo/beta-catenin repeat family protein / U-box domain-containing protein contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain (88416.m00877)
1943	Not regulated	NC-NC-NC	25907360	Al3g07360	expressed protein (88416.m00892)
1944	Not regulated	NC-NC-NC	259016_at	Al3g07480	expressed protein (88416.m00871)
1945	Not regulated	NC-NC-NC	259017_at	Al3g07310	tetratricopeptide repeat (TPR)-containing protein / U-box domain-containing protein similar to serologically defined colon cancer antigen 7 GB:5031963 Gi:3170178 [Homo sapiens]; (88416.m00879)
1946	Not regulated	NC-NC-NC	259019_at	Al3g07370	oxysterol-binding family protein similar to SPIP22059 Oxysterol-binding protein 1 (Homo sapiens); contains Pfam profile PF01237: oxysterol-binding protein (88416.m01104)
1947	Not regulated	NC-NC-NC	259029_at	Al3g09300	KOW domain-containing transcription factor family protein; est match (88416.m01095)
1948	Not regulated	NC-NC-NC	259038_at	Al3g09320	expressed protein (88416.m01099)
1949	Not regulated	NC-NC-NC	259039_at	Al3g09250	60S acidic ribosomal protein P0 (RPP0B) similar to putative 60S acidic ribosomal protein P0 GB:P50346 [Glycine max] (88416.m01094)
1950	Not regulated	NC-NC-NC	259006_at	Al3g09200	myb family transcription factor (MYB3R3) contains Pfam profile: Myb DNA-binding proteins; identical to cDNA putative c-myp-like transcription factor (MYB3R3) GI:15375265 (88416.m01111)
1951	Not regulated	NC-NC-NC	259007_at	Al3g09370	zinc finger (DHC type) family protein similar to Colgi-specific DHC zinc finger protein [Mus musculus] GI:21728103; contains Pfam profile PF01529: DHC zinc finger domain (88416.m01108)
1952	Not regulated	NC-NC-NC	259078_at	Al3g09320	expressed protein contains Pfam profile PF04398: Protein of unknown function, DUFS38 (88416.m01034)
1953	Not regulated	NC-NC-NC	259088_at	Al3g08890	rhodanese-like domain-containing protein contains rhodanese-like domain PF:00581 (88416.m01038)
1954	Not regulated	NC-NC-NC	259099_at	Al3g08920	LMBR1 integral membrane family protein contains 5 transmembrane domains; contains Pfam PF04781: LMBR1-like conserved region; similar to unknown protein GB:BA483351 [Oryza sativa] (88416.m01039)
1955	Not regulated	NC-NC-NC	259092_at	Al3g08930	chlorophyll A-B binding protein (LHCBA-2) contains Pfam profile: PF00504 chlorophyll A-B binding protein; identical to Lhcb4.2 protein GB:AA028774 [Arabidopsis thaliana] (88416.m01041)
1956	Not regulated	NC-NC-NC	259093_at	Al3g08940	adenylate kinase family protein contains Pfam profile: PF00406 adenylate kinase (88416.m00124)
1957	Not regulated	NC-NC-NC	259098_at	Al3g01820	expressed protein (88416.m00130)
1958	Not regulated	NC-NC-NC	259000_at	Al3g01860	yrkC family protein contains Pfam PF01300: yrkC domain; similar to Protein ykO (Swiss-Prot:P45847) [Shigella flexneri]; similar to Chain A, Crystall Structure Of E. Coli Yoo Length [GI:27573707] [Escherichia coli] (88416.m00141)
1959	Not regulated	NC-NC-NC	259072_at	Al3g01920	WRKY family transcription factor similar to WRKY1 GB:AA049527 [Petroselinum crispum] (88416.m00153)
1960	Not regulated	NC-NC-NC	259075_at	Al3g01970	aspartate kinase, lysine-sensitive, putative similar to aspartate kinase gi:2257743 (Arabidopsis thaliana) (88416.m00164)
1961	Not regulated	NC-NC-NC	259077_s_at	Al3g02020	sulfite oxidase, putative similar to sulfite oxidase GB:3212610 SPIP07850 [Callus gallus]; Moco containing protein [Oryza sativa japonica cultivar-group] GI:22759594; contains Pfam profiles: PF00174: Oxidoreductase molybdopter binding domain and PF03404: Mo-co oxidoreductase dimerisation domain (88416.m00139)
1962	Not regulated	NC-NC-NC	259048_at	Al3g01910	

1963	Not regulated	NC-NC-NC	258950_at	A13g01460	PHD finger family protein / methyl-CpG binding domain-containing protein contains Pfam profiles PF00628: PHD-finger (2 copies), PF01429: Methyl-CpG binding domain (88416.m00070)
1964	Not regulated	NC-NC-NC	258954_at	A13g01400	armadillo/beta-catenin repeat family protein contains Pfam profile: PF00514: armadillo/beta-catenin-like repeats (4 copies) (88416.m00083)
1965	Not regulated	NC-NC-NC	258958_at	A13g01390	vacuolar ATP synthase subunit G 1 (VATG1) / V-ATPase G subunit 1 (VAG1) / vacuolar proton pump G subunit 1 (VMA10) identical to SWISS-PROT:O62628 vacuolar ATP synthase subunit G 1 (V-ATPase G subunit 1, Vacuolar proton pump G subunit 1) (Arabidopsis thaliana) (88416.m00061)
1966	Not regulated	NC-NC-NC	258965_at	A13g10530	transducin family protein / WD-40 repeat family protein contains 2 WD-40 repeats (PF00400); BING4 (gi:3811380) [Mus musculus]; similar to hypothetical protein GB:P40055 [Saccharomyces cerevisiae] (88416.m01284)
1967	Not regulated	NC-NC-NC	258970_at	A13g10410	serine carboxypeptidase III, putative similar to serine carboxypeptidase III from <i>Oryza sativa</i> SPIP27891, <i>Maizitania charnilla</i> GI:6960455, <i>Hordeum vulgare</i> SPIP21529, <i>Triticum aestivum</i> SPIP11515; contains Pfam profile PF0450: serine carboxypeptidase (88416.m01248)
1968	Not regulated	NC-NC-NC	258916_at	A13g10670	ABC transporter family protein similar to ABC transporter ATPase GB:AA068280 [Chlamydia trachomatis] (88416.m01283)
1969	Not regulated	NC-NC-NC	258919_at	A13g10525	expressed protein (88416.m01263)
1970	Not regulated	NC-NC-NC	258924_at	A13g10620	diadenosine 5',5''-P ₁ ,P ₄ -tetraphosphate hydrolase, putative similar to diadenosine 5',5''-P ₁ ,P ₄ -tetraphosphate hydrolase from <i>Lupinus angustifolius</i> [GI:1888557, <i>Hordeum vulgare</i> subsp. vulgare] GI:2564253; contains Pfam profile PF00283: NUDIX domain (88416.m01277)
1971	Not regulated	NC-NC-NC	258927_at	A13g10160	hydrofolate synthetase/polyglutamate synthetase (DHFS/PPGSS) nearly identical to gi:17978757 (88416.m01218)
1972	Not regulated	NC-NC-NC	258929_at	A13g10050	immunophilin, putative / FKBP-type peptidyl-prolyl isomerase, putative Pfam:PF-254: FKBP-type peptidyl-prolyl isomerase (88416.m01206)
1973	Not regulated	NC-NC-NC	258936_at	A13g10080	germin-like protein, putative similar to germin-like protein 2 [<i>Oryza sativa</i>] GI:2655287 (88416.m01208)
1974	Not regulated	NC-NC-NC	258893_at	A13g09970	calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149: Calcineurin-like phosphoesterase (88416.m01198)
1975	Not regulated	NC-NC-NC	258892_at	A13g05670	PHD finger family protein contains Pfam domain, PF00628: PHD-finger (88416.m00631)
1976	Not regulated	NC-NC-NC	258900_at	A13g05590	60S ribosomal protein L18 (RPL18B) similar to GB:P42781 (88416.m00621)
1977	Not regulated	NC-NC-NC	258902_at	A13g06483	pyruvate dehydrogenase (lipoamide) kinase (PDHK) nearly identical to pyruvate dehydrogenase kinase [Arabidopsis thaliana] GI:3641834 (88416.m00751)
1978	Not regulated	NC-NC-NC	258903_at	A13g06410	zinc finger (CCH-type) family protein contains Pfam domain, PF00842: Zinc finger C-x ₂ -C-x ₅ -C-x ₃ -H type (and similar) (88416.m00739)
1979	Not regulated	NC-NC-NC	258905_at	A13g06390	integral membrane family protein similar to hypothetical protein GB:CAB10339 [Arabidopsis thaliana]; contains TIGRFAM TIGR01569: plant integral membrane protein TIGR01569; contains Pfam PF04535: Domain of unknown function (DUF588) (88416.m00737)
1980	Not regulated	NC-NC-NC	258906_at	A13g06380	F-box family protein / tubby family protein similar to phosphodiesterase (GI:487578) [Mus musculus]; similar to C-terminal half of tubby protein (A mutation in the tub gene causes maturity-onset obesity, insulin resistance, and sensory deficits) (GB:P50568) [GI:6730159] [Mus musculus]; contains Pfam PF00948: F-box domain and Pfam PF01167: Tub family, similar to Tubby protein homolog [Swiss-Prot:O88808] [Rattus norvegicus] (88416.m00736)
1981	Not regulated	NC-NC-NC	258910_at	A13g06460	DEAD box RNA helicase, putative similar to RNA helicase DRH1 [Arabidopsis thaliana] GI:3149952; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain, PF00397: VW domain (88416.m00750)
1982	Not regulated	NC-NC-NC	258911_at	A13g06470	GNS1/SUR4 membrane family protein similar to SPIP39540 Elongation of fatty acids protein 1 [Saccharomyces cerevisiae]; contains Pfam profile PF01151: GNS1/SUR4 family (88416.m00749)
1983	Not regulated	NC-NC-NC	258913_at	A13g06450	anion exchange family protein similar to putative Anion exchanger family members: GB:AA039873, GB:AA055295 [Arabidopsis thaliana] (88416.m00746)
1984	Not regulated	NC-NC-NC	258881_at	A13g06310	NADH-ubiquinone oxidoreductase 19 kDa subunit (NDUFA8) family protein contains Pfam profile PF05850: NADH-ubiquinone oxidoreductase 19 kDa subunit (NDUFA8); similar to NADH-ubiquinone oxidoreductase 19 kDa subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-19KD) (CI-19KD) (Complex I-PGV) (CI-PGV) [Swiss-Prot:P51970] [Homo sapiens] (88416.m00725)
1985	Not regulated	NC-NC-NC	258882_at	A13g06330	zinc finger (C3HC4-type RING finger) family protein contains InterPro Entry IPR001841 Zn-finger, RING: contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger) (88416.m00729)
1986	Not regulated	NC-NC-NC	258855_at	A13g02070	OTU-like cysteine protease family protein contains Pfam profile PF02338: OTU-like cysteine protease (88416.m00172)
1987	Not regulated	NC-NC-NC	258857_at	A13g02110	serine carboxypeptidase S10 family protein similar to serine carboxypeptidase II (CP-MII) GB:CAA70815 (SP:P08818) [Hordeum vulgare] (88416.m00177)
1988	Not regulated	NC-NC-NC	258859_at	A13g02120	hydroxyproline-rich glycoprotein family protein (88416.m00317)
1989	Not regulated	NC-NC-NC	258864_at	A13g03210	expressed protein (88416.m00312)
1990	Not regulated	NC-NC-NC	258875_at	A13g03160	ADP-ribosylation factor, putative similar to ADP-ribosylation factor 1; ARF 1 (GP:385340) [Drosophila melanogaster] (88416.m00308)
1991	Not regulated	NC-NC-NC	258876_at	A13g03120	expansin, putative (EXP13) similar to expansin precursor GB:AA013631 from [<i>Lycopersicon esculentum</i>]; alpha-expansin gene family, PMID:11641069 (88416.m00318)
1992	Not regulated	NC-NC-NC	258877_at	A13g03220	universal stress protein (USP) family protein / early nodulin ENOD18 family protein contains Pfam profile PF00582: universal stress protein family, similar to early nodulin ENOD18 (GI:1602747) [Nicotiana glauca] (88416.m00323)
1993	Not regulated	NC-NC-NC	258879_at	A13g03270	NADH-ubiquinone oxidoreductase family protein contains Pfam PF05071: NADH-ubiquinone oxidoreductase 17.2 kD subunit; similar to ethylene-regulated ER6 protein [GI:5689854] [Lycopersicon esculentum]; identical to Probable NADH-ubiquinone oxidoreductase subunit B17.2 (EC 1.6.99.3) (Complex I-B17.2) (CI-B17.2) (Swiss-Prot:Q9M6M9) [Arabidopsis thaliana] (88416.m00306)
1994	Not regulated	NC-NC-NC	258847_at	A13g03100	

1995	Not regulated	NC-NC-NC	258848_at	A13g03305	calciurein-like phosphodiesterase family protein contains Pfam profile: PF00149 calciurein-like phosphodiesterase (68416.m00328)
1996	Not regulated	NC-NC-NC	258850_at	A13g03050	cellulose synthase family protein (CslD3) similar to cellulose synthase catalytic subunit gl:2827143 from [Arabidopsis thaliana], cellulose synthase-7 (gl:3622868) from Zea mays, contains Pfam profile PF03552: Cellulose synthase (68416.m00301)
1997	Not regulated	NC-NC-NC	258823_at	A13g07200	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger) (68416.m00659)
1998	Not regulated	NC-NC-NC	258834_at	A13g07270	GTP cyclohydrolase I identical to GTP cyclohydrolase I (gl:19909132 from [Arabidopsis thaliana]; contains Pfam profile: PF01227 (68416.m00885)
1999	Not regulated	NC-NC-NC	258839_at	A13g07170	GTP cyclohydrolase I (68416.m00885)
2000	Not regulated	NC-NC-NC	258844_at	A13g04740	sterile alpha motif (SAM) domain-containing protein contains Pfam profile PF00536: SAM domain (Sterile alpha motif) (68416.m00854)
2001	Not regulated	NC-NC-NC	258819_at	A13g04590	expressed protein (SWP1) (68416.m00510)
2002	Not regulated	NC-NC-NC	258820_at	A13g04600	DNA-binding family protein contains a AT hook motif (DNA binding motifs with a preference for A/T rich regions), Pfam:PF02178 (68416.m00488)
2003	Not regulated	NC-NC-NC	258790_at	A13g04610	tRNA synthetase class I (W and Y) family protein contains Pfam profile: PF00579 tRNA synthetase class I (W and Y) (68416.m00490)
2004	Not regulated	NC-NC-NC	258793_at	A13g04780	KH domain-containing protein similar putative nucleic acid binding protein GB:CA33665 [Arabidopsis thaliana]; Pfam HMM hit: KH domain family of RNA binding proteins (68416.m00493)
2005	Not regulated	NC-NC-NC	258794_at	A13g04710	expressed protein (68416.m00515)
2006	Not regulated	NC-NC-NC	258796_at	A13g04630	ankyrin repeat family protein contains Pfam profile: PF00023 ankyrin repeat (68416.m00505)
2007	Not regulated	NC-NC-NC	258800_at	A13g04550	expressed protein (68416.m00495)
2008	Not regulated	NC-NC-NC	258801_at	A13g04590	expressed protein (68416.m00483)
2009	Not regulated	NC-NC-NC	258803_at	A13g04670	WRKY family transcription factor similar to elicitor response element binding protein WRKY3 isoform GB:AA83078 [Arabidopsis thaliana] (68416.m00500)
2010	Not regulated	NC-NC-NC	258810_at	A13g03870	expressed protein (68416.m00416)
2011	Not regulated	NC-NC-NC	258811_at	A13g03990	esterase/lipase/thioesterase family protein low similarity to 3-oxoacyl-CoA thioesterase (Pseudomonas sp. B13) (68416.m00420)
2012	Not regulated	NC-NC-NC	258812_at	A13g03950	GI:17738948, esterase V (Pseudomonas sp.) GI:402521, contains Interpro entry IPR000379 (68416.m00420)
2013	Not regulated	NC-NC-NC	258814_at	A13g03980	expressed protein contains Pfam profile PF04146: YTS21-B-like family (68416.m00413)
2014	Not regulated	NC-NC-NC	258815_at	A13g04000	short-chain dehydrogenase/reductase (SDR) family protein similar to short-chain type dehydrogenase/reductase SP:Q08632 [Picea abies] (68416.m00419)
2015	Not regulated	NC-NC-NC	258757_at	A13g10810	short-chain dehydrogenase/reductase (SDR) family protein similar to SP:Q08632 Short-chain type dehydrogenase/reductase (EC 1.1.1.1) [Picea abies], contains Pfam:PF00106 oxidoreductase, short chain dehydrogenase/reductase family (68416.m00421)
2016	Not regulated	NC-NC-NC	258758_at	A13g10810	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger) (68416.m01313)
2017	Not regulated	NC-NC-NC	258759_at	A13g10800	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger) (68416.m01301)
2018	Not regulated	NC-NC-NC	258771_at	A13g10770	bZIP transcription factor family protein contains Pfam profile: PF00170 bZIP transcription factor, contains similarity to TGACG-sequence specific DNA-binding protein TGA-1B (HSBF) GB:P14233 [Nicotiana tabacum] (68416.m01300)
2019	Not regulated	NC-NC-NC	258772_at	A13g10860	expressed protein (68416.m01296)
2020	Not regulated	NC-NC-NC	258773_at	A13g10730	ubiquinol-cytochrome C reductase complex ubiquinol-binding protein, putative / ubiquinol-cytochrome C reductase complex 8.2 kDa protein, putative similar to ubiquinol-cytochrome c reductase GI:633687 from [Solanum tuberosum] (68416.m01308)
2021	Not regulated	NC-NC-NC	258780_at	A13g11910	sad1/lunc-84-like 2 family protein contains 1 transmembrane domain; similar to Sad1 unc-84 domain protein 2 (GI:6538749) [Homo sapiens]; similar to Sad1/lunc-84-like protein 2 (Fragment) (Swiss-Prot:Q9UH99) [Homo sapiens] (68416.m01292)
2022	Not regulated	NC-NC-NC	258784_at	A13g11770	ubiquitin-specific protease, putative strong similarity to ubiquitin-specific protease 12 (UBP12) [Arabidopsis thaliana] (GI:11983471; contains Pfam profiles PF00443: Ubiquitin carboxyl-terminal hydrolase, PF00817: MATN domain (68416.m01460)
2023	Not regulated	NC-NC-NC	258786_at	A13g11820	expressed protein (68416.m01444)
2024	Not regulated	NC-NC-NC	258755_at	A13g11950	syntaxin 121 (SYP121) / syntaxin-related protein (SYR1) contains Pfam profiles: PF00804 syntaxin and PF05739: SNARE domain; identical to cDNA syntaxin-related protein At-SYR1 (At-SYR1) GI:4205788, SP:Q8ZSD4 Syntaxin 121 (AISYP121) (Syntaxin-related protein At-SYR1) [Arabidopsis thaliana] (68416.m01448)
2025	Not regulated	NC-NC-NC	258726_at	A13g11800	UbaA prenyltransferase family protein contains Pfam profile PF01040: UbaA prenyltransferase family (68416.m01473)
2026	Not regulated	NC-NC-NC	258729_at	A13g11900	expressed protein (68416.m01448)
2027	Not regulated	NC-NC-NC	258730_at	A13g11730	amino acid transporter family protein low similarity to proton/amine acid transporter 1 [Mus musculus] GI:21908024; belongs to INTERPRO:IPR002422 amino acid/polyamine transporter, family II (68416.m01459)
2028	Not regulated	NC-NC-NC	258747_at	A13g05810	Ras-related GTP-binding protein, putative similar to Rab1-like small GTP-binding protein GI:4096662 from [Petunia x hybrida] (68416.m01439)
2029	Not regulated	NC-NC-NC	258749_at	A13g05760	expressed protein (68416.m00652)
2030	Not regulated	NC-NC-NC	258706_at	A13g05950	expressed protein (68416.m00647)
2031	Not regulated	NC-NC-NC	258708_at	A13g05950	amine oxidase family protein low similarity to SP:IP28553 Phytoene dehydrogenase, chloroplast precursor (Phytoene desaturase) from Glycine max, contains Pfam profile PF01593 amine oxidase, flavin-containing (68416.m01138)
2032	Not regulated	NC-NC-NC	258710_s_at	A13g05980	clathrin adaptor complex small chain family protein contains Pfam profile: PF01217 clathrin adaptor complex small chain (68416.m01165)

2033	Not regulated	NC-NC-NC	258713_at	A13g08735	DNA-binding S1FA family protein contains Pfam profile: PF04689 DNA binding protein S1FA (88416.m01153)
2034	Not regulated	NC-NC-NC	258715_at	A13g08830	60S ribosomal protein L4L1 (RPL4A) strong similarity to 60S ribosomal protein L1 (88416.m01142)
2035	Not regulated	NC-NC-NC	258891_at	A13g08830	expressed protein (88416.m01002)
2036	Not regulated	NC-NC-NC	258865_at	A13g08710	thioredoxin family protein similar to thioredoxin H-type GB:P29448 SPIP29448 [Arabidopsis thaliana], Thioredoxin H-type 2 (TRX-H2) SPIQ07090 (Nicotiana tabacum); contains Pfam profile: PF00085 Thioredoxin (88416.m01012)
2037	Not regulated	NC-NC-NC	258874_at	A13g08740	elongation factor P (EF-P) family protein similar to SPIP33398 Elongation factor P (EF-P) [Escherichia coli O157:H7]; contains Pfam profile PF01132; Elongation factor P (EF-P) (88416.m01018)
2038	Not regulated	NC-NC-NC	258875_at	A13g08770	lipid transfer protein 6 (LTP6) identical to Gi:8571927 (88416.m01019)
2039	Not regulated	NC-NC-NC	258877_at	A13g08730	serine/threonine protein kinase (PK1) (PK6) identical to serine/threonine-protein kinase AIPK1/AIPK8 (ribosomal-protein S8 kinase ATPK6) [Arabidopsis thaliana] SWISS-PROT:P42818 (88416.m01015)
2040	Not regulated	NC-NC-NC	258878_at	A13g08690	ubiquitin-conjugating enzyme 11 (UBC11) E2; identical to gi:12643427, SP:P35134 (88416.m01010)
2041	Not regulated	NC-NC-NC	258879_at	A13g08590	2,3-bisphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative strong similarity to SPIQ42908 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1) (Phosphoglyceromutase) [Mesembryanthemum crystallinum]; contains Pfam profile PF01876; Metalloenzyme superfamily (88416.m00987)
2042	Not regulated	NC-NC-NC	258880_at	A13g08580	ADP, ATP carrier protein 1, mitochondrial / ADP/ATP translocase 1 / adenine nucleotide translocator 1 (ANT1) identical to SWISS-PROT:P31187 ADP,ATP carrier protein 1 (Adenine nucleotide translocator 1) [Arabidopsis thaliana] (88416.m00995)
2043	Not regulated	NC-NC-NC	258881_at	A13g08810	expressed protein (88416.m01000)
2044	Not regulated	NC-NC-NC	258882_at	A13g08720	serine/threonine protein kinase (PK19) identical to serine/threonine-protein kinase AIPK19 (Ribosomal-protein S8 kinase homolog [Arabidopsis thaliana] SWISS-PROT:Q39030 (88416.m01013)
2045	Not regulated	NC-NC-NC	258883_at	A13g08760	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (88416.m01018)
2046	Not regulated	NC-NC-NC	258836_at	A13g07890	RabGAP/TBC domain-containing protein similar to plant adhesion molecule 1 [Arabidopsis thaliana] Gi:3511223; contains Pfam profile PF00566; TBC domain (88416.m00984)
2047	Not regulated	NC-NC-NC	258837_at	A13g07880	Rho GDP-dissociation inhibitor family protein similar to SPIP52563 Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) (Homo sapiens); contains Pfam profile PF02115; RHO protein GDP dissociation inhibitor (88416.m00983)
2048	Not regulated	NC-NC-NC	258838_at	A13g07950	homodimer protein-related contains 6 transmembrane domains; similar to phosphatidylinositol glycan class T (Gi:14456615) [Homo sapiens] (88416.m00972)
2049	Not regulated	NC-NC-NC	258842_at	A13g07910	sapient3 (88416.m00986)
2050	Not regulated	NC-NC-NC	258843_at	A13g08010	expressed protein (88416.m00978)
2051	Not regulated	NC-NC-NC	258844_at	A13g07810	heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative contains Pfam profile: PF00078 RNA recognition motif (a.k.a. RRM, RBD, or RNP domain) (88416.m00955)
2052	Not regulated	NC-NC-NC	258850_at	A13g09830	protein kinase, putative similar to protein kinase [Lophopyrum elongatum] gi13022177[gbIAAK11874 (88416.m01172)
2053	Not regulated	NC-NC-NC	258851_at	A13g09920	phosphatidylinositol-4-phosphate 5-kinase family protein similar to phosphatidylinositol-4-phosphate 5-kinase AIP5K1 [Arabidopsis thaliana] Gi:3702691; contains Pfam profiles PF01504; Phosphatidylinositol-4-phosphate 5-Kinase, PF02493; MORN repeat (88416.m01183)
2054	Not regulated	NC-NC-NC	258854_at	A13g09880	expressed protein (88416.m01176)
2055	Not regulated	NC-NC-NC	258856_at	A13g09900	Ras-related GTP-binding protein, putative similar to GTP-binding protein Gi:871510 from [Pisum sativum]; contains Pfam profile: PF00071 Ras family (88416.m01180)
2056	Not regulated	NC-NC-NC	258858_at	A13g09820	adenosine kinase 1 (ADK1) / adenosine 5'-phosphotransferase 1 identical to adenosine kinase 1 / adenosine 5'-phosphotransferase 1 SP:Q8SF85 from [Arabidopsis thaliana] (88416.m01170)
2057	Not regulated	NC-NC-NC	258860_at	A13g09850	D111/G-patch domain-containing protein contains Pfam profile PF01585; G-patch domain (88416.m01175)
2058	Not regulated	NC-NC-NC	258862_at	A13g02900	expressed protein (88416.m00285)
2059	Not regulated	NC-NC-NC	258607_at	A13g02730	thioredoxin, putative similar to SPIP29450 Thioredoxin F-type, chloroplast precursor (TRX-F) [Pisum sativum]; contains Pfam profile: PF00085 Thioredoxin (88416.m00285)
2060	Not regulated	NC-NC-NC	258812_at	A13g02820	replication protein-related similar to replication protein A 30kDa [Oryza sativa (japonica cultivar-group)] Gi:13516748; contains InterPro entry IPR004365; OB-fold nucleic acid binding domain (88416.m00287)
2061	Not regulated	NC-NC-NC	258814_at	A13g02770	dimethylmenaquinone methyltransferase family protein similar to bacterial S-adenosylmethionine-2-demethylmenaquinone methyltransferases; contains Pfam profile PF03737; Dimethylmenaquinone methyltransferase (88416.m00289)
2062	Not regulated	NC-NC-NC	258815_at	A13g02740	aspartyl protease family protein contains Pfam profile: PF00026 eukaryotic aspartyl protease (88416.m00266)
2063	Not regulated	NC-NC-NC	258819_at	A13g02780	isopentenyl-diphosphate delta-isomerase II / isopentenyl diphosphate:dimethylallyl diphosphate isomerase II (IPF2) identical to isopentenyl diphosphate:dimethylallyl diphosphate isomerase (IPF2) GB:UA9259 [Arabidopsis thaliana] (88416.m00270)
2064	Not regulated	NC-NC-NC	258822_at	A13g02720	DL-1 family protein / protease-related similar to intracellular Protease [Pyrococcus horikoshii] Gi:11513902; contains Pfam profile: PF01965 ThiL/PPi family (88416.m00283)
2065	Not regulated	NC-NC-NC	258595_at	A13g04500	InterPro entry IPR000504; RNA-binding region RNP-1 (RNA recognition motif) (RRM) (88416.m00477)
2066	Not regulated	NC-NC-NC	258599_at	A13g04520	threonine aldolase family protein similar to L-allo-threonine aldolase SP:C07051 from [Aeromonas jandaei] (88416.m00478)
2067	Not regulated	NC-NC-NC	258598_at	A13g04470	expressed protein (88416.m00474)
2068	Not regulated	NC-NC-NC	258573_at	A13g04290	SAP domain-containing protein contains Pfam profile PF02037; SAP domain (88416.m00450)
2069	Not regulated	NC-NC-NC	258576_at	A13g04230	40S ribosomal protein S16 (RPS16B) similar to 40S ribosomal protein S16 GB:AA022896 [Arabidopsis thaliana] (88416.m00447)
2070	Not regulated	NC-NC-NC	258565_at	A13g04350	expressed protein (88416.m00460)
2071	Not regulated	NC-NC-NC	258566_at	A13g04110	glutamate receptor family protein (GLR1.1) (GLR1) identical to putative glutamate receptor (GLR1) GB:AF078988 [Arabidopsis thaliana]; plant glutamate receptor family, PMID:11379826 (88416.m00435)
2072	Not regulated	NC-NC-NC	258538_at	A13g06950	RNA pseudouridine synthase family protein similar to SPIP07649 RNA pseudouridine synthase A (EC 4.2.1.70) [Urcei hydrolyase] (Escherichia coli); contains Pfam profile PF01416; RNA pseudouridine synthase (88416.m00825)

2073 Not regulated	NC-NC-NC	258548_at	A13g06930	protein arginine N-methyltransferase family protein similar to protein arginine methyltransferase [Mus musculus] GI:5257221 (88416.m00822)
2074 Not regulated	NC-NC-NC	258554_at	A13g06980	DEAD/DEAH box helicase, putative contains Pfam profile: PF00270 DEAD/DEAH box helicase (88416.m00829)
				fatty acid multifunctional protein (MF2), identical to fatty acid multifunctional protein (AMFP2) GB:AF123254 (gi:4337027) (Arabidopsis thaliana) (fatty acid beta-oxidation); contains Pfam profiles PF02737 (3-hydroxyacyl-CoA dehydrogenase, NAD binding domain), PF00378 (enoyl-CoA hydratase/isomerase family protein), PF00725 (3-hydroxyacyl-CoA dehydrogenase) (88416.m00814)
2075 Not regulated	NC-NC-NC	258555_at	A13g06980	long-chain-fatty-acid-CoA ligase / long-chain acyl-CoA synthetase (LACS8) strong similarity to AMP-binding protein (MF38P) gi:161724 from Brassica napus, similar to putative long-chain-fatty-acid-CoA ligase (brain isoform) GB:P33124 [Rattus norvegicus]; contains Pfam AMP-binding enzyme domain PF00501; identical to cDNA ALAC58 for long-chain acyl-CoA synthetase expressed protein (88416.m00681)
2076 Not regulated	NC-NC-NC	258563_at	A13g06970	glycosyl hydrolase family 1 protein similar to Beta-galactosidase (SP:P22498) [Sulfolobus solfataricus]; almost identical to beta-glucosidase GB:AAF23823 GI:6085165 from [Arabidopsis thaliana] (88416.m00755)
2077 Not regulated	NC-NC-NC	258571_at	A13g06950	DNA-binding enhancer protein-related similar to huntingtin interacting protein HYPK (GI:3329429) [Homo sapiens]; identical to Egd2p (GI:172043) [Saccharomyces cerevisiae] similar to EGD2 protein (GAL4 DNA-binding enhancer protein 2) [Swiss-Prot:P36879] [Saccharomyces cerevisiae] (88416.m00768)
2079 Not regulated	NC-NC-NC	258514_at	A13g06610	ATP-citrate synthase, putative / ATP-citrate (pro-S)-lyase, putative / citrate cleavage enzyme, putative strong similarity to ATP-citrate lyase [Capsicum annuum] GI:13160653; contains Pfam profiles PF00549; CoA-ligase, PF02629; CoA binding domain (88416.m00774)
2080 Not regulated	NC-NC-NC	258515_at	A13g06650	galactokinase (GAL1) identical to galactokinase (Galactose kinase) [Arabidopsis thaliana] SWISS-PROT:Q8SEE5 (88416.m00764)
2081 Not regulated	NC-NC-NC	258517_at	A13g06580	PAPA-1-like family protein / zinc finger (HIT type) family protein contains Pfam domains, PF04795: PAPA-1-like conserved region and PF04438: HIT zinc finger (88416.m00784)
2082 Not regulated	NC-NC-NC	258522_at	A13g06660	acyl-CoA dehydrogenase-related low similarity to acyl-CoA dehydrogenase [Acinetobacter sp. NCIM89871] GI:14587418; contains Pfam profiles PF01636: Phosphotransferase enzyme family, PF00441: Acyl-CoA dehydrogenase C-terminal domain, PF02770: acyl-CoA dehydrogenase middle domain (88416.m00808)
2083 Not regulated	NC-NC-NC	258524_at	A13g06810	plastid developmental protein DAG; putative similar to DAG protein, chloroplast precursor [Garden snail] SWISS-PROT:Q38732 (88416.m00806)
2084 Not regulated	NC-NC-NC	258526_at	A13g06790	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein weak similarity to polygalacturonase [Pensea americana] GI:166951; contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases) (88416.m00802)
2085 Not regulated	NC-NC-NC	258528_at	A13g06770	importin alpha-1 subunit, putative (IMP1) similar to importin alpha-1 subunit [Karyophen alpha-1 subunit, KAP alpha] [Arabidopsis thaliana] SWISS-PROT:Q86321 (88416.m00786)
2086 Not regulated	NC-NC-NC	258531_at	A13g06720	thioredoxin family protein contains Pfam profile: PF00085 Thioredoxin (88416.m00788)
2087 Not regulated	NC-NC-NC	258534_at	A13g06730	hydroxyproline-rich glycoprotein family protein contains proline-rich extensin domains, INTERPRO:IPR002965 (88416.m00800)
2088 Not regulated	NC-NC-NC	258535_at	A13g06750	tRNA synthetase class I (W and Y) family protein similar to SPIP00952 Tyrosyl-tRNA synthetase (EC 6.1.1) (Tyrosine-tRNA ligase) (TyRS) [Bacillus stearothermophilus]; contains Pfam profiles PF00578: tRNA synthetases class I (W and Y), PF01478: S4 domain (88416.m00257)
2089 Not regulated	NC-NC-NC	258475_at	A13g02660	Chaperonin, putative similar to SWISS-PROT:P80317: T-complex protein 1, zeta subunit (TCP-1-zeta) [Mus musculus]; contains Pfam-PF00118 domain, TCP-1/cpn60 chaperonin family (88416.m00241)
2090 Not regulated	NC-NC-NC	258482_at	A13g02530	expressed protein (88416.m00229)
2091 Not regulated	NC-NC-NC	258488_at	A13g02420	14-3-3 protein GF14 nu (GRF7) identical to 14-3-3 protein GF14 nu GI:1531631 from [Arabidopsis thaliana] (88416.m00240)
2092 Not regulated	NC-NC-NC	258489_at	A13g02520	NC domain-containing protein contains Pfam domain, PF04970: NC domain (88416.m00281)
2093 Not regulated	NC-NC-NC	258491_at	A13g02700	cell division protein tsH, putative similar to SWISS-PROT:P46469 cell division protein tsH homolog [Lactococcus lactis]; contains Pfam domain, PF00004: ATPase, AAA family (ATPases 'A' associated with diverse cellular 'A' activities) (88416.m00232)
2094 Not regulated	NC-NC-NC	258494_at	A13g02450	integral membrane family protein similar to PcdM protein (GI:5852331) [Vogelia indigofera] and PcdM protein (SP:P42194) [Erwinia chrysanthemi] (88416.m00280)
2095 Not regulated	NC-NC-NC	258495_at	A13g02690	plant adhesion molecule, putative strong similarity to plant adhesion molecule 1 [Arabidopsis thaliana] GI:3511223; contains Pfam profile PF00566: TBC domain (88416.m00233)
2096 Not regulated	NC-NC-NC	258496_at	A13g02460	short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family IPR002188 short-chain dehydrogenase/reductase (SDR) superfamily (88416.m00693)
2097 Not regulated	NC-NC-NC	258467_at	A13g06060	alkyl hydroperoxide reductase/ethiol specific antioxidant (Ahpc/TSA)/mal allergen family protein identical to SPIQ9M770 Putative peroxidase, mitochondrial precursor [Arabidopsis thaliana]; similar to thioredoxin peroxidase [Capsicum annuum] GI:18654477; contains Pfam profile: PF00578 Ahpc/TSA (alkyl hydroperoxide reductase and thiol-specific antioxidant) family (88416.m00692)
2098 Not regulated	NC-NC-NC	258469_at	A13g06050	expressed protein (88416.m02816)
2099 Not regulated	NC-NC-NC	258448_at	A13g02290	hydroxyproline-rich glycoprotein family protein identical to hydroxyproline-rich glycoprotein [Arabidopsis thaliana]
2100 Not regulated	NC-NC-NC	258455_at	A13g02440	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (88416.m02829)
2101 Not regulated	NC-NC-NC	258456_at	A13g02240	dihydropyrimidine dehydrogenase 2, mitochondrial / liponamide dehydrogenase 2 (MTLDP2) nearly identical to GB:AAF34796 (gi:6994216) from [Arabidopsis thaliana]; alternative splice form exons (88416.m02202)
2102 Not regulated	NC-NC-NC	258439_at	A13g17240	expressed protein (88416.m02211)
2103 Not regulated	NC-NC-NC	258413_at	A13g17300	expressed protein (88416.m02129)
2104 Not regulated	NC-NC-NC	258418_at	A13g16660	expressed protein (88416.m02129)

2105	Not regulated	NC-NC-NC	258430_at	A13g16785	phospholipase D zeta1 / PLDzeta1 (PLDP1) identical to phospholipase D zeta1 [Arabidopsis thaliana] Gi:15723315. SPOBLRZ5 Phospholipase D p1 (EC 3.1.4.4) (APLDP1) (Phospholipase D1 PHOX and PX containing domain) (Phospholipase D zeta 1) (PLDzeta1) [Arabidopsis thaliana]; supported by cDNA gi:15723314; non-consensus splice site (GC) at the beginning of first intron. (68416.m02143)
2106	Not regulated	NC-NC-NC	258432_at	A13g16570	rapid alkalization factor (RALF) family protein similar to RALF precursor [Nicotiana tabacum] Gi:16560316 (68416.m02119) translationally controlled tumor family protein similar to translationally controlled tumor protein GB:AA10032 from [Hevea brasiliensis] (68416.m02127)
2107	Not regulated	NC-NC-NC	258433_at	A13g16640	F-box family protein contains F-box domain Pfam:PF00846 (68416.m02137)
2108	Not regulated	NC-NC-NC	258435_at	A13g16740	protein phosphatase 2C-related / PP2C-related contains protein phosphatase 2C domain (68416.m02116)
2109	Not regulated	NC-NC-NC	258437_at	A13g16560	peptidyl-prolyl cis-trans isomerase TL P38, chloroplast / thylakoid lumen PPIase of 38 kDa / cyclophilin / rotamase cyclophilin-type; identical to SPIP82869 Thylakoid lumenal 38 kDa protein, chloroplast precursor (P38) [Arabidopsis thaliana] (68416.m01987) leucine-rich repeat family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains leucine-rich repeat family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, identical to leucine-rich repeat protein [Arabidopsis thaliana] gi:2760084 (68416.m01955)
2110	Not regulated	NC-NC-NC	258386_at	A13g15520	similarity to Hcr2-5D [Lycopodium obscurum] gi:3894333 (68416.m01955)
2111	Not regulated	NC-NC-NC	258390_at	A13g15410	expressed protein (68416.m01963)
2112	Not regulated	NC-NC-NC	258393_at	A13g15480	expressed protein (68416.m01968)
2113	Not regulated	NC-NC-NC	258394_at	A13g15530	brx domain-containing protein contains Pfam domain, PF04427: Brx domain (68416.m01981)
2114	Not regulated	NC-NC-NC	258396_at	A13g15460	regulator of chromosome condensation (RCC1) family protein low similarity to UVB-resistance protein UVR8 [Arabidopsis thaliana] (68416.m01957)
2115	Not regulated	NC-NC-NC	258401_at	A13g15430	regulator of chromosome condensation (RCC1) family protein low similarity to UVB-resistance protein UVR8 [Arabidopsis thaliana] (68416.m01957)
2116	Not regulated	NC-NC-NC	258403_at	A13g15380	choline transporter-related contains weak similarity to CD92 protein [Homo sapiens] gi:16845323 (68416.m01950)
2117	Not regulated	NC-NC-NC	258406_at	A13g17815	leucine-rich repeat transmembrane protein kinase, putative similar to leucine-rich repeat transmembrane protein kinase 1 (68416.m01814)
2118	Not regulated	NC-NC-NC	258357_at	A13g14350	GB:AA227894 from [Zea mays] (68416.m01814)
2119	Not regulated	NC-NC-NC	258365_s_at	A13g14390	diaminopimelate decarboxylase, putative / DAP carboxylase, putative similar to diaminopimelate decarboxylase [Arabidopsis thaliana] Gi:8562332; contains Pfam profiles PF02784: Pyridoxal-dependent decarboxylase pyridoxal binding domain, PF00278: Pyridoxal-dependent decarboxylase C-terminal sheet domain (68416.m01820)
2120	Not regulated	NC-NC-NC	258371_at	A13g14410	transporter-related low similarity to SPIQ86A29 GDP-Lucose transporter 1 (Homo sapiens), phosphoenolpyruvate/phosphate translocator precursor [Mesembryanthemum crystallinum] Gi:9295275; contains 10 predicted transmembrane domains; (68416.m01823)
2121	Not regulated	NC-NC-NC	258373_at	A13g14290	20S proteasome alpha subunit E2 (PAE2) identical to 20S proteasome subunit PAE2 GB:AA32081 from [Arabidopsis thaliana] (68416.m01808)
2122	Not regulated	NC-NC-NC	258375_at	A13g22750	protein kinase, putative similar to protein kinase ATM/K1 [Arabidopsis thaliana] gi:2351097 (68416.m02889)
2123	Not regulated	NC-NC-NC	258324_at	A13g22780	CXC domain protein (TSO1) identical to CXC domain protein TSO1 [Arabidopsis thaliana] Gi:7787425 (68416.m02872)
2124	Not regulated	NC-NC-NC	258329_at	A13g16110	thioredoxin family protein similar to protein disulfide isomerase Gi:5902592 from [Volvox carterii f. nagariensis], Gi:2708314 from [Chlamydomonas reinhardtii]; contains Pfam profile: PF00085 Thioredoxin (68416.m02035)
2125	Not regulated	NC-NC-NC	258313_at	A13g15970	Ran-binding protein 1 domain-containing protein / RanBP1 domain (68416.m02019)
2126	Not regulated	NC-NC-NC	258314_at	A13g16100	Gi:824232; contains Pfam profile PF00638: RanBP1 domain (68416.m02019)
2127	Not regulated	NC-NC-NC	258285_at	A13g16140	Ras-related GTP-binding family protein contains Pfam profile: PF00071 Ras family (68416.m02034)
2128	Not regulated	NC-NC-NC	258293_at	A13g23430	photosystem I reaction center subunit VI, chloroplast, putative / PSI-H, putative (PSAH1) identical to PSIQ9SU7; similar to PSI-H precursor [Nicotiana sylvestris] Gi:407353; contains Pfam profile PF03244: Photosystem I reaction center subunit VI (68416.m02038)
2129	Not regulated	NC-NC-NC	258295_at	A13g23400	phosphate transporter, putative (PHO1) identical to PHO1 protein [Arabidopsis thaliana] Gi:20069032; supporting cDNA gi:20069031 (68416.m02038)
2130	Not regulated	NC-NC-NC	258297_at	A13g23325	plastid-lipid associated protein PAP / fibrillin family protein contains Pfam profile PF04755: PAP_fibrillin (68416.m02850)
2131	Not regulated	NC-NC-NC	258298_at	A13g23300	splicing factor, putative similar to Splicing factor 3B subunit 10 (SF3b10) (Pre-mRNA splicing factor SF3b 10 kDa subunit) (Swiss-Prot:Q8BWJ5) [Homo sapiens] (68416.m02942)
2132	Not regulated	NC-NC-NC	258310_at	A13g26744	dehydration-responsive protein-related similar to early-responsive to dehydration stress ERD3 protein [Arabidopsis thaliana] Gi:15320410; contains Pfam profile PF03141: Putative methyltransferase (68416.m02939)
2133	Not regulated	NC-NC-NC	258311_at	A13g26810	basix helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain (68416.m03344)
2134	Not regulated	NC-NC-NC	258281_at	A13g26900	transport inhibitor response protein, putative E3 ubiquitin ligase SCF complex F-box subunit; similar to transport inhibitor response 1 Gi:2352492 from [Arabidopsis thaliana] (68416.m03354)
2135	Not regulated	NC-NC-NC	258253_at	A13g26760	shikimate kinase family protein similar to shikimate kinase precursor GB:CAA45121 [Lycopodium obscurum]; contains Pfam shikimate kinase domain PF01202 (68416.m03368)
2136	Not regulated	NC-NC-NC	258256_at	A13g26890	short-chain dehydrogenase/reductase (SDR) family protein similar to sex determination protein tasselseed 2 SP:PS0180 from [Zea mays] (68416.m03347)
2137	Not regulated	NC-NC-NC	258266_at	A13g15880	expressed protein (68416.m03384)
2138	Not regulated	NC-NC-NC	258269_at	A13g15690	WD-40 repeat family protein contains Pfam profile: PF00400 WD domain, G-beta repeat (7 copies) (68416.m02008)
2139	Not regulated	NC-NC-NC	258273_at	A13g15660	biotin carboxyl carrier protein of acetyl-CoA carboxylase-related contains weak similarity to Biotin carboxyl carrier protein of acetyl-CoA carboxylase, chloroplast precursor (BCCP) [Swiss-Prot:Q42533] [Arabidopsis thaliana] (68416.m01988)
2140	Not regulated	NC-NC-NC	258275_at	A13g15760	glutaredoxin family protein contains Pfam profile PF00462: Glutaredoxin (68416.m01985)
2141	Not regulated	NC-NC-NC	258249_s_at	A13g15820	expressed protein (68416.m01986)
					phosphatidic acid phosphatase-related / PAP2-related contains Pfam profile PF01568: PAP2 superfamily (68416.m02002)

2142 Not regulated	NC-NC-NC	258250_at	A3g15850	fatty acid desaturase family protein similar to delta 9 acyl-lipid desaturase (ADS1) Gi:2970034 from [Arabidopsis thaliana] (68416.m02005)
2143 Not regulated	NC-NC-NC	258251_at	A3g15810	expressed protein contains Pfam profile PF04525: Protein of unknown function (DUF567) (68416.m02001)
2144 Not regulated	NC-NC-NC	258223_at	A3g15840	expressed protein (68416.m02004)
				chlorophyll A-B binding protein (LHC82-4) nearly identical to Lhc2 protein [Arabidopsis thaliana] Gi:4741950; similar to chlorophyll A-B binding protein 151 precursor (LHCP) GB:P27518 from [Gossypium hirsutum]; contains Pfam PF00504: Chlorophyll A-B binding protein (68416.m03457)
2145 Not regulated	NC-NC-NC	258239_at	A3g27890	glycine-rich protein / oleosin identical to oleosin isoform GB:S71286 from [Arabidopsis thaliana], identical to cDNA oleosin (isoform Ato2) Gi:987013 (68416.m03454)
2146 Not regulated	NC-NC-NC	258240_at	A3g27860	expressed protein (68416.m03457)
2147 Not regulated	NC-NC-NC	258244_at	A3g27770	expressed protein (68416.m03465)
				Snr1-related protein kinase (KIN11) identical to protein kinase AKin11 Gi:1729444 from [Arabidopsis thaliana] (68416.m03852)
2148 Not regulated	NC-NC-NC	258221_at	A3g29160	pectinesterase family protein similar to pectinesterase precursor GB:Q43043 [Petunia integrifolia]; contains Pfam profile: PF01095 pectinesterase (68416.m03842)
2149 Not regulated	NC-NC-NC	258193_at	A3g29090	expressed protein contains Pfam PF05915: Eukaryotic protein of unknown function (DUF872) (68416.m03855)
2150 Not regulated	NC-NC-NC	258194_at	A3g29170	expressed protein (68416.m01757)
2151 Not regulated	NC-NC-NC	258201_at	A3g13910	expressed protein weak similarity to DNA-directed RNA polymerase I 49 kDa polypeptide (EC 2.7.7.8) (A49) (Swiss-Prot:O14086) [Schizosaccharomyces pombe]; similar to Nuclear pore complex protein Nup107 (Nucleoporin Nup107) (107 kDa nucleoporin) (p105) (Swiss-Prot:P52590) [Rattus norvegicus] (68416.m01780)
				hydroxyproline-rich glycoprotein family protein similar to Mra16p (Gi:2737884) [Saccharomyces cerevisiae]; weak similarity to ataxin 2 related protein (Gi:1679686) [Homo sapiens] (68416.m01789)
2152 Not regulated	NC-NC-NC	258202_at	A3g13940	RelA/Spot1 protein, putative (RSH2) nearly identical to RelA/Spot1 homolog RSH2 [Arabidopsis thaliana] Gi:7141306; contains Pfam profiles PF01986: HD domain, PF04607: Region found in RelA / Spot1 proteins (68416.m01773)
2153 Not regulated	NC-NC-NC	258206_at	A3g14010	eukaryotic translation initiation factor 4A-1 / eIF-4A-1 gi:15293046, gi:15450485; contains Pfam profile PF00270: DEAD/DEAH box helicase; contains Pfam profile PF00271: Helicase conserved C-terminal domain (68416.m01758)
2154 Not regulated	NC-NC-NC	258207_at	A3g14050	expressed protein (68416.m02279)
2155 Not regulated	NC-NC-NC	258210_at	A3g13920	leucine-rich repeat family protein contains leucine rich repeat (LRR) domains, Pfam:PF00560 (68416.m02282)
2156 Not regulated	NC-NC-NC	258211_at	A3g17890	tetratricoredoxin (TRX-H) identical to tetratricoredoxin [Arabidopsis thaliana] Gi:18041544; similar to SPIQ42443 Thoredoxin H-type (TRX-H) (Phloem sap 13 kDa protein-1) [Oryza sativa]; contains Pfam profile: PF00085 Thoredoxin (68416.m02278)
2157 Not regulated	NC-NC-NC	258212_at	A3g17830	expressed protein (68416.m02276)
				expressed protein (68416.m02283)
				dihydroorotate dehydrogenase family protein / dihydroorotate oxidase family protein low similarity to SPIQ12862 Dihydropyrimidine dehydrogenase [NADP+] precursor (EC 1.3.1.2) (DPD) (DHPDase) (Dihydroorotate dehydrogenase) (Dihydrothymine dehydrogenase) [Homo sapiens]; contains Pfam profile PF01180: Dihydroorotate dehydrogenase (68416.m02271)
2161 Not regulated	NC-NC-NC	258162_at	A3g17810	aldose 1-epimerase family protein similar to ALDOSE-1-EPIMERASE PRECURSOR GB:POS149 [SP POS149] from [Acinetobacter calcoaceticus]; contains Pfam profile PF01263 Aldose 1-epimerase (68416.m02284)
2162 Not regulated	NC-NC-NC	258163_at	A3g17940	expressed protein (68416.m02280)
2163 Not regulated	NC-NC-NC	258165_at	A3g17900	UDP-glucosyltransferase, putative similar to UDP-glucose:sinapate glucosyltransferase Gi:9794913 from [Brassica napus] (68416.m02719)
2164 Not regulated	NC-NC-NC	258167_at	A3g21560	senescence/dehydration-associated protein-related similar to senescence-associated protein 12 [Hemerocallis hybrid cultivar] (68416.m02718)
				gi:3551858[gb AAC34857], similar to early-responsive to dehydration stress ERD7 protein [Arabidopsis thaliana]
2165 Not regulated	NC-NC-NC	258170_at	A3g21600	gi:15320412[dbj BA863916] (68416.m02724)
2166 Not regulated	NC-NC-NC	258171_at	A3g21810	expressed protein contains Pfam domain, PF02681: Uncharacterized BCR, COG1983 (68416.m02726)
2167 Not regulated	NC-NC-NC	258173_at	A3g21830	protein kinase family protein contains protein kinase domain, Pfam:PF00089 (68416.m02728)
				serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative similar to SWISS-PROT:Q28653 serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, delta isoform (PP2A, B subunit, B' delta isoform, PP2A, B subunit, B56 delta isoform, PP2A, B subunit, PR81 delta isoform, PP2A, B subunit, R5 delta isoform, PP2A, B subunit, B' gamma) [Cytococcus curculius]; contains Pfam profile PF01603: Protein phosphatase 2A regulatory B subunit (B56 family) (68416.m02730)
2168 Not regulated	NC-NC-NC	258176_at	A3g21650	nitrate transporter (NTPs) nearly identical to nitrate transporter [Arabidopsis thaliana] Gi:4490323; contains Pfam profile: PF00854 POT family (68416.m02732)
2169 Not regulated	NC-NC-NC	258181_at	A3g21670	peroxisomal membrane 22 kDa family protein contains Mpv17 / PMP22 family domain, Pfam:PF04117 (68416.m03087)
2170 Not regulated	NC-NC-NC	258127_at	A3g24570	signal peptidase I family protein contains Pfam profile: PF00461 signal peptidase I (68416.m03088)
2171 Not regulated	NC-NC-NC	258128_at	A3g24590	aldohydroxy dehydrogenase (ALDH1a) identical to aldohydroxy dehydrogenase ALDH1a [Arabidopsis thaliana]
2172 Not regulated	NC-NC-NC	258140_at	A3g24503	transducin family protein / WD-40 repeat family protein similar to 66 kDa stress protein (SP:P80587) [Physarum polycephalum]
				gi:20530143[gb AA027004] (68416.m03074)
				transducin family protein / WD-40 repeat family protein similar to 66 kDa stress protein (SP:P80587) [Physarum polycephalum]
2173 Not regulated	NC-NC-NC	258146_at	A3g18060	(Slime mold); similar to WDR1 protein GB:AA005042 [Gallus gallus] [Genomics 56 (1), 59-68 (1996)]; contains 11 WD-40 repeats (PF00400) (68416.m02287)
2174 Not regulated	NC-NC-NC	258149_at	A3g18110	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile: PF01535 PPR repeat (68416.m02303)
				expressed protein similar to DAM1 (Gi:39859530) [Homo sapiens]; contains Pfam profile PF05700: Breast carcinoma amplified sequence 2 (BCAS2) (68416.m02311)
2175 Not regulated	NC-NC-NC	258153_at	A3g18165	expressed protein contains Pfam profile PF04654: Protein of unknown function, DUF599 (68416.m02317)
2176 Not regulated	NC-NC-NC	258124_at	A3g18215	expressed protein; expression supported by MPSS (68416.m02982)
2177 Not regulated	NC-NC-NC	258099_at	A3g23540	dienelactone hydrolase family protein similar to SPIQ92768 Endo-1,3,1,4-beta-D-glucanase precursor (EC 3.2.1.-) [Zea mays]; contains Pfam profile: PF01738 Dienelactone hydrolase family (68416.m02988)
2178 Not regulated	NC-NC-NC	258102_at	A3g23600	

2179	Not regulated	NC-NC-NC	258104_at	A13g23620	bix domain-containing protein contains Pfam domain, PF04427; Bix domain (68416.m02971)
2180	Not regulated	NC-NC-NC	258106_at	A13g23580	ribonucleoside-diphosphate reductase small chain / ribonucleoside reductase nearly identical to SPIP50631 Ribonucleoside-diphosphate reductase small chain (EC 1.17.4.1) (Ribonucleoside reductase) (R2 subunit) (Arabidopsis thaliana) (68416.m02966)
2181	Not regulated	NC-NC-NC	258108_at	A13g23570	dieneleone hydrolase family protein similar to SPIQ82766 Endo-1,3;1,4-beta-D-glucanase precursor (EC 3.2.1.-) (Zea mays); contains Pfam profile: PF01736 dieneleone hydrolase family (68416.m02965)
2182	Not regulated	NC-NC-NC	258113_at	A13g14650	cytochrome P450, putative similar to GB:Q05047 from [Catharanthus roseus] (68416.m01854)
2183	Not regulated	NC-NC-NC	258092_at	A13g14595	expressed protein (68416.m01848)
2184	Not regulated	NC-NC-NC	258094_at	A13g14680	cytochrome P450, putative similar to GB:Q05047 from [Catharanthus roseus] (68416.m01857)
2185	Not regulated	NC-NC-NC	258071_s_at	A13g26070	plasma-lipid associated protein PAP / fibrillin family protein contains Pfam profile PF04755: PAP_fibrillin (68416.m03246)
2186	Not regulated	NC-NC-NC	258072_at	A13g26090	expressed protein (68416.m03249)
2187	Not regulated	NC-NC-NC	258075_at	A13g25900	homocysteine S-methyltransferase 1 (HMT-1) identical to GB:AAF23821 from [Arabidopsis thaliana] (68416.m03227)
2188	Not regulated	NC-NC-NC	258076_at	A13g25920	SOS ribosomal protein L15, chloroplast (CL15) identical to GB:P25873 from [Arabidopsis thaliana] (68416.m03231)
2189	Not regulated	NC-NC-NC	258081_at	A13g26085	CAAX amino terminal protease family protein contains Pfam profile PF02517 CAAX amino terminal protease family protein (68416.m03248)
2190	Not regulated	NC-NC-NC	258088_at	A13g25860	hydrolytic S-acetyltransferase (LTA2) identical to dihydroisopropylamide S-acetyltransferase (LTA2) [Arabidopsis thaliana] (68416.m03222)
2191	Not regulated	NC-NC-NC	258087_at	A13g26060	peroxiredoxin Q, putative similar to peroxiredoxin Q [Sedum lineare] GI:6899842; contains Pfam profile: PF00578 AhpC/TSA (alkyl hydroperoxide reductase and thiol-specific antioxidant) family (68416.m03245)
2192	Not regulated	NC-NC-NC	258061_at	A13g25910	expressed protein (68416.m03230)
2193	Not regulated	NC-NC-NC	258062_at	A13g26000	F-box family protein contains Pfam PF00648: F-box domain; similar to SKP1 interacting partner 2 (SKIP2) TGR_Ath1A15g67250 (68416.m03239)
2194	Not regulated	NC-NC-NC	258033_at	A13g21250	ABC transporter family protein similar to MRP-like ABC transporter GB:AAAC49781 from [Arabidopsis thaliana] (68416.m02865)
2195	Not regulated	NC-NC-NC	258038_at	A13g21260	glycolipid transfer protein-related contains weak similarity to Glycolipid transfer protein (GLTP) (Swiss-Prot P17403) [Sus scrofa] (68416.m02886)
2196	Not regulated	NC-NC-NC	258039_at	A13g21200	expressed protein (68416.m02679)
2197	Not regulated	NC-NC-NC	258044_at	A13g21270	Dof-type zinc finger domain-containing protein (ADOE2) identical to Dof zinc finger protein ADOF2 GI:3608263 from [Arabidopsis thaliana]; identical to cDNA adoz2 mRNA for Dof zinc finger protein GI:3608262; contains Pfam profile PF02701: Dof domain, zinc finger (68416.m02688)
2198	Not regulated	NC-NC-NC	258045_at	A13g21280	ubiquitin-specific protease 7, putative (UBP7) similar to GI:11963487 (68416.m02689)
2199	Not regulated	NC-NC-NC	258046_at	A13g18220	expressed protein similar to CG1-18 protein GB:AA027727 [Homo sapiens] (68416.m02047)
2200	Not regulated	NC-NC-NC	258050_at	A13g18200	expressed protein (68416.m02045)
2201	Not regulated	NC-NC-NC	258052_at	A13g18190	isochromatase hydrolase family protein low similarity to SPIP32400 N-carbamoylcarbamate amidase (EC 3.5.1.59) (N-carbamoylcarbamate amidohydrolase) (Arthrobacter sp); contains Pfam profile PF00857: isochromatase family protein (68416.m02044)
2202	Not regulated	NC-NC-NC	258054_at	A13g18240	delta tonoplast integral protein (delta-TIP) identical to delta tonoplast integral protein (delta-TIP) (GI:9278707) (GB:U39485) [Arabidopsis thaliana] (Plant Cell 8 (4): 587-599 (1996)) (68416.m02049)
2203	Not regulated	NC-NC-NC	258055_at	A13g18250	ferredoxin-related contains Pfam profile: PF00111 2Fe-2S iron-sulfur cluster binding domains (68416.m02050)
2204	Not regulated	NC-NC-NC	258057_at	A13g26970	expressed protein contains Pfam domain PF03556: Domain of unknown function (DUF288) (68416.m03821)
2205	Not regulated	NC-NC-NC	258020_at	A13g19490	sodium hydrogen antiporter, putative similar to NhaD [Vibrio parahaemolyticus] gi 3123728 dbj BAJ25964; Na+/H+ antiporter (NhaD) family member, PMID:11500563 (68416.m02470)
2206	Not regulated	NC-NC-NC	258022_at	A13g19460	reticulon family protein (RTNLB11) weak similarity to neuroendocrine-specific protein C [Homo sapiens] (GI:307311; identical to cDNA RTNLB11 GI:32331878 (68416.m02467)
2207	Not regulated	NC-NC-NC	258026_at	A13g19290	ABA-responsive element-binding protein 2 (AREB2) almost identical (one amino acid) to GB:AAF27182 from [Arabidopsis thaliana]; contains Pfam profile PF00170 bZIP transcription factor; identical to cDNA abscisic acid responsive element-binding factor (ABRE) mRNA, partial cds GI:6739282 (68416.m02446)
2208	Not regulated	NC-NC-NC	257972_at	A13g27560	protein kinase (ATN1) almost identical (1 amino acid difference) to protein kinase ATN1 [Arabidopsis thaliana]
2209	Not regulated	NC-NC-NC	257973_at	A13g20720	gi 1054633 emb CAA63387 (68416.m03444)
2210	Not regulated	NC-NC-NC	257981_at	A13g20770	expressed protein (68416.m02622)
2211	Not regulated	NC-NC-NC	257983_at	A13g20790	ethylene-insensitive 3 (EIN3) identical to ethylene-insensitive3 GI:2224933 from [Arabidopsis thaliana] (68416.m02627)
2212	Not regulated	NC-NC-NC	257984_at	A13g20800	oxidoreductase family protein weak similarity to SPIQ07982 Glucose-fructose oxidoreductase precursor (EC 1.1.99.28) (Zymomonas mobilis); contains Pfam profiles PF01408: Oxidoreductase family NAD-binding Rossmann fold, PF02894: Oxidoreductase family C-terminal alpha/beta domain (68416.m02829)
2213	Not regulated	NC-NC-NC	257988_at	A13g20800	rdc1-like cell differentiation protein, putative similar to protein involved in sexual development [Schizosaccharomyces pombe]
2214	Not regulated	NC-NC-NC	257989_at	A13g18770	GI:1620896; contains Pfam profile PF04078: Cell differentiation family, Rcd1-like (68416.m02630)
2215	Not regulated	NC-NC-NC	257996_at	A13g18860	vacuolar sorting protein 9 domain-containing protein / VPS9 domain-containing protein contains Pfam domain PF02204: Vacuolar sorting protein 8 (VPS8) domain (68416.m02502)
2216	Not regulated	NC-NC-NC	257998_at	A13g18860	basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain (68416.m02515)
2217	Not regulated	NC-NC-NC	257982_at	A13g19950	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00087: Zinc finger, C3HC4 type (RING finger) (68416.m02525)
2218	Not regulated	NC-NC-NC	257984_at	A13g19850	hypothetical protein; expression supported by MPSS (68416.m02506)
2219	Not regulated	NC-NC-NC	257985_at	A13g19800	phototropic-responsive NPH3 family protein contains NPH3 family domain, Pfam:PF03000 (68416.m02514)
2220	Not regulated	NC-NC-NC	257986_at	A13g19800	expressed protein (68416.m02502)

2220	Not regulated	NC-NC-NC	257987_at	A13g19910	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00087 zinc finger, C3HC4 type (RING finger) (88416.m02521)
2221	Not regulated	NC-NC-NC	257937_at	A13g18810	expressed protein contains Pfam PF02620: Uncharacterized ACR, COG1399 (88416.m02509)
2222	Not regulated	NC-NC-NC	257939_at	A13g19930	sugar transport protein (STP4) identical to GB_S25009 Gi:16524 from [Arabidopsis thaliana] (88416.m02523)
2223	Not regulated	NC-NC-NC	257940_at	A13g21790	UDP-glucuronosyl(UDP-glucosyl) transferase family protein contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase (88416.m02748)
2224	Not regulated	NC-NC-NC	257953_at	A13g21865	expressed protein (88416.m02756)
2225	Not regulated	NC-NC-NC	257954_at	A13g21760	UDP-glucuronosyl(UDP-glucosyl) transferase family protein contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase (88416.m02745)
2226	Not regulated	NC-NC-NC	257933_at	A13g25585	aminoalcoholphosphotransferase, putative strong similarity to aminoalcoholphosphotransferase [Arabidopsis thaliana] (Gi:3681593); contains Pfam profile PF01066: CDP-alcohol phosphatidyltransferase (88416.m03182)
2227	Not regulated	NC-NC-NC	257906_at	A13g25520	60S ribosomal protein L5 similar to 60S ribosomal protein L5 GB:P46825 from [Onyza sativa] (88416.m03173)
2228	Not regulated	NC-NC-NC	257907_at	A13g25470	bacterial hemolysin-related similar to hemolysin GB:AA036643 from [Thermotoga maritima], contains Pfam profile: PF01479 S4 domain (88416.m03166)
2229	Not regulated	NC-NC-NC	257909_at	A13g25480	rhodanese-like domain-containing protein contains Rhodanese-like domain PF:00581 (88416.m03167)
2230	Not regulated	NC-NC-NC	257911_at	A13g25530	6-phosphogluconate dehydrogenase NAD-binding domain-containing protein low similarity to SPIP23523 2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) (Tarronate semialdehyde reductase) [Escherichia coli]; contains Pfam profile PF03446: NAD binding domain of 6-phosphogluconate dehydrogenase; supporting cDNA gil15375087/gilAY044183.1] (88416.m03174)
2231	Not regulated	NC-NC-NC	257913_at	A13g25540	longevity-assurance (LAG1) family protein similar to Alternaria stem canker resistance protein (ASC1) [Lycopersicon esculentum] (Gi:7688742); contains Pfam profile PF03798: Longevity-assurance protein (LAG1); supporting cDNA
2232	Not regulated	NC-NC-NC	257914_at	A13g25545	expressed protein (88416.m03175)
2233	Not regulated	NC-NC-NC	257916_at	A13g23210	basic helix-loop-helix (bHLH) family protein similar to hypothetical protein GB:CAB10220 from [Arabidopsis thaliana] (88416.m02926)
2234	Not regulated	NC-NC-NC	257924_at	A13g23190	lesion inducing protein-related similar to ORF, able to induce HR-like lesions [Nicotiana tabacum] (88416.m02924)
2235	Not regulated	NC-NC-NC	257926_at	A13g23280	zinc finger (C3HC4-type RING finger) family protein / ankyrin repeat family protein contains Pfam profile: PF00087 zinc finger, C3HC4 type (RING finger) and Pfam profile: PF00023 ankyrin repeat (88416.m02934)
2236	Not regulated	NC-NC-NC	257932_at	A13g17040	tetrahelical repeat (TPR)-containing protein low similarity to SP-IC8PNSA P5bB mRNA maturation factor Mbb1, chloroplast precursor (Chlamydomonas reinhardtii); contains Pfam profile: PF00515: TPR Domain (88416.m02175)
2237	Not regulated	NC-NC-NC	257878_at	A13g17160	expressed protein (88416.m02189)
2238	Not regulated	NC-NC-NC	257880_at	A13g16910	AMP-dependent synthetase and ligase family protein similar to AMP-binding protein Gi:1903034 from [Brassica napus]; contains Pfam AMP-binding domain PF00501; identical to cDNA adenosine monophosphate binding protein 7 AMPBP7 (AMPBP7) (88416.m02162)
2239	Not regulated	NC-NC-NC	257887_at	A13g17090	protein phosphatase 2C family protein / PP2C family protein similar to Ser/Thr protein phosphatase 2C (PP2C8) (Gi:15020818) [Arabidopsis thaliana]; similar to protein phosphatase 2C (Gi:3608412) [Mesembryanthemum crystallinum]; contains Pfam PF00481 : Protein phosphatase 2C domain; (88416.m02180)
2240	Not regulated	NC-NC-NC	257892_at	A13g17020	universal stress protein (USP) family protein similar to early nodulin ENOD18 [Vicia faba] (Gi:11602747); contains Pfam profile PF00552: universal stress protein family (88416.m02173)
2241	Not regulated	NC-NC-NC	257893_at	A13g17000	ubiquitin-conjugating enzyme, putative similar to Non-Canonical Ubiquitin Conjugating Enzyme 1 (NCUBE1) from [Gallus gallus] : enzyme (88416.m02171)
2242	Not regulated	NC-NC-NC	257894_at	A13g17100	Gi:7382937, [Mus musculus] Gi:7383050, [Homo sapiens] Gi:7382973; contains Pfam profile PF00178: Ubiquitin-conjugating expressed protein (88416.m02181)
2243	Not regulated	NC-NC-NC	257895_at	A13g16950	dihydrolipoamide dehydrogenase 1, plastidic / liposamide dehydrogenase 1 (PTLPD1) identical to plastidic liposamide dihydrolipoamide dehydrogenase 1, plastidic [gi:7159282] (88416.m02166)
2244	Not regulated	NC-NC-NC	257897_at	A13g18030	halotolerance protein (HAL3A) identical to GB:AA051616 from [Arabidopsis thaliana]; similar to Halotolerance protein Hal3b (SP:P94063)[Arabidopsis thaliana]; contains Pfam PF02441: Flavoprotein (88416.m02291)
2245	Not regulated	NC-NC-NC	257902_at	A13g28450	leucine-rich repeat transmembrane protein kinase, putative similar to receptor kinase GB:AA020501 from [Arabidopsis thaliana] (88416.m03554)
2246	Not regulated	NC-NC-NC	257844_at	A13g28480	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to prolyl 4-hydroxylase, alpha subunit, from Gallus gallus (Gi:212530), Rattus norvegicus (Gi:474940), Mus musculus (SP:Q60715); contains PF03171 2OG-Fe(II) oxygenase superfamily domain (88416.m03558)
2247	Not regulated	NC-NC-NC	257854_at	A13g12960	Histone acetyltransferase 5 (HAC5) identical to HAC5 (Gi:21105780) [Arabidopsis thaliana]; similar to CREB-binding protein GB:S39162 from [Homo sapiens] (88416.m01617)
2248	Not regulated	NC-NC-NC	257856_at	A13g12930	expressed protein contains Pfam domain PF02410: Domain of unknown function DUF143 (88416.m01611)
2249	Not regulated	NC-NC-NC	257860_at	A13g13062	expressed protein weak similarity to SPIQBUKL6 Phosphatidylcholine transfer protein (PC-TP) (Homo sapiens) (88416.m01629)
2250	Not regulated	NC-NC-NC	257865_at	A13g17750	protein kinase family protein contains Pfam profile: PF00069 Eukaryotic protein kinase domain (88416.m02285)
2251	Not regulated	NC-NC-NC	257866_at	A13g17770	dihydroxyacetone kinase family protein contains Pfam domains, PF02733: DAK1 domain and PF02734: DAK2 domain (88416.m02267)
2252	Not regulated	NC-NC-NC	257867_at	A13g17780	expressed protein (88416.m02268)
2253	Not regulated	NC-NC-NC	257868_at	A13g25070	RPM1-interacting factor 4 (RIN4) identical to SPIQBGYN5 RPM1-interacting protein 4 (Arabidopsis thaliana) (88416.m03132)
2254	Not regulated	NC-NC-NC	257817_at	A13g25150	nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein contains Pfam profile: PF00076 RNA recognition motif, (a.k.a. RRM, RBD, or RNP domain); similar to ras-GTPase-activating protein (GAP-120^v) SH3-domain-binding protein 2 GB:NP_035946 [Mus musculus] (88416.m03140)

2255	Not regulated	NC-NC-NC	257818_at	Al3g25120	mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein contains Pfam PF02466; Mitochondrial import inner membrane translocase subunit Tim17 (68416.m03137)
2256	Not regulated	NC-NC-NC	257820_at	Al3g25220	FK506-binding protein 2-1 (FKBP15-1) / immunophilin / peptidyl-prolyl cis-trans isomerase / rotamase identical to SPIQ38935 FK506-binding protein 2-1 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (15 kDa FKBP) (FKBP-15-1) (Arabidopsis thaliana), immunophilin (FKBP15-1) GB:U52046 [Arabidopsis thaliana] (Proc. Natl. Acad. Sci. U.S.A. 83 (14), 6964-6969 (1986)) (68416.m03150)
2257	Not regulated	NC-NC-NC	257826_at	Al3g26730	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00087 zinc finger, C3HC4 type (RING finger) (68416.m03342)
2258	Not regulated	NC-NC-NC	257827_at	Al3g26630	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile: PF01535 PPR repeat (68416.m03328)
2259	Not regulated	NC-NC-NC	257830_at	Al3g26690	MutT/nudix family protein similar to SPIQ09790 Diadenosine 5',5'-P ₁ P ₆ -hexaphosphate hydrolase (EC 3.6.1.-) (Ap6A hydrolase) (Schizosaccharomyces pombe), contains Pfam profile PF00293: NUDIX domain (68416.m03337)
2260	Not regulated	NC-NC-NC	257831_at	Al3g26710	expressed protein (68416.m03340)
2261	Not regulated	NC-NC-NC	257833_at	Al3g26640	transducin family protein / WD-40 repeat family protein contains 3 WD-40 repeats (PF00400); similar to ATAN11 (GI:2290528) [Arabidopsis thaliana] (Genes Dev. 11 (11), 1422-1434 (1997)); contains Pfam profile: PF00400 WD domain, G-beta repeat (3 copies) (68416.m03329)
2262	Not regulated	NC-NC-NC	257834_at	Al3g26720	glycosyl hydrolase family 38 protein similar to lysosomal alpha-mannosidase GI:3522887 from Homo sapiens (68416.m03341)
2263	Not regulated	NC-NC-NC	257807_at	Al3g26650	glyceraldehyde 3-phosphate dehydrogenase A, chloroplast (GAP) / NADP-dependent glyceraldehydephosphate dehydrogenase subunit A identical to SPIP25656 Glyceraldehyde 5,5'-P ₁ P ₆ -hexaphosphate dehydrogenase A, chloroplast precursor (EC 1.2.1.13) (NADP-dependent glyceraldehydephosphate dehydrogenase subunit A) (Arabidopsis thaliana) (68416.m03330)
2264	Not regulated	NC-NC-NC	257780_at	Al3g27100	expressed protein (68416.m03390)
2265	Not regulated	NC-NC-NC	257783_at	Al3g26950	expressed protein (68416.m03374)
2266	Not regulated	NC-NC-NC	257784_at	Al3g26970	ubiquitin family protein contains INTERPRO:IPR000626 ubiquitin domain (68416.m03378)
2267	Not regulated	NC-NC-NC	257785_at	Al3g26980	oligopeptide transporter OPT family protein similar to iron-phytosiderophore transporter protein yellow stripe 1 [Zea mays] (GI:10770865; contains Pfam profile PF03169: OPT oligopeptide transporter protein (68416.m03380)
2268	Not regulated	NC-NC-NC	257789_at	Al3g27020	peptidase M48 family protein contains Pfam domain, PF01435: Peptidase family M48 (68416.m03391)
2269	Not regulated	NC-NC-NC	257791_at	Al3g27110	expressed protein (68416.m03384)
2270	Not regulated	NC-NC-NC	257794_at	Al3g27050	expressed protein (68416.m03384)
2271	Not regulated	NC-NC-NC	257797_at	Al3g15940	glycosyl transferase family 1 protein contains Pfam profile: PF00534 Glycosyl transferases group 1 (68416.m02018)
2272	Not regulated	NC-NC-NC	257800_at	Al3g15900	expressed protein (68416.m02011)
2273	Not regulated	NC-NC-NC	257805_at	Al3g18830	mannitol transporter, putative similar to mannitol transporter (Agium graveolens var. dulcea) [GI:12004316; contains Pfam profile PF00083; major facilitator superfamily protein (68416.m02381)
2274	Not regulated	NC-NC-NC	257749_at	Al3g18780	actin 2 (ACT2) identical to SPIQ96282 Actin 2 (Arabidopsis thaliana); nearly identical to SPIQ96283 Actin 8 [Arabidopsis thaliana] (GI:1669387 and to A11g48240 (68416.m02385)
2275	Not regulated	NC-NC-NC	257754_at	Al3g18820	Ras-related GTP-binding protein, putative similar to Ras-related protein RAB7 [GI:1370186 from Pisum sativum], Plant Mol. Biol. 21 (6), 1195-1199 (1993); contains Pfam profile: PF00071 Ras family (68416.m02390)
2276	Not regulated	NC-NC-NC	257756_at	Al3g18880	aspartate/glutamate/oxidate kinase family protein similar to UMP-kinase GB:CA838122 gi:4488812 from [Lactococcus lactis] ; contains Pfam profile PF00896: Amino acid kinase family (68416.m02372)
2277	Not regulated	NC-NC-NC	257758_at	Al3g22880	elongation factor Tu family protein similar to eukaryotic translation elongation factor 2 GB:NP_001952 [Homo sapiens] (68416.m02898)
2278	Not regulated	NC-NC-NC	257766_at	Al3g23030	auxin-responsive protein / indoleacetic acid-induced protein 2 (IAA2) identical to SPIP49878 Auxin-responsive protein IAA2 (Indoleacetic acid-induced protein 2) (Arabidopsis thaliana) (68416.m02803)
2279	Not regulated	NC-NC-NC	257769_at	Al3g23050	auxin-responsive protein / indoleacetic acid-induced protein 7 (IAA7) identical to SPIQ36825/AXIT_ARATH Auxin-responsive protein IAA7 (Indoleacetic acid-induced protein 7) (68416.m02805)
2280	Not regulated	NC-NC-NC	257772_at	Al3g23080	expressed protein weak similarity to SPIQ8UKL6 Phosphatidylcholine transfer protein (PC-TP) (Homo sapiens) (68416.m02806)
2281	Not regulated	NC-NC-NC	257773_at	Al3g29185	expressed protein (68416.m03658)
2282	Not regulated	NC-NC-NC	257745_at	Al3g29240	expressed protein similar to A11g33780 [Arabidopsis thaliana]; contains Pfam profile PF02622: Uncharacterized ACR, COG1878 (68416.m03668)
2283	Not regulated	NC-NC-NC	257723_at	Al3g18500	nodulin-related contains weak similarity to Nodulin (CCR4 protein homolog) (Swiss-Prot C35710) [Mus musculus] (68416.m02351)
2284	Not regulated	NC-NC-NC	257727_at	Al3g18380	expressed protein (68416.m02337)
2285	Not regulated	NC-NC-NC	257729_at	Al3g18520	histone deacetylase family protein similar to SPIP53973 Histone deacetylase HDA1 (Saccharomyces cerevisiae); contains Pfam profile PF00850: Histone deacetylase family; AT-acceptor splice site at intron 7 (68416.m02353)
2286	Not regulated	NC-NC-NC	257731_at	Al3g18430	calcium-binding EF hand family protein similar to Calcineurin B subunit (Protein phosphatase 2B regulatory subunit) (Calcineurin regulatory subunit) SP-P42322 from [Naegleria gruber]; contains Pfam profile PF00036: EF hand (68416.m02343)
2287	Not regulated	NC-NC-NC	257732_at	Al3g18480	CCAAT displacement protein-related / CDP-related similar to CCAAT displacement protein (CDP) (Cut-like 1) (Swiss-Prot P39880) [Homo sapiens]; contains Pfam:PF00904 Involutin repeat (68416.m02348)
2288	Not regulated	NC-NC-NC	257711_at	Al3g27430	20S proteasome beta subunit B (PBB1) identical to 20S proteasome beta subunit PBB1 (PBB1) GB:AAC32066 [Arabidopsis thaliana] (Genetics 149 (2), 677-692 (1998)); contains Pfam profile: PF00227 proteasome A-type and B-type; (68416.m03428)
2289	Not regulated	NC-NC-NC	257713_at	Al3g27380	succinate dehydrogenase, iron-sulphur subunit, mitochondrial (SDH2-1) nearly identical to mitochondrial succinate dehydrogenase iron-sulphur subunit (sdh2-1) [gi:12049598] from Arabidopsis thaliana (68416.m03423)
2290	Not regulated	NC-NC-NC	257714_at	Al3g27360	histone H3 identical to histone H3 from Zea mays SPIP05203, Medicago sativa GI:166394, Eriophthalmus alsestiensis SPIP08903, Pisum sativum SPIP02300; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4 (68416.m03421)

2291	Not regulated	NC-NC-NC	257686_at	A13g12790	short-chain dehydrogenase/reductase (SDR) family protein contains Pfam profile PF00108: oxidoreductase, short chain dehydrogenase/reductase family (88416.m01597)
2292	Not regulated	NC-NC-NC	257687_at	A13g12800	floral homeotic protein (HUA1) identical to floral homeotic protein HUA1 [Arabidopsis thaliana] gi 1679786 gb AAK01470 (88416.m01582)
2293	Not regulated	NC-NC-NC	257688_at	A13g12880	asparaginyl protease family protein contains Pfam PF00026: Eukaryotic asparaginyl protease, similar to CND41, chloroplast nucleoid DNA binding protein (Gi2541816) [Nicotiana tabacum] (88416.m01587)
2294	Not regulated	NC-NC-NC	257689_at	A13g12700	phosphoglycerate kinase, putative similar to SPIP41758 Phosphoglycerate kinase, chloroplast precursor (EC 2.7.2.3) (Chlamydomonas reinhardtii); contains Pfam profile PF00162: phosphoglycerate kinase (88416.m01598)
2295	Not regulated	NC-NC-NC	257699_at	A13g12780	CTP synthase, putative / UTP--ammonia ligase, putative similar to SPIP17812 CTP synthase (EC 6.3.4.2) (UTP--ammonia ligase) (Homo sapiens); contains Pfam profile PF00117: glutamine amidotransferase class-I (88416.m01578)
2296	Not regulated	NC-NC-NC	257702_at	A13g12870	RNA recognition motif (RRM)-containing protein contains InterPro entry IPRO00504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) (88416.m01573)
2297	Not regulated	NC-NC-NC	257703_at	A13g12840	expressed protein similar to RP42 protein [Homo sapiens] (Gi:9896488; contains Pfam profile PF00827: UBA7S-N domain, PF03558: Domain of unknown function (DUF298) (88416.m01593)
2298	Not regulated	NC-NC-NC	257705_at	A13g12760	expressed protein (88416.m01575)
2299	Not regulated	NC-NC-NC	257707_at	A13g12850	DNAJ heat shock N-terminal domain-containing protein similar to J11 protein [Arabidopsis thaliana] Gi:9843641; contains Pfam profile: PF00228 DNAJ domain (88416.m01676)
2300	Not regulated	NC-NC-NC	257708_at	A13g13330	ubiquitin family protein contains INTERPRO:IPRO00626 ubiquitin domain (88416.m01686)
2301	Not regulated	NC-NC-NC	257654_at	A13g13310	regulatory protein RecX family protein contains Pfam PF02831: regulatory protein RecX (88416.m01682)
2302	Not regulated	NC-NC-NC	257657_at	A13g13235	calcium exchanger (CAX2) almost identical to low affinity calcium antiporter CAX2 (Gi:1488287) [Arabidopsis thaliana];
2303	Not regulated	NC-NC-NC	257659_at	A13g13228	Ca2+-Cation Antiporter (CaCA) Family member PMID:11500563 (88416.m01677)
2304	Not regulated	NC-NC-NC	257662_at	A13g13320	endonuclease L-PSP family protein contains Pfam domain PF01042: Endonuclease L-PSP (88416.m02583)
2305	Not regulated	NC-NC-NC	257674_at	A13g20380	ethylene-responsive element-binding family protein similar to SPI080339 Ethylene responsive element binding factor 3 (AERF3) (Arabidopsis thaliana); contains Pfam profile PF00847: AP2 domain (88416.m02573)
2306	Not regulated	NC-NC-NC	257675_at	A13g20310	mice-related family protein contains Pfam PF02470: mice related protein (88416.m02574)
2307	Not regulated	NC-NC-NC	257676_at	A13g20320	calcium-binding EF hand family protein similar to EH-domain containing protein 1 from (Mus musculus) SPI08WVK4 and (Homo sapiens) SPI08HAM8; receptor-mediated endocytosis 1 from (Caenorhabditis elegans) (Gi:13487775, Gi:13487777, Gi:13487778; contains INTERPRO:IPRO02048 calcium-binding EF-hand domain (88416.m02571)
2308	Not regulated	NC-NC-NC	257677_at	A13g20290	aspartate carbamoyltransferase, chloroplast / aspartate transcarbamylase / ATCase (PYRB) identical to SPIP49077 Aspartate carbamoyltransferase, chloroplast precursor (EC 2.1.3.2) (Aspartate transcarbamylase) (ATCase) [Arabidopsis thaliana]
2309	Not regulated	NC-NC-NC	257680_at	A13g20330	(88416.m02576)
2310	Not regulated	NC-NC-NC	257621_at	A13g20410	calmodulin-domain protein kinase isoform 9 (CPK9) identical to calmodulin-domain protein kinase CDPK isoform 8 [Arabidopsis thaliana] gi 1399285 gb AA803242 (88416.m02585)
2311	Not regulated	NC-NC-NC	257623_at	A13g28210	cytochrome P450 71B23, putative (CYP71B23) identical to Cytochrome P450 71B23 (SP-Q8LTM0)[Arabidopsis thaliana]; contains Pfam profile: PF00067 cytochrome P450 (88416.m03270)
2312	Not regulated	NC-NC-NC	257628_at	A13g28290	Cytochrome P450 71B26, putative (CYP71B26) identical to cytochrome P450 71B26 (SP-Q8LTL0) [Arabidopsis thaliana]; contains Pfam profile: PF00087 cytochrome P450 (88416.m03280)
2313	Not regulated	NC-NC-NC	257647_at	A13g25805	expressed protein (88416.m03212)
2314	Not regulated	NC-NC-NC	257648_at	A13g16840	DEAD/DEAH box helicase, putative (RH13) similar to RNA helicase GB:CAA08204 from [Arabidopsis thaliana]; identical to cDNA DEAD box RNA helicase, RH13 Gi:3776002 (88416.m02150)
2315	Not regulated	NC-NC-NC	257651_at	A13g16850	Polygalacturonase 2A precursor (EC 3.2.1.15) (Pectinase) (Lycopersicon esculentum); contains PF00285: Glycosyl hydrolases family 28 (88416.m02151)
2316	Not regulated	NC-NC-NC	257652_at	A13g16810	Pumilio/Puf RNA-binding domain-containing protein contains Pfam profile PF00808 Pumilio-family RNA binding domains (88416.m02147)
2317	Not regulated	NC-NC-NC	257654_at	A13g24740	expressed protein (88416.m03106)
2318	Not regulated	NC-NC-NC	257588_at	A13g24800	PRT1 protein (PRT1) E3, N-end rule ubiquitin ligase, contains two RING finger domain; identical to PRT1 [Arabidopsis thaliana] Gi:3319884 (88416.m03112)
2319	Not regulated	NC-NC-NC	257598_at	A13g24830	60S ribosomal protein L13A (RPL 13aB) similar to 60S RIBOSOMAL PROTEIN L13A GB:P55427 from [Rattus norvegicus] (88416.m03115)
2320	Not regulated	NC-NC-NC	257600_at	A13g24770	CLE41, putative CLAVATE/RES-Related 41 (CLE41) (88416.m03108)
2321	Not regulated	NC-NC-NC	257608_at	A13g13860	chaperonin, putative similar to SWISS-PROT:P29197: chaperonin CPN60, mitochondrial precursor (HSP60) [Arabidopsis thaliana];
2322	Not regulated	NC-NC-NC	257609_at	A13g13845	contains Pfam:PF00118 domain, TCP-1cpn60 chaperonin family (88416.m03315)
2323	Not regulated	NC-NC-NC	257611_at	A13g26580	expressed protein (88416.m01748)
2324	Not regulated	NC-NC-NC	257310_at	A13g26560	ATP-dependent RNA helicase, contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain, PF00575: S1 RNA binding domain (88416.m03315)
2325	Not regulated	NC-NC-NC	257291_at	A13g15590	DNA-binding protein, putative similar to DNA-binding protein [Triticum aestivum] Gi:6958202; contains Pfam profile: PF01535 PPR repeat (88416.m01975)
2326	Not regulated	NC-NC-NC	257293_at	A13g15580	autophagy 8 (APG8) identical to autophagy 8 [Arabidopsis thaliana] Gi:19912167; contains Pfam profile PF02991: Microtubule associated protein 1A/1B, light chain 3; supporting cDNA gi 21636957 gb AF492760.1 (88416.m01974)
2327	Not regulated	NC-NC-NC	257295_at	A13g17420	protein kinase family protein contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPRO02280 (88416.m02225)

2328	Not regulated	NC-NC-NC	257269_at	A13g17440	novel plant SNARE 13 (NPSN13) identical to Novel plant SNARE 13 (ANPSN13) (SP-QBLRP1) (Arabidopsis thaliana); contains Plam profile: PF001190 11S plant seed storage protein (68416.m02227)
2329	Not regulated	NC-NC-NC	257238_at	A13g17430	phosphate translocator-related low similarity to phosphoenolpyruvate/phosphate translocator precursor (Mesembryanthemum crystallinum) GI:9295275, SPI52178 These phosphatidylphosphate translocator, non-green plastid, chloroplast precursor (CTPT) (Brassica oleracea) (68416.m02228)
2330	Not regulated	NC-NC-NC	257240_at	A13g24200	monooxygenase family protein low similarity to VisC (Escherichia coli) (G1216829); contains Plam profile: PF01360 Monooxygenase (68416.m03037)
2331	Not regulated	NC-NC-NC	257249_at	A13g24180	expressed protein contains Plam domain PF04885: Protein of unknown function, DUF608 (68416.m03035)
2332	Not regulated	NC-NC-NC	257250_at	A13g24120	myb family transcription factor contains Plam profile: PF00249 myb-like DNA-binding domain (68416.m03028)
2333	Not regulated	NC-NC-NC	257252_at	A13g24170	glutathione reductase, putative identical to GB-P48641 from (Arabidopsis thaliana) (68416.m03034)
2334	Not regulated	NC-NC-NC	257266_at	A13g15010	RNA recognition motif (RRM)-containing protein similar to UBP1 interacting protein 1a (Arabidopsis thaliana) GI:19574236; contains Plam profile: PF00076 RNA recognition motif (a.k.a. RRM, RBD, or RNP domain) (68416.m01898)
2335	Not regulated	NC-NC-NC	257235_at	A13g15060	Ras-related GTP-binding family protein similar to GTP-binding protein GI:303742 from (Pisum sativum); contains Plam profile: PF00071 ras family (68416.m01903)
2336	Not regulated	NC-NC-NC	257236_at	A13g15095	expressed protein (68416.m01908)
2337	Not regulated	NC-NC-NC	257211_at	A13g15080	exonuclease family protein contains exonuclease domain, Plam:PF00829 (68416.m01907)
2338	Not regulated	NC-NC-NC	257212_at	A13g15090	oxido-reductase, zinc-binding dehydrogenase family protein low similarity to NCOG-interacting mitochondrial protein from Mus musculus (gi:14522884); contains Plam profile: PF00107 zinc-binding dehydrogenases (68416.m01908)
2339	Not regulated	NC-NC-NC	257214_at	A13g15040	expressed protein contains Plam profile PF04520: Protein of unknown function, DUF584 (68416.m01903)
2340	Not regulated	NC-NC-NC	257219_at	A13g14930	uroporphyrinogen decarboxylase, putative / UPO, putative similar to uroporphyrinogen decarboxylase (chloroplast) from Nicotiana tabacum (SPIQ42867), Hordeum vulgare (SPIQ42855), Zea mays (SPIQ81220); contains Plam domain uroporphyrinogen decarboxylase (URO-D) PF01208 (68416.m01887)
2341	Not regulated	NC-NC-NC	257225_s_at	A13g27850	SOS ribosomal protein L12-3, chloroplast (CL12-C) identical to ribosomal protein L12 GB:X68046 (Arabidopsis thaliana) (J. Biol. Chem. 269 (10), 7330-7336 (1994)) (68416.m03478)
2342	Not regulated	NC-NC-NC	257226_at	A13g27880	expressed protein (68416.m03478)
2343	Not regulated	NC-NC-NC	257227_at	A13g27820	monodehydroascorbate reductase, putative similar to cytosolic monodehydroascorbate reductase GB:BAA77214 (Oryza sativa) (68416.m03470)
2344	Not regulated	NC-NC-NC	257228_at	A13g27890	NADPH-dependent FMN reductase family protein contains Plam profile: PF03358 NADPH-dependent FMN reductase (68416.m03479)
2345	Not regulated	NC-NC-NC	257232_at	A13g16500	auxin-responsive AUX/IAA family protein similar to SPIQ24408/AUX/IAA Auxin-responsive protein IAA18 (Indoleacetic acid-induced protein 18) (Arabidopsis thaliana); contains Plam profile: PF02309: AUX/IAA family (68416.m02106)
2346	Not regulated	NC-NC-NC	257177_at	A13g23490	cyanate lyase family contains Plam profile: PF02560 cyanate lyase C-terminal domain (68416.m02859)
2347	Not regulated	NC-NC-NC	257178_at	A13g13070	CBS domain-containing protein / transporter associated domain-containing protein similar to SPIQ54318 Hemolysin C (Serpulina hyodysenteriae) (Treponema hyodysenteriae); contains Plam profiles PF00571: CBS domain, PF03471: Transporter associated domain, PF01595: Domain of unknown function (68416.m01634)
2348	Not regulated	NC-NC-NC	257189_at	A13g13222	expressed protein (68416.m01655)
2349	Not regulated	NC-NC-NC	257190_at	A13g13120	30S ribosomal protein S10, chloroplast, putative similar to 30S ribosomal protein S10 GB:P02384 (Escherichia coli) (est matches suggest the N-terminal extension) (68416.m01642)
2350	Not regulated	NC-NC-NC	257182_at	A13g13200	Cw15 / Cwc15 cell cycle control family protein contains Plam profile PF04889: Cw15/Cwc15 cell cycle control protein, similar to Cell cycle control protein cwf15 (Swiss-Prot:P78794) (Schizosaccharomyces pombe) (68416.m01652)
2351	Not regulated	NC-NC-NC	257194_at	A13g13110	serine O-acetyltransferase (SAT-1) identical to serine acetyltransferase (Sat-1) GI:1184048 (Arabidopsis thaliana) (68416.m01641)
2352	Not regulated	NC-NC-NC	257199_at	A13g23710	chloroplast inner membrane import protein Tic22, putative similar to Tic22 (Pisum sativum) gi1376871 (68416.m02881)
2353	Not regulated	NC-NC-NC	257204_at	A13g23805	rapid alkalization factor (RALF) family protein similar to RALF precursor (Nicotiana tabacum) GI:16566316 (68416.m02992)
2354	Not regulated	NC-NC-NC	257172_at	A13g23700	S1 RNA-binding domain-containing protein contains Plam domain, PF00575: S1 RNA binding domain (68416.m02890)
2355	Not regulated	NC-NC-NC	257144_at	A13g27300	glucose-6-phosphate 1-dehydrogenase / G6PD (ACG39) identical to glucose-6-phosphate 1-dehydrogenase (ecg9) (Arabidopsis thaliana) GI:5732195 (68416.m03412)
2356	Not regulated	NC-NC-NC	257146_at	A13g27260	DNA-binding bromodomain-containing protein contains bromodomain, INTERPRO (IPR001487) (68416.m03407)
2357	Not regulated	NC-NC-NC	257149_at	A13g27280	prohibitin, putative strongly similar to prohibitin (Arabidopsis thaliana) GI:1946331; contains Plam profile PF01145: SPFH domain / Band 7 family (68416.m03409)
2358	Not regulated	NC-NC-NC	257150_at	A13g27230	expressed protein (68416.m03404)
2359	Not regulated	NC-NC-NC	257152_at	A13g27310	expressed protein (68416.m03413)
2360	Not regulated	NC-NC-NC	257154_at	A13g27210	expressed protein (68416.m03402)
2361	Not regulated	NC-NC-NC	257157_at	A13g24350	synaptin, putative (SYF32) similar to SPIQ6FFK1 Synaptin 31 (ASYP31) (AISED5) (Arabidopsis thaliana), syntaxin 5A GB:NP_003155 from (Homo sapiens) (J. Mol. Neurosci. (1997) 8 (2), 159-161) (68416.m03057)
2362	Not regulated	NC-NC-NC	257168_at	A13g24430	expressed protein contains Plam profile PF01883: Domain of unknown function (68416.m03066)
2363	Not regulated	NC-NC-NC	257169_at	A13g24315	sec20 family protein contains Plam PF03908: Sec20 (68416.m03053)
2364	Not regulated	NC-NC-NC	257122_at	A13g20250	pumilio/Puf RNA-binding domain-containing protein contains Plam profile: PF00806 Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain) (8 copies at C-terminus) (68416.m02585)
2365	Not regulated	NC-NC-NC	257132_at	A13g20230	SOS ribosomal protein L18 family similar to ribosomal protein L18 (GI:29342325) (Enterococcus faecalis V583); similar to SOS ribosomal protein L18 (Swiss-Prot:O24704) (Synchococcus sp.) (68416.m02593)
2366	Not regulated	NC-NC-NC	257088_at	A13g20510	expressed protein contains Plam profile PF03647: Uncharacterised protein family (UPF0136) (68416.m02597)
2367	Not regulated	NC-NC-NC	257092_at	A13g20550	forkhead-associated domain-containing protein / FHA domain-containing protein weak similarity to SPIQ28147 Nuclear inhibitor of protein phosphatase-1 (NIPP-1) (Protein phosphatase 1, regulatory inhibitor subunit 8) (Bos taurus); contains Plam profile PF00498: FHA domain (68416.m02601)

2368 Not regulated	237083_at	NC-NC-NC	plastocyanin-like domain-containing protein (88416.m02604)
2369 Not regulated	257095_at	NC-NC-NC	thioredoxin family protein contains Pf00085; Thioredoxin (88416.m02603)
2370 Not regulated	257105_at	NC-NC-NC	VQ motif-containing protein contains PF05878; VO motif (88416.m01932)
2371 Not regulated	257052_at	NC-NC-NC	3-hydroxybutyryl-CoA dehydrogenase, putative similar to S(+)-beta-hydroxybutyryl CoA dehydrogenase (3-hydroxybutyryl-CoA dehydrogenase) [Paracoccus denitrificans] GI:12003336; contains Pfam profiles PF02737: 3-hydroxyacyl-CoA dehydrogenase NAD binding; PF00725: 3-hydroxyacyl-CoA dehydrogenase C-terminal (88416.m01931)
2372 Not regulated	257053_at	NC-NC-NC	ethylene-responsive element-binding factor 4 (ERF4) identical to ethylene responsive element binding factor 4 SP_O80340 from Arabidopsis thaliana (88416.m01922)
2373 Not regulated	257054_at	NC-NC-NC	metallothionein protein, putative (88416.m01944)
2374 Not regulated	257055_at	NC-NC-NC	expressed protein (88416.m01941)
2375 Not regulated	257058_at	NC-NC-NC	cytochrome c oxidase copper chaperone-related contains similarity to cytochrome c oxidase copper chaperone [Mus musculus]
2376 Not regulated	257062_at	NC-NC-NC	SWISS-PROT: P56394 (88416.m01943)
2377 Not regulated	257066_at	NC-NC-NC	zinc finger protein-related weak alignment to Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies) (88416.m02326)
2378 Not regulated	257072_at	NC-NC-NC	protease inhibitor/seed storage lipid transfer protein (LTP) family protein similar to TED4 [Zinnia elegans] GI:483721; contains Pfam protease inhibitor/seed storage LTP family domain PF00234 (88416.m02325)
2379 Not regulated	257074_at	NC-NC-NC	GDSL-motif lipase/hydrolase family protein similar to myrosinase-associated proteins GI:1769968, GI:1769970 from Brassica napus; contains InterPro Entry IPR011087 Lipolytic enzyme, G-D-S-L family, contains 1 predicted transmembrane domain; (88416.m01797)
2380 Not regulated	257046_at	NC-NC-NC	expressed protein (88416.m02491)
2381 Not regulated	257018_at	NC-NC-NC	AAA-type ATPase family protein contains Pfam domain, PF00004: ATPase, AAA family (88416.m02496)
2382 Not regulated	257019_at	NC-NC-NC	radical SAM domain-containing protein similar to florfenicol resistance protein [Staphylococcus sciui] GI:9009980; contains Pfam profile PF04055: radical SAM domain protein (88416.m02488)
2383 Not regulated	257029_at	NC-NC-NC	magnesium transporter CorA-like family protein (MRS2-3) low similarity to SPIQ01928 RNA splicing protein MRS2, mitochondrial precursor (Saccharomyces cerevisiae); contains Pfam profile PF01544: CorA-like Mg2+ transporter protein (88416.m02489)
2384 Not regulated	257038_at	NC-NC-NC	expressed protein (88416.m02441)
2385 Not regulated	257016_at	NC-NC-NC	longevity-assurance (LAG1) family protein similar to Alternaria stem canker resistance protein (ASC1) [Lyopercaria esculentum] GI:7688742; contains Pfam profile PF03788: Longevity-assurance protein (LAG1) (88416.m02443)
2386 Not regulated	256988_s_at	NC-NC-NC	protein kinase, putative similar to protein kinase APK1A [Arabidopsis thaliana] Swiss-Prot: Q06548 (88416.m03580)
2387 Not regulated	257003_at	NC-NC-NC	H+-transporting two-sector ATPase, putative similar to SPIP54641 Vacuolar ATP synthase subunit d (EC 3.6.3.14) [Vacuolar protein pump d subunit] (V-ATPase 41 kDa accessory protein) [Dictyostelium discoideum]; contains Pfam profile PF01682: ATP synthase (C/AC39) subunit (88416.m03584)
2388 Not regulated	257007_at	NC-NC-NC	tetratricopeptide repeat (TPR)-containing protein contains Pfam profile PF00515: TPR Domain (88416.m01783)
2389 Not regulated	257010_at	NC-NC-NC	phosphoinositide phosphatase family protein contains similarity to phosphoinositide phosphatase SAC1 [Rattus norvegicus] GI:1095248 [gb AAAG288.10], contains Pfam domain, PF02383: Sac1 homology domain; identical to SAC domain protein 2 (SAC2) GI:31415720 (88416.m01785)
2390 Not regulated	256983_at	NC-NC-NC	exocyst subunit EXO70 family protein contains Pfam domain PF03081: Exo70 exocyst complex subunit; (88416.m01781)
2391 Not regulated	256984_at	NC-NC-NC	chaperonin, putative similar SWISS-PROT: P21240: Rubisco subunit binding-protein beta subunit, chloroplast precursor (60 kDa) chaperonin beta subunit, CPN-60 beta [Arabidopsis thaliana]; contains Pfam: PF00118 domain, TCP-1/cpn60 chaperonin family (88416.m01695)
2392 Not regulated	256954_at	NC-NC-NC	expressed protein; expression supported by MPSS (88416.m01696)
2393 Not regulated	256956_at	NC-NC-NC	ubiquitin-conjugating enzyme (COP10) identical to ubiquitin-conjugating enzyme COP10 [Arabidopsis thaliana] GI:20065778; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme (88416.m01703)
2394 Not regulated	256958_at	NC-NC-NC	expressed protein (88416.m01686)
2395 Not regulated	256959_at	NC-NC-NC	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger) (88416.m01688)
2396 Not regulated	256961_at	NC-NC-NC	transcription initiation factor IID-1 (TFIID-1) / TATA-box factor 1 / TATA sequence-binding protein 1 (TBP-1) identical to Swiss-thaliana (88416.m01691)
2397 Not regulated	256972_at	NC-NC-NC	expressed protein (88416.m02671)
2398 Not regulated	256978_at	NC-NC-NC	phosphonitrosylamidimidazole-succinocarboxamide synthase / SAICAR synthetase (PUR7) identical to phosphonitrosylamidimidazole-succinocarboxamide synthase, chloroplast [precursor] SP_P38025 from [Arabidopsis thaliana] (88416.m02668)
2399 Not regulated	256979_at	NC-NC-NC	photosystem II 5 MD protein, putative identical to Swiss-Prot: Q39195 photosystem II 5 kDa protein, chloroplast precursor (PSII-T) [Arabidopsis thaliana] (88416.m02661)
2400 Not regulated	256928_at	NC-NC-NC	RNA pol II accessory factor Cdc73 family protein contains Pfam PF05178: RNA pol II accessory factor, Cdc73 family (88416.m02654)
2401 Not regulated	256932_at	NC-NC-NC	expressed protein (88416.m02846)
2402 Not regulated	256934_at	NC-NC-NC	expressed protein contains Pfam profile: PF00011 HSP20-Hsc20/alpha crystallin family (88416.m02847)
2403 Not regulated	256936_at	NC-NC-NC	prefoldin-related KE2 family protein similar to Swiss-Prot: Q3UHV9 prefoldin subunit 2 (Protein HSPC231) [Homo sapiens]; contains Pfam domain, PF01920: KE2 family protein (88416.m02841)
2404 Not regulated	256942_at	NC-NC-NC	expressed protein contains Pfam profile PF04852: Protein of unknown function (DUF640) (88416.m02836)
2405 Not regulated	256944_at	NC-NC-NC	transcriptional factor B3 family protein contains Pfam profile PF02962: B3 DNA binding domain (88416.m02410)
2406 Not regulated	256900_at	NC-NC-NC	pectate lyase family protein similar to pectate lyase GP_14531288 from [Fragaria x ananassa] (88416.m03097)
2407 Not regulated	256902_s_at	NC-NC-NC	expressed protein (88416.m03004)

2408	Not regulated	NC-NC-NC	256905_at	Al3g23890	chaperonin (CPN60) (HSP60) identical to SWISS-PROT:P29197: chaperonin CPN60, mitochondrial precursor (HSP60) [Arabidopsis thaliana] (88416.m03013)
2409	Not regulated	NC-NC-NC	256907_at	Al3g24030	hydroxyethylthiazole kinase family protein contains Pfam profile: PF02110 hydroxyethylthiazole kinase family (88416.m03018)
2410	Not regulated	NC-NC-NC	256908_at	Al3g24040	enzymic (88416.m03019)
2411	Not regulated	NC-NC-NC	256914_at	Al3g23880	F-box family protein contains F-box domain Pfam:PF00646 (88416.m03001)
2412	Not regulated	NC-NC-NC	256915_at	Al3g23900	RNA recognition motif (RRM)-containing protein (88416.m03003)
2413	Not regulated	NC-NC-NC	256890_at	Al3g23830	glycine-rich RNA-binding protein, putative similar to Glycine-rich RNA-binding protein 2, mitochondrial precursor (AIGRP2) (Swiss-Prot:O8SVN8) [Arabidopsis thaliana], contains Pfam profile: PF00076 RNA recognition motif (e.k.a. RRM, RBD, or RNP domain) (88416.m02895)
2414	Not regulated	NC-NC-NC	256891_at	Al3g23920	beta-amylase, putative / 1,4-alpha-D-glucan maltohydrolase, putative similar to beta-amylase enzyme [Arabidopsis thaliana] (88416.m03005)
2415	Not regulated	NC-NC-NC	256898_at	Al3g26400	eukaryotic translation initiation factor 4B, putative/ eIF-4B, putative similar to eukaryotic initiation factor 4B [Arabidopsis thaliana] (88416.m03292)
2416	Not regulated	NC-NC-NC	256870_at	Al3g26300	cytochrome P450 family protein contains Pfam profile: PF00067 cytochrome P450 (88416.m03282)
2417	Not regulated	NC-NC-NC	256876_at	Al3g26360	ribosomal protein-related similar to SPIB2354 30S ribosomal protein S21 (Rizobium meliloti) (88416.m03288)
2418	Not regulated	NC-NC-NC	256877_at	Al3g26470	expressed protein (88416.m03300)
2419	Not regulated	NC-NC-NC	256878_at	Al3g26460	major latex protein-related / MLP-related low similarity to major latex protein (Papaver somniferum)(Gi:284060) contains Pfam profile PF00407: Pathogenesis-related protein Bet v 1 family (88416.m03298)
2420	Not regulated	NC-NC-NC	256879_at	Al3g26370	expressed protein contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown;
2421	Not regulated	NC-NC-NC	256881_at	Al3g26410	expressed protein (88416.m03293)
2422	Not regulated	NC-NC-NC	256882_at	Al3g26420	glycine-rich RNA-binding protein similar to RNA-binding protein (RZ-1) GB.BAA12064 (Nicotiana sylvestris); contains Pfam profile: PF00076 RNA recognition motif (e.k.a. RRM, RBD, or RNP domain) (88416.m03285)
2423	Not regulated	NC-NC-NC	256885_at	Al3g15160	expressed protein (88416.m01917)
2424	Not regulated	NC-NC-NC	256885_at	Al3g15190	chloroplast 30S ribosomal protein S20, putative contains Pfam profile: PF01649 ribosomal protein S20 (88416.m01920)
2425	Not regulated	NC-NC-NC	256828_at	Al3g22850	expressed protein similar to auxin down-regulated protein ARG10 [Vigna radiata] (Gi:2970051), wall7 (aluminum-induced protein) (Triticum aestivum) (Gi:451193) (88416.m02881)
2426	Not regulated	NC-NC-NC	256832_at	Al3g22880	meiotic recombination protein, putative similar to Swiss-Prot:Q14565 meiotic recombination protein DMC1/LJM15 homolog [Homo sapiens]; contains non-consensus ATAC non-consensus splice sites at intron 14 (88416.m02884)
2427	Not regulated	NC-NC-NC	256836_at	Al3g22860	pyruvate kinase, putative similar to pyruvate kinase isozyme A, chloroplast precursor [Ricinus communis] SWISS-PROT:Q43117 (88416.m02895)
2428	Not regulated	NC-NC-NC	256838_at	Al3g22850	ADP-ribosylation factor, putative similar to ADP-ribosylation factor GB:P91824 [Dugesia japonica] (88416.m02893)
2429	Not regulated	NC-NC-NC	256797_at	Al3g18600	DEAD/DEAH box helicase, putative non-consensus acceptor splice site AT at exon 2; similar to DEAD box helicase protein GB:NP_008784 from [Homo sapiens], contains Pfam profile: PF00270 DEAD/DEAH box helicase (88416.m02364)
2430	Not regulated	NC-NC-NC	256799_at	Al3g18560	expressed protein (88416.m02360)
2431	Not regulated	NC-NC-NC	256804_at	Al3g20920	translocation protein-related contains weak similarity to Drosophila melanogaster protein 1 (Gi:556181) [Drosophila melanogaster] (88416.m02844)
2432	Not regulated	NC-NC-NC	256807_at	Al3g20970	nitrogen fixation NifU-like family protein similar to HIRA-interacting protein 5 (NIFU FAMILY) (SP:080223) [Mus musculus]; contains Pfam profile: PF01106 NifU-like domain (88416.m02850)
2433	Not regulated	NC-NC-NC	256819_at	Al3g21390	mitochondrial substrate carrier family protein (88416.m02700)
2434	Not regulated	NC-NC-NC	256823_at	Al3g22220	hAT dimerisation domain-containing protein contains Pfam profiles PF04837: Protein of unknown function (DUF 859), PF05699
2435	Not regulated	NC-NC-NC	256793_at	Al3g22160	hAT family dimerisation domain (88416.m02803)
2436	Not regulated	NC-NC-NC	256794_at	Al3g22230	VQ motif-containing protein contains PF05678: VQ motif (88416.m02797)
2437	Not regulated	NC-NC-NC	256769_at	Al3g13690	60S ribosomal protein L27 (RPL27B) similar to 60S RIBOSOMAL PROTEIN L27 GB:P41101 from [Solanum tuberosum] (88416.m02804)
2438	Not regulated	NC-NC-NC	256771_at	Al3g13710	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (88416.m01729)
2439	Not regulated	NC-NC-NC	256776_at	Al3g13772	prenylated rab acceptor (PRA1) family protein weak similarity to prenylated Rab acceptor [Mus musculus] (Gi:7716652; contains Pfam profile PF03208: Prenylated rab acceptor (PRA1) (88416.m01730)
2440	Not regulated	NC-NC-NC	256783_at	Al3g13670	endomembrane protein 70, putative TM4 family; (88416.m01738)
2441	Not regulated	NC-NC-NC	256785_at	Al3g13720	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (88416.m01729)
2442	Not regulated	NC-NC-NC	256783_at	Al3g16860	prenylated rab acceptor (PRA1) family protein contains Pfam profile PF03208: Prenylated rab acceptor (PRA1) (88416.m01732)
2443	Not regulated	NC-NC-NC	256744_at	Al3g28350	phytohelatin synthetase-related contains Pfam PF04833: Phytohelatin synthetase-like conserved region (88416.m02156)
2444	Not regulated	NC-NC-NC	256747_at	Al3g28180	two-component phosphorelay mediator 1 (HP1) identical to ATP1 [Arabidopsis thaliana] (Gi:4156241) (88416.m03085)
2445	Not regulated	NC-NC-NC	256751_at	Al3g27170	expressed protein (88416.m03657)
2446	Not regulated	NC-NC-NC	256752_at	Al3g27160	chloride channel protein (CLC-b) identical to CLC-b chloride channel protein GB:CAA9058 from [Arabidopsis thaliana] (J. Biol. Chem. 271 (52), 33632-33638 (1996)) (88416.m03338)
2447	Not regulated	NC-NC-NC	256753_at	Al3g27180	expressed protein (88416.m03399)
2448	Not regulated	NC-NC-NC	256755_at	Al3g25600	ribosomal protein S21 family protein contains Pfam profile: PF01165 ribosomal protein S21 (88416.m03387)
2449	Not regulated	NC-NC-NC	256728_at	Al3g25660	calmodulin, putative similar to calmodulin (Gi:239841 from [Paramedusa tetraurelia] (88416.m03187)
2450	Not regulated	NC-NC-NC	256724_at	Al2g34040	glutathionyl-RNA(Gin) amidotransferase, putative similar to SPI006491 Glutathionyl-RNA(Gin) amidotransferase subunit A (EC 6.3.5.-) [Bacillus subtilis]; contains Pfam profile PF01425: Amidase (88416.m03194)
		NC-NC-NC			apoptosis inhibitory 5 (API5) family protein contains Pfam domain PF05918 Apoptosis inhibitory protein 5 (API5) (88415.m04187)

2451	Not regulated	NC-NC-NC	256727_at	A1g522240	expressed protein (68416.m05741)
2452	Not regulated	NC-NC-NC	256671_at	A1g522280	calmodulin-binding family protein similar to SF16 protein [Helianthus annuus] Gi:590150; contains Pfam profile PF00612; IQ calmodulin-binding motif (68416.m05747)
2453	Not regulated	NC-NC-NC	256673_at	A1g523370	beta-Ig-H3 domain-containing protein / fasciclin domain-containing protein weak similarity to osteoblast specific factor 2 [Homo sapiens] Gi:393319; contains Pfam profile PF02469; Fasciclin domain; supporting cDNA gi26450289[gbjAK117608.1]
2454	Not regulated	NC-NC-NC	256674_at	A1g523600	expressed protein (68416.m05756)
2455	Not regulated	NC-NC-NC	256678_at	A1g523300	ATP synthase D chain-related contains weak similarity to ATP synthase D chain, mitochondrial (EC 3.6.3.14) [Swiss-Prot:P31399]
2456	Not regulated	NC-NC-NC	256680_at	A1g522330	[Rattus norvegicus] (68416.m05748)
2457	Not regulated	NC-NC-NC	256681_at	A1g523340	expressed protein (68416.m05739)
					sucrose-phosphatase 2 (SPP2) identical to sucrose-phosphatase (SPP2) [Arabidopsis thaliana] Gi:13811669; supporting cDNA gi113811668[gbjAF356816.1]AF356816 (68416.m05752)
2458	Not regulated	NC-NC-NC	256682_at	A1g522000	dihydrolipoyl S-acyltransferase, putative similar to dihydrolipoyl acetyltransferase (E2) subunit of PDC [Arabidopsis thaliana] Gi:556935; contains Pfam profiles PF00198: 2-oxo acid dehydrogenases acyltransferase (catalytic domain), PF00384: Biotin-requiring enzyme, PF02817: ad binding domain; supporting cDNA gi15861864[gbjAF066080.1]AF066080 (68416.m05733)
2459	Not regulated	NC-NC-NC	256683_at	A1g522220	expressed protein (68416.m05737)
2460	Not regulated	NC-NC-NC	256686_at	A1g206500	mRNA capping enzyme family protein contains Pfam PF03291: mRNA capping enzyme, large subunit (68416.m02813)
2461	Not regulated	NC-NC-NC	256688_at	A1g208700	histone H2A, putative strong similarity to histone H2A GBAAAF84418 Gi:7595337 from Arabidopsis thaliana, Tribolium aestivum Gi:536892; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4 (68416.m02816)
2462	Not regulated	NC-NC-NC	256649_at	A1g313570	SC35-like splicing factor, 30a KD (SCL30a) almost identical to SC35-like splicing factor SCL30a Gi:9843681 from [Arabidopsis thaliana]; contains Pfam profile PF00076: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) (68416.m01707)
2463	Not regulated	NC-NC-NC	256655_at	A1g318890	expressed protein similar to UV-B and ozone similarly regulated protein 1 UOS1 [Pisum sativum] Gi:20339364 (68416.m02399)
2464	Not regulated	NC-NC-NC	256637_at	A1g3120300	expressed protein similar to membrane protein GB:BA86974 Gi:6467175 from [Homo sapiens] (68416.m01482)
2465	Not regulated	NC-NC-NC	256611_at	A1g329270	expressed protein (68416.m03674)
2466	Not regulated	NC-NC-NC	256612_at	A1g329280	expressed protein; expression supported by MPSS (68416.m03678)
2467	Not regulated	NC-NC-NC	256629_at	A1g319980	serine/threonine protein phosphatase (STPP) identical to serine/threonine protein phosphatase [Arabidopsis thaliana]
2468	Not regulated	NC-NC-NC	256603_at	A1g328270	Gi:14582206; very similar to serine/threonine protein phosphatase GB:247076 Gi:1143510 [Malus domestica]; contains Pfam profile PF00149: Ser/Thr protein phosphatase (68416.m02528)
2469	Not regulated	NC-NC-NC	256607_at	A1g332930	expressed protein similar to A114a protein (Gi:11994571 and Gi:11994573) [Arabidopsis thaliana] (68416.m03530)
2470	Not regulated	NC-NC-NC	256590_at	A1g328730	structure-specific recognition protein 1 / high mobility group protein / HMG protein nearly identical to SPQ05153 Structure-specific recognition protein 1 homolog (HMG protein) [Arabidopsis thaliana]; contains Pfam profile PF00505: HMG (high mobility group) box; contains Pfam profile PF03531: Structure-specific recognition protein (68416.m03587)
2471	Not regulated	NC-NC-NC	256598_at	A1g303180	Cytochrome P450, putative similar to cytochrome P450 homolog (SP:U54770) [Lycopersicon esculentum] (68416.m03808)
2472	Not regulated	NC-NC-NC	256573_at	A1g314860	NHL repeat-containing protein contains Pfam profile PF01436: NHL repeat (68416.m01878)
2473	Not regulated	NC-NC-NC	256575_at	A1g314790	NAD-dependent epimerase/dehydratase family protein similar to dTDP-glucose 4,8-dehydratase from Aneurinibacillus thermoaerophilus Gi:16357461, Saccharopolyspora spinosa Gi:15077647, RmB from Lepidospira borgpetersenii Gi:4234803; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family (68416.m01869)
2474	Not regulated	NC-NC-NC	256587_at	A1g319553	amino acid permease family protein weak similarity to aspartate/glutamate transporter 1 [Mus musculus] Gi:21322754; contains amino acid permease (68416.m02479)
2475	Not regulated	NC-NC-NC	256588_at	A1g319520	Pfam profile PF00324: Amino acid permease (68416.m02479)
2476	Not regulated	NC-NC-NC	256570_at	A1g319540	expressed protein contains Pfam profile PF04778: Protein of unknown function (DUF628) (68416.m02475)
2477	Not regulated	NC-NC-NC	256541_at	A1g425400	expressed protein contains Pfam profile PF04788: Protein of unknown function (DUF620) (68416.m02477)
2478	Not regulated	NC-NC-NC	256542_at	A1g425500	glutamate receptor family protein (GLR3.3) plant glutamate receptor family, PMID:11379628 (68414.m04905)
2479	Not regulated	NC-NC-NC	256525_at	A1g661800	expressed protein (68414.m04906)
					aspartyl protease family protein contains Pfam PF00026: Eukaryotic aspartyl protease profile; similar to CND41, chloroplast nucleoid DNA binding protein (Gi:2541876) [Nicotiana tabacum] (68414.m07512)
2480	Not regulated	NC-NC-NC	256530_at	A1g332900	sporulation protein-related isoform contains non-consensus AT-donor acceptor site at intron 6; similar to Stage III sporulation protein AA. (Swiss-Prot:Q01387) [Bacillus subtilis]; similar to SpoIIAA (Gi:1303904) [Bacillus subtilis]; similar to stage III sporulation protein AA. (Gi:18145497) [Clostridium perfringens str. 13] (68414.m04117)
2481	Not regulated	NC-NC-NC	256534_at	A1g332700	palatin-related contains Palatin domain PF01734 (68414.m04114)
2482	Not regulated	NC-NC-NC	256538_at	A1g333330	peptide chain release factor, putative similar to peptide chain release factor 2 [Campylobacter jejuni] Gi:6468628; contains Pfam profile PF00472: Peptidyl-RNA hydrolase domain (68414.m04123)
2483	Not regulated	NC-NC-NC	256485_at	A1g314400	SH3 domain-containing protein 1 (SH3P1) nearly identical to SH3 domain-containing protein 1 [Arabidopsis thaliana] Gi:16974876; contains Pfam profile PF00018: SH3 domain (68414.m03850)
2484	Not regulated	NC-NC-NC	256497_at	A1g315800	expressed protein identical to ORF1 [Arabidopsis thaliana] gi457718[embICA50905 (68414.m03875)]
2485	Not regulated	NC-NC-NC	256451_s_at	A1g751700	SEC14 cytosolic factor family protein / phosphoglycyl transfer factor protein similar to polyphosphonitide binding protein Shp1p (Gi:2739044) [Glycine max]; similar to SEC14 cytosolic factor (Phosphatidylinositol/phosphatidylcholine transfer protein) [P1CPT] (SP:P24859) [Kuyveromyces lacticus] and to SEC14 cytosolic factor (SP:P53989) [Candida glabrata] (68414.m08731)
2486	Not regulated	NC-NC-NC	256455_at	A1g751900	expressed protein (68414.m08735)
2487	Not regulated	NC-NC-NC	256456_at	A1g751800	expressed protein (68414.m08732)
2488	Not regulated	NC-NC-NC	256458_at	A1g752200	integral membrane protein, putative strong similarity to integral membrane protein Gi:1209756 from [Beta vulgaris]; contains Pfam profile PF00083: major facilitator superfamily protein (68414.m08738)

2489	Not regulated	NC-NC-NC	256468_at	ferredoxin family protein similar to ferredoxin from <i>Synechocystis</i> sp. [GI:48019]; contains Pfam profile PF00111 2Fe-2S iron-sulfur cluster binding domain (88414.m04017)
2490	Not regulated	NC-NC-NC	256424_at	expressed protein (88414.m04145)
2491	Not regulated	NC-NC-NC	256439_at	superoxide dismutase [Mn], mitochondrial (SOD4) / manganese superoxide dismutase (MSD1) identical to manganese superoxide dismutase [Arabidopsis thaliana] gi27373751 gb AA24832.6 (88416.m01317)
2492	Not regulated	NC-NC-NC	256440_at	haloacid dehalogenase-like hydrolase family protein similar to genetic modifier [Zea mays] GI:10444400; contains InterPro accession IPRO05834; Haloacid dehalogenase-like hydrolase (88416.m01322)
2493	Not regulated	NC-NC-NC	256415_at	GDSL-motif lipase/hydrolase family protein contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif (88416.m01382)
2494	Not regulated	NC-NC-NC	256387_at	TMS membrane family protein / tumour differentially expressed (TDE) family protein contains Pfam domain, PF03348: TMS membrane protein/tumour differentially expressed protein (TDE) (88416.m00709)
2495	Not regulated	NC-NC-NC	256394_at	SAC3/GANP family protein contains Pfam profile: PF03398 SAC3/GANP family (88416.m00722)
2496	Not regulated	NC-NC-NC	256397_at	dual specificity protein phosphatase family protein contains Pfam profile: PF00782 dual specificity phosphatase, catalytic domain (88416.m00701)
2497	Not regulated	NC-NC-NC	256402_at	heavy-metal-associated domain-containing protein contains Pfam heavy metal associated domain PF00403 (88416.m00704)
2498	Not regulated	NC-NC-NC	256406_at	expressed protein (88414.m05702)
2499	Not regulated	NC-NC-NC	256411_at	ATP-dependent Clp protease proteolytic subunit (ClpP3) identical to ATP-dependent Clp protease (nC1pP3) GI:5360591 [Arabidopsis thaliana] (88414.m07577)
2500	Not regulated	NC-NC-NC	256385_at	arginyl-RNA synthetase, putative / arginine-RNA ligase, putative similar to SPIP37880 Arginyl-RNA synthetase (EC 6.1.1.19) (Arginine-RNA ligase) (ArgRS) [Cicobulus longicaudatus]; contains Pfam profiles PF00750: arginyl-RNA synthetase, PF03485: arginyl-RNA synthetase N-terminal domain (88414.m07559)
2501	Not regulated	NC-NC-NC	256386_at	serine/threonine protein kinase family protein contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPRO02290 (88414.m07601)
2502	Not regulated	NC-NC-NC	256373_at	ASF1-like anti-silencing protein, putative similar to SPIP32447 Anti-silencing protein 1 [Saccharomyces cerevisiae]; contains Pfam profile PF04728: Anti-silencing protein, ASF1-like; supporting cDNA gi27530835 dbj AB078339.1 (88414.m07586)
2503	Not regulated	NC-NC-NC	256380_at	S locus-linked protein, putative similar to S locus-linked protein SL2 [Brassica napus] GI:1518113 (88414.m07579)
2504	Not regulated	NC-NC-NC	256327_at	glycosyl transferase family 8 protein contains Pfam profile: PF01501 glycosyl transferase family 8 (88416.m00218)
2505	Not regulated	NC-NC-NC	256329_at	expressed protein (88414.m08943)
2506	Not regulated	NC-NC-NC	256333_at	small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative similar to SWISS-PROT:Q8Y4Z1 U8 snRNP-associated Sm-like protein LSM3 (MDS017) [Mouse] (88414.m08944)
2507	Not regulated	NC-NC-NC	256338_at	GCN5-related N-acetyltransferase (GNAT) family protein contains Pfam profile PF00583: acetyltransferase, GNAT family expressed protein (88414.m08326)
2508	Not regulated	NC-NC-NC	256342_at	expressed protein (88414.m08325)
2509	Not regulated	NC-NC-NC	256343_at	radical SAM domain-containing protein / TRAM domain-containing protein contains Pfam profiles PF00919: UPF0004 family protein, PF04055: radical SAM domain protein, PF01838: TRAM domain (88414.m08333)
2510	Not regulated	NC-NC-NC	256351_at	NPK1-related protein kinase, putative (ANP2) similar to protein kinase [Nicotiana tabacum] gi456308 dbj BAA05648; identical to cDNA NPK1-related protein kinase 2, partial cds GI:2342424 (88414.m06277)
2511	Not regulated	NC-NC-NC	256353_at	peptidoglycan-binding LysM domain-containing protein contains Pfam profile PF01476: LysM domain (88414.m06282)
2512	Not regulated	NC-NC-NC	256294_at	early-responsive to dehydration protein-related / ERD protein-related low similarity to ERD4 protein (early-responsive to dehydration stress) [Arabidopsis thaliana] GI:15375406; contains Pfam profile PF02714: Domain of unknown function DUF221 (88414.m07880)
2513	Not regulated	NC-NC-NC	256301_at	expressed protein (88414.m07887)
2514	Not regulated	NC-NC-NC	256309_at	photosystem I reaction center subunit psak, chloroplast, putative / photosystem I subunit X, putative / PSI-K, putative (PSAK) identical to SPIQ85U5; strong similarity to SPIP36896 Photosystem I reaction center subunit psak, chloroplast precursor (Photosystem I subunit X) [PSI-K] (Light-harvesting complex I 7 kDa protein)[Hordeum vulgare]; contains Pfam profile PF01241: Photosystem I psak / psak (88414.m03714)
2515	Not regulated	NC-NC-NC	256286_at	cornichon family protein contains Pfam profile: PF03311 cornichon protein (88416.m01518)
2516	Not regulated	NC-NC-NC	256288_at	protein arginine N-methyltransferase family protein similar to protein arginine N-methyltransferase 3 from (Rattus norvegicus) SPIO70467, (Homo sapiens) SPIO60678 (88416.m01532)
2517	Not regulated	NC-NC-NC	256291_at	protein kinase family protein contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPRO02290 (88416.m01521)
2518	Not regulated	NC-NC-NC	256283_at	tetrahydrofolate dehydrogenase/cyclohydrolase, putative similar to SPIP07245 C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) [includes: Methylene-tetrahydrofolate dehydrogenase (EC 1.5.1.5); Methylene-tetrahydrofolate cyclohydrolase (EC 3.5.4.9); Formyltetrahydrofolate synthetase (EC 6.3.4.3)] [Saccharomyces cerevisiae]; contains Pfam profiles PF02882: Tetrahydrofolate dehydrogenase/cyclohydrolase, NAD(P)-binding domain, PF00783: Tetrahydrofolate dehydrogenase/cyclohydrolase, catalytic domain (88416.m01534)
2519	Not regulated	NC-NC-NC	256287_at	complex 1 family protein / LVR family protein contains Pfam PF05347: Complex 1 protein (LYR family) (88416.m01531)
2520	Not regulated	NC-NC-NC	256288_at	retinoblastoma-related protein (RBR1) nearly identical to retinoblastoma-related protein [Arabidopsis thaliana] GI:8777927; contains Pfam profiles: PF01858 retinoblastoma-associated protein A domain, PF01857 retinoblastoma-associated protein B domain (88416.m01533)
2521	Not regulated	NC-NC-NC	256270_at	expressed protein (88416.m01535)
2522	Not regulated	NC-NC-NC	256272_at	cation efflux family protein / metal tolerance protein, putative member of the cation diffusion facilitator (CDF) family, or cation efflux (CE) family, PMID:11500563 (88416.m01506)
2523	Not regulated	NC-NC-NC	256273_at	senescence-associated protein 5 [Hemerocallis hybrid cultivar] gi3551954 gb AAC34855 (88416.m01505)

2524	Not regulated	NC-NC-NC	256279_at	Al3g12620	protein phosphatase 2C family protein / PP2C family protein similar to Ser/Thr protein phosphatase 2C (PP2C) (GI:15020818) [Arabidopsis thaliana]; similar to protein phosphatase 2C (GI:3608412) [Mesembryanthemum crystallinum]; contains Pfam PF00481
2525	Not regulated	NC-NC-NC	256258_at	Al3g12480	: Protein phosphatase 2C domain; (88416.m01571)
2526	Not regulated	NC-NC-NC	256232_at	Al3g12570	transcription factor, putative (88416.m01553)
2527	Not regulated	NC-NC-NC	256233_at	Al3g12380	expressed protein (88416.m01564)
2528	Not regulated	NC-NC-NC	256234_at	Al3g12370	ankyrin repeat family protein contains ankyrin repeat domains. Pfam:PF00023 (88416.m01541)
2529	Not regulated	NC-NC-NC	256235_at	Al3g12490	ribosomal protein L10 family protein similar to 50S ribosomal protein L10 (Oryza sativa) [GB:AA084971 GI:3777602] (Oryza sativa) (88416.m01542)
2530	Not regulated	NC-NC-NC	256236_at	Al3g12350	cysteine protease inhibitor, putative / cystatin, putative similar to PRL-Interacting factor M (Arabidopsis thaliana) GI:1139270.
2531	Not regulated	NC-NC-NC	256237_at	Al3g12360	cysteine protease inhibitor [Brassica rapa] GI:762785; contains Pfam profile PF00031: Cystatin domain (88416.m01554)
2532	Not regulated	NC-NC-NC	256241_at	Al3g12390	F-box family protein : similar to SKP1 interacting partner 2 (SKP2) TIGR. A011A05087250 (88416.m01540)
2533	Not regulated	NC-NC-NC	256242_at	Al3g12380	tumour susceptibility gene 101 (TSG101) family protein contains Pfam profile PF05743: Tumour susceptibility gene 101 protein (TSG101); similar to Tumor susceptibility gene 101 protein (Swiss-Prot:Q98816) (Homo sapiens) (88416.m01545)
2534	Not regulated	NC-NC-NC	256249_at	Al3g11270	nascent polypeptide associated complex alpha chain protein, putative / alpha-NAC, putative similar to alpha-NAC, non-muscle form [Mus musculus] GI:1666890; contains Pfam profiles PF01849: NAC domain, PF00627: UBA/TS-N domain (88416.m01544)
2535	Not regulated	NC-NC-NC	256252_at	Al3g11340	actin/actin-like family protein similar to SPIP53948 Actin-like protein ARP5 (Saccharomyces cerevisiae); contains Pfam profile PF00022: Actin (88416.m01543)
2536	Not regulated	NC-NC-NC	256253_at	Al3g11250	26S proteasome non-ATPase regulatory subunit 7, putative / 26S proteasome regulatory subunit S12, putative / MOV24 protein, putative contains similarity to 26S proteasome regulatory subunit S12 (MOV24) SP:P26518 from [Mus musculus] (88416.m01370)
2537	Not regulated	NC-NC-NC	256255_at	Al3g11280	UDP-glucuronosyl-UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase (88416.m01379)
2538	Not regulated	NC-NC-NC	256256_at	Al3g11230	60S acidic ribosomal protein P0 (RPP0C) similar to 60S acidic ribosomal protein P0 GI:2088654 [Arabidopsis thaliana] (88416.m01368)
2539	Not regulated	NC-NC-NC	256229_at	Al1g56200	myb family transcription factor contains Pfam profile: PF00249 Myb-like DNA-binding domain (88416.m01371)
2540	Not regulated	NC-NC-NC	256209_at	Al1g50940	yppee family protein similar to ydp1-1 [Colinus coturnix] GI:10441650. Yppee protein [Homo sapiens] GI:5713281; contains Pfam profile PF03226: Yppee putative zinc-binding protein (88416.m01368)
2541	Not regulated	NC-NC-NC	256215_at	Al1g50900	mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein contains Pfam profile PF00824: Mechanosensitive ion channel (88414.m06808)
2542	Not regulated	NC-NC-NC	256217_at	Al1g56320	electron transfer flavoprotein alpha subunit family protein contains Pfam profile: PF00768 electron transfer flavoprotein, alpha subunit (88414.m05727)
2543	Not regulated	NC-NC-NC	256223_at	Al1g56200	expressed protein (88414.m05723)
2544	Not regulated	NC-NC-NC	256169_at	Al1g51800	expressed protein (88414.m06474)
2545	Not regulated	NC-NC-NC	256170_at	Al1g51700	expressed protein (88414.m06459)
2546	Not regulated	NC-NC-NC	256173_at	Al1g51730	leucine-rich repeat protein kinase, putative similar to light repressible receptor protein kinase [Arabidopsis thaliana]
2547	Not regulated	NC-NC-NC	256179_at	Al1g51710	gi1321686[lemb]CAAG6378; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, leucine-rich repeat protein kinase, putative similar to light repressible receptor protein kinase [Arabidopsis thaliana]
2548	Not regulated	NC-NC-NC	256184_at	Al1g51650	Pfam:PF00069 (88414.m05837)
2549	Not regulated	NC-NC-NC	256191_at	Al1g50130	leucine-rich repeat protein kinase, putative similar to light repressible receptor protein kinase [Arabidopsis thaliana]
2550	Not regulated	NC-NC-NC	256160_at	Al1g30120	gi1321686[lemb]CAAG6378; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069 (88414.m05838)
2551	Not regulated	NC-NC-NC	256142_at	Al1g48790	RWD domain-containing protein contains Pfam profile PF05773: RWD domain; similar to GCN2 eIF2alpha kinase (GI:6086595) [Mus musculus]; similar to GCN2beta (GI:10764163) [Mus musculus]; similar to RING finger protein 25 (RING finger protein A07) (Swiss-Prot:Q9QZ00) [Mus musculus]; similar to RING finger protein 25 (Swiss-Prot:Q988B1) [Homo sapiens] (88414.m05628)
2552	Not regulated	NC-NC-NC	256143_at	Al1g48830	ubiquitin-specific protease 6, putative (UBP6) similar to GI:11963465 (88414.m05827)
2553	Not regulated	NC-NC-NC	256145_at	Al1g48750	ATP synthase epsilon chain, mitochondrial identical to ATP synthase epsilon chain, mitochondrial SP:Q96253 from [Arabidopsis thaliana] (88414.m05819)
2554	Not regulated	NC-NC-NC	256149_at	Al1g55110	expressed protein similar to hypothetical protein GI:1489227 from [Brassica oleracea] (88414.m03882)
2555	Not regulated	NC-NC-NC	256152_at	Al1g55150	pyruvate dehydrogenase E1 component beta subunit, chloroplast identical to pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana] GI:2454184; identical to cDNA pyruvate dehydrogenase E1 beta subunit mRNA, nuclear gene encoding plastid protein GI:2454183 (88414.m03881)
2556	Not regulated	NC-NC-NC	256158_at	Al1g13590	mov34 family protein similar to AMSH [Homo sapiens] GI:4058124; contains Pfam profile PF01398: Mov34/MNPAD-1 family (88414.m05460)
2557	Not regulated	NC-NC-NC	256134_at	Al1g13560	40S ribosomal protein S7 (RPS7A) similar to 40S ribosomal protein S7 homolog GI:5532505 from [Brassica oleracea] (88414.m05464)
					protease inhibitor/seed storage/LTP family protein similar to TED4 [Zinnia elegans] GI:493721; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234 (88414.m05455)
					zinc finger (C2H2 type) family protein contains Pfam domain, PF00098: Zinc finger, C2H2 type (88414.m06284)
					DEAD box RNA helicase, putative (RH20) similar to ethylene-responsive RNA helicase GI:5689638 from [Lycopersicon esculentum]; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain (88414.m06288)
					phytosulfokines-related similar to SPIQ9AR88 Phytosulfokines 4 precursor [Contains: Phytosulfokine-alpha (PSK- alpha) (Phytosulfokine- α), Phytosulfokine-beta (PSK-beta) (Oryza sativa) (88414.m01583)]
					aminocyclitolphosphotransferase (AAPT1) identical to aminocyclitolphosphotransferase GI:3861593 from [Arabidopsis thaliana] (88414.m01589)

2558	Not regulated	NC-NC-NC	256106_at	A11g16870	mitochondrial 28S ribosomal protein S29-related contains weak similarity to Swiss-Prot:P51398 mitochondrial 28S ribosomal protein S29 (MRP-S29, Death-associated protein 3, DAP-3) [Homo sapiens] (68414.m02037)
2559	Not regulated	NC-NC-NC	256112_at	A11g16820	Ras-related GTP-binding protein, putative similar to GTP binding protein Gi:218228 from [Vicia faba]; identical to cDNA small GTP-binding protein (Rab11) Gi:451859 (68414.m02051)
2560	Not regulated	NC-NC-NC	256113_at	A11g16810	expressed protein (68414.m02019)
2561	Not regulated	NC-NC-NC	256115_at	A11g16880	undecyltransferase-related similar to [Protein-Pil] undecyltransferase (Pil undecyl- transferase) (Undecyl removing enzyme) (UTase)[SP:Q8AC53] [Caulobacter crescentus] (68414.m02039)
2562	Not regulated	NC-NC-NC	256117_at	A11g16840	expressed protein (68414.m02025)
2563	Not regulated	NC-NC-NC	256118_at	A11g16970	Ku70-like protein identical to Ku70-like protein Gi:12008424 from [Arabidopsis thaliana]; contains Pfam profiles PF03731; Ku70/Ku80 N-terminal alphabeta domain, PF02735; Ku70/Ku80 beta-barrel domain, PF03730; Ku70/Ku80 C-terminal arm, and PF02037; SAP domain, contains TIGRfam profile TIGR00578: ATP-dependent DNA helicase II, 70 kDa subunit (68414.m02061)
2564	Not regulated	NC-NC-NC	256119_at	A11g18070	EF-1-alpha-related GTP-binding protein, putative similar to EF-1-alpha-related GTP-binding protein gi1009232[gb]AAA79032 (68414.m02236)
2565	Not regulated	NC-NC-NC	256121_at	A11g18160	protein kinase family protein contains Pfam domain, PF00069; Protein kinase domain (68414.m02256)
2566	Not regulated	NC-NC-NC	256125_at	A11g18250	thumatin, putative identical to SPIP50699 Thumatin-like protein precursor (Arabidopsis thaliana); strong similarity to patugenesis-related group 5 protein Gi:2748943 from [Brassica rapa] (68414.m02276)
2567	Not regulated	NC-NC-NC	256129_at	A11g18210	calcium-binding protein, putative similar to SPIC9M7R0 Calcium-binding allergen Ole a 8 (PCA18PCA23) (Olea europaea); contains INTERPRO:IPR002048 calcium-binding EF-hand domain (68414.m02266)
2568	Not regulated	NC-NC-NC	256075_at	A11g18150	mitogen-activated protein kinase, putative / MAPK, putative (MPK8) identical to ATMPK8 [Arabidopsis thaliana]
2569	Not regulated	NC-NC-NC	256086_at	A11g20770	gi17106542[dbj]BAA82222; mitogen-activated protein kinase (MAPK), PMID:12119187; similar to mitogen-activated protein kinase Gi:5815410 from [Oryza sativa] (68414.m02252)
2570	Not regulated	NC-NC-NC	256088_at	A11g20810	expressed protein (68414.m02601)
2571	Not regulated	NC-NC-NC	256091_at	A11g20693	immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein identical to Probable FKBP-type peptidyl-prolyl cis-trans isomerase 1, chloroplast precursor (Ppiase) (Rotamase) (SP:O8LM71)[Arabidopsis thaliana]; similar to SPIP25138 FK508-binding protein (Peptidyl-prolyl cis-trans isomerase) (PPIase) (EC 5.2.1.8) (Rotamase) (Nissaria meningibidis); contains Pfam PF00254; peptidyl-prolyl cis-trans isomerase, FKBP-type (68414.m02606)
2572	Not regulated	NC-NC-NC	256092_at	A11g20686	high mobility group protein beta1 (HMGbeta1) / HMG protein beta1 nearly identical to HMG protein (HMGbeta1) [Arabidopsis thaliana] Gi:2832359 (68414.m02592)
2573	Not regulated	NC-NC-NC	256097_at	A11g13870	high mobility group protein beta2 (HMGbeta2) / HMG protein beta2 nearly identical to HMG protein (HMGbeta2) [Arabidopsis thaliana] Gi:2832361 (68414.m02593)
2574	Not regulated	NC-NC-NC	256068_at	A11g13690	expressed protein (68414.m01607)
2575	Not regulated	NC-NC-NC	256041_at	A11g07230	RNA recognition motif (RRM)-containing protein contains Pfam profile: PF00078 RNA recognition motif (68414.m01809)
2576	Not regulated	NC-NC-NC	256043_at	A11g07210	phosphotase family protein low similarity to SPIP95246 Phospholipase C 2 precursor (EC 3.1.4.3) [Mycobacterium tuberculosis]; contains Pfam profile PF04185: Phosphotase family (68414.m00769)
2577	Not regulated	NC-NC-NC	256045_at	A11g07150	30S ribosomal protein S18 family contains Pfam profile: PF01084 ribosomal protein S18; similar to 30S ribosomal protein S18 (SP:P80382) (Thermus thermophilus) (68414.m00767)
2578	Not regulated	NC-NC-NC	256057_at	A11g07180	protein kinase family protein contains eukaryotic protein kinase domain, INTERPRO:IPR000719 (68414.m00761)
2579	Not regulated	NC-NC-NC	256058_at	A11g07240	pyridine nucleotide-disulphide oxidoreductase family protein contains similarity to alternative NADH-dehydrogenase Gi:3718005 from [Yarrowia lipolytica], SPIP23240 Rotenone-insensitive NADH-ubiquinone oxidoreductase, mitochondrial precursor (EC 1.6.5.3) (Internal NADH dehydrogenase) (Saccharomyces cerevisiae); contains Pfam profile PF00070: Pyridine nucleotide-disulphide oxidoreductase (68414.m00764)
2580	Not regulated	NC-NC-NC	256064_at	A11g07020	UDP-glucuronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase (68414.m00770)
2581	Not regulated	NC-NC-NC	256065_at	A11g07070	expressed protein (68414.m00747)
2582	Not regulated	NC-NC-NC	256067_at	A11g07170	60S ribosomal protein L35a (RPL35a) similar to ribosomal protein L35a Gi:57118 from [Rattus norvegicus] (68414.m00753)
2583	Not regulated	NC-NC-NC	256033_at	A11g07250	expressed protein contains Pfam domain PF03660: Uncharacterised protein family (UFP0123) (68414.m00763)
2584	Not regulated	NC-NC-NC	256034_at	A11g07080	UDP-glucuronosyl/UDP-glucosyl transferase family protein similar to UDP-glucose glucosyltransferase Gi:453245 from [Manduca sexta] (68414.m00771)
2585	Not regulated	NC-NC-NC	256035_at	A11g07140	gamma interferon responsive lysosomal thiol reductase family protein / GILT family protein similar to SPIP13284 Gamma-interferon inducible lysosomal thiol reductase precursor (Homo sapiens); contains Pfam profile PF03227: Gamma interferon inducible Ran-binding protein 1a (RanBP1a) identical to Ran-binding protein (atranbp1a) Gi:2058282 from [Arabidopsis thaliana] (68414.m00760)
2586	Not regulated	NC-NC-NC	256038_at	A11g07110	Ran-binding protein 1a (RanBP1a) identical to Ran-binding protein (atranbp1a) Gi:2058282 from [Arabidopsis thaliana]
2587	Not regulated	NC-NC-NC	256015_at	A11g19150	fructose-6-phosphate 2-kinase / fructose-2,6-bisphosphatase (F2KP) identical to fructose-6-phosphate 2-kinase/fructose-2,6-bisphosphatase (F2KP) [Arabidopsis thaliana] Gi:13090908 (68414.m00756)
2588	Not regulated	NC-NC-NC	256016_at	A11g19240	chlorophyll A-B binding protein, putative / LHCII type II, putative very strong similarity to PSI type II chlorophyll a/b-binding protein Lhca2*1 Gi:541565 from [Arabidopsis thaliana]; contains Pfam profile: PF00504 chlorophyll A-B binding protein (68414.m02394)
2589	Not regulated	NC-NC-NC	256022_at	A11g58360	expressed protein (68414.m02394)
2590	Not regulated	NC-NC-NC	255979_at	A11g33980	amino acid permease I (AAP1) identical to amino acid permease I Gi:22641 from [Arabidopsis thaliana] (68414.m06938)
2591	Not regulated	NC-NC-NC	255981_at	A11g34020	Sng-4/UFP3 family protein contains Pfam PF03487: Sng-4/UFP3 family, similar to NUPF3B (Gi:12232324) [Homo sapiens] (68414.m04213)
					transporter-related low similarity to UDP-sugar transporter [Drosophila melanogaster] Gi:14871008. UDP-glucuronic acid transporter [Homo sapiens] Gi:11463948 (68414.m04218)

2592	Not regulated	NC-NC-NC	255982_at	A11g34000	light stress-responsive one-helix protein (OHP2) contains similarity to photosystem II 22 kDa protein G16008279 from [Arabidopsis thaliana] (88414.m04215) hydrolase, alpha/beta fold family protein similar to polyneuridine aldehyde esterase G16651383 from [Rauvolfia serpentina]. SPIQ40708 PIRTA protein (Oryza sativa), ethylene-induced esterase [Citrus sinensis] G1:14278437; contains Pfam profile PF00561: hydrolase, alpha/beta fold family (88414.m04214) expressed protein (88414.m03842) expressed protein (88414.m03839) chlorophyll A-B binding protein 2, chloroplast / LHClI type 1 CAB-2 / CAB-140 (CAB2A) identical to SPIQ40778 Chlorophyll A-B chlorophyll A-B binding protein 2, chloroplast (LHClI type 1 CAB-2) (LHCP) (Arabidopsis thaliana) (88414.m03855) binding protein 2, chloroplast precursor (LHClI type 1 CAB-2) (LHCP) (Arabidopsis thaliana) (88414.m03855) glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolase, putative similar to serine hydroxymethyltransferase [Chlamydomonas reinhardtii] G1:17066748; contains Pfam profile PF00464: serine to serine hydroxymethyltransferase (88414.m02755) hydroxymethyltransferase (88414.m02767) expressed protein (88414.m02767) 14-3-3 protein GF14 epsilon (GRF10) identical to 14-3-3 protein GF14 epsilon G1:5602798, SP-P48347 from [Arabidopsis thaliana] (88414.m02788) protein phosphatase 2C, putative / PP2C, putative similar to protein phosphatase type 2C G1:4336438 from [Lotus japonicus] (88414.m02785) pumilioPur RNA-binding domain-containing protein contains Pfam profile: PF00808 pumilio-family RNA binding domain (88414.m02780) expressed protein (88414.m02776) AP2 domain-containing transcription factor, putative similar to AP2 domain containing protein RAP2.4 G1:2281633 from [Arabidopsis thaliana] (88414.m02775) membrane bound O-acyl transferase (MBOAT) family protein low similarity to porcupine from [Xenopus laevis] G1:8714514, G1:8714520, G1:8714518, G1:8714516; contains Pfam profile PF03062: MBOAT family (88414.m01468) rhomboid family protein contains PFAM domain PF01694, Rhomboid family (88414.m01480) protein kinase family protein contains protein kinase domain, Pfam:PF00089 (88414.m01472) prolyl oligopeptidase, putative / prolyl endopeptidase, putative / post-proline cleaving enzyme, putative similar to SPIP48147 Prolyl oligopeptidase (EC 3.4.21.26) (Post-proline cleaving enzyme) (Homo sapiens); contains Pfam profiles PF00328: prolyl oligopeptidase family, PF02897: Prolyl oligopeptidase, N-terminal beta-propeller domain (88414.m02542) endopeptidase (EC 3.4.21.26) (Post-proline cleaving enzyme) (Homo sapiens); contains Pfam profiles PF00328: prolyl oligopeptidase family, PF02897: Prolyl oligopeptidase, N-terminal beta-propeller domain (88414.m02542) plastocyanin similar to plastocyanin G1:1865683 from [Arabidopsis thaliana] (88414.m02538) GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase, putative similar to GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase (GER1)G1:6016479 from [Arabidopsis thaliana] (88414.m02213) nascent polypeptide-associated complex (NAC) domain-containing protein / BTF3-like transcription factor / BTF3-like transcription factor 3 (Homo sapiens); contains Pfam profile PF01648: SPIP20290 Transcription factor BTF3 (NAC) domain-containing protein (88414.m02212) NAC domain; identical to CDNA BTF30-like factor G1:5912423 (88414.m02228) expressed protein contains 11 transmembrane domains; putative (QIN8) contains Pfam profile: PF01238 phosphomannose isomerase type 1; similar to phosphomannose isomerase G1:10834550 from [Arabidopsis thaliana]; identical to CDNA phosphomannose isomerase (din8) partial cds G1:10834549 (88414.m07627) glycerophosphoryl diester phosphodiesterase family protein contains Pfam PF03009: Glycerophosphoryl diester phosphodiesterase family (88414.m07615) expressed protein (88414.m07628) zinc finger (C2H2 type) family protein (ZFP6) identical to zinc finger protein, ZFP6 g1:7908983(gb)AAA87302; contains Pfam domain, PF00096: Zinc finger, C2H2 type (88414.m07622) expressed protein contains Pfam profile PF04525: Protein of unknown function (DUF587) (88415.m03685) small nuclear ribonucleoprotein U2B, putative / spliceosomal protein, putative similar to spliceosomal protein [Solanum tuberosum] G1:169589 (88415.m03684) expressed protein (88415.m05003) expansin, putative (EXP8) similar to expansin 2 G1:7025493 from [Zinnia elegans]; alpha-expansin gene family, PMID:11641069 (88415.m05009) uroporphyrinogen decarboxylase, putative / UROD, putative similar to uroporphyrinogen decarboxylase (chloroplast) from Nicotiana glauca (SPIQ42867), Hordeum vulgare (SPIQ42855), Zea mays (SPJ081220); contains Pfam domain uroporphyrinogen decarboxylase (URO-D) PF01208 (88415.m04897)
2593	Not regulated	NC-NC-NC	255983_at	A12g40600	appr-1-p processing enzyme family protein contains Pfam domain PF01661: Appr-1-p processing enzyme family (88415.m05008) potassium transporter, putative (KT2) identical to putative potassium transporter AKKT2p [Mesembryanthemum crystallinum] G1:14091471; g1:2384671(gb)AAC48845, strong similarity to potassium transporter HAK2p [Mesembryanthemum crystallinum] G1:14091471; KUPHA/KAT Transporter family member, PMID:11500563 (88415.m05002) transducin family protein 1 / WD-40 repeat family protein contains 5 WD-40 repeats (PF00400); similar to cell cycle control protein cwR (SP-O14011) [Schizosaccharomyces pombe (Fission yeast)] (88415.m04086) cinnamoyl-CoA reductase family similar to cinnamoyl-CoA reductase from Pinus taeda [G1:17978648], Eucalyptus gunnii [G1:2056311] (88415.m04118) 50S ribosomal protein L28, chloroplast (CL28) (88415.m04100) glycolipid transfer protein-related similar to phosphorinositol 4-phosphate adaptor protein-2 (G1:14165198) [Homo sapiens]; similar to Glycolipid transfer protein (GLTP) (Swiss-Prot:Q8N2D2) [Homo sapiens] (88415.m04102) Prot:Q8N2D2) [Homo sapiens] (88415.m04102)
2594	Not regulated	NC-NC-NC	255984_at	A12g40540	
2595	Not regulated	NC-NC-NC	255985_at	A12g40540	
2596	Not regulated	NC-NC-NC	255986_at	A12g40540	
2597	Not regulated	NC-NC-NC	255987_at	A12g40540	
2598	Not regulated	NC-NC-NC	255988_at	A12g40540	
2599	Not regulated	NC-NC-NC	255989_at	A12g40540	
2600	Not regulated	NC-NC-NC	255990_at	A12g40540	
2601	Not regulated	NC-NC-NC	255991_at	A12g40540	
2602	Not regulated	NC-NC-NC	255992_at	A12g40540	
2603	Not regulated	NC-NC-NC	255993_at	A12g40540	
2604	Not regulated	NC-NC-NC	255994_at	A12g40540	
2605	Not regulated	NC-NC-NC	255995_at	A12g40540	
2606	Not regulated	NC-NC-NC	255996_at	A12g40540	
2607	Not regulated	NC-NC-NC	255997_at	A12g40540	
2608	Not regulated	NC-NC-NC	255998_at	A12g40540	
2609	Not regulated	NC-NC-NC	255999_at	A12g40540	
2610	Not regulated	NC-NC-NC	256000_at	A12g40540	
2611	Not regulated	NC-NC-NC	256001_at	A12g40540	
2612	Not regulated	NC-NC-NC	256002_at	A12g40540	
2613	Not regulated	NC-NC-NC	256003_at	A12g40540	
2614	Not regulated	NC-NC-NC	256004_at	A12g40540	
2615	Not regulated	NC-NC-NC	256005_at	A12g40540	
2616	Not regulated	NC-NC-NC	256006_at	A12g40540	
2617	Not regulated	NC-NC-NC	256007_at	A12g40540	
2618	Not regulated	NC-NC-NC	256008_at	A12g40540	
2619	Not regulated	NC-NC-NC	256009_at	A12g40540	
2620	Not regulated	NC-NC-NC	256010_at	A12g40540	
2621	Not regulated	NC-NC-NC	256011_at	A12g40540	
2622	Not regulated	NC-NC-NC	256012_at	A12g40540	
2623	Not regulated	NC-NC-NC	256013_at	A12g40540	
2624	Not regulated	NC-NC-NC	256014_at	A12g40540	
2625	Not regulated	NC-NC-NC	256015_at	A12g40540	
2626	Not regulated	NC-NC-NC	256016_at	A12g40540	

2627	Not regulated	NC-NC-NC	255787_at	A2g333590	cinnamoyl-CoA reductase family similar to cinnamoyl-CoA reductase from <i>Pinus taeda</i> [GI:17878648], <i>Eucalyptus gunnii</i> [GI:2058311] (68415.m04117)
2628	Not regulated	NC-NC-NC	255788_at	A2g333310	auxin-responsive protein 1 / indoleacetic acid-induced protein 13 (IAA13) identical to SPIQ38831 Auxin-responsive protein IAA13 (Indoleacetic acid-induced protein 13) [Arabidopsis thaliana] (68415.m04082)
2629	Not regulated	NC-NC-NC	255791_at	A2g333430	plastid developmental protein DAG, putative similar to DAG protein, chloroplast precursor [Garden snapdragon] SWISS-PROT:Q38732 (68415.m04097)
2630	Not regulated	NC-NC-NC	255792_at	A2g333820	DNA-binding family protein / AT-hook protein 1 (AHP1) identical to AT-hook protein 1 [Arabidopsis thaliana]
2631	Not regulated	NC-NC-NC	255793_at	A2g333250	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; (68415.m04104)
2632	Not regulated	NC-NC-NC	255794_at	A2g333480	3-beta hydroxysteroid dehydrogenase/isomerase family protein contains Pfam PF01073 3-beta hydroxysteroid dehydrogenase/isomerase domain; similar to NAD(P)-dependent cholesterol dehydrogenase [Nocardia sp.] [GI:216809] (68415.m04123)
2633	Not regulated	NC-NC-NC	255797_at	A2g333630	haloacid dehalogenase-like hydrolase family protein contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase (68415.m04075)
2634	Not regulated	NC-NC-NC	255798_at	A2g333255	light-mediated development protein 1 / deetiolated1 (DET1) identical to Light-mediated development protein DET1 (Deetiolated1) (Swiss-Prot:P48732) [Arabidopsis thaliana] (68417.m01686)
2635	Not regulated	NC-NC-NC	255799_at	A4g101080	expressed protein (68417.m01684)
2636	Not regulated	NC-NC-NC	255808_at	A4g1010300	expressed protein (68417.m01659)
2637	Not regulated	NC-NC-NC	255810_at	A4g101140	expressed protein (68414.m02005)
2638	Not regulated	NC-NC-NC	255764_at	A1g161720	expressed protein contains Pfam PF04784: Protein of unknown function, DUF547 (68414.m02011)
2639	Not regulated	NC-NC-NC	255766_at	A1g161750	60S ribosomal protein L6 (RPL6A) similar to 60S ribosomal protein L6 GI:7208784 from <i>Cicer arietinum</i> (68414.m02313)
2640	Not regulated	NC-NC-NC	255776_at	A1g1618540	glycine-rich RNA-binding protein, putative similar to glycine-rich RNA-binding protein from <i>Sorghum bicolor</i> SPIQ89070, GI:1778373 from <i>Pisum sativum</i> ; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) (68414.m02322)
2641	Not regulated	NC-NC-NC	255777_at	A1g168630	3-phosphoserine phosphatase (PSP) nearly identical to 3-phosphoserine phosphatase GI:3759177 from <i>Arabidopsis thaliana</i> (68414.m02323)
2642	Not regulated	NC-NC-NC	255778_at	A1g168840	glycosyl hydrolase family protein 17 similar to beta-1,3-glucanase GI:15150341 from <i>Camellia sinensis</i> ; C-terminal homology only (68414.m02325)
2643	Not regulated	NC-NC-NC	255779_at	A1g168650	phytochrome and flowering time regulatory protein (PFT1) PMID: 12815435 (68414.m03171)
2644	Not regulated	NC-NC-NC	255725_at	A1g255440	mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein (68414.m03150)
2645	Not regulated	NC-NC-NC	255736_at	A1g255380	expressed protein contains Pfam profile: PF03398 eukaryotic protein of unknown function, DUF282 (68414.m03155)
2646	Not regulated	NC-NC-NC	255737_at	A1g25420	leucine-rich repeat protein-related contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001811; contains some similarity to light repressible receptor protein kinase [Arabidopsis thaliana] gi1321688[emb]CAA68376 (68414.m03174)
2647	Not regulated	NC-NC-NC	255738_at	A1g255570	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (68414.m03152)
2648	Not regulated	NC-NC-NC	255740_at	A1g255390	secretory carrier membrane protein (SCAMP) family protein contains Pfam domain, PF04144: SCAMP family (68414.m03943)
2649	Not regulated	NC-NC-NC	255752_at	A1g32050	GCN5-related N-acetyltransferase (GNAT) family protein / nuclear shuttle interacting protein (NSI) very low similarity to SPIP09453 Ribosomal-protein-alanine acetyltransferase (EC 2.3.1.128) [Escherichia coli]; contains Pfam profile PF00583: acetyltransferase, GNAT family; PMID 12837850, identical to cDNA nuclear shuttle interacting protein (NSI) GI: 30780420 (68414.m03945)
2650	Not regulated	NC-NC-NC	255718_at	A1g32070	membrane protein, putative contains 12 transmembrane domains; similar to yohK (GI:405873) [Escherichia coli] (68414.m03947)
2651	Not regulated	NC-NC-NC	255719_at	A1g32080	expressed protein (68414.m03925)
2652	Not regulated	NC-NC-NC	255721_at	A1g31940	NAD-dependent epimerase/dehydratase family protein similar to nucleotide sugar epimerase from <i>Vibrio vulnificus</i> GI:3093975 [PID:3093975], WbnF [Escherichia coli] GI:5738472, CAP1 protein (Staphylococcus aureus) SPIP39856; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family (68417.m00011)
2653	Not regulated	NC-NC-NC	255696_at	A4g00110	scarecrow-like transcription factor 8 (SCL8) (68417.m00015)
2654	Not regulated	NC-NC-NC	255698_at	A4g00150	vesicle-associated membrane family protein / VAMP family protein similar to VAP27 GI:6888926 [Nicotiana glauca] (68417.m00018)
2655	Not regulated	NC-NC-NC	255704_at	A4g00170	transducin family protein / WD-40 repeat family protein similar to Transducin beta-like 2 protein (WS beta-transducin repeats protein) (WS-betaTRP) (Williams-Beuren syndrome chromosome region 13 protein) (SP:Q8Y4P3) [Homo sapiens] (68417.m00009)
2656	Not regulated	NC-NC-NC	255711_at	A4g00080	fringe-related protein + weak similarity to Fringe [Schistosoma gregana] (GI:6573138); Fringe encodes an extracellular protein that regulates Notch signalling. (68417.m00037)
2657	Not regulated	NC-NC-NC	255714_at	A4g00300	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (68417.m00042)
2658	Not regulated	NC-NC-NC	255716_at	A4g00330	phospholipid/glycerol acyltransferase family protein (68417.m00054)
2659	Not regulated	NC-NC-NC	255692_at	A4g00400	malate oxidoreductase, putative similar to NAD-dependent malic enzyme 59 kDa isoform, mitochondrial precursor (EC 1.1.1.39) (NAD-ME) (SP:P37225) [Solanum tuberosum] (68417.m00080)
2660	Not regulated	NC-NC-NC	255683_at	A4g000570	terahydrofolate dehydrogenase/cyclohydrolase, putative similar to SPIP08440 C-1-terahydrofolate synthase, mitochondrial precursor (C1-THF synthase) [includes: Methylenetetrahydrofolate dehydrogenase (EC 1.5.1.5); Methylenetetrahydrofolate cyclohydrolase (EC 3.5.4.9); Formyltetrahydrofolate synthetase (EC 6.3.4.3) (Saccharomyces cerevisiae)]; contains Pfam profiles PF02882: Tetrahydrofolate dehydrogenase/cyclohydrolase, NAD(P)-binding domain, PF00763: Tetrahydrofolate dehydrogenase/cyclohydrolase, catalytic domain (68417.m00084)
2661	Not regulated	NC-NC-NC	255685_s_at	A4g00600	dehydrogenase/cyclohydrolase, catalytic domain (68417.m00084)
2662	Not regulated	NC-NC-NC	255830_at	A4g00700	C2 domain-containing protein contains INTERPRO:IPR000008 C2 domain (68417.m00096)
2663	Not regulated	NC-NC-NC	255633_at	A4g00585	expressed protein (68417.m00082)

2664	Not regulated	NC-NC-NC	255635_at	AI4g00720	shaggy-related protein kinase theta / ASK-theta (ASK-theta) identical to shaggy-related protein kinase theta (ASK-theta) [Arabidopsis thaliana] SWISS-PROT:Q86287 (88417.m00098)
2665	Not regulated	NC-NC-NC	255645_at	AI4g00880	auxin-responsive family protein similar to small auxin up RNA (GI:546362) [Arabidopsis thaliana] (88417.m00118)
2666	Not regulated	NC-NC-NC	255657_at	AI4g00810	60S acidic ribosomal protein P1 (RPP1B) similar to acidic ribosomal protein p1 (88417.m00111)
2667	Not regulated	NC-NC-NC	255628_at	AI4g00850	SSXT family protein low similarity to synovial sarcoma associated SS18-delta [Mus musculus] GI:17978535; contains Pfam profile PF05030: SSXT protein (N-terminal region) (88417.m00116)
2668	Not regulated	NC-NC-NC	255628_at	AI4g00880	stress-related ozone-induced protein (OZ11) / stress-related ozone-responsive protein identical to stress-related ozone-induced protein AQZ11 (mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection); putative pathogenesis-related protein (GI:790583) [Arabidopsis thaliana] (88417.m00117)
2669	Not regulated	NC-NC-NC	255598_at	AI4g00830	RNA recognition motif (RRM)-containing protein similar to nucleolin protein; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) (88417.m00114)
2670	Not regulated	NC-NC-NC	255600_s_at	AI5g10370	glycosyl hydrolase family 18 protein contains Pfam profile PF00704: Glycosyl hydrolases family 18 (88417.m00141)
2671	Not regulated	NC-NC-NC	255603_at	AI4g01040	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA binding domain (88417.m00169)
2672	Not regulated	NC-NC-NC	255614_at	AI4g01280	Helicase domain-containing protein / IBR domain-containing protein (GI: 439562; contains Pfam profiles PF04408: Helicase associated ATPase/helicase Cdc28p [Schizosaccharomyces pombe] GI: 439562; contains Pfam profiles PF00089: contains serine/threonine protein kinase domain, domain (HA2), PF00271: Helicase conserved C-terminal domain, weak hit to PF00097: Zinc finger, C3HC4 type (RING finger), PF01485: IBR domain (88418.m01203)
2673	Not regulated	NC-NC-NC	255617_at	AI4g01330	ribosomal protein L5 family protein contains Pfam profiles PF00673: ribosomal L5P family C-terminus, PF00281: ribosomal protein L5 (88417.m00171)
2674	Not regulated	NC-NC-NC	255623_at	AI4g01310	mitogen-activated protein kinase, putative / MAPK, putative (MPK4) identical to mitogen-activated protein kinase homolog (AIMP4)[Arabidopsis thaliana] SWISS-PROT:Q39024; PMID:12119167 (88417.m00177)
2675	Not regulated	NC-NC-NC	255624_at	AI4g01370	expressed protein (88417.m00153)
2676	Not regulated	NC-NC-NC	255567_at	AI4g01150	CAAX protease, putative (STE24) contains Pfam domain, PF01435: Peptidase family M48 (88417.m00172)
2677	Not regulated	NC-NC-NC	255569_at	AI4g01320	mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein (88417.m00148)
2678	Not regulated	NC-NC-NC	255570_at	AI4g01100	hydroxyproline-rich glycoprotein family protein (88417.m00142)
2679	Not regulated	NC-NC-NC	255572_at	AI4g01050	nodulin MIN21 family protein similar to MIN21 GI:2598575 (root nodule development) from [Medicago truncatula] (88417.m00183)
2680	Not regulated	NC-NC-NC	255575_at	AI4g01430	nodulin MIN21 family protein similar to MIN21 GI:2598575 (root nodule development) from [Medicago truncatula] (88417.m00188)
2681	Not regulated	NC-NC-NC	255578_at	AI4g01450	no apical meristem (NAM) family protein similar to NAC1 (GI:7716952) [Medicago truncatula]; contains Pfam PF02365: No apical meristem (NAM) protein (88417.m00201)
2682	Not regulated	NC-NC-NC	255585_at	AI4g01550	brx domain-containing protein contains Pfam domain, PF04427: Brx domain (88417.m00202)
2683	Not regulated	NC-NC-NC	255586_at	AI4g01560	inorganic pyrophosphatase, putative [soluble] / pyrophosphate phospho-hydrolase, putative / PPase, putative strong similarity to inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-hydrolase) (PPase) [Solanum tuberosum]; SPIQ43187 Soluble inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-hydrolase) (PPase) (88417.m00191)
2684	Not regulated	NC-NC-NC	255587_at	AI4g01480	contains Pfam profile PF00718: inorganic pyrophosphatase (88417.m00191)
2685	Not regulated	NC-NC-NC	255590_at	AI4g01810	cathepsin B-like cysteine protease, putative similar to cathepsin B-like cysteine protease (88417.m00210)
2686	Not regulated	NC-NC-NC	255594_at	AI4g01660	contains an unusually short, 5nt exon (88417.m00210)
2687	Not regulated	NC-NC-NC	255597_at	AI4g01730	ABC1 family protein contains Pfam domain, PF03108: ABC1 family (88417.m00216)
2688	Not regulated	NC-NC-NC	255537_at	AI4g01690	zinc finger (DHC type) family protein contains Pfam profile PF01528: DHC zinc finger domain (88417.m00224)
2689	Not regulated	NC-NC-NC	255552_at	AI4g01850	protoporphyrinogen oxidase (PPOX) identical to SPIP55628 (88417.m00219)
2690	Not regulated	NC-NC-NC	255553_at	AI4g01960	S-adenosylmethionine synthetase 2 (SAM2) identical to S-adenosylmethionine synthetase 2 (Methionine adenosyltransferase 2, AdoMet synthetase 2) [Arabidopsis thaliana] SWISS-PROT:P17562 (88417.m00242)
2691	Not regulated	NC-NC-NC	255556_at	AI4g01940	expressed protein (88417.m00261)
2692	Not regulated	NC-NC-NC	255558_at	AI4g02030	nitrogen fixation NifU-like family protein similar to apricot NifU homolog partial CDS, GenBank accession number U85179; contains Pfam profile: PF01108 NifU-like domain (88417.m00259)
2693	Not regulated	NC-NC-NC	255561_at	AI4g02050	expressed protein (88417.m00273)
2694	Not regulated	NC-NC-NC	255529_at	AI4g02120	sugar transporter, putative similar to SPIQ10710 Sugar carrier protein A (Ricinus communis), glucose transporter [Saccharum hybrid cultivar H65-7052] GI:347855; contains Pfam profile PF00083: major facilitator superfamily protein (88417.m00275)
2695	Not regulated	NC-NC-NC	255505_at	AI4g02080	CTP synthase, putative / UTP--ammonia ligase, putative similar to SPIP17812 CTP synthase (EC 6.3.4.2) (UTP--ammonia ligase) (Homo sapiens); contains Pfam profile PF00117: glutamine amidotransferase class-I (88417.m00283)
2696	Not regulated	NC-NC-NC	255516_at	AI4g02270	GTP-binding protein (SAR1A) identical to SP:O04834 GTP-binding protein SAR1A. [Arabidopsis thaliana] (88417.m00279)
2697	Not regulated	NC-NC-NC	255525_at	AI4g02340	pollen Ole e 1 allergen and extensin family protein contains Pfam domain, PF01190: Pollen proteins Ole e 1 family (88417.m00308)
2698	Not regulated	NC-NC-NC	255526_at	AI4g02350	epoxide hydrolase, putative similar to epoxide hydrolases from Glycine max GI:2784806; Solanum tuberosum GI:407938; contains Pfam profile PF00561: hydrolase, alpha/beta fold family (88417.m00318)
2699	Not regulated	NC-NC-NC	255473_at	AI4g02450	exocyst complex subunit Sec15-like family protein contains Pfam profile PF04081: Exocyst complex subunit Sec15-like (88417.m00319)
2700	Not regulated	NC-NC-NC	255477_at	AI4g02370	glycine-rich protein similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807) (88417.m00332)
2701	Not regulated	NC-NC-NC	255478_at	AI4g02440	expressed protein contains Pfam profile PF04398: Protein of unknown function, DUF538 (88417.m00321)
2702	Not regulated	NC-NC-NC	255484_at	AI4g02540	F-box family protein to circadian clock coupling factor ZGT (GI:14210078) [Nicotiana glauca]; contains Pfam PF00846: F-box domain (88417.m00331)
2703	Not regulated	NC-NC-NC	255495_at	AI4g02720	DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain (88417.m00347)
					expressed protein temporary automated functional assignment (88417.m00368)

2704	Not regulated	NC-NC-NC	255498_at	vacuolar ATPase subunit F family protein contains weak similarity to vacuolar ATP synthase subunit F (EC 3.6.3.14) (V-ATPase F subunit) [Vacuolar proton pump F subunit] (V-ATPase 14 kDa subunit) (Swiss-Prot:P50408) [Rattus norvegicus]; contains Pfam PF01890: ATP synthase (F14-kDa) subunit (88417.m00356)
2705	Not regulated	NC-NC-NC	255442_at	NADH-ubiquinone oxidoreductase 24 kDa subunit, putative similar to NADH-ubiquinone oxidoreductase 24 kDa subunit, (88417.m00352)
2706	Not regulated	NC-NC-NC	255447_at	mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Polypeptide II) [Swiss-Prot:P04394] [Bos taurus] (88417.m00352)
2707	Not regulated	NC-NC-NC	255448_at	GTP-binding family protein contains Pfam domain, PF01926: GTPase of unknown function (88417.m00378)
2708	Not regulated	NC-NC-NC	255451_at	phenazine biosynthesis PhzC/PhzF family protein contains Pfam profile, PF02587: phenazine biosynthesis-like protein (88417.m00388)
2709	Not regulated	NC-NC-NC	255457_at	photosystem I reaction center subunit II, chloroplast, putative / photosystem I 20 kDa subunit, putative / PSI-D, putative (PSAD1) similar to SPIP12353 Photosystem I reaction center subunit II, chloroplast precursor (Photosystem I 20 kDa subunit) (PSI-D) (Spinacia oleracea); contains Pfam profile PF02531: PsaD (88417.m00377)
2710	Not regulated	NC-NC-NC	255458_at	small nuclear ribonucleoprotein D1, putative / snRNP core protein D1, putative / Sm protein D1, putative similar to small nuclear ribonucleoprotein Sm D1 (snRNP core protein D1, Sm-D1, Sm-D1 autoantigen) (Mouse) SWISS-PROT:P13841 (88417.m00384)
2711	Not regulated	NC-NC-NC	255462_at	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to A. thaliana hypothetical protein T13L18.2, GenBank accession number 2708738; contains Pfam domain PF03171: 2OG-Fe(II) oxygenase superfamily (88417.m00401)
2712	Not regulated	NC-NC-NC	255465_at	mitochondrial transcription termination factor family protein / mTERF family protein weak similarity to mTERF protein [Paracentrotus lividus] GI:4584695; contains Pfam profile PF02536: mTERF (88417.m00406)
2713	Not regulated	NC-NC-NC	255468_at	transducin family protein / WD-40 repeat family protein contains 8 WD-40 repeats (PF00400); similar to L. erythrorhizon LEC14B, GenBank accession number O40153 (88417.m00410)
2714	Not regulated	NC-NC-NC	255469_at	kelch repeat-containing F-box family protein contains Pfam profiles PF01344: Kelch motif, PF00846: F-box domain (88417.m00411)
2715	Not regulated	NC-NC-NC	255411_at	RNA-binding protein, putative similar to Etr-1 [Dario reno] GI:7870536, BRUNO-like 8 RNA-binding protein [Homo sapiens] GI:15341327, CUG-BP and ETR-3 like factor 3 [Homo sapiens] GI:12746392; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) (88417.m00420)
2716	Not regulated	NC-NC-NC	255412_at	auxin-binding protein 1 (ABP1) identical to Auxin-binding protein 1 precursor (ABP) (Swiss-Prot:P33487) [Arabidopsis thaliana] (88417.m00405)
2717	Not regulated	NC-NC-NC	255420_at	frataxin protein-related contains weak similarity to Frataxin, mitochondrial precursor (Friedreich's ataxia protein) (Fxn) (Swiss-Prot:Q16595) [Homo sapiens] (88417.m00443)
2718	Not regulated	NC-NC-NC	255431_at	proline-rich family protein similar to U1 small nuclear ribonucleoprotein C; contains proline rich extensin domains, INTERPRO:IPR002965 (88417.m00425)
2719	Not regulated	NC-NC-NC	255435_at	cytochrome B6-F complex iron-sulfur subunit, chloroplast / Rieske iron-sulfur protein / plastocyanin-plastoquinone reductase (petC) identical to gi:9843639; identical to cDNA rieske iron-sulfur protein precursor (petC) GI:5725449 (88417.m00447)
2720	Not regulated	NC-NC-NC	255379_at	thioredoxin M-type 2, chloroplast (TRX-M2) nearly identical to SPIQ95E08 Thioredoxin M-type 2, chloroplast precursor (TRX-M2) (Arabidopsis thaliana) (88417.m00480)
2721	Not regulated	NC-NC-NC	255380_at	two-pore calcium channel (TPC1) identical to two-pore calcium channel (TPC1) [Arabidopsis thaliana] gi14041819[dbj]BAB55460 (88417.m00488)
2722	Not regulated	NC-NC-NC	255382_at	pre-mRNA splicing factor-related similar to pre-mRNA splicing factor pre-mRNA splicing factor prp1 (SP:Q12361) [Fission yeast] (88417.m00470)
2723	Not regulated	NC-NC-NC	255365_at	pyrophosphate-fructose-6-phosphate 1-phosphotransferase beta subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative strong similarity to SPIQ41141 Pyrophosphate-fructose 6-phosphate 1-phosphotransferase beta subunit (EC 2.7.1.80) (PFP) (6-phosphofructokinase, pyrophosphate-dependent) (Pyrophosphate-dependent 6-phosphofructose-1-kinase) (PPI-PFK) (Ricinua communis) (88417.m00574)
2724	Not regulated	NC-NC-NC	255327_at	malonyl-CoA decarboxylase family protein contains weak similarity to Malonyl-CoA decarboxylase, mitochondrial precursor (EC 4.1.1.9) (MCD) (Swiss-Prot:O95822) [Homo sapiens]; contains Pfam profile PF05282: Malonyl-CoA decarboxylase (MCD) (88417.m00616)
2725	Not regulated	NC-NC-NC	255328_at	leucyl-RNA synthetase, putative / leucine-RNA ligase, putative similar to SPIP36430 Leucyl-RNA synthetase (EC 6.1.1.4) (Leucine-RNA ligase) (LeuRS) (Bacillus subtilis); contains Pfam profile PF00133: RNA synthetases class I (L, M and V) (88417.m00622)
2726	Not regulated	NC-NC-NC	255338_at	peroxisomal membrane protein 22 kDa (PMP22) identical to peroxisomal membrane protein [Arabidopsis thaliana] gi13860254[emb]CAA06834 (88417.m00649)
2727	Not regulated	NC-NC-NC	255283_at	autophagy 8b (APG8b) identical to autophagy 8b [Arabidopsis thaliana] GI:19812153; contains Pfam profile PF02991: Microtubule associated protein 1A/1B, light chain 3 (88417.m00675)
2728	Not regulated	NC-NC-NC	255288_at	Met-10+ like family protein / kelch repeat-containing protein contains Pfam profiles PF01344: Kelch motif, PF02475: Met-10+ like-protein (88417.m00663)
2729	Not regulated	NC-NC-NC	255300_at	CDP-alcohol phosphatidyltransferase family protein similar to SPIQ07560 Cardiolipin synthetase (EC 2.7.8.-) [Saccharomyces cerevisiae]; contains Pfam profile PF01066: CDP-alcohol phosphatidyltransferase (88417.m00709)
2730	Not regulated	NC-NC-NC	255301_at	methionine sulfoxide reductase domain-containing protein / Self domain-containing protein low similarity to plin-like transcription methionine sulfoxide reductase domain-containing protein (88417.m00707)
2731	Not regulated	NC-NC-NC	255303_at	factor [Homo sapiens] GI:5059082, SPIP14930 Peptide methionine sulfoxide reductase msrA/msrB (EC 1.8.4.6) [Neisseria gonorrhoeae]; contains Pfam profile PF01641: SsrR domain (88417.m00702)
2732	Not regulated	NC-NC-NC	255304_at	Der1-like family protein / degradation in the ER-like family protein contains Pfam profile: PF04511 Der1-like family (88417.m00708)
2733	Not regulated	NC-NC-NC	255305_at	K+ efflux antiporter, putative (KEA3) similar to A. thaliana K+ antiporter KEA1, GenBank accession number AF003382; Monovalent cation/proton antiporter family 2 (CPA2 family) member, PMID:11500563 (88417.m00707)
				ATP-binding-cassette transporter (ABC1) identical to the protein described in PMID:11159608 and note that sequence was not deposited into GenBank by the authors. (88417.m00698)

2734	Not regulated	NC-NC-NC	255308_at	A14g04910	AAA-type ATPase family protein similar to SPIP18708 Vesicular-tusion protein NSF (N-ethylmaleimide-sensitive fusion protein) (NEM-sensitive fusion protein) [Cricetulus griseus]; contains Pfam profiles PF00004: ATPase AAA family, PF02359: Cell division protein 48 (CDC48) N-terminal domain; contains non-consensus AT-AC splice sites at intron 2 (68417.m00714)
2735	Not regulated	NC-NC-NC	255253_at	A14g05000	vacuolar protein sorting-associated protein 28 family protein / VPS28 family protein contains similarity to Swiss-Prot:Q02767 vacuolar protein sorting-associated protein VPS28 [Saccharomyces cerevisiae] (68417.m00730)
2736	Not regulated	NC-NC-NC	255256_at	A14g05060	vesicle-associated membrane protein / VAMP family protein similar to VAMP27 Gi:6688926 [Nicotiana plumbaginifolia] (68417.m00746)
2737	Not regulated	NC-NC-NC	255259_at	A14g05020	NADH dehydrogenase-related similar to alternative NA DH-dehydrogenase [Yarrowia lipolytica] Gi:3718005, 64 kDa mitochondrial NADH dehydrogenase [Neurospora crassa] Gi:4753821; contains Pfam profile PF00070: Pyridine nucleotide-disulphide oxidoreductase (68417.m00736)
2738	Not regulated	NC-NC-NC	255263_at	A14g05160	4-coumarate-CoA ligase, putative / 4-coumaroyl-CoA synthase, putative similar to 4CL2 [gi:12229665] from Arabidopsis thaliana, 4CL1 [gi:12229631] from Nicotiana tabacum; contains Pfam AMP-binding enzyme domain PF00501; acyl-activating enzyme superfamily; identical to cDNA 4-coumarate-CoA ligase-like protein (A14g05160) Gi:28893226 (68417.m00775)
2739	Not regulated	NC-NC-NC	255248_at	A14g05180	oxygen-evolving enhancer protein 3, chloroplast, putative (PSBQ2) identical to SPIQ41832 Oxygen-evolving enhancer protein 3-2, chloroplast precursor (OEE3) (16 kDa subunit of oxygen evolving system of photosystem II) (OEC 16 kDa subunit) [Arabidopsis thaliana]; similar to SPIP12301 Oxygen-evolving enhancer protein 3, chloroplast precursor (OEE3) (16 kDa subunit of oxygen evolving system of photosystem II) (OEC 16 kDa subunit) [Spinacia oleracea]; contains Pfam profile PF05757: Oxygen evolving enhancer protein 3 (PsbQ) (68417.m00778)
2740	Not regulated	NC-NC-NC	255249_at	A14g05090	inositol monophosphatase family protein low similarity to SPIQ42546 3'(2',5'-bisphosphate nucleotidase (EC 3.1.3.7) (DPNPase) [Arabidopsis thaliana]; contains Pfam profile PF00459: Inositol monophosphatase family (68417.m00756)
2741	Not regulated	NC-NC-NC	255220_at	A14g05320	polyubiquitin (UBQ10) (SEN3) senescence-associated protein; identical to GI:870791 (68417.m00810)
2742	Not regulated	NC-NC-NC	255221_at	A14g05150	octacosapeptide/Phox/Bem1p (PB1) domain-containing protein various predicted proteins contains Pfam profile PF00564: PB1 domain (68417.m00773)
2743	Not regulated	NC-NC-NC	255227_at	A14g05440	temperature sensing protein-related contains weak similarity to D123 (GI:1236114) [Rattus norvegicus] (68417.m00826)
2744	Not regulated	NC-NC-NC	255231_at	A14g05460	F-box family protein (FBL20) contains similarity to N7 protein GI:3273101 from [Medicago truncatula] (68417.m00828)
2745	Not regulated	NC-NC-NC	255240_at	A14g05530	short-chain dehydrogenase/reductase (SDR) family protein similar to peroxisomal short-chain alcohol dehydrogenase GI:4105180 from [Homo sapiens] (68417.m00842)
2746	Not regulated	NC-NC-NC	255243_at	A14g05590	expressed protein contains Pfam domain, PF03650: Uncharacterized protein family (UPF0041) (68417.m00884)
2747	Not regulated	NC-NC-NC	255199_at	A14g07390	PQ-loop repeat family protein / transmembrane family protein similar to SPIQ60441 Mannose-6-phosphate utilization defect 1 protein (Suppressor of Lec15 and Lec35 glycosylation mutation) [Cricetulus griseus], Lec35 protein [Cricetulus griseus] (GI:9858721; contains Pfam profile PF04193: PQ loop repeat (68417.m01134)
2748	Not regulated	NC-NC-NC	255171_at	A14g07980	DNAJ heat shock N-terminal domain-containing protein similar to SPIQ9QV15 DnaJ homolog subfamily B member 10 Mus musculus; contains Pfam profile PF00226 DnaJ domain (68417.m01280)
2749	Not regulated	NC-NC-NC	255176_s_at	A14g07950	DNA-directed RNA polymerase III family protein similar to SPIQ9Y2Y1 DNA-directed RNA polymerases III 12.5 kDa polypeptide (EC 2.7.6) (RNA polymerase III C11 subunit) [Homo sapiens]; RNA polymerases M15 Kd subunit, PF01096: Transcription factor S-II (TFIIS) (68417.m01275)
2750	Not regulated	NC-NC-NC	255151_at	A14g08180	oysterol-binding family protein similar to SPIQ969R2 Oysterol-binding protein 2 [Homo sapiens]; contains Pfam profiles PF00169: PH domain, PF01237: Oysterol-binding protein (68417.m01351)
2751	Not regulated	NC-NC-NC	255154_at	A14g08220	nodulin MN21 family protein similar to MN21 Gi:2598575 (root nodule development) from [Medicago truncatula] (68417.m01369)
2752	Not regulated	NC-NC-NC	255129_at	A14g08290	expressed protein (68417.m01359)
2753	Not regulated	NC-NC-NC	255130_at	A14g08240	tetratricopeptide repeat (TPR)-containing protein glutamine-rich tetratricopeptide repeat (TPR) containing protein (SGT) - Rattus norvegicus, PID:e1285298 (SPIQ70593); contains Pfam profile PF00515 TPR Domain (68417.m01373)
2754	Not regulated	NC-NC-NC	255133_at	A14g08320	KOW domain-containing transcription factor family protein chromatin structural protein homolog Sup5hp - Mus musculus, PID:q2754752 (68417.m01380)
2755	Not regulated	NC-NC-NC	255136_s_at	A14g08350	proline-rich extensin-like family protein contains proline-rich extensin domains, INTERPRO:IPR002985; (68417.m01390)
2756	Not regulated	NC-NC-NC	255140_x_at	A14g08410	expressed protein (68417.m01398)
2757	Not regulated	NC-NC-NC	255147_at	A14g08460	mitogen-activated protein kinase, putative similar to mitogen-activated protein kinase [Arabidopsis thaliana] gi:1255448 [BAA05057]; contains Pfam PF00069: Protein kinase domain (68417.m01398)
2758	Not regulated	NC-NC-NC	255148_at	A14g08470	pollen Ole e 1 allergen and extensin family protein contains Pfam domain, PF01190: Pollen proteins Ole e 1 family (68417.m01430)
2759	Not regulated	NC-NC-NC	255104_at	A14g08685	thioredoxin-related contains weak similarity to Swiss-Prot:Q39239 thioredoxin H-type 4 (TRX-H4) [Mouse-ear cross] (68417.m01470)
2760	Not regulated	NC-NC-NC	255061_at	A14g08930	F-box family protein (FBW2) contains similarity to N7 protein GI:3273101 from [Medicago truncatula] (68417.m01478)
2761	Not regulated	NC-NC-NC	255066_at	A14g08980	T-complex protein 11 contains Pfam PF05794: T-complex protein 11 (68417.m01515)
2762	Not regulated	NC-NC-NC	255077_at	A14g09150	L-ascorbate peroxidase, chloroplast, putative identical to SPIP82281 [TL29_ARATH (EC 1.1.1.11) [Arabidopsis thaliana]; ascorbate peroxidase - Spinacia oleracea, (gi:1669585); contains Pfam domain PF00141: Peroxidase; contains TIGRfam domain TIGR01409: Tat (twin-arginine translocation) pathway signal sequence; identical to ascorbate peroxidase APX4 (A14g09010) mRNA, partial cds GI:31980498 (68417.m01488)
2763	Not regulated	NC-NC-NC	255078_at	A14g09010	14-3-3-like protein GF14 chi / general regulatory factor 1 (GRF1) identical to 14-3-3 protein GF14 chi chain GI:1702986, SP:P428643 from [Arabidopsis thaliana] (68417.m01487)
2764	Not regulated	NC-NC-NC	255079_s_at	A14g09000	arabinogalactan-protein (AGP10) identical to gi:10880487 [gb AAAG24278; supported by Ceres cDNA 265772 (68417.m01490)
2765	Not regulated	NC-NC-NC	255080_at	A14g09030	

2768	Not regulated	NC-NC-NC	255039_at	A14g09570	calcium-dependent protein kinase, putative / CDPK, putative similar to calcium-dependent protein kinase [Arabidopsis thaliana] gi604881[dbj]BA04830; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048 (68417.m01575)
2767	Not regulated	NC-NC-NC	255041_at	A14g09620	expressed protein hypothetical protein F5E13.15 - Arabidopsis thaliana, PIR2:T00682 (68417.m01581) ATP synthase delta chain, chloroplast, putative / H(+)-translocating two-sector A1Pase, delta (OSCP) subunit, putative similar to SPI32980 ATP synthase delta chain, chloroplast precursor (EC 3.6.3.14) (Nicotiana tabacum); contains Pfam profile PF00213: ATP synthase F1, delta subunit (68417.m01585)
2766	Not regulated	NC-NC-NC	255046_at	A14g09650	oxido-reductase family protein similar to AX110P [Daucus carota] Gi:285739; contains Pfam profiles PF01408: Oxido-reductase family NAD-binding Rossmann fold, PF02894: Oxido-reductase family C-terminal alpha/beta domain (68417.m01588) hydrolase, alpha/beta fold family protein similar to ethylene-induced esterase [Citrus sinensis] Gi:14279437; polyneurine aldehyde esterase [Rauvolfia serpentina] Gi:6651393; SPIQ40708 PIR7A protein (Oryza sativa); contains Pfam profile PF00561: choline kinase, putative similar to GmCK2p choline kinase gi1438881[gb AAC49375 (68417.m01602)
2765	Not regulated	NC-NC-NC	255047_at	A14g09670	expressed protein (68417.m01612) 40S ribosomal protein S18 (RPS18C) (68417.m01609) cytochrome c, putative similar to cytochrome c [Pumpkin, Winter squash] SWISS-PROT:P00051 (68417.m01641) hydrolase, alpha/beta fold family protein contains Pfam profile PF00561: hydrolase, alpha/beta fold family (68417.m01640) expressed protein (68417.m01651) glycine-rich protein (68417.m01698) expressed protein (68417.m01701)
2770	Not regulated	NC-NC-NC	255025_at	A14g09800	chlorophyll A-B binding protein CP26, chloroplast / light-harvesting complex II protein 5 / LHCB5 identical to SPIQ8XF89 Chlorophyll A-B binding protein CP26, chloroplast precursor (Light-harvesting complex II protein 5) (LHCB5) (LHCIIc) (Arabidopsis thaliana); contains Pfam profile: PF00504 chlorophyll A-B binding protein; chlorophyll a/b-binding protein CP26 in PS II, Brassica juncea, gb:X95727 (68417.m01699)
2771	Not regulated	NC-NC-NC	254998_at	A14g09760	60S ribosomal protein L9 (RPL90D) ribosomal protein L9, cytosolic - garden pea, PIR2:S19878 (68417.m01717)
2772	Not regulated	NC-NC-NC	254999_at	A14g09830	RNA-binding protein, putative (68417.m01735)
2773	Not regulated	NC-NC-NC	255000_at	A14g09800	UBX domain-containing protein low similarity to SPIQ8UNNS FAS-associated factor 1 (FAF1 protein) (Homo sapiens); contains Pfam profile PF00788: UBX domain (68417.m01759)
2774	Not regulated	NC-NC-NC	255011_at	A14g10040	expressed protein (68417.m01772)
2775	Not regulated	NC-NC-NC	255012_at	A14g10030	expressed protein (68417.m01781)
2776	Not regulated	NC-NC-NC	255018_at	A14g10090	UDP-glucose 4-epimerase, putative / UDP-glucose 4-epimerase, putative / Galactose-4-epimerase, putative similar to UDP-galactose 4-epimerase from Arabidopsis thaliana SPIQ42605; Cymopopsis tetragoloba Gi:3021357 [AJ005082] (68417.m01781)
2777	Not regulated	NC-NC-NC	255021_at	A14g10330	F-box family protein contains Pfam PF00646: F-box domain (68417.m01776)
2778	Not regulated	NC-NC-NC	254970_at	A14g10340	expressed protein (68417.m01783)
2779	Not regulated	NC-NC-NC	254980_at	A14g10450	vacuolar ATP synthase subunit E / V-ATPase E subunit / vacuolar proton pump E subunit (VATE) identical to SPIQ39258 Vacuolar ATP synthase subunit E (EC 3.6.3.14) (V-ATPase E subunit) (Vacuolar proton pump E subunit) (Arabidopsis thaliana)
2780	Not regulated	NC-NC-NC	254980_at	A14g10610	ATP synthase subunit E (68417.m01807)
2781	Not regulated	NC-NC-NC	254990_at	A14g10810	translation initiation factor IF-1, chloroplast, putative similar to Swiss-Prot:P08698 translation initiation factor IF-1, chloroplast [Spinacia oleracea]; contains Pfam profile PF00575: S1 RNA binding domain (68417.m01810) cysteine proteinase, putative contains similarity to cysteine proteinase RD21A (thiol protease) Gi:435618, SP:P43287 from [Arabidopsis thaliana] (68417.m01827)
2782	Not regulated	NC-NC-NC	254936_at	A14g10790	phosphatase-related low similarity to protein phosphatase T [Saccharomyces cerevisiae] Gi:897806; contains Pfam profiles PF00515: TPR Domain, PF05002: SGS domain, PF04989: CS domain (68417.m01822)
2783	Not regulated	NC-NC-NC	254943_at	A14g10890	reticulon family protein (RTNLB2) similar to SPIQ84548 Reticulon 1 (Neuroendocrine-specific protein) (Rettus norvegicus); contains Pfam profile PF02453: Reticulon (68417.m01818)
2784	Not regulated	NC-NC-NC	254950_at	A14g10810	short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family IPR002188 Short-chain dehydrogenase/reductase (SDR) superfamily (68417.m01839)
2785	Not regulated	NC-NC-NC	254952_at	A14g11150	protein kinase family protein contains Pfam PF00069: Protein kinase domain (68417.m01844)
2786	Not regulated	NC-NC-NC	254953_at	A14g11410	serine racemase, putative similar to serine racemase [Mus musculus] Gi:6448965; contains Pfam profile PF00291: Pyridoxal-phosphate dependent enzyme (68417.m01861)
2787	Not regulated	NC-NC-NC	254957_at	A14g11175	phosphate dependent enzyme (68417.m01861)
2788	Not regulated	NC-NC-NC	254903_at	A14g11310	expressed protein contains Pfam PF05964: Protein of unknown function (DUF810) (68417.m01865)
2789	Not regulated	NC-NC-NC	254910_at	A14g11280	area4-interacting protein, putative (SAY1) similar to Area4-interacting protein [Arabidopsis thaliana] Gi:13160608; contains Pfam profiles PF00765: UBX domain, PF02806: Ubiquitin interaction motif (68417.m01872)
2790	Not regulated	NC-NC-NC	254915_s_at	A14g11220	calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase (68417.m01879)
2791	Not regulated	NC-NC-NC	254918_at	A14g11460	expressed protein hypothetical protein F7H19.70 - Arabidopsis thaliana, PIR2:e1310057 (68417.m01904)
2792	Not regulated	NC-NC-NC	254920_at	A14g11560	DNA-binding family protein contains a AT hook motif (DNA binding motifs with a preference for A/T rich regions), Pfam:PF02178 (68417.m01820)
2793	Not regulated	NC-NC-NC	254928_at	A14g12080	Cip amino terminal domain-containing protein contains Pfam profile: PF02881 Cip amino terminal domain (68417.m01918)
2794	Not regulated	NC-NC-NC	254931_at	A14g12060	sterol desaturase family protein similar to sterol 4-alpha-methyl-oxidase Gi:16973471 from [Arabidopsis thaliana]; contains Pfam profile PF01598: Sterol desaturase (68417.m01923)
2795	Not regulated	NC-NC-NC	254872_at	A14g12110	bile acid sodium symporter family protein low similarity to SPIQ12908 ileal sodium/bile acid cotransporter (Homo sapiens); contains Pfam profile PF01758: Sodium Bile acid symporter family (68417.m01913)
2796	Not regulated	NC-NC-NC	254877_at	A14g11640	cytochrome P450, putative similar to P450 monooxygenase Gi:14334057 from [Gossypium arboreum] (68417.m01949)
2797	Not regulated	NC-NC-NC	254878_at	A14g11670	
2798	Not regulated	NC-NC-NC	254891_at	A14g11740	
2799	Not regulated	NC-NC-NC	254892_at	A14g11800	
2800	Not regulated	NC-NC-NC	254848_at	A14g11960	
2801	Not regulated	NC-NC-NC	254853_at	A14g12080	
2802	Not regulated	NC-NC-NC	254859_at	A14g12060	
2803	Not regulated	NC-NC-NC	254860_at	A14g12110	
2804	Not regulated	NC-NC-NC	254862_at	A14g12030	
2805	Not regulated	NC-NC-NC	254835_s_at	A14g12310	

2806	Not regulated	NC-NC-NC	254814_at	Al4g12340	expressed protein (68417.m01952)
2807	Not regulated	NC-NC-NC	254827_at	Al4g12850	endomembrane protein 70, putative TMA family, (68417.m01990)
2808	Not regulated	NC-NC-NC	254830_at	Al4g12590	expressed protein contains Pfam PF05883: Eukaryotic protein of unknown function (DUF850) (68417.m01985)
2809	Not regulated	NC-NC-NC	254778_at	Al4g12750	expressed protein (68417.m02002)
2810	Not regulated	NC-NC-NC	254788_at	Al4g12790	ATP-binding family protein contains Pfam domain, PF03029: Conserved hypothetical ATP binding protein (68417.m02006) photosystem I reaction center subunit XI, chloroplast (PSI-L) / PSI subunit V identical to Photosystem I reaction center subunit XI; contains Pfam profile PF02805: ATP-binding family protein contains Pfam domain, PF03029: Conserved hypothetical ATP binding protein (68417.m02006) photosystem I reaction center subunit XI; contains 2 transmembrane domains (68417.m02008)
2811	Not regulated	NC-NC-NC	254790_at	Al4g12800	photosystem I reaction center subunit XI; contains 2 transmembrane domains (68417.m02008)
2812	Not regulated	NC-NC-NC	254791_at	Al4g12910	photosystem I reaction center subunit XI; contains 2 transmembrane domains (68417.m02008)
2813	Not regulated	NC-NC-NC	254798_at	Al4g13050	serine carboxypeptidase S10 family protein SERINE CARBOXYPEPTIDASE I PRECURSOR - Hordeum vulgare, SWAILCBP1_HORVU (68417.m02019)
2814	Not regulated	NC-NC-NC	254804_at	Al4g13010	acyl-ACP thioesterase, putative / acyl-ACP thioesterase, putative / oleoyl-acyl-carrier protein] hydrolase, putative / S-acyl fatty acid synthase thioesterase, putative strong similarity to acyl-ACP thioesterase; oleoyl-acyl-carrier protein] hydrolase (Brassica napus) (G1:435011; contains Pfam profile PF01643: Acyl-ACP thioesterase (68417.m02036)
2815	Not regulated	NC-NC-NC	254747_at	Al4g13020	oxido-reductase, zinc-binding dehydrogenase family protein low similarity to probable NADP-dependent oxido-reductase (zeta-oxido-reductase, zinc-binding dehydrogenase family (68417.m02030)
2816	Not regulated	NC-NC-NC	254750_at	Al4g13140	crystallin homolog P1 [SPIQ39172] (G1:886428) and P2 [SPIQ39173] (G1:886430); contains Pfam profile PF00107: oxido-reductase, zinc-binding dehydrogenase family (68417.m02030)
2817	Not regulated	NC-NC-NC	254755_at	Al4g13220	serine/threonine protein kinase (MHK) identical to serine/threonine-protein kinase MHK (Arabidopsis thaliana) SWISS-PROT: P43284 (68417.m02031)
2818	Not regulated	NC-NC-NC	254760_at	Al4g13200	expressed protein (68417.m02046)
2819	Not regulated	NC-NC-NC	254763_at	Al4g13170	expressed protein (68417.m02056)
2820	Not regulated	NC-NC-NC	254764_at	Al4g13250	expressed protein hypothetical protein sll1769 - Synechocystis sp. P.D.1018408 (68417.m02053)
2821	Not regulated	NC-NC-NC	254765_at	Al4g13270	60S ribosomal protein L13a (RPL13aC) ribosomal protein L13a -Lupinus luteus.PID.e12378/1 (68417.m02049) short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily (68417.m02060)
2822	Not regulated	NC-NC-NC	254776_at	Al4g13360	expressed protein (68417.m02076)
2823	Not regulated	NC-NC-NC	254745_at	Al4g13460	enoyl-CoA hydratase/isomerase family protein similar to CoA-thioester hydrolase CHY1 (beta-hydroxyacylbutyryl-CoA hydrolase) (Arabidopsis thaliana) (G1:8572769; contains Pfam profile PF00378: enoyl-CoA hydratase/isomerase family protein (68417.m02089)
2824	Not regulated	NC-NC-NC	254721_at	Al4g13520	SET domain-containing protein (SUVH9) identical to SUVH9 [Arabidopsis thaliana] (G1:13517759; contains Pfam profiles PF00856: SET domain, PF05033: Pre-SET motif, PF02182: YDGSRA domain; identical to cDNA SUVH9 (SUVH9) (G1:13517758)
2825	Not regulated	NC-NC-NC	254722_at	Al4g13530	expressed protein (68417.m02102)
2826	Not regulated	NC-NC-NC	254727_at	Al4g13670	expressed protein (68417.m02108)
2827	Not regulated	NC-NC-NC	254730_at	Al4g13730	expressed protein predicted protein, Arabidopsis thaliana (68417.m02109)
2828	Not regulated	NC-NC-NC	254737_at	Al4g13840	peptidoglycan-binding domain-containing protein similar to spore cortex-lytic enzyme prepeptide (G1:1644192) [Bacillus cereus]; contains Pfam PF01471: Putative peptidoglycan binding domain; contains Pfam PF00684: DnaJ central domain (4 repeats) (68417.m02125)
2829	Not regulated	NC-NC-NC	254738_at	Al4g13860	RabGAP1B domain-containing protein low similarity to SPIQ08484 GTPase-activating protein GYP1 [Saccharomyces cerevisiae]; contains Pfam profile PF00568: TEC domain (68417.m02131)
2830	Not regulated	NC-NC-NC	254682_at	Al4g13940	transferase family protein low similarity to acetyl-CoA:benzylalcohol acetyltransferase [Clarkia concinna] (G1:6168328; contains Pfam profile PF02458: Transferase family (68417.m02144)
2831	Not regulated	NC-NC-NC	254686_at	Al4g13720	glycine-rich RNA-binding protein, putative similar to Glycine-rich RNA-binding protein 2, mitochondrial precursor (AIGRP2) (Swiss-Prot:Q8VNM6) [Arabidopsis thaliana]; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) (68417.m02147)
2832	Not regulated	NC-NC-NC	254691_at	Al4g17840	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain (68417.m02122)
2833	Not regulated	NC-NC-NC	254656_at	Al4g18070	inosine triphosphate pyrophosphatase, putative / HAM1 family protein contains Pfam profile PF01725: Ham1 family; similar to inosine triphosphate pyrophosphatase (G1:13398328) [Homo sapiens] (68417.m02130)
2834	Not regulated	NC-NC-NC	254659_at	Al4g18240	expressed protein (68417.m02661)
2835	Not regulated	NC-NC-NC	254665_at	Al4g18340	expressed protein (68417.m02688)
2836	Not regulated	NC-NC-NC	254669_at	Al4g18370	starch synthase-related protein contains similarity to starch synthase G1:4582783 from [Vigna unguiculata] (68417.m02709)
2837	Not regulated	NC-NC-NC	254673_at	Al4g18430	glycosyl hydrolase family 17 protein similar to elicitor-inducible chitinase Nt-SubE76 G1:11071974 from [Nicotiana tabacum] (68417.m02721)
2838	Not regulated	NC-NC-NC	254644_at	Al4g18510	protease HhaA, chloroplast (SPPA) (HHAO) identical to SPIQ08SEL7 Protease HhaA, chloroplast precursor (EC 3.4.21.-) (Arabidopsis thaliana) (68417.m02724)
2839	Not regulated	NC-NC-NC	254649_at	Al4g18570	Ras-related GTP-binding protein, putative similar to GTP-binding protein G1:303742 from [Pisum sativum] (68417.m02735)
2840	Not regulated	NC-NC-NC	254623_at	Al4g18480	Clavata3 / ESR-Related-2 (CLE2) CLAVATA3/ESR-Related-2 (CLE2) (68417.m02744)
2841	Not regulated	NC-NC-NC	254628_at	Al4g18400	proline-rich family protein common family members: A15g04980, A15g04980 [Arabidopsis thaliana] (68417.m02749) magnesium-chelatase subunit chl, chloroplast / Mg-protoporphyrin IX chelatase (ChL) (CS) (CH42) identical to SPIP161127 [thaliana] (68417.m02741)
2842	Not regulated	NC-NC-NC	254628_at	Al4g18593	Magnesium-chelatase subunit chl, chloroplast precursor (Mg-protoporphyrin IX chelatase) (Protein CSCH-42) (Arabidopsis thaliana) (68417.m02741)
					expressed protein (68417.m02731)
					dual specificity protein phosphatase-related contains weak similarity to Dual specificity protein phosphatase 12 (EC 3.1.3.48) (EC 3.1.3.16) (Dual-specificity tyrosine phosphatase YVH1) (Swiss-Prot:Q8UNB8) [Homo sapiens] (68417.m02753)

2843	Not regulated	NC-NC-NC	254636_at	A14g18700	CBL-interacting protein kinase 12 (CIPK12) identical to CBL-interacting protein kinase 12 [Arabidopsis thaliana] gi13249123 gbAAK16987; contains Pfam profile PF00069; protein kinase domain and PF03822: NAF domain; identical to cDNA
2844	Not regulated	NC-NC-NC	254638_at	A14g18740	expressed protein (68417.m02769)
2845	Not regulated	NC-NC-NC	254617_s_at	A14g18730	60S ribosomal protein L11 (RPL11C) (68417.m02768)
2846	Not regulated	NC-NC-NC	254598_at	A14g18975	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535; PPR repeat (68417.m02795) aquaglyceroporin / NOD26-like major intrinsic protein 2 (NLM2) contains Pfam profile: MIP PF00230; similar to SP-P08995 (Glycine max) Nodulin-26 (N-26); identical to cDNA aquaglyceroporin (nln2 gene) Gi:11071655, aquaglyceroporin [Arabidopsis thaliana]
2847	Not regulated	NC-NC-NC	254608_at	A14g18910	GI:11071656 (68417.m02788)
2848	Not regulated	NC-NC-NC	254612_at	A14g19100	expressed protein (68417.m02818)
2849	Not regulated	NC-NC-NC	254615_at	A14g19210	RNase L inhibitor protein, putative similar to 68 kDa protein HP08 Gi:18755057 from <i>Triticum aestivum</i> (68417.m02834)
2850	Not regulated	NC-NC-NC	254559_at	A14g19200	proline-rich family protein contains proline rich extension domains, INTERPRO:IPR002965 (68417.m02833)
2851	Not regulated	NC-NC-NC	254580_at	A14g19390	expressed protein (68417.m02854)
2852	Not regulated	NC-NC-NC	254584_at	A14g19490	expressed protein (68417.m02860)
2853	Not regulated	NC-NC-NC	254553_at	A14g19530	disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein. (68417.m02873)
2854	Not regulated	NC-NC-NC	254530_at	A14g19640	Ras-related GTP-binding protein, putative similar to GTP-binding protein RAB5A Gi:1370178 from <i>[Lotus japonicus]</i> (68417.m02884)
2855	Not regulated	NC-NC-NC	254532_at	A14g19660	ankyrin repeat family protein / BTB/POZ domain-containing protein contains Pfam domain, PF00023: Ankyrin repeat and Pfam domain, PF00651: BTB/POZ domain (68417.m02888)
2856	Not regulated	NC-NC-NC	254533_at	A14g19870	zinc finger (C3HC4-type RING finger) family protein contains a Prosite PS00518 Zinc finger, C3HC4 type (RING finger), signature and Pfam domain PF01485: IIR domain (68417.m02889)
2857	Not regulated	NC-NC-NC	254535_at	A14g19710	bi-functional aspartate kinase/homoserine dehydrogenase, putative / AK-HSDH, putative similar to gbX71364 [PIR]S46497
2858	Not regulated	NC-NC-NC	254551_at	A14g19840	aspartate kinase / homoserine dehydrogenase from <i>Arabidopsis thaliana</i> (68417.m02894)
2859	Not regulated	NC-NC-NC	254498_at	A14g20070	lectin-related similar to PP2 lectin polypeptide [Cucurbita maxima] Gi:410437 (68417.m02908)
2860	Not regulated	NC-NC-NC	254500_at	A14g20110	peptidase M20/M25/M40 family protein contains similarity to hydantoin utilization protein C [Pseudomonas sp.] SWISS-PROT:Q01284; contains Pfam profile PF01546: Peptidase family M20/M25/M40 (68417.m02836)
2861	Not regulated	NC-NC-NC	254503_at	A14g20010	vacuolar sorting receptor, putative similar to BP-80 vacuolar sorting receptor [Plasmodium satum] Gi:1737222; identical to vacuolar sorting receptor-like protein (GI:2827665) [Arabidopsis thaliana] (68417.m02943)
2862	Not regulated	NC-NC-NC	254505_at	A14g19985	expressed protein contains Pfam PF05329: Protein of unknown function (DUF731) (68417.m02928)
2863	Not regulated	NC-NC-NC	254492_at	A14g20260	GCN5-related N-acetyltransferase (GNAT) family protein contains Pfam profile PF00583: acetyltransferase, GNAT family (68417.m02926)
2864	Not regulated	NC-NC-NC	254482_at	A14g20150	DREPP plasma membrane polypeptide family protein contains Pfam profile: PF05558 DREPP plasma membrane polypeptide (68417.m02959)
2865	Not regulated	NC-NC-NC	254494_at	A14g20400	expressed protein (68417.m02948)
2866	Not regulated	NC-NC-NC	254474_at	A14g20390	transcription factor jumonji (jmi) family protein / zinc finger (C5HC2 type) family protein contains Pfam domains, PF02375: jmi domain, PF02373: iMiC domain and PF02828: C5HC2 zinc finger (68417.m02978)
2867	Not regulated	NC-NC-NC	254475_at	A14g20440	integral membrane family protein contains TIGRFAM TIGR01569 - plant integral membrane protein TIGR01569; contains Pfam PF04535: Domain of unknown function (DUF588) (68417.m02977)
2868	Not regulated	NC-NC-NC	254476_at	A14g20410	small nuclear ribonucleoprotein associated protein B, putative / snRNP-B, putative / Sm protein B, putative similar to SP Q05856 Small nuclear ribonucleoprotein associated protein B (snRNP-B) (Sm-B) (SmB) (Drosophila melanogaster) (68417.m02982)
2869	Not regulated	NC-NC-NC	254477_at	A14g20380	gamma-soluble NSF attachment protein / gamma-SNAP identical to gamma-soluble NSF attachment protein; gamma-SNAP (68417.m02982)
2870	Not regulated	NC-NC-NC	254478_at	A14g20330	zinc finger protein (LSD1) identical to zinc-finger protein Lsd1 [Arabidopsis thaliana] gi1875251 gb AAC49660 (68417.m02974)
2871	Not regulated	NC-NC-NC	254481_at	A14g20480	transcription initiation factor-related contains weak similarity to Transcription initiation factor IIE, beta subunit (TFIIE-beta) (Swiss-Prot:P29084) [Homo sapiens] (68417.m02988)
2872	Not regulated	NC-NC-NC	254438_at	A14g20990	expressed protein contains Pfam profile PF04398: Protein of unknown function, DUF537 (68417.m02987)
2873	Not regulated	NC-NC-NC	254444_at	A14g20980	eukaryotic translation initiation factor 3 subunit 7, putative / eIF-3 zeta, putative / eIF3d, putative similar to initiation factor 3d [Arabidopsis thaliana] Gi:12407755, SP Q15371 Eukaryotic translation initiation factor 3 subunit 7 (eIF-3 zeta) (eIF3 p66) (eIF3d) [Homo sapiens]; contains Pfam profile PF05091: Eukaryotic translation initiation factor 3 subunit 7 (eIF-3) (68417.m03037)
2874	Not regulated	NC-NC-NC	254446_at	A14g20890	cytidine/deoxycytidylate deaminase family protein contains SP P25539 Riboflavin biosynthesis protein ribD [includes: Daminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.4.26) (Riboflavin-specific deaminase); 5-amino-6-(5-phosphoribosylamino)uracil reductase (EC 1.1.1.193) (HTP reductase)] [Escherichia coli]; contains Pfam profile PF00383: Cytidine and deoxycytidylate deaminase zinc-binding region (68417.m03035)
2875	Not regulated	NC-NC-NC	254447_at	A14g20860	tubulin beta-9 chain (TUBB9) nearly identical to SP P29517 Tubulin beta-9 chain (Arabidopsis thaliana) (68417.m03028)
2876	Not regulated	NC-NC-NC	254448_at	A14g20870	FAD-binding domain-containing protein similar to SP P20988 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) [Tetrahydropyridoxylamine synthase] [Escherichia coli]; contains PF01565 FAD binding domain (68417.m03026)
2877	Not regulated	NC-NC-NC	254480_at	A14g21210	fatty acid hydroxylase, putative similar to fatty acid hydroxylase Fdh1p GB AF021804 Gi:2736147 from [Arabidopsis thaliana] (68417.m03027)
2878	Not regulated	NC-NC-NC	254428_at	A14g21160	expressed protein contains Pfam domain PF03618: Domain of unknown function (DUF299) (68417.m03066)
2879	Not regulated	NC-NC-NC	254429_at	A14g21105	zinc finger and C2 domain protein (ZAC) identical to zinc finger and C2 domain protein Gi:9857238 from [Arabidopsis thaliana] (68417.m03058)

2880	Not regulated	NC-NC-NC	254398_at	oxygen-evolving enhancer protein 3, chloroplast, putative (PSBQ) identical to SPIQ8XFT3 Oxygen-evolving enhancer protein 3-1, chloroplast precursor (OE3) (16 kDa subunit of photosystem II) (OE3 16 kDa subunit) (Arabidopsis thaliana); similar to SPIP12301 Oxygen-evolving enhancer protein 3, chloroplast precursor (OE3) (16 kDa subunit of photosystem II) (OE3 16 kDa subunit) (Spinacia oleracea); contains Pfam profile PF05757: Oxygen evolving system of photosystem II (PF05757)
2881	Not regulated	NC-NC-NC	254399_at	evolving enhancer protein 3 (P3BQ) (68417.m03075)
2882	Not regulated	NC-NC-NC	254410_at	G10 family protein contains Pfam profile: PF01125 G10 protein (68417.m03053)
2883	Not regulated	NC-NC-NC	254414_at	protein kinase family protein contains Pfam PF00069: Protein kinase domain (68417.m03093)
2884	Not regulated	NC-NC-NC	254417_at	(2R)-phospho-3-sulfolactate synthase-related contains weak similarity to Swiss-Prot.Q57703 (2R)-phospho-3-sulfolactate synthase (PSL synthase) [Methanococcus jannaschii] (68417.m03079)
2885	Not regulated	NC-NC-NC	254425_at	ribitol kinase/FAD synthetase family protein contains Pfam profiles PF01687: Ribitol kinase / FAD synthetase, PF00702: halocacid dehalogenase-like hydrolase (68417.m03105)
2886	Not regulated	NC-NC-NC	254392_at	vesicle-associated membrane family protein / VAMP family protein similar to VAP27 Gi:6688928 [Nicotiana glauca] (68417.m03102)
2887	Not regulated	NC-NC-NC	254393_at	bifunctional nuclease, putative similar to bifunctional nuclease [Zinnia elegans] gi4099833[gbAAAD00694 (68417.m03128)] (68417.m03102)
2888	Not regulated	NC-NC-NC	254370_at	oxidoreductase, zinc-binding dehydrogenase family protein Pig3 Homo sapiens, PID:G2754812; contains Pfam zinc-binding dehydrogenase domain PF00107 (68417.m03122)
2889	Not regulated	NC-NC-NC	254378_at	L1 specific homeobox gene (ML1) / ovule-specific homeobox protein A20 nearly identical to mentem L1 layer homeobox protein A20 (A1ML1) [Arabidopsis thaliana] Gi:181536; protodermal factor2 (PDF2) [Arabidopsis thaliana] Gi:14276060 (68417.m03148)
2890	Not regulated	NC-NC-NC	254375_at	ATP-binding family protein contains Pfam domain, PF03028: Conserved hypothetical ATP binding protein (68417.m03153)
2891	Not regulated	NC-NC-NC	254378_at	transmembrane protein-related (TOM1) contains some similarity to transmembrane protein TOM3 Gi:15425641 from [Arabidopsis thaliana]; identical to cDNA TOM1 Gi:9967414 (68417.m03152)
2892	Not regulated	NC-NC-NC	254383_at	Der1-like family protein / degradation in the ER-like family protein contains Pfam profile: PF04511 Der1-like family (68417.m03155)
2893	Not regulated	NC-NC-NC	254341_at	multi-copper oxidase type I family protein similar to pollen-specific BP10 protein [SPIQ00824][Brassica napus]; contains Pfam profile: PF00394 Multicopper oxidase (68417.m03185)
2894	Not regulated	NC-NC-NC	254345_at	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (68417.m03199)
2895	Not regulated	NC-NC-NC	254346_at	expressed protein (68417.m03184)
2896	Not regulated	NC-NC-NC	254347_at	autophagy 8a (APC8a) identical to autophagy 8a [Arabidopsis thaliana] Gi:19912151; contains Pfam profile PF02891: Microtubule associated protein 1A/1B, light chain 3 (68417.m03182)
2897	Not regulated	NC-NC-NC	254348_at	WRKY family transcription factor identical to WRKY transcription factor 31 (WRKY31) Gi:15990589 from [Arabidopsis thaliana] (68417.m03182)
2898	Not regulated	NC-NC-NC	254355_at	UBX domain-containing protein similar to XY40 protein [Rattus norvegicus] Gi:2547025; contains Pfam profile PF00789: UBX domain (68417.m03201)
2899	Not regulated	NC-NC-NC	254356_at	ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein similar to NHP2/L7Ae family proteins, see SWISSPROT:P32495 and PMID:2063628 (68417.m03234)
2900	Not regulated	NC-NC-NC	254358_at	expressed protein (68417.m03208)
2901	Not regulated	NC-NC-NC	254335_at	expressed protein contains Pfam domain, PF03650: Uncharacterized protein family (UPF0041) (68417.m03226)
2902	Not regulated	NC-NC-NC	254306_at	alternative oxidase, putative / immunins protein (IM) identical to IMMUTANS from Arabidopsis thaliana [gi.4138855]; contains Pfam profile PF01786 alternative oxidase (68417.m03220)
2903	Not regulated	NC-NC-NC	254321_at	alkaline phosphatase family / aPHC family contains Pfam profile: PF05875: alkaline phosphatase (aPHC) (68417.m03228)
2904	Not regulated	NC-NC-NC	254327_at	trehalase-5-phosphate phosphatase, putative similar to trehalase-5-phosphate phosphatase (ATPPA) Gi:2944178; contains Pfam profile PF02358: Trehalase-phosphatase (68417.m03259)
2905	Not regulated	NC-NC-NC	254328_at	protease inhibitor/seed storage lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storageLTP family domain PF00234 (68417.m03247)
2906	Not regulated	NC-NC-NC	254329_at	adenine phosphoribosyltransferase, putative strong similarity to Adenine phosphoribosyltransferase [Hordeum vulgare] subsp. vulgare] Gi:9711921; contains Pfam profile PF00156: Phosphoribosyl transferase domain (68417.m03257)
2907	Not regulated	NC-NC-NC	254273_at	oxysterol-binding family protein similar to SPIP16258 Oxysterol-binding protein 1 [Oryctolagus cuniculus]; contains Pfam profiles PF00169: PH domain, PF01237: Oxysterol-binding protein (68417.m03252)
2908	Not regulated	NC-NC-NC	254278_at	glycoproteinase M22 family protein similar to salivaryglycoproteinase [Haemophilus ducreyi] Gi:6942294; contains Pfam profile PF00814: glycoproteinase M22 family (68417.m03277)
2909	Not regulated	NC-NC-NC	254279_at	glycine-rich protein (68417.m03280)
2910	Not regulated	NC-NC-NC	254281_at	zinc finger (DHHC type) family protein contains DHHC zinc finger domain PF01529 (68417.m03283)
2911	Not regulated	NC-NC-NC	254291_at	bile acid:sodium symporter family protein low similarity to SPIQ12908 ileal sodium/bile acid cotransporter [Homo sapiens]; contains Pfam profile PF01758: Sodium bile acid symporter family (68417.m03298)
2912	Not regulated	NC-NC-NC	254293_at	UDP-galactose transporter-related contains weak similarity to UDP-galactose transporter related isozyme 1 (Gi:1669562) [Mus musculus] (68417.m03319)
2913	Not regulated	NC-NC-NC	254298_at	calmodulin-binding family protein contains Pfam profile PF00612: IQ calmodulin-binding motif (68417.m03325)
2914	Not regulated	NC-NC-NC	254299_at	expressed protein (68417.m03305)
2915	Not regulated	NC-NC-NC	254267_at	expressed protein (68417.m03310)
2916	Not regulated	NC-NC-NC	254269_at	dihydroorotase, mitochondrial / DHase (PYR4) identical to SPIQ04904 Dihydroorotase, mitochondrial precursor (EC 3.5.2.3) (DHase) [Arabidopsis thaliana] (68417.m03311)
2917	Not regulated	NC-NC-NC	254248_at	protein kinase, putative similar to MAP3K delta-1 protein kinase [Arabidopsis thaliana] gi2253010[embCAA74591]; contains Pfam PF00069 Protein kinase domain and PF00889 PAS domain (68417.m03323)
		NC-NC-NC		protein kinase family protein contains Pfam PF00069: Protein kinase domain (68417.m03354)

2918	Not regulated	NC-NC-NC	254249_at	A14g23280	protein kinase, putative similar to receptor-like protein kinase 4 (gi:13508745), 5 (gi:13508747), and 6 (gi:13508749) from Arabidopsis thaliana; contains Pfam protein kinase domain PF00089 (88417.m03355)
2919	Not regulated	NC-NC-NC	254259_s_at	A14g23420	short-chain dehydrogenase/reductase (SDR) family protein similar to WW-domain oxidoreductase [Mus musculus] (gi:8834274, WW domain-containing oxidoreductase isoform FORI [Homo sapiens] gi:15667686; contains Pfam PF00106: oxidoreductase, short chain dehydrogenase/reductase family (88417.m03375)
2920	Not regulated	NC-NC-NC	254261_at	A14g23460	beta-adaptin, putative strong similarity to SPQ10567 Adapter-related protein complex 1 beta 1 subunit (Beta-adaptin 1) [Homo sapiens], beta-adaptin [Drosophila melanogaster] gi:434902; contains Pfam profile: PF01602: Adaptin N terminal region (88417.m03381)
2921	Not regulated	NC-NC-NC	254262_at	A14g23460	
2922	Not regulated	NC-NC-NC	254239_at	A14g23400	
2923	Not regulated	NC-NC-NC	254211_at	A14g23570	major intrinsic family protein / MIP family protein contains Pfam profile: MIP PF00230 (88417.m03373)
2924	Not regulated	NC-NC-NC	254214_at	A14g23640	phosphatase-related low similarity to phosphoprotein phosphatase [Mus musculus] gi:567040; contains Pfam profiles PF00515: TPR Domain, PF05002: SCS domain, PF04969: CS domain (88417.m03395)
2925	Not regulated	NC-NC-NC	254215_at	A14g23700	potassium transporter / tiny root hair 1 protein (TRH1) identical to tiny root hair 1 protein [Arabidopsis thaliana]
2926	Not regulated	NC-NC-NC	254216_at	A14g23710	1 protein (trh1) gi:1181957 (88417.m03404)
2927	Not regulated	NC-NC-NC	254218_at	A14g23740	cation/hydrogen exchanger, putative (CHX17) similar to Na+/H+-exchanging protein srl1595 - Synchocystis sp., EMBL:D80902; monovalent cation/proton antiporter family 2 (CPA2) member, PMID:11500563 (88417.m03411)
2928	Not regulated	NC-NC-NC	254223_at	A14g23730	vacuolar ATP synthase subunit G 2 (VATG2) / V-ATPase G subunit 2 (VAG2) / vacuolar proton pump G subunit 2 identical to Swiss Prot:O82628 vacuolar ATP synthase subunit G 2 (V-ATPase G subunit 2, Vacuolar proton pump G subunit 2) [Arabidopsis thaliana] (88417.m03412)
2929	Not regulated	NC-NC-NC	254224_at	A14g23650	leucine-rich repeat transmembrane protein kinase, putative receptor-like protein kinase - Arabidopsis thaliana RKL1, PID g4008006 (88417.m03415)
2930	Not regulated	NC-NC-NC	254228_at	A14g23620	aldose 1-epimerase family protein similar to aspartate-associated protein C; APOC (Chlamydomonas reinhardtii) gi:6970044 Pfam profile PF01263: Aldose 1-epimerase (88417.m03414)
2931	Not regulated	NC-NC-NC	254232_at	A14g23600	calcium-dependent protein kinase, putative / CDPK, putative similar to calcium-dependent protein kinase [Marchantia polymorpha] gi:162877 (dbjBAA81748; contains protein kinase domain, Pfam:PF00089; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048 (88417.m03405)
2932	Not regulated	NC-NC-NC	254233_at	A14g23600	50S ribosomal protein-related contains weak similarity to 50S ribosomal protein L25 (TLS), (Swiss-Prot:P56930) [Thermus thermophilus] (88417.m03402)
2933	Not regulated	NC-NC-NC	254178_at	A14g23910	coronatine-responsive tyrosine aminotransferase / tyrosine transaminase similar to nicotianamine aminotransferase from Hordeum vulgare (gi:8488122, gi:8469087); contains Pfam profile PF00155: aminotransferase, classes I and II; identical to CDNA coronatine-regulated tyrosine aminotransferase (F0016.70) gi:15076652 (88417.m03398)
2934	Not regulated	NC-NC-NC	254190_at	A14g23885	high mobility group (HMG1/2) family protein similar to HMG2B [Homo sapiens] gi:32335; contains Pfam profile PF00505: HMG expressed protein various predicted proteins, Arabidopsis thaliana (88417.m03439)
2935	Not regulated	NC-NC-NC	254198_at	A14g24090	expressed protein (88417.m03435)
2936	Not regulated	NC-NC-NC	254147_at	A14g24270	RNA recognition motif (RRM) containing protein low similarity to tumor-rejection antigen SART3 [Mus musculus] gi:7637845; contains INTERPRO:IPR005004 RNA-binding region RNP-1 (RNA recognition motif) domain (88417.m03483)
2937	Not regulated	NC-NC-NC	254148_at	A14g24280	heat shock protein 70, putative / HSP70, putative strong similarity to heat shock protein 70 [Arabidopsis thaliana] gi:6746592; similar to heat shock 70 protein - Spinacia oleracea, PID:g2654208 (88417.m03486)
2938	Not regulated	NC-NC-NC	254154_at	A14g24460	expressed protein (88417.m03506)
2939	Not regulated	NC-NC-NC	254160_at	A14g24210	F-box family protein / SLEEPY1 protein contains Pfam PF00646: F-box domain; similar to F-box protein Fbx8 (gi:6164735) [Homo sapiens]; identified as SLEEPY1 in McGinnis, et al, Plant Cell (2003) 15: 1120-1130, (88417.m03475)
2940	Not regulated	NC-NC-NC	254161_at	A14g24370	transcription initiation factor IIA gamma chain / TFIIA-gamma (TFIIA-S) identical to transcription initiation factor IIA gamma chain SP_Q35236 from [Arabidopsis thaliana], (88417.m03503)
2941	Not regulated	NC-NC-NC	254162_at	A14g24440	phosphorylase family protein contains Pfam PF01048: Phosphorylase family (88417.m03493)
2942	Not regulated	NC-NC-NC	254163_s_at	A14g24340	zinc finger (GATA type) protein ZIM (ZIM) identical to zinc-finger protein expressed in Inflorescence Meristem, ZIM gi:8918533 from [Arabidopsis thaliana] (88417.m03507)
2943	Not regulated	NC-NC-NC	254164_at	A14g24470	cathrin adaptor complexes medium subunit family protein contains Pfam profile: PF00928 adaptor complexes medium subunit family (88417.m03518)
2944	Not regulated	NC-NC-NC	254172_at	A14g24550	calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase (88417.m03538)
2945	Not regulated	NC-NC-NC	254116_at	A14g24730	expressed protein (88417.m03542)
2946	Not regulated	NC-NC-NC	254117_at	A14g24750	pectate lyase family protein similar to pectate lyase GP:14289189 from [Salix gilgiana] (88417.m03548)
2947	Not regulated	NC-NC-NC	254119_at	A14g24780	31 kDa ribonucleoprotein, chloroplast / RNA-binding protein RNP-T, putative / RNA-binding protein 12/3, putative / RNA-binding protein cp31, putative similar to SPQ04836 31 kDa ribonucleoprotein, chloroplast precursor (RNA-binding protein RNP-T) (RNA-binding protein 12/3) (A1RB933) (RNA-binding protein cp31) [Arabidopsis thaliana]; contains InterPro entry IPR00504: RNA binding region RNP-1 (RNA recognition motif) (RRM) (88417.m03546)
2948	Not regulated	NC-NC-NC	254126_at	A14g24770	NADPH-cytochrome P450 reductase, putative / NADPH-ferrihemoprotein reductase, putative similar to NADPH-ferrihemoprotein reductase NADPH-cytochrome P450 oxidoreductase isoform 1 [Populus balsamifera subsp. trichocarpa x Populus deltoides] gi:13183562, SPIP37116 NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) [Vigna radiata] (Phaseolus aureus)
2949	Not regulated	NC-NC-NC	254127_at	A14g24520	protein kinase (AFC2) identical to protein kinase AFC2 [Arabidopsis thaliana] SWISS-PROT:P51587 (88417.m03540)
2950	Not regulated	NC-NC-NC	254131_at	A14g24740	arginosuccinate synthase family contains Pfam profile: PF00764 arginosuccinate synthase (88417.m03557)
2951	Not regulated	NC-NC-NC	254134_at	A14g24830	

2952	Not regulated	NC-NC-NC	254137_at	Alq24930	thylakoid lumenal 17.9 kDa protein, chloroplast SP-Q85W33; Gi:17369630; PMID:11719511; similar to expressed protein gi:12321169 (Oryza sativa) (68417.m03570)
2953	Not regulated	NC-NC-NC	254083_at	Alq24920	protein transport protein SEC61 gamma subunit, putative similar to Swiss-Prot Q19887 protein transport protein SEC61 gamma subunit (Caenorhabditis elegans) (68417.m03568)
2954	Not regulated	NC-NC-NC	254086_at	Alq24820	26S proteasome regulatory subunit, putative (RPN7) contains similarity to ubiquitin activating enzyme Gi:3647283 from [Lycopersicon esculentum] (68417.m03555)
2955	Not regulated	NC-NC-NC	254087_at	Alq24840	expressed protein (68417.m03558)
2956	Not regulated	NC-NC-NC	254103_at	Alq25030	expressed protein (68417.m03590)
2957	Not regulated	NC-NC-NC	254105_at	Alq25080	magnesium-protoporphyrin O-methyltransferase, putative / magnesium-protoporphyrin IX methyltransferase, putative similar to SPIQ55467 Magnesium-protoporphyrin O-methyltransferase (EC 2.1.1.1) (Magnesium-protoporphyrin IX methyltransferase) (Synchocystis sp.) (68417.m03596)
2958	Not regulated	NC-NC-NC	254108_at	Alq25230	zinc finger (C3HC4-type RING finger) family protein similar to autocrine motility factor receptor [Mus musculus] Gi:5931853; contains Pfam profiles PF00097: Zinc finger, C3HC4 type (RING finger), PF02845: CUE domain (68417.m03630)
2959	Not regulated	NC-NC-NC	254057_at	Alq25170	expressed protein (68417.m03624)
2960	Not regulated	NC-NC-NC	254058_at	Alq25210	expressed protein weak similarity to storekeeper protein [Solanum tuberosum] Gi:14268478; contains Pfam profile PF04504: Protein of unknown function, DUF573 (68417.m03628)
2961	Not regulated	NC-NC-NC	254068_at	Alq25450	ABC transporter family protein similar to multidrug resistance protein 2 SP P21440 from [Mus musculus] (68417.m03665)
2962	Not regulated	NC-NC-NC	254073_at	Alq25500	arginine/serine-rich splicing factor RSP40 (RSP40) identical to SPIP2985 Arginine/serine-rich splicing factor RSP40 (Arabidopsis thaliana) (68417.m03673)
2963	Not regulated	NC-NC-NC	254076_at	Alq25340	immunophilin-related / FKBP-type peptidyl-prolyl cis-trans isomerase-related immunophilin FKBP46 - Spodoptera frugiperda (fall armyworm); PIR2.A55320 (68417.m03647)
2964	Not regulated	NC-NC-NC	254077_at	Alq25840	MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] Gi:12231298; contains Pfam profile PF01554: Uncharacterized membrane protein family (68417.m03692)
2965	Not regulated	NC-NC-NC	254082_at	Alq25720	glutamine cyclotransferase family protein contains Pfam profile: PF05096 glutamine cyclotransferase (68417.m03702)
2966	Not regulated	NC-NC-NC	254049_at	Alq25740	40S ribosomal protein S10 (RPS10A) 40S ribosomal protein S10 - Lumbricus rubellus, PID.e1328701 (68417.m03706)
2967	Not regulated	NC-NC-NC	254050_s_at	Alq25870	expressed protein (68417.m03696)
2968	Not regulated	NC-NC-NC	254030_at	Alq25980	60S acidic ribosomal protein P3 (RPP3A) acidic ribosomal protein P3a - maize, PIR2.T02037 (68417.m03723)
2969	Not regulated	NC-NC-NC	254034_at	Alq25960	multidrug resistance P-glycoprotein, putative similar to multidrug resistant P-glycoprotein Gi:4204793 from [Solanum tuberosum] (68417.m03735)
2970	Not regulated	NC-NC-NC	254038_at	Alq25910	nitrogen fixation protein, putative nitrogen fixation protein nifU (SP-Q43885) [Anabaena sp.]; contains Pfam profile: PF01106 NifU-like domain (68417.m03725)
2971	Not regulated	NC-NC-NC	254039_at	Alq25840	haloacid dehalogenase-like hydrolase family protein low similarity to SPIQ0823 GS1 protein [Homo sapiens]; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase (68417.m03717)
2972	Not regulated	NC-NC-NC	254040_at	Alq25900	aldose 1-epimerase family protein similar to asporosy-associated protein C; APOC (Chlamydomonas reinhardtii) Gi:6870044 Pfam profile PF01283: Aldose 1-epimerase (68417.m03724)
2973	Not regulated	NC-NC-NC	254041_at	Alq25830	integral membrane protein contains TIGRFAM TIGR01569: plant integral membrane protein TIGR01569; contains Pfam PF04535: Domain of unknown function (DUF588) (68417.m03715)
2974	Not regulated	NC-NC-NC	254044_at	Alq25920	xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (XTR9) identical to xyloglucan endotransglycosylase Gi:4218963 from [Arabidopsis thaliana] (68417.m03714)
2975	Not regulated	NC-NC-NC	253991_at	Alq26000	KH domain-containing protein single-stranded nucleic acid-binding protein CBP - mouse, PIR2.S78515 (68417.m03745)
2976	Not regulated	NC-NC-NC	253992_at	Alq26060	expressed protein (68417.m03751)
2977	Not regulated	NC-NC-NC	253993_at	Alq26070	mitogen-activated protein kinase kinase (MAPKK) (MEK1) identical to MEK1 [Arabidopsis thaliana]
2978	Not regulated	NC-NC-NC	253994_at	Alq26080	protein phosphatase 2C AB1 / PP2C AB1 / abscisic acid-insensitive 1 (ABI1) nearly identical to SPIP48597 Protein phosphatase 2C AB1 (EC 3.1.3.16) (PP2C) (Abcscic acid-insensitive 1) (Arabidopsis thaliana) (68417.m03755)
2979	Not regulated	NC-NC-NC	253995_at	Alq26100	casein kinase, putative similar to casein kinase I, delta isoform [Arabidopsis thaliana] SWISS-PROT: P42156; contains protein kinase domain, Pfam:PF00069 (68417.m03757)
2980	Not regulated	NC-NC-NC	253996_at	Alq26110	nucleosome assembly protein (NAP), putative similar to nucleosome assembly protein 1 [Glycine max] Gi:1161252; contains Pfam profile PF00956: Nucleosome assembly protein (NAP) (68417.m03759)
2981	Not regulated	NC-NC-NC	253998_at	Alq26010	peroxidase, putative peroxidase ATP13a - Arabidopsis thaliana, PID.e264765; identical to cDNA class III peroxidase ATP35, Gi:17530565 (68417.m03748)
2982	Not regulated	NC-NC-NC	254004_at	Alq26200	arginyl-RNA synthetase, putative / arginine-RNA ligase, putative similar to SPIP37880 Arginyl-RNA synthetase (EC 6.1.1.19) (Arginine-RNA ligase) (ArgRS) [Cricetus longicaudatus]; contains Pfam profiles PF00750: arginyl-RNA synthetase, PF03485: arginyl-RNA synthetase N-terminal domain (68417.m03783)
2983	Not regulated	NC-NC-NC	254010_at	Alq26240	expressed protein (68417.m03777)
2984	Not regulated	NC-NC-NC	254012_at	Alq26230	60S ribosomal protein L31 (RPL31B) ribosomal protein L31, Nicotiana glauca, U23784 (68417.m03776)
2985	Not regulated	NC-NC-NC	253986_at	Alq26210	mitochondrial ATP synthase g subunit family protein contains Pfam profile: PF04718 mitochondrial ATP synthase g subunit (68417.m03773)
2986	Not regulated	NC-NC-NC	253959_at	Alq26410	expressed protein (68417.m03801)
2987	Not regulated	NC-NC-NC	253984_at	Alq26480	KH domain-containing protein qkl-7, Mus musculus (68417.m03810)
2988	Not regulated	NC-NC-NC	253967_at	Alq26550	expressed protein probable membrane protein YBL102w, yeast, PIR2.S45393 (68417.m03824)
2989	Not regulated	NC-NC-NC	253972_at	Alq26500	Bola-like family protein / Fe-S metabolism associated domain-containing protein similar to SurE protein [Erwinia chrysanthemi] Gi:11342550; contains Pfam profiles PF02857: Fe-S metabolism associated domain, PF01722: Bola-like protein (68417.m03813)

2980	Not regulated	NC-NC-NC	253973_at	immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein similar to FK506-binding protein (Peptidyl-prolyl cis-trans isomerase) (PPIase) (SP-P25138) [(Neisseria meningitidis); contains Pfam profile: PF00254 FKBP-type peptidyl-prolyl cis-trans isomerase; similar to FK506-binding protein 39 kDa (Peptidyl-prolyl cis-trans isomerase) (PPIase) (EC 5.2.1.8) (SP-O74191) (Schizosaccharomyces pombe) (68417.m03828)
2981	Not regulated	NC-NC-NC	253976_at	protein kinase, putative similar to protein kinase G11A [Oryza sativa] SWISS-PROT:P47997 (68417.m03835)
2982	Not regulated	NC-NC-NC	253980_at	sucrose-related (68417.m03836)
2983	Not regulated	NC-NC-NC	253981_at	mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein weak similarity to SPIQ820V8
2984	Not regulated	NC-NC-NC	253982_at	mitochondrial import inner membrane translocase subunit TIM17 A [Mus musculus]; contains Pfam profile PF02468; Mitochondrial import inner membrane translocase subunit Tim17 (68417.m03842)
2985	Not regulated	NC-NC-NC	253983_at	calcineurin B-like protein 3 (CBL3) identical to calcineurin B-like protein 3 (GI:22136404) [Arabidopsis thaliana] (68417.m03830)
2986	Not regulated	NC-NC-NC	253925_at	WRKY family transcription factor contains Pfam profile: PF03108 WRKY DNA-binding domain (68417.m03838)
2987	Not regulated	NC-NC-NC	253927_at	glycerophosphoryl diester phosphodiesterase family protein weak similarity to glycerophosphodiester phosphodiesterase [Borrelia hermslii] GI:1399038; contains Pfam profile PF03009; Glycerophosphoryl diester phosphodiesterase family (68417.m03846)
2988	Not regulated	NC-NC-NC	253928_at	ATP synthase subunit H family protein contains similarity to Swiss-Prot:O15342 Vacuolar ATP synthase subunit H (V-ATPase H subunit) [Vacuolar proton pump H subunit] (V-ATPase M9.2 subunit) (V-ATPase 9.2 kDa membrane accessory protein) [Homo sapiens] (68417.m03849)
2989	Not regulated	NC-NC-NC	253935_at	serine/threonine protein phosphatase PP-X isozyme 1 (PPX1) identical to SPIP48528 Serine/threonine protein phosphatase PP-X isozyme 1 (EC 3.1.3.16) [Arabidopsis thaliana]; contains Pfam profile PF00148: Ser/Thr protein phosphatase (68417.m03851)
2990	Not regulated	NC-NC-NC	253943_at	asparaginyl-RNA synthetase, putative / aspartate-RNA ligase, putative similar to aspartate-RNA ligase (EC 6.1.1.12) from Drosophila melanogaster GI:4512034; Homo sapiens SPIP14688; Rattus norvegicus SPIP15178; contains Pfam profile PF00152 tRNA synthetases class II (D, K and N) (68417.m03887)
2991	Not regulated	NC-NC-NC	253944_at	expressed protein (68417.m03888)
3002	Not regulated	NC-NC-NC	253950_at	2-oxoacid dehydrogenase family protein similar to SPIP38957 Dihydroisopamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial precursor (EC 2.3.1.61) [Homo sapiens]; contains Pfam profiles PF00198: 2-oxo acid dehydrogenases acyltransferase (catalytic domain), PF00384: Biotin-requiring enzyme (68417.m03871)
3003	Not regulated	NC-NC-NC	253951_at	alanine racemase family protein contains Pfam domain, PF01168: Alanine racemase, N-terminal domain (68417.m03886)
3004	Not regulated	NC-NC-NC	253952_at	ubiquitin-like protein (SMT3) identical to Ubiquitin-like protein SMT3 SP:P55652 from [Arabidopsis thaliana]; identical to cDNA SMT3 protein GI:1707371 (68417.m03884)
3005	Not regulated	NC-NC-NC	253953_at	hydroxyproline-rich glycoprotein family protein (68417.m03854)
3006	Not regulated	NC-NC-NC	253954_at	sconitoxyl hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative strong similarity to SPIP49608 Aconitase hydratase, cytoplasmic (EC 4.2.1.3) [Citrate hydro-lyase] (Aconitase) [Cucurbita maxima]; contains Pfam profiles PF00330: Aconitase family (aconitase hydratase), PF00694: Aconitase C-terminal domain (68417.m03881)
3007	Not regulated	NC-NC-NC	253955_at	RNA-binding protein 45 (RBP45), putative DNA binding protein ACBF - Nicotiana tabacum, PID:G1899188 (68417.m03884)
3008	Not regulated	NC-NC-NC	253956_at	fimbria-like protein (FIM1) identical to fimbria-like protein (ATFIM1) [Arabidopsis thaliana] GI:2905683 (68417.m03848)
3009	Not regulated	NC-NC-NC	253921_at	imidazole glycerol phosphate synthase hsfH, chloroplast / IGP synthase / IGP synthase / IGP synthase identical to SPIQ8S230
3010	Not regulated	NC-NC-NC	253923_at	expressed protein (68417.m03891)
3011	Not regulated	NC-NC-NC	253924_at	thioredoxin family protein contains Pfam PF00085: Thioredoxin (68417.m03893)
3012	Not regulated	NC-NC-NC	253901_at	60S ribosomal protein L14 (RPL14B) ribosomal protein L14 - Human, PIR3:JCS854 (68417.m03894)
3013	Not regulated	NC-NC-NC	253908_at	auxin-responsive GH3 family protein similar to auxin-responsive GH3 product [Glycine max] GI:18591; contains Pfam profile PF03321: GH3 auxin-responsive promoter (68417.m03913)
3014	Not regulated	NC-NC-NC	253918_at	universal stress protein (USP) family protein low similarity to ER8 protein [Lycopersicon esculentum] GI:5669854; early nodulin
3015	Not regulated	NC-NC-NC	253919_at	ENOD18 [Vicia faba] GI:11602747; contains Pfam profile PF00582: universal stress protein family (68417.m03920)
3016	Not regulated	NC-NC-NC	253985_at	expressed protein (68417.m03925)
3017	Not regulated	NC-NC-NC	253986_at	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (68417.m03947)
3018	Not regulated	NC-NC-NC	253875_at	expressed protein non-consensus GA donor splice site at exon 6 (68417.m03950)
3019	Not regulated	NC-NC-NC	253885_at	plastocyanin-like domain-containing protein similar to PIRJUC7196 phytylcytin-related protein Pn14 [Ipomoea nil]; contains Pfam profile PF02298: Plastocyanin-like domain (68417.m03952)
3020	Not regulated	NC-NC-NC	253886_at	vacuolar protein sorting-associated protein 28, putative / VPS28, putative similar to vacuolar sorting protein 28 [Homo sapiens] GI:9622852; contains Pfam profile PF03643: Vacuolar protein sorting-associated protein 28 (68417.m03981)
3021	Not regulated	NC-NC-NC	253890_s_at	expressed protein (68417.m03987)
3022	Not regulated	NC-NC-NC	253890_s_at	band 7 family protein similar to stomatin-like protein [Zea mays] GI:7718464; contains Pfam profile PF01145: SPFH domain / Band 7 family (68418.m06736)
3023	Not regulated	NC-NC-NC	253858_at	pH8-type carbohydrate kinase family protein contains Pfam profile: PF00294 pH8 family carbohydrate kinase (68417.m03966)
3024	Not regulated	NC-NC-NC	253861_at	MSP1 protein, putative / intramitochondrial sorting protein, putative similar to Swiss-Prot:P28737 MSP1 protein (TAT-binding homolog 4) [Saccharomyces cerevisiae]; contains Pfam domain, PF00004: ATPase, AAA family (68417.m03980)
3025	Not regulated	NC-NC-NC	253862_at	protein phosphatase 2C PPH1 / PP2C PPH1 (PPH1) identical to SPIP49599/PP2C_3_ARATH Protein phosphatase 2C PPH1 (EC 3.1.3.16) (PP2C) [Arabidopsis thaliana]; similar to protein phosphatase-2C; PP2C (GI:3643090) [Mesembryanthemum crystallinum] (68417.m03992)
3026	Not regulated	NC-NC-NC	253834_at	

3025	Not regulated	NC-NC-NC	253838_at	A14g27880	seven in absentia (SINA) family protein similar to uah-1A protein [Mus musculus] GI:287035; contains Pfam profile PF03145; Seven in absentia protein family (68417.m04002)
3026	Not regulated	NC-NC-NC	253841_at	A14g27830	glycosyl hydrolase family 1 protein contains Pfam PF00232; Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233; 6-phospho-beta-galactosidase, similar to hydroxyisourate hydrolase (GI:19568603) (Glycine max) (68417.m03997)
3027	Not regulated	NC-NC-NC	253855_at	A14g28050	senescence-associated protein, putative similar to senescence-associated protein 5 [Hemerocallis hybrid cultivar] gi 3551954 gb AAC34855 (68417.m04024)
3028	Not regulated	NC-NC-NC	253857_at	A14g27990	YGGT family protein contains Pfam profile PF02325; YGGT family (unknown function) (68417.m04015)
3029	Not regulated	NC-NC-NC	253823_at	A14g28030	GCN5-related N-acetyltransferase (GNAT) family protein contains Pfam profile PF00583; acetyltransferase, GNAT family (68417.m04021)
3030	Not regulated	NC-NC-NC	253803_at	A14g28200	expressed protein (68417.m04042)
3031	Not regulated	NC-NC-NC	253805_at	A14g28260	expressed protein (68417.m04048)
3032	Not regulated	NC-NC-NC	253808_at	A14g28300	hydroxyproline-rich glycoprotein family protein (68417.m04052)
3033	Not regulated	NC-NC-NC	253810_at	A14g28220	NADH dehydrogenase-related similar to 64 kDa mitochondrial NADH dehydrogenase [Neurospora crassa] GI:4753821, alternative
3034	Not regulated	NC-NC-NC	253812_at	A14g28240	NADH dehydrogenase [Yarrowia lipolytica] GI:3718005; contains Pfam profile PF00070; Pyridine nucleotide-disulphide
3035	Not regulated	NC-NC-NC	253816_at	A14g28210	oxidoreductase (68417.m04044)
3036	Not regulated	NC-NC-NC	253797_at	A14g28470	wound-responsive protein-related wound-induced protein - tomato (fragment), PIR2-S19773 (68417.m04046)
3037	Not regulated	NC-NC-NC	253773_s_at	A14g28360	expressed protein (68417.m04043)
3038	Not regulated	NC-NC-NC	253775_at	A14g28440	26S proteasome regulatory subunit, putative contains Pfam domain PF01851; Proteasome/cyclosome repeat (68417.m04073)
3039	Not regulated	NC-NC-NC	253780_at	A14g28400	ribosomal protein L22 family protein (68417.m04059)
3040	Not regulated	NC-NC-NC	253783_at	A14g28600	DNA-binding protein-related contains weak similarity to G-quartet DNA binding protein 3 [Tetrahymena thermophila]
3041	Not regulated	NC-NC-NC	253784_at	A14g28610	gi 4583503 gb AAJ025098 (68417.m04070)
3042	Not regulated	NC-NC-NC	253790_at	A14g28660	protein phosphatase 2C, putative / PP2C, putative protein phosphatase 2C-fission yeast, PIR2:S54297 (68417.m04085)
3043	Not regulated	NC-NC-NC	253765_at	A14g28740	calmodulin-binding protein similar to pollen-specific calmodulin-binding protein MPCBP GI:10086280 from [Zea mays] (68417.m04090)
3044	Not regulated	NC-NC-NC	253738_at	A14g28750	myb family transcription factor, putative / phosphate starvation response regulator, putative (PHR1) contains Pfam profile: PF00248
3045	Not regulated	NC-NC-NC	253784_at	A14g28610	mvp-like DNA-binding domain; identical to cDNA phosphate starvation response regulator 1 (phr1 gene) GI:15384675 (68417.m04091)
3046	Not regulated	NC-NC-NC	253740_at	A14g28706	photosystem II reaction centre subunit IV / PsaE (68417.m04111)
3047	Not regulated	NC-NC-NC	253748_at	A14g28990	photosystem I reaction center subunit IV, chloroplast, putative / PSL-E, putative (PSAE1) identical to SPIQ8S931; similar to SPIP12354 Photosystem I reaction center subunit IV, chloroplast precursor (PSI-E) [Spinacia oleracea]; contains Pfam profile PF02427; Photosystem I reaction centre subunit IV / PsaE (68417.m04111)
3048	Not regulated	NC-NC-NC	253749_at	A14g29080	pikB-type carbohydrate kinase family protein contains Pfam profile: PF00284 pikB family carbohydrate kinase (68417.m04103)
3049	Not regulated	NC-NC-NC	253751_at	A14g29070	RNA-binding protein-related contains weak similarity to Swiss-Prot:Q01844 RNA-binding protein EWS (EWS oncogene)(Ewing sarcoma breakpoint region 1 protein) [Homo sapiens] (68417.m04143)
3050	Not regulated	NC-NC-NC	253752_at	A14g28910	auxin-responsive AUX/IAA family protein similar to SPIQ38626 Auxin-responsive protein IAA8, SPIQ38827 Auxin-responsive protein IAA9 from Arabidopsis thaliana; contains Pfam profile: PF02309; AUX/IAA family (68417.m04161)
3051	Not regulated	NC-NC-NC	253755_at	A14g29040	expressed protein (68417.m04131)
3052	Not regulated	NC-NC-NC	253756_at	A14g28980	26S proteasome AAA-ATPase subunit (RPT2a) almost identical to 26S proteasome AAA-ATPase subunit RPT2a (GI:6652880) (Arabidopsis thaliana); Drosophila melanogaster 26S proteasome subunit 4 ATPase, PID.g1060065 (68417.m04153)
3053	Not regulated	NC-NC-NC	253706_at	A14g29120	cyclin-dependent kinase-activating kinase 1A1 / CDK-activating kinase 1A1 (CAK1) identical to Cdk-activating kinase 1A1 (Arabidopsis thaliana) gi 3218550 db BAA28775 (68417.m04139)
3054	Not regulated	NC-NC-NC	253709_at	A14g29220	SNF7 family protein contains Pfam domain, PF03357; SNF7 family (68417.m04172)
3055	Not regulated	NC-NC-NC	253712_at	A14g29330	6-phosphogluconate dehydrogenase NAD-binding domain-containing protein similar to SPIP23523 2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) (Tartronate semialdehyde reductase) [Escherichia coli]; contains Pfam profile PF03446; NAD binding domain of 6-phosphogluconate dehydrogenase (68417.m04168)
3056	Not regulated	NC-NC-NC	253715_at	A14g29390	phosphofructokinase family protein similar to phosphofructokinase [Amycolatopsis methanolica] GI:17432243; contains Pfam profile PF00365; Phosphofructokinase (68417.m04180)
3057	Not regulated	NC-NC-NC	253720_at	A14g29270	Der1-like family protein / degradation in the ER-like family protein contains Pfam profile: PF04511 Der1-like family (68417.m04181)
3058	Not regulated	NC-NC-NC	253728_at	A14g29410	40S ribosomal protein S30 (RPS30B) RIBOSOMAL PROTEIN S30 - Arabidopsis thaliana, PID.g1358183 (68417.m04188)
3059	Not regulated	NC-NC-NC	253730_at	A14g29480	acid phosphatase class B family protein similar to acid phosphatase (Glycine max) GI:3341443; contains Pfam profile PF03767; 40S ribosomal protein S30 (RPS30B) RIBOSOMAL PROTEIN S30 - Arabidopsis thaliana, PID.g1358183 (68417.m04188)
3060	Not regulated	NC-NC-NC	253731_at	A14g29260	HAD superfamily (subfamily IIB) phosphatase (68417.m04185)
3061	Not regulated	NC-NC-NC	253704_at	A14g29500	HAD superfamily (subfamily IIB) phosphatase (Glycine max) GI:3341443; contains Pfam profile PF03767; prolidase-related contains similarity to prolidase GI:3114968 from [Suberites domuncula] (68417.m04209)
3062	Not regulated	NC-NC-NC	253691_at	A14g29660	60S ribosomal protein L28 (RPL28C) unknown protein chromosome II BAC F8F22 - Arabidopsis thaliana, PID.g3887251 (68417.m04200)

3063	Not regulated	NC-NC-NC	253692_at	A14g29720	amine oxidase family protein similar to polyamine oxidase isoform-2 [Homo sapiens] GI:16554063; contains Pfam profile PF01593; amine oxidase, flavin-containing (88417.m04232)
3064	Not regulated	NC-NC-NC	253693_at	A14g29670	thiodoxin family protein contains Pfam profile PF00895; Thiodoxin (88417.m04226)
3065	Not regulated	NC-NC-NC	253694_at	A14g29735	expressed protein contains Pfam domain PF05251; Uncharacterised protein family (UPF0197) (88417.m04234)
3066	Not regulated	NC-NC-NC	253695_at	A14g29510	protein arginine N-methyltransferase, putative similar to protein arginine N-methyltransferase 1-variant 2 [Homo sapiens] GI:7453575 (88417.m04210)
3067	Not regulated	NC-NC-NC	253700_at	A14g28840	threonine synthase, chloroplast identical to SPIQ857B5 Threonine synthase, chloroplast precursor (EC 4.2.3.1) (TS) [Arabidopsis thaliana] (88417.m04247)
3068	Not regulated	NC-NC-NC	253642_at	A14g29660	expressed protein (88417.m04282)
3068	Not regulated	NC-NC-NC	253644_at	A14g29870	expressed protein predicted protein, Arabidopsis thaliana, PIR2:TO1282 (88417.m04251)
3070	Not regulated	NC-NC-NC	253645_at	A14g29830	transducin family protein / WD-40 repeat family protein contains 7 WD-40 repeats (PF00400); G protein beta subunit-like protein, Schistosoma mansoni, gi:U30261 (88417.m04246)
3071	Not regulated	NC-NC-NC	253646_at	A14g29810	mitogen-activated protein kinase kinase (MAPKK) identical to MAP kinase kinase 2 [Arabidopsis thaliana] gi:3219267[dbj]BAA28828; mitogen-activated protein kinase kinase (MAPKK) family, PMID:12119167 (88417.m04244)
3072	Not regulated	NC-NC-NC	253647_at	A14g29950	microtubule-associated protein identical to microtubule-associated protein GI:5032258 from [Arabidopsis thaliana]; similar to TBC1 domain family member 5 (Swiss-Prot:Q26809) [Homo sapiens]; contains Pfam profile PF00566; TBC domain (88417.m04260)
3073	Not regulated	NC-NC-NC	253668_at	A14g30020	small nuclear ribonucleoprotein F, putative / snRNP-F, putative / Sm protein F, putative similar to SWISS-PROT:Q15356 small nuclear ribonucleoprotein F (snRNP-F, Sm protein F, Sm-F, SmF) [Mouse] (88417.m04288)
3074	Not regulated	NC-NC-NC	253610_at	A14g30200	expressed protein contains weak similarities to Pfam profiles: PF00041 Fibronectin type III domain, PF00828 PHD-finger; supporting cDNA gi:1117136[dbj]AB050977.1 (88417.m04293)
3075	Not regulated	NC-NC-NC	253612_at	A14g30310	ribitol kinase, putative similar to ribitol kinase [Klebsiella pneumoniae] gi:2905643[gb]AAC26495 (88417.m04307)
3076	Not regulated	NC-NC-NC	253618_at	A14g30420	nodulin MtN21 family protein similar to MtN21 [Medicago truncatula] GI:2596575; contains Pfam profile PF00892; Integral membrane protein (88417.m04321)
3077	Not regulated	NC-NC-NC	253624_at	A14g30580	phospholipid/glycerol acyltransferase family protein (88417.m04339)
3078	Not regulated	NC-NC-NC	253625_at	A14g30600	signal recognition particle receptor alpha subunit family protein similar to Signal recognition particle receptor alpha subunit (SR-alpha) (Docking protein alpha) (DP-alpha) (SP-P08240) [Homo sapiens]; similar to Signal recognition particle receptor alpha subunit (SR-alpha) (Docking protein alpha) (DP-alpha) (SP-P08625) [Canis familiaris]; contains Pfam PF04086; Signal recognition particle, alpha subunit, N-terminal; contains Pfam PF00448; SRP54-type protein, GTPase domain (88417.m04341)
3079	Not regulated	NC-NC-NC	253628_at	A14g30450	glycine-rich protein (88417.m04324)
3080	Not regulated	NC-NC-NC	253633_at	A14g30480	tetrathiopeptide repeat (TPR)-containing protein similar to SP Q98614 Tetrathiopeptide repeat protein 1 [Homo sapiens]; contains Pfam profile PF00515; TPR Domain (88417.m04327)
3081	Not regulated	NC-NC-NC	253637_at	A14g30390	expressed protein (88417.m04317)
3082	Not regulated	NC-NC-NC	253639_at	A14g30550	glutamine amidotransferase class-1 domain-containing protein similar to defense-related protein [Brassica carinata] GI:14009280; component of aniline dioxygenase (GMP synthase like protein) - Acinetobacter sp., PID:01013698; contains Pfam profile PF00117; glutamine amidotransferase class-1 (88417.m04336)
3083	Not regulated	NC-NC-NC	253579_at	A14g30610	serine carboxypeptidase S10 family protein similar to Serine carboxypeptidase II chains A and B (SP-P08819) (EC 3.4.18.6) [Triticum aestivum (Wheat)]; (88417.m04342)
3084	Not regulated	NC-NC-NC	253592_at	A14g30840	WD-40 repeat protein family (88417.m04375)
3085	Not regulated	NC-NC-NC	253593_at	A14g30760	expressed protein contains Pfam profile PF04396; Protein of unknown function, DUF537 (88417.m04358)
3086	Not regulated	NC-NC-NC	253597_at	A14g30690	translation initiation factor 3 (IF-3) family protein similar to SPIP33319 Translation initiation factor IF-3 (Proteus vulgaris); contains Pfam profiles PF00707; Translation initiation factor IF-3, C-terminal domain, PF05198; Translation initiation factor IF-3, N-terminal domain (88417.m04350)
3087	Not regulated	NC-NC-NC	253603_at	A14g30935	WRKY family transcription factor contains Pfam profile: PF03106 WRKY DNA-binding domain (88417.m04382)
3088	Not regulated	NC-NC-NC	253548_at	A14g30993	omega-6 fatty acid desaturase, chloroplast (FAD6) (FAD6) identical to GI:493068 (88417.m04394)
3089	Not regulated	NC-NC-NC	253549_at	A14g30930	expressed protein (88417.m04399)
3090	Not regulated	NC-NC-NC	253552_at	A14g30930	50S ribosomal protein L21, mitochondrial (RPL21M) identical to SP Q8L9A0 50S ribosomal protein L21, mitochondrial precursor [Arabidopsis thaliana] (88417.m04391)
3091	Not regulated	NC-NC-NC	253552_at	A14g30890	ubiquitin-specific protease 24, putative (UBP24) identical to ubiquitin-specific protease 24 [Arabidopsis thaliana] GI:11993488 (88417.m04386)
3092	Not regulated	NC-NC-NC	253555_at	A14g31090	expressed protein (88417.m04413)
3093	Not regulated	NC-NC-NC	253558_at	A14g31120	Skb1 methyltransferase family protein contains Pfam profile: PF05185 Sbk1 methyltransferase (88417.m04417)
3094	Not regulated	NC-NC-NC	253566_at	A14g31210	DNA topoisomerase family protein similar to DNA Topoisomerase I (SP-Q9X3X7) [Zymomonas mobilis] (88417.m04432)
3095	Not regulated	NC-NC-NC	253545_at	A14g31310	avirulence-responsive protein-related / avirulence induced gene (AIG) protein-related similar to SPIP54121 AIG2 protein [Arabidopsis thaliana] (88417.m04442)
3096	Not regulated	NC-NC-NC	253522_at	A14g31290	ChaC-like family protein contains Pfam profile: PF04752 ChaC-like protein (88417.m04440)
3097	Not regulated	NC-NC-NC	253523_at	A14g31340	myosin heavy chain-related contains weak similarity to Myosin heavy chain, nonmuscle type A [Cellular myosin heavy chain, type A] (Nonmuscle myosin heavy chain-A) (NMHC-A) (Swiss-Prot:P35579) [Homo sapiens] (88417.m04445)
3098	Not regulated	NC-NC-NC	253526_at	A14g31420	zinc finger (C2H2 type) family protein contains Pfam profile: PF00096 zinc finger, C2H2 type (88417.m04460)
3099	Not regulated	NC-NC-NC	253530_at	A14g31530	expressed protein (88417.m04477)
3100	Not regulated	NC-NC-NC	253533_at	A14g31590	glycosyl transferase family 2 protein similar to cellulose synthase from Agrobacterium tumefaciens [gi:710492] and Agrobacterium radiobacter [gi:710493]; contains Pfam glycosyl transferase, group 2 family protein domain PF00535 (88417.m04487)
3101	Not regulated	NC-NC-NC	253535_at	A14g31550	WRKY family transcription factor contains Pfam profile: PF03106 WRKY DNA-binding domain (88417.m04479)
3102	Not regulated	NC-NC-NC	253537_at	A14g31560	expressed protein (88417.m04482)

3103	Not regulated	NC-NC-NC	253538_at	Alq31460	ribosomal protein L28 family protein ribosomal protein Yml14 precursor, mitochondrial - Saccharomyces cerevisiae, PIR2:S50921 (88417.m04470)
3104	Not regulated	NC-NC-NC	253539_at	Alq31450	zinc finger (C3HC4-type RING finger) family protein similar to Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger) (88417.m04469)
3105	Not regulated	NC-NC-NC	253512_at	Alq31750	protein phosphatase 2C, putative / PP2C, putative protein phosphatase 2C, Medicago sativa, PID:q2582800 (88417.m04508)
3106	Not regulated	NC-NC-NC	253484_at	Alq31720	transcription initiation factor IID (TFIID) 23-30kDa subunit (TAF2H) family protein contains Pfam profile: PF03540 transcription initiation factor TFIID 23-30kDa (88417.m04502)
3107	Not regulated	NC-NC-NC	253486_at	Alq31800	UDP-glucuronic acid/UDP-N-acetylgalactosamine transporter-related contains weak similarity to UDP-glucuronic acid/UDP-N-acetylgalactosamine transporter (UDP-GCA/UDP-GalNAc transporter) (Swiss-Prot:Q8NTN3) (Homo sapiens) (88417.m04489)
3108	Not regulated	NC-NC-NC	253489_at	Alq31780	1,2-diacylglycerol 3-beta-galactosyltransferase, putative / monogalactosyltransferase, putative / MGDT synthase, putative similar to MGD synthase type A from Arabidopsis thaliana [gi:9827297], similar to monogalactosyltransferase, putative, Cucumis sativus, PID:q1805254 (88417.m04509)
3109	Not regulated	NC-NC-NC	253490_at	Alq31790	diphthine synthase, putative (DPHS) similar to Diphthine synthase (Diphthamide biosynthesis methyltransferase) (DPHS) (SP:P32469) (Saccharomyces cerevisiae); similar to CGI-30 protein (GI:4680599) [Homo sapiens], similar to methyltransferase DPH5, Saccharomyces cerevisiae, PIR2:S30890; contains Pfam PF00590: Tetrahydropyran (CornuPophyrin) Methylases domain; contains TIGRFAM5 TIGR00522: diphthine synthase (88417.m04513)
3110	Not regulated	NC-NC-NC	253496_at	Alq31870	glutathione peroxidase, putative glutathione peroxidase, Arabidopsis thaliana, PIR2:S71250 (88417.m04528)
3111	Not regulated	NC-NC-NC	253487_at	Alq31880	expressed protein (88417.m04531)
3112	Not regulated	NC-NC-NC	253506_at	Alq31980	expressed protein contains Pfam profile PF03140: Plant protein of unknown function (88417.m04547)
3113	Not regulated	NC-NC-NC	253480_at	Alq31840	plastocyanin-like domain-containing protein (88417.m04524)
3114	Not regulated	NC-NC-NC	253453_at	Alq31860	protein phosphatase 2C, putative / PP2C, putative protein phosphatase 2C, Schizosaccharomyces pombe, PIR2:S54287 (88417.m04526)
3115	Not regulated	NC-NC-NC	253460_at	Alq32130	expressed protein (88417.m04571)
3116	Not regulated	NC-NC-NC	253466_at	Alq32040	homeobox protein knotted-1 like 5 (KNA15) / homeobox domain containing protein 1 (H1) identical to homeobox protein knotted-1 like 5 (KNA15) SP:P48002 from Arabidopsis thaliana (88417.m04581)
3117	Not regulated	NC-NC-NC	253467_at	Alq32140	expressed protein (88417.m04572)
3118	Not regulated	NC-NC-NC	253468_at	Alq32160	phox (PX) domain-containing protein contains Pfam profile PF00787: PX domain (88417.m04574)
3119	Not regulated	NC-NC-NC	253469_at	Alq32180	eukaryotic pantothene kinase family protein similar to pantothene kinase [Emicella nidulans] GI:4191500; contains Pfam profiles PF03630: Fumble, PF01937: Protein of unknown function (88417.m04580)
3120	Not regulated	NC-NC-NC	253470_s_at	Alq32210	protein kinase family protein contains protein kinase domain, Pfam:PF00089 (88417.m04588)
3121	Not regulated	NC-NC-NC	253473_at	Alq32250	UDP-sugar transporter-related contains weak similarity to Swiss-Prot:Q95Y15 UDP-sugar transporter UST74c [Drosophila melanogaster] (88417.m04591)
3122	Not regulated	NC-NC-NC	253474_at	Alq32270	peroxidase family protein similar to L-ascorbate peroxidase [Arabidopsis thaliana] gi 1523789 emb CAA68925; contains Pfam profile PF00141: Peroxidase (88417.m04597)
3123	Not regulated	NC-NC-NC	253477_at	Alq32320	ATP synthase family protein contains Pfam profile: PF00430 ATP synthase subunit C (88417.m04590)
3124	Not regulated	NC-NC-NC	253420_at	Alq32260	chain precursor (atpG) GI:5730140 (88417.m04587)
3125	Not regulated	NC-NC-NC	253422_at	Alq32240	expressed protein (88417.m04587)
3126	Not regulated	NC-NC-NC	253424_at	Alq32330	expressed protein (88417.m04589)
3127	Not regulated	NC-NC-NC	253425_at	Alq32190	centromeric protein-related low similarity to SPIQ02224 Centromeric protein E (CENP-E protein) (Homo sapiens) (88417.m04581)
3128	Not regulated	NC-NC-NC	253427_at	Alq32380	phosphate translocator-related low similarity to phosphoenolpyruvate/phosphate translocator precursor [Mesembryanthemum crystallinum] GI:9285275, SPIP52178 Those phosphate/phosphate translocator, non-green plastid, chloroplast precursor (CTPT) (Brassicaceae) (88417.m04612)
3129	Not regulated	NC-NC-NC	253435_at	Alq32400	mitochondrial substrate carrier family protein (88417.m04613)
3130	Not regulated	NC-NC-NC	253436_at	Alq32470	ubiquinol-cytochrome C reductase complex 14 kDa protein, putative similar to SPIP48502 Ubiquinol-cytochrome C reductase complex 14 kDa protein (EC 1.10.2.2) (CR14) (Solanum tuberosum); contains Pfam profile PF02271: Ubiquinol-cytochrome C reductase complex 14kD subunit (88417.m04622)
3131	Not regulated	NC-NC-NC	253437_at	Alq32460	expressed protein contains Pfam profile PF04862: Protein of unknown function, DUF642 (88417.m04620)
3132	Not regulated	NC-NC-NC	253438_at	Alq32520	glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolase, putative similar to serine hydroxymethyltransferase [Chlamydomonas reinhardtii] GI:17066746; contains Pfam profile PF00464: serine hydroxymethyltransferase (88417.m04629)
3133	Not regulated	NC-NC-NC	253442_at	Alq32530	vacuolar ATP synthase, putative / V-ATPase, putative SPIP23988 Vacuolar ATP synthase 22 kDa proteolipid subunit (EC 3.6.3.14) (Saccharomyces cerevisiae); contains Pfam profile PF00137: ATP synthase subunit C (88417.m04631)
3134	Not regulated	NC-NC-NC	253443_at	Alq32551	WD-40 repeat family protein (LEUNG) contains seven G-protein beta WD-40 repeats; beta transducin-like protein, Podospora anserina, gi L28125; contains Pfam profiles PF04503: Single-stranded DNA binding protein, SSCP; PF00400: WD domain, G-beta repeat; identical to cDNA LEUNG (LEUNG) GI:1141804 (88417.m04633)
3135	Not regulated	NC-NC-NC	253444_at	Alq32800	zinc finger (C3HC4-type RING finger) family protein low similarity to RING finger protein 38 [Homo sapiens] GI:21668412; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger) (88417.m04639)
3136	Not regulated	NC-NC-NC	253391_at	Alq32580	ferredoxin-related contains Pfam profile: PF00111 2Fe-2S iron-sulfur cluster binding domain (88417.m04642)
3137	Not regulated	NC-NC-NC	253392_at	Alq32850	inward rectifying potassium channel, putative (KAT3) (KAT1) (KAT1) identical to K ⁺ inward rectifying channel protein KC1 [Arabidopsis thaliana] gi 4090537 tblAAC98810; similar to (KAT1) K ⁺ channel [Arabidopsis thaliana] gi 1165000 emb CAA63601; Shaker-type channel (IP6TM), PMID:11500563 (88417.m04647)

3138	Not regulated	253394_at	NC-NC-NC	locophoral cyclase, chloroplast / vitamin E deficient 1 (VTE1) / sucrose export defective 1 (SXD1) identical to SPI084FY7 Tocopherol cyclase, chloroplast precursor (Vitamin E deficient 1) (Sucrose export defective 1) [Arabidopsis thaliana] (68417.m04682)
3139	Not regulated	253395_at	NC-NC-NC	protein kinase (AFC3) (AME3) identical to protein kinase AFC3 [Arabidopsis thaliana] SWISS-PROT:P51568 (68417.m04849)
3140	Not regulated	253403_at	NC-NC-NC	protein kinase, putative similar to protein kinase p40XIEg22 [Xenopus laevis] gi 809280 emb CAA78914; contains protein kinase domain, Pfam:PF00069 (68417.m04688)
3141	Not regulated	253412_at	NC-NC-NC	calcineurin B-like protein 10 (CBL10) identical to calcineurin B-like protein 10 [Arabidopsis thaliana] Gi:29150248 (68417.m04693)
3142	Not regulated	253384_at	NC-NC-NC	expressed protein (68417.m04694)
3143	Not regulated	253385_at	NC-NC-NC	expressed protein predicted protein, Caenorhabditis elegans, gb.Z70780 (68417.m04686)
3144	Not regulated	253386_at	NC-NC-NC	UDP-sulfoliquinose synthase / sulfite:UDP-glucose sulfoliquinase / sulfite:UDP-glucose sulfoliquinase protein (SQD1) identical to gi:2736155 (68417.m04699)
3145	Not regulated	253388_at	NC-NC-NC	expressed protein (68417.m04683)
3146	Not regulated	253389_at	NC-NC-NC	expressed protein (68417.m04683)
3147	Not regulated	253387_at	NC-NC-NC	expressed protein (68417.m04683)
3148	Not regulated	253388_at	NC-NC-NC	expressed protein (68417.m04683)
3149	Not regulated	253389_at	NC-NC-NC	expressed protein (68417.m04683)
3150	Not regulated	253390_at	NC-NC-NC	expressed protein (68417.m04683)
3151	Not regulated	253391_at	NC-NC-NC	expressed protein (68417.m04683)
3152	Not regulated	253392_at	NC-NC-NC	expressed protein (68417.m04683)
3153	Not regulated	253393_at	NC-NC-NC	expressed protein (68417.m04683)
3154	Not regulated	253394_at	NC-NC-NC	expressed protein (68417.m04683)
3155	Not regulated	253395_at	NC-NC-NC	expressed protein (68417.m04683)
3156	Not regulated	253396_at	NC-NC-NC	expressed protein (68417.m04683)
3157	Not regulated	253397_at	NC-NC-NC	expressed protein (68417.m04683)
3158	Not regulated	253398_at	NC-NC-NC	expressed protein (68417.m04683)
3159	Not regulated	253399_at	NC-NC-NC	expressed protein (68417.m04683)
3160	Not regulated	253400_at	NC-NC-NC	expressed protein (68417.m04683)
3161	Not regulated	253401_at	NC-NC-NC	expressed protein (68417.m04683)
3162	Not regulated	253402_at	NC-NC-NC	expressed protein (68417.m04683)
3163	Not regulated	253403_at	NC-NC-NC	expressed protein (68417.m04683)
3164	Not regulated	253404_at	NC-NC-NC	expressed protein (68417.m04683)
3165	Not regulated	253405_at	NC-NC-NC	expressed protein (68417.m04683)
3166	Not regulated	253406_at	NC-NC-NC	expressed protein (68417.m04683)
3167	Not regulated	253407_at	NC-NC-NC	expressed protein (68417.m04683)
3168	Not regulated	253408_at	NC-NC-NC	expressed protein (68417.m04683)
3169	Not regulated	253409_at	NC-NC-NC	expressed protein (68417.m04683)
3170	Not regulated	253410_at	NC-NC-NC	expressed protein (68417.m04683)
3171	Not regulated	253411_at	NC-NC-NC	expressed protein (68417.m04683)
3172	Not regulated	253412_at	NC-NC-NC	expressed protein (68417.m04683)
3173	Not regulated	253413_at	NC-NC-NC	expressed protein (68417.m04683)
3174	Not regulated	253414_at	NC-NC-NC	expressed protein (68417.m04683)

3175	Not regulated	NC-NC-NC	253278_at	A14g34220	leucine-rich repeat transmembrane protein kinase, putative protein kinase TMKL1, Arabidopsis thaliana, P1D.E353150 (88417.m04862)
3176	Not regulated	NC-NC-NC	253282_at	A14g34120	CBS domain-containing protein contains Pfam profile PF00571; CBS domain (88417.m04840)
3177	Not regulated	NC-NC-NC	253283_at	A14g34080	expressed protein (88417.m04836)
3178	Not regulated	NC-NC-NC	253286_at	A14g34260	expressed protein (88417.m04869)
3179	Not regulated	NC-NC-NC	253257_at	A14g34350	extra-large guanine nucleotide binding protein, putative / G-protein, putative similar to extra-large G-protein (XLG) [Arabidopsis thaliana] GI:3201680; contains Pfam profile PF00503; G-protein alpha subunit (88417.m04885)
3180	Not regulated	NC-NC-NC	253234_at	A14g34265	expressed protein (88417.m04870)
3181	Not regulated	NC-NC-NC	253235_at	A14g34350	LYB family protein contains Pfam profile: PF02401 LYB protein (88417.m04881)
3182	Not regulated	NC-NC-NC	253237_at	A14g34240	aldehyde dehydrogenase (ALDH3) similar to aldehyde dehydrogenase [Arabidopsis thaliana] gi17065878[emb]CAC84903; contains Pfam profile PF00171; aldehyde dehydrogenase (NAD) family protein; identical to cDNA aldehyde dehydrogenase (ALDH3 gene) GI:17065875, aldehyde dehydrogenase [Arabidopsis thaliana] GI:17065878 (88417.m04886)
3183	Not regulated	NC-NC-NC	253248_at	A14g34670	40S ribosomal protein S3A (RPS3A) (88417.m04822)
3184	Not regulated	NC-NC-NC	253251_at	A14g34730	ribosome-binding factor A family protein contains Pfam PF02033; Ribosome-binding factor A (88417.m04829)
3185	Not regulated	NC-NC-NC	253255_at	A14g34760	auxin-responsive family protein auxin-induced protein X15, Glycine max, PIR2-JQ1087 (88417.m04834)
3186	Not regulated	NC-NC-NC	253228_at	A14g34630	expressed protein (88417.m04918)
3187	Not regulated	NC-NC-NC	253200_at	A14g34720	vacuolar ATP synthase 16 kDa proteolipid subunit 1 / V-ATPase 16 kDa proteolipid subunit 1 (AVAP1) (AVA-P1) identical to SPIP59227 Vacuolar ATP synthase 16 kDa proteolipid subunit 1/35 (EC 3.6.3.14) (V-ATPase 16 kDa proteolipid subunit 1/35) [Arabidopsis thaliana]; contains Pfam profile PF00137; ATP synthase subunit C (88417.m04928)
3188	Not regulated	NC-NC-NC	253204_at	A14g34460	guanine nucleotide-binding protein beta subunit (Gβ1) / GTP-binding protein beta subunit (AGB1) / transducin contains 7 WD-40 repeats (PF00400); identical to Guanine nucleotide-binding protein beta subunit SP-P49177 [Arabidopsis thaliana]; Weiss, CA et al, PNAS 91:9854 (1994) (88417.m04898)
3189	Not regulated	NC-NC-NC	253206_at	A14g34640	farnesyl-diphosphate farnesyltransferase 1 / squalene synthase 1 (SQS1) identical to SPIP53789 Farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) (Squalene synthetase) (SQS) (FPP:FPP farnesyltransferase) (Arabidopsis thaliana); non-consensus GC donor splice site at exon 3, squalene synthase 2 (SQS2), Arabidopsis thaliana (88417.m04819)
3190	Not regulated	NC-NC-NC	253212_s_at	A14g34890	xanthine dehydrogenase, putative similar to xanthine dehydrogenase from Gallus gallus, PIR:XOCHDH [SPIP47890]; contains Pfam profile PF02738 Aldehyde oxidase and xanthine dehydrogenase, molybdopter binding domain (88417.m04948)
3191	Not regulated	NC-NC-NC	253220_s_at	A14g34920	1-phosphatidylinositol phosphodiesterase-related contains weak similarity to 1-phosphatidylinositol phosphodiesterase precursor (EC 3.1.4.10) (Phosphatidylinositol-specific phospholipase C) (PI-PLC) (Swiss-Prot:P34024) [Listeria monocytogenes] (88417.m04951)
3192	Not regulated	NC-NC-NC	253221_at	A14g34870	peptidyl-prolyl cis-trans isomerase / cyclophilin (CYP1) / rotamase identical to cyclophilin (CYP1) gi1992643[gb]AA75512; similar to PROT:Q39613 (88417.m04946)
3193	Not regulated	NC-NC-NC	253223_at	A14g35000	L-ascorbate peroxidase 3 (APX3) identical to ascorbate peroxidase 3 [Arabidopsis thaliana] (GI:2444018, L-ascorbate peroxidase 3 [Arabidopsis thaliana] gi1523791[emb]CAA66926; similar to ascorbate peroxidase [Gossypium hirsutum] gi1019946[gb]AA52854 [Arabidopsis thaliana] (88417.m04963)
3194	Not regulated	NC-NC-NC	253225_at	A14g35020	Rac-like GTP-binding protein (ARAC3) / Rho-like GTP-binding protein (ROP6) identical to SPIQ38912 RAC-like GTP binding protein ARAC3 (GTP-binding protein ROP6) (Arabidopsis thaliana); identical to cDNA Rho-like GTP binding protein (Rop6) GI:2645642 (88417.m04967)
3195	Not regulated	NC-NC-NC	253171_at	A14g35040	bZIP transcription factor family protein contains Pfam profile: PF00170 bZIP transcription factor (88417.m04872)
3196	Not regulated	NC-NC-NC	253172_at	A14g35060	heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related low similarity to copper homeostasis factor [GI:3168840][PMID:9701579]; similar to farnesylated proteins GMFP7 (Glycine max)[GI:4087573] and ATFP6 (GI:4087553); contains heavy-metal-associated domain PF00403 (88417.m04977)
3197	Not regulated	NC-NC-NC	253183_at	A14g35220	cyclase family protein contains Pfam profile: PF04199 putative cyclase (88417.m05005)
3198	Not regulated	NC-NC-NC	253184_at	A14g35230	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (88417.m05007)
3199	Not regulated	NC-NC-NC	253188_at	A14g35300	transporter-related low similarity to hexose transporter [Solanum tuberosum] GI:8347246; contains Pfam profile PF00083; major facilitator superfamily protein (88417.m05017)
3200	Not regulated	NC-NC-NC	253197_at	A14g35250	vestibone reductase-related low similarity to vestibone reductase [Medicago sativa subsp. sativa] GI:973249 (88417.m05010)
3201	Not regulated	NC-NC-NC	253138_at	A14g35490	ribosomal protein L11 family protein several ribosomal proteins L11 (88417.m05043)
3202	Not regulated	NC-NC-NC	253139_at	A14g35450	ankyrin repeat family protein / AFT protein (AFT) contains ankyrin repeats, Pfam:PF00023; identical to cDNA AFT protein (AFT) GI:3478698 (88417.m05036)
3203	Not regulated	NC-NC-NC	253140_at	A14g35480	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain PF00097; Zinc finger, C3HC4 type (RING finger) (88417.m05042)
3204	Not regulated	NC-NC-NC	253147_at	A14g35600	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (88417.m05057)
3205	Not regulated	NC-NC-NC	253159_at	A14g35570	high mobility group protein delta (HMGdelta) / HMG protein delta identical to HMG protein (HMGdelta) [Arabidopsis thaliana] GI:2832363 (88417.m05054)
3206	Not regulated	NC-NC-NC	253160_at	A14g35760	expressed protein (88417.m05076)
3207	Not regulated	NC-NC-NC	253109_at	A14g35920	expressed protein contains Pfam profile PF04749; Protein of unknown function, DUF814; isoform contains AT-acceptor splice site at intron 8 (88417.m05105)
3208	Not regulated	NC-NC-NC	253118_at	A14g35950	Rac-like GTP-binding protein (ARAC6) identical to rac-like GTP binding protein Arac6 GI:3408757 from [Arabidopsis thaliana] (88417.m05115)
3209	Not regulated	NC-NC-NC	253119_at	A14g35980	expressed protein (88417.m05119)
3210	Not regulated	NC-NC-NC	253120_at	A14g35790	phospholipase D delta / PLD delta (PLDDELTA) identical to phospholipase D delta SP: QBC5Y0 from [Arabidopsis thaliana]; supporting cDNA gi11761141[db]JA8031047.1 (88417.m05084)

3211	Not regulated	NC-NC-NC	253121_at	A14g35890	La domain-containing protein contains Pfam PF05383; La domain (88417.m05097) pathogenesis-related thaumatin family protein similar to receptor serine/threonine kinase PRSK [Arabidopsis thaliana] (G1:1235880); contains Pfam profile PF00314; Thaumatin family (88417.m05127)
3212	Not regulated	NC-NC-NC	253104_at	A14g36010	expressed protein contains Pfam PF05277; Protein of unknown function (DUF726) (88417.m05151)
3213	Not regulated	NC-NC-NC	253081_at	A14g36210	cytochrome P450 84A1 (CYP84A1) (ferulate-5-hydroxylase) (FAH1) identical to Cytochrome P450 84A1 (Ferulate-5-hydroxylase) (SP1C42600) [Arabidopsis thaliana] (88417.m05153)
3214	Not regulated	NC-NC-NC	253088_at	A14g36220	teratocoeptide repeat (TPR)-containing protein contains Pfam profile PF00515; TPR Domain (88417.m05302)
3215	Not regulated	NC-NC-NC	253093_at	A14g37460	cytochrome P450 family protein (88417.m05287)
3216	Not regulated	NC-NC-NC	253096_at	A14g37330	formamidase, putative / formamide amidohydrolyase, putative similar to SPIQ50228 Formamidase (EC 3.5.1.49) (Formamide amidohydrolyase) [Methylophilus methylotrophus]; contains Pfam profile PF03069; Acetamidase/Formamidase family (88417.m05314)
3217	Not regulated	NC-NC-NC	253042_at	A14g37550	formamidase, putative / formamide amidohydrolyase, putative similar to SPIQ50228 Formamidase (EC 3.5.1.49) (Formamide amidohydrolyase) [Methylophilus methylotrophus]; contains Pfam profile PF03069; Acetamidase/Formamidase family (88417.m05316)
3218	Not regulated	NC-NC-NC	253048_at	A14g37560	cytochrome P450, putative (88417.m05283)
3219	Not regulated	NC-NC-NC	253052_at	A14g37310	expressed protein contains Pfam domain, PF03006; Uncharacterised protein family (Hly-III / UFP0073) (88417.m05416)
3220	Not regulated	NC-NC-NC	253059_s_at	A14g38320	calcium-transporting ATPase 2, plasma membrane-type / Ca(2+)-ATPase isoform 2 (ACA2) identical to SPIQ81108 Calcium-transporting ATPase 2, plasma membrane-type (EC 3.6.3.8) [Ca(2+)-ATPase isoform 2] (Arabidopsis thaliana) (88417.m05324)
3221	Not regulated	NC-NC-NC	253083_at	A14g37640	bZIP transcription factor family protein contains Pfam profile: PF00170 bZIP transcription factor (88417.m05342)
3222	Not regulated	NC-NC-NC	253084_at	A14g37730	homeobox-leucine zipper protein 22 (HAT22) / HD-ZIP protein 22 identical to homeobox-leucine zipper protein HAT22 (HD-ZIP protein 22) (SP:P46604) [Arabidopsis thaliana] (88417.m05348)
3223	Not regulated	NC-NC-NC	253038_at	A14g37790	phosphoenolpyruvate carboxylase [ATP], putative / PEP carboxylase, putative / PEPC, putative similar to phosphoenolpyruvate carboxylase [Lycopodium obscurum] (G1:16950587; SPIQ8SL20 Phosphoenolpyruvate carboxylase [ATP] (EC 4.1.1.49) (PEP carboxylase) (Phosphoenolpyruvate carboxylase) (PEPC) [Zea mays]; contains Pfam profile PF01293; phosphoenolpyruvate carboxylase (88417.m05356)
3224	Not regulated	NC-NC-NC	253041_at	A14g37870	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535; PPR repeat (88417.m05388)
3225	Not regulated	NC-NC-NC	253027_at	A14g38150	mitochondrial transcription termination factor-related / mTERF-related contains Pfam profile PF02536; mTERF (88417.m05387) aminoacylase, putative / N-acyl-L-amino-acid amidohydrolyase, putative similar to aminoacylase-1 (N-acyl-L-amino-acid amidohydrolyase, ACY-1) [Homo sapiens] SWISS-PROT:Q03154 (88417.m05384)
3226	Not regulated	NC-NC-NC	253028_at	A14g38160	amino acid transporter family protein low similarity to lysosomal amino acid transporter 1 [Rattus norvegicus] (G1:14571904; contains amino acid transporter family protein (88417.m05402)
3227	Not regulated	NC-NC-NC	253033_at	A14g38220	expressed protein contains Pfam PF01205; Uncharacterized protein family UPP0028 (88417.m05379)
3228	Not regulated	NC-NC-NC	253006_at	A14g38250	glycine hydroxymethyltransferase / serine hydroxymethyltransferase / semineurotheone aldolase (SHN1) identical to serine hydroxymethyltransferase [Arabidopsis thaliana] (G1:6899845 (88417.m05383)
3229	Not regulated	NC-NC-NC	253007_at	A14g38090	exostosin family protein contains Pfam profile: PF03018 Exostosin family (88417.m05373)
3230	Not regulated	NC-NC-NC	253008_at	A14g37930	expressed protein contains Pfam PF05742; Protein of unknown function (DUF633) (88417.m05404)
3231	Not regulated	NC-NC-NC	252980_at	A14g38040	histone deacetylase (RPD3A) identical to SPIQ22448 Histone deacetylase (HD) (Arabidopsis thaliana) (88417.m05384)
3232	Not regulated	NC-NC-NC	252981_at	A14g38260	mannitol dehydrogenase, putative (ELIS-1) identical to G1:16267 (88417.m05387)
3233	Not regulated	NC-NC-NC	252982_at	A14g38130	geranylgeranyl pyrophosphate synthase, putative / GGPP synthetase, putative / farnesyltransferase, putative 65% similar to geranylgeranyl pyrophosphate synthase (G1:413730); (88417.m05434)
3234	Not regulated	NC-NC-NC	252983_at	A14g37960	expressed protein contains Pfam profile: PF04785 protein of unknown function (DUF616) (88417.m05444)
3235	Not regulated	NC-NC-NC	252998_s_at	A14g38460	expressed protein (88417.m05440)
3236	Not regulated	NC-NC-NC	252999_at	A14g38500	expressed protein contains Pfam profile PF03759; Domain of unknown function (DUF315) (88417.m05431)
3237	Not regulated	NC-NC-NC	253001_at	A14g38490	expressed protein (88417.m05402)
3238	Not regulated	NC-NC-NC	252975_s_at	A14g38430	expressed protein contains Pfam profile PF03759; Domain of unknown function (DUF315) (88417.m05431)
3239	Not regulated	NC-NC-NC	252976_s_at	A14g38550	1-phosphatidylinositol phosphodiesterase-related contains weak similarity to 1-phosphatidylinositol phosphodiesterase precursor (EC 4.8.1.13) (Phosphatidylinositol diacylglycerol-lyase) (Phosphatidylinositol-specific phospholipase C) (PI-PLC), (Swiss-Prot:P34024) [Listeria monocytogenes] (88417.m05478)
3240	Not regulated	NC-NC-NC	252950_at	A14g38890	CDP-diacylglycerol-inositol 3-phosphatidyltransferase, putative / phosphatidylinositol synthase, putative similar to phosphatidylinositol synthase (PIS1) - Arabidopsis thaliana, PID a1313354 (g1:3387632) (88417.m05460)
3241	Not regulated	NC-NC-NC	252953_at	A14g38570	26S proteasome regulatory subunit S5A (RPN10) identical to multiubiquitin chain binding protein (MBP1) SP:P55034, G1:1185208 (88417.m05467)
3242	Not regulated	NC-NC-NC	252955_at	A14g38630	heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related low similarity to copper homeostasis factor (PMID:9701579) [G1:168840]; nearly identical to farnesylated protein TFP6 (G1:4087553); contains Heavy-metal-associated domain PF00403 (88417.m05461)
3243	Not regulated	NC-NC-NC	252956_at	A14g38580	cholesterol transporter-related contains weak similarity to CD82 protein [Homo sapiens] g1:16945321emb(CAC82175 (88417.m05469)
3244	Not regulated	NC-NC-NC	252959_at	A14g38640	dihydrouridine synthase family protein contains Pfam domain, PF01207; Dihydrouridine synthase (Dus) (88417.m05508)
3245	Not regulated	NC-NC-NC	252968_at	A14g38900	bZIP protein var-1 protein, Lycopodium obscurum, PIR2:552203 (88417.m05510)
3246	Not regulated	NC-NC-NC	252969_at	A14g38900	autin-responsive protein, putative autin-inducible SAUR gene, Raphanus sativus A8000708 (88417.m05488)
3247	Not regulated	NC-NC-NC	252972_at	A14g38840	peptidyl-prolyl cis-trans isomerase / cyclophilin / rotamase / cyclosporin A-binding protein (ROC1) identical to SPIP34790 Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclosporin A-binding protein) (Arabidopsis thaliana) (88417.m05487)
3248	Not regulated	NC-NC-NC	252973_s_at	A14g38740	phosphorylase family protein contains weak similarity to Swiss-Prot:O51931 nucleosidase [includes: 5'-methylthioadenosine nucleosidase (EC 3.2.2.16); S-adenosylhomocysteine nucleosidase [Buchnera aphidicola] (88417.m05483)
3249	Not regulated	NC-NC-NC	252974_at	A14g38800	

3250 Not regulated	NC-NC-NC	252915_at	A14g38810	calcium-binding EF hand family protein contains INTERPRO:IPR002048 calcium-binding EF-hand domain (68417.m05404)
3251 Not regulated	NC-NC-NC	252922_at	A14g39040	expressed protein contains PF01985; Uncharacterised protein family (68417.m05529)
3252 Not regulated	NC-NC-NC	252925_at	A14g39100	PHD finger family protein / bromo-adjacent homology (BAH) domain-containing protein contains Pfam domain, PF00828; PHD-finger and PF01426; BAH domain (68417.m05536)
3253 Not regulated	NC-NC-NC	252926_at	A14g38920	vacuolar ATP synthase 16 kDa proteolipid subunit 1/3/5 (EC 3.6.3.14) (V-ATPase 16 kDa proteolipid subunit 1/3/5) (Arabidopsis thaliana); contains Pfam profile PF00137; ATP synthase subunit C (68417.m05515)
3254 Not regulated	NC-NC-NC	252929_at	A14g38970	fructose-bisphosphate aldolase, putative strong similarity to plastidic fructose-bisphosphate aldolase (EC 4.1.2.13) from Nicotiana glauca (NPALDP1) [GI:4827251]; Onyza sativa, PIR2.T02057 [SPIQ40877] (68417.m05521)
3255 Not regulated	NC-NC-NC	252931_at	A14g38930	ubiquitin fusion degradation UFD1 family protein similar to SPIP70362 Ubiquitin fusion degradation protein 1 homolog (UB fusion protein 1) (Mus musculus); contains Pfam profile PF03152; Ubiquitin fusion degradation protein UFD1 (68417.m05516)
3256 Not regulated	NC-NC-NC	252935_at	A14g39150	DNAJ heat shock N-terminal domain-containing protein similar to SPIP39101; CAJ1 protein, Saccharomyces cerevisiae, PIR2.S46085; contains Pfam profile PF00228 DnaJ domain (68417.m05545)
3257 Not regulated	NC-NC-NC	252939_at	A14g39230	isoflavone reductase, putative similar to allergenic isoflavone reductase-like protein Bel v 6.0102 (Beta pendula)[GI:10764481]; contains Pfam profile PF02718; isoflavone reductase (68417.m05541)
3258 Not regulated	NC-NC-NC	252945_at	A14g39140	expressed protein (68417.m05541)
3259 Not regulated	NC-NC-NC	252912_at	A14g39200	40S ribosomal protein S25 (RPS25E) ribosomal protein S25, Lycopersicon esculentum, PIR2.S40089 (68417.m05550)
3260 Not regulated	NC-NC-NC	252913_at	A14g39220	RER1A protein identical to SPIQ40870 RER1A protein (AIRER1A) (Arabidopsis thaliana) (68417.m05552)
3261 Not regulated	NC-NC-NC	252984_at	A14g39170	SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative similar to phosphatidylinositol transfer-like protein IV (GI:14486707) (Lotus japonicus) and phosphatidylinositol-phosphatidylcholine transfer protein SEC14, Yarrowia lipolytica, PIR2.S43745; contains Pfam PF00650; CRAUTRIO domain; contains Pfam PF03785; CRAUTRIO, N-terminus (68417.m05547)
3262 Not regulated	NC-NC-NC	252987_at	A14g39240	Kelch repeat-containing F-box family protein similar to SKP1 interacting partner 6 [Arabidopsis thaliana] GI:10718957; contains Pfam profiles PF01344; Kelch motif, PF00646; F-box domain (68417.m05555)
3263 Not regulated	NC-NC-NC	252990_at	A14g39540	shikimate kinase family protein similar to shikimate kinase precursor from Lycopersicon esculentum [SPIQ00497]; contains Pfam shikimate kinase domain PF01202 (68417.m05590)
3264 Not regulated	NC-NC-NC	252990_at	A14g39570	Kelch repeat-containing F-box family protein contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344 (68417.m05595)
3265 Not regulated	NC-NC-NC	252911_at	A14g39510	Cytochrome P450 family protein contains Pfam PF00067; Cytochrome P450, similar to Cytochrome P450 88A2 (SP-O23086) [Arabidopsis thaliana] (68417.m05587)
3266 Not regulated	NC-NC-NC	252978_at	A14g39480	mitochondrial substrate carrier family protein (68417.m05583)
3267 Not regulated	NC-NC-NC	252879_at	A14g39390	transporter-related low similarity to glucose-6-phosphate/phosphate-translocator precursor [Solanum tuberosum] GI:2897593 (68417.m05575)
3268 Not regulated	NC-NC-NC	252980_at	A14g39730	lipid-associated family protein contains PLAT/LH2 (Polycystin-1, Lipoxigenase, Alpha-Toxin/Lipoxygenase homology) domain Pfam:PF01477 (68417.m05824)
3269 Not regulated	NC-NC-NC	252983_at	A14g39520	GTP-binding protein, putative similar to SPIQ97295 Developmentally regulated GTP-binding protein 1 (DRG 1) (Homo sapiens); contains Pfam profiles PF02824; TGS domain, PF01018; GTP10B8 family (68417.m05588)
3270 Not regulated	NC-NC-NC	252956_at	A14g39690	expressed protein (68417.m05616)
3271 Not regulated	NC-NC-NC	252976_at	A14g39970	haloacid dehalogenase-like hydrolase family protein low similarity to SPIP95649 CbbY protein (Rhodobacter sphaeroides) (68417.m05661)
3272 Not regulated	NC-NC-NC	252950_at	A14g39880	ribosomal protein L23 family protein contains Pfam profile PF00276; ribosomal protein L23 (68417.m05650)
3273 Not regulated	NC-NC-NC	252952_at	A14g39900	expressed protein (68417.m05652)
3274 Not regulated	NC-NC-NC	252922_at	A14g39955	hydrolase, alpha/beta fold family protein low similarity to SPIP24640LIP3_MORSP Lipase 3 precursor (EC 3.1.1.3) (Triacylglycerol lipase) (Moraxella sp); contains Pfam profile PF00561; hydrolase, alpha/beta fold family (68417.m05659)
3275 Not regulated	NC-NC-NC	252923_at	A14g40045	expressed protein (68417.m05670)
3276 Not regulated	NC-NC-NC	252924_at	A14g40030	histone H3.2 identical to Histone H3.2, minor Lolium temulentum SPIP11105, nearly identical to histone H3.2 Mus pahari GI:515005; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4 (68417.m05687)
3277 Not regulated	NC-NC-NC	252928_at	A14g39980	DNAJ heat shock family protein similar to SPIQ955A3 Chaperone protein dnaJ (Listeria monocytogenes); contains Pfam profiles PF00228 DnaJ domain, PF01558 DnaJ C terminal region, PF00884 DnaJ central domain (4 repeats) (68417.m05680)
3278 Not regulated	NC-NC-NC	252929_at	A14g40060	homeobox-leucine zipper protein 16 (HB-16) / HD-ZIP transcription factor 16 identical to homeodomain leucine-zipper protein ATHB 16 (GP:5668909) (Arabidopsis thaliana) (68417.m05672)
3279 Not regulated	NC-NC-NC	252932_at	A14g39910	ubiquitin-specific protease 3 (UBP3) identical to GI:2347098 (68417.m05653)
3280 Not regulated	NC-NC-NC	252745_at	A14g43230	zinc finger (FYVE type) family protein contains Pfam domain PF01363; FYVE zinc finger (68416.m04563)
3281 Not regulated	NC-NC-NC	252754_at	A14g43510	expressed protein (68417.m05670)
3282 Not regulated	NC-NC-NC	252723_at	A14g43520	expressed protein contains Pfam profile PF03647; Uncharacterised protein family (UPF0136) (68416.m04614)
3283 Not regulated	NC-NC-NC	252703_at	A14g43740	leucine-rich repeat family protein contains leucine-rich repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to somatic embryogenesis receptor-like kinase 2 (Arabidopsis thaliana) gi14573457(gbJAAK68073) (68416.m04672)
3284 Not regulated	NC-NC-NC	252711_at	A14g43720	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage/LTP family domain PF00234 (68416.m04668)
3285 Not regulated	NC-NC-NC	252687_at	A14g44200	protein kinase family protein contains Pfam protein kinase domain, Pfam:PF00068; contains serine/threonine protein kinase domain, INTERPRO:IPR002280 (68416.m04739)
3286 Not regulated	NC-NC-NC	252669_at	A14g44100	MD-2-related lipid recognition domain-containing protein / ML domain-containing protein contains Pfam profile PF02221; ML domain (68416.m04726)

3287	Not regulated	NC-NC-NC	252676_at	A13g44280	expressed protein (68416.m04755)
3288	Not regulated	NC-NC-NC	252677_at	A13g44320	nitrilase 3 (NIT3) identical to SPIP46010 Nitrilase 3 (EC 3.5.5.1) (Arabidopsis thaliana) (68416.m04760)
3289	Not regulated	NC-NC-NC	252678_s_at	A13g44330	nitrilase 2 (NIT2) identical to SPIP32982 Nitrilase 2 (EC 3.5.5.1) (Arabidopsis thaliana) (68416.m04757)
3290	Not regulated	NC-NC-NC	252680_at	A13g44330	expressed protein (68416.m04763)
3291	Not regulated	NC-NC-NC	252683_at	A13g44380	expressed protein predicted proteins, Arabidopsis thaliana (68416.m04766)
3292	Not regulated	NC-NC-NC	252683_x_at	A13g44490	histone deacetylase-related / HD-related similar to SPIQ09106 Histone deacetylase 1 (HD1) (Mus musculus) (68416.m04782)
3293	Not regulated	NC-NC-NC	252647_at	A13g44620	low molecular weight phosphotyrosine protein phosphatase family protein contains Pfam profile: PF01451 low molecular weight phosphotyrosine protein phosphatase (68416.m04797)
3294	Not regulated	NC-NC-NC	252601_s_at	A13g45030	40S ribosomal protein S20 (RPS20A) 40S ribosomal proteinS20, Arabidopsis thaliana, pir.T12992 (68416.m04851)
3295	Not regulated	NC-NC-NC	252603_at	A13g45050	expressed protein (68416.m04853)
3296	Not regulated	NC-NC-NC	252619_at	A13g45210	expressed protein contains Pfam profile PF04520: Protein of unknown function, DJF584 (68416.m04878)
3297	Not regulated	NC-NC-NC	252573_at	A13g45260	zinc finger (C2H2 type) family protein contains Pfam domain, PF00086: Zinc finger, C2H2 type (68416.m04887)
3298	Not regulated	NC-NC-NC	252587_at	A13g45820	transducin family protein / WD-40 repeat family protein contains 7 WD-40 repeats, similar to PC326 protein (GI:200241) (PIR2:IS37694) [Mus musculus]; Human (H326) translated mRNA - Homo sapiens, EMBL:HS06631 (68416.m04927)
3299	Not regulated	NC-NC-NC	252591_at	A13g45800	senescence-associated family protein similar to senescence-associated protein 5 [Hemerocallis hybrid cultivar] gi 3551954 gb AAC34855 (68416.m04925)
3300	Not regulated	NC-NC-NC	252542_at	A13g45770	oxidoreductase, zinc-binding dehydrogenase family protein similar to nuclear receptor binding factor-1 NRBF-1 - Rattus norvegicus, EMBL:AB015724; contains Pfam zinc-binding dehydrogenase domain PF00107 (68416.m04947)
3301	Not regulated	NC-NC-NC	252548_at	A13g45850	kinesin motor protein-related kinesin-related protein TKRP125, Nicotiana tabacum, PIR: T02017 (68416.m04962)
3302	Not regulated	NC-NC-NC	252560_at	A13g46030	histone H2B, putative strong similarity to histone H2B Arabidopsis thaliana GI:2407802, Gossypium hirsutum SPIQ22562, Lycopodium esculentum GI:3021489; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4 (68416.m04980)
3303	Not regulated	NC-NC-NC	252561_at	A13g45980	histone H2B identical to histone H2B Arabidopsis thaliana GI:2407802; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4 (68416.m04975)
3304	Not regulated	NC-NC-NC	252564_at	A13g46010	actin-depolymerizing factor 1 (ADF1) identical to SPIQ39250 Actin-depolymerizing factor 1 (ADF-1) (Arabidopsis thaliana) (68416.m04978)
3305	Not regulated	NC-NC-NC	252565_at	A13g46000	actin-depolymerizing factor, putative (ADF2) strong similarity to SPIQ82SK3 Actin-depolymerizing factor 4 (ADF-4) (Arabidopsis thaliana); contains Pfam profile PF00241: Cofilin/tropomyosin-type actin-binding protein (68416.m04877)
3306	Not regulated	NC-NC-NC	252568_at	A13g46040	40S ribosomal protein S15A (RPS15aD) cytoplasmic ribosomal protein S15a, Arabidopsis thaliana, EMBL:ATAF1412 (68416.m04981)
3307	Not regulated	NC-NC-NC	252513_at	A13g46220	expressed protein (68416.m05003)
3308	Not regulated	NC-NC-NC	252514_at	A13g46060	Ras-related protein (ARA-3) / small GTP-binding protein, putative identical to SPIP28168 Ras-related protein ARA-3 (Arabidopsis thaliana); contains Pfam profile: PF00071 Ras family (68416.m04984)
3309	Not regulated	NC-NC-NC	252516_at	A13g46100	histidyl-IRNA synthetase / histidine-IRNA ligase identical to histidyl-IRNA synthetase [Arabidopsis thaliana] GI:3659908 (68416.m04988)
3310	Not regulated	NC-NC-NC	252524_at	A13g46430	expressed protein (68416.m05033)
3311	Not regulated	NC-NC-NC	252525_at	A13g46450	SEC14 cytosolic factor family protein / phosphoglycerate transfer family protein contains Pfam PF00650: CRAU/TRIO domain; similar to polyphosphoinositide binding protein Sah1p (GI:2739044) (Glycine max) (68416.m05035)
3312	Not regulated	NC-NC-NC	252527_at	A13g46440	NAD-dependent epimerase/dehydratase family protein similar to UDP-glucuronic acid decarboxylase Uxa1p from Filobasidiella neoformans GI:14318327; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family (68416.m05034)
3313	Not regulated	NC-NC-NC	252528_at	A13g46460	ubiquitin-conjugating enzyme 13 (UBC13) E2; identical to gi:992706 (68416.m05037)
3314	Not regulated	NC-NC-NC	252504_at	A13g46590	telomere repeat-binding protein, putative similar to telomere repeat-binding protein TRP1 [Arabidopsis thaliana] gi 5459298 emb CA850690 (68416.m05057)
3315	Not regulated	NC-NC-NC	252478_at	A13g46540	epsin N-terminal homology (ENTH) domain-containing protein / dalttrin assembly protein-related contains Pfam PF01417: ENTH domain, ENTH (Epsin N-terminal homology) domain; similar to Chain A Of The Epsin N-Terminal Homology (Entb) Domain (GI:8569264) [Rattus Norvegicus]; similar to A110-protein (GI:1724114) [Avena sativa] (68416.m05052)
3316	Not regulated	NC-NC-NC	252481_at	A13g46830	expressed protein contains similarity to defective chloroplasts and leaves protein SP:Q42463 from [Lycopodium esculentum] (68416.m05062)
3317	Not regulated	NC-NC-NC	252471_at	A13g46820	serine/threonine protein phosphatase PP1 isozyme 5 (TOPP5) / phosphoprotein phosphatase 1 identical to SPIP48485 Serine/threonine protein phosphatase PP1 isozyme 5 (EC 3.1.3.1) (Arabidopsis thaliana), phosphoprotein phosphatase 1 deoxyuridine 5'-triphosphate nucleotidohydrolase family contains Pfam profile: PF00692 deoxyuridine 5'-triphosphate nucleotidohydrolase (68416.m05095)
3318	Not regulated	NC-NC-NC	252442_at	A13g46940	transporter-related low similarity to brain specific Na+-dependent inorganic phosphate cotransporter from [Rattus norvegicus] GI:507415, [Homo sapiens] GI:7328925; vesicular glutamate transporter 3 from [Rattus norvegicus] GI:21685382; contains Pfam profile PF00083; major facilitator superfamily protein (68416.m05101)
3319	Not regulated	NC-NC-NC	252444_at	A13g46980	glycosyl hydrolase family 3 protein beta-D-glucan exohydrolase, Nicotiana tabacum, TREMBL:AB017502_1 (68416.m05104)
3320	Not regulated	NC-NC-NC	252445_at	A13g47000	expressed protein contains Pfam profile PF03140: Plant protein of unknown function (68416.m05130)
3321	Not regulated	NC-NC-NC	252462_at	A13g47250	expressed protein similar to MTD2 [Medicago truncatula] GI:9294812; supporting cDNA gi 25083983 gb ET002136.1 (68416.m05120)
3322	Not regulated	NC-NC-NC	252464_at	A13g47160	expressed protein (68416.m05112)
3323	Not regulated	NC-NC-NC	252467_at	A13g47080	peroxisomal biogenesis factor 11 family protein / PEX11 family protein contains Pfam PF05648: Peroxisomal biogenesis factor 11 (PEX11) (68416.m05157)
3324	Not regulated	NC-NC-NC	252411_at	A13g47430	HNH endonuclease domain-containing protein contains Pfam domain PF01844: HNH endonuclease (68416.m05164)
3325	Not regulated	NC-NC-NC	252418_at	A13g47490	

3326	Not regulated	NC-NC-NC	252421_at	A13g47540	chitinase, putative similar to basic endochitinase CHB4 precursor SP_Q06208 from [Brassica napus] (68416.m05170)
3327	Not regulated	NC-NC-NC	252423_at	A13g47590	esterase/lipase/thioesterase family protein low similarity to cinnamoyl ester hydrolase Clnl [Butyrivibrio fibrisolvens] Gi:1622732; contains InterPro entry IPR000379 (68416.m05181)
3328	Not regulated	NC-NC-NC	252427_at	A13g47840	basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain (68416.m05186)
3329	Not regulated	NC-NC-NC	252430_at	A13g47470	chlorophyll A-B binding protein 4, chloroplast / LHCI type III CAB-4 (CAB4) identical to SPIP27521 Chlorophyll A-B binding protein 4, chloroplast precursor (LHCI type III CAB-4) (LHCP) (Arabidopsis thaliana) (68416.m05162)
3330	Not regulated	NC-NC-NC	252433_at	A13g47560	esterase/lipase/thioesterase family protein low similarity to cinnamoyl ester hydrolase Clnl [Butyrivibrio fibrisolvens] Gi:1622732; contains InterPro entry IPR000379 (68416.m05177)
3331	Not regulated	NC-NC-NC	252409_at	A13g47650	bundle-sheath defective protein 2 family / bsd2 family similar to bundle sheath defective protein 2 [Zea mays] Gi:4732091 (68416.m05187)
3332	Not regulated	NC-NC-NC	252383_at	A13g47780	ABC transporter family protein transport protein ABC-C, Homo sapiens, PIR2:S71363 (68416.m05205)
3333	Not regulated	NC-NC-NC	252385_at	A13g47810	calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase (68416.m05208)
3334	Not regulated	NC-NC-NC	252387_at	A13g47800	aldose 1-epimerase family protein similar to ALDOSE 1-EPIMERASE PRECURSOR GB_P05148 [SPIP05148] from [Acinetobacter calcoaceticus]; contains Pfam profile PF01283 Aldose 1-epimerase (68416.m05207)
3335	Not regulated	NC-NC-NC	252389_at	A13g47833	expressed protein (68416.m05213)
3336	Not regulated	NC-NC-NC	252391_at	A13g47860	apolipoprotein D-related contains weak similarity to Apolipoprotein D precursor (ApoD) (Swiss-Prot P51910) [Mus musculus] (68416.m05217)
3337	Not regulated	NC-NC-NC	252398_at	A13g47890	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00087 zinc finger, C3HC4 type (RING finger) (68416.m05232)
3338	Not regulated	NC-NC-NC	252400_at	A13g48020	expressed protein (68416.m05235)
3339	Not regulated	NC-NC-NC	252402_s_at	A13g48050	bromo-adjacent homology (BAH) domain-containing protein contains Pfam profile PF01426 BAH domain (68416.m05238)
3340	Not regulated	NC-NC-NC	252371_at	A13g48070	expressed protein (68416.m05241)
3341	Not regulated	NC-NC-NC	252348_at	A13g48140	senescence-associated protein, putative similar to B12D protein [Ipomoea batatas] GB:AA222104 (68416.m05250)
3342	Not regulated	NC-NC-NC	252349_at	A13g48150	cell division cycle family protein / CDC family protein similar to cell division cycle protein 23 [Homo sapiens] Gi:3283051, anaphase-promoting complex subunit 8 [Homo sapiens] Gi:6180017; contains Pfam profile PF00515: TPR Domain (68416.m05251)
3343	Not regulated	NC-NC-NC	252353_at	A13g48200	expressed protein (68416.m05259)
3344	Not regulated	NC-NC-NC	252354_at	A13g48170	betaine-aldehyde dehydrogenase, putative similar to betaine-aldehyde dehydrogenase, chloroplast precursor (BADH) [Arabidopsis thaliana] SWISS-PROT:Q85785 (68416.m05254)
3345	Not regulated	NC-NC-NC	252362_at	A13g48500	expressed protein (68416.m05294)
3346	Not regulated	NC-NC-NC	252363_at	A13g48460	GDOL-motif lipase/hydrolase family protein similar to lipase [Arabidopsis thaliana] Gi:1145627; contains InterPro Entry IPR001087
3347	Not regulated	NC-NC-NC	252366_at	A13g48420	Lipolytic enzyme, G-D-S-L family (68416.m05290)
3348	Not regulated	NC-NC-NC	252324_at	A13g48565	haloacid dehalogenase-like hydrolase family protein low similarity to SPIP95649 CbbY protein [Rhodobacter sphaeroides]; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase (68416.m05285)
3349	Not regulated	NC-NC-NC	252328_at	A13g48570	protein transport protein SEC61 gamma subunit, putative similar to Swiss-Prot Q19887 protein transport protein SEC61 gamma subunit [Caenorhabditis elegans] (68416.m05303)
3350	Not regulated	NC-NC-NC	252329_at	A13g48760	zinc finger (C2HC2 type) family protein contains Pfam profile PF01526: DHHC zinc finger domain (68416.m05325)
3351	Not regulated	NC-NC-NC	252335_at	A13g48860	expressed protein (68416.m05336)
3352	Not regulated	NC-NC-NC	252336_at	A13g48880	F-box family protein N7 protein - Medicago truncatula, EMBL:CAA76808; similar to SKP1 interacting partner 2 (SKIP2) [TIGR, Ath1:A15g07250 (68416.m05339)]
3353	Not regulated	NC-NC-NC	252337_at	A13g48750	cell division control protein 2 homolog A (CDC2A) identical to cell division control protein 2 homolog A [Arabidopsis thaliana] SWISS-PROT:P24100 (68416.m05324)
3354	Not regulated	NC-NC-NC	252338_at	A13g48890	cytochrome b5 domain-containing protein similar to SPIP00284 Membrane associated progesterone receptor component (mPR) (Homo sapiens); contains Pfam profile PF00173: HemeStereoid binding domain (68416.m05341)
3355	Not regulated	NC-NC-NC	252287_at	A13g49080	ribosomal protein S9 family protein contains Pfam profile PF00380: ribosomal protein S9 (68416.m05362)
3356	Not regulated	NC-NC-NC	252294_at	A13g49010	60S ribosomal protein L13 (RPL13B) / breast basic conserved protein 1-related (BBC1) (68416.m05353)
3357	Not regulated	NC-NC-NC	252295_at	A13g49100	signal recognition particle 9 kDa protein, putative / SRP9, putative similar to SPIP49458 Signal recognition particle 9 kDa protein (SRP9) (Homo sapiens); contains Pfam PF05486: Signal recognition particle 9 kDa protein (SRP9) (68416.m05363)
3358	Not regulated	NC-NC-NC	252303_at	A13g49210	expressed protein (68416.m05378)
3359	Not regulated	NC-NC-NC	252308_at	A13g49310	expressed protein contains PF05631: Protein of unknown function (DUF791) (68416.m05391)
3360	Not regulated	NC-NC-NC	252280_at	A13g49260	calmodulin-binding family protein low similarity to SF16 protein [Helianthus annuus] Gi:560150; contains Pfam profile PF00812: IQ glucosamine/galactosamine-6-phosphate isomerase family protein similar to SPIP095338 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL) (Homo sapiens); contains Pfam profile PF01182: Glucosamine-6-phosphate isomerase/6-phosphogluconolactonase (68416.m05396)
3361	Not regulated	NC-NC-NC	252282_at	A13g49360	expressed protein (68416.m05419)
3362	Not regulated	NC-NC-NC	252264_at	A13g49580	expressed protein (68416.m05418)
3363	Not regulated	NC-NC-NC	252269_at	A13g49580	mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein contains Pfam PF02466: Mitochondrial import inner membrane translocase subunit Tim17 (68416.m05418)
3364	Not regulated	NC-NC-NC	252270_at	A13g49560	Got1-like family protein contains Pfam profile: PF04178 Got1-like family (68416.m05402)
3365	Not regulated	NC-NC-NC	252271_s_at	A13g49420	branched-chain amino acid aminotransferase 3 / branched-chain amino acid transaminase 3 (BCAT3) identical to SPIP08M401 Branched-chain amino acid aminotransferase 3, chloroplast precursor (EC 2.6.1.42) (Atbcat-3)(Arabidopsis thaliana) (68416.m05431)
3366	Not regulated	NC-NC-NC	252274_at	A13g49680	

3367	Not regulated	NC-NC-NC	252278_at	A13g49480	expressed protein (68416.m05409) nascent polypeptide-associated complex (NAC) domain-containing protein similar to alpha-NAC, non-muscle form [Mus musculus]
3368	Not regulated	NC-NC-NC	252277_at	A13g49470	GI:1666690; contains Pfam profile PF01848: NAC domain (68416.m05407)
3369	Not regulated	NC-NC-NC	252278_at	A13g49530	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain, similar to NAC2 - Arabidopsis thaliana. EMBL:AF201456 (68416.m05413)
3370	Not regulated	NC-NC-NC	252225_at	A13g49870	ADP-ribosylation factor, putative similar to ADP-ribosylation factor-like protein 1 (SP-P40816) [Homo sapiens]; ARF3 ADP-ribosylation factor, putative similar to ADP-ribosylation factor family RIBOSYLATION FACTOR, GP-453191 Arabidopsis thaliana; contains domain PF00025: ADP-ribosylation factor family (68416.m05452)
3371	Not regulated	NC-NC-NC	252231_at	A13g49720	expressed protein (68416.m05436)
3372	Not regulated	NC-NC-NC	252189_at	A13g50070	cyclin family protein similar to cyclin D3.1 protein [Nicotiana tabacum] GI:4160300, CycD3.2 [Lycopersicon esculentum] GI:6434198; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain (68416.m05474)
3373	Not regulated	NC-NC-NC	252192_at	A13g50000	casein kinase II alpha chain 2 identical to casein kinase II, alpha chain 2 (CK II) [Arabidopsis thaliana] SWISS-PROT:Q08466 (68416.m05467)
3374	Not regulated	NC-NC-NC	252213_at	A13g50210	2-oxoacid-dependent oxidase, putative strong similarity to partial cds of 2-oxoacid-dependent oxidase (din11) from GI:10834554 [Arabidopsis thaliana] (68416.m05490)
3375	Not regulated	NC-NC-NC	252214_at	A13g50260	AP2 domain-containing transcription factor, putative EREBP-3 homolog, Stylosanthes hamata, EMBL:U91882 (68416.m05498)
3376	Not regulated	NC-NC-NC	252157_at	A13g50430	expressed protein (68416.m05516)
3377	Not regulated	NC-NC-NC	252158_at	A13g50530	calcium-dependent protein kinase, putative / CDPK, putative similar to calcium/calmodulin-dependent protein kinase CαMK3 [Nicotiana tabacum] gi16804226ipbAAL30820 (68416.m05526)
3378	Not regulated	NC-NC-NC	252166_at	A13g50500	protein kinase, putative similar to abscisic acid-activated protein kinase [Vicia faba] gi18739828ipbIAAF27340 (68416.m05523)
3379	Not regulated	NC-NC-NC	252167_at	A13g50560	short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family IPR002188 short-chain dehydrogenase/reductase (SDR) superfamily (68416.m05530)
3380	Not regulated	NC-NC-NC	252168_at	A13g50440	hydrolase, alpha/beta fold family protein similar to ethylene-induced esterase [Citrus sinensis] GI:14279437 polynucleotide aldehyde esterase [Rauvolfia serpentina] GI:6651393; contains Pfam profile PF00561: hydrolase, alpha/beta fold family (68416.m05517)
3381	Not regulated	NC-NC-NC	252169_at	A13g50520	phosphoglycerate/bisphosphoglycerate mutase family protein similar to SPIP00950 Phosphoglycerate mutase 1 (EC 5.4.2.1) [Saccharomyces cerevisiae]; contains Pfam profile PF00300: phosphoglycerate mutase family (68416.m05525)
3382	Not regulated	NC-NC-NC	252174_at	A13g50680	leucine-rich repeat family protein (68416.m05548)
3383	Not regulated	NC-NC-NC	252178_at	A13g50750	brassinosteroid signalling positive regulator-related contains similarity to BZR1 protein [Arabidopsis thaliana]
3384	Not regulated	NC-NC-NC	252181_at	A13g50685	expressed protein (68416.m05545)
3385	Not regulated	NC-NC-NC	252184_at	A13g50680	steroid 22-alpha-hydroxylase (CYP90B1) (DMF4) identical to gi:2835342 (68416.m05541)
3386	Not regulated	NC-NC-NC	252154_at	A13g50880	HhH-GPD base excision DNA repair family protein contains weak similarity to DNA-3-methyladenine glycosylase 1 (EC 3.2.2.21) (3-methyladenine DNA glycosylase 1) (3MEA DNA glycosylase 1) (Swiss-Prot:Q82383) [Schizosaccharomyces pombe]; contains oxygen-evolving enhancer protein, chloroplast, putative / 33 kDa subunit of oxygen evolving system of photosystem II, putative (PSB2) identical to SP-Q8S841 Oxygen-evolving enhancer protein 1-2, chloroplast precursor (OEE1) [Arabidopsis thaliana]; strong similarity to SPIP23321 Oxygen-evolving enhancer protein 1-1, chloroplast precursor (OEE1) (33 kDa subunit of oxygen evolving system of photosystem II) (OEC 33 kDa subunit) (33 kDa thylakoid membrane protein) [Arabidopsis thaliana]
3387	Not regulated	NC-NC-NC	252130_at	A13g50820	late embryogenesis abundant protein, putative / LEA protein, putative similar to Picea glauca late embryogenesis abundant protein (EMB8), PID.g1350545 SPIQ40863; contains Pfam profile PF00561: hydrolase, alpha/beta fold family (68416.m05562)
3388	Not regulated	NC-NC-NC	252132_at	A13g50790	expressed protein (68416.m05573)
3389	Not regulated	NC-NC-NC	252133_at	A13g50900	expressed protein (68416.m05573)
3390	Not regulated	NC-NC-NC	252134_at	A13g50910	expressed protein (68416.m05574)
3391	Not regulated	NC-NC-NC	252135_at	A13g50830	stress-responsive protein, putative similar to cold acclimation WCOR413-like protein gamma form [Hordeum vulgare]
3392	Not regulated	NC-NC-NC	252136_at	A13g50770	gi18449100ipbAAL8998; similar to stress-regulated protein SAP1 [Xerophyta viscosa] gi21360378ipbIAAM47505; identical to cDNA cold acclimation protein WCOR413-like protein beta form GI:10121842 (68416.m05568)
3393	Not regulated	NC-NC-NC	252139_at	A13g51050	calmodulin-related protein, putative similar to regulator of gene silencing calmodulin-related protein GI:12963415 from [Nicotiana tabacum] (68416.m05560)
3394	Not regulated	NC-NC-NC	252141_at	A13g51050	FC-GAP repeat-containing protein (68416.m05590)
3395	Not regulated	NC-NC-NC	252147_at	A13g51100	expressed protein (68416.m05595)
3396	Not regulated	NC-NC-NC	252150_at	A13g51310	RIO1 family protein contains Pfam profile PF01163: RIO1 family (68416.m05612)
3397	Not regulated	NC-NC-NC	252121_at	A13g51160	vacuolar protein sorting-associated protein 35 family protein / VPS35 family protein similar to vacuolar protein sorting 35 [Mus musculus] GI:1875394; contains Pfam profile PF03635: Vacuolar protein sorting-associated protein 35 (68416.m05618)
3398	Not regulated	NC-NC-NC	252122_at	A13g51140	GDP-D-mannose-4,6-dehydratase (MUR1) almost identical to GDP-D-mannose-4,6-dehydratase (MUR1) GI:1764100 from [Arabidopsis thaliana] (68416.m05602)
3399	Not regulated	NC-NC-NC	252124_at	A13g51010	expressed protein (68416.m05600)
3400	Not regulated	NC-NC-NC	252125_at	A13g51040	expressed protein contains Pfam PF05608: Protein of unknown function (DUF778) (68416.m05588)
3401	Not regulated	NC-NC-NC	252095_at	A13g51000	epoxide hydrolase, putative similar to epoxide hydrolase [Glycine max] GI:2764808; contains Pfam profile PF00561: hydrolase, alpha/beta fold family (68416.m05584)

3402	Not regulated	NC-NC-NC	252098_at	A13g51330	aspartyl protease family protein contains Eukaryotic and viral aspartyl proteases active site, PROSITE:PS00141 (88416.m05818) senescence/dehydration-associated protein-related similar to senescence-associated protein 12 [Hemerocallis hybrid cultivar]
3403	Not regulated	NC-NC-NC	252099_at	A13g51250	g13551958[gb]AAC34857, similar to early-responsive to dehydration stress ERD7 protein [Arabidopsis thaliana]
3404	Not regulated	NC-NC-NC	252104_at	A13g51460	g115320412[db]BAB83916 (88416.m05610) phosphoinositide phosphatase family protein contains similarity to phosphoinositide phosphatase SAC1 [Rattus norvegicus]
3405	Not regulated	NC-NC-NC	252113_at	A13g51820	g111095248[gb]AAG29810, contains Pfam domain, PF02383: Sac homology domain; contains non-consensus AT-AC splice sites at intron 8 (88416.m05636)
3406	Not regulated	NC-NC-NC	252116_at	A13g51510	expressed protein (88416.m05658)
3407	Not regulated	NC-NC-NC	252091_at	A13g51390	expressed protein (88416.m05641)
3408	Not regulated	NC-NC-NC	252092_at	A13g51420	zinc finger (DHH type) family protein contains Pfam profile PF01529: DHH zinc finger domain (88416.m05629)
3409	Not regulated	NC-NC-NC	252093_at	A13g51500	serpinin[SPIP15324]; contains stictosidine synthase domain PF03088 (88416.m05632)
3410	Not regulated	NC-NC-NC	252064_at	A13g51520	serpinin[SPIP15324]; contains stictosidine synthase domain PF03088 (88416.m05632)
3411	Not regulated	NC-NC-NC	252065_at	A13g51610	expressed protein predicted protein, Oryza sativa, EMBL:AP000387 (88416.m05640)
3412	Not regulated	NC-NC-NC	252067_at	A13g51370	diacylglycerol acyltransferase family protein contains Pfam PF03982: Diacylglycerol acyltransferase (88416.m05642)
3413	Not regulated	NC-NC-NC	252069_s_at	A13g51640	expressed protein (88416.m05656)
3414	Not regulated	NC-NC-NC	252076_at	A13g51660	protein phosphatase 2C, putative / PP2C, putative similar to Ser/Thr protein phosphatase 2C (PF208) (GI:15020818) [Arabidopsis thaliana]; similar to protein phosphatase 2C (GI:3608412) [Mesembryanthemum crystallinum]; contains Pfam PF00481 : Protein phosphatase 2C domain (88416.m05626)
3415	Not regulated	NC-NC-NC	252086_at	A13g52030	macrophage migration inhibitory factor family protein / MIF family protein contains Pfam profile: PF01187 Macrophage migration inhibitory factor family(MIF) (88416.m05665)
3416	Not regulated	NC-NC-NC	252032_at	A13g52150	F-box family protein / WD-40 repeat family protein (88416.m05707)
3417	Not regulated	NC-NC-NC	252033_at	A13g51950	RNA recognition motif (RRM)-containing protein similar to chloroplast RNA-binding protein cp33 [Arabidopsis thaliana] GI:881812; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) domain (88416.m05724)
3418	Not regulated	NC-NC-NC	252038_at	A13g52120	zinc finger (CCHC-type) family protein / RNA recognition motif (RRM)-containing protein contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM), PF00842: Zinc finger C-x8-C-x5-C-x3-H type (and similar) (88416.m05688)
3419	Not regulated	NC-NC-NC	252041_at	A13g52080	SWAP (Suppressor-of-White-APRicot)/surp domain-containing protein / D111VC-patch domain-containing protein contains Pfam profiles PF01585: G-patch domain, PF01805: Surp module (88416.m05721)
3420	Not regulated	NC-NC-NC	252044_at	A13g52420	DNA-directed RNA polymerase II 13.6 kDa subunit (RPB13.6) identical to SP1Q38859 DNA-directed RNA polymerase II 13.6 kDa polypeptide (EC 2.7.7.6) [Arabidopsis thaliana] (88416.m05716)
3421	Not regulated	NC-NC-NC	252055_at	A13g52580	outer envelope membrane protein, putative similar to outer envelope membrane protein g1703236[gb]AAA63414 (88416.m05765)
3422	Not regulated	NC-NC-NC	252059_at	A13g52560	40S ribosomal protein S14 (RPS14C) ribosomal protein S14 -Zea mays,PIR2:A30097 (88416.m05780)
3423	Not regulated	NC-NC-NC	252001_at	A13g52750	ubiquitin-conjugating enzyme family protein similar to DNA-binding protein CROC-1B [Homo sapiens] GI:1066082; contains Pfam profile PF00178: Ubiquitin-conjugating enzyme (88416.m05784)
3424	Not regulated	NC-NC-NC	252002_at	A13g52760	chloroplast division protein, putative strong similarity to plastid division protein Flaz [Arabidopsis thaliana] GI:14195704, chloroplast division protein AIF422-1 [Arabidopsis thaliana] GI:15636809 (88416.m05812)
3425	Not regulated	NC-NC-NC	252008_at	A13g52810	integral membrane Yip1 family protein contains Pfam domain, PF04893: Yip1 domain (88416.m05813)
3426	Not regulated	NC-NC-NC	252012_at	A13g52730	expressed protein (88416.m05796)
3427	Not regulated	NC-NC-NC	252028_at	A13g53030	ubiquinol-cytochrome C reductase UQCRC/UCR9-like family protein contains Pfam profile: PF05365 ubiquinol-cytochrome C reductase, UQCRC/UCR9 like (88416.m05810)
3428	Not regulated	NC-NC-NC	251996_at	A13g52840	protein kinase family protein contains eukaryotic protein kinase domain, INTERPRO:IPR000719 (88416.m05845)
3429	Not regulated	NC-NC-NC	251987_at	A13g53020	beta-galactosidase, putative / lactase, putative similar to beta-galactosidase precursor GI:3869280 from [Carica papaya] (88416.m05823)
3430	Not regulated	NC-NC-NC	251989_at	A13g53130	60S ribosomal protein L24 (RPL24B) 60S ribosomal protein L24, Arabidopsis thaliana, EMBL:AC006282 (88416.m05844)
3431	Not regulated	NC-NC-NC	251973_at	A13g53180	cytochrome P450 family protein similar to Cytochrome P450 97B2 (SP:048921) [Glycine max] (88416.m05855)
3432	Not regulated	NC-NC-NC	251975_at	A13g53230	glutamine synthetase, putative similar to glutamine synthetase (glutamate-ammonia ligase) [Bacillus subtilis] SWISS-PROT:P12425 (88416.m05860)
3433	Not regulated	NC-NC-NC	251982_at	A13g53190	cell division cycle protein 48, putative / CDC48, putative very strong similarity to SPIP54609 Cell division cycle protein 48 homolog domain (88416.m05865)
3434	Not regulated	NC-NC-NC	251989_at	A13g53110	(Arabidopsis thaliana); contains Pfam profiles PF00004: ATPase AAA family, PF02359: Cell division protein 48 (CDC48) N-terminal domain (88416.m05865)
3435	Not regulated	NC-NC-NC	251981_at	A13g53340	pectate lyase family protein similar to pectate lyase 2 GP:6606534 from [Musa acuminata] (88416.m05881)
3436	Not regulated	NC-NC-NC	251938_at	A13g53430	DEAD/DEAH box helicase, putative RNA helicase, Mus musculus, PIR:149731 (88416.m05853)
3437	Not regulated	NC-NC-NC	251941_at	A13g53470	CCAAT-box binding transcription factor, putative similar to CAAAT-box DNA binding protein subunit B (NF-YB) (SP:P25209) (GI:22380) [Zea mays]; contains Pfam PF08088 : Histone-like transcription factor (CBF/NF-Y) and archaeal histone (88416.m05885)
3438	Not regulated	NC-NC-NC	251945_at	A13g53520	60S ribosomal protein L12 (RPL12B) 60S RIBOSOMAL PROTEIN L12, Prunus americana, SWISSPROT:RL12_PRUAR (88416.m05896)
3439	Not regulated	NC-NC-NC	251946_at	A13g53540	expressed protein ribosomal protein S25, cytosolic, Arabidopsis thaliana, PIR:T08568 (88416.m05902)
3440	Not regulated	NC-NC-NC	251948_at	A13g53580	NAD-dependent epimerase/dehydratase family protein similar to UDP-glucuronic acid decarboxylase Uxs'p from Fibrobacillus neofiformans GI:14318327; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family (88416.m05912)
					expressed protein (88416.m05912)
					diaminopimelate epimerase family protein contains Pfam profile PF01678: Diaminopimelate epimerase (88416.m05918)

3441	Not regulated	NC-NC-NC	251951_s_at	A13g53630	expressed protein predicted proteins, Arabidopsis thaliana (88416.m05924) 29 kDa ribonucleoprotein, chloroplast / RNA-binding protein cp 29 nearly identical to SPQ43349 29 kDa ribonucleoprotein, chloroplast precursor (RNA-binding protein cp29) [Arabidopsis thaliana] (88416.m05900)
3442	Not regulated	NC-NC-NC	251956_at	A13g53460	Ras-related GTP-binding protein, putative similar to Ras-related protein ARA-3 SP-P28186 from [Arabidopsis thaliana] (88416.m05921)
3443	Not regulated	NC-NC-NC	251960_at	A13g53610	plasma membrane intrinsic protein 2A (PIP2A) / aquaporin PIP2.1 (PIP2.1) identical to plasma membrane intrinsic protein 2A SP-P43286 from [Arabidopsis thaliana] (88416.m05985)
3444	Not regulated	NC-NC-NC	251962_at	A13g53420	ARF GAP-like zinc finger-containing protein ZIGA2 (ZIGA2) nearly identical to ARF GAP-like zinc finger-containing protein ZIGA2 from GI:10441356 [Arabidopsis thaliana], contains InterPro accession IPR001184; Human Rev interacting-like protein (hRIP) (88416.m05933)
3445	Not regulated	NC-NC-NC	251905_at	A13g53710	arnadillobeta-catenin repeat family protein contains Pfam profile: PF00514 arnadillobeta-catenin-like repeat (88416.m05944) uracil phosphoribosyltransferase, putative / UMP pyrophosphorylase, putative / UPRase, putative similar to SP-P50928 Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRase) [Lactococcus lactis]; contains Pfam profile PF00156; Phosphoribosyl transferase domain (88416.m05954)
3447	Not regulated	NC-NC-NC	251920_at	A13g53900	aldoketo reductase family protein similar to chalcone reductase [Sesbania rostrata] (GI:2782155), and aldose reductase ALDRXV4 (88416.m05954)
3448	Not regulated	NC-NC-NC	251923_at	A13g53880	[Xerophyta viscosa] (GI:4539944), [Hordium vulgare] (GI:728592) and [Schizosaccharomyces pombe, swissprot-Q82365]
3449	Not regulated	NC-NC-NC	251926_at	A13g53740	60S ribosomal protein L36 (RPL36B) 60S RIBOSOMAL PROTEIN L36 - Schizosaccharomyces pombe, swissprot-Q82365 (88416.m05936)
3450	Not regulated	NC-NC-NC	251932_at	A13g54010	peptidyl-prolyl cis-trans isomerase, putative / FK506-binding protein, putative / pasticcino 1-D (PAS1-D) nearly identical to pasticcino 1-D [Arabidopsis thaliana] (GI:3080740) (88416.m05971)
3451	Not regulated	NC-NC-NC	251935_at	A13g54090	piRb-type carbohydrate kinase family protein contains Pfam profile: PF00294 piRb family carbohydrate kinase (88416.m05980) synaptobrevin family protein similar to vesicle-associated membrane protein 7B (At VAMP7B), Arabidopsis thaliana, EMBL-AFD25333 (88416.m06001)
3452	Not regulated	NC-NC-NC	251877_at	A13g54300	expressed protein hin1 protein, Nicotiana tabacum, PIR:T03265 (88416.m05991)
3453	Not regulated	NC-NC-NC	251879_at	A13g54200	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family (88416.m05985)
3454	Not regulated	NC-NC-NC	251882_at	A13g54140	ribosomal protein L17 family protein contains Pfam profile: PF01186 ribosomal protein L17 (88416.m05992)
3455	Not regulated	NC-NC-NC	251883_at	A13g54210	embryo-abundant protein-related similar to embryo-abundant protein [Picea glauca] (GI:1350531) (88416.m05988)
3458	Not regulated	NC-NC-NC	251884_at	A13g54150	fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative strong similarity to fructose-1,6-bisphosphatase [Brassica napus] (GI:289367) identical to SP-P25951 Fructose-1,6-bisphosphatase, chloroplast precursor (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase) [Arabidopsis thaliana]; contains Pfam profile PF00316; fructose-1,6-bisphosphatase (88416.m05978)
3457	Not regulated	NC-NC-NC	251885_at	A13g54050	expressed protein GTP-binding regulatory protein beta chain, Dictyostelium discoideum, PIR:A47370 (88416.m05980)
3458	Not regulated	NC-NC-NC	251880_at	A13g54190	expressed protein DNA-binding Mel-18 protein, Homo sapiens, PIR:JN0717 (88416.m06008)
3459	Not regulated	NC-NC-NC	251893_at	A13g54370	SKP1 interacting partner 5 (SKP5) identical to GP:14348816 SKP1-interacting partner 5 [Arabidopsis thaliana] (88416.m06027)
3460	Not regulated	NC-NC-NC	251897_at	A13g54360	proline-rich extensin-like family protein contains proline-rich extensin domains, INTERPRO:IPR002385 (88416.m06040)
3461	Not regulated	NC-NC-NC	251867_at	A13g54480	ABC transporter family protein similar to ABC50 GI:10863747 from [Rattus norvegicus] (88416.m06035)
3462	Not regulated	NC-NC-NC	251843_x_at	A13g54590	histone H2A.F.Z identical to GI:2407800 (88416.m06037)
3463	Not regulated	NC-NC-NC	251845_at	A13g54540	arnadillobeta-catenin repeat family protein / U-box domain-containing protein contains Pfam domain, PF00514; Arnadillobeta-catenin-like repeats and Pfam, PF04564; U-box domain (88416.m06063)
3464	Not regulated	NC-NC-NC	251846_at	A13g54560	pectate lyase, putative / powdery mildew susceptibility protein (PMR8) identical to powdery mildew susceptibility protein [Arabidopsis thaliana] (GI:22508901; similar to pectate lyase 2 GP-8608534 from [Musa acuminata] (88416.m06088)
3465	Not regulated	NC-NC-NC	251852_at	A13g54750	AP2 domain-containing transcription factor, putative similar to (SP-P47827) Floral homeotic protein APETALA2, Arabidopsis thaliana, U12546 (88416.m06102)
3466	Not regulated	NC-NC-NC	251853_at	A13g54790	tonneau family protein similar to tonneau 1b (GI:11484367) [Arabidopsis thaliana] (88416.m06104)
3467	Not regulated	NC-NC-NC	251864_at	A13g54920	chlorophyll A-B binding protein / LHCl type I (CAB) identical to chlorophyll A/B-binding protein [Arabidopsis thaliana] (GI:16207; contains Pfam profile: PF00504 chlorophyll A-B binding protein (88416.m06081)
3468	Not regulated	NC-NC-NC	251811_at	A13g54990	CAX-interacting protein 1 (CAXIP1) identical to cDNA CAXIP1 protein (CAXIP1) (GI:27752304, CAXIP1 protein [Arabidopsis thaliana] (GI:27752305) (88416.m06084)
3469	Not regulated	NC-NC-NC	251813_at	A13g55000	Rab GTPase (ARA8) identical to small GTPase ARA8 [Arabidopsis thaliana] (GI:13160603) (88416.m06076)
3470	Not regulated	NC-NC-NC	251814_at	A13g54890	phosphatidylglycerolphosphate synthase, putative similar to phosphatidylglycerolphosphate synthase GI:13365518 from [Arabidopsis thaliana]; contains non-consensus CG acceptor splice site at exon 4 (88416.m06111)
3471	Not regulated	NC-NC-NC	251815_at	A13g54900	ln2-1 protein, putative similar to ln2-1 protein, Zea mays, P48248 (88416.m06112)
3472	Not regulated	NC-NC-NC	251817_at	A13g54840	serine/threonine protein phosphatase 2C (PP2C8) identical to Ser/Thr protein phosphatase 2C (PP2C8) (GI:15020818) [Arabidopsis thaliana]; similar to protein phosphatase 2C (GI:3608412) [Mesembryanthemum crystallinum]; contains Pfam PF00481
3473	Not regulated	NC-NC-NC	251819_at	A13g55030	SET domain-containing protein low similarity to ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I [Suaeda elaeagnifolia] (GI:3403238; contains Pfam profile PF00856; SET domain (88416.m06117)
3474	Not regulated	NC-NC-NC	251820_at	A13g55040	chalcone-flavanone isomerase / chalcone isomerase (CHI) identical to SP-P41088 (88416.m06121) pectate lyase family protein similar to pollen allergen Amb a 1.3 SP-P27761 from [Ambrosia artemisiifolia] (88416.m06123) exocyst subunit EXO70 family protein contains Pfam domain PF03081; Exo70 exocyst complex subunit; tomato leucine zipper-containing protein, Lycopersicon esculentum, PIR:S21495 (88416.m06125)
3475	Not regulated	NC-NC-NC	251821_at	A13g55050	
3476	Not regulated	NC-NC-NC	251823_at	A13g55080	
3477	Not regulated	NC-NC-NC	251827_at	A13g55120	
3478	Not regulated	NC-NC-NC	251831_at	A13g55140	
3479	Not regulated	NC-NC-NC	251832_at	A13g55150	

3480	Not regulated	NC-NC-NC	251834_at	A13g55170	60S ribosomal protein L35 (RPL35C) various ribosomal L35 proteins (88416.m08127)
3481	Not regulated	NC-NC-NC	251810_at	A13g55250	expressed protein predicted peccate-lyase, Arabidopsis thaliana, PIR:T08728 (88416.m08136)
3482	Not regulated	NC-NC-NC	251783_at	A13g55280	60S ribosomal protein L23a (RPL23aB) various ribosomal L23a proteins (88416.m08139)
3483	Not regulated	NC-NC-NC	251784_at	A13g55330	photosystem II reaction center P680 family protein contains Pfam profile PF01789; P68P (88416.m08145)
3484	Not regulated	NC-NC-NC	251785_at	A13g55130	ABC transporter family protein breast cancer resistance protein 1 BCRP1, Mus musculus, EMBL:NP_036050 (88416.m08122)
3485	Not regulated	NC-NC-NC	251786_at	A13g55420	expressed protein (88416.m08155)
3486	Not regulated	NC-NC-NC	251789_at	A13g55450	protein kinase, putative similar to protein kinase APK1B [Arabidopsis thaliana] SWISS-PROT:P46573 (88416.m08158)
3487	Not regulated	NC-NC-NC	251790_at	A13g55470	C2 domain-containing protein similar to phloem protein Gl:4164533 from [Cucurbita maxima] (88416.m08160)
3488	Not regulated	NC-NC-NC	251796_at	A13g55380	3-oxo-5-alpha-steroid 4-dehydrogenase family protein / steroid 5-alpha-reductase family protein similar to synaptic glycoprotein SC2 spliced variant from Homo sapiens [EMBL:AF038958], SC2 from Rattus sp. [gi:256894]; contains Pfam 3-oxo-5-alpha-steroid 4-dehydrogenase domain PF02544 (88416.m08148)
3489	Not regulated	NC-NC-NC	251797_at	A13g55560	DNA-binding protein-related contains Pfam domain PF03479; Domain of unknown function (DUF298), found in AT-hook motifs Pfam:PF02178 (88416.m08169)
3490	Not regulated	NC-NC-NC	251798_at	A13g55460	SC35-like splicing factor, 30 kD (SCL30) nearly identical to SC35-like splicing factor SCL30, 30 kD [Arabidopsis thaliana] GI:9843657; Serine/arginine-rich protein/putative splicing factor, Arabidopsis thaliana, EMBL:AF068940; contains Pfam profile PF00078; RNA recognition motif (a.k.a. RRM, RBD, or RNP domain) (88416.m08159)
3491	Not regulated	NC-NC-NC	251801_at	A13g55440	triophosphate isomerase, cytosolic, putative strong similarity to triophosphate isomerase, cytosolic from Petunia hybrida [SPJP48495], from Coptis japonica [SPJP21820] (88416.m08157)
3492	Not regulated	NC-NC-NC	251802_at	A13g55380	ubiquitin-conjugating enzyme 14 (UBC14) E2: UbcA73; identical to gi:2129757, S46656 (88416.m08151)
3493	Not regulated	NC-NC-NC	251804_at	A13g55430	glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative similar to beta-1,3 glucanase Gl:7414433 from [Pisum sativum]; contains Pfam profile PF00332; Glycosyl hydrolases family 17 (88416.m08156)
3494	Not regulated	NC-NC-NC	251805_at	A13g55530	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (88416.m08166)
3495	Not regulated	NC-NC-NC	251807_at	A13g55400	methylionine-IRNA synthetase / methionine-IRNA ligase / MeIRS (cpMeIRS) identical to methionyl-IRNA synthetase MEIRS [Arabidopsis thaliana] GI:2266985 (88416.m08153)
3496	Not regulated	NC-NC-NC	251809_at	A13g55600	expressed protein predicted proteins, Arabidopsis thaliana (88416.m08175)
3497	Not regulated	NC-NC-NC	251775_s_at	A13g55610	delta 1-pyruvate-5-carboxylate synthetase B / P5CS B (P5CS2) identical to SPJP54888 (88416.m08177)
3498	Not regulated	NC-NC-NC	251776_at	A13g55620	eukaryotic translation initiation factor 6, putative / eIF-6, putative similar to SPJ05135 Eukaryotic translation initiation factor 6 (eIF-6) (B4 integrin interactor) [Mus musculus]; contains Pfam profile PF01912; eIF-6 family (88416.m08178)
3499	Not regulated	NC-NC-NC	251758_at	A13g55570	LIM domain-containing protein similar to pollen specific LIM domain protein 1b [Nicotiana tabacum] GI:8467905; PGPS/D1 [Petunia hybrida] GI:4105772; contains Pfam profile PF00412; LIM domain (88416.m08187)
3500	Not regulated	NC-NC-NC	251759_at	A13g55630	x hybrid2 synthetase/serine/ubiquitin synthetase (DHES/PGCS4) nearly identical to x hybrid2 synthetase/serine/ubiquitin synthetase (DHES/PGCS4) (88416.m08179)
3501	Not regulated	NC-NC-NC	251762_at	A13g55800	synthetase [Arabidopsis thaliana] GI:17976761 (88416.m08181)
3502	Not regulated	NC-NC-NC	251763_at	A13g55730	sedoheptulose-1,7-bisphosphatase, chloroplast / sedoheptulose-bisphosphatase (SBPASE) (SED1.7)P2ASE [Arabidopsis thaliana] (88416.m08200)
3503	Not regulated	NC-NC-NC	251764_at	A13g55830	myb family transcription factor (MYB109) contains Pfam profile: PF00249 myb-like DNA-binding domain (88416.m08191)
3504	Not regulated	NC-NC-NC	251773_at	A13g55960	glycosyltransferase family protein 47 similar to exostose-related protein 2, Homo sapiens, PIR:JC5935 [SPJ083063], EXT12, Mus musculus [GI:10443933] (88416.m08203)
3505	Not regulated	NC-NC-NC	251740_at	A13g56070	NU1 interacting factor (NIF) family protein contains Pfam profile PF03031; NU1 interacting factor (88416.m08218)
3506	Not regulated	NC-NC-NC	251744_at	A13g56010	peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative similar to peptidyl-prolyl cis-trans isomerase, putative (88416.m08223)
3507	Not regulated	NC-NC-NC	251719_at	A13g56140	PIIase (cyclophilin, cyclosporin A-binding protein) [Catharanthus roseus] SWISS-PROT:Q39613 (88416.m08231)
3508	Not regulated	NC-NC-NC	251721_s_at	A13g56190	expressed protein A12g04000 - Arabidopsis thaliana, EMBL:AC007020 (88416.m08240)
3509	Not regulated	NC-NC-NC	251722_at	A13g56200	expressed protein A12g04000 - Arabidopsis thaliana, EMBL:AC007020 (88416.m08240)
3510	Not regulated	NC-NC-NC	251728_at	A13g56310	alpha-soluble NSF attachment protein 2 / alpha-SNAP2 identical to alpha-soluble NSF attachment protein 2 / alpha-SNAP2 SP-Q8SPE6 from [Arabidopsis thaliana] (88416.m08245)
3511	Not regulated	NC-NC-NC	251732_at	A13g56110	amino acid transporter family protein low similarity to N system amino acids transporter NAT-1 [Mus musculus] GI:7408850; belongs to INTERPRO:IPR002422; amino acid/polyamine transporter, family II (88416.m08246)
3512	Not regulated	NC-NC-NC	251735_at	A13g56090	alpha-galactosidase, putative / melibiose, putative / alpha-D-galactoside galactohydrolase, putative similar to alpha-galactosidase SP-Q42656 from [Coffee arabica] (88416.m08259)
3513	Not regulated	NC-NC-NC	251736_at	A13g56130	prenylated rab acceptor (PRA1) family protein weak similarity to prenylated Rab acceptor 1 (PRA1) [Homo sapiens] GI:4877285; contains Pfam profile PF03208; Prenylated rab acceptor (PRA1) (88416.m08236)
3514	Not regulated	NC-NC-NC	251737_at	A13g56340	ferritin, putative similar to ferritin subunit cowpea2 precursor [Vigna unguiculata] GI:2970654; contains Pfam profile PF00210; Ferritin-like domain (88416.m08234)
3515	Not regulated	NC-NC-NC	251739_at	A13g56170	biotin/tyrosyl attachment domain-containing protein low similarity to SPJQ08881 Biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP) [Arabidopsis sp.]; contains Pfam profile PF00364; Biotin-requiring enzyme (88416.m08238)
3516	Not regulated	NC-NC-NC	251687_at	A13g56460	40S ribosomal protein S26 (RPS26C) several 40S ribosomal protein S26 (88416.m08264)
3517	Not regulated	NC-NC-NC	251695_at	A13g56585	Cal(2+)-dependent nuclease identical to Cal(2+)-dependent nuclease [Arabidopsis thaliana] GI:7894282; supporting cDNA gi77684281[dbj]D84228.1 (88416.m08243)
3518	Not regulated	NC-NC-NC	251696_at	A13g56590	oxido-reductase, zinc-binding dehydrogenase family protein low similarity to probable NADP-dependent oxido-reductase (zeta-crystallin homolog) P1 [SPJQ39172] [gi:886428]; zeta-crystallin / quinone reductase (NADPH) - Mus musculus, PIR:A54932; contains Pfam profile PF00107; oxido-reductase, zinc-binding dehydrogenase family (88416.m08278)

3518	Not regulated	NC-NC-NC	251701_at	A13g56650	thylakoid luminal 20 kDa protein SP-QBLXXS; PMID:11719511; F22K20.16 - Arabidopsis thaliana, EMBL:AC002291; (88416.m06239)
3519	Not regulated	NC-NC-NC	251707_at	A13g56490	zinc-binding protein, putative / protein kinase C inhibitor, putative similar to 14 kDa zinc-binding protein (Protein kinase C inhibitor, PKC1) [Zea mays] Swiss-Prot:P42956 (88416.m06282)
3520	Not regulated	NC-NC-NC	251679_at	A13g57030	strictosidine synthase family protein similar to strictosidine synthase [Rauvolfia serpentina][SP15324] (88416.m06348)
3521	Not regulated	NC-NC-NC	251657_at	A13g57000	nucleolar essential protein-related contains weak similarity to Nucleolar essential protein 1 (Essential for mitotic growth 1) [Swiss-Prot:Q06287] [Saccharomyces cerevisiae] (88416.m06345)
3522	Not regulated	NC-NC-NC	251659_at	A13g57090	expressed protein (88416.m06356)
3523	Not regulated	NC-NC-NC	251661_at	A13g56950	small basic membrane integral family protein contains similarity to small basic membrane integral protein ZnSIP2.1 (GI:13447817) [Zea mays] (88416.m06336)
3524	Not regulated	NC-NC-NC	251662_at	A13g57080	eukaryotic rpb5 RNA polymerase subunit family protein similar to SP1P19388 DNA-directed RNA polymerase II 23 kDa polypeptide (EC 2.7.7.6) [Homo sapiens]; contains Pfam profiles PF03871: RNA polymerase Rpb5 N-terminal domain, PF01191: RNA polymerase Rpb5 C-terminal domain (88416.m06355)
3525	Not regulated	NC-NC-NC	251663_at	A13g57070	glutaredoxin family protein contains Pfam profile PF00462: Glutaredoxin (88416.m06354)
3526	Not regulated	NC-NC-NC	251664_at	A13g56940	disuboxylate diiron protein, putative (Crd1) similar to leucine-containing zipper protein At103 GP.6911984; contains Pfam profile PF05447: Copper response defect 1 (CRD1) (88416.m06334)
3527	Not regulated	NC-NC-NC	251666_at	A13g57050	cystathionine beta-lyase, chloroplast / beta-cyathionase / cysteine lyase (CBL) identical to SP1P53780 Cystathionine beta-lyase, chloroplast precursor (EC 4.4.1.8) (CBL) (Beta-cyathionase) (Cysteine lyase) (Arabidopsis thaliana) (88416.m06350)
3528	Not regulated	NC-NC-NC	251672_at	A13g57230	MADS-box protein (AGL16) MADS-box transcription factor DEFH125 - Antirrhinum majus, PIR:T17028; contains Pfam domain PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain); contains Pfam domain PF01488: K-box region (88416.m06371)
3529	Not regulated	NC-NC-NC	251649_at	A13g57330	calcium-modulating ATPase, plasma membrane-type, putative / Ca2+-ATPase, putative (ACA11) identical to SP1Q9M2L4JACAB_ARATH Potential calcium-transporting ATPase 11, plasma membrane-type (EC 3.6.3.8) (Ca2+-ATPase isoform 11) (Arabidopsis thaliana); strong similarity to calmodulin-stimulated calcium-ATPase [Brassica oleracea] GI:1805654 (88416.m06381)
3530	Not regulated	NC-NC-NC	251622_at	A13g57340	DNAJ heat shock N-terminal domain-containing protein similar to SP1Q9QY14 DnaJ homolog subfamily B member 12 Mus musculus; contains Pfam profile PF00226 DnaJ domain (88416.m06382)
3531	Not regulated	NC-NC-NC	251624_at	A13g57280	expressed protein contains Pfam profile PF03847: Uncharacterised protein family (UPOF136) (88416.m06378)
3532	Not regulated	NC-NC-NC	251628_at	A13g57290	eukaryotic translation initiation factor 3E / eIF3e (TIF3E1) identical to eukaryotic initiation factor 3E subunit (Arabidopsis thaliana) gi12407658gb AAG53613 (88416.m06377)
3533	Not regulated	NC-NC-NC	251630_at	A13g57420	expressed protein contains Pfam domain PF03385: Protein of unknown function, DUF288 (88416.m06383)
3534	Not regulated	NC-NC-NC	251639_at	A13g57560	aspartate/glutamate/uridylylate kinase family protein similar to acetylglutamate kinase from Porphyra purpurea [SP1P31595], Campylobacter jejuni (GI:6650364) contains Pfam profile PF00696: Amino acid kinase family (88416.m06409)
3535	Not regulated	NC-NC-NC	251640_at	A13g57450	expressed protein (88416.m06396)
3536	Not regulated	NC-NC-NC	251643_at	A13g57550	guanylate kinase 2 (GK-2) identical to guanylate kinase (GK-2) [Arabidopsis thaliana] gi17861798gb AAFF70409 (88416.m06408)
3537	Not regulated	NC-NC-NC	251645_at	A13g57790	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein weak similarity to SP1P15922 Exo-poly-alpha-D-galacturonidase precursor (EC 3.2.1.82) (Exo-PG) [Ewinia chrysanthemi]; contains PF00295: Glycosyl hydrolases family 28 (88416.m06438)
3538	Not regulated	NC-NC-NC	251596_at	A13g57650	acyl-CoA:1-acylglycerol-3-phosphate acyltransferase, putative similar to acyl-CoA:1-acylglycerol-3-phosphate acyltransferase GI:4583544 from [Brassica napus] (88416.m06423)
3539	Not regulated	NC-NC-NC	251602_at	A13g57785	expressed protein (88416.m06437)
3540	Not regulated	NC-NC-NC	251619_at	A13g58050	expressed protein (88416.m06471)
3541	Not regulated	NC-NC-NC	251536_at	A13g57810	OTU-like cysteine protease family protein contains Pfam profile PF02338: OTU-like cysteine protease (88416.m06444)
3542	Not regulated	NC-NC-NC	251559_at	A13g58010	expressed protein (88416.m06465)
3543	Not regulated	NC-NC-NC	251573_at	A13g58140	phenylalanine-tryptophan synthetase class Iic family protein similar to phenylalanine-tryptophan synthetase [Homo sapiens] GI:3983103; contains Pfam profile PF01409: tRNA synthetases class II core domain (F) (88416.m06483)
3544	Not regulated	NC-NC-NC	251578_at	A13g58180	PBS lyase HEAT-like repeat-containing protein contains Pfam profile: PF03130: PBS lyase HEAT-like repeat; contains alternative donor splice site TT at exon 2, hypothetical protein C14A4.1 - Caenorhabditis elegans, PIR:T19243 (88416.m06487)
3545	Not regulated	NC-NC-NC	251579_at	A13g58170	Ber1-like SNARE 1-1 / Ber1 / Slt1-like SNARE 14a / BS14a (BET11) identical to SP1Q9M2J9 Ber1-like SNARE 1-1 (ABET11) (Ber1/Slt1-like SNARE 14a) (AIBS14a) [Mouse-ear cross] [Arabidopsis thaliana]; supporting cDNA gi14030602gb AF368175.1AF368175 (88416.m06486)
3546	Not regulated	NC-NC-NC	251582_at	A13g58580	endonuclease/exonuclease/phosphatase family protein similar to SP1P31384 Glucose-repressible alcohol dehydrogenase transcriptional effector [Carbon catabolite repressor protein 4] [Saccharomyces cerevisiae]; contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family (88416.m06529)
3547	Not regulated	NC-NC-NC	251528_at	A13g58600	expressed protein hypothetical protein F21M11.17 - Arabidopsis thaliana, EMBL:AC003027 (88416.m06531)
3548	Not regulated	NC-NC-NC	251532_at	A13g58530	F-box family protein-related contains weak similarity to F-box protein FBL2 (GI:6010699) [Rattus norvegicus] (88416.m06524)
3549	Not regulated	NC-NC-NC	251533_at	A13g58460	rhomboid family protein / Ubiquitin-associated (UBA)/TSN domain-containing protein contains Pfam profiles PF01694: Rhomboid family, PF00827: UBA/TSN domain (88416.m06516)
3550	Not regulated	NC-NC-NC	251536_at	A13g58610	ketol-acid reductoisomerase identical to ketol-acid reductoisomerase, chloroplast precursor (EC 1.1.1.86) (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylal reductoisomerase) (Swiss-Prot:Q05758) [Arabidopsis thaliana] (88416.m06532)
3551	Not regulated	NC-NC-NC	251541_at	A13g58750	citrate synthase, glyoxysomal, putative strong similarity to SP1P48298 Citrate synthase, glyoxysomal precursor [Cucurbita maxima]; contains Pfam profile PF00285: Citrate synthase (88416.m06548)

3552	Not regulated	NC-NC-NC	251546_at	Al3g58830	haloacid dehalogenase (HAD) superfamily protein contains TIGRfam TIGR01688: HAD superfamily (subfamily IIIA) phosphatase, TIGR01688 and TIGR01692: hydrolase, HAD-superfamily, subfamily IIIA (88416.m06557)
3553	Not regulated	NC-NC-NC	251551_at	Al3g58880	ethylene-responsive transcriptional coactivator, putative similar to ethylene-responsive transcriptional coactivator (Lycopodium esculentum) gii5669634 gb AA046402 (88416.m06540)
3554	Not regulated	NC-NC-NC	251553_at	Al3g58770	WRKY family transcription factor contains Pfam profile: PF03108 WRKY DNA-binding domain (88416.m06543)
3555	Not regulated	NC-NC-NC	251505_at	Al3g59050	amine oxidase family protein similar to polyamine oxidase (EC 1.5.3.11) precursor - Zea mays [SPO64411], contains Pfam profile PF01593 amine oxidase, flavin-containing (88416.m06582)
3556	Not regulated	NC-NC-NC	251508_at	Al3g58870	magnesium transporter CorA-like family protein contains Pfam profile PF01544: CorA-like Mg2+ transporter protein (88416.m06572)
3557	Not regulated	NC-NC-NC	251519_at	Al3g59400	expressed protein (88416.m06625)
3558	Not regulated	NC-NC-NC	251520_at	Al3g59410	protein kinase family protein low similarity to GCN2 eIF2alpha kinase [Mus musculus] Gi:6066585; contains Pfam profiles PF03128: Anticodon binding domain, PF00069: Protein kinase domain (88416.m06628)
3559	Not regulated	NC-NC-NC	251492_at	Al3g59280	signaling molecule-related contains similarity to mitochondria-associated granule cytochrome macrophage CSF signaling molecule, mitochondrial precursor (CGI-136) [Mus musculus] SWISS-PROT:Q8CQV1 (88416.m06690)
3560	Not regulated	NC-NC-NC	251493_at	Al3g59300	expressed protein hypothetical protein T2J13.20 - Arabidopsis thaliana, PIR-T46116 (88416.m06610)
3561	Not regulated	NC-NC-NC	251494_at	Al3g59350	serine/threonine protein kinase, putative similar to Pto kinase interactor 1 (Pti1)[Lycopodium esculentum]
3562	Not regulated	NC-NC-NC	251464_at	Al3g59380	gii668069 gb AAC81805 (88416.m06617)
3563	Not regulated	NC-NC-NC	251465_at	Al3g59360	farnesyltransferase alpha subunit, putative / FTA, putative / protein farnesyltransferase, putative similar to farnesyltransferase alpha subunit [Gi:2246442][Pisum sativum] (88416.m06622)
3564	Not regulated	NC-NC-NC	251475_at	Al3g59660	nucleotide-sugar transporter family protein low similarity to SPIP78382 CMP-sialic acid transporter (Homo sapiens); contains Pfam profile PF04142: Nucleotide-sugar transporter (88416.m06619)
3565	Not regulated	NC-NC-NC	251484_at	Al3g59640	C2 domain-containing protein / GRAM domain-containing protein low similarity to GLUT4 vesicle protein [Rattus norvegicus] Gi:4193489; contains Pfam profiles PF00168: C2 domain, PF02893: GRAM domain (88416.m06656)
3566	Not regulated	NC-NC-NC	251460_at	Al3g58770	glycine-rich protein (88416.m06654)
3567	Not regulated	NC-NC-NC	251439_at	Al3g59950	sad homology domain-containing protein / WW domain-containing protein contains Pfam profiles PF00387: WW domain, PF02383: Sad homology domain, identical to cDNA SAC domain protein 9 (SAC9) Gi:31415734 (88416.m06670)
3568	Not regulated	NC-NC-NC	251442_at	Al3g59980	autophagy 4b (APC4b) identical to autophagy 4b [Arabidopsis thaliana] gii19812145 db BAB88384 (88416.m06690)
3569	Not regulated	NC-NC-NC	251444_at	Al3g59990	tRNA-binding region domain-containing protein similar to SPO54873 Multisynthetase complex auxiliary component p43 [Contains: Endothelial-monocyte activating polypeptide II (EMAP-II) (Small inducible cytokine subfamily E member 1)] [Crotalaria gineensis]
3570	Not regulated	NC-NC-NC	251446_at	Al3g59840	contains Pfam profile PF01598: Putative tRNA binding domain (88416.m06698)
3571	Not regulated	NC-NC-NC	251447_at	Al3g59810	methionyl aminopeptidase, putative / methionine aminopeptidase, putative / peptidase M, putative similar to Methionine aminopeptidase 2 (EC 3.4.11.18) from [Rattus norvegicus] SPIP28062 (Homo sapiens) contains Pfam profile PF05078: contains Pfam profile PF00557: metalloprotease family M24; supporting cDNA gii1344921 gb AF300880 (88416.m06697)
3572	Not regulated	NC-NC-NC	251453_at	Al3g60070	expressed protein (88416.m06677)
3573	Not regulated	NC-NC-NC	251454_at	Al3g60080	small nuclear ribonucleoprotein F, putative / U6 snRNA-associated Sm-like protein, putative / Sm protein F, putative similar to SWISS-PROT:Q9Y4Y8 U6 snRNA-associated Sm-like protein LSm6 [Mus musculus] (88416.m06674)
3574	Not regulated	NC-NC-NC	251425_at	Al3g60210	lactose permease-related contains weak similarity to Lactose permease (Lactose-proton symport) (Lactose transport protein). (Swiss-Prot:Q33814) [Staphylococcus xylosum] (88416.m06708)
3575	Not regulated	NC-NC-NC	251426_at	Al3g60180	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (88416.m06709)
3576	Not regulated	NC-NC-NC	251427_at	Al3g60130	chloroplast chaperonin 10, putative similar to chloroplast chaperonin 10 Gi:14041813 from [Arabidopsis thaliana] (88416.m06728)
3577	Not regulated	NC-NC-NC	251428_at	Al3g60190	uridylylate kinase, putative / uridine monophosphate kinase (UMP kinase) (UMP/CMP kinase) (Swiss-Prot:Q04805) [Arabidopsis thaliana] (GI:18757866) [Prunus serotina]; identical to cDNA YLS1 mRNA for beta-glucosidase, partial cds Gi:13122279 (88416.m06714)
3578	Not regulated	NC-NC-NC	251429_at	Al3g60290	glycosyl hydrolase family 1 protein / beta-glucosidase, putative (YLS1) contains Pfam PF00232: Glycosyl hydrolase family 1 domain, TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to amygdalin hydrolase isoform AH1 precursor (GI:18757866) [Prunus serotina]; identical to cDNA YLS1 mRNA for beta-glucosidase, partial cds Gi:13122279 (88416.m06714)
3579	Not regulated	NC-NC-NC	251403_at	Al3g60300	dynamitin-like protein E (DL1E) nearly identical to dynamitin-like protein E [Arabidopsis thaliana] Gi:19423872; contains Pfam profiles PF01031: Dynamitin central region, PF00350: Dynamitin family, PF02212: Dynamitin GTPase effector domain (88416.m06724)
3580	Not regulated	NC-NC-NC	251408_at	Al3g60340	oxido-reductase, 2OG-Fe(II) oxygenase family protein similar to flavonol synthase 1 [SPIQ86330], gibberellin 20-oxidase (GI:9791198); contains PF03171 2OG-Fe(II) oxygenase superfamily domain (88416.m06738)
3581	Not regulated	NC-NC-NC	251409_at	Al3g60245	RWD domain-containing protein contains weak similarity to RING finger protein 25 (RING finger protein AOT) [Swiss-Prot:Q8QZRO] [Mus musculus] (88416.m06740)
3582	Not regulated	NC-NC-NC	251411_at	Al3g60250	palmitoyl protein thioesterase family protein palmitoyl-protein thioesterase precursor, Mus musculus, EMBL:AF071025 (88416.m06745)
3583	Not regulated	NC-NC-NC	251422_at	Al3g60540	80S ribosomal protein L37a (RPL37aC) (88416.m06733)
3584	Not regulated	NC-NC-NC	251400_at	Al3g60420	casein kinase II beta chain, putative (CKB3) similar to casein kinase II beta-3 chain (CK II) [Arabidopsis thaliana SWISS-PROT:Q81275 (88416.m06734)]
3585	Not regulated	NC-NC-NC	251369_at	Al3g60480	sec63 beta family protein similar to SPIP52870 Protein transport protein SEC61 beta 1 subunit [Saccharomyces cerevisiae]; contains Pfam profile PF03911: Sec63 beta family (88416.m06771)
3586	Not regulated	NC-NC-NC	251376_at	Al3g60630	expressed protein (88416.m06758)
3587	Not regulated	NC-NC-NC	251386_at	Al3g60800	scarecrow transcription factor family protein contains DHHC zinc finger domain PF01529 (88416.m06801)

3588	Not regulated	NC-NC-NC	251391_at	A13g608910	expressed protein low similarity to PIR146078 endothelin converting enzyme from <i>Bos primigenius taurus</i> (68416.m06814) autophagy 8g (APG8g) identical to autophagy 8g [Arabidopsis thaliana] GI:19912163; contains Pfam profile PF02991; Microtubule associated protein 1A/1B, light chain 3; supporting cDNA gl119912162[dbj AB073181.1] (68416.m06785)
3589	Not regulated	NC-NC-NC	251393_at	A13g60640	20S proteasome beta subunit F1 (PBF1) (68416.m06804)
3590	Not regulated	NC-NC-NC	251337_at	A13g60820	actin-related protein 7 (ARP7) identical to actin-related protein 7 (ARP7) [Arabidopsis thaliana] GI:21427489; contains Pfam profile PF00022; Actin (68416.m06805)
3591	Not regulated	NC-NC-NC	251340_at	A13g60830	40S ribosomal protein S13 (RPS13A) AIRPS13A mRNA for cytoplasmic ribosomal protein S13, <i>Arabidopsis thaliana</i> .AB031739 (68416.m06798)
3592	Not regulated	NC-NC-NC	251341_at	A13g60770	auxin-responsive family protein similar to auxin-induced protein SAUR-AC1 (GP:546362) (PIR:T08084)[<i>Arabidopsis thaliana</i>] PIR:T08084 (68416.m06790)
3593	Not regulated	NC-NC-NC	251342_at	A13g60690	penicillin-binding protein (PBP) repeat-containing protein contains Pfam profile PF01535; PPR repeat (68416.m06824)
3594	Not regulated	NC-NC-NC	251346_at	A13g60980	peroxisomal biogenesis factor 11 family protein / PEX11 family protein contains Pfam PF05648; Peroxisomal biogenesis factor 11 (PEX11) (68416.m06835)
3595	Not regulated	NC-NC-NC	251352_at	A13g61070	fructosamine kinase family protein contains Pfam PF03831; Fructosamine kinase (68416.m06836)
3596	Not regulated	NC-NC-NC	251353_at	A13g61080	expressed protein contains Pfam profile PF04396; Protein of unknown function, DUF537 (68416.m06838)
3597	Not regulated	NC-NC-NC	251355_at	A13g61100	U-box domain-containing protein several hypothetical proteins - <i>Arabidopsis thaliana</i> (68416.m06871)
3598	Not regulated	NC-NC-NC	251334_at	A13g61390	thioesterase family protein contains Pfam profile PF03061; thioesterase family protein (68416.m06849)
3599	Not regulated	NC-NC-NC	251307_at	A13g61200	short-chain dehydrogenase/reductase (SDR) family protein similar to carbonyl reductase Gl:1049108 from [<i>Mus musculus</i>] (68416.m06851)
3600	Not regulated	NC-NC-NC	251309_at	A13g61220	zinc finger (C3HC4-type RING finger) family protein low similarity to RNFB protein [<i>Mus musculus</i>] GI:20530241; contains Pfam profile PF00097; Zinc finger, C3HC4 type (RING finger) (68416.m06847)
3601	Not regulated	NC-NC-NC	251314_at	A13g61180	zinc finger (C3HC4-type RING finger) family protein (BRH1) identical to BRH1 RING finger protein [<i>Arabidopsis thaliana</i>] GI:4889366; identical to cDNA BRH1 RING finger protein, GI:4889365
3602	Not regulated	NC-NC-NC	251321_at	A13g61460	delta-8 sphingolipid desaturase (SLD1) identical to delta-8 sphingolipid desaturase Gl:3819710 from [<i>Arabidopsis thaliana</i>]; contains Pfam profile PF00487; Fatty acid desaturase; contains Pfam profile PF00173; Heme/Staroid binding domain (68416.m06897)
3603	Not regulated	NC-NC-NC	251323_at	A13g61580	plasma membrane intrinsic protein 1A (PIP1A) / aquaporin PIP1.1 (PIP1.1) (AQ1) identical to plasma membrane intrinsic protein 1A SP:P43285 from [<i>Arabidopsis thaliana</i>] (68416.m06880)
3604	Not regulated	NC-NC-NC	251324_at	A13g61430	chlorophyll A-B binding protein (LHCA2) identical to LHCA2 protein [<i>Arabidopsis thaliana</i>] GI:4741940; similar to chlorophyll A-B binding protein, chloroplast [Precursor] SP:P13989 from [<i>Petunia hybrida</i>]; contains Pfam profile: PF00504 chlorophyll A-B binding protein (68416.m06884)
3605	Not regulated	NC-NC-NC	251325_s_at	A13g61470	zinc finger (C3HC4-type RING finger) family protein similar to RING-H2 zinc finger protein ATL6 [<i>Arabidopsis thaliana</i>] GI:4828403; contains Pfam profile PF00097; Zinc finger, C3HC4 type (RING finger) (68416.m06894)
3606	Not regulated	NC-NC-NC	251330_at	A13g61550	expressed protein contains Pfam domain, PF02681; Uncharacterized BCR, COG1963 (68416.m06929)
3607	Not regulated	NC-NC-NC	251285_at	A13g61770	exonuclease RRP41 (RRP41) identical to exonuclease RRP41 [<i>Arabidopsis thaliana</i>] GI:6164938 (68416.m06908)
3608	Not regulated	NC-NC-NC	251288_at	A13g61820	serine protease inhibitor, Kazal-type family protein contains Pfam domain PF00050; Kazal-type serine protease inhibitor domain (68416.m06961)
3609	Not regulated	NC-NC-NC	251300_at	A13g61880	peptidyl-prolyl cis-trans isomerase, chloroplast / cyclophilin / rotamase / cyclosporin A-binding protein (ROCA) identical to peptidyl-prolyl cis-trans isomerase, chloroplast precursor, PPIase (cyclophilin, cyclosporin A-binding protein) [<i>Arabidopsis thaliana</i>] SWISS-PROT:P34791; identical to cDNA nuclear-encoded chloroplast stromal cyclophilin (ROCA) GI:405130 (68416.m06987)
3610	Not regulated	NC-NC-NC	251305_at	A13g62030	arginine/serine-rich splicing factor RSP31 (RSP31) identical to SLIP92864 Arginine/serine-rich splicing factor RSP31 [<i>Arabidopsis thaliana</i>] (68416.m06947)
3611	Not regulated	NC-NC-NC	251242_at	A13g61860	expressed protein; expression supported by MPSS (68416.m06982)
3612	Not regulated	NC-NC-NC	251247_at	A13g62140	zinc finger (C2H2 type) family protein contains Pfam PF00096; Zinc finger, C2H2 type (68416.m06992)
3613	Not regulated	NC-NC-NC	251253_at	A13g62240	anion exchange family protein contains similarity to anion exchanger 3, cardiac splice form - <i>Rattus norvegicus</i> , PIR:A42487 (68416.m06996)
3614	Not regulated	NC-NC-NC	251254_at	A13g62270	protein phosphatase 2C, putative / PP2C, putative phosphoprotein phosphatase (EC 3.1.3.16) 1A-alpha - <i>Homo sapiens</i> , PIR:S22423 (68416.m06994)
3615	Not regulated	NC-NC-NC	251259_at	A13g62260	RNA helicase, putative similar to SLIP53131 Pre-mRNA splicing factor RNA helicase PRP43 (Helicase JA1) (<i>Saccharomyces cerevisiae</i>); contains Pfam profiles PF04408; Helicase associated domain (HA2), PF00271; Helicase conserved C-terminal domain (68416.m07000)
3616	Not regulated	NC-NC-NC	251265_at	A13g62310	expressed protein (68416.m07005)
3617	Not regulated	NC-NC-NC	251269_at	A13g62360	expressed protein (68416.m07008)
3618	Not regulated	NC-NC-NC	251270_at	A13g62370	bZIP transcription factor family protein similar to common plant regulatory factor 8 (G1:9650828 from [<i>Petroselinum crispum</i>] (68416.m07012)
3619	Not regulated	NC-NC-NC	251237_at	A13g62420	expressed protein (68416.m07015)
3620	Not regulated	NC-NC-NC	251240_at	A13g62450	expressed protein contains Pfam profile PF04396; Protein of unknown function, DUF537 (68416.m07017)
3621	Not regulated	NC-NC-NC	251241_s_at	A13g62460	GTP-binding protein, putative similar to GTP-binding protein SAR1A (SP:Q04834) [<i>Arabidopsis thaliana</i>]; small GTP-binding protein Bsa1a - <i>Brassica campestris</i> , EMBL:U55035 (68416.m07028)
3622	Not regulated	NC-NC-NC	251217_at	A13g62560	expressed protein (68416.m07030)
3623	Not regulated	NC-NC-NC	251222_at	A13g62580	double-stranded RNA-binding domain (DRBD)-containing protein weak similarity to SLIP19525 Interferon-induced, double-stranded RNA-activated protein kinase (EC 2.7.1.-) (<i>Homo sapiens</i>); contains Pfam profile PF00035; Double-stranded RNA binding motif (68416.m07055)
3624	Not regulated	NC-NC-NC	251233_at	A13g62800	mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein contains Pfam PF02460; mitochondrial import inner membrane translocase subunit Tim17 (68416.m07084)
3625	Not regulated	NC-NC-NC	251208_at	A13g62880	expressed protein (68416.m07035)
3626	Not regulated	NC-NC-NC	251183_at	A13g62630	

3627	Not regulated	NC-NC-NC	251185_at	A13g62870	60S ribosomal protein L7A (RPL7aB) 60S RIBOSOMAL PROTEIN L7A - <i>Oryza sativa</i> , SWISSPROT:RL7A_ORYSA (68416.m07063)
3628	Not regulated	NC-NC-NC	251186_at	A13g62790	NADH-ubiquinone oxidoreductase-related contains weak similarity to NADH-ubiquinone oxidoreductase 15 kDa subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex 1-15 kDa) (Ci-15 kDa) (Swiss-Prot:Q43920) [Homo sapiens] (68416.m07054)
3629	Not regulated	NC-NC-NC	251189_at	A13g62850	expressed protein putative mitochondrial carrier protein A2q47480 - Arabidopsis thaliana, EMBL:AC002535 (68416.m07037)
3630	Not regulated	NC-NC-NC	251192_at	A13g62720	galactosyl transferase GMA12/MNN10 family protein low similarity to alpha-1,2-galactosyltransferase, <i>Schizosaccharomyces pombe</i> [SPIQ09174] (68416.m07045)
3631	Not regulated	NC-NC-NC	251198_at	A13g62970	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain PF00097, Zinc finger, C3HC4 type (RING finger) (68416.m07074)
3632	Not regulated	NC-NC-NC	251205_at	A13g63080	glutathione peroxidase, putative phospholipid-hydroperoxide glutathione peroxidase, spinach, PIR:JC5818 (68416.m07085)
3633	Not regulated	NC-NC-NC	251150_at	A13g63120	Cydl family protein similar to cydl 2 [Trypanosoma brucei] (GI:7339572, cydl 6 [Trypanosoma cruzi] (GI:12005317, contains Pfam profile PF00134; Cydlin, N-terminal domain (68416.m07089)
3634	Not regulated	NC-NC-NC	251151_at	A13g63170	expressed protein (68416.m07095)
3635	Not regulated	NC-NC-NC	251153_at	A13g63000	NPL4 family protein contains Pfam domain, PF05021; NPL4 family (68416.m07077)
3636	Not regulated	NC-NC-NC	251155_at	A13g63160	expressed protein (68416.m07083)
3637	Not regulated	NC-NC-NC	251158_at	A13g63150	GTP-binding protein-related low similarity to SPIQ38912 RAC-like GTP binding protein ARAC3 (GTP-binding protein ROP6) (Arabidopsis thaliana); contains Pfam profile PF00036; EF hand (domain) (68416.m07092)
3638	Not regulated	NC-NC-NC	251161_at	A13g63290	expressed protein low similarity to N-methyl-D-aspartate receptor-associated protein [Drosophila melanogaster] (GI:587104; expressed protein (68416.m07113)
3639	Not regulated	NC-NC-NC	251163_at	A13g63310	contains Pfam profile PF01027; Uncharacterized protein family UPF0005 (68416.m07121)
3640	Not regulated	NC-NC-NC	251169_at	A13g63210	expressed protein identical to senescence-associated protein SAG102 (GI:22331931) [Arabidopsis thaliana] (unpublished); contains Pfam profile PF04570; Protein of unknown function (DUF581) (68416.m07101)
3641	Not regulated	NC-NC-NC	251170_at	A13g63260	protein kinase, putative (MRK1) identical to ATM/K1 [Arabidopsis thaliana] (gi2351097) [idjBA322079 (68416.m07108)
3642	Not regulated	NC-NC-NC	251171_at	A13g63220	kelch repeat-containing F-box family protein contains Pfam profiles PF01344; Kelch motif, PF00946; F-box domain (68416.m07102)
3643	Not regulated	NC-NC-NC	251172_at	A13g63190	ribosome recycling factor, chloroplast, putative / ribosome releasing factor, chloroplast, putative similar to SPIP82231 Ribosome recycling factor, chloroplast precursor (Ribosome releasing factor, chloroplast) (RRF) (CpFm) (RRFHCP) [Spinacia oleracea]; contains Pfam profile PF01765; ribosome recycling factor (68416.m07098)
3644	Not regulated	NC-NC-NC	251178_at	A13g63380	calcium-transporting ATPase, ATPase, plasma membrane-type, putative / Ca(2+)-ATPase, putative (ACA12) identical to SPIQ8LY77 Potential calcium-transporting ATPase 12, plasma membrane-type (EC 3.6.3.8) (Ca(2+)-ATPase isoform 12) (Arabidopsis thaliana); similar to SPIQ8LF79 Calcium-transporting ATPase 8, plasma membrane-type (EC 3.6.3.8) (Ca2+-ATPase, isoform 8) (Arabidopsis thaliana); contains InterPro Accession IPR006068; Carbon transporting ATPase (68416.m07135)
3645	Not regulated	NC-NC-NC	251177_at	A13g63400	peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein similar to cyclophilin [Digitalis lanata] (GI:1563719; contains Pfam profile PF00160; peptidyl-prolyl cis-trans isomerase, cyclophilin-type; contains A1-donor splice site at intron 9 (68416.m07137)
3646	Not regulated	NC-NC-NC	251145_at	A13g63500	expressed protein (68416.m07152)
3647	Not regulated	NC-NC-NC	251148_at	A13g63520	9-cis-epoxycarotenoid dioxygenase / neoxanthin cleavage enzyme / NCED1 / carotenoid cleavage dioxygenase 1 (CCD1) identical to putative 9-cis-epoxy-carotenoid dioxygenase (GI:3086810); contains Pfam profile PF03055; Retinal pigment epithelial membrane protein (68416.m07155)
3648	Not regulated	NC-NC-NC	251117_at	A13g63380	expressed protein (68416.m07136)
3649	Not regulated	NC-NC-NC	251121_at	A13g63420	heterotrimeric G protein gamma-subunit (AGG1) (68416.m07140)
3650	Not regulated	NC-NC-NC	251125_at	A15g01060	protein kinase family protein contains eukaryotic protein kinase domain, INTERPRO:IPR000719 (68416.m00009)
3651	Not regulated	NC-NC-NC	251138_at	A15g01160	e-cadherin binding protein-related contains weak similarity to E-cadherin binding protein E7 [Mus musculus]
3652	Not regulated	NC-NC-NC	251142_at	A15g01015	GPI9822093gpiAFAF89617 (68416.m00020)
3653	Not regulated	NC-NC-NC	251089_at	A15g01380	expressed protein (68416.m00003)
3654	Not regulated	NC-NC-NC	251091_at	A15g01410	DNAJ heat shock protein, putative similar to SPIQ8QYJ3 DnaJ homolog subfamily B member 1 (Heat shock 40 kDa protein 1) (Mus musculus); contains Pfam profile PF00226; DnaJ domain (68416.m00052)
3655	Not regulated	NC-NC-NC	251094_at	A15g01350	stress-responsive protein, putative similar to ethylene-inducible protein HEVER [Hvea brasiliensis] SWISS-PROT:Q39863 (68416.m00054)
3656	Not regulated	NC-NC-NC	251106_at	A15g01500	expressed protein (68416.m00048)
3657	Not regulated	NC-NC-NC	251108_at	A15g01620	mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein (68416.m00064)
3658	Not regulated	NC-NC-NC	251082_at	A15g01530	expressed protein several hypothetical proteins - Arabidopsis thaliana (68416.m00077)
3659	Not regulated	NC-NC-NC	251058_at	A15g01790	chlorophyll A-B binding protein CP29 (LHC84) identical to CP29 [Arabidopsis thaliana] (GI:298036; contains Pfam profile: PF00504 chlorophyll A-B binding protein (68416.m00098)
3660	Not regulated	NC-NC-NC	251077_at	A15g01980	expressed protein (68416.m00098)
3661	Not regulated	NC-NC-NC	251022_at	A15g02150	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (68416.m00117)
3662	Not regulated	NC-NC-NC	251028_at	A15g02050	expressed protein (68416.m00136)
3663	Not regulated	NC-NC-NC	251032_at	A15g02030	mitochondrial glycoprotein family protein / MAM33 family protein low similarity to SUAPRGA1 [Emeticella nidulans] (GI:6562378; contains Pfam profile PF02330; Mitochondrial glycoprotein (68416.m00126)
3664	Not regulated	NC-NC-NC	251034_at	A15g02040	homeodomain protein (BELLINGER) several homeodomain proteins; (68416.m00123)
3665	Not regulated	NC-NC-NC	251037_at	A15g02100	prenylated rab acceptor (PRA1) family protein contains Pfam PF03208; PRA1 family protein (68416.m00124)
3666	Not regulated	NC-NC-NC	251038_at	A15g02240	oxysterol-binding family protein similar to SWH1 [Saccharomyces cerevisiae] (GI:402658; contains Pfam profile PF01237; Oxysterol-binding protein (68416.m00131)

3667	Not regulated	NC-NC-NC	251048_at	A15g02410	DIE2/ALG10 family contains Pfam PF04922; DIE2/ALG10 family (68418.m00164) metallothionein protein 2B (MT-2B) identical to SWISS-PROT:Q38805 metallothionein-like protein 2B (MT-2B) [Arabidopsis thaliana] (68418.m00161)
3668	Not regulated	NC-NC-NC	250981_at	A15g02380	expansin, putative (EXP6) similar to expansin precursor Gl:4138914 from [Lycopersicon esculentum]; alpha-expansin gene family, thaliana] (68418.m00161)
3669	Not regulated	NC-NC-NC	250982_at	A15g02280	PMID:11841069 (68418.m00148)
3670	Not regulated	NC-NC-NC	250983_at	A15g02280	syndecin, putative similar to Swiss-Prot Q9ES56 syndecin (TRSD3 homolog) [Mus musculus] (68418.m00151)
3671	Not regulated	NC-NC-NC	250986_at	A15g02820	ankyrin repeat family protein contains ankyrin repeat domains, Pfam:PF00023 (68418.m00198)
3672	Not regulated	NC-NC-NC	251008_at	A15g02710	expressed protein contains Pfam PF03692; Uncharacterized protein family (UPF0153) (68418.m00210)
3673	Not regulated	NC-NC-NC	251011_at	A15g02560	histone H2A, putative similar to histone H2A from Pisum sativum SPIP25470, Zea mays SPIP40280, Petroselinum crispum SPIP19177; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4 (68418.m00180)
3674	Not regulated	NC-NC-NC	251013_at	A15g02540	short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily (68418.m00188)
3675	Not regulated	NC-NC-NC	250987_at	A15g02850	hydroxyproline-rich glycoprotein family protein (68418.m00228)
3676	Not regulated	NC-NC-NC	250988_at	A15g02880	HECT-domain-containing protein / ubiquitin-transferase family protein / armadillo-beta-catenin-like repeat-containing protein similar to SPIQ14869 Thyroid receptor interacting protein 12 (TRIP12) (Homo sapiens); contains Pfam profiles PF00632; HECT-domain (ubiquitin-transferase), PF00514; Armadillo-beta-catenin-like repeat (68418.m00231)
3677	Not regulated	NC-NC-NC	250987_at	A15g02790	In2-1 protein, putative similar to In2-1, Zea mays; EMBL:X58573 (68418.m00221)
3678	Not regulated	NC-NC-NC	250971_at	A15g02810	pseudo-response regulator 7 (APRR7) identical to pseudo-response regulator 7 Gl:10281004 from [Arabidopsis thaliana] (68418.m00223)
3679	Not regulated	NC-NC-NC	250972_at	A15g02840	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA binding domain (68418.m00226)
3680	Not regulated	NC-NC-NC	250928_at	A15g03320	ethylene-insensitive 2 (EIN2) identical to EIN2 [Arabidopsis thaliana] gl:5231113gl:AA041076; member of the natural resistance-associated macrophage protein (NRAIP) metal transporter family, PMID:11500563; metal transport capacity has not been shown, PMID:11500563, PMID:1038174 (68418.m00277)
3681	Not regulated	NC-NC-NC	250929_at	A15g03290	isocitrate dehydrogenase, putative / NAD+ isocitrate dehydrogenase, putative strong similarity to isocitrate dehydrogenase (NAD+) (Nicotiana tabacum) Gl:3021506 (68418.m00278)
3682	Not regulated	NC-NC-NC	250931_at	A15g03200	zinc finger (C3HC4-type RING finger) family protein contains weak similarity to zinc finger proteins (68418.m00268)
3683	Not regulated	NC-NC-NC	250932_s_at	A15g03220	transcriptional co-activator-related contains weak similarity to CoRator required for Sp1 transcriptional activation subunit 9 (Transcriptional co-activator CRSP33) (RNA polymerase transcriptional regulation mediator subunit 7 homolog) (HIMED7) (Activator-repressed cofactor 34 kDa component) (ARCS4) (Swiss-Prot:O43513) [Homo sapiens] (68418.m00270)
3684	Not regulated	NC-NC-NC	250934_at	A15g03030	DNAJ heat shock N-terminal domain-containing protein contains Pfam profile PF00226 DNAJ domain; DNAJ domain-containing protein kinase, putative similar to serine/threonine protein kinase NAK [Arabidopsis thaliana] SWISS-PROT:PA3293 (68418.m00283)
3685	Not regulated	NC-NC-NC	250941_at	A15g03320	Ras-related GTP-binding protein, putative similar to GTP-binding protein Gl:871508 from [Pisum sativum] (68418.m00308)
3686	Not regulated	NC-NC-NC	250954_at	A15g03520	expressed protein (68418.m00302)
3687	Not regulated	NC-NC-NC	250921_at	A15g03480	rhodanese-like domain-containing protein contains Rhodanese-like domain PF:00581 (68418.m00301)
3688	Not regulated	NC-NC-NC	250923_at	A15g03455	phosphadenosine phosphosulfate (PAPS) reductase family protein low similarity to SPIP38913 FAD synthetase (EC 2.7.7.2) (Saccharomyces cerevisiae); contains Pfam profiles PF01507; Phosphadenosine phosphosulfate reductase family, PF00694; Probable molybdopterin binding domain (68418.m00296)
3689	Not regulated	NC-NC-NC	250987_at	A15g03430	cell division cycle protein 48, putative / CDC48, putative very strong similarity to SPIP54609 Cell division cycle protein 48 homolog (Arabidopsis thaliana); contains Pfam profiles PF00004; ATPase AAA family, PF02358; Cell division protein 48 (CDC48) N-terminal domain; supporting cDNA gl:26449351dbjAK117125-1] (68418.m00286)
3690	Not regulated	NC-NC-NC	250899_at	A15g03340	serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B' (B'alpha) similar to SWISS-PROT:Q28653 serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, delta isoform (PP2A, B subunit, B' delta isoform, PP2A, B subunit, B56 delta isoform, PP2A, B subunit, PR61 delta isoform, PP2A, B subunit, R5 delta isoform, PP2A, B subunit, B-gamma) [Oryctolagus cuniculus]; contains Pfam domain, PF01603; Protein phosphatase 2A regulatory B subunit (B56 family) (68418.m00303)
3691	Not regulated	NC-NC-NC	250900_at	A15g03470	zinc finger (C2H2 type) family protein contains Pfam domain, PF00086; Zinc finger, C2H2 type (68418.m00335)
3692	Not regulated	NC-NC-NC	250912_at	A15g03740	monodehydroascorbate reductase, putative monodehydroascorbate reductase (NADH), cucumber, PIR:J00182 (68418.m00322)
3693	Not regulated	NC-NC-NC	250916_at	A15g03630	expressed protein low similarity to outer surface protein F [Borrelia burgdorferi] Gl:466482; contains Pfam profile PF04948; Family of unknown function (DUF662) (68418.m00325)
3694	Not regulated	NC-NC-NC	250919_at	A15g03660	HesB-like domain-containing protein low similarity to HesB [Cyanospora sp. PCC 8801] Gl:2183308; contains Pfam profile PF01521; HesB-like domain (68418.m00370)
3695	Not regulated	NC-NC-NC	250886_at	A15g03905	palatin-related contains Palatin domain PF01734 (68418.m00384)
3696	Not regulated	NC-NC-NC	250877_at	A15g04040	F-box family protein predicted proteins, Arabidopsis thaliana (68418.m00377)
3697	Not regulated	NC-NC-NC	250883_at	A15g03970	signal recognition particle 54 kDa protein, chloroplast / SRP54 (54 chloroplast protein) (S4CP) (FFC) [Arabidopsis thaliana] recognition particle 54 kDa protein, chloroplast precursor (SRP54) (54 chloroplast protein) (S4CP) (FFC) [Arabidopsis thaliana] (68418.m00374)
3698	Not regulated	NC-NC-NC	250884_at	A15g03940	expressed protein (68418.m00441)
3699	Not regulated	NC-NC-NC	250886_at	A15g04440	phosphatidate cytidyltransferase family protein contains Pfam profile: PF01148 phosphatidate cytidyltransferase (68418.m00448)
3700	Not regulated	NC-NC-NC	250842_at	A15g04480	KH domain-containing protein NOVA, putative astrocytic NOVA-like RNA-binding protein, Homo sapiens, U70477 (68418.m00437)
3701	Not regulated	NC-NC-NC	250843_at	A15g04430	expressed protein (68418.m00445)
3702	Not regulated	NC-NC-NC	250844_at	A15g04470	RNA recognition motif (RRM)-containing protein contains InterPro entry IPR000504; RNA-binding region RNP-1 (RNA recognition motif) (RRM) (68418.m00460)
3703	Not regulated	NC-NC-NC	250845_at	A15g04600	

3704 Not regulated	250848_at	NC-NC-NC	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) protein; supporting cDNA
3705 Not regulated	250856_at	NC-NC-NC	gib8456750(gib)AF201456 (68418.m00433)
3706 Not regulated	250858_at	NC-NC-NC	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile: PF01535 PPR repeat (68418.m00503)
			myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain (68418.m00490)
3707 Not regulated	250862_s_at	NC-NC-NC	40S ribosomal protein S17 (RPS17D) 40S ribosomal protein S17, Lycopersicon esculentum, EMBL:AF161704 (68418.m00498)
			F1FO-ATPase inhibitor protein, putative similar to F1FO-ATPase inhibitor protein [Oryza sativa (japonica cultivar-group)]
3708 Not regulated	250863_at	NC-NC-NC	gij5106371(gij)BAAB1661 (68418.m00498)
3709 Not regulated	250829_at	NC-NC-NC	disease resistance protein (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists, suggestive of a disease
			resistance protein, (68418.m00482)
3710 Not regulated	250811_t_at	NC-NC-NC	cysteine protease inhibitor, putative / cystatin, putative similar to cysteine protease inhibitor [Glycine max] Gi:1944342; contains Pfam profile PF00031: Cystatin domain (68418.m00542)
			short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily (68418.m00515)
3711 Not regulated	250812_at	NC-NC-NC	translocase of chloroplast 34 (TOC34) / GTP-binding protein (OEP34) contains Pfam PF04548: AIG1 family; contains TIGRFAM TIGR00891: GTP-binding protein and TIGR00231: small GTP-binding protein domain; 99.7% identical to atToc34 protein (Gi:11557975) [Arabidopsis thaliana]; similar to Chlamy. A. Pea Toc34 - A Novel GTPase Of The Chloroplast Protein Translocon (Gi:1885556) [Pisum sativum]; almost identical to SP-Q38906 Translocase of chloroplast 34; identical to cDNA GTP-binding protein (OEP34) Gi:1151243 (68418.m00529)
3712 Not regulated	250813_at	NC-NC-NC	ubiquitin-conjugating enzyme, putative similar to SPIQ18763 Ubiquitin-conjugating enzyme E2-24 kDa (EC 6.3.2.19) (Ubiquitin-protein ligase) (Ubiquitin carrier protein) (Homo sapiens); contains Pfam profile PF00178: Ubiquitin-conjugating enzyme (68418.m00539)
			expressed protein (68418.m00537)
3713 Not regulated	250814_at	NC-NC-NC	expressed protein (68418.m00537)
3714 Not regulated	250815_s_at	NC-NC-NC	clathrin adaptor complexes medium subunit-related contains pfam profile: PF00928 adaptor complexes medium subunit family (68418.m00532)
3715 Not regulated	250816_at	NC-NC-NC	ABC1 family protein contains Pfam domain, PF03109: ABC1 family (68418.m00554)
3716 Not regulated	250824_at	NC-NC-NC	outer membrane OMP85 family protein contains Pfam profile PF01103: outer membrane protein, OMP85 family (68418.m00588)
			expressed protein (68418.m00623)
3717 Not regulated	250792_at	NC-NC-NC	26S proteasome non-ATPase regulatory subunit 7, putative / 26S proteasome regulatory subunit S12, putative / MOV34 protein, putative contains similarity to 26S proteasome regulatory subunit s12 (proteasome subunit p40) (mov34 protein) SP-P26516 from [Mus musculus]; contains Pfam profile PF01396: Mov34/MNP/PAD-1 family (68418.m00636)
3718 Not regulated	250768_at	NC-NC-NC	UDP-glucuronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase (68418.m00644)
3719 Not regulated	250742_at	NC-NC-NC	UDP-glucuronosyl/UDP-glucosyl transferase 1 / arginyltransferase 1 / arginyl-RNA-protein transferase 1 (ATE1) identical to SPIQ92749 arginine-RNA-protein transferase 1 (EC 2.3.2.8) (R-transferase 1) (Arginyltransferase 1) (Arginyl-RNA-protein transferase 1) (Arabidopsis thaliana) (68418.m00627)
3720 Not regulated	250749_at	NC-NC-NC	dihydrodipicolinate synthetase/polyphosphatase synthetase (dhfr/pdp2 gene) Gi:17876704 (68418.m00682)
3721 Not regulated	250753_at	NC-NC-NC	eukaryotic translation initiation factor 3G, putative / eIF-3g, putative similar to eukaryotic translation initiation factor 3g [Arabidopsis thaliana] Gi:12407751; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) (68418.m00665)
3722 Not regulated	250754_at	NC-NC-NC	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage/LTP family domain PF00234 (68418.m00659)
3723 Not regulated	250757_at	NC-NC-NC	guanylyl cyclase-related (GC1) similar to guanylyl cyclase (GC1) Gi:21436488 from [Arabidopsis thaliana]; identical to cDNA putative guanylate cyclase Gi:21436486 (68418.m00655)
			expressed protein (68418.m00658)
3724 Not regulated	250758_at	NC-NC-NC	DNA J heat shock N-terminal domain-containing protein / cell division protein-related similar to GISA [Volvox carter] f. nagantensis] Gi:4633129; contains Pfam profiles PF00226 DnaJ domain, PF00249 Myb-like DNA-binding domain (68418.m00679)
3725 Not regulated	250764_at	NC-NC-NC	chaperone protein dnaJ-related similar to unknown protein (pif1T00468); contains Pfam PF00684 : DnaJ central domain (4 repeats) (68418.m00681)
3726 Not regulated	250765_at	NC-NC-NC	phox (PX) domain-containing protein similar to SPQ60749 Sorting nexin 2 (Homo sapiens); contains Pfam profile PF00787: PX domain (68418.m00683)
3727 Not regulated	250707_at	NC-NC-NC	RNA-binding protein, putative contains similarity to RNA-binding protein from [Nicotiana tabacum] Gi:15822703, [Nicotiana sylvestris] Gi:624925, [Solanum tuberosum] Gi:15822705; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) (68418.m00693)
3728 Not regulated	250711_at	NC-NC-NC	lysine decarboxylase family protein contains Pfam profile PF00641: lysine decarboxylase family (68418.m00708)
3729 Not regulated	250713_at	NC-NC-NC	thioredoxin-related contains weak similarity to Swiss-Prot:Q9SEU7 thioredoxin M-type 3, chloroplast precursor (TRX-M3) [Arabidopsis thaliana] (68418.m00720)
3730 Not regulated	250714_at	NC-NC-NC	expressed protein (68418.m00702)
3731 Not regulated	250721_at	NC-NC-NC	expressed protein similar to unknown protein (pif1T08447) (68418.m00703)
3732 Not regulated	250723_at	NC-NC-NC	zinc finger (CCHC-type/C3HC4-type RING finger) family protein contains Pfam domains PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar) and PF00097: Zinc finger, C3HC4 type (RING finger) (68418.m00718)
3733 Not regulated	250727_at	NC-NC-NC	ribosomal protein S8a family protein contains Pfam profile PF01201: Ribosomal protein S8a (68418.m00712)
3734 Not regulated	250734_at	NC-NC-NC	
3735 Not regulated	250735_at	NC-NC-NC	
3736 Not regulated	250736_s_at	NC-NC-NC	
3737 Not regulated	250703_at	NC-NC-NC	

3738	Not regulated	NC-NC-NC	250675_at	A15g06280	nucleolar protein-related contents weak similarity to nucleolar protein CTC (GI:13540302) [Rattus norvegicus] (68418.m00700)
3739	Not regulated	NC-NC-NC	250680_at	A15g06570	expressed protein similar to PMc3 [Pinus radiata] (GI:5487873) (68418.m00741)
3740	Not regulated	NC-NC-NC	250682_x_at	A15g06630	proline-rich extensin-like family protein contains proline-rich extensin domains, INTERPRO:IPR002985 (68418.m00749)
3741	Not regulated	NC-NC-NC	250683_x_at	A15g06640	proline-rich extensin-like family protein contains proline-rich extensin domains, INTERPRO:IPR002985 (68418.m00750)
3742	Not regulated	NC-NC-NC	250687_at	A15g06660	expressed protein contains PF05809: Eukaryotic protein of unknown function (DUF841) (68418.m00752)
3743	Not regulated	NC-NC-NC	250692_at	A15g06560	expressed protein contains Pfam profile PF04576: Protein of unknown function, DUF593 (68418.m00740)
3744	Not regulated	NC-NC-NC	250643_at	A15g06780	enry1 N terminus domain-containing protein / ENT domain-containing protein contains Pfam profile PF03735: ENT domain protein phosphatase 2C family protein / PP2C family protein similar to Ser/Thr protein phosphatase 2C (PP2C6) (GI:15020818) [Arabidopsis thaliana], similar to protein phosphatase 2C (GI:3608412) [Mesembryanthemum crystallinum], contains Pfam PF00481 [Arabidopsis thaliana]
3745	Not regulated	NC-NC-NC	250644_at	A15g06750	Protein phosphatase 2C domain; (68418.m00783)
3746	Not regulated	NC-NC-NC	250649_at	A15g06690	thioredoxin family protein low similarity to SpP34723 Thioredoxin (Penicillium chrysogenum); contains Pfam profile: PF00085
3747	Not regulated	NC-NC-NC	250663_at	A15g07110	prenylated rab acceptor (PRA1) family protein weak similarity to prenylated Rab acceptor 1 (PRA1) [Homo sapiens] GI:4877285; contains Pfam profile PF03208: Prenylated rab acceptor (PRA1) (68418.m00810)
3748	Not regulated	NC-NC-NC	250687_at	A15g07090	40S ribosomal protein S4 (RPS4B) (68418.m00804)
3749	Not regulated	NC-NC-NC	250669_at	A15g06870	polygalacturonase inhibiting protein 2 (PGIP2) identical to polygalacturonase inhibiting protein 2 (PGIP2) [Arabidopsis thaliana] gi 700201 gb AAAF6882; contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611 (68418.m00777)
3750	Not regulated	NC-NC-NC	250672_at	A15g06910	DNAJ heat shock protein, putative (J6) identical to DnaJ homologue [Arabidopsis thaliana] GI:2688720; contains Pfam profile PF00226 DnaJ domain (68418.m00781)
3751	Not regulated	NC-NC-NC	250615_at	A15g07270	ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023 (68418.m00828)
3752	Not regulated	NC-NC-NC	250618_at	A15g07220	BAG domain-containing protein contains Pfam:PF02179 BAG domain (68418.m00823)
3753	Not regulated	NC-NC-NC	250621_at	A15g07250	Romboid family protein contains PFAM PF01694, Romboid family (68418.m00827)
3754	Not regulated	NC-NC-NC	250626_at	A15g07350	tudor domain-containing protein / nuclease family protein contains Pfam domains PF00567: Tudor domain and PF00565: Staphylococcal nuclease homologue (68418.m00839)
3755	Not regulated	NC-NC-NC	250627_at	A15g07360	amidase family protein low similarity to enantiomerase-selective amidase [Rhodococcus sp.] GI:152052; contains Pfam profile PF01425: Amidase (68418.m00840)
3756	Not regulated	NC-NC-NC	250607_at	A15g07370	inositol polyphosphate 6-/3-/5-kinase 2a (IPK2a) contains Pfam domain, PF03770: inositol polyphosphate kinase (68418.m00841)
3757	Not regulated	NC-NC-NC	250581_at	A15g07300	copine, putative strong similarity to BGNZA11 [Arabidopsis thaliana] GI:15487382; contains Pfam profile PF00168: C2 domain (68418.m00834)
3758	Not regulated	NC-NC-NC	250582_at	A15g07580	ethylene-responsive element-binding family protein contains similarity to ethylene responsive element binding factor 5 (AERF5) (Swiss-Prot:O80341) [Arabidopsis thaliana]; contains Pfam PF00847: AP2 domain (68418.m00868)
3759	Not regulated	NC-NC-NC	250584_at	A15g07590	WD-40 repeat protein family contains 3 WD-40 repeats (PF00400); similarity to WD-repeat protein 8 (WDR8) (SP:Q8PZS5) [Homo sapiens] (68418.m00870)
3760	Not regulated	NC-NC-NC	250590_at	A15g07710	SAPIENS (68418.m00870)
3761	Not regulated	NC-NC-NC	250604_at	A15g07830	exonuclease family protein contains exonuclease domain, Pfam:PF00929 (68418.m00884)
3762	Not regulated	NC-NC-NC	250577_at	A15g07910	glycosyl hydrolase family 79 N-terminal domain-containing protein similar to beta-glucuronidase GI:8918740 from [Scutellaria baicalensis] (68418.m00898)
3763	Not regulated	NC-NC-NC	250553_at	A15g07980	leucine-rich repeat family protein contains leucine rich repeat (LRR) domains, Pfam:PF00560 (68418.m00914)
3764	Not regulated	NC-NC-NC	250582_at	A15g08040	expressed protein contains Pfam PF03989: Uncharacterised protein family (UFP0139) (68418.m00924)
3765	Not regulated	NC-NC-NC	250583_at	A15g08050	expressed protein predicted protein, Arabidopsis thaliana (68418.m00938)
3766	Not regulated	NC-NC-NC	250564_at	A15g08060	expressed protein sigma factor F inhibitor spoliAB, Bacillus megaterium, PIR:B48402 (68418.m00940)
3767	Not regulated	NC-NC-NC	250565_at	A15g08000	glycosyl hydrolase family protein 17 similar to beta-1,3-glucanase GI:15150341 from [Camellia sinensis]; C-terminal homology only (68418.m00931)
3768	Not regulated	NC-NC-NC	250569_at	A15g08130	basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain (68418.m00946)
3769	Not regulated	NC-NC-NC	250575_at	A15g08240	expressed protein (68418.m00987)
3770	Not regulated	NC-NC-NC	250543_at	A15g08190	TATA-binding protein-associated phosphoprotein Dr1 protein, putative similar to Dr1 protein homolog (SP:P46592) [Arabidopsis thaliana]; similar to TATA-binding protein-associated phosphoprotein (Down-regulator of transcription 1) (DR1 protein) (SP:Q01858) [Homo sapiens]; contains Pfam PF00808 : Histone-like transcription factor (CBF/NFY) and archaean histone (68418.m00957)
3771	Not regulated	NC-NC-NC	250544_at	A15g08080	synlaxin, putative (SYP132) similar to SP Q8ZSD4 Synlaxin 121 (A1SYP121) (Synlaxin-related protein At-Syr1) [Arabidopsis thaliana] (68418.m00942)
3772	Not regulated	NC-NC-NC	250545_at	A15g08160	serine/threonine protein kinase, putative identical to serine/threonine protein kinase [Arabidopsis thaliana]
3773	Not regulated	NC-NC-NC	250546_at	A15g08180	gi 2109293 gb LA689123 (68418.m00952)
3774	Not regulated	NC-NC-NC	250547_at	A15g08100	ribosomal protein L7AE130w/S12e/Gadd45 family protein Similar to NHP2/L7AE family proteins, see SWISSPROT:P32465 and PMID:2063928. (68418

3778	Not regulated	NC-NC-NC	250528_at	A15g08570	pyruvate kinase, putative similar to pyruvate kinase, cytosolic isoforms [Glycine max] SWISS-PROT:Q42806 (68418.m01020) DEAD box RNA helicase (RH26) strong similarity to RNA helicase RH26 [Arabidopsis thaliana] GI:3776025; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain; identical to cDNA DEAD box RNA helicase, RH26 GI:3776024 (68418.m01024)
3779	Not regulated	NC-NC-NC	250529_at	A15g08610	GTP-binding protein LepA, putative (68418.m01023)
3780	Not regulated	NC-NC-NC	250531_at	A15g08650	expressed protein similar to unknown protein [pilT] (72191) (68418.m01016)
3781	Not regulated	NC-NC-NC	250532_at	A15g08540	D111/G-patch domain-containing protein contains Pfam profile PF01585: G-patch domain; contains a 2nt micro-exon, as identified using GeneSeqer. (68418.m01014)
3782	Not regulated	NC-NC-NC	250536_at	A15g08535	DEAD box RNA helicase (RH25) identical to RNA helicase [Arabidopsis thaliana] GI:3776023; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain (68418.m01025)
3783	Not regulated	NC-NC-NC	250538_at	A15g08620	transducin family protein / WD-40 repeat family protein contains 7 WD-40 repeats (PF00400); similar to wild die slowly protein (WDS) (SP-Q9VJL8) [Drosophila melanogaster] (68418.m01018)
3784	Not regulated	NC-NC-NC	250539_at	A15g08560	calcium-binding EF hand family protein contains INTERPRO:IPR002048 calcium-binding EF-hand domain (68418.m01021) octicosapeptidePhox/Ben1p (PB1) domain-containing protein predicted proteins, Arabidopsis thaliana and Drosophila melanogaster contains Pfam profile PF00564: PB1 domain (68418.m01113)
3786	Not regulated	NC-NC-NC	250516_at	A15g08620	pectinesterase family protein contains Pfam profile: PF01095 pectinesterase (68418.m01130)
3787	Not regulated	NC-NC-NC	250490_at	A15g09760	ribosomal protein L17 family protein contains Pfam profile: PF01198 ribosomal protein L17 (68418.m01131)
3788	Not regulated	NC-NC-NC	250495_at	A15g09770	inorganic pyrophosphatase family protein similar to SPIQ15181 inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphatase (Homo sapiens); contains Pfam profile PF00718: inorganic pyrophosphatase (68418.m01116)
3789	Not regulated	NC-NC-NC	250496_at	A15g09650	heat shock protein 70 / HSP70 (HSC70-5) identical to heat shock protein 70 [Arabidopsis thaliana] GI:6746590 (68418.m01110)
3790	Not regulated	NC-NC-NC	250502_at	A15g09590	expressed protein (68418.m01155)
3791	Not regulated	NC-NC-NC	250512_at	A15g09995	BolA-like family protein contains Pfam profile: PF01722 BolA-like protein (68418.m01137)
3792	Not regulated	NC-NC-NC	250454_at	A15g09830	RNA recognition motif (RRM)-containing protein (68418.m01142)
3793	Not regulated	NC-NC-NC	250457_at	A15g09880	nuclear matrix protein-related low similarity to nuclear matrix protein p84 [Homo sapiens] GI:550056 (68418.m01140)
3794	Not regulated	NC-NC-NC	250459_at	A15g09860	transcription elongation factor-related low similarity to SPIP10712 Transcription elongation factor S-II (Transcription elongation factor A) [Mus musculus] (68418.m01139)
3795	Not regulated	NC-NC-NC	250460_at	A15g09850	beta-hydroxyacyl-ACP dehydratase, putative similar to beta-hydroxyacyl-ACP dehydratase from Toxoplasma gondii (GI:3850997); contains Pfam profile PF01377 Thioester dehydratase (68418.m01176)
3796	Not regulated	NC-NC-NC	250470_at	A15g10160	expressed protein (68418.m01183)
3797	Not regulated	NC-NC-NC	250472_at	A15g10210	sulfate transporter identical to sulfate transporter [Arabidopsis thaliana] GI:2114104 (68418.m01178)
3798	Not regulated	NC-NC-NC	250475_at	A15g10180	asparagine synthetase 3 (ASN3) identical to asparagine synthetase (ASN3) [Arabidopsis thaliana] GI:3859534 (68418.m01189)
3799	Not regulated	NC-NC-NC	250484_at	A15g10240	elongation factor 1-alpha, putative / EF-1-alpha, putative contains similarity to SWISS-PROT:Q9YAV0 elongation factor 1-alpha (EF-1-alpha) [Aeropyrum pernix] (68418.m01231)
3800	Not regulated	NC-NC-NC	250452_at	A15g10630	DNA-binding bromodomain-containing protein low similarity to kinase [Gallus gallus] GI:1370092; contains Pfam profile PF00439: Bromodomain (68418.m01221)
3801	Not regulated	NC-NC-NC	250424_at	A15g10550	protein tyrosine phosphatase-like protein, putative (PAS2) identical to PEPINOPASTICIN2 protein GI:24411183, GI:24575153 from [Arabidopsis thaliana]; contains Pfam profile PF04387: protein tyrosine phosphatase-like protein (68418.m01214)
3802	Not regulated	NC-NC-NC	250428_at	A15g10480	haloacid dehalogenase-like hydrolase family protein contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase (68418.m01212)
3803	Not regulated	NC-NC-NC	250430_at	A15g10460	histone H3 identical to several histone H3 proteins, including Zea mays SPIP05203, Medicago sativa GI:166384, Encaphalartos altensteinii SPIP08903, Pisum sativum SPIP02300; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4 (68418.m01208)
3804	Not regulated	NC-NC-NC	250433_at	A15g10400	histone H3 identical to histone H3 from Zea mays SPIP05203, Medicago sativa GI:166384, Encaphalartos altensteinii SPIP08903, Pisum sativum SPIP02300; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4 (68418.m01208)
3805	Not regulated	NC-NC-NC	250434_at	A15g10390	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (68418.m01204)
3806	Not regulated	NC-NC-NC	250435_at	A15g10380	polyadenylate-binding protein family protein / PABP family protein contains weak similarity to poly(A) binding protein II from [Mus musculus] GI:2351846; [Xenopus laevis] GI:11527140; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) (68418.m01200)
3807	Not regulated	NC-NC-NC	250436_at	A15g10350	expressed protein contains Pfam profile PF04654: Protein of unknown function, DUF599 (68418.m01224)
3808	Not regulated	NC-NC-NC	250438_at	A15g10580	40S ribosomal protein S6 (RPS6B) (68418.m01202)
3809	Not regulated	NC-NC-NC	250440_at	A15g10360	peptidase M3 family protein / hirnet oligopeptidase family protein similar to SPIP27237 Oligopeptidase A (EC 3.4.24.70)
3810	Not regulated	NC-NC-NC	250441_at	A15g10540	mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein contains Pfam profile PF00924: Mechanosensitive ion channel (68418.m01215)
3811	Not regulated	NC-NC-NC	250442_at	A15g10490	integral membrane transporter family protein contains 11 transmembrane domains; similar to folate/methotrexate transporter FT1 (GI:5813863) [Leishmania donovani]; lignostilbene-alpha,beta-dioxygenase gene, Synecococcus PCC7942, EMBL:AF055873 (68418.m01257)
3812	Not regulated	NC-NC-NC	250448_at	A15g10820	mRNA methylase family protein contains Pfam profile PF01795: mRNA methylase family (68418.m01268)
3813	Not regulated	NC-NC-NC	250394_at	A15g10910	protein phosphatase 2C-related / PP2C-related protein phosphatase 2C, atafra, PIR:1059640 (68418.m01245)
3814	Not regulated	NC-NC-NC	250400_at	A15g10740	expressed protein HSPC184, Homo sapiens, EMBL:AF151018 (68418.m01253)
3815	Not regulated	NC-NC-NC	250401_at	A15g10780	argininosuccinate lyase, putative / argininosuccinate lyase, putative similar to argininosuccinate lyase [Nostoc punctiforme] GI:7672743; contains Pfam profile PF00206: Lyase (68418.m01267)
3816	Not regulated	NC-NC-NC	250403_at	A15g10820	

3817	Not regulated	NC-NC-NC	250404_at	Al5g10960	CCR4-NOT transcription complex protein, putative similar to SWISS-PROT:Q9UFF9 CCR4-NOT transcription complex, subunit 8 (CAF1-like protein, CALIFP) [Homo sapiens] (68418.m01273) enhancer of rudimentary protein, putative identical to enhancer of rudimentary homolog SP:Q86319 from [Arabidopsis thaliana]; contains Pfam profile: PF01133 enhancer of rudimentary (68418.m01256) CBS domain-containing protein contains Pfam profile PF00571: CBS domain (68418.m01261)
3818	Not regulated	NC-NC-NC	250406_at	Al5g10810	
3819	Not regulated	NC-NC-NC	250409_at	Al5g10860	
3820	Not regulated	NC-NC-NC	250413_at	Al5g11160	adenine phosphoribosyltransferase, putative strong similarity to SPIQ42563 Adenine phosphoribosyltransferase 2 (EC 2.4.2.7) (APRT) [Arabidopsis thaliana]; contains Pfam profile PF00156: Phosphoribosyl transferase domain (68418.m01304)
3821	Not regulated	NC-NC-NC	250390_at	Al5g11340	GCN5-related N-acetyltransferase (GNAT) family protein low similarity to SPIQ03503 L-A virus GAG protein N-acetyltransferase (EC 2.3.1.-) [Saccharomyces cerevisiae]; contains Pfam profile PF00583: acetyltransferase, GNAT family (68418.m01324)
3822	Not regulated	NC-NC-NC	250368_at	Al5g11280	oxygen-evolving complex-related 23 kDa polypeptide of water-oxidizing complex of photosystem II, Nicotiana tabacum, expressed protein (68418.m01317) EMBL:NT23WOP28 (68418.m01337)
3823	Not regulated	NC-NC-NC	250371_at	Al5g11450	expressed protein (68418.m01340)
3824	Not regulated	NC-NC-NC	250383_at	Al5g11480	adaplin family protein similar to SPIQ9WV78 Adapter-related protein complex 4 beta 1 subunit (Beta subunit of AP-4) [Mus musculus]; beta-adaplin Drosophila 1 [Drosophila melanogaster] GI:434902; contains Pfam profile: PF01602 Adaplin N terminal region (68418.m01341)
3825	Not regulated	NC-NC-NC	250384_at	Al5g11500	expressed protein (68418.m01360)
3826	Not regulated	NC-NC-NC	250352_at	Al5g11490	glycine-rich protein predicted protein, Arabidopsis thaliana (68418.m01367)
3827	Not regulated	NC-NC-NC	250353_at	Al5g11630	
3828	Not regulated	NC-NC-NC	250355_at	Al5g11700	
3829	Not regulated	NC-NC-NC	250329_at	Al5g11800	K+ efflux antiporter, putative (KEA9) Monovalent cation-proton antiporter family 2 (CPA2 family) member, PMID:11500563; similar to glutathione-regulated potassium-efflux system protein KEF8, Escherichia coli, SWISSPROT:P45522 (68418.m01377)
3830	Not regulated	NC-NC-NC	250330_at	Al5g11810	expressed protein (68418.m01378)
3831	Not regulated	NC-NC-NC	250333_at	Al5g11690	mitochondrial import inner membrane translocase subunit Tim17 (Arabidopsis thaliana); contains Pfam profile PF02468: Mitochondrial import inner membrane translocase subunit Tim17 (68418.m01368)
3832	Not regulated	NC-NC-NC	250334_at	Al5g11770	NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondrial identical to NADH-ubiquinone oxidoreductase 20 kDa subunit (68418.m01374)
3833	Not regulated	NC-NC-NC	250336_at	Al5g11760	expressed protein (68418.m01373)
3834	Not regulated	NC-NC-NC	250340_at	Al5g11840	expressed protein predicted proteins in Synechococcus, Cyanophora and other organisms (68418.m01384)
3835	Not regulated	NC-NC-NC	250341_at	Al5g11850	protein kinase family protein contains Pfam domain, PF00069: Protein kinase domain; identical to cDNA MAP3K delta-1 protein kinase GI:2253009 (68418.m01385)
3836	Not regulated	NC-NC-NC	250347_at	Al5g11960	expressed protein (68418.m01399)
3837	Not regulated	NC-NC-NC	250350_at	Al5g12010	expressed protein (68418.m01404)
3838	Not regulated	NC-NC-NC	250326_at	Al5g12080	mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein contains Pfam profile PF00624: Mechanosensitive ion channel (68418.m01414)
3839	Not regulated	NC-NC-NC	250287_at	Al5g11980	conserved oligomeric Golgi complex component-related / COG complex component-related similar to SPIQ96MW5 Conserved oligomeric Golgi complex component 8 (Homo sapiens); contains Pfam profile PF04124: Dori-like family (68418.m01401)
3840	Not regulated	NC-NC-NC	250298_at	Al5g11860	NLI interacting factor (NIF) family protein contains Pfam profile PF03031: NLI interacting factor (68418.m01386)
3841	Not regulated	NC-NC-NC	250299_at	Al5g11910	asterase/lipase/rhoesterase family protein low similarity to cineromyl ester hydrolase Cni [Buynivibrio fibrisolvens] GI:1622732; contains Interpro entry IPR000379 (68418.m01393)
3842	Not regulated	NC-NC-NC	250301_at	Al5g11970	expressed protein (68418.m01400)
3843	Not regulated	NC-NC-NC	250305_at	Al5g12150	pleckstrin homology (PH) domain-containing protein / RhoGAP domain-containing protein weak similarity to glucocorticoid receptor DNA binding factor 1 [Canis familiaris] GI:23268717; contains Pfam profiles PF00169: PH domain, PF00620: RhoGAP domain (68418.m01426)
3844	Not regulated	NC-NC-NC	250307_at	Al5g12170	expressed protein similar to unknown protein (pirIT09909) (68418.m01428)
3845	Not regulated	NC-NC-NC	250315_at	Al5g12130	integral membrane TerC family protein contains Pfam profile PF03741: Integral membrane protein TerC family (68418.m01424)
3846	Not regulated	NC-NC-NC	250318_at	Al5g12200	dihydropyrimidinase / DHPase / dihydropyrimidine amidohydrolase / hydantoinase (PYD2) identical to dihydropyrimidine amidohydrolase (PYD2) [Arabidopsis thaliana] GI:28194047; similar to SPIQ9EQF5 Dihydropyrimidinase (EC 3.5.2.2) (DHPase) (Hydantoinase) (DHP) [Mus musculus]; contains Pfam profile PF01979: Amidohydrolase family (68418.m01431)
3847	Not regulated	NC-NC-NC	250319_at	Al5g12120	ubiquitin-associated (UBA)/ITS-N domain-containing protein contains Pfam profile PF00627: UBA/ITS-N domain (68418.m01423)
3848	Not regulated	NC-NC-NC	250320_at	Al5g12840	CCAAT-binding transcription factor (CBF-BNF-YA) family protein contains Pfam profile PF02045 CCAAT-binding transcription factor (CBF-BNF-YA) subunit B (68418.m01467)
3849	Not regulated	NC-NC-NC	250323_at	Al5g12860	proline-rich family protein similar to hydroxyproline-rich glycoprotein gi168345[gbIAA33763 (68418.m01478)
3850	Not regulated	NC-NC-NC	250273_at	Al5g13010	RNA helicase, putative similar to DEAH-box RNA helicase [Chlamydomonas reinhardtii] GI:12044832; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain (68418.m01461)
3851	Not regulated	NC-NC-NC	250278_at	Al5g12860	oxoglutarate/malate translocator, putative similar to 2-oxoglutarate/malate translocator precursor, spinach, SWISSPROT:Q41364 (68418.m01476)
3852	Not regulated	NC-NC-NC	250282_at	Al5g13280	expressed protein (68418.m01523)

3853	Not regulated	NC-NC-NC	250287_at	A15g13330	AP2 domain-containing transcription factor family protein similar to AP2 domain containing protein RAP2.6, Arabidopsis thaliana, EMBL:AF003099; contains Pfam profile PF00847; AP2 domain (88418.m01533)
3854	Not regulated	NC-NC-NC	250289_at	A15g13280	aspartate kinase identical to aspartate kinase [Arabidopsis thaliana] GI:4376156 (88418.m01525)
3855	Not regulated	NC-NC-NC	250293_s_at	A15g13360	auxin-responsive GH3 family protein similar to auxin-responsive GH3 product [Glycine max] GI:18591; contains Pfam profile PF03321; GH3 auxin-responsive promotor (88418.m01539)
3856	Not regulated	NC-NC-NC	250291_at	A15g13400	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family (88418.m01543)
3857	Not regulated	NC-NC-NC	250282_at	A15g13410	immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein SP:QBLYR5; similar to FK506-binding protein (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (SP:P25138) [Neisseria meningitidis]; peptidyl-prolyl cis-trans isomerase, Spodoptera frugiperda, EMBL:SF15038; contains Pfam PF00254; peptidyl-prolyl cis-trans isomerase, FKBP-type (88418.m01544)
3858	Not regulated	NC-NC-NC	250234_at	A15g13420	transaldolase, putative similar to transaldolase [Solanum tuberosum] gi2078350lpbAA54016 (88418.m01545)
3859	Not regulated	NC-NC-NC	250235_s_at	A15g13430	ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondrial, putative / Rieske iron-sulfur protein, putative similar to ubiquinol-cytochrome-c reductase from Solanum tuberosum [SP:IP37841], Nicotiana tabacum [SP:IP51132] [SP:IP51133]; non-consensus AT acceptor splice site at exon 2 (88418.m01546)
3860	Not regulated	NC-NC-NC	250236_at	A15g13450	ATP synthase delta chain, mitochondrial, putative / H(+)-transporting two-sector ATPase, delta (OSCP) subunit, putative identical to SPIQ86251; similar to SPIP27278 ATP synthase delta chain, mitochondrial precursor (EC 3.6.3.14) (Oligomycin sensitivity conferral protein) (OSCP) (Ipomoea batatas); contains Pfam profile PF00213; ATP synthase F1, delta subunit (88418.m01548)
3861	Not regulated	NC-NC-NC	250237_at	A15g13560	expressed protein weak similarity to SPIQ42184 Reslin (Cytoplasmic linker protein-170) (CLIP-170) (Gallus gallus) (88418.m01566)
3862	Not regulated	NC-NC-NC	250247_at	A15g13720	expressed protein (88418.m01587)
3863	Not regulated	NC-NC-NC	250254_at	A15g13710	steroid 24-C-methyltransferase, putative similar to SP:P25087 Steroid 24-C-methyltransferase, Delta(24)-sterol C-methyltransferase, Saccharomyces cerevisiae (88418.m01596)
3864	Not regulated	NC-NC-NC	250256_at	A15g13650	elongation factor family protein contains Pfam profiles: PF00009 elongation factor Tu GTP binding domain, PF00879 elongation factor G C-terminus, PF03144 elongation factor Tu domain 2 (88418.m01584)
3865	Not regulated	NC-NC-NC	250257_at	A15g13770	pentapeptide (PPR) repeat-containing protein contains Pfam profile PF01535; PPR repeat (88418.m01606)
3866	Not regulated	NC-NC-NC	250228_at	A15g13780	GCN5-related N-acetyltransferase, putative similar to SPIP07347 N-terminal acetyltransferase complex ARD1 subunit (Arrest-defective protein 1) (Saccharomyces cerevisiae); contains Pfam profile PF00583; acetyltransferase, GNAT family (88418.m01607)
3867	Not regulated	NC-NC-NC	250229_at	A15g13850	nascent polypeptide-associated complex (NAC) domain-containing protein similar to alpha-NAC, non-muscle form [Mus musculus] GI:1686690; contains Pfam profile PF01849; NAC domain (88418.m01619)
3868	Not regulated	NC-NC-NC	250231_at	A15g13910	AP2/EREBP-like transcription factor LEAFY PETIOLE, putative nearly identical to AP2/EREBP-like transcription factor LEAFY
3869	Not regulated	NC-NC-NC	250202_at	A15g13970	PETIOLE [Arabidopsis thaliana] GI:6942018 (88418.m01627)
3870	Not regulated	NC-NC-NC	250203_at	A15g13980	expressed protein (88418.m01633)
3871	Not regulated	NC-NC-NC	250209_at	A15g14030	glycosyl hydrolase family 38 protein similar to alpha-mannosidase GI:1419374 from [Homo sapiens] (88418.m01634)
3872	Not regulated	NC-NC-NC	250210_at	A15g13890	translocin-associated protein beta (TRAPB) family protein low similarity to SPIP23438 Translocin-associated protein, beta subunit precursor (TRAP-beta) (Signal sequence receptor beta subunit) (Canis familiaris); contains Pfam profile PF05753; Translocin-associated protein beta (TRAPB) (88418.m01640)
3873	Not regulated	NC-NC-NC	250216_at	A15g14090	expressed protein contains Pfam profile PF04819; Family of unknown function (DUF716) (Plant viral-response family) (88418.m01623)
3874	Not regulated	NC-NC-NC	250218_at	A15g14170	hypothetical protein (88418.m01648)
3875	Not regulated	NC-NC-NC	250220_at	A15g14210	SWIB complex BAF60b domain-containing protein similar to brahma associated protein 60 kDa [Drosophila melanogaster] GI:3378134, SWISNF-related, matrix-associated, actin-dependent regulator of chromatin D1 [Homo sapiens] GI:4566530; contains Pfam profile PF02201; BAF60b domain of the SWIB complex (88418.m01657)
3876	Not regulated	NC-NC-NC	250221_at	A15g14220	leucine-rich repeat transmembrane protein kinase, putative (88418.m01660)
3877	Not regulated	NC-NC-NC	250222_at	A15g14050	protoporphyrinogen oxidase, putative similar to protoporphyrinogen IX oxidase, mitochondrial (PPO II) from Nicotiana tabacum [SP:Q24164], Glycine max, AB025102, Spinacia oleracea [GI:14349153]; contains Pfam profile PF05477; Surfeit locus protein 2 (SURF2) [PF015930] (88418.m01661)
3878	Not regulated	NC-NC-NC	250225_at	A15g14105	transducin family protein / WD-40 repeat family protein contains 4 WD-40 repeats (PF00400); similar to unknown protein (refNP_057085.1) (88418.m01644)
3879	Not regulated	NC-NC-NC	250200_at	A15g14130	expressed protein (88418.m01650)
3880	Not regulated	NC-NC-NC	250172_at	A15g14330	peroxidase, putative identical to peroxidase ATP20a [Arabidopsis thaliana] gi1546894IembICAA467338 (88418.m01653)
3881	Not regulated	NC-NC-NC	250177_at	A15g14420	expressed protein (88418.m01675)
3882	Not regulated	NC-NC-NC	250179_at	A15g14440	copine-related low similarity to SPIQ9828 Copine I [Homo sapiens] (88418.m01684)
3883	Not regulated	NC-NC-NC	250181_at	A15g14460	surfeit locus 2 protein-related / SURF2 protein-related contains weak hit to Pfam profile PF05477; Surfeit locus protein 2 (SURF2) (88418.m01690)
3884	Not regulated	NC-NC-NC	250184_at	A15g14420	pseudouridylyl synthase TruB family protein similar to SPIP09171 tRNA pseudouridylation synthase B (EC 4.2.1.70) (RNA pseudouridylation 55 synthase) (Pseudouridylyl synthase) (Uracil hydrolyase) (Escherichia coli O157:H7); contains Pfam profile PF01509; TruB family pseudouridylyl synthase (N terminal domain) (88418.m01692)
3885	Not regulated	NC-NC-NC	250188_at	A15g14250	expressed protein (88418.m01684)
3886	Not regulated	NC-NC-NC	250190_at	A15g14320	COP9 signalosome complex subunit 3 / CSN complex subunit 3 (CSN3) / FUSCA protein (FUS11) CSN3, FUS11; identical to contains Pfam profile PF01399; PCI domain (88418.m01665)
					30S ribosomal protein S13, chloroplast (CS13) ribosomal protein S13 precursor, chloroplast Arabidopsis thaliana, PIR:S59594; identical to cDNA ribosomal protein S13 GI:1515106 (88418.m01674)

3887	Not regulated	NC-NC-NC	250197_at	Al5g14590	isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative strong similarity to isocitrate dehydrogenase (NADP+) [Nicotiana glauca] Gi:3021512; contains Pfam domain PF00180: dehydrogenase, isocitrate/isopyruvate family (88418.m01711)
3888	Not regulated	NC-NC-NC	250141_at	Al5g14640	protein kinase family protein similar to glycogen synthase kinase-3 homolog Msk-3 Sp-P51139 from [Medicago sativa]; contains Pfam profile PF00068: Protein kinase domain (88418.m01715)
3889	Not regulated	NC-NC-NC	250144_at	Al5g14680	universal stress protein (USP) family protein similar to ER6 protein [Lycopersicon esculentum] Gi:5663654; contains Pfam profile PF00582: universal stress protein family (88418.m01720)
3890	Not regulated	NC-NC-NC	250148_at	Al5g14660	peptide deformylase, chloroplast / polypeptide deformylase 1B (PDF1B) identical to SPIQ8FUZZ Peptide deformylase, chloroplast precursor (EC 3.5.1.88) (PDF) (Polypeptide deformylase) [Arabidopsis thaliana]; supporting cDNA
3891	Not regulated	NC-NC-NC	250150_at	Al5g14710	gi11320685 gbIAF269165.1 AF269165 (88418.m01717)
3892	Not regulated	NC-NC-NC	250151_at	Al5g14570	expressed protein (88418.m01725)
3893	Not regulated	NC-NC-NC	250159_at	Al5g15200	transporter, putative similar to trans-membrane nitrate transporter protein ANRT2.1 [Arabidopsis thaliana] Gi:3747058; high-affinity nitrate transporter ACH1 [Arabidopsis thaliana] Gi:3608382; contains Pfam profile PF00083: Sugar (and other) transporter (88418.m01708)
3894	Not regulated	NC-NC-NC	250167_at	Al5g15310	40S ribosomal protein S9 (RPS9B) 40S ribosomal protein S9, Chlamydomonas sp., EMBL:AU066528 (88418.m01781)
3895	Not regulated	NC-NC-NC	250168_at	Al5g15320	myb family transcription factor contains PFAM profile: myb DNA-binding domain PF00249 (88418.m01793)
3896	Not regulated	NC-NC-NC	250137_at	Al5g15390	expressed protein predicted protein, Arabidopsis thaliana (88418.m01794)
3897	Not regulated	NC-NC-NC	250111_at	Al5g16290	tRNA/RNA methyltransferase (SpuU) family protein similar to SP1P19398 tRNA (Guanosine-2-O)-methyltransferase (EC 2.1.1.34) [Escherichia coli Q157.H7]; contains Pfam profile PF00588: SpoU RNA Methylase (RNA methyltransferase, TrmH) family (88418.m01800)
3898	Not regulated	NC-NC-NC	250112_at	Al5g16300	acetylactate synthase small subunit, putative similar to gi:5031781 from Nicotiana glauca [Nicotiana glauca] (88418.m01803)
3899	Not regulated	NC-NC-NC	250125_at	Al5g16390	biotin carboxyl carrier protein 1 (BCCP1) identical to biotin carboxyl carrier protein of acetyl-CoA carboxylase precursor [Arabidopsis thaliana] gi1875912 dbj BA09606 (88418.m01815)
3900	Not regulated	NC-NC-NC	250129_at	Al5g16450	dimethylmenaquinone methyltransferase family protein similar to bacterial S-adenosylmethionine:2-demethylmenaquinone methyltransferase; contains Pfam profile PF03737: Dimethylmenaquinone methyltransferase (88418.m01822)
3901	Not regulated	NC-NC-NC	250130_at	Al5g16510	reversibly glycosylated polypeptide, putative similar to reversibly glycosylated polypeptide (RGP1) [Pisum sativum] Gi:2130521; contains Pfam profile PF03214: Reversibly glycosylated polypeptide (88418.m01830)
3902	Not regulated	NC-NC-NC	250131_at	Al5g16550	expressed protein (88418.m01837)
3903	Not regulated	NC-NC-NC	250133_at	Al5g16400	thioredoxin, putative similar to SP1P29450 Thioredoxin F-type, chloroplast precursor (TRX-F) [Pisum sativum]; contains Pfam profile: PF00085 Thioredoxin (88418.m01817)
3904	Not regulated	NC-NC-NC	250134_at	Al5g16505	expressed protein (88418.m01850)
3905	Not regulated	NC-NC-NC	250076_at	Al5g16660	PHD finger family protein contains Pfam domain, PF00628: PHD-finger (88418.m01851)
3906	Not regulated	NC-NC-NC	250077_at	Al5g16680	DNAJ heat shock N-terminal domain-containing protein similar to SPIP30725 Chaperone protein dnaJ Clostridium acetobutylicum; contains Pfam profile PF00228: DnaJ domain (88418.m01849)
3907	Not regulated	NC-NC-NC	250079_at	Al5g16650	hydroxyproline-rich glycoprotein family protein contains proline rich extensin domains, INTERPRO:IPR002965 (88418.m01946)
3908	Not regulated	NC-NC-NC	250080_at	Al5g16620	autophagy protein Apg5 family contains Pfam profile: PF04108 autophagy protein Apg5 (88418.m02025)
3909	Not regulated	NC-NC-NC	250088_at	Al5g17290	glutamate decarboxylase 1 (GAD 1) sp Q42521 (88418.m02030)
3910	Not regulated	NC-NC-NC	250090_at	Al5g17330	expressed protein similar to unknown protein (gb AAAF26109.1) (88418.m02014)
3911	Not regulated	NC-NC-NC	250096_at	Al5g17190	expressed protein similar to unknown protein (gi 1741892) (88418.m02024)
3912	Not regulated	NC-NC-NC	250097_at	Al5g17280	expressed protein similar to unknown protein (gi 1741892) (88418.m02024)
3913	Not regulated	NC-NC-NC	250073_at	Al5g17170	rubredoxin family protein contains Pfam profile PF00301: Rubredoxin (88418.m02012)
3914	Not regulated	NC-NC-NC	250074_at	Al5g17310	UTP-glucose-1-phosphate uridylyltransferase, putative / UDP-glucose pyrophosphorylase, putative / UGPase, putative strong similarity to SPIP19595 UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase) (UDPGP) (UGPase) [Solanum tuberosum]; contains Pfam profile PF01704: UTP-glucose-1-phosphate uridylyltransferase (88418.m02027)
3915	Not regulated	NC-NC-NC	250075_at	Al5g17670	expressed protein (88418.m02071)
3916	Not regulated	NC-NC-NC	250057_at	Al5g17840	chaperone protein dnaJ-related similar to bundle sheath defective protein 2 (Gi:4732081) [Zea mays] (88418.m02091)
3917	Not regulated	NC-NC-NC	250018_at	Al5g18100	superoxide dismutase [Cu-Zn] / copper/zinc superoxide dismutase (CSD3) identical to copper/zinc superoxide dismutase Gi:3273755 (88418.m02125)
3918	Not regulated	NC-NC-NC	250017_at	Al5g18140	DNAJ heat shock N-terminal domain-containing protein similar to DnaJ protein Trd-1 [Homo sapiens] Gi:17066575; contains Pfam profile PF00228 DnaJ domain (88418.m02130)
3919	Not regulated	NC-NC-NC	250018_at	Al5g18150	expressed protein similar to unknown protein (emb CA887627.1) (88418.m02131)
3920	Not regulated	NC-NC-NC	250021_at	Al5g18190	protein kinase family protein contains Pfam domains, PF00069: Protein kinase domain (88418.m02135)
3921	Not regulated	NC-NC-NC	250027_at	Al5g18250	expressed protein similar to unknown protein (db BAAG0342.1) (88418.m02145)
3922	Not regulated	NC-NC-NC	250028_at	Al5g18130	expressed protein similar to unknown protein (gb AAAF00631.1) (88418.m02128)
3923	Not regulated	NC-NC-NC	250034_at	Al5g18280	aprase (APY2) identical to aprase Gi:6006801, Gi:782685 from [Arabidopsis thaliana] (88418.m02149)
3924	Not regulated	NC-NC-NC	250035_at	Al5g18230	transcription regulator NOT2/NOT3/NOT5 family protein contains Pfam domain PF04153: NOT2 / NOT3 / NOT5 family (88418.m02139)
3925	Not regulated	NC-NC-NC	250042_at	Al5g18420	expressed protein non-consensus GC donor splice site at exon 1, unknown (C40) protein, Homo sapiens, EMBL:AF103788 (88418.m02188)
3926	Not regulated	NC-NC-NC	249982_at	Al5g18520	expressed protein (88418.m02187)
3927	Not regulated	NC-NC-NC	249984_at	Al5g18400	expressed protein contains Pfam profile PF05093: Protein of unknown function (DUF689) (88418.m02164)
3928	Not regulated	NC-NC-NC	250001_at	Al5g18680	F-box family protein / tubby family protein similar to phosphodiesterase (Gi:487578) [Mus musculus]; similar to Chain A, C-Terminal Domain Of Mouse Brain Tubby Protein (Gi:6730158) [Mus musculus]; contains Pfam PF00648: F-box domain and Pfam PF01167: Tub family (88418.m02217)

3929	Not regulated	NC-NC-NC	250005_at	A15g18760	zinc finger (C3HC4-type RING finger) family protein predicted proteins, Arabidopsis thaliana ; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger) (68418.m02228)
3930	Not regulated	NC-NC-NC	250007_at	A15g18670	beta-amylase, putative (BMV3) / 1,4-alpha-D-glucan maltohydrolase, putative almost identical to beta-amylase BMV3 GI:15148457 from Arabidopsis thaliana; identical to cDNA putative beta-amylase BMV3 (BMV3) GI:15148456 (68418.m02216)
3931	Not regulated	NC-NC-NC	250008_at	A15g18630	lipase class 3 family protein low similarity to Triacylglycerol Acylhydrolase (E.C.3.1.1.3) [Rhizomucor miehei] GI:230346; contains Pfam profile PF01764: Lipase (68418.m02208)
3932	Not regulated	NC-NC-NC	249875_s_at	A15g18790	ribosomal protein L33 family protein ribosomal protein L33, Rickettsia prowazekii, PIR:E71650 (68418.m02232)
3933	Not regulated	NC-NC-NC	249856_at	A15g18940	Mo25 family protein similar to SPJ008138 Mo25 protein [Mus musculus]; contains Pfam profile PF03204: Mo25 protein family (68418.m02249)
3934	Not regulated	NC-NC-NC	249857_at	A15g18900	oxido-reductase, 2OG-Fe(II) oxygenase family protein similar to prolyl 4-hydroxylase, alpha subunit, from Rattus norvegicus [GI:474940], Mus musculus [SPI060715], Homo sapiens [GI:18073925]; contains PF03171 2OG-Fe(II) oxygenase superfamily domain (68418.m02245)
3935	Not regulated	NC-NC-NC	249859_at	A15g18800	NADH-ubiquinone oxidoreductase 19 kDa subunit (NDUFA8) family protein contains Pfam profile: PF05850 NADH-ubiquinone oxidoreductase 19 kDa subunit (68418.m02233)
3936	Not regulated	NC-NC-NC	249860_at	A15g18830	squamosa promoter-binding protein-like 7 (SP17) identical to squamosa promoter binding protein-like 7 [Arabidopsis thaliana] GI:5931635; contains Pfam profile PF03110: SBP domain (68418.m02237)
3937	Not regulated	NC-NC-NC	249863_at	A15g19000	speckle-type POZ protein-related contains Pfam PF00851 : BTB/POZ domain; contains Pfam PF00917: MATH domain; similar to Speckle-type POZ protein (SP-OC43791) [Homo sapiens] (68418.m02257)
3938	Not regulated	NC-NC-NC	249864_at	A15g19010	mitogen-activated protein kinase, putative / MAPK, putative (MPK16) mitogen-activated protein kinase (MAPK)(A1MPK16), PMID:12119167; similar to ATPMK9, Arabidopsis thaliana, ENBL:AB038694 (68418.m02258)
3939	Not regulated	NC-NC-NC	249868_at	A15g19070	expressed protein (68418.m02287)
3940	Not regulated	NC-NC-NC	249869_at	A15g19080	heavy-metal-associated domain-containing protein contains Pfam heavy-metal-associated domain PF00403: glycine-rich protein GRP22, rape, PIR:S31415; isoform contains a non-consensus TG-acceptor splice site at intron 3 (68418.m02289)
3941	Not regulated	NC-NC-NC	249818_at	A15g19250	expressed protein (68418.m02292)
3942	Not regulated	NC-NC-NC	249827_at	A15g19220	glucose-1-phosphate adenylyltransferase large subunit 1 (APL1) / ADP-glucose pyrophosphorylase (ADG2) identical to SPJP55229 (68418.m02289)
3943	Not regulated	NC-NC-NC	249828_at	A15g22340	expressed protein (68418.m02606)
3944	Not regulated	NC-NC-NC	249830_at	A15g22360	synaptobrevin family protein similar to Synaptobrevin-like protein 1 (SP-P51809) [Homo sapiens] (68418.m02609)
3945	Not regulated	NC-NC-NC	249838_at	A15g22330	TATA box-binding protein-interacting protein-related similar to TATA box-binding protein-interacting protein SP-O35753 from [Mus musculus] (68418.m02605)
3946	Not regulated	NC-NC-NC	249842_at	A15g22300	nitrilase 4 (NIT4) identical to SPIP46011 Nitrilase 4 (EC 3.5.5.1) [Arabidopsis thaliana] (68418.m02601)
3947	Not regulated	NC-NC-NC	249843_at	A15g22280	expressed protein (68418.m02597)
3948	Not regulated	NC-NC-NC	249845_at	A15g22440	60S ribosomal protein L10A (RPL10aC) (68418.m02617)
3949	Not regulated	NC-NC-NC	249884_at	A15g22580	expressed protein (68418.m02637)
3950	Not regulated	NC-NC-NC	249885_at	A15g22500	acyl CoA reductase, putative / male-sterility protein, putative similar to acyl CoA reductase [Simmondsia chinensis] GI:5020215; contains Pfam profile PF03015: Male sterility protein; identical to cDNA male sterility 2-like protein GI:1491614 (68418.m02628)
3951	Not regulated	NC-NC-NC	249888_at	A15g22510	beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative similar to neutral invertase [Daucus carota] GI:4200165; contains Pfam profile PF04653: Plant neutral invertase (68418.m02627)
3952	Not regulated	NC-NC-NC	249800_at	A15g22640	MORN (Membrane Occupation and Recognition Nexus) repeat-containing protein contains Pfam profile PF02483: MORN repeat (68418.m02645)
3953	Not regulated	NC-NC-NC	249809_s_at	A15g22770	adaplin family protein similar to SPJP18484 adaptor-related protein complex 2 alpha 2 subunit (Alpha-adaptin C) (Clatrin assembly protein complex 2 alpha-C large chain) (Rattus norvegicus); contains Pfam profiles PF01602: Adaplin N terminal region, PF02863: Adaplin C-terminal domain (68418.m02659)
3954	Not regulated	NC-NC-NC	249810_at	A15g22630	prephenate dehydratase family protein contains Pfam profile PF00800: prephenate dehydratase (68418.m02644)
3955	Not regulated	NC-NC-NC	249816_at	A15g22880	histone H2B, putative strong similarity to histone H2B-3 Lycopodium obscurum GI:3021485, H2B Gossypium hirsutum SPI022582; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4 (68418.m02676)
3956	Not regulated	NC-NC-NC	249859_at	A15g22840	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (68418.m02670)
3957	Not regulated	NC-NC-NC	249861_at	A15g22875	expressed protein (68418.m02675)
3958	Not regulated	NC-NC-NC	249863_at	A15g22850	SNF7 family protein contains Pfam domain, PF03357: SNF7 family (68418.m02683)
3959	Not regulated	NC-NC-NC	249864_at	A15g22830	magnesium transporter CorA-like family protein weak similarity to SPIQ01928 RNA splicing protein MRS2, mitochondrial precursor (Saccharomyces cerevisiae); contains Pfam profile PF01544: CorA-like Mg2+ transporter protein; supporting cDNA gll12007446ipJA1F322255.11AF322255 (68418.m02669)
3960	Not regulated	NC-NC-NC	249873_at	A15g23140	ATP-dependent CIP protease proteolytic subunit, putative nCip2nCipP7; similar to SP-Q8XW8 ATP-dependent CIP protease proteolytic subunit (EC 3.4.21.82) (Endopeptidase CIP) from [Azospirillum brasilense] (68418.m02706)
3961	Not regulated	NC-NC-NC	249874_at	A15g23070	thymidine kinase, putative similar to thymidine kinase [Oryza sativa] SWISS-PROT:O81263 (68418.m02697)
3962	Not regulated	NC-NC-NC	249875_at	A15g23120	photosystem II stability/assembly factor, chloroplast (HCF136) identical to SPI082660 Photosystem II stability/assembly factor HCF136, chloroplast precursor (Arabidopsis thaliana) (68418.m02704)
3963	Not regulated	NC-NC-NC	249847_at	A15g23210	serine carboxypeptidase S10 family protein similar to Serine carboxypeptidase II chains A and B (SP-P08818) (EC 3.4.16.6) [Triticum aestivum (Wheat)]; (68418.m02714)
3964	Not regulated	NC-NC-NC	249834_at	A15g23440	ferredoxin-thioredoxin reductase, putative similar to ferredoxin-thioredoxin reductase, variable chain (FTR-V, Ferredoxin-thioredoxin reductase subunit A, FTR-A) [Zea mays] SWISS-PROT:P06080 (68418.m02750)
3965	Not regulated	NC-NC-NC	249835_s_at	A15g23510	expressed protein (68418.m02758)
3966	Not regulated	NC-NC-NC	249842_at	A15g23550	expressed protein (68418.m02764)

3967	Not regulated	NC-NC-NC	249846_at	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein similar to SPO14072 Cation-transporting ATPase 4 (EC 3.6.3.-) (Schizosaccharomyces pombe); contains InterPro accession IPR001757: ATPase, E1-E2 type; contains Pfam profile PF00702: haloacid dehalogenase-like hydrolase (68418.m02771)
3968	Not regulated	NC-NC-NC	249795_at	40S ribosomal protein S11 (RPS11C) (68418.m02784)
3969	Not regulated	NC-NC-NC	249796_at	26S proteasome, non-ATPase subunit [Mus musculus] GI:2505940; contains Pfam profile PF01398: Mv34/MPN/PAD-1 family (68418.m02763)
3970	Not regulated	NC-NC-NC	249798_at	transducin family protein / WD-40 repeat family protein contains similarity to photomorphogenesis repressor protein; contains Pfam profile PF00400: WD domain, G-beta repeat (5 copies) (68418.m02782)
3971	Not regulated	NC-NC-NC	249799_at	serine C-palmitoyltransferase (LCE2) identical to serine palmitoyltransferase [Arabidopsis thaliana] GI:9309380; similar to serine palmitoyltransferase from Solanum tuberosum (GI:4995890); Homo sapiens [SPO15270]; Mus musculus [SP197363]; contains Pfam profile PF00155: aminotransferase, classes I and II (68418.m02775)
3972	Not regulated	NC-NC-NC	249810_at	expressed protein (68418.m02809)
3973	Not regulated	NC-NC-NC	249815_at	60S ribosomal protein L13 (RPL13D) (68418.m02807)
3974	Not regulated	NC-NC-NC	249765_at	C4-dicarboxylate transporter/malic acid transport family protein weak similarity to SP125398 Tellurite resistance protein tetaA (Escherichia coli); contains Pfam profile PF05595: C4-dicarboxylate transporter/malic acid transport protein (68418.m02823)
3975	Not regulated	NC-NC-NC	249775_at	squalene monooxygenase 1.2 / squalene epoxidase 1.2 (SQEP1.2) identical to SPO85402 (68418.m02842)
3976	Not regulated	NC-NC-NC	249776_at	expressed protein (68418.m02844)
3977	Not regulated	NC-NC-NC	249778_at	expressed protein (68418.m02843)
3978	Not regulated	NC-NC-NC	249790_at	integral membrane family protein contains Pfam domain PF01988: Integral membrane protein (68418.m02857)
3979	Not regulated	NC-NC-NC	249733_at	glucosamine/galactosamine-6-phosphate isomerase family protein low similarity to SPO95336 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL) (Homo sapiens); contains Pfam profile PF01182: Glucosamine-6-phosphate isomerase/6-phosphogluconolactonase (68418.m02878)
3980	Not regulated	NC-NC-NC	249735_at	transcription factor-related low similarity to transcription factor IIC23 (Homo sapiens) GI:5281318 (68418.m02882)
3981	Not regulated	NC-NC-NC	249736_at	expressed protein (68418.m02883)
3982	Not regulated	NC-NC-NC	249739_at	transparent testa glabra 1 protein (TTG1) identical to transparent testa glabra 1 (Ttg1) protein (GI:10177852) (Arabidopsis thaliana); contains Pfam PF00400: WD domain, G-beta repeat (4 copies, 1 weak); (68418.m02891)
3983	Not regulated	NC-NC-NC	249748_at	tunip crinkle virus-interacting protein / TVC-interacting protein (TIP) contains Pfam PF02365: No apical membrane (NAM) domain; similar to NAC2 (GI:6456751) (Arabidopsis thaliana); identical to cDNA TIP mRNA, GI:9408900 (68418.m02904)
3984	Not regulated	NC-NC-NC	249750_at	expressed protein (68418.m02901)
3985	Not regulated	NC-NC-NC	249751_at	mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein contains Pfam PF02468: Mitochondrial import inner membrane translocase subunit Tim17 (68418.m02911)
3986	Not regulated	NC-NC-NC	249753_at	expressed protein similar to unknown protein (embICA862458.1) (68418.m02907)
3987	Not regulated	NC-NC-NC	249754_at	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to flavanone 3-hydroxylase [Pensea americana] (GI:727410); contains PF03171 2OG-Fe(II) oxygenase superfamily domain (68418.m02897)
3988	Not regulated	NC-NC-NC	249723_at	40S ribosomal protein S3 (RPS3C) (68418.m04226)
3989	Not regulated	NC-NC-NC	249700_at	expressed protein (68418.m04217)
3990	Not regulated	NC-NC-NC	249701_at	DENN (AEX-3) domain-containing protein contains Pfam domain PF02141: DENN (AEX-3) domain; this cDNA may contain an anomalously spliced intron, will require further examination; (68418.m04231)
3991	Not regulated	NC-NC-NC	249703_at	glutamine synthetase (GS2) identical to glutamine synthetase, chloroplast precursor (glutamate- ammonia ligase, GS2) (Arabidopsis thaliana) SWISS-PROT:Q43127 (68418.m04253)
3992	Not regulated	NC-NC-NC	249710_at	eukaryotic translation initiation factor 1A, putative / eIF-1A, putative / eIF-4C, putative strong similarity to translation initiation factor (eIF-1A) [Beta vulgaris] GI:7977875; contains Pfam profile PF01176: Eukaryotic initiation factor 1A (68418.m04283)
3993	Not regulated	NC-NC-NC	249711_at	EXS family protein / ERD1/XPR1/SYG1 family protein low similarity to xenotropic and polytropic murine leukemia virus receptor [Mus musculus] GI:6093318; contains Pfam profile PF03124: EXS family (68418.m04274)
3994	Not regulated	NC-NC-NC	249717_at	[Mus musculus] GI:6093318; contains Pfam profile PF03124: EXS family (68418.m04274)
3995	Not regulated	NC-NC-NC	249694_at	glucose-6-phosphate 1-dehydrogenase / G6PD (APG1) identical to SPO43727 Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform (EC 1.1.1.49) (G6PD) (Arabidopsis thaliana) (68418.m04292)
3996	Not regulated	NC-NC-NC	249674_at	AMP-dependent synthetase and ligase family protein similar to harn A synthetase C [Bacillus subtilis] GI:16040972; contains Pfam profile PF00501: AMP-binding enzyme (68418.m04322)
3997	Not regulated	NC-NC-NC	249678_at	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (68418.m04333)
3998	Not regulated	NC-NC-NC	249679_at	YGGT family protein contains Pfam profile PF02325: YGGT family (unknown function) (68418.m04352)
3999	Not regulated	NC-NC-NC	249685_at	aminotransferase-related similar to nicotianamine aminotransferase B GI:8469087 from [Hordeum vulgare subsp. vulgare] (68418.m04357)
4000	Not regulated	NC-NC-NC	249688_at	peptide chain release factor, putative similar to SP128387 Peptide chain release factor 2 (RF-2) [Bacillus subtilis]; contains Pfam profiles PF00472: Peptidyl-RNA hydrolase domain, PF03462: PCRF domain (68418.m04358)
4001	Not regulated	NC-NC-NC	249691_at	phosphoglycolate phosphatase, putative similar to phosphoglycolate phosphatase precursor [Chlamydomonas reinhardtii] GI:15982558; contains InterPro accession IPR005634: Haloacid dehalogenase-like hydrolase (68418.m04392)
4002	Not regulated	NC-NC-NC	249658_s_at	glycosyl hydrolase family 1 protein contains Pfam PF00232: Glycosyl hydrolase family 1 domain; similar to amygdalin hydrolase isoform AH1 precursor (GI:16757966) [Prunus serotina]; prunasin hydrolase isoform PHA precursor, Prunus serotina, EMBL:AF221528 (68418.m04419)
4003	Not regulated	NC-NC-NC	249636_at	acetyl-CoA synthetase, putative / acylate-CoA ligase, putative similar to SP127550 (Escherichia coli) and GI:8439651 (Homo sapiens); contains Pfam AMP-binding enzyme domain PF00501 (68418.m04418)
4004	Not regulated	NC-NC-NC	249638_at	auxin-responsive factor (ARF8) identical to auxin response factor 8 GI:4104931 from [Arabidopsis thaliana] (68418.m04440)
4005	Not regulated	NC-NC-NC	249651_at	

4008	Not regulated	NC-NC-NC	249652_at	A15g37070	expressed protein contains Pfam profile PF04398; Protein of unknown function, DUF538 (88418.m04450)
4007	Not regulated	NC-NC-NC	249610_at	A15g37360	expressed protein (88418.m04488)
4008	Not regulated	NC-NC-NC	249811_at	A15g37370	pre-mRNA splicing factor PRP38 family protein (SRL1) contains Pfam profile PF03371; PRP38 family (88418.m04489)
4009	Not regulated	NC-NC-NC	249576_at	A15g37690	GDSL-motif lipase/hydrolase family protein similar to family II lipase EXL3 (GI:15054382), EXL2 (GI:15054384) [Arabidopsis thaliana] (88418.m04539)
4010	Not regulated	NC-NC-NC	249583_at	A15g37770	touch-responsive protein / calmodulin-related protein 2, touch-induced (TCH2) identical to calmodulin-related protein 2, touch-induced SP:P25070 from [Arabidopsis thaliana] (88418.m04547)
4011	Not regulated	NC-NC-NC	249589_at	A15g37850	p1kB-type carboxylate kinase family protein contains Pfam profile: PF00294 p1kB family carboxylate kinase (88418.m04557)
4012	Not regulated	NC-NC-NC	249595_at	A15g37930	seven in absentia (SINA) family protein similar to SIAH1 protein [Brassica napus var. napus] (GI:7657876); contains Pfam profile PF03145; Seven in absentia protein family (88418.m04569)
4013	Not regulated	NC-NC-NC	249562_at	A15g38350	disease resistance protein (NBS-LRR class), putative domain signature NBS-LRR exists, suggestive of a disease resistance protein. (88418.m04628)
4014	Not regulated	NC-NC-NC	249508_at	A15g38380	expressed protein (88418.m04635)
4015	Not regulated	NC-NC-NC	249510_at	A15g38510	hormonal protein RAD23, putative similar to DNA repair by nucleotide excision (NER) RAD23 protein, isoform I (GI:1914883 from [Daucus carota] (88418.m04650)
4016	Not regulated	NC-NC-NC	249512_at	A15g38470	tryptophan synthase-related low similarity to tryptophan synthases, beta subunit, from Lactococcus lactis [SP1001888], Pyrococcus kodakarensis [SP109YGB0], Thermus thermophilus [SP1p16609]; contains Pfam pyridoxal-phosphate dependent enzyme domain PF00291 (88418.m04659)
4017	Not regulated	NC-NC-NC	249515_at	A15g38530	expressed protein similar to unknown protein (pf01575762) (88418.m04675)
4018	Not regulated	NC-NC-NC	249519_at	A15g38680	cytochrome B561 family protein contains Pfam domain, PF03188; Cytochrome b561 (88418.m04672)
4019	Not regulated	NC-NC-NC	249523_at	A15g38630	hydrolase, alpha/beta fold family protein low similarity to hydrolase [Ternabacter sp. DBF63] (GI:14198240); contains Pfam profile PF00561; hydrolase, alpha/beta fold family (88418.m04658)
4020	Not regulated	NC-NC-NC	249524_at	A15g38520	proteasome maturation factor UMP1 family protein contains Pfam profile PF05348; Proteasome maturation factor UMP1 (88418.m04674)
4021	Not regulated	NC-NC-NC	249525_at	A15g38650	RNA synthetase class I (C) family protein similar to SP1008752 Cysteine-RNA synthetase (EC 6.1.1.18) (Cysteine-RNA ligase) (CysRS) [Bacillus subtilis]; contains Pfam profile PF01406; RNA synthetases class I (C) (88418.m04697)
4022	Not regulated	NC-NC-NC	249537_at	A15g38830	exoribonuclease-related similar to SP1P3859 3'-5' exoribonuclease CSL4 (EC 3.1.13.-) [Saccharomyces cerevisiae]
4023	Not regulated	NC-NC-NC	249475_at	A15g38880	protein kinase family protein contains protein kinase domain, Pfam:PF00089 (88418.m04717)
4024	Not regulated	NC-NC-NC	249480_s_at	A15g38990	DSBA oxidoreductase family protein contains Pfam profile: PF01323 DSBA-like thioester domain (88418.m04705)
4025	Not regulated	NC-NC-NC	249481_at	A15g38900	UDP-glucose 6-dehydrogenase, putative very strong similarity to SPIQ86558 UDP-glucose 6-dehydrogenase (EC 1.1.2.2) (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH) (Glycine max); contains Pfam profiles PF03721: UDP-glucose/GDP-mannose dehydrogenase family NAD binding domain, PF00984: UDP-glucose/GDP-mannose dehydrogenase family central domain, PF03720: UDP-glucose/GDP-mannose dehydrogenase family UDP binding domain (88418.m04781)
4026	Not regulated	NC-NC-NC	249469_at	A15g39320	expressed protein (88418.m04749)
4027	Not regulated	NC-NC-NC	249472_at	A15g39210	two-component phosphorelay mediator 2 (HP2) nearly identical to ATP2 (Arabidopsis thaliana) (GI:4156243) (88418.m04784)
4028	Not regulated	NC-NC-NC	249473_at	A15g39340	pattern formation protein, putative similar to SP1Q42510 Pattern formation protein EMB30 [Arabidopsis thaliana]; contains Pfam profile PF01369; Sec7 domain (88418.m04783)
4029	Not regulated	NC-NC-NC	249452_at	A15g39500	vesicle transport v-SNARE 11 (VNT11) / vesicle soluble NSF attachment protein receptor VTI1a (VTI1a) identical to SPIQ8SEL6 receptor VTI1a (VNT11a) [Arabidopsis thaliana] (88418.m04784)
4030	Not regulated	NC-NC-NC	249453_at	A15g39510	60S ribosomal protein L5 (RPL5B) ribosomal protein L5, rice (88418.m04813)
4031	Not regulated	NC-NC-NC	249466_at	A15g39740	avirulence-responsive protein-related / avirulence induced gene (AIG) protein-related similar to SPIP54121 AIG3 protein [Arabidopsis thaliana] (88418.m04811)
4032	Not regulated	NC-NC-NC	249441_at	A15g39730	expressed protein (88418.m04796)
4033	Not regulated	NC-NC-NC	249443_at	A15g39600	Dof-type zinc finger domain-containing protein similar to H-protein promoter binding factor-2a (GI:3386546 from [Arabidopsis thaliana] (88418.m04802)
4034	Not regulated	NC-NC-NC	249415_at	A15g39660	60S ribosomal protein-related contains weak similarity to 60S ribosomal protein L27, mitochondrial precursor (Yml27) (Swiss-Prot:P36526) [Saccharomyces cerevisiae] (88418.m04821)
4035	Not regulated	NC-NC-NC	249424_s_at	A15g39800	5'-AMP-activated protein kinase beta-1 subunit-related contains similarity to Swiss-Prot:P80387 5'-AMP-activated protein kinase, beta-1 subunit (AMPK beta-1 chain) (AMPKb) (40 kDa subunit) [Sus scrofa] (88418.m04820)
4036	Not regulated	NC-NC-NC	249425_at	A15g39790	40S ribosomal protein S9 (RPS9C) 40S ribosomal protein S9 - Chlamydomonas sp. EMBL:AU066528 (88418.m04829)
4037	Not regulated	NC-NC-NC	249427_at	A15g39850	thioredoxin H-type 2 (TRX-H-2) (G12) identical to SPIQ38878 Thioredoxin H-type 2 (TRX-H-2) [Arabidopsis thaliana]; identical to cDNA (G12) mRNA for thioredoxin (GI:992963) (88418.m04844)
4038	Not regulated	NC-NC-NC	249385_at	A15g39950	disease resistance family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; similar to Cf-4 [Lycopersicon hirsutum] (GI:2806863) (88418.m04875)
4039	Not regulated	NC-NC-NC	249393_at	A15g40170	calmodulin-binding protein (88418.m04877)
4040	Not regulated	NC-NC-NC	249395_at	A15g40190	DegP protease, putative contains similarity to RING-H2 finger protein RHX1a [Arabidopsis thaliana] (GI:3790591); zinc finger (C3HC4-type RING finger) family protein similar to RING-H2 finger protein RHX1a [Arabidopsis thaliana] (GI:3790591); contains Pfam profile PF00097; Zinc finger, C3HC4 type (RING finger) (88418.m04883)
4041	Not regulated	NC-NC-NC	249396_at	A15g40200	refinase synthase family protein similar to galactinol:raffinose galactosyltransferase [Vigna angulata] (GI:6634701, seed inhibition protein GB:AAA32975 GI:167100 from [Hordeum vulgare]; contains Pfam profile PF05691; Raffinase synthase or seed inhibition protein Sio1 (88418.m04899)
4042	Not regulated	NC-NC-NC	249398_at	A15g40250	glutaredoxin, putative similar to glutaredoxin [Ricinur communis] SWISS-PROT:P55143 (88418.m04897)
4043	Not regulated	NC-NC-NC	249411_at	A15g40390	
4044	Not regulated	NC-NC-NC	249380_at	A15g40370	

4045	Not regulated	NC-NC-NC	249355_at	AT5g40500	expressed protein (88418.m04912)	expressed protein (88418.m04912)
4046	Not regulated	NC-NC-NC	249358_at	AT5g40510	expressed protein (88418.m04914)	expressed protein (88418.m04914)
4047	Not regulated	NC-NC-NC	249360_at	AT5g40530	PQ-loop repeat family protein / transmembrane family protein similar to SPI060931 Cystinosin (Homo sapiens); contains Pfam profile PF04193; PQ loop repeat (88418.m04937)	PQ-loop repeat family protein / transmembrane family protein similar to SPI060931 Cystinosin (Homo sapiens); contains Pfam profile PF04193; PQ loop repeat (88418.m04937)
4048	Not regulated	NC-NC-NC	249373_at	AT5g40670	ATP12 protein-related weak similarity to SPI22135 ATP12 protein, mitochondrial precursor (Saccharomyces cerevisiae)	ATP12 protein-related weak similarity to SPI22135 ATP12 protein, mitochondrial precursor (Saccharomyces cerevisiae)
4049	Not regulated	NC-NC-NC	249342_at	AT5g40660	succinate dehydrogenase, iron-sulphur subunit, mitochondrial (SDH2-2) nearly identical to mitochondrial succinate dehydrogenase iron-sulphur subunit (sdh2-2) [gi:12049600] from Arabidopsis thaliana (88418.m04935)	succinate dehydrogenase, iron-sulphur subunit, mitochondrial (SDH2-2) nearly identical to mitochondrial succinate dehydrogenase iron-sulphur subunit (sdh2-2) [gi:12049600] from Arabidopsis thaliana (88418.m04935)
4050	Not regulated	NC-NC-NC	249343_at	AT5g40650	prohibitin identical to prohibitin [Arabidopsis thaliana] GI:1946331 (88418.m04948)	prohibitin identical to prohibitin [Arabidopsis thaliana] GI:1946331 (88418.m04948)
4051	Not regulated	NC-NC-NC	249344_at	AT5g40770	mitochondrial import receptor subunit TOM20-4 / translocase of outer membrane 20 kDa subunit 4 identical to mitochondrial import receptor subunit TOM20-4 SP-P82805 from Arabidopsis thaliana (88418.m04989)	mitochondrial import receptor subunit TOM20-4 / translocase of outer membrane 20 kDa subunit 4 identical to mitochondrial import receptor subunit TOM20-4 SP-P82805 from Arabidopsis thaliana (88418.m04989)
4052	Not regulated	NC-NC-NC	249322_at	AT5g40830	cytochrome c1, putative cytochrome c1, heme protein, mitochondrial precursor (Clone PC13III) [Solanum tuberosum] SWISS-PROT:P25078 (88418.m04955)	cytochrome c1, putative cytochrome c1, heme protein, mitochondrial precursor (Clone PC13III) [Solanum tuberosum] SWISS-PROT:P25078 (88418.m04955)
4053	Not regulated	NC-NC-NC	249324_at	AT5g40810	chloride channel protein (CLC-a) identical to GI:1742952 (dbIAAC05742.1) (88418.m04985)	chloride channel protein (CLC-a) identical to GI:1742952 (dbIAAC05742.1) (88418.m04985)
4054	Not regulated	NC-NC-NC	249327_at	AT5g40890	SOS ribosomal protein L27, chloroplast, putative (RPL27) identical to SPIQ9FLN4 ribosomal protein L27, chloroplast precursor (Arabidopsis thaliana); similar to SPI230155 50S ribosomal protein L27, chloroplast precursor (CL27) [Nicotiana glauca] (88418.m04975)	SOS ribosomal protein L27, chloroplast, putative (RPL27) identical to SPIQ9FLN4 ribosomal protein L27, chloroplast precursor (Arabidopsis thaliana); similar to SPI230155 50S ribosomal protein L27, chloroplast precursor (CL27) [Nicotiana glauca] (88418.m04975)
4055	Not regulated	NC-NC-NC	249331_at	AT5g40950	expressed protein (88418.m04996)	expressed protein (88418.m04996)
4056	Not regulated	NC-NC-NC	249339_at	AT5g41100	zinc finger (DHC type) family protein contains Pfam profile PF01528: DHC zinc finger domain (88418.m04991)	zinc finger (DHC type) family protein contains Pfam profile PF01528: DHC zinc finger domain (88418.m04991)
4057	Not regulated	NC-NC-NC	249289_at	AT5g41060	glutathione S-transferase (GST10) identical to glutathione transferase AGST 10 [Arabidopsis thaliana] GI:4049401 (88418.m05008)	glutathione S-transferase (GST10) identical to glutathione transferase AGST 10 [Arabidopsis thaliana] GI:4049401 (88418.m05008)
4059	Not regulated	NC-NC-NC	249291_at	AT5g41210	ubiquitin-conjugating enzyme 4 (UBC4) E2; identical to gi:431265, SP-P42748 (88418.m05024)	ubiquitin-conjugating enzyme 4 (UBC4) E2; identical to gi:431265, SP-P42748 (88418.m05024)
4060	Not regulated	NC-NC-NC	249298_at	AT5g41340	40S ribosomal protein S10 (RPS10B) contains similarity to 40S ribosomal protein S10 (88418.m05044)	40S ribosomal protein S10 (RPS10B) contains similarity to 40S ribosomal protein S10 (88418.m05044)
4061	Not regulated	NC-NC-NC	249310_at	AT5g41520	reticulin family protein (RTNLB4) weak similarity to Nogo-C protein [Rattus norvegicus] GI:8822251, SPI095187 Reticulon protein 3 (Neuroendocrine-specific protein-like) (Homo sapiens); contains Pfam profile PF02453: Reticulon (88418.m05054)	reticulin family protein (RTNLB4) weak similarity to Nogo-C protein [Rattus norvegicus] GI:8822251, SPI095187 Reticulon protein 3 (Neuroendocrine-specific protein-like) (Homo sapiens); contains Pfam profile PF02453: Reticulon (88418.m05054)
4062	Not regulated	NC-NC-NC	249267_at	AT5g41800	mitochondrial import receptor subunit TOM7 / translocase of outer membrane 7 kDa subunit (TOM7.1) identical to SPIQ8ASY8 (88418.m05066)	mitochondrial import receptor subunit TOM7 / translocase of outer membrane 7 kDa subunit (TOM7.1) identical to SPIQ8ASY8 (88418.m05066)
4063	Not regulated	NC-NC-NC	249268_at	AT5g41885	Mitochondrial import receptor subunit TOM7 (Translocase of outer membrane 7 kDa subunit) [Arabidopsis thaliana]	Mitochondrial import receptor subunit TOM7 (Translocase of outer membrane 7 kDa subunit) [Arabidopsis thaliana]
4064	Not regulated	NC-NC-NC	249281_at	AT5g41940	RabGAP/TBC domain-containing protein similar to GTPase activating protein [Yarrowia lipolytica] GI:2370595; contains Pfam profile PF00568: TBC domain (88418.m05106)	RabGAP/TBC domain-containing protein similar to GTPase activating protein [Yarrowia lipolytica] GI:2370595; contains Pfam profile PF00568: TBC domain (88418.m05106)
4065	Not regulated	NC-NC-NC	249282_at	AT5g41760	nucleotide-sugar transporter family protein low similarity to SPIQ81420 CMP-sialic acid transporter [Mus musculus]; contains Pfam profile PF04142: Nucleotide-sugar transporter (88418.m05084)	nucleotide-sugar transporter family protein low similarity to SPIQ81420 CMP-sialic acid transporter [Mus musculus]; contains Pfam profile PF04142: Nucleotide-sugar transporter (88418.m05084)
4066	Not regulated	NC-NC-NC	249284_at	AT5g41810	expressed protein (88418.m05090)	expressed protein (88418.m05090)
4067	Not regulated	NC-NC-NC	249285_at	AT5g41960	mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein (88418.m05128)	mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein (88418.m05128)
4068	Not regulated	NC-NC-NC	249224_at	AT5g42130	peroxidase 64 (PER64) (P64) (PRXR4) identical to SPIQ43872 Peroxidase 64 precursor (EC 1.11.1.7) (Alperox P64) (PRXR4) (ATP17a) [Arabidopsis thaliana] (88418.m05134)	peroxidase 64 (PER64) (P64) (PRXR4) identical to SPIQ43872 Peroxidase 64 precursor (EC 1.11.1.7) (Alperox P64) (PRXR4) (ATP17a) [Arabidopsis thaliana] (88418.m05134)
4069	Not regulated	NC-NC-NC	249227_at	AT5g42180	E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (A2) / UFO-binding protein (UFP2) E3 ubiquitin ligase; skp1b; identical to UFP2 GI:3719211 from [Arabidopsis thaliana]; contains Pfam profiles PF01468: Skp1 family, dimethylase domain and PF03931: Skp1 family, tetramensation domain; identical to cDNA UFO binding protein UFP2 mRNA, partial cds GI:3719210 (88418.m05135)	E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (A2) / UFO-binding protein (UFP2) E3 ubiquitin ligase; skp1b; identical to UFP2 GI:3719211 from [Arabidopsis thaliana]; contains Pfam profiles PF01468: Skp1 family, dimethylase domain and PF03931: Skp1 family, tetramensation domain; identical to cDNA UFO binding protein UFP2 mRNA, partial cds GI:3719210 (88418.m05135)
4070	Not regulated	NC-NC-NC	249228_at	AT5g42190	expressed protein (88418.m05124)	expressed protein (88418.m05124)
4071	Not regulated	NC-NC-NC	249229_at	AT5g42090	expressed protein similar to unknown protein (dbjBAA92898.1) (88418.m05121)	expressed protein similar to unknown protein (dbjBAA92898.1) (88418.m05121)
4072	Not regulated	NC-NC-NC	249230_at	AT5g42070	expressed protein similar to unknown protein (embjCAB66408.1) (88418.m05117)	expressed protein similar to unknown protein (embjCAB66408.1) (88418.m05117)
4073	Not regulated	NC-NC-NC	249231_at	AT5g42030	expressed protein (88418.m05108)	expressed protein (88418.m05108)
4074	Not regulated	NC-NC-NC	249236_at	AT5g41890	expressed protein contains Pfam profile PF03690: Uncharacterised protein family (UFP0160) (88418.m05110)	expressed protein contains Pfam profile PF03690: Uncharacterised protein family (UFP0160) (88418.m05110)
4075	Not regulated	NC-NC-NC	249239_at	AT5g41970	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (88418.m05112)	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (88418.m05112)
4076	Not regulated	NC-NC-NC	249239_at	AT5g41990	zinc carboxypeptidase family protein contains Pfam domain, PF00246: Zinc carboxypeptidase (88418.m05150)	zinc carboxypeptidase family protein contains Pfam domain, PF00246: Zinc carboxypeptidase (88418.m05150)
4077	Not regulated	NC-NC-NC	249248_at	AT5g42320	serine carboxypeptidase S10 family protein similar to Serine carboxypeptidase II-3 precursor (SP-P52711) (CP-MII.3, [Hordseum vulgare] (88418.m05142)	serine carboxypeptidase S10 family protein similar to Serine carboxypeptidase II-3 precursor (SP-P52711) (CP-MII.3, [Hordseum vulgare] (88418.m05142)
4078	Not regulated	NC-NC-NC	249216_at	AT5g42240	metalloendopeptidase identical to chloroplast processing enzyme metalloendopeptidase [Arabidopsis thaliana]	metalloendopeptidase identical to chloroplast processing enzyme metalloendopeptidase [Arabidopsis thaliana]
4079	Not regulated	NC-NC-NC	249218_at	AT5g42390	gi 2827039 gb AAAC39482 (88418.m05181)	gi 2827039 gb AAAC39482 (88418.m05181)
4080	Not regulated	NC-NC-NC	249220_at	AT5g42420	transporter-related low similarity to phosphoenolpyruvate/phosphate translocator precursor [Mesembryanthemum crystallinum] GI:9295275, glucose-6-phosphate/phosphate-translocator precursor [Solanum tuberosum] GI:2897593 (88418.m05184)	transporter-related low similarity to phosphoenolpyruvate/phosphate translocator precursor [Mesembryanthemum crystallinum] GI:9295275, glucose-6-phosphate/phosphate-translocator precursor [Solanum tuberosum] GI:2897593 (88418.m05184)
4081	Not regulated	NC-NC-NC	249192_at	AT5g42470	expressed protein low similarity to BRE alpha 1 isoform [Homo sapiens] GI:16326573 (88418.m05170)	expressed protein low similarity to BRE alpha 1 isoform [Homo sapiens] GI:16326573 (88418.m05170)
4082	Not regulated	NC-NC-NC	249193_at	AT5g42480	DNAJ domain (88418.m05171)	DNAJ domain (88418.m05171)
4083	Not regulated	NC-NC-NC	249195_s_at	AT5g42500	disease resistance-responsive family protein similar to disease resistance response protein 208-d [Pisum sativum]	disease resistance-responsive family protein similar to disease resistance response protein 208-d [Pisum sativum]
4084	Not regulated	NC-NC-NC	249196_at	AT5g42560	abscisic acid-responsive HVA22 family protein weak similarity to SPIQ00705 Polyposis locus protein 1 (TB2 protein) (Homo sapiens); contains Pfam profile PF03134: TB2/DP1, HVA22 family (88418.m05180)	abscisic acid-responsive HVA22 family protein weak similarity to SPIQ00705 Polyposis locus protein 1 (TB2 protein) (Homo sapiens); contains Pfam profile PF03134: TB2/DP1, HVA22 family (88418.m05180)
4085	Not regulated	NC-NC-NC	249199_at	AT5g42520	expressed protein (88418.m05178)	expressed protein (88418.m05178)

4086	Not regulated	4086	NC-NC-NC	249204_at	A15g42570	expressed protein low similarity to SPIP51572 B-cell receptor-associated protein 31 (BC6-AG tumor-associated antigen) (DXS1357E) (Homo sapiens) (88418.m05183)
4087	Not regulated	4087	NC-NC-NC	249210_at	A15g42870	agouti domain-containing protein contains Pfam PF05841; Agouti domain (88418.m05188)
4088	Not regulated	4088	NC-NC-NC	249214_at	A15g42720	glycosyl hydrolase family 17 protein similar to glucan endo-1,3-beta-glucosidase precursor SP.P52409 from [Triticum aestivum] (88418.m05203)
4089	Not regulated	4089	NC-NC-NC	249188_at	A15g42830	transferase family protein similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus [gi:2239061]; contains Pfam transferase family domain PF002458 (88418.m05219)
4090	Not regulated	4090	NC-NC-NC	249161_at	A15g42780	20S proteasome alpha subunit F1 (PAF1) (gbIAAC32082.1) (88418.m05212)
4091	Not regulated	4091	NC-NC-NC	249162_at	A15g42765	expressed protein (88418.m05208)
4092	Not regulated	4092	NC-NC-NC	249163_at	A15g42740	glucose-6-phosphate isomerase, cytosolic (PGIC) identical to SPIP34795 Glucose-6-phosphate isomerase, cytosolic (EC 5.3.1.9) (GPI) (Phosphoglucose isomerase) (GPI) (Phosphoglucose isomerase) (88418.m05205)
4093	Not regulated	4093	NC-NC-NC	249165_at	A15g42810	PF00342: glucose-6-phosphate isomerase (88418.m05214)
4094	Not regulated	4094	NC-NC-NC	249171_at	A15g42940	expressed protein similar to unknown protein (pirlT26506) (88418.m05214)
4095	Not regulated	4095	NC-NC-NC	249175_at	A15g42970	zinc finger (C3HC4-type RING finger) family protein similar to Pfam domain, PF00087: Zinc finger, C3HC4 type (RING finger) (88418.m05235)
4096	Not regulated	4096	NC-NC-NC	249176_at	A15g42980	COP9 signalosome complex subunit 4 / CSN complex subunit 4 (CSN4) (COP9) (FUS4) FUSC4, COP8, CSN4; identical to CSN complex subunit 4 [Arabidopsis thaliana] GI:18056659, COP8 [Arabidopsis thaliana] GI:5802627; contains Pfam profile PF01399; PCI domain; identical to cDNA CSN complex subunit 4 (CSN4) GI:18056658 (88418.m05241)
4097	Not regulated	4097	NC-NC-NC	249177_at	A15g42850	thioredoxin H-type 3 (TRX-H-3) (GIF1) identical to SPIQ42403 Thioredoxin H-type 3 (TRX-H-3) (Arabidopsis thaliana); identical to cDNA (GIF1) mRNA for thioredoxin GI:982961 (88418.m05242)
4098	Not regulated	4098	NC-NC-NC	249178_at	A15g42890	expressed protein (88418.m05222)
4099	Not regulated	4099	NC-NC-NC	249180_at	A15g43010	sterol carrier protein 2 (SCP-2) family protein similar to sterol carrier protein-2 [Homo sapiens] GI:432973; contains Pfam profile PF02036: SCP-2 sterol transfer family (88418.m05227)
4100	Not regulated	4100	NC-NC-NC	249181_at	A15g42920	26S proteasome AAA-ATPase subunit (RPT4a) gbIAAF2524.1 (88418.m05245)
4101	Not regulated	4101	NC-NC-NC	249182_at	A15g42960	expressed protein (88418.m05232)
4102	Not regulated	4102	NC-NC-NC	249183_at	A15g42980	expressed protein (88418.m05239)
4103	Not regulated	4103	NC-NC-NC	249133_at	A15g43130	ubiquitin-conjugating enzyme 18 (UBC18) E2; identical to gi:2801448 (88418.m05243)
4104	Not regulated	4104	NC-NC-NC	249136_at	A15g43180	transcription initiation factor IID (TFIID) component TAF4 family protein weak similarity to SPIQ00288 Transcription initiation factor TFIIID 135 kDa subunit (Homo sapiens); contains Pfam profile PF05236: Transcription initiation factor TFIID component TAF4 family (88418.m05265)
4105	Not regulated	4105	NC-NC-NC	249138_at	A15g43070	expressed protein contains Pfam profile PF04654: Protein of unknown function, DUF589 (88418.m05272)
4106	Not regulated	4106	NC-NC-NC	249140_at	A15g43190	MFP1 attachment factor, putative contains similarity to MFP1 attachment factor 1 similar to MFP1 attachment factor 1 [Glycine max] (88418.m05276)
4107	Not regulated	4107	NC-NC-NC	249147_at	A15g43330	F-box family protein (FBX6) contains similarity to unusual floral organs (UFO) GI:4376159 from [Arabidopsis thaliana]
4108	Not regulated	4108	NC-NC-NC	249158_at	A15g43430	malate dehydrogenase, cytosolic, putative strong similarity to cytosolic malate dehydrogenase (EC 1.1.1.37) SPIQ24047 (Mesembryanthemum crystallinum), SPIQ48905 (Medicago sativa), [Prunus pensilv] GI:15882848; contains InterPro entry IPK001236: Lactate/malate dehydrogenase (88418.m05296)
4109	Not regulated	4109	NC-NC-NC	249159_at	A15g43460	electron transfer flavoprotein beta subunit family protein contains Pfam profile: PF01012 electron transfer flavoprotein, beta subunit (88418.m05310)
4110	Not regulated	4110	NC-NC-NC	249128_at	A15g43440	lesion inducing protein-related similar to ORF, able to induce HR-like lesions [Nicotiana tabacum] (88418.m05313)
4111	Not regulated	4111	NC-NC-NC	249100_at	A15g43560	2-oxoglutarate-dependent dioxygenase, putative similar to 2A6 (GI:598822) and tomato ethylene synthesis regulatory protein E8 (SPIP10867) (88418.m05311)
4112	Not regulated	4112	NC-NC-NC	249103_at	A15g43600	meprin and TRAF homology domain-containing protein / MATH domain-containing protein weak similarity to ubiquitin-specific protease 12 [Arabidopsis thaliana] GI:11993471; contains Pfam profile PF00917: MATH domain (88418.m05325)
4113	Not regulated	4113	NC-NC-NC	249120_at	A15g43750	N-carbamyl-L-amino acid hydrolase, putative similar to N-carbamoyl-L-amino acid hydrolase [Bacillus stearothermophilus] SWISS-PROT:Q53389 (88418.m05330)
4114	Not regulated	4114	NC-NC-NC	249121_at	A15g43830	expressed protein (88418.m05350)
4115	Not regulated	4115	NC-NC-NC	249124_at	A15g43740	expressed protein similar to auxin down-regulated protein ARG10 [Vigna radiata] GI:2970051; wall7 (aluminum-induced protein) [Triticum aestivum] GI:451193 (88418.m05359)
4116	Not regulated	4116	NC-NC-NC	249083_at	A15g43880	disease resistance protein (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein, (88418.m05347)
4117	Not regulated	4117	NC-NC-NC	249072_at	A15g44060	expressed protein (88418.m05396)
4118	Not regulated	4118	NC-NC-NC	249075_at	A15g44000	expressed protein similar to unknown protein (gbIAAD10670.1) (88418.m05391)
4119	Not regulated	4119	NC-NC-NC	249077_at	A15g43940	glutathione S-transferase C-terminal domain-containing protein contains Pfam domain PF00043: Glutathione S-transferase, C-terminal domain (88418.m05384)
4120	Not regulated	4120	NC-NC-NC	249081_at	A15g44090	alcohol dehydrogenase class III / glutathione-dependent formaldehyde dehydrogenase / GSH-FDH (ADHIII) identical to gi:1143388 (88418.m05376)
4121	Not regulated	4121	NC-NC-NC	249089_at	A15g44240	calcium-binding EF hand family protein, putative / protein phosphatase 2A 62 kDa B" regulatory subunit, putative contains Pfam profile: PF00036 EF hand; identical to cDNA protein phosphatase 2A 62 kDa B" regulatory subunit GI:5533378 (88418.m05394)
4122	Not regulated	4122	NC-NC-NC	249093_at	A15g44110	haloacid dehalogenase-like hydrolase family protein similar to Potential phospholipid-transporting ATPase (EC 3.6.3.1) from (Musa musculus) SPIP70704, [Bos taurus] SPQ28449; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase (88418.m05412)
4123	Not regulated	4123	NC-NC-NC	249094_at	A15g44250	ABC transporter family protein (88418.m05397)
						expressed protein contains Pfam PF05705: Eukaryotic protein of unknown function (DUF629) (88418.m05413)

4124	Not regulated	NC-NC-NC	249036_at	A15g44200	nuclear cap-binding protein, putative similar to SPIP2298 20 kDa nuclear cap binding protein (CBP20) (NCBP interacting protein 1) (Homo sapiens), non-consensus AT donor splice site at exon 4, AC acceptor splice site at exon 5; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RIM) (68418.m05408)
4125	Not regulated	NC-NC-NC	249040_at	A15g44320	eukaryotic translation initiation factor 3 subunit 7, putative / eIF-3 zeta, putative similar to initiation factor 3d [Arabidopsis thaliana] GI:12407755; SPI015371 Eukaryotic translation initiation factor 3 subunit 7 (eIF-3 zeta) (eIF3 p66) (eIF3d) (Homo sapiens); contains Pfam profile PF05091: Eukaryotic translation initiation factor 3 subunit 7 (eIF-3) (68418.m05427)
4126	Not regulated	NC-NC-NC	249049_at	A15g44340	tubulin beta-4 chain (TUBA4) nearly identical to SPIP24836 Tubulin beta-4 chain (Arabidopsis thaliana) (68418.m05428)
4127	Not regulated	NC-NC-NC	249050_at	A15g44290	protein kinase family protein contains Pfam domain, PF00069: Protein kinase domain (68418.m05421)
4128	Not regulated	NC-NC-NC	249057_at	A15g44480	NAD-dependent epimerase/dehydratase family protein similar to SPIP55180 UDP-glucose 4-epimerase (EC 5.1.3.2) from <i>Bacillus subtilis</i> , GI:3021357 UDP-glucose 4-epimerase from <i>Cyanopsis tetragonoloba</i> ; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family (68418.m05450)
4129	Not regulated	NC-NC-NC	249010_at	A15g44580	expressed protein (68418.m05463)
4130	Not regulated	NC-NC-NC	249014_at	A15g44710	expressed protein similar to unknown protein (refNP_011731.1) (68418.m05478)
4131	Not regulated	NC-NC-NC	249026_at	A15g44785	expressed protein contains Pfam PF05329: Protein of unknown function (DUF731) (68418.m05469)
4132	Not regulated	NC-NC-NC	249029_at	A15g44870	disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein. (68418.m05501)
4133	Not regulated	NC-NC-NC	249033_at	A15g44920	Toll-interleukin-Resistance (TIR) domain-containing protein domain signature TIR exists, suggestive of a disease resistance protein. (68418.m05507)
4134	Not regulated	NC-NC-NC	249037_at	A15g45070	disease resistance protein (TIR class), putative domain signature TIR exists, suggestive of a disease resistance protein. (68418.m05527)
4135	Not regulated	NC-NC-NC	249081_at	A15g45110	ankyrin repeat family protein / BTB/POZ domain-containing protein contains Pfam domain, PF00023: Ankyrin repeat and Pfam domain, PF00651: BTB/POZ domain (68418.m05536)
4136	Not regulated	NC-NC-NC	249083_at	A15g45130	Ras-related protein (RHA1) / small GTP-binding protein identical to Ras-related protein RHA1 SP:P31582 from [Arabidopsis thaliana] (68418.m05540)
4137	Not regulated	NC-NC-NC	249086_at	A15g45170	CbbY protein-related low similarity to SPIP40119 CbbY protein, chromosomal (Alcaligenes eutrophus) (68418.m05545)
4138	Not regulated	NC-NC-NC	249050_at	A15g45390	ATP-dependent Clp protease proteolytic subunit (ClpP4) identical to nClpP4 GI:5360583 from [Arabidopsis thaliana] (68418.m05578)
4139	Not regulated	NC-NC-NC	249051_at	A15g45550	mob 1/phocin family protein contains Pfam profile, PF03637 Mob 1/phocin family (68418.m05594)
4140	Not regulated	NC-NC-NC	249055_at	A15g45600	YEATS family protein contains Pfam domain PF03366: YEATS family (68418.m05603)
4141	Not regulated	NC-NC-NC	249057_at	A15g45620	26S proteasome regulatory subunit, putative (RPN6) contains similarity to 26S proteasome subunit p40.5 GI:3618343 from [Homo sapiens] (68418.m05607)
4142	Not regulated	NC-NC-NC	249058_at	A15g45590	expressed protein (68418.m05601)
4143	Not regulated	NC-NC-NC	249058_at	A15g45800	leucine-rich repeat transmembrane protein kinase, putative (68418.m05632)
4144	Not regulated	NC-NC-NC	249014_at	A15g45750	Ras-related GTP-binding protein, putative similar to GTP-binding protein GI:303744 from [Pisum sativum] (68418.m05624)
4145	Not regulated	NC-NC-NC	249020_at	A15g45930	magnesium-chelatase subunit chl, chloroplast, putative / Mg-protoporphyrin IX chelatase, putative similar to SPIP161127 from <i>Arabidopsis thaliana</i> , SPIP93162 from Glycine max, SPIQ22436 from <i>Nicotiana glauca</i> ; non-consensus AA donor splice site at exon 1, TG acceptor splice site at exon 2 (68418.m05648)
4146	Not regulated	NC-NC-NC	249023_at	A15g45940	MutT/nudix family protein contains Pfam profile PF00293: NUDIX domain (68418.m05649)
4147	Not regulated	NC-NC-NC	249027_at	A15g45900	autophagy 7 (APG7) nearly identical to autophagy 7 [Arabidopsis thaliana] GI:19912147; contains Pfam profile PF00898: Thif family (68418.m05645)
4148	Not regulated	NC-NC-NC	249078_at	A15g46160	ribosomal protein L14 family protein / huelienlos paralog (HLP) contains Pfam profile PF00238: Ribosomal protein L14pL23e; identical to cDNA HUELLENLOS PARALOG (HLP) nuclear gene for mitochondrial product GU:18140859 (68418.m05677)
4149	Not regulated	NC-NC-NC	249079_at	A15g46180	ornithine aminotransferase, putative / ornithine--oxo-acid aminotransferase, putative similar to SPIQ82413 Ornithine aminotransferase (EC 2.6.1.13) (Ornithine--oxo-acid aminotransferase) [Aspergillus nidulans]; contains Pfam profile PF00202: aminotransferase, class III (68418.m05680)
4150	Not regulated	NC-NC-NC	249084_at	A15g46030	expressed protein contains Pfam profile PF05129: Putative zinc binding domain (DUF701) (68418.m05661)
4151	Not regulated	NC-NC-NC	249086_at	A15g46110	phosphate/triose-phosphate translocator, putative identical to phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana] GI:3983125 [giAAC38315]; similar to those phosphate/phosphate translocator, chloroplast precursor (CTPT)[Cauliflower/Brassica oleracea] SWISS-PROT:PS2177 (68418.m05669)
4152	Not regulated	NC-NC-NC	249096_at	A15g46350	WRKY family transcription factor contains similarity to WRKY-type DNA-binding protein (68418.m05705)
4153	Not regulated	NC-NC-NC	249093_at	A15g46290	3-oxoacyl-CoA-carrier-protein synthase I identical to Swis-Prot:PS2410 3-oxoacyl-CoA-carrier-protein synthase I, chloroplast precursor (EC 2.3.1.41) (Beta-ketoacyl-ACP synthase I) (KAS I) [Arabidopsis thaliana] (68418.m05688)
4154	Not regulated	NC-NC-NC	249005_at	A15g46250	RNA recognition motif (RRM)-containing protein contains similarity to RNA-binding protein; contains InterPro entry IPR000504: RNA binding region RNP-1 (RNA recognition motif) (RRM) (68418.m05693)
4155	Not regulated	NC-NC-NC	249008_at	A15g46420	16S rRNA processing protein RlmM family contains weak similarity to Swiss-Prot:Q74833 UDP-N-acetylglucosamine pyrophosphorylase [Candida albicans]; contains Pfam profiles PF01782: 16S rRNA processing protein RlmM, PF05239: PRC-barrel domain (68418.m05713)
4156	Not regulated	NC-NC-NC	249054_at	A15g46580	pentapeptide (PPR) repeat-containing protein contains similarity to 67kD chloroplastic RNA-binding protein, P67.1 [Rapanus sativus] GI:9755886; contains Pfam profile PF01535: PPR repeat (68418.m05735)
4157	Not regulated	NC-NC-NC	249056_at	A15g46620	expressed protein similar to unknown protein (pfIT05082) (68418.m05739)
4158	Not regulated	NC-NC-NC	249058_at	A15g46630	clathrin adaptor complexes medium subunit family protein contains Pfam profile: PF00928 adaptor complexes medium subunit family (68418.m05740)
4159	Not regulated	NC-NC-NC	249061_at	A15g46700	senescence-associated protein, putative similar to senescence-associated protein 5 [Hemerocallis hybrid cultivar] GI:3551954 [giAAC34855 (68418.m05754)]

4160	Not regulated	NC-NC-NC	248983_at	A15g46750	human Rev interacting-like family protein / hRIP family protein contains Pfam profile PF01412: Putative GTP-ase activating protein for Arf (68418.m05753)
4161	Not regulated	NC-NC-NC	248985_at	A15g46790	expressed protein similar to unknown protein (pifT05073) (68418.m05764)
4162	Not regulated	NC-NC-NC	248989_at	A15g46940	RNA recognition motif (RRM)-containing protein contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) (68418.m05771)
4163	Not regulated	NC-NC-NC	248938_at	A15g46800	mitochondrial carnitine/acyl carrier, putative / a bout de souille (BOU) / CAC-like protein identical to SPIQ93XM7 Mitochondrial carnitine/acylcarnitine carrier-like protein (A BOUT DE SOUFFLE) (Carnitine/acylcarnitine translocase-like protein) (CAC-like protein) [Arabidopsis thaliana], contains Pfam profile: PF00153 mitochondrial carrier protein (68418.m05766)
4164	Not regulated	NC-NC-NC	248813_at	A15g46980	syntaxin 22 (SYP22) (VAM3) identical to GPI809669; syntaxin related protein AtVam3p [Arabidopsis thaliana] (68418.m05774)
4165	Not regulated	NC-NC-NC	248818_at	A15g47040	Lon protease homolog 1, mitochondrial (LON) identical to Lon protease homolog 1 mitochondrial precursor SP-Q64948 from [Arabidopsis thaliana] (68418.m05797)
4166	Not regulated	NC-NC-NC	248820_at	A15g47060	senescence-associated protein-related similar to senescence-associated protein SAG102 (GI:22331831) [Arabidopsis thaliana]; (68418.m05799)
4167	Not regulated	NC-NC-NC	248825_at	A15g47030	ATP synthase delta' chain, mitochondrial identical to SPIQ96252 ATP synthase delta' chain, mitochondrial precursor (EC 3.6.3.14) [Arabidopsis thaliana]; contains Pfam profile PF02823: ATP synthase, Delta/Epsilon chain, beta-sandwich domain (68418.m05796)
4168	Not regulated	NC-NC-NC	248826_at	A15g47080	casein kinase II beta chain, putative similar to casein kinase II beta chain (CK II) [Arabidopsis thaliana] SWISS-PROT:P40228 (68418.m05802)
4169	Not regulated	NC-NC-NC	248827_at	A15g47100	calneurin B-like protein 9 (CBL9) identical to calneurin B-like protein 9 (GI:5866278) and calcium-binding protein AICBL9 (GI:16151825) [Arabidopsis thaliana]; similar to calneurin B-like protein 1 (GI:3309082) [Arabidopsis thaliana] (68418.m05807)
4170	Not regulated	NC-NC-NC	248828_at	A15g47110	it3 protein, putative similar to L13 protein [Arabidopsis thaliana] gi4741966 [giAA028780] (68418.m05808)
4171	Not regulated	NC-NC-NC	248792_at	A15g47200	Ras-related GTP-binding protein, putative similar to GTP-binding protein GI:303750 from [Pisum sativum] (68418.m05820)
4172	Not regulated	NC-NC-NC	248795_at	A15g47390	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain (68418.m05840)
4173	Not regulated	NC-NC-NC	248796_at	A15g47180	vesicle-associated membrane family protein / VAMP family protein similar to VAP27 GI:9688928 [Nicotiana glauca] (68418.m05841)
4174	Not regulated	NC-NC-NC	248798_at	A15g47190	VAMP-associated protein B GI:4240464 [Rattus norvegicus] and to Vesicle-associated membrane protein/Vynaptobrevin binding protein (VAP-33) (SP-Q16943) [Aplysia californica] (68418.m05817)
4175	Not regulated	NC-NC-NC	248800_at	A15g47320	ribosomal protein L18 family protein similar to plastid ribosomal protein L19 precursor [Spinacia oleracea] gi17582403 [giAA184312] (68418.m05819)
4176	Not regulated	NC-NC-NC	248801_at	A15g47370	30S ribosomal protein S19, mitochondrial (RPS19) (68418.m05833)
4177	Not regulated	NC-NC-NC	248802_at	A15g47435	homeobox-leucine zipper protein 2 (HAT2) / HD-ZIP protein 2 identical to homeobox-leucine zipper protein HAT2 (HD-ZIP protein 2) [Arabidopsis thaliana] SP-P46801; contains Pfam profile PF04618: HD-ZIP protein N terminus, PF02183: Homeobox associated leucine zipper, PF00046: Homeobox domain (68418.m05838)
4178	Not regulated	NC-NC-NC	248805_at	A15g47480	formyltetrahydrofolate deformylase, putative similar to formyltetrahydrofolate deformylase [strain PCC 6803- Synecchocystis sp.] expressed protein (68418.m05845)
4179	Not regulated	NC-NC-NC	248751_at	A15g47540	SWISS-PROT:Q55135 (68418.m05845)
4180	Not regulated	NC-NC-NC	248757_at	A15g47680	Mo25 family protein similar to Mo25 protein (early mouse development protein family) [Mouse] SWISS-PROT:Q06138 (68418.m05869)
4181	Not regulated	NC-NC-NC	248759_at	A15g47810	expressed protein contains Pfam profile PF04243: Protein of unknown function (DUF425) (68418.m05868)
4182	Not regulated	NC-NC-NC	248760_at	A15g47570	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00087 zinc finger, C3HC4 type (RING finger) (68418.m05876)
4183	Not regulated	NC-NC-NC	248764_at	A15g47640	expressed protein (68418.m05872)
4184	Not regulated	NC-NC-NC	248767_at	A15g47710	CCAAT-box binding transcription factor subunit B (NF-YB) (HAP3) (AHAP3) family (Hap3b) similar to CAAT-box DNA binding protein subunit B (NF-YB) (SP-P25209) (GI:22380) [Zea mays]; contains Pfam PF00808 : Histone-like transcription factor (CBF/NF-Y) and archaeal histone; identical to cDNA transcription factor Hap3b (Hap3b) mRNA, partial cds GI:985734 (68418.m05882)
4185	Not regulated	NC-NC-NC	248768_at	A15g47700	C2 domain-containing protein contains similarity to CLB1 [Lycopodium obscurum] GI:2769434; contains Pfam profile PF00168: C2 domain (68418.m05891)
4186	Not regulated	NC-NC-NC	248769_at	A15g47730	60S acidic ribosomal protein P1 (RPP1C) (68418.m05889)
4187	Not regulated	NC-NC-NC	248748_at	A15g47840	SEC14 cytosolic factor, putative / polyphosphoinositide-binding protein, putative similar to polyphosphoinositide binding protein SEC14 homolog Ssh1p (GI:2739044) [Glycine max] (68418.m05897)
4188	Not regulated	NC-NC-NC	248749_at	A15g47880	adenylate kinase, chloroplast, putative / ATP-AMP transphosphorylase, putative similar to SPIP43188 Adenylate kinase, chloroplast (EC 2.7.4.3) (ATP-AMP transphosphorylase) [Zea mays]; contains Pfam profile PF00406: Adenylate kinase (68418.m05911)
4189	Not regulated	NC-NC-NC	248718_at	A15g47770	eukaryotic peptide chain release factor subunit 1-1 (ERF1-1) identical to SPIQ39097 Eukaryotic peptide chain release factor subunit 1-1 (eRF1-1) [Eukaryotic release factor 1-1] (Ornithine suppressor protein 1 homolog 1) (SUP1 homolog 1) [Arabidopsis thaliana], eukaryotic release factor 1 homolog GI:1155281 from [Arabidopsis thaliana]; contains Pfam profiles: PF03463 eRF1 domain 1, PF03464 eRF1 domain 2, PF03465 eRF1 domain 3 (68418.m05915)
4190	Not regulated	NC-NC-NC	248719_at	A15g47910	farnesyl pyrophosphate synthetase 1, mitochondrial (FPS1) / FPP synthetase 1 / farnesyl diphosphate synthase 1 identical to SPIQ08152 Farnesyl pyrophosphate synthetase 1, mitochondrial precursor (FPP synthetase 1) (FPS 1) (Farnesyl diphosphate synthetase 1) [includes: Dimethylallyltransferase (EC 2.5.1.1); Geranyltransferase (EC 2.5.1.10)] [Arabidopsis thaliana] (68418.m05901)
4191	Not regulated	NC-NC-NC	248737_at	A15g48120	respiratory burst oxidase protein D (RbohD) / NADPH oxidase identical to respiratory burst oxidase protein D from Arabidopsis thaliana [gi:3242769] (68418.m05918)
					expressed protein low similarity to MMS19 [Mus musculus] GI:14029390 (68418.m05944)

4192	Not regulated	NC-NC-NC	248738_at	A15g48020	expressed protein (68418.m05934) DNAJ heat shock protein, mitochondrially targeted (GFA2) 99.8% identical to mitochondrially targeted DnaJ protein GFA2 [Arabidopsis thaliana] GI:21429604; contains Pfam profiles PF00228: DnaJ domain, PF01556: DnaJ C terminal region, PF00684: DnaJ central domain (4 repeats) (68418.m05935) indole-3-glycerol phosphate synthase, putative similar to SPIP49572 (68418.m05957) phytochrome A signal transduction 1 (PAT1) (68418.m05947) acetyl-CoA C-acetyltransferase, putative / 3-ketoacyl-CoA thiolase, putative strong similarity to Acetoacetyl-coenzyme A thiolase (E.C. 2.3.1.9) [Rachanus sativus] GI:1542941; contains InterPro accession IPR002155: Thiolase (68418.m05958) leucine-rich repeat family protein / protein kinase family protein contains protein kinase domain, Pfam:PF00088; contains leucine-rich repeats, Pfam:PF00560 (68418.m05978) glutamate receptor family protein (GLR1.2) plant glutamate receptor family, PMID:11379628 (68418.m05984) glutamate receptor family protein (GLR1.3) plant glutamate receptor family, PMID:11379628 (68418.m05986) cyclin family protein similar to SPIP55168 Cyclin C [Gallus gallus]; contains Pfam profile PF00134: Cyclin, N-terminal domain (68418.m06015) expressed protein (68418.m06010) cyclin family protein similar to SPIP55168 Cyclin C [Gallus gallus]; contains Pfam profile PF00134: Cyclin, N-terminal domain (68418.m06014) small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative similar to U6 snRNA-associated Sm-like protein LSmt5 [Homo sapiens] SWISS-PROT:Q8Y4Y8 (68418.m06045) pectate lyase family protein similar to pectate lyase GP:14531298 from [Fragaria x ananassa]; non-consensus AG donor splice site at exon 2 (68418.m06049) 60S ribosomal protein L13a (RPL13aD) (68418.m06034) expressed protein (68418.m06037) drought-responsive family protein similar to drought-induced mRNA, D19 [Arabidopsis thaliana] gi469110[emb]CAA55321 (68418.m06094) zinc knuckle (CCHC-type) family protein contains Pfam domain, PF00098: Zinc knuckle (68418.m06113) ATP-citrate lyase, putative / ATP-citrate (pro-S)-lyase, putative / citrate cleavage enzyme, putative strong similarity to ATP-citrate lyase [Capsicum annuum] GI:13160653; contains Pfam profiles PF00549: CoA-ligase, PF02828: CoA binding domain (68418.m06119) SIN-like family protein low similarity to Sex-lethal interactor [Drosophila melanogaster] GI:6048274; contains Pfam profile PF04801: SIN-like protein conserved region (68418.m06130) transglutaminase-like family protein low similarity to peptide-N-glycanase PNGase [Mus musculus] GI:8347622; contains Pfam profile PF01841: Transglutaminase-like superfamily (68418.m06135) expressed protein (68418.m06132) VHL binding protein, putative / pifelin, putative similar to Swas-Prot:Q15765 pifelin subunit 3 (Von Hippel-Lindau binding protein 1; VHL binding protein-1; VBP-1; HIBB46) [Mus musculus] (68418.m06127) xylose lyase, putative similar to D-xylose lyase [Pichia stipitis] gi8100400[gb]AAT73238 (68418.m06145) expressed protein similar to unknown protein (pif1105575) (68418.m06154) expressed protein (68418.m06171) ATP-dependent Clp protease ATP-binding subunit ClpX, putative similar to Clp protease regulatory subunit CLPX GI:2674203 from [Arabidopsis thaliana]; non-consensus splice donor GC at exon 4; non-consensus splice donor AA at exon 7 (68418.m06172) chloride channel protein (CLC-c) identical to gi:1742956 (68418.m06178) zinc knuckle (CCHC-type) family protein contains Pfam domain, PF00098: Zinc knuckle (68418.m06182) pyridoxamine 5'-phosphate oxidase-related contains weak similarity to Pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5) (PNP/PMPOxidase) (PNPOX), (Swiss-Prot:P28225) [Shigella flexneri] (68418.m06187) protein kinase, putative similar to protein kinase ATM/K1 [Arabidopsis thaliana] gi2351097[db]BAA22079 (68418.m06191) nitrogen fixation NifU-like family protein similar to Nitrogen fixation protein nifU (SP:Q43885) [Anabaena azollae]; contains Pfam profile: PF01106 NifU-like domain (68418.m06183) expressed protein contains Pfam domain PF04134: Protein of unknown function, DUF393 (68418.m06204) transducin family protein / WD-40 repeat family protein contains 7 WD-40 repeats (PF00400); similar to T1PD PROTEIN (SP:O15736)[Dicyostelium discoideum] (68418.m06221) quinolinate synthetase A-related contains weak similarity to Swiss-Prot:P11458 quinolinate synthetase A [Escherichia coli] (68418.m06219) expressed protein similar to unknown protein (pif1105562) isoform contains a non-consensus AT acceptor splice site at intron 1 (68418.m06216) 31 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein RNP-T, putative / RNA-binding protein 1/23, putative / RNA-binding protein q31, putative similar to SP Q04836 31 kDa ribonucleoprotein, chloroplast precursor (RNA-binding protein RNP-T) (1/23) (AIRBP33) (cp31) [Arabidopsis thaliana]; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) (68418.m06223) expressed protein (68418.m06236) exocyst subunit EXO70 family protein contains Pfam domain PF03081: Exo70 exocyst complex subunit; (68418.m06240) calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase (68418.m06242) expressed protein (68418.m06243) expressed protein strong similarity to unknown protein (gb AA050008.1) (68418.m06244)
4193	Not regulated	NC-NC-NC	248739_at	A15g48030	
4194	Not regulated	NC-NC-NC	248688_at	A15g48220	
4195	Not regulated	NC-NC-NC	248689_at	A15g48150	
4196	Not regulated	NC-NC-NC	248690_at	A15g48230	
4197	Not regulated	NC-NC-NC	248698_at	A15g48380	
4198	Not regulated	NC-NC-NC	248700_at	A15g48760	
4199	Not regulated	NC-NC-NC	248701_at	A15g48410	
4200	Not regulated	NC-NC-NC	248699_at	A15g48640	
4201	Not regulated	NC-NC-NC	248693_at	A15g48590	
4202	Not regulated	NC-NC-NC	248696_at	A15g48630	
4203	Not regulated	NC-NC-NC	248678_at	A15g48670	
4204	Not regulated	NC-NC-NC	248681_at	A15g48900	
4205	Not regulated	NC-NC-NC	248655_at	A15g48760	
4206	Not regulated	NC-NC-NC	248624_at	A15g48790	
4207	Not regulated	NC-NC-NC	248595_at	A15g48230	
4208	Not regulated	NC-NC-NC	248601_at	A15g49400	
4209	Not regulated	NC-NC-NC	248608_at	A15g49460	
4210	Not regulated	NC-NC-NC	248612_at	A15g49530	
4211	Not regulated	NC-NC-NC	248615_at	A15g49570	
4212	Not regulated	NC-NC-NC	248597_at	A15g49550	
4213	Not regulated	NC-NC-NC	248589_at	A15g49510	
4214	Not regulated	NC-NC-NC	248591_at	A15g49650	
4215	Not regulated	NC-NC-NC	248565_at	A15g49710	
4216	Not regulated	NC-NC-NC	248574_at	A15g48830	
4217	Not regulated	NC-NC-NC	248575_at	A15g48840	
4218	Not regulated	NC-NC-NC	248580_at	A15g49890	
4219	Not regulated	NC-NC-NC	248593_at	A15g49930	
4220	Not regulated	NC-NC-NC	248590_at	A15g49970	
4221	Not regulated	NC-NC-NC	248529_at	A15g50000	
4222	Not regulated	NC-NC-NC	248532_at	A15g49940	
4223	Not regulated	NC-NC-NC	248537_at	A15g50100	
4224	Not regulated	NC-NC-NC	248543_at	A15g50230	
4225	Not regulated	NC-NC-NC	248550_at	A15g50210	
4226	Not regulated	NC-NC-NC	248551_at	A15g50200	
4227	Not regulated	NC-NC-NC	248552_at	A15g50250	
4228	Not regulated	NC-NC-NC	248556_at	A15g50350	
4229	Not regulated	NC-NC-NC	248497_at	A15g50380	
4230	Not regulated	NC-NC-NC	248499_at	A15g50400	
4231	Not regulated	NC-NC-NC	248500_at	A15g50410	
4232	Not regulated	NC-NC-NC	248507_at	A15g50420	

4233	Not regulated	NC-NC-NC	248508_at	A15g50320	radical SAM domain-containing protein / GON5-related N-acetyltransferase (GNAT) family protein contains Pfam profiles PF00583; acetyltransferase, GNAT family, PF04055; Radical SAM superfamily (88418.m06232)
4234	Not regulated	NC-NC-NC	248511_at	A15g50375	cytopropyl isomerase (CPI1) (88418.m06239)
4235	Not regulated	NC-NC-NC	248521_s_at	A15g50630	nodulin family protein similar to nodulin-like protein [Arabidopsis thaliana] GI:3329388, nodule-specific protein Nt70 [Lotus japonicus] GI:3329368 (88418.m06272)
4236	Not regulated	NC-NC-NC	248523_s_at	A15g50580	SUMO activating enzyme, putative nearly identical to SUMO activating enzyme 1b [Arabidopsis thaliana] GI:22652852; nearly identical to A15g50680, contains Pfam profile PF00899; Thif family (88418.m06285)
4237	Not regulated	NC-NC-NC	248528_at	A15g50780	auxin-responsive family protein similar to auxin-induced protein TCSAUR22 (GI:10185820) [Tulipa gesneriana] (88418.m06288)
4238	Not regulated	NC-NC-NC	248471_at	A15g50840	expressed protein (88418.m06288)
4239	Not regulated	NC-NC-NC	248473_at	A15g50810	mitochondrial import inner membrane translocase (TIM8) identical to mitochondrial import inner membrane translocase subunit Tim8 [Arabidopsis thaliana] Swiss-Prot:Q9XGY4; contains Pfam domain, PF02953; Tim10/ODD family zinc finger (88418.m06285)
4240	Not regulated	NC-NC-NC	248474_at	A15g50850	pyruvate dehydrogenase E1 component beta subunit, mitochondrial / PDHE1-B (PDH2) identical to SPIQ38799 Pyruvate dehydrogenase E1 component beta subunit, mitochondrial precursor (EC 1.2.4.1) (PDHE1-B) [Arabidopsis thaliana]
4241	Not regulated	NC-NC-NC	248477_at	A15g50900	dehydrogenase E1 component beta subunit, mitochondrial precursor (EC 1.2.4.1) (PDHE1-B) [Arabidopsis thaliana]
4242	Not regulated	NC-NC-NC	248478_at	A15g50870	armadillo/beta-catenin repeat family protein armadillo/beta-catenin-like repeats, Pfam:PF00514 (88418.m06310)
4243	Not regulated	NC-NC-NC	248491_at	A15g51010	ubiquitin-conjugating enzyme, putative strong similarity to ubiquitin conjugating enzyme [Lycopersicon esculentum] GI:886678; contains Pfam profile PF00179; Ubiquitin-conjugating enzyme (88418.m06304)
4244	Not regulated	NC-NC-NC	248492_at	A15g51040	rubredoxin family protein similar to SPIP04170 Rubredoxin (Rd) [Desulfovibrio desulfuricans]; contains Pfam profile PF00301; rubredoxin (88418.m06324)
4245	Not regulated	NC-NC-NC	248493_at	A15g51100	expressed protein (88418.m06327)
4246	Not regulated	NC-NC-NC	248495_at	A15g51020	superoxide dismutase [Fe], putative / iron superoxide dismutase, putative similar to Fe-superoxide dismutase precursor [Medicago sativa] GI:16974682 [p]AAL32441 (88418.m06335)
4247	Not regulated	NC-NC-NC	248462_at	A15g50860	expressed protein similar to unknown protein [p]IIS76207 (88418.m06325)
4248	Not regulated	NC-NC-NC	248465_at	A15g51200	nucleotide-binding family protein similar to Nucleotide-binding protein 1 (NBP 1) (SP-QBR060) [Mus musculus]; contains Pfam PF00991; Para family ATPase (88418.m06320)
4249	Not regulated	NC-NC-NC	248445_at	A15g51170	expressed protein (88418.m06349)
4250	Not regulated	NC-NC-NC	248448_at	A15g51110	expressed protein (88418.m06344)
4251	Not regulated	NC-NC-NC	248433_at	A15g51400	expressed protein (88418.m06338)
4252	Not regulated	NC-NC-NC	248403_at	A15g51410	expressed protein contains Pfam profile PF04749; Protein of unknown function, DUF614 (88418.m06372)
					LUC7 N_terminus domain-containing protein similar to dispirin resistance-associated overexpressed protein [Homo sapiens] GI:6899846; contains Pfam profile PF03184; LUC7 N_terminus (88418.m06373)
4253	Not regulated	NC-NC-NC	248409_at	A15g51540	peptidase M3 family protein / bimetalloprotease family protein low similarity to SPIQ9787 Mitochondrial intermediate peptidase, mitochondrial precursor (EC 3.4.24.59) (Homo sapiens); contains Pfam profile PF01432; Peptidase family M3 (88418.m06381)
4254	Not regulated	NC-NC-NC	248415_at	A15g51620	expressed protein (88418.m06398)
4255	Not regulated	NC-NC-NC	248421_at	A15g51510	expressed protein (88418.m06398)
4256	Not regulated	NC-NC-NC	248422_at	A15g51640	leaf senescence protein-related (YLS7) annotation temporarily based on supporting cDNA [p]I1322291 [dbj]AB047810.1; identical to cDNA YLS7 leaf-senescence-related protein GI:1312291 (88418.m06403)
4257	Not regulated	NC-NC-NC	248426_at	A15g51740	peptidase M48 family protein contains Pfam domain, PF01435; Peptidase family M48 (88418.m06416)
4258	Not regulated	NC-NC-NC	248376_at	A15g51880	expressed protein (88418.m06434)
4259	Not regulated	NC-NC-NC	248379_at	A15g51700	RAR1 disease resistance protein (RAR1) Contains a 3 nt micro-exon at exon 2. (88418.m06411)
4260	Not regulated	NC-NC-NC	248382_at	A15g51890	peroxidase-related similar to peroxidase [Spinacia oleracea] GI:29590707 [emb]CAA76376 (88418.m06436)
					DNA-directed RNA polymerase II, putative similar to SPIQ8828 DNA-directed RNA polymerase II 14.4 kDa polypeptide (EC 2.7.7.6) (RPB8) (RPB14.4) (Rattus norvegicus); contains Pfam profile PF01192; RNA polymerases K / 14 to 18 kDa subunit (88418.m06444)
4261	Not regulated	NC-NC-NC	248386_at	A15g51940	expressed protein (88418.m06448)
4262	Not regulated	NC-NC-NC	248387_at	A15g51860	dihydrodipicolinate reductase family protein weak similarity to dihydrodipicolinate reductase [Corynebacterium glutamicum] GI:311768; contains Pfam profiles PF01113; Dihydrodipicolinate reductase N-terminus, PF05173; Dihydrodipicolinate reductase C-terminus (88418.m06467)
4263	Not regulated	NC-NC-NC	248402_at	A15g52100	ADP-ribosylation factor, putative similar to art-related protein (ARP) (SP-Q63055) [Rattus norvegicus]; contains Pfam domain PF00025; ADP-ribosylation factor family (88418.m06480)
4264	Not regulated	NC-NC-NC	248346_at	A15g52210	sugar isomerase (SIS) domain-containing protein similar to 8-phospho-3-hexulose isomerase [Mycobacterium gastri] GI:6899880; contains Pfam profile PF01380; SIS domain (88418.m06478)
4265	Not regulated	NC-NC-NC	248348_at	A15g52190	cytochrome b5 domain-containing protein similar to SPIP70560 Membrane associated progesterone receptor component 1 [Rattus norvegicus]; contains Pfam profile PF00173; Helme/Steroid binding domain (88418.m06484)
4266	Not regulated	NC-NC-NC	248349_at	A15g52240	expressed protein (88418.m06479)
4267	Not regulated	NC-NC-NC	248351_at	A15g52200	expressed protein (88418.m06505)
4268	Not regulated	NC-NC-NC	248336_at	A15g52420	RNA synthetase class II (G, H, P and S) family protein similar to SPIP07814 Bifunctional aminoacyl-tRNA synthetase [includes: Glutamyl-tRNA synthetase (EC 6.1.17) (Glutamate-IRNA ligase); Prolyl-tRNA synthetase (EC 6.1.1.15) (Proline-IRNA ligase)] (Homo sapiens); contains Pfam profiles PF00587; RNA synthetase class II core domain (G, H, P, S and T), PF03128; Anticodon binding domain (88418.m06516)
4269	Not regulated	NC-NC-NC	248339_at	A15g52520	WD-40 repeat family protein / notchless protein, putative similar to notchless [Xenopus laevis] GI:3687833; contains Pfam PF00400; WD domain, G-beta repeat (8 copies) (88418.m06556)
4270	Not regulated	NC-NC-NC	248326_at	A15g52820	UDP-N-acetylglucosamine pyrophosphorylase-related contains weak similarity to UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23) (Swiss-Prot:O74933) [Candida albicans] (88418.m06527)
4271	Not regulated	NC-NC-NC	248305_at	A15g52560	

4272	Not regulated	NC-NC-NC	248283_at	A15g52920	pyruvate kinase, putative similar to pyruvate kinase isozyme G, chloroplast precursor [Nicotiana tabacum] [SWISS-PROT:Q40546 (88418.m06567)]
4273	Not regulated	NC-NC-NC	248285_at	A15g52960	expressed protein similar to unknown protein (pir S77140 (88418.m06571))
4274	Not regulated	NC-NC-NC	248287_at	A15g52970	thylakoid lumen 13.0 kDa protein SP-39L/VV5; similar to unknown protein (pir S77462 (88418.m06575))
4275	Not regulated	NC-NC-NC	248288_at	A15g52980	NADH-ubiquinone oxidoreductase-related contains weak similarity to NADH-ubiquinone oxidoreductase 13 kDa-B subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex 1-13kDa-B) (Complex 1 subunit B13) (Swiss-Prot:Q63362) [Rattus norvegicus] (88418.m06559)
4276	Not regulated	NC-NC-NC	248300_at	A15g53000	protein phosphatase 2A-associated 48 kDa protein / PP2A regulatory subunit (TAP46) identical to PP2A regulatory subunit (48 kDa like family (88418.m06583))
4277	Not regulated	NC-NC-NC	248302_at	A15g53160	expressed protein similar to unknown protein (pir T02893 (88418.m06608))
4278	Not regulated	NC-NC-NC	248303_at	A15g53170	Fish protease, putative similar to ATP-dependent metalloprotease Fish1 [G:3600100 from [Mus musculus] (88418.m06610)]
4279	Not regulated	NC-NC-NC	248304_at	A15g53180	polypyridine tract-binding protein, putative / heterogeneous nuclear ribonucleoprotein, putative similar to Polypyridine tract-binding protein 1 (PTB) (Heterogeneous nuclear ribonucleoprotein 1) (hnRNP 1) from [Rattus norvegicus] SPIQ00438; (Homo sapiens) SPIP26596; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) (88418.m06611)
4280	Not regulated	NC-NC-NC	248250_at	A15g53130	cyclic nucleotide-regulated ion channel / cyclic nucleotide-gated channel (CNGC1) almost identical to cyclic nucleotide-regulated ion channel 1 pir:T51354, GI:11357236 from [Arabidopsis thaliana] (88418.m06604)
4281	Not regulated	NC-NC-NC	248258_at	A15g53400	nuclear movement family protein contains Pfam profile: PF03593 nuclear movement protein (88418.m06635)
4282	Not regulated	NC-NC-NC	248259_at	A15g53330	expressed protein (88418.m06628)
4283	Not regulated	NC-NC-NC	248264_at	A15g53310	myosin heavy chain-related contains weak similarity to Myosin IB heavy chain (Swiss-Prot:P34092) [Dicyostelium discoideum] (88418.m06628)
4284	Not regulated	NC-NC-NC	248266_at	A15g53440	expressed protein (88418.m06641)
4285	Not regulated	NC-NC-NC	248270_at	A15g53450	protein kinase family protein contains protein kinase domain, Pfam:PF00069 (88418.m06642)
4286	Not regulated	NC-NC-NC	248271_at	A15g53420	expressed protein (88418.m06639)
4287	Not regulated	NC-NC-NC	248276_at	A15g53550	transporter, putative similar to iron-phytochelator transporter protein yellow stripe 1 [Zea mays] GI:10770865; contains Pfam profile PF03169: OPT oligopeptide transporter protein (88418.m06654)
4288	Not regulated	NC-NC-NC	248242_at	A15g53580	aldoketo reductase family protein contains Pfam profile PF00248: oxidoreductase, aldoketo reductase family (88418.m06657)
4289	Not regulated	NC-NC-NC	248243_at	A15g53590	auxin-responsive family protein similar to indole-3-acetic acid induced protein ARG7 (SP:P32285) [Vigna radiata] (88418.m06658)
4290	Not regulated	NC-NC-NC	248217_at	A15g53560	cytochrome b5 isoform 1 identical to SPIQ42342 Cytochrome b5 isoform 1 [Arabidopsis thaliana] (88418.m06655)
4291	Not regulated	NC-NC-NC	248219_at	A15g53650	expressed protein (88418.m06664)
4292	Not regulated	NC-NC-NC	248220_at	A15g53540	MSP1 protein, putative / intramitochondrial sorting protein, putative similar to Swiss-Prot:P28737 MSP1 protein (TAT-binding homolog 4) [Saccharomyces cerevisiae]; contains Pfam domain, PF00004: ATPase, AAA family (88418.m06653)
4293	Not regulated	NC-NC-NC	248221_at	A15g53530	vacuolar protein sorting-associated protein 26, putative / VPS26, putative similar to vacuolar sorting protein 26 [Homo sapiens] GI:9822852; contains Pfam profile PF03643: Vacuolar protein sorting-associated protein 26 (88418.m06652)
4294	Not regulated	NC-NC-NC	248223_at	A15g53620	expressed protein (88418.m06661)
4295	Not regulated	NC-NC-NC	248234_at	A15g53850	haloacid dehalogenase-like hydrolase family protein low similarity to endo-1,4-phosphatase E-1 enzyme [Klebsiella oxytoca] GI:401712; contains InterPro accession IPR005634: Haloacid dehalogenase-like hydrolase (88418.m06691)
4296	Not regulated	NC-NC-NC	248235_at	A15g53880	expressed protein (88418.m06697)
4297	Not regulated	NC-NC-NC	248238_at	A15g53900	expressed protein similar to unknown protein (gb AAAF34833.1 (88418.m06705))
4298	Not regulated	NC-NC-NC	248187_at	A15g53940	yippee family protein similar to mdg1-1 [Mus musculus] GI:10441848; Yippee protein [Drosophila melanogaster] GI:5713279; contains Pfam profile PF03226: Yippee putative zinc-binding protein (88418.m06711)
4299	Not regulated	NC-NC-NC	248191_at	A15g54130	calcium-binding EF hand family protein contains INTERPRO:IPR002048 calcium-binding EF-hand domain (88418.m06739)
4300	Not regulated	NC-NC-NC	248193_at	A15g54080	homogentisate 1,2-dioxygenase / homogentisate/homogentisate oxygenase / homogentisic acid oxidase (HGO) identical to SPIQ92A2 Homogentisate 1,2-dioxygenase (EC 1.13.11.5) (Homogentisate oxygenase) (Homogentisic acid oxidase) [Arabidopsis thaliana]; contains Pfam profile PF04209: homogentisate 1,2-dioxygenase (88418.m06732)
4301	Not regulated	NC-NC-NC	248195_at	A15g54110	vesicle-associated membrane family protein / VAMP family protein similar to VAP27 [Nicotiana glauca] (88418.m06737)
4302	Not regulated	NC-NC-NC	248181_at	A15g54290	cytochrome c biogenesis protein family low similarity to cytochrome c biogenesis protein Coda [Paracoccus pantotrophus] GI:11095328; contains Pfam profile PF02693: Cytochrome C biogenesis protein transmembrane region (88418.m06782)
4303	Not regulated	NC-NC-NC	248151_at	A15g54270	chlorophyll A-B binding protein / LHCII type III (LHC3) identical to Lhc3 protein [Arabidopsis thaliana] GI:4741852; contains Pfam profile PF00504: Chlorophyll A-B binding protein (88418.m06760)
4304	Not regulated	NC-NC-NC	248155_at	A15g54390	inositol monophosphatase family protein similar to SPIQ42546 3(2),5-bisphosphate nucleotidase (EC 3.1.3.7) [Arabidopsis thaliana]; contains Pfam profile PF00459: Inositol monophosphatase family; supporting cDNA gi 1354509 gb U55205.1 ATU55205 (88418.m06773)
4305	Not regulated	NC-NC-NC	248158_at	A15g54440	expressed protein (88418.m06780)
4306	Not regulated	NC-NC-NC	248165_at	A15g54430	universal stress protein (USP) family protein low similarity to early nodulin ENOD18 [Vicia faba] GI:11602747; ER8 protein [Lycopersicon esculentum] GI:5695654; contains Pfam profile PF00582: universal stress protein family (88418.m06779)
4307	Not regulated	NC-NC-NC	248171_at	A15g54680	basic helix-loop-helix (bHLH) family protein similar to unknown protein (pir B71406 (88418.m06809))
4308	Not regulated	NC-NC-NC	248173_at	A15g54580	RNA recognition motif (RRM)-containing protein low similarity to RNA-binding protein RGP-3 [Nicotiana sylvestris] GI:1009363; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) (88418.m06794)

4309	Not regulated	NC-NC-NC	248174_at	A15g54800	50S ribosomal protein L24, chloroplast (CL24) identical to SPIP92859 50S ribosomal protein L24, chloroplast precursor (Arabidopsis thaliana) (68418.m06786)
4310	Not regulated	NC-NC-NC	248175_at	A15g54640	histone H2A identical to histone H2A Arabidopsis thaliana GI:7595337 (68418.m06803)
4311	Not regulated	NC-NC-NC	248120_at	A15g54540	expressed protein (68418.m06790)
4312	Not regulated	NC-NC-NC	248124_at	A15g54730	eukaryotic translation initiation factor SU11, putative similar to SPIP32911 Protein translation factor SU11 (Saccharomyces cerevisiae); contains Pfam profile PF01253: Translation initiation factor SU11 (68418.m06820)
4313	Not regulated	NC-NC-NC	248126_at	A15g54760	transport protein particle (TRAPP) component Bet3, putative similar to SPIP36149 Transport protein particle 22 kDa subunit (TRAPP 22 kDa subunit) (Saccharomyces cerevisiae); contains Pfam profile PF04051: Transport protein particle (TRAPP)
4314	Not regulated	NC-NC-NC	248127_at	A15g54750	component, Bet3 (68418.m06818)
4315	Not regulated	NC-NC-NC	248132_at	A15g54840	GTP-binding family protein similar to SPIP87027 Septum-promoting GTP-binding protein 1 (GTPase spg1) (Sidi3 protein) (Schizosaccharomyces pombe) (68418.m06830)
4316	Not regulated	NC-NC-NC	248134_at	A15g54880	integral membrane transporter family protein contains 10 transmembrane domains; contains Pfam PF03092: BT1 family, contains (Leishmania tarentolae) (68418.m06834)
4317	Not regulated	NC-NC-NC	248139_at	A15g54970	expressed protein (68418.m06846)
4318	Not regulated	NC-NC-NC	248140_at	A15g54980	membrane protein TIGR01593: contains Pfam PF04535: Domain of unknown function (DUF588) (68418.m06847)
4319	Not regulated	NC-NC-NC	248142_at	A15g55030	expressed protein (68418.m06855)
4320	Not regulated	NC-NC-NC	248144_at	A15g54800	glucose-6-phosphate/phosphate translocator, putative identical to glucose 6 phosphate/phosphate translocator (Arabidopsis thaliana) gi1229875gbIAAF42936 (68418.m06826)
4321	Not regulated	NC-NC-NC	248147_at	A15g54900	RNA-binding protein 45 (RBP45), putative contains similarity to polyadenylate-binding protein 5 (68418.m06838)
4322	Not regulated	NC-NC-NC	248149_at	A15g54855	pollen Ole e 1 allergen and extensin family protein contains Pfam domain, PF01190: Pollen proteins Ole e 1 family (68418.m06833)
4323	Not regulated	NC-NC-NC	248115_at	A15g54870	expressed protein strong similarity to unknown protein (pf1704825) (68418.m06835)
4324	Not regulated	NC-NC-NC	248117_at	A15g55000	potassium channel tetramerisation domain-containing protein / pentapeptide repeat-containing protein contains Pfam profiles PF02214: K+ channel tetramerisation domain, PF08005: Pentapeptide repeats (8 copies) (68418.m06849)
4325	Not regulated	NC-NC-NC	248087_at	A15g55060	expressed protein (68418.m06862)
4326	Not regulated	NC-NC-NC	248091_at	A15g55120	expressed protein strong similarity to unknown protein (pf1704913) (68418.m06871)
4327	Not regulated	NC-NC-NC	248092_at	A15g55170	identical to cDNA small ubiquitin-like modifier 3 (SUMO) GI:22652845 (68418.m06878)
4328	Not regulated	NC-NC-NC	248093_at	A15g55210	expressed protein similar to unknown protein (pf1704913) (68418.m06882)
4329	Not regulated	NC-NC-NC	248094_at	A15g55220	trigger factor type chaperone family protein contains Pfam profiles PF05697: Bacterial trigger factor protein (TF), PF05698: Bacterial trigger factor protein (TF) C-terminus, PF00254: peptidyl-prolyl cis-trans isomerase, FKBP-type (68418.m06883)
4330	Not regulated	NC-NC-NC	248098_at	A15g55290	ATP synthase subunit H family protein contains weak similarity to Vacuolar ATP synthase subunit H (EC 3.6.3.14) (V-ATPase H subunit) (Vacuolar proton pump H subunit) (V-ATPase M8.2 subunit) (V-ATPase 9.2 kDa membrane accessory protein) (Swiss-Prot:P81103) (Bot tauris); contains Pfam profile PF05493: ATP synthase subunit H (68418.m06890)
4331	Not regulated	NC-NC-NC	248099_at	A15g55300	DNA topoisomerase I identical to Swiss-Prot:P30181 DNA topoisomerase I (Arabidopsis thaliana) (68418.m06889)
4332	Not regulated	NC-NC-NC	248101_at	A15g55200	co-chaperone GrpE protein, putative similar to chaperone GrpE type 2 (Nicotiana tabacum) GI:3851640; contains Pfam profile PF01025: co-chaperone GrpE (68418.m06881)
4333	Not regulated	NC-NC-NC	248102_at	A15g55140	ribosomal protein L30 family protein contains similarity to 50S ribosomal protein L30 (68418.m06875)
4334	Not regulated	NC-NC-NC	248103_at	A15g55160	small ubiquitin-like modifier 2 (SUMO) similar to ubiquitin-like protein SMT3 SP-P55852 from [Arabidopsis thaliana]; identical to cDNA small ubiquitin-like modifier 2 (SUMO) GI:22652843; contains Pfam profile PF00240: Ubiquitin family (68418.m06877)
4335	Not regulated	NC-NC-NC	248105_at	A15g55280	cell division protein Flz2, chloroplast, putative (FTS2) identical to SPIQ42545 Cell division protein flz2 homolog, chloroplast precursor (Arabidopsis thaliana); similar to Flz21 (Tagetes erecta) GI:8896066; contains Pfam profiles PF00091: Tubulin/Fliz family, GTPase domain, PF03953: Tubulin/Fliz family, C-terminal domain (68418.m06889)
4336	Not regulated	NC-NC-NC	248107_at	A15g55190	Ras-related GTP-binding protein (RANK) identical to atran3 (Arabidopsis thaliana) GI:20583280 (68418.m06880)
4337	Not regulated	NC-NC-NC	248108_at	A15g55130	molybdenum cofactor synthesis protein 3 / molybdopterin synthase sulphurase (CNX5) identical to SPIQ92NWO Molybdenum cofactor synthesis protein 3 (Molybdopterin synthase sulphurase) (MPT synthase sulfurylase) (Arabidopsis thaliana); contains Pfam profiles PF00899: ThiF family, PF00581: Rhodanese-like domain, PF05237: MoeZ/MoeB domain (68418.m06872)
4338	Not regulated	NC-NC-NC	248109_at	A15g55310	DNA topoisomerase I, putative similar to Swiss-Prot:P30181 DNA topoisomerase I (Arabidopsis thaliana) (68418.m06893)
4339	Not regulated	NC-NC-NC	248080_at	A15g55380	membrane bound O-acyl transferase (XylT) identical to SPIQ9LDH0 (68418.m06912)
4340	Not regulated	NC-NC-NC	248056_at	A15g55500	Simmondsia chinensis (68418.m06900)
4341	Not regulated	NC-NC-NC	248058_at	A15g55530	C2 domain-containing protein low similarity to cold-regulated gene SRC2 [Glycine max] (Glycine max) GI:20552230; contains Pfam profile PF00168: C2 domain (68418.m06916)
4342	Not regulated	NC-NC-NC	248062_at	A15g55450	protease inhibitor/seed storage lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage/LTP family domain PF00234 (68418.m06907)
4343	Not regulated	NC-NC-NC	248068_at	A15g55610	expressed protein (68418.m06933)
4344	Not regulated	NC-NC-NC	248074_at	A15g55730	fasciclin-like arabinogalactan-protein (FLA1) identical to gll1337778IAAK208571337775gbIAF333970 (68418.m06947)
4345	Not regulated	NC-NC-NC	248079_at	A15g55790	expressed protein: expression supported by MPSS (68418.m06953)
4346	Not regulated	NC-NC-NC	248025_at	A15g55850	nitrate-responsive NOI protein, putative similar to nitrate-induced NOI protein [Zea mays] GI:2642213 (68418.m06960)
4347	Not regulated	NC-NC-NC	248026_at	A15g55710	expressed protein (68418.m06945)
4348	Not regulated	NC-NC-NC	248028_at	A15g55820	expressed protein similar to unknown protein (gbIAAF04428.1) (68418.m06935)
4349	Not regulated	NC-NC-NC	248031_at	A15g55840	expressed protein (68418.m06938)

4350	Not regulated	NC-NC-NC	248041_at	A15g55940	expressed protein contains Pfam PF03685: Uncharacterised protein family (UPF0172) (68418.m06877); expressed protein (68418.m06878); expressed protein (68418.m06890)
4351	Not regulated	NC-NC-NC	248042_at	A15g55960	expressed protein (68418.m06990)
4352	Not regulated	NC-NC-NC	248044_at	A15g56020	KH domain-containing protein (68418.m07003)
4353	Not regulated	NC-NC-NC	247994_at	A15g56140	expressed protein contains similarity to GP-anchored protein (68418.m07007)
4354	Not regulated	NC-NC-NC	247996_at	A15g56170	actin-related protein, putative (ARP8) strong similarity to actin-related protein 8a (ARP8) [Arabidopsis thaliana] GI:21427473; contains Pfam profile PF00022: Actin, supporting cDNA gi21427470/gbIAF5079.1 (68418.m07008)
4355	Not regulated	NC-NC-NC	247997_at	A15g56180	WD-40 repeat family protein contains 3 (2 significant) WD-40 repeats (PF0400): similar to beta transducin-like protein HET-EC2*40 (GI:17225208) [Podospira anserina] (68418.m07010)
4356	Not regulated	NC-NC-NC	248000_at	A15g56190	expressed protein (68418.m07018)
4357	Not regulated	NC-NC-NC	248005_at	A15g56240	dimethylmenaquinone methyltransferase family protein similar to bacterial S-adenosylmethionine:2-demethylmenaquinone methyltransferase; contains Pfam profile PF03737: Dimethylmenaquinone methyltransferase (68418.m07021)
4358	Not regulated	NC-NC-NC	248007_at	A15g56260	peroxisomal targeting signal type 1 receptor (PEX5) identical to GI:3603333; contains Pfam profile PF00515 TPR Domain (68418.m07026)
4359	Not regulated	NC-NC-NC	248010_at	A15g56290	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger) (68418.m07032)
4360	Not regulated	NC-NC-NC	248014_at	A15g56340	pyruvate kinase, putative similar to pyruvate kinase, cytosolic isozyme [Nicotiana tabacum] SWISS-PROT Q42954 (68418.m07033)
4361	Not regulated	NC-NC-NC	247989_at	A15g56350	glycosyl hydrolase family 17 protein similar to elicitor inducible chitinase Nt-SubE78 GI:11071974 from [Nicotiana tabacum] (68418.m07063)
4362	Not regulated	NC-NC-NC	247963_at	A15g56590	profilin 5 (PRO5) identical to SPIQ9FE83 Profilin 5 [Arabidopsis thaliana] (68418.m07065)
4363	Not regulated	NC-NC-NC	247964_at	A15g56600	40S ribosomal protein S30 (RPS30C) (68418.m07074)
4364	Not regulated	NC-NC-NC	247968_at	A15g56670	phosphofructokinase family protein similar to phosphofructokinase [Amycolatopsis methanolica] GI:17432243; contains Pfam profile PF00365: Phosphofructokinase (68418.m07070)
4365	Not regulated	NC-NC-NC	247983_at	A15g56630	protein kinase family protein contains protein kinase domain, Pfam.PF00069 (68418.m07087)
4366	Not regulated	NC-NC-NC	247985_at	A15g56790	CwJ-like family protein / zinc finger (CCCH-type) family protein contains Pfam domain, Pfam.PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar), PF04677: Protein similar to CwJ C-terminus 1, PF04678: Protein similar to CwJ C-terminus 2 (68418.m07100)
4367	Not regulated	NC-NC-NC	247987_at	A15g56900	expressed protein (68418.m07104)
4368	Not regulated	NC-NC-NC	247988_at	A15g56910	expressed protein (68418.m07122)
4369	Not regulated	NC-NC-NC	247930_at	A15g57060	lactoylglycine lyase family protein / glyoxalase I family protein contains Pfam PF00903: glyoxalase family protein (68418.m07120)
4370	Not regulated	NC-NC-NC	247931_at	A15g57040	expressed protein similar to unknown protein (gbIA4E21159.1) (68418.m07114)
4371	Not regulated	NC-NC-NC	247934_at	A15g57000	ribosomal protein S16 family protein contains Pfam profile PF00888: ribosomal protein S16 (68418.m07108)
4372	Not regulated	NC-NC-NC	247935_at	A15g56940	lycopene epsilon cyclase identical to lycopene epsilon cyclase [GI:1399181] (68418.m07116)
4373	Not regulated	NC-NC-NC	247936_at	A15g57030	macrophage migration inhibitory factor family protein / MIF family protein contains Pfam profile: PF01187 Macrophage migration inhibitory factor(MIF) (68418.m07141)
4374	Not regulated	NC-NC-NC	247943_at	A15g57170	basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain (68418.m08531)
4375	Not regulated	NC-NC-NC	247945_at	A15g57150	expressed protein (68418.m07150)
4376	Not regulated	NC-NC-NC	247950_at	A15g57230	expressed protein (68418.m07156)
4377	Not regulated	NC-NC-NC	247926_at	A15g57280	aldose 1-epimerase family protein contains Pfam profile PF01283 Aldose 1-epimerase (68418.m07161)
4378	Not regulated	NC-NC-NC	247929_at	A15g57330	F-box family protein / LOV ketch protein 1 (LKP1) E3 ubiquitin ligase SCF complex F-box subunit, identical to clock-associated PAS protein ZTL; ZEITLUPE GI:7839456, LOV ketch protein 1 GI:11610573; Adagio 1 GI:13487068 from [Arabidopsis thaliana]; contains Pfam profile PF01344: Ketch motif, identical to cDNA Adagio 1 (ADO1) GI:13487067; identical to cDNA LKP1 mRNA for LOV ketch protein 1, GI:11610572 (68418.m07166)
4379	Not regulated	NC-NC-NC	247898_at	A15g57360	expressed protein (68418.m07184)
4380	Not regulated	NC-NC-NC	247899_at	A15g57345	Ubiquitin/ubiquitin-like protein family protein similar to ubiquitin biosynthesis methyltransferase COQ5 [Saccharomyces cerevisiae]SPIP49017; ubiquitin/ubiquitin-like protein biosynthesis methyltransferase ubiE [Escherichia coli]SP127851; contains Pfam profile PF01209: methyltransferase, Ubiquitin/ubiquitin-like protein family (68418.m07158)
4381	Not regulated	NC-NC-NC	247901_at	A15g57300	putative similar to 36kDa protein II [Solanum tuberosum] GI:515360; contains Pfam profile PF01458: Eukaryotic protein (68418.m07184)
4382	Not regulated	NC-NC-NC	247923_at	A15g57490	calmodulin-binding protein similar to calmodulin-binding protein TC860 GI:1988548 from [Nicotiana tabacum] (68418.m07184)
4383	Not regulated	NC-NC-NC	247870_at	A15g57580	CER1 protein, putative (WAX2) similar to maize glossy1 homolog GI:2213643 from [Oryza sativa]; contains Pfam profile PF01598: Sierid desaturase (68418.m07226)
4384	Not regulated	NC-NC-NC	247884_at	A15g57800	aminotransferase class IV family protein contains Pfam profile: PF01063 aminotransferase class IV (68418.m07234)
4385	Not regulated	NC-NC-NC	247886_at	A15g57850	expressed protein (68418.m07246)
4386	Not regulated	NC-NC-NC	247889_at	A15g57930	phosphatase-related weak similarity to CTD phosphatase-like 3 [Arabidopsis thaliana] GI:22212705; contains Pfam profiles PF02453: Reclucan, PF00533: BRCA1 C Terminus (BRCT) domain, PF03031: NLI interacting factor (68418.m07256)
4387	Not regulated	NC-NC-NC	247894_at	A15g58000	SKP1/ASK1 interacting partner 1 (SKP1) / SCF (Skp1-cullin-F-box) ubiquitin ligase identical to SKP1 interacting partner 1 (68418.m07242)
4388	Not regulated	NC-NC-NC	247863_at	A15g57900	anthranilate synthase beta subunit, putative similar to anthranilate synthase beta chain GI:403434 [Arabidopsis thaliana]
4389	Not regulated	NC-NC-NC	247864_s_at	A15g57890	cytochrome c oxidase subunit 6b, putative similar to subunit 6b of cytochrome c oxidase [Arabidopsis thaliana]
4390	Not regulated	NC-NC-NC	247865_at	A15g57815	gi16518353/dbjBAAB7883 (68418.m07230)
4391	Not regulated	NC-NC-NC	247835_at	A15g57910	expressed protein similar to unknown protein (emb CA87978.1) (68418.m07244)

4392	Not regulated	NC-NC-NC	247836_at	A15g57860	ubiquitin family protein contains Pfam profile PF00240; Ubiquitin family (68418.m07235)
4393	Not regulated	NC-NC-NC	247838_at	A15g57890	ubiquitin-specific protease 23, putative (UBP23) identical to GI:11963466 (68418.m07255)
4394	Not regulated	NC-NC-NC	247840_at	A15g58020	expressed protein contains PF04641; Protein of unknown function, DUF602 (68418.m07260)
4395	Not regulated	NC-NC-NC	247842_at	A15g58030	transport protein particle (TRAPP) component Bet3 family protein very strong similarity to SPP30 (Solanum pollinatum pistil)
4396	Not regulated	NC-NC-NC	247845_at	A15g58090	transport protein particle (TRAPP) component Bet3 family protein particle (TRAPP) component, Bet3 (Solanum tuberosum) GI:4959712; contains Pfam profile PF04051; Transport protein particle (TRAPP) component, Bet3 (Solanum tuberosum) GI:4959712
4397	Not regulated	NC-NC-NC	247847_at	A15g58110	glycosyl hydrolase family 17 protein similar to 3-glucanase GI:184832322 from [Sorghum bicolor] (68418.m07269)
4398	Not regulated	NC-NC-NC	247849_at	A15g58130	expressed protein predicted proteins, Homo sapiens and Drosophila melanogaster (68418.m07271)
4399	Not regulated	NC-NC-NC	247854_at	A15g58200	RNA recognition motif (RRM)-containing protein (68418.m07285)
4400	Not regulated	NC-NC-NC	247858_at	A15g58220	expressed protein (68418.m07289)
4401	Not regulated	NC-NC-NC	247860_at	A15g58240	bis(5'-adenosyl)-triphosphatase, putative similar to bis(5'-adenosyl)-triphosphatase (Diadenosine 5',5'-P1-P2-triphosphate hydrolase, Dinucleoside triphosphatase, AP3A hydrolase, AP3AAASE, Fragile histidine triad protein) [Homo sapiens] Swiss-Prot:P49789 (68418.m07291)
4402	Not regulated	NC-NC-NC	247862_at	A15g58250	expressed protein (68418.m07293)
4403	Not regulated	NC-NC-NC	247868_at	A15g58270	mitochondrial half-ABC transporter (STA1) identical to half-molecule ABC transporter ATM3 GI:9964121 from [Arabidopsis thaliana]; almost identical to mitochondrial half-ABC transporter STA1 GI:9187883 from [Arabidopsis thaliana]; identical to cDNA
4404	Not regulated	NC-NC-NC	247810_at	A15g58290	mitochondrial half-ABC transporter (STA1) gene(GI:9187882 (68418.m07295))
4405	Not regulated	NC-NC-NC	247811_at	A15g58430	26S proteasome AAA-ATPase subunit (RPT3) identical to 26S proteasome AAA-ATPase subunit RPT3 GI:6852882 from [Arabidopsis thaliana] (68418.m07297)
4406	Not regulated	NC-NC-NC	247812_at	A15g58390	exocyst subunit EXO70 family protein leucine zipper-containing protein, Lycopersicon esculentum, PIR:S21495; contains Pfam domain PF03081; Exo70 exocyst complex subunit, similar to exo70 (GI:2827160) [Rattus norvegicus] (68418.m07317)
4407	Not regulated	NC-NC-NC	247813_at	A15g58330	peroxidase, putative similar to peroxidase (Nicotiana tabacum) gi15381253dbj[BAAB2306 (68418.m07312)
4408	Not regulated	NC-NC-NC	247815_at	A15g58420	malate dehydrogenase [NADP], chloroplast, putative strong similarity to chloroplast NADP-dependent malate dehydrogenase (EC 1.1.1.82) SPIQ48902 (Medicago sativa), SPIP21528 (Pisum sativum), SPIQ05145 (Mesembryanthemum crystallinum), SPIP46489 (Flavaria bidentis), [Flavaria tinervia] (GI:726334, SPIP17606) [Sorghum bicolor]; contains InterPro entry IPR001236; Lactate/malate dehydrogenase (68418.m07302)
4409	Not regulated	NC-NC-NC	247817_at	A15g58375	40S ribosomal protein S4 (RPS40) ribosomal protein S4, Arabidopsis thaliana, PIR:T48480 (68418.m07315)
4410	Not regulated	NC-NC-NC	247819_at	A15g58350	expressed protein (68418.m07310)
4411	Not regulated	NC-NC-NC	247821_at	A15g58230	protein kinase family protein contains protein kinase domain, Pfam:PF00089 (68418.m07306)
4412	Not regulated	NC-NC-NC	247823_at	A15g58450	WD-40 repeat protein (MS1) contains 6 WD-40 repeats (PF04000); identical to WD-40 repeat protein (SP:O22467) [Arabidopsis thaliana] (68418.m07290)
4413	Not regulated	NC-NC-NC	247825_at	A15g58470	expressed protein predicted proteins from D. melanogaster, C. elegans and S. pombe (68418.m07320)
4414	Not regulated	NC-NC-NC	247828_at	A15g58480	zinc finger (Ran-binding) family protein weak similarity to SPIQ01844 RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma breakpoint region 1 protein) [Homo sapiens]; contains Pfam profiles PF00076: RNA recognition motif, (a.k.a. RRM, RBD, or RNP domain), PF00641: Zn-finger in Ran binding protein and others (68418.m07322)
4415	Not regulated	NC-NC-NC	247834_at	A15g58490	glycosyl hydrolase family 17 protein similar to elicitor inducible chitinase Ni-SubE76 GI:11071974 from [Nicotiana tabacum]
4416	Not regulated	NC-NC-NC	247800_at	A15g58570	(68418.m07324)
4417	Not regulated	NC-NC-NC	247771_at	A15g58590	cinnamoyl-CoA reductase family similar to cinnamoyl-CoA reductase from Pinus taeda [GI:17878848], Eucalyptus gunnii [GI:2058311] (68418.m07325)
4418	Not regulated	NC-NC-NC	247776_at	A15g58600	expressed protein (68418.m07337)
4419	Not regulated	NC-NC-NC	247777_at	A15g58740	Ran-binding protein 1, putative / RanBP1, putative strong similarity to Ran binding proteins from Arabidopsis thaliana atranbp1a [Arabidopsis thaliana] (GI:2058282, atranbp1b [Arabidopsis thaliana] (GI:2058284; contains Pfam profile PF00638: RanBP1 domain (68418.m07342)
4420	Not regulated	NC-NC-NC	247783_at	A15g58800	phosphoinositide-specific phospholipase C family protein contains Pfam profile: PF00388 phosphatidylinositol-specific phospholipase C (68418.m07354)
4421	Not regulated	NC-NC-NC	247786_at	A15g58600	nuclear movement family protein contains Pfam profile: PF03593 nuclear movement protein (68418.m07358)
4422	Not regulated	NC-NC-NC	247787_at	A15g58640	quinone reductase family protein similar to 1,4-benzoquinone reductase [Phanerochaete chrysosporium] (GI:4454983); similar to
4423	Not regulated	NC-NC-NC	247788_at	A15g58730	Trp repressor binding protein [Escherichia coli] (SPIP30848); contains flavodoxin domain PF00258 (68418.m07367)
4424	Not regulated	NC-NC-NC	247792_at	A15g58787	expressed protein various predicted proteins, Arabidopsis thaliana and Oryza sativa (68418.m07343)
4425	Not regulated	NC-NC-NC	247793_at	A15g58650	selenoprotein-related contains weak similarity to Selenoprotein W (Swiss-Prot:P48904) [Rattus norvegicus] (68418.m07348)
4426	Not regulated	NC-NC-NC	247794_at	A15g58670	pH6-type carbohydrate kinase family protein contains Pfam profile: PF00294 pH6 family carbohydrate kinase (68418.m07357)
4427	Not regulated	NC-NC-NC	247770_at	A15g58830	zinc finger (C3HC4-type RING finger) family protein similar to MTD2 [Medicago truncatula] (GI:9294812; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger) (68418.m07365)
4428	Not regulated	NC-NC-NC	247745_at	A15g59030	expressed protein (68418.m07349)
4429	Not regulated	NC-NC-NC	247761_at	A15g59160	phosphoinositide-specific phospholipase C (PLC1) identical to phosphoinositide specific phospholipase C [Arabidopsis thaliana] (GI:902923 (68418.m07351)
4430	Not regulated	NC-NC-NC	247762_at	A15g59180	expressed protein contains Pfam PF05340: Protein of unknown function (DUF740) (68418.m07382)
4431	Not regulated	NC-NC-NC	247763_at	A15g59190	copper transporter 1 (COPT1) nearly identical to SPIQ39065 Copper transporter 1 (COPT1) [Arabidopsis thaliana] (68418.m07395)
4432	Not regulated	NC-NC-NC	247764_at	A15g59200	serine/threonine protein phosphatase PP1 isozyme 2 (TOPP2) identical to SPIP48482 Serine/threonine protein phosphatase PP1 isozyme 2 (EC 3.1.3.16) [Arabidopsis thaliana] (68418.m07414)

4430	Not regulated	NC-NC-NC	247709_at	A15g59250	sugar transporter family protein similar to D-xylase-H+ symporter from <i>Lactobacillus brevis</i> GI:2895858, sugar-porter family protein 2 (Arabidopsis thaliana) GI:1458570; contains Pfam profile PF00063: major facilitator superfamily protein (68418.m07425); UDP-glucuronic acid decarboxylase (UXS3) identical to UDP-glucuronic acid decarboxylase [Arabidopsis thaliana] GI:14595666; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family; identical to cDNA UDP-glucuronic acid decarboxylase (UXS3) GI:14595665 (68418.m07428)
4431	Not regulated	NC-NC-NC	247720_at	A15g59290	SKP1 family protein similar to elongin C, <i>Drosophila melanogaster</i> , GI:2780365 PIR-JC5794; contains Pfam profile PF01468: Skp1 family, dimensin domain (68418.m07412)
4432	Not regulated	NC-NC-NC	247721_at	A15g59140	Ras-related GTP-binding protein, putative similar to Ras-related protein Rab11C SP-Q40193 from [Lotus japonicus] (68418.m07413)
4433	Not regulated	NC-NC-NC	247722_at	A15g59150	expressed protein (68418.m07445)
4434	Not regulated	NC-NC-NC	247725_at	A15g59410	scarecrow-like transcription factor 11 (SCL11) identical to cDNA scarecrow-like 11 (SCL11) mRNA, partial cds gi:4580528 (68418.m07452)
4435	Not regulated	NC-NC-NC	247705_at	A15g59460	oxygen-binding family protein similar to SPIP16258 Oxygen-binding protein 1 (Oryctolagus cuniculus); contains Pfam profile PF01237: Oxygen-binding protein (68418.m07446)
4436	Not regulated	NC-NC-NC	247877_at	A15g59420	zinc transporter (ZIP2) identical to zinc transporter ZIP2 [Arabidopsis thaliana] gi3252866[gb AAC24188; member of the Zinc (Zn2+)-Iron (Fe2+) permease (ZIP) family, PMID:11500563 (68418.m07459)
4437	Not regulated	NC-NC-NC	247878_at	A15g59520	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to desacetoxyindole-4-hydroxylase [Catharanthus roseus] GI:2352812; contains Pfam profile PF03171: oxidoreductase, 2OG-Fe(II) oxygenase family (68418.m07461)
4438	Not regulated	NC-NC-NC	247879_at	A15g59540	expressed protein (68418.m07491)
4439	Not regulated	NC-NC-NC	247889_at	A15g59770	histone H4 identical to histone H4 from <i>Lycopodium obscurum</i> GI:297150, <i>Lolium temulentum</i> SPIP02308, <i>Acropora formosa</i> GI:4555652, <i>Citrus jambhiri</i> GI:16797797 (68418.m07483)
4440	Not regulated	NC-NC-NC	247892_s_at	A15g59890	riboflavin biosynthesis protein, putative similar to SPIP50855 Riboflavin biosynthesis protein rbaA [includes: GTP cyclohydrolase II (EC 3.5.4.25); 3,4-dihydroxy-2-butanone 4-phosphate synthase (DHP synthase)] [Acetobacterium pleurononumoniae]; contains Pfam profiles PF00925: GTP cyclohydrolase II, PF00926: 3,4-dihydroxy-2-butanone 4-phosphate synthase (68418.m07489)
4441	Not regulated	NC-NC-NC	247894_at	A15g59750	Ras-related GTP-binding family protein contains Pfam profile: PF00071 Ras family (68418.m07503)
4442	Not regulated	NC-NC-NC	247899_at	A15g59840	expressed protein (68418.m07520)
4443	Not regulated	NC-NC-NC	247850_at	A15g59960	histone H2B nearly identical to histone H2B Arabidopsis thaliana GI:2407802; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4 (68418.m07513)
4444	Not regulated	NC-NC-NC	247852_at	A15g59910	40S ribosomal protein S15a (RPS15a) cytoplasmic ribosomal protein S15a, Arabidopsis thaliana, EMBL:ATAF1412 (68418.m07505)
4445	Not regulated	NC-NC-NC	247854_at	A15g59850	actin-depolymerizing factor 4 (ADF4) identical to SPIQ8ZSK3 Actin-depolymerizing factor 4 (ADF-4) (Arabidopsis thaliana) (68418.m07510)
4446	Not regulated	NC-NC-NC	247856_at	A15g59890	actin-depolymerizing factor 3 (ADF3) identical to SPIQ8ZSK4 Actin-depolymerizing factor 3 (ADF-3) (Arabidopsis thaliana) (68418.m07508)
4447	Not regulated	NC-NC-NC	247858_at	A15g59880	aspartyl aminopeptidase, putative similar to SPIQ9ULAO Aspartyl aminopeptidase (EC 3.4.11.21) (Homo sapiens); contains Pfam profile PF02127: Aminopeptidase / zinc metalloprotease (M16) (68418.m07542)
4448	Not regulated	NC-NC-NC	247824_at	A15g60160	lectin protein kinase family protein contains Pfam domains, PF00089: Protein kinase domain and PF00139: Legume lectin beta domain (68418.m07557)
4449	Not regulated	NC-NC-NC	247826_at	A15g60300	cysteine proteinase, putative / AALP protein (AALP) identical to AALP protein GI:7230640 from [Arabidopsis thaliana]; similar to barley aleurain (68418.m07568)
4450	Not regulated	NC-NC-NC	247827_at	A15g60360	sec81 beta family protein similar to SPIP52870 Protein transport protein SEC81 beta 1 subunit (Saccharomyces cerevisiae); contains Pfam profile PF03911: Sec81 beta family (68418.m07583)
4451	Not regulated	NC-NC-NC	247830_at	A15g60420	fascidin-like arabinogalactan-protein (FLA12) (68418.m07586)
4452	Not regulated	NC-NC-NC	247832_at	A15g60460	SNO glutamine amidotransferase family protein similar to pyridoxine synthesis protein PDX2 [Cercospora nicotianae] GI:9854418; contains Pfam profile PF01174: SNO glutamine amidotransferase family (68418.m07591)
4453	Not regulated	NC-NC-NC	247838_at	A15g60490	elongation factor 1-alpha / EF-1-alpha identical to SWISS-PROT:P13805 elongation factor 1-alpha (EF-1-alpha) [Arabidopsis thaliana] (68418.m07574)
4454	Not regulated	NC-NC-NC	247841_at	A15g60540	CAAX amino terminal protease family protein contains Pfam profile PF02517 CAAX amino terminal protease family protein (68418.m07622)
4455	Not regulated	NC-NC-NC	247844_s_at	A15g60390	major intrinsic family protein / MIP family protein similar to mipC protein GI:1657848 from [Mesembryanthemum crystallinum] (68418.m07622)
4456	Not regulated	NC-NC-NC	247583_at	A15g60750	phospholipid/glycerol acyltransferase family protein contains Pfam profile PF01553: Acyltransferase (68418.m07608)
4457	Not regulated	NC-NC-NC	247586_at	A15g60660	regulator of chromosome condensation (RCC1) family protein weak similarity to UVB-resistance protein UVR8 [Arabidopsis thaliana] GI:5478530; contains Pfam profile PF00415: Regulator of chromosome condensation (RCC1) (68418.m07635)
4458	Not regulated	NC-NC-NC	247587_at	A15g60620	phytochelatin synthetase-related contains Pfam profile PF04833: Phytochelatin synthetase-like conserved region (68418.m07646)
4459	Not regulated	NC-NC-NC	247598_at	A15g60870	DEAD/DEAH box helicase, putative (RH10) probable replication protein A1, <i>Oryza sativa</i> , EMBL:AF009179 (68418.m07651)
4460	Not regulated	NC-NC-NC	247604_at	A15g60950	nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein G3BP ras-GTPase-activating protein SH3-domain binding protein, <i>Mus musculus</i> , EMBL:MMU65313 (68418.m07649)
4461	Not regulated	NC-NC-NC	247608_at	A15g60990	glycosyl hydrolase family protein 17 similar to beta-1,3-glucanase GI:15150341 from [Carnellia sinensis]; C-terminal homology only (68418.m07669)
4462	Not regulated	NC-NC-NC	247551_at	A15g60980	
4463	Not regulated	NC-NC-NC	247563_at	A15g61130	

4464	Not regulated	NC-NC-NC	247565_at	A15g01150	leo1-like family protein weak similarity to SPIP38439, LEO1 protein (Saccharomyces cerevisiae); contains Pfam profile PF04004; Leo1-like protein; supporting cDNA gi21828714 gb AF480422.1 (68418.m07871)
4465	Not regulated	NC-NC-NC	247571_at	A15g01210	SNAP25 homologous protein SNAP33 (SNAP33) (SNAP33) / synaptosomal-associated protein SNAP25-like 1 / snap25a identical to SNAP25 homologous protein SNAP33 (SNAP33) (SNAP33) / synaptosomal-associated protein SNAP25-like 1 (SNAP-25 like protein 1) (Snap25a) (Swiss-Prot:Q85TP9) [Arabidopsis thaliana] (68418.m07878)
4466	Not regulated	NC-NC-NC	247572_at	A15g01220	complex 1 family protein / LVR family protein contains Pfam PF05347; complex 1 protein (LYR family) (68418.m07878)
4467	Not regulated	NC-NC-NC	247547_at	A15g01360	expressed protein (68418.m07898)
4468	Not regulated	NC-NC-NC	247520_at	A15g01310	Cytochrome c oxidase subunit Vc, putative / COX5C, putative similar to cytochrome c oxidase subunit 5c (Helianthus annuus) [GI:184059602; contains Pfam profile PF05799; Cytochrome c oxidase subunit Vc (COX5C) (68418.m07893)
4469	Not regulated	NC-NC-NC	247522_at	A15g01340	expressed protein (68418.m07897)
4470	Not regulated	NC-NC-NC	247523_at	A15g01410	ribulose-phosphate 3-epimerase, chloroplast, putative / pentose-5-phosphate 3-epimerase, putative strong similarity to SPI043157 (Spinacia oleracea); contains Pfam profile PF00834; Ribulose-phosphate 3-epimerase family (68418.m07704)
4471	Not regulated	NC-NC-NC	247532_at	A15g01560	phosphofructokinase family protein contains protein kinase domain, Pfam:PF00069 (68418.m07725)
4472	Not regulated	NC-NC-NC	247534_at	A15g01580	profile PF00365; Phosphofructokinase (68418.m07727)
4473	Not regulated	NC-NC-NC	247544_at	A15g01670	expressed protein (68418.m07737)
4474	Not regulated	NC-NC-NC	247513_at	A15g01510	NADP-dependent oxidoreductase, putative similar to zeta-crystallin homolog TED3 from Zinnia elegans [gi:531098]; contains Pfam zinc-binding dehydrogenase domain PF00107 (68418.m07718)
4475	Not regulated	NC-NC-NC	247493_at	A15g01900	copine BONZA1 (BON1) nearly identical to BONZA1 [Arabidopsis thaliana] [GI:15487382; contains Pfam profile PF00168; C2 domain (68418.m07786)
4476	Not regulated	NC-NC-NC	247496_at	A15g01840	exostosin family protein contains Pfam profile: PF03016 exostosin family; supported by cDNA gi23821293 dbj AB080693.1 ; (68418.m07759)
4477	Not regulated	NC-NC-NC	247486_at	A15g02140	expressed protein (68418.m07799)
4478	Not regulated	NC-NC-NC	247480_at	A15g02150	peptidoglycan-binding LysM domain-containing protein contains Pfam profile PF01478; LysM domain (68418.m07800)
4479	Not regulated	NC-NC-NC	247487_at	A15g02150	embryo-specific protein-related contains weak similarity to embryo-specific protein 3 (GI:3335171) [Arabidopsis thaliana]
4480	Not regulated	NC-NC-NC	247459_at	A15g02200	embryo-specific protein-related contains weak similarity to embryo-specific protein 3 (GI:3335171) [Arabidopsis thaliana]
4481	Not regulated	NC-NC-NC	247460_at	A15g02050	OXAL1 protein (OXAL1) identical to AOXAL1 [Arabidopsis thaliana] [GI:6624207 (68418.m07788)
4482	Not regulated	NC-NC-NC	247477_at	A15g02340	invertase/pectin methylesterase inhibitor family protein similar to SPQ42534 Pectinesterase 2 precursor (EC 3.1.1.11) (Pectin methylesterase 2) (PE 2) [Arabidopsis thaliana]; contains Pfam profile PF04043; Plant invertase/pectin methylesterase inhibitor (68418.m07825)
4483	Not regulated	NC-NC-NC	247449_at	A15g02290	nucleotide-sensitive chloride conductance regulator (ClCn) family protein contains PF03517; Nucleotide-sensitive chloride conductance regulator (ClCn) (68418.m07820)
4484	Not regulated	NC-NC-NC	247450_at	A15g02350	invertase/pectin methylesterase inhibitor family protein / DC 1.2 homolog (FLS-2122) similar to SPI042534 Pectinesterase 2 precursor (EC 3.1.1.11) (Pectin methylesterase 2) (PE 2) [Arabidopsis thaliana]; contains Pfam profile PF04043; Plant invertase/pectin methylesterase inhibitor (68418.m07837)
4485	Not regulated	NC-NC-NC	247427_at	A15g02580	expressed protein (68418.m07837)
4486	Not regulated	NC-NC-NC	247428_at	A15g02590	expressed protein (68418.m07855)
4487	Not regulated	NC-NC-NC	247430_at	A15g02610	basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain (68418.m07857)
4488	Not regulated	NC-NC-NC	247434_at	A15g02575	expressed protein (68418.m07853)
4489	Not regulated	NC-NC-NC	247435_at	A15g02480	glutathione S-transferase, putative (68418.m07841)
4490	Not regulated	NC-NC-NC	247436_at	A15g02530	delta-1-pyrroline-5-carboxylate dehydrogenase (P5CDH) identical to delta-1-pyrroline-5-carboxylate dehydrogenase precursor [Arabidopsis thaliana] [gi1538374 gb AAK73756; identical to cDNA delta-1-pyrroline-5-carboxylate dehydrogenase precursor (P5CDH) nuclear gene for mitochondrial product GI:15383743; contains Pfam profile PF00171; aldehyde dehydrogenase (NAD) family protein (68418.m07846)
4491	Not regulated	NC-NC-NC	247438_at	A15g02460	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097; Zinc finger, C3HC4 type (RING finger) (68418.m07838)
4492	Not regulated	NC-NC-NC	247444_at	A15g02630	expressed protein (68418.m07861)
4493	Not regulated	NC-NC-NC	247445_at	A15g02640	proline-rich family protein contains proline-rich extensin domains, INTERPRO:IPR002965 (68418.m07862)
4494	Not regulated	NC-NC-NC	247446_at	A15g02650	expressed protein (68418.m07863)
4495	Not regulated	NC-NC-NC	247422_at	A15g02810	peroxisomal protein (PEX14) identical to PEX14 [Arabidopsis thaliana] [GI:1094252; contains Pfam profile PF04895; Peroxisomal membrane anchor protein (Pex14p) conserved region; supporting cDNA gi11094253 dbj AB037538.1 (68418.m07884)
4496	Not regulated	NC-NC-NC	247396_at	A15g02930	GDSL-motif lipase/hydrolase family protein similar to SPIP41734 Isomyl acetate-hydrolyzing esterase (EC 3.1.-) [Saccharomyces cerevisiae]; contains Pfam profile PF00657; Lipase/Acylhydrolase with GDSL-like motif (68418.m07896)
4497	Not regulated	NC-NC-NC	247398_at	A15g02950	expressed protein (68418.m07896)
4498	Not regulated	NC-NC-NC	247403_at	A15g02740	band 7 family protein strong similarity to hypersensitive-induced response protein [Zea mays] [GI:7716470; contains Pfam profile PF01145; SPFH domain / Band 7 family; supporting cDNA gi17065547 gb AY062850.1 (68418.m07876)
4499	Not regulated	NC-NC-NC	247405_at	A15g02880	Rac-like GTP-binding protein (ARAC10) identical to Rac GTP binding protein Arac10 [Arabidopsis thaliana] [GI:3702984; rac-like GTP binding protein (68418.m07893)
4500	Not regulated	NC-NC-NC	247407_at	A15g02900	expressed protein (68418.m07893)
4501	Not regulated	NC-NC-NC	247411_at	A15g03000	expressed protein (68418.m07904)
4502	Not regulated	NC-NC-NC	247414_at	A15g03050	expressed protein (68418.m07910)

4503	Not regulated	NC-NC-NC	247418_at	A15g63030	glutaredoxin, putative similar to glutaredoxin [Ricinus communis] gll1732424[emb]CAA89898 (68418.m07907)
4504	Not regulated	NC-NC-NC	247366_at	A15g63280	zinc finger (CCH-type) family protein contains Pfam domain, PF00842; Zinc finger C-x-C-x5-C-x3-H type (end similar) (68418.m07940)
4505	Not regulated	NC-NC-NC	247373_at	A15g63150	expressed protein (68418.m07929)
4506	Not regulated	NC-NC-NC	247374_at	A15g63180	MA3 domain-containing protein low similarity to programmed cell death 4 protein [Gallus gallus] Gi:12959584; contains Pfam profile PF02847; MA3 domain (68418.m07933)
4507	Not regulated	NC-NC-NC	247380_at	A15g63380	4-coumarate-CoA ligase family protein / 4-coumaroyl-CoA synthase family protein similar to 4CL2 [gi:12229665] from Arabidopsis thaliana, 4CL1 [gi:12229631] from Nicotiana tabacum; contains Pfam AMP-binding enzyme domain PF00501 (68418.m07955)
4508	Not regulated	NC-NC-NC	247384_at	A15g63370	protein kinase family protein contains protein kinase domain, Pfam:PF00089 (68418.m07954)
4509	Not regulated	NC-NC-NC	247389_at	A15g63490	CBS domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein contains Pfam profiles: PF00571 CBS domain, PF00564; PB1 domain (68418.m07970)
4510	Not regulated	NC-NC-NC	247392_at	A15g63570	glutamate-1-semialdehyde 2,1-aminomutase 1 (GSA 1) / glutamate-1-semialdehyde aminotransferase 1 (GSA-AT 1) identical to GSA 1 [SPIP42799] (68418.m07979)
4511	Not regulated	NC-NC-NC	247359_at	A15g63560	transferase family protein similar to hypersensitivity-related gene product HSR201 - Nicotiana tabacum, EMBL:X95343; contains Pfam transferase family domain PF00248 (68418.m07977)
4512	Not regulated	NC-NC-NC	247330_at	A15g63510	Bacterial transferase hexapeptide repeat-containing protein contains similarity to acetyltransferase; contains Pfam profile PF00132; Bacterial transferase hexapeptide (four repeats) (68418.m07972)
4513	Not regulated	NC-NC-NC	247332_at	A15g63440	expressed protein contains Pfam PF02594; Uncharacterized ACR_YggU family COG:1872 (68418.m07983)
4514	Not regulated	NC-NC-NC	247334_at	A15g63610	protein kinase, putative similar to cytochrome-dependent kinase cdc2McE [Medicago sativa] gll180814[emb]CAA65981; contains protein kinase domain, Pfam:PF00069 (68418.m07986)
4515	Not regulated	NC-NC-NC	247336_at	A15g63640	VHS domain-containing protein / GAT domain-containing protein weak similarity to hepatocyte growth factor-regulated tyrosine kinase substrate HRS isoform 2 [Homo sapiens] Gi:9022389; contains Pfam profiles PF00790; VHS domain, PF03127; GAT domain (68418.m07980)
4516	Not regulated	NC-NC-NC	247347_at	A15g63780	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) domain (68418.m08005)
4517	Not regulated	NC-NC-NC	247353_at	A15g63620	oxidoreductase, zinc-binding dehydrogenase family protein contains PFAM zinc-binding dehydrogenase domain PF00107 (68418.m07987)
4518	Not regulated	NC-NC-NC	247355_at	A15g63670	transcription initiation protein-related contains weak similarity to Transcription initiation protein SPT4 homolog 1 [Swiss-Prot:Q16550] [Mus musculus] (68418.m07993)
4519	Not regulated	NC-NC-NC	247356_at	A15g63800	glycosyl hydrolase family 35 protein similar to beta-galactosidase Gi:7939821 from [Lycopodium obscurum]; contains Pfam profile PF01301; Glycosyl hydrolases family 35 (68418.m08007)
4520	Not regulated	NC-NC-NC	247298_at	A15g63840	alpha-glucosidase, putative similar to alpha-glucosidase Gi:2848032 from [Solanum tuberosum] (68418.m08014)
4521	Not regulated	NC-NC-NC	247300_at	A15g63910	expressed protein (68418.m08025)
4522	Not regulated	NC-NC-NC	247302_at	A15g63880	SNF7 family protein contains Pfam domain, PF03357; SNF7 family (68418.m08020)
4523	Not regulated	NC-NC-NC	247303_at	A15g63890	histidinol dehydrogenase, putative / HDH; putative strong similarity to SPIP24228 Histidinol dehydrogenase, chloroplast precursor (EC 1.1.1.23) (HDH) [Brassica oleracea var capitata]; contains Pfam profile PF00815; histidinol dehydrogenase (68418.m08021)
4524	Not regulated	NC-NC-NC	247306_at	A15g63870	serine/threonine protein phosphatase (PP7) identical to PP7 [Arabidopsis thaliana] Gi:2791900 (68418.m08017)
4525	Not regulated	NC-NC-NC	247307_at	A15g63860	UVB-resistance protein (UVR8) identical to UVB-resistance protein UVR8 [Gi:5478530; GB:AAAD43920.1] [Arabidopsis thaliana]; contains Pfam 00415; Regulator of chromosome condensation (RCC1) (68418.m08016)
4526	Not regulated	NC-NC-NC	247312_at	A15g63970	copine-related low similarity to SPIQ99829 Copine I [Homo sapiens] (68418.m08032)
4527	Not regulated	NC-NC-NC	247310_at	A15g64030	dehydration-responsive protein-related similar to early-responsive to dehydration stress ERD3 protein [Arabidopsis thaliana] Gi:15320410; contains Pfam profile PF03141; Putative methyltransferase (68418.m08039)
4528	Not regulated	NC-NC-NC	247319_at	A15g64050	glutamate-tRNA ligase family protein / glutamyl-tRNA synthetase family protein similar to SPIP22250 from Bacillus subtilis, SPIP22249 from Bacillus stearothermophilus; contains Pfam tRNA synthetases class I (E and Q), catalytic domain PF00749 (68418.m08042)
4529	Not regulated	NC-NC-NC	247325_at	A15g64200	arginine/serine-rich splicing factor SC35 contains similarity to splicing factor, contains Pfam profile PF00078; RNA recognition motif (a.k.a. RRM, RBD, or RNP domain) (68418.m08062)
4530	Not regulated	NC-NC-NC	247326_at	A15g64110	peroxidase, putative similar to peroxidase ATP3a [Arabidopsis thaliana] gll1546698[emb]CAA67340 (68418.m08051)
4531	Not regulated	NC-NC-NC	247328_at	A15g64130	expressed protein (68418.m08053)
4532	Not regulated	NC-NC-NC	247295_at	A15g64180	expressed protein (68418.m08058)
4533	Not regulated	NC-NC-NC	247296_at	A15g64160	expressed protein (68418.m08058)
4534	Not regulated	NC-NC-NC	247275_at	A15g64370	beta-ureidopropionase, putative / beta-alanine synthase, putative similar to beta-alanine synthase [Dictyostelium discoideum] Gi:14334061; contains Pfam profile PF00795; hydrolase, carbon-nitrogen family (68418.m08086)
4535	Not regulated	NC-NC-NC	247277_at	A15g64420	DNA polymerase V family contains Pfam domain PF04931; DNA polymerase V (68418.m08092)
4536	Not regulated	NC-NC-NC	247278_at	A15g64380	fructose-1,6-bisphosphatase family protein similar to SPIP22418 Fructose-1,6-bisphosphatase, chloroplast precursor (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase) [Spinacia oleracea]; contains Pfam profile PF00316; fructose-1,6-bisphosphatase (68418.m08087)
4537	Not regulated	NC-NC-NC	247280_at	A15g64260	phosphate-responsive protein, putative similar to phi-1 (phosphate-induced gene) [Nicotiana tabacum] Gi:3759184; contains Pfam profile PF04874; Phosphate-induced protein 1 conserved region (68418.m08073)
4538	Not regulated	NC-NC-NC	247281_at	A15g64350	FK506-binding protein (FKBP-12) / immunophilin identical to immunophilin [Gi:2104957] [Arabidopsis thaliana] (68418.m08082)
4539	Not regulated	NC-NC-NC	247282_at	A15g64240	late-abundant family protein (AMC3) / caspase family protein contains similarity to late-abundant protein [Hvea brasiliensis] gb:AA013216; contains Pfam profile PF00656; ICE-like protease (caspase) p20 domain (68418.m08089)
4540	Not regulated	NC-NC-NC	247286_at	A15g64280	oxoglutarate/malate translocator, putative similar to SWISS-PROT:Q41384 2-oxoglutarate/malate translocator, chloroplast precursor [Spinacia oleracea] (68418.m08075)

4541	Not regulated	NC-NC-NC	247288_at	A15g64330	non-photosynthetic hypocotyl 3 (NPH3); identical to non-photosynthetic hypocotyl 3 [Arabidopsis thaliana] gi6224712[bbAAFO5914, PMID:10542152 (88418.m08080)]
4542	Not regulated	NC-NC-NC	247280_at	A15g64500	membrane protein-related contains weak similarity to spinster type IV (GI:12003976) [Drosophila melanogaster] (88418.m08103)
4543	Not regulated	NC-NC-NC	247241_at	A15g64680	expressed protein (88418.m08128) inverted/pectin methyltransferase inhibitor family protein low similarity to SPIP83328 Pectinesterase inhibitor (Pectin methyltransferase inhibitor) (PMEI) (Actinidia chinensis); contains Pfam profile PF04043; Plant invertase/pectin methyltransferase inhibitor (88418.m08120)
4544	Not regulated	NC-NC-NC	247246_at	A15g64620	ribosomal protein L17 family protein contains Pfam profile: PF01196 ribosomal protein L17 (88418.m08125)
4545	Not regulated	NC-NC-NC	247247_at	A15g64650	expressed protein similar to unknown protein (pf1704031) (88418.m08145)
4546	Not regulated	NC-NC-NC	247255_at	A15g64780	26S proteasome regulatory subunit, putative (RPN5) (88418.m08143)
4547	Not regulated	NC-NC-NC	247257_at	A15g64760	expressed protein (88418.m08153)
4548	Not regulated	NC-NC-NC	247258_at	A15g64816	CPR5 protein, putative Constitutive expressor of Pathogenesis Related genes 5 (cpr5); regulator of disease resistance and senescence (Plant J. (2001)28(4)409-420. (88418.m08167)
4549	Not regulated	NC-NC-NC	247259_at	A15g64930	nucleotide-sugar transporter family protein low similarity to SPIQSY202 UDP N-acetylglucosamine transporter (Homo sapiens); contains Pfam profile PF04142; Nucleotide-sugar transporter (88418.m08175)
4550	Not regulated	NC-NC-NC	247207_at	A15g65000	expressed protein (88418.m08161)
4551	Not regulated	NC-NC-NC	247211_at	A15g64880	senescence-associated protein-related similar to senescence-associated protein SAG102 (GI:22331831) [Arabidopsis thaliana] (88418.m08181)
4552	Not regulated	NC-NC-NC	247212_at	A15g65040	expressed protein (88418.m08163)
4553	Not regulated	NC-NC-NC	247213_at	A15g64900	expressed protein (88418.m08158)
4554	Not regulated	NC-NC-NC	247214_at	A15g64850	
4555	Not regulated	NC-NC-NC	247219_at	A15g64920	COP1-interacting protein (CIP8) / zinc finger (C3HC4-type RING finger) family protein identical to COP1-interacting protein CIP8 [Arabidopsis thaliana] gi5929806[gbAA056638; contains Pfam profile: PF00087 zinc finger, C3HC4 type (88418.m08186)]
4556	Not regulated	NC-NC-NC	247220_at	A15g64960	cyclin-dependent kinase, putative / CDK, putative similar to cyclin dependent kinase C [Lycopersicon esculentum]
4557	Not regulated	NC-NC-NC	247222_at	A15g64840	gi15215944[emb CAC51391 (88418.m08171) ABC transporter family protein (88418.m08157) bZIP family transcription factor (TGA1) identical to transcription factor (TGA1) GI:16550 from [Arabidopsis thaliana] (88418.m08203)
4558	Not regulated	NC-NC-NC	247198_at	A15g65210	ribosomal protein L29 family protein contains Pfam profile PF00831; ribosomal protein L29 (88418.m08205)
4559	Not regulated	NC-NC-NC	247201_at	A15g65220	Ras-related GTP-binding family protein similar to GTP-binding protein RAB11A GI:1370142 from [Lotus japonicus]; contains Pfam profile: PF00071 Ras family (88418.m08210)
4560	Not regulated	NC-NC-NC	247202_at	A15g65270	expressed protein contains Pfam PF03136; Plant protein family. The function of this family of plant proteins is unknown;
4561	Not regulated	NC-NC-NC	247186_at	A15g65470	(88418.m08233)
4562	Not regulated	NC-NC-NC	247188_at	A15g65430	14-3-3 protein GF14 kappa (GRF8) identical to 14-3-3 protein GF14 kappa GI:5802784, SP:P46348 from [Arabidopsis thaliana] (88418.m08228)
4563	Not regulated	NC-NC-NC	247193_at	A15g65380	ripening-responsive protein, putative similar to ripening regulated protein DDTR18 [Lycopersicon esculentum] GI:12231296; contains Pfam profile PF01554; Uncharacterized membrane protein family (88418.m08223)
4564	Not regulated	NC-NC-NC	247194_at	A15g65480	expressed protein (88418.m08234)
4565	Not regulated	NC-NC-NC	247151_at	A15g65640	basic helix-loop-helix (bHLH) family protein (88418.m08257)
4566	Not regulated	NC-NC-NC	247154_at	A15g65710	leucine-rich repeat transmembrane protein kinase, putative (88418.m08270)
4567	Not regulated	NC-NC-NC	247156_at	A15g65760	serine carboxypeptidase S28 family protein similar to SPIP42785 Lysosomal Pro-X carboxypeptidase precursor (EC 3.4.16.2) (Poly(carboxypeptidase) (PRCP) (Proline carboxypeptidase) (Homo sapiens); contains Pfam profile PF05577; Serine carboxypeptidase S28 (88418.m08275)
4568	Not regulated	NC-NC-NC	247162_at	A15g65730	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative similar to endo-xyloglucan transferase GI:2244732 from [Gossypium hirsutum] (88418.m08272)
4569	Not regulated	NC-NC-NC	247163_at	A15g65685	soluble glycogen synthase-related contains weak similarity to Soluble glycogen synthase, chloroplast precursor (EC 2.4.1.11) (SS III) (Swiss-Prot:Q43848) [Solanum tuberosum] (88418.m08266)
4570	Not regulated	NC-NC-NC	247110_at	A15g65830	leucine-rich repeat family protein contains leucine rich repeat domains Pfam:PF00560, INTERPRO:IPR001811; contains similarity to receptor protein kinase-like protein (88418.m08302)
4571	Not regulated	NC-NC-NC	247112_at	A15g65950	expressed protein (88418.m08303)
4572	Not regulated	NC-NC-NC	247113_at	A15g65960	expressed protein (88418.m08302)
4573	Not regulated	NC-NC-NC	247114_at	A15g65910	BSD domain-containing protein contains Pfam profile PF03909; BSD domain (88418.m08298)
4574	Not regulated	NC-NC-NC	247117_at	A15g65940	3-hydroxyisobutyryl-coenzyme A hydrolase / CoA-thioester hydrolase (CHY1) identical to gi:8572780; contains Pfam profile PF00388 enoyl-CoA hydratase/isomerase family protein (88418.m08301)
4575	Not regulated	NC-NC-NC	247120_at	A15g65980	amino acid transporter family protein similar to proton/amino acid transporter 1 [Mus musculus] GI:21908024; contains Pfam profile PF01480; Transmembrane amino acid transporter protein (88418.m08308)
4576	Not regulated	NC-NC-NC	247121_at	A15g66010	heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative similar to Heterogeneous nuclear ribonucleoprotein SPIP5785, SPIP31943, SPIP52597 (Homo sapiens); contains InterPro IPR000504; RNA-binding region RNP-1 (RNA recognition motif) (RRM) domain (88418.m08312)
4577	Not regulated	NC-NC-NC	247123_at	A15g66050	expressed protein (88418.m08318)
4578	Not regulated	NC-NC-NC	247125_at	A15g66070	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (88418.m08324)
4579	Not regulated	NC-NC-NC	247139_at	A15g66090	expressed protein (88418.m08326)
4580	Not regulated	NC-NC-NC	247106_at	A15g66240	transducin family protein / WD-40 repeat family protein contains Pfam PF00400; WD domain, G-beta repeat (4 copies, 1 weak); similar to Will die slowly protein. [Drosophila melanogaster] (SP:Q9VJ38) [Drosophila melanogaster] (88418.m08344)

4581	Not regulated	NC-NC-NC	247079_at	A15g66055	ankyrin repeat protein / AKRP (AKR) identical to ankyrin repeat protein (AKRP) [Arabidopsis thaliana] SWISS-PROT:Q05753 (88418.m08321)
4582	Not regulated	NC-NC-NC	247082_at	A15g66030	Golgi-localized GRIP domain-containing protein contains Pfam profile PF01485: GRIP domain; supporting cDNA gi20303028(gb1AF49634.1) (88418.m08314)
4583	Not regulated	NC-NC-NC	247091_at	A15g66390	peroxidase 72 (PER72) (PRXR8) identical to SPIQ9F.J29 Peroxidase 72 precursor (EC 1.11.1.7) (Aberox P72) (PRXR8) (ATPGA) [Arabidopsis thaliana] (88418.m08372)
4584	Not regulated	NC-NC-NC	247092_at	A15g66380	mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein (88418.m08370)
4585	Not regulated	NC-NC-NC	247101_at	A15g66530	aldose 1-epimerase family protein similar to asposy-associated protein C, APOC [Chlamydomonas reinhardtii] GI:6870044; contains Pfam profile PF01263: Aldose 1-epimerase (88418.m08388)
4586	Not regulated	NC-NC-NC	247072_at	A15g66490	expressed protein (88418.m08384)
4587	Not regulated	NC-NC-NC	247073_at	A15g66570	oxygen-evolving enhancer protein 1-1, chloroplast / 33 kDa subunit of oxygen evolving system of photosystem II (PSBO1) (PSBO) identical to SP-P23321 Oxygen-evolving enhancer protein 1-1, chloroplast precursor (OEE1) (33 kDa subunit of oxygen evolving system of photosystem II) (OEC 33 kDa subunit) (33 kDa thylakoid membrane protein) [Arabidopsis thaliana] (88418.m08382)
4588	Not regulated	NC-NC-NC	247075_at	A15g66410	expressed protein (88418.m08378)
4589	Not regulated	NC-NC-NC	247077_at	A15g66420	expressed protein (88418.m08377)
4590	Not regulated	NC-NC-NC	247049_at	A15g66440	zinc finger (C2H2 type) family protein contains Pfam domain, PF00096: Zinc finger, C2H2 type (88418.m08412)
4591	Not regulated	NC-NC-NC	247054_at	A15g66730	expressed protein (88418.m08425)
4592	Not regulated	NC-NC-NC	247063_at	A15g66820	disease resistance protein (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein, (88418.m08433)
4593	Not regulated	NC-NC-NC	247065_s_at	A15g66900	expressed protein similar to unknown protein (phf1738383) (88418.m08436)
4594	Not regulated	NC-NC-NC	247045_at	A15g66930	zeaxanthin epoxidase (ZEP) (ABA1) identical to GI:9857296 ABA1; controls Pfam profiles PF01360: Monooxygenase and PF00498: FHA domain; identical to cDNA AABA1, GI:9857295 (88418.m08450)
4595	Not regulated	NC-NC-NC	247025_at	A15g67030	SKP1 interacting partner 2 (SKIP2) identical to SKP1 interacting partner 2 GI:10716948 from [Arabidopsis thaliana] (88418.m08477)
4596	Not regulated	NC-NC-NC	247033_at	A15g67250	cydin family protein similar to cydin D3.1 protein [Nicotiana tabacum] GI:4160300; contains Pfam profiles PF00134: Cydin, N-terminal domain, PF02884: Cydin, C-terminal domain (88418.m08478)
4597	Not regulated	NC-NC-NC	247034_at	A15g67260	expressed protein (88418.m08463)
4598	Not regulated	NC-NC-NC	247036_at	A15g67130	nitrogen regulation family protein similar to unknown protein (gb1AAF51525.1); contains Pfam domain PF01207: Dihydropyridine synthase (Dua); similar to (SP-P45672) NFR3-like protein (SP-P45672) [Azospirillum brasilense] (88418.m08473)
4599	Not regulated	NC-NC-NC	247042_at	A15g67220	FAD-dependent oxidoreductase family protein contains Pfam profile PF01268: FAD dependent oxidoreductase (88418.m08484)
4600	Not regulated	NC-NC-NC	246985_at	A15g67280	leucine-rich repeat transmembrane protein kinase, putative (88418.m08483)
4601	Not regulated	NC-NC-NC	246986_at	A15g67280	zinc finger (C2H2 type) protein 1 (AZF1) identical to Cy2/H2A2-type zinc finger protein 1 [Arabidopsis thaliana]
4602	Not regulated	NC-NC-NC	246993_at	A15g67450	gi6009887(dblBA485108) (88418.m08504)
4603	Not regulated	NC-NC-NC	247000_at	A15g67380	casein kinase II alpha chain 1 identical to casein kinase II, alpha chain 1 (CK II) [Arabidopsis thaliana] SWISS-PROT:Q08467; contains protein kinase domain, Pfam:PF00069 (88418.m08496)
4604	Not regulated	NC-NC-NC	247001_at	A15g67330	NRAMP metal ion transporter 4 (NRAMP4) identical to metal transporter Nramp4 [Arabidopsis thaliana] gi6468014(gb1AAF13278; member of the natural resistance-associated macrophage protein (NRAMP) metal transporter family, PMID:11500563 (88418.m08491)
4605	Not regulated	NC-NC-NC	247006_at	A15g67480	expressed protein (88418.m08511)
4606	Not regulated	NC-NC-NC	247007_at	A15g67500	porin, putative similar to SPIPA2055 34 kDa outer mitochondrial membrane protein porin (Voltage-dependent anion-selective channel protein) (VDAC) [Solanum tuberosum]; contains Pfam profile PF01459: Eukaryotic porin (88418.m08512)
4607	Not regulated	NC-NC-NC	247011_at	A15g67590	NADH-ubiquinone oxidoreductase-related contains weak similarity to NADH-ubiquinone oxidoreductase 21 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex 1-2 KD) (GI-21KD). (Swiss-Prot:P25711) [Neurospora crassa]; contains Pfam PF04800: ETC complex 1 subunit conserved region (88418.m08523)
4608	Not regulated	NC-NC-NC	247014_at	A15g67630	DNA helicase, putative similar to RuvB-like DNA helicase region (88418.m08523)
4609	Not regulated	NC-NC-NC	246953_at	A15g04850	GI:7243682 (88418.m08527)
4610	Not regulated	NC-NC-NC	246958_at	A15g24690	SNF7 family protein contains Pfam domain, PF03357: SNF7 family (88418.m00508)
4611	Not regulated	NC-NC-NC	246945_s_at	A15g25040	integral membrane transporter family protein similar to biotin transporter (GI:3377706) [Leishmania mexicana]; contains Pfam PF03052: B11 family; contains TIGRFAM5 TIGR00786: folate/biotin transporter, InterPro IPR001991/ PRO0173
4612	Not regulated	NC-NC-NC	246927_s_at	A15g25260	Sodium/dicarboxylate symporter family (88418.m02987)
4613	Not regulated	NC-NC-NC	246928_at	A15g25280	expressed protein (88418.m02984)
4614	Not regulated	NC-NC-NC	246931_at	A15g25270	expressed protein (88418.m02986)
4615	Not regulated	NC-NC-NC	246936_at	A15g25360	expressed protein (88418.m02984)
4616	Not regulated	NC-NC-NC	246939_at	A15g25520	transcription elongation factor-related contains weak similarity to transcription elongation factors (88418.m03036)
4617	Not regulated	NC-NC-NC	246895_at	A15g25540	expressed protein (88418.m03039)
4618	Not regulated	NC-NC-NC	246897_at	A15g25560	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain PF00097: Zinc finger, C3HC4 type (RING finger) (88418.m03041)
4619	Not regulated	NC-NC-NC	246908_at	A15g25610	dehydration-responsive protein (RD22) identical to SPIQ08298 Dehydration-responsive protein RD22 precursor (Arabidopsis thaliana) (88418.m03047)
4620	Not regulated	NC-NC-NC	246909_at	A15g25770	expressed protein (88418.m03058)

4621	Not regulated	NC-NC-NC	246911_at	A15g25810	AP2 domain-containing transcription factor TINY (TINY) identical to transcription factor TINY (GP:1246403) [Arabidopsis thaliana] (68418.m03063)
4622	Not regulated	NC-NC-NC	246861_at	A15g25890	auxin-responsive protein / indoleacetic acid-induced protein 28 (IAA28) identical to SPIQ9XFM0JAXIS_ARATH Auxin-responsive protein IAA28 (Indoleacetic acid-induced protein 28) [Arabidopsis thaliana] (68418.m03073)
4623	Not regulated	NC-NC-NC	246862_at	A15g25760	ubiquitin-conjugating enzyme, putative similar to SPIQ60015 Ubiquitin-conjugating enzyme E2-21 kDa (EC 6.3.2.19) (Ubiquitin-ligase) (Ubiquitin carrier protein) [Pichia angusta]; contains Pfam profile PF00178: Ubiquitin-conjugating enzyme (68418.m03057)
4624	Not regulated	NC-NC-NC	246863_at	A15g25940	early nodulin-related contains weak similarity to Swiss-Prot Q02821 early nodulin 93 (N-93) [Glycine max] (68418.m03083)
4625	Not regulated	NC-NC-NC	246864_at	A15g25900	ent-laurene oxidase, putative (GA3) / cyclochrome P450 identical to GA3 [Arabidopsis thaliana] Gi:3342249; similar to ent-laurene oxidase [Cucurbita maxima] Gi:11934675; contains Pfam profile PF00687: Cyclochrome P450 (68418.m03075)
4626	Not regulated	NC-NC-NC	246865_s_at	A15g25780	eukaryotic translation initiation factor 3 subunit 9, putative / eIF-3 eta, putative / eIF3b, putative nearly identical to SPIQ8C5Z1 (68418.m03106)
4627	Not regulated	NC-NC-NC	246879_at	A15g26110	expressed protein (68418.m030313)
4628	Not regulated	NC-NC-NC	246886_at	A15g26270	PHD finger family protein contains Pfam domain, PF06828: PHD-finger (68418.m03119)
4629	Not regulated	NC-NC-NC	246856_at	A15g26210	expressed protein (68418.m03203)
4630	Not regulated	NC-NC-NC	246832_at	A15g26595	RNA/RNA methyltransferase (SpuU) family protein low similarity to tRNA (Gm18) methyltransferase [Thermus thermophilus] Gi:11079208; contains Pfam profile PF00588: SpoU RNA Methylase (RNA methyltransferase, TmH) family (68418.m03206)
4631	Not regulated	NC-NC-NC	246843_at	A15g26734	drought-responsive family protein non-consensus AT donor site at exon 3, AC acceptor splice site at exon 4; similar to drought-induced mRNA, D19 [Arabidopsis thaliana] gi468110lembICAA55321 (68418.m03220)
4632	Not regulated	NC-NC-NC	246849_at	A15g26850	protein transport protein-related low similarity to SPIP25386 Intracellular protein transport protein USO1 [Saccharomyces cerevisiae] (68418.m03247)
4633	Not regulated	NC-NC-NC	246852_at	A15g26880	zinc finger (DNL type) family protein contains Pfam profile PF05180: DNL zinc finger (68418.m03256)
4634	Not regulated	NC-NC-NC	246824_at	A15g26990	expressed protein predicted proteins, Arabidopsis thaliana (68418.m03258)
4635	Not regulated	NC-NC-NC	246815_at	A15g27220	sodium proton exchanger / Na+/H+ antiporter (NHEX1) identical to Na+/H+ exchanger [Arabidopsis thaliana] gi4324587 [gb]AAD16948; Member of The
4636	Not regulated	NC-NC-NC	246791_at	A15g27280	Monovalent Cation:Proton Antiporter (CPA1) Family, PMID:11500563 (68418.m03240)
4637	Not regulated	NC-NC-NC	246792_at	A15g27290	expressed protein predicted proteins - different species (68418.m03271)
4638	Not regulated	NC-NC-NC	246763_at	A15g27150	mevalonate kinase (MK) identical to mevalonate kinase [Arabidopsis thaliana] SWISS-PROT:P46086 (68418.m03276)
4639	Not regulated	NC-NC-NC	246768_at	A15g27400	serY-RNA synthetase / serine-tRNA ligase identical to SPIQ39230 SerY-RNA synthetase (EC 6.1.1.11) (Serine-tRNA ligase) (SerRS) [Arabidopsis thaliana] (68418.m03281)
4640	Not regulated	NC-NC-NC	246778_at	A15g27450	sugar-porter family protein 1 (SFP1) identical to sugar-porter family protein 1 [Arabidopsis thaliana] Gi:14595698 (68418.m03286)
4641	Not regulated	NC-NC-NC	246780_at	A15g27470	signal peptidase subunit family protein contains Pfam profile: PF04573 signal peptidase subunit (68418.m03274)
4642	Not regulated	NC-NC-NC	246781_at	A15g27350	AMP-binding protein, putative similar to AMP-binding protein (MF389) gi:1617274 from Brassica napus, long-chain-fatty-acid-CoA
4643	Not regulated	NC-NC-NC	246784_at	A15g27430	ligase - Brassica napus, EMBL:Z72152; contains Pfam AMP-binding enzyme domain PF00501 (68418.m03305)
4644	Not regulated	NC-NC-NC	246789_at	A15g27600	histone H2A, putative similar to histone H2A Lycopersicon esculentum SPIP25469, Pisum sativum SPIP25470, Petroselinum
4645	Not regulated	NC-NC-NC	246735_at	A15g27670	crispin SPIP19177; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4 (68418.m03317)
4646	Not regulated	NC-NC-NC	246735_at	A15g27720	small nuclear ribonucleoprotein, putative / snRNP; putative / Sn protein, putative similar to SWISS-PROT:Q9QXAS U8 snRNA-associated Sm-like protein LSM4 [Mus musculus] (68418.m03325)
4647	Not regulated	NC-NC-NC	246741_at	A15g27720	serine/threonine protein phosphatase PP1 isozyme 8 (TOPP8) identical to SPIQ82734 Serine/threonine protein phosphatase PP1 isozyme 8 (EC 3.1.3.16) [Arabidopsis thaliana] (68418.m03337)
4648	Not regulated	NC-NC-NC	246742_at	A15g27840	ribosomal protein L18 family protein similar to SPIP52883 50S ribosomal protein L18 [Aeromonas proteolytica] (Vibrio proteolyticus) (68418.m03335)
4649	Not regulated	NC-NC-NC	246746_at	A15g27820	expressed protein (68418.m03336)
4650	Not regulated	NC-NC-NC	246749_at	A15g27830	F-box family protein contains similarity to leucine-rich repeats containing F-box protein FBL3 Gi:5919219 from [Homo sapiens] (68418.m03354)
4651	Not regulated	NC-NC-NC	246755_at	A15g27920	expressed protein (68418.m03369)
4652	Not regulated	NC-NC-NC	246790_at	A15g27970	expressed protein predicted proteins, Saccharomyces cerevisiae and Schizosaccharomyces pombe (68418.m03371)
4653	Not regulated	NC-NC-NC	246699_at	A15g27990	cysteine synthase, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative similar to O-acetylserine(thiol) lyase (EC 4.2.99.8) [Brassica juncea] Gi:2245144; contains Pfam profile PF00291: Pyridoxal-phosphate dependent enzyme (68418.m03374)
4654	Not regulated	NC-NC-NC	246701_at	A15g28020	expressed protein (68418.m03402)
4655	Not regulated	NC-NC-NC	246708_at	A15g28150	chloride channel-like (CLC) protein, putative similar to CLC-c, A15g49890 [Arabidopsis thaliana] and chloride channel protein CLC-1. Nicotiana tabacum, PIR: T02939 (68418.m03944)
4656	Not regulated	NC-NC-NC	246873_at	A15g29771	calciuretic-like phosphodiesterase family protein contains Pfam profile: PF00149 calcein-like phosphodiesterase (68418.m04090)
4657	Not regulated	NC-NC-NC	246681_at	A15g33280	peptidyl-prolyl cis-trans isomerase cytochrome-type family protein contains Pfam domain, PF00190: peptidyl-prolyl cis-trans isomerase, cytochrome-type (68418.m04153)
4658	Not regulated	NC-NC-NC	246636_at	A15g34650	
4659	Not regulated	NC-NC-NC	246644_at	A15g35100	

4660	Not regulated	NC-NC-NC	246853_at	A15g35200	epsin N-terminal homology (ENTH) domain-containing protein contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain, similar to clathrin assembly protein short form, Rattus norvegicus, EMBL:AF041373 similar to Chain A, Calm-N sapiens) (68418.m04171)
4661	Not regulated	NC-NC-NC	246854_s_at	A15g35210	peptidase M50 family protein / sterol-regulatory element binding protein (SREBP) site 2 protease family protein contains Pfam PF02163: sterol-regulatory element binding protein (SREBP) site 2 protease (68418.m04174)
4662	Not regulated	NC-NC-NC	246867_at	A15g35370	lectin protein kinase family protein contains Pfam domains, PF01453: Lectin (probable mannose binding) and PF000069: Protein kinase domain (68418.m04204)
4663	Not regulated	NC-NC-NC	246811_at	A15g35330	methy-CpG-binding domain-containing protein similar to methyl-CpG binding protein MBD4 [Mus musculus] G1:3800807: contains Pfam profile PF01429: Methyl-CpG binding domain (68418.m04187)
4664	Not regulated	NC-NC-NC	246613_at	A15g35360	acetyl-CoA carboxylase, biotin carboxylase subunit (CAC2) identical to acetyl-CoA carboxylase, biotin carboxylase subunit (CAC2) [Arabidopsis thaliana] G1:1905878 (68418.m04203)
4665	Not regulated	NC-NC-NC	246619_at	A15g36290	expressed protein contains Pfam profile PF01189: Uncharacterized protein family UPF0018 (68418.m04378)
4666	Not regulated	NC-NC-NC	246620_at	A15g36220	cytochrome P450 81D1 (CYP81D1) (CYP81A1) identical to Cytochrome P450 (SP:Q8FC65) [Arabidopsis thaliana]; eIF4-gamma/eIF5
4667	Not regulated	NC-NC-NC	246821_at	A15g36230	subunit (eIF-2B GDP-GTP exchange factor) (Homo sapiens); contains Pfam profile PF02020: eIF-4-gamma/eIF5/eIF2-epsilon subunit (68418.m04371)
4668	Not regulated	NC-NC-NC	246822_at	A15g36250	protein phosphatase 2C, putative / PP2C, putative (68418.m04373)
4669	Not regulated	NC-NC-NC	246823_at	A11g48920	nucleolin, putative similar to nuM1 protein G1:1279562 from [Medicago sativa] (68414.m05480)
4670	Not regulated	NC-NC-NC	246830_at	A11g48920	expressed protein (68414.m05705)
4671	Not regulated	NC-NC-NC	246575_at	A11g31660	bystin family contains Pfam profile: PF05291 Bystin (68414.m03887)
4672	Not regulated	NC-NC-NC	246576_at	A11g31650	expressed protein contains Pfam profile PF03759: Domain of unknown function (DUF315) (68414.m03888)
4673	Not regulated	NC-NC-NC	246591_at	A15g14880	potassium transporter, putative similar to potassium transporter HAK2p [Mesembryanthemum crystallinum]
4674	Not regulated	NC-NC-NC	246593_at	A15g14790	g114091471gbJAAK53759; KUP/HAK/KT Transporter family member, PMID:11500563; contains Pfam profile PF02705: K+
4675	Not regulated	NC-NC-NC	246597_at	A15g14950	potassium transporter (68418.m01745) expressed protein (68418.m01735) glycosyl hydrolase family 38 protein similar to alpha-mannosidase II SP:P27048 from [Mus musculus] (68418.m01754)
4676	Not regulated	NC-NC-NC	246546_at	A15g15090	porin, putative / voltage-dependent anion-selective channel protein, putative similar to SP:P42055 34 kDa outer mitochondrial membrane protein porin (Voltage-dependent anion-selective channel protein) (VDAC) (Solanum tuberosum); contains Pfam profile PF01459: Eukaryotic porin; identical to cDNA voltage-dependent anion-selective channel protein G1:4006940 (68418.m01768)
4677	Not regulated	NC-NC-NC	246548_at	A15g14910	heavy-metal-associated domain-containing protein Pfam profile PF00403: Heavy-metal-associated domain (68418.m01749)
4678	Not regulated	NC-NC-NC	246549_at	A15g15050	glycosyltransferase family 14 protein / core-2/1-branching enzyme family protein contains Pfam profile: PF02485 Core-2/1-branching enzyme (68418.m01764)
4679	Not regulated	NC-NC-NC	246553_at	A15g15440	circadian clock coupling factor-related similar to circadian clock coupling factor ZGT [Nicotiana glauca] G1:14210079 (68418.m01807)
4680	Not regulated	NC-NC-NC	246559_at	A15g15550	transducin family protein / WD-40 repeat family protein similar to YTM1 - Homo sapiens, EMBL:AF242546; contains Pfam PF00400: WD domain, G-beta repeat (7 copies, 1 weak); (68418.m01820)
4681	Not regulated	NC-NC-NC	246564_at	A15g15610	proteasome family protein contains Pfam domain, PF01398: PCI domain (68418.m01826)
4682	Not regulated	NC-NC-NC	246565_at	A15g15530	biotin carboxyl carrier protein 2 (BCCP2) identical to biotin carboxyl carrier protein isoform 2 [Arabidopsis thaliana]
4683	Not regulated	NC-NC-NC	246538_at	A15g15520	g18866691gbJAAAF80592 (68418.m01816) 40S ribosomal protein S19 (RPS19B) 40S RIBOSOMAL PROTEIN S19 - Oryza sativa, SWISSPROT:RS19_ORYSA (68418.m01817)
4684	Not regulated	NC-NC-NC	246519_at	A15g15780	pollen Ole e 1 allergen and extensin family protein contains Pfam profile PF01190: Pollen proteins Ole e 1 family (68418.m01845)
4685	Not regulated	NC-NC-NC	246521_at	A15g15810	N2,N2-dimethylguanosine RNA methyltransferase family protein similar to SP:Q8P804 N(2),N(2)-dimethylguanosine RNA methyltransferase (EC 2.1.1.32) (tRNA(guanine-26 N(2)-N(2)) methyltransferase) (Schizosaccharomyces pombe); contains Pfam profile PF02005: N2,N2-dimethylguanosine RNA methyltransferase (68418.m01850)
4686	Not regulated	NC-NC-NC	246527_at	A15g15750	RNA-binding S4 domain-containing protein 40S RIBOSOMAL PROTEIN - different species (68418.m01842)
4687	Not regulated	NC-NC-NC	246528_at	A15g15640	mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein (68418.m01830)
4688	Not regulated	NC-NC-NC	246533_at	A15g15880	expressed protein (68418.m01858)
4689	Not regulated	NC-NC-NC	246479_at	A15g16060	expressed protein (68418.m01877)
4690	Not regulated	NC-NC-NC	246480_at	A15g16070	chaperonin, putative similar to SWISS-PROT:P80317 T-complex protein 1, zeta subunit (TCP-1-zeta) [Mus musculus]; contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family (68418.m01874)
4691	Not regulated	NC-NC-NC	246487_at	A15g16030	expressed protein (68418.m01874)
4692	Not regulated	NC-NC-NC	246489_at	A15g16050	14-3-3 protein GF14 upslon (GRF5) identical to 14-3-3 protein GF14 upslon G1:2232148 from [Arabidopsis thaliana] (68418.m01876)
4693	Not regulated	NC-NC-NC	246490_at	A15g15950	adenosylmethionine decarboxylase family protein contains Pfam profile: PF01536 adenosylmethionine decarboxylase (68418.m01865)
4694	Not regulated	NC-NC-NC	246492_at	A15g16140	peptidyl-RNA hydrolase family protein contains Pfam profile PF01195: peptidyl-RNA hydrolase (68418.m01885)
4695	Not regulated	NC-NC-NC	246497_at	A15g16220	octicosapeptide/Phox/Bem1p (PB1) domain-containing protein hypothetical proteins - Arabidopsis thaliana contains Pfam profile PF00564: PB1 domain (68418.m01895)
4696	Not regulated	NC-NC-NC	246503_at	A15g16130	40S ribosomal protein S7 (RPS7C) 40S ribosomal protein S7 homolog - Brassica oleracea, EMBL:AF144752 (68418.m01884)
4697	Not regulated	NC-NC-NC	246505_at	A15g16250	expressed protein (68418.m01898)

4698	Not regulated	NC-NC-NC	246506_at	A15g16110	expressed protein hypothetical protein T26J14.6 - Arabidopsis thaliana, EMBL:AC011915 (68418.m01882) hydrolase, alphabeta fold family protein similar to monoglyceride lipase from Homo sapiens [GI:14594904, [Mus musculus] GI:2632162, contains Pfam profile PF00561: hydrolase, alphabeta fold family (68418.m01883) hexose transporter, putative strong similarity to hexose transporter [Arabidopsis thaliana] GI:8347250; contains Pfam profile PF00083: major facilitator superfamily protein (68418.m01886)
4699	Not regulated	NC-NC-NC	246507_at	A15g16120	GCN5-related N-acetyltransferase (GNAT) family protein very low similarity to SPIP39009 Spermine/spermidine acetyltransferase (EC 2.3.1.57) [Bacillus subtilis]; contains Pfam profile PF00583: acetyltransferase, GNAT family (68418.m01887) inositol 1,3,4-trisphosphate 5b-kinase identical to inositol 1,3,4-trisphosphate 5b-kinase [Spinacia oleracea] gi:10952512 (68418.m01882)
4700	Not regulated	NC-NC-NC	246508_at	A15g16150	RNA recognition motif (RRM)-containing protein predicted proteins - Arabidopsis thaliana (68418.m01973)
4701	Not regulated	NC-NC-NC	246448_at	A15g16800	synthase 21 (SYP21) / PEP12 homolog identical to Synthase homolog (PEP12 homolog) (SP_Q39233) and synthase of plants 21 (GP_899122) [Arabidopsis thaliana]; contains Pfam profiles PF05739: SNARE domain and PF00804: Synthase (68418.m01972)
4702	Not regulated	NC-NC-NC	246451_at	A15g16760	dehydroascorbate reductase, putative Strong similarity to dehydroascorbate reductase [Spinacia oleracea] gi:10952512 (68418.m01982)
4703	Not regulated	NC-NC-NC	246452_at	A15g16840	gp-AAG24945 (68418.m01956) cellulose synthase-7 from Zea mays (68418.m01982)
4704	Not regulated	NC-NC-NC	246453_at	A15g16830	expressed protein contains Pfam profile PF04828: Protein of unknown function (DUF636) (68418.m01985) cellulose synthase-7 from Zea mays (68418.m01982)
4705	Not regulated	NC-NC-NC	246454_at	A15g16710	expressed protein contains Pfam profile PF04828: Protein of unknown function (DUF636) (68418.m01985) cellulose synthase-7 from Zea mays (68418.m01982)
4706	Not regulated	NC-NC-NC	246460_at	A15g16910	sugar transporter family protein similar to D-xylose proton-symporter [Lactobacillus brevis] GI:2895856; contains Pfam profile PF00083: major facilitator superfamily protein (68418.m01992)
4707	Not regulated	NC-NC-NC	246462_at	A15g16940	UDP-glucuronosylUDP-glucosyl transferase family protein similar to UDP glucose:flavonoid 3-O-glucosyltransferase, Vitis vinifera, EMBL:AF000372 (68418.m01998)
4708	Not regulated	NC-NC-NC	246466_at	A15g17010	expressed protein (68418.m02000)
4709	Not regulated	NC-NC-NC	246468_at	A15g17050	NADP-dependent oxidoreductase, putative strong similarity to probable NADP-dependent oxidoreductase (zeta-crystallin homolog) P1 [SPQ39172] (gi:886428) and P2 [SPQ39173] (gi:886430); Arabidopsis thaliana (68418.m01990)
4710	Not regulated	NC-NC-NC	246469_at	A15g17070	VHS domain-containing protein / GAT domain-containing protein weak similarity to hepatocyte growth factor-regulated tyrosine kinase substrate [Homo sapiens] GI:2731383; contains Pfam profiles PF00780: VHS domain, PF03127: GAT domain (68418.m01977)
4711	Not regulated	NC-NC-NC	246417_at	A15g16990	ADP-ribosylation factor, putative similar to ADP-ribosylation factor 1, ARF 1 (GP_365340) [Drosophila melanogaster] (68418.m01977)
4712	Not regulated	NC-NC-NC	246421_at	A15g16880	ADP-ribosylation factor, putative similar to ADP-ribosylation factor 1, ARF 1 (GP_365340) [Drosophila melanogaster] (68418.m01977)
4713	Not regulated	NC-NC-NC	246422_at	A15g17060	root cap 1 (RCP1) identical to Gi:6137138 (68418.m02055)
4714	Not regulated	NC-NC-NC	246434_at	A15g17520	glycine/proline-rich protein glycine/proline-rich protein GRP - Arabidopsis thaliana, EMBL:X64315 (68418.m02069)
4715	Not regulated	NC-NC-NC	246440_at	A15g17650	BolA-like family protein contains Pfam profile: PF01722 BolA-like protein (68418.m02060)
4716	Not regulated	NC-NC-NC	246441_at	A15g17560	BolA-like family protein contains Pfam profile: PF01722 BolA-like protein (68418.m02060)
4717	Not regulated	NC-NC-NC	246442_at	A15g17610	expressed protein (68418.m02065)
4718	Not regulated	NC-NC-NC	246443_at	A15g17620	expressed protein (68418.m02066)
4719	Not regulated	NC-NC-NC	246446_at	A15g17640	phosphoglucosamine mutase family protein low similarity to phosphoglucosamine/phosphomannomutase [Sphingomonas paucimobilia] GI:6103619; contains InterPro accession IPR006352: Phosphoglucosamine mutase (68418.m02056)
4720	Not regulated	NC-NC-NC	246412_at	A15g17530	expressed protein (68418.m02068)
4721	Not regulated	NC-NC-NC	246391_at	A11g17350	TCP family transcription factor, putative similar to auxin-induced basic helix-loop-helix transcription factor GI:5731257 from [Oenothera lutea] (68414.m06585)
4722	Not regulated	NC-NC-NC	246398_at	A11g58100	expressed protein contains similarity to T-box domain GI:5931592 from [Cynops pyrrhogaster] (68414.m06525) membrane bound O-acyl transferase (MBOAT) family protein low similarity to skinny hedgehog [Drosophila melanogaster] GI:15420842; contains Pfam profile PF03062: MBOAT family (68414.m06536)
4723	Not regulated	NC-NC-NC	246400_at	A11g57540	disease resistance protein (TIR class), putative domain signature TIR exists, suggestive of a disease resistance protein. (68414.m06540)
4724	Not regulated	NC-NC-NC	246404_at	A11g57600	emp24gpp25Up24 family protein similar to SPIP49755 Transmembrane protein Tmp21 precursor (21 kDa Transmembrane trafficking protein) [Homo sapiens]; contains Pfam profile PF01105: emp24gpp25Up24 family (68414.m06539)
4725	Not regulated	NC-NC-NC	246405_at	A11g57630	60S ribosomal protein L21 (RPL21E) similar to 60S ribosomal protein L21 GB_Q43281 GI:2851508 from [Arabidopsis thaliana] (68414.m06543)
4726	Not regulated	NC-NC-NC	246378_at	A11g57620	auxin-responsive protein / indoleacetic acid-induced protein 18 (IAA18) identical to SPIQ24408AXII_ARATH Auxin-responsive protein IAA18 (Indoleacetic acid-induced protein 18) [Arabidopsis thaliana] (68414.m05856)
4727	Not regulated	NC-NC-NC	246379_s_at	A11g57690	glycosyl transferase family 1 protein contains similarity to mannosyltransferase GI:1800223 from Dicotyledon discoidium; contains Pfam glycosyl transferase, group 1 family protein domain PF00534 (68414.m01986)
4728	Not regulated	NC-NC-NC	246376_at	A11g51950	Per1-like family protein contains Pfam profile PF04080: Per1-like (68414.m01983)
4729	Not regulated	NC-NC-NC	246351_at	A11g16570	protein kinase family protein contains protein kinase domain, Pfam:PF00068; similar to receptor-like serine/threonine kinase GI:2465923 from [Arabidopsis thaliana] (68414.m01996)
4730	Not regulated	NC-NC-NC	246320_at	A11g16560	Rieske [2Fe-2S] domain-containing protein similar to lethal leaf-spot 1 from Zea mays [gi:1935908]; contains Pfam PF00355 (68414.m06543)
4731	Not regulated	NC-NC-NC	246327_at	A11g16670	Rieske [2Fe-2S] domain (68416.m04835)
4732	Not regulated	NC-NC-NC	246335_at	A13g44880	50S ribosomal protein L9, chloroplast (CL9) contains Pfam profile PF03948: Ribosomal protein L9, C-terminal domain; contains Pfam profile PF01281: ribosomal protein L9, N-terminal domain; contains TIGRfam profile TIGR00158: ribosomal protein L9 (68418.m04836)
4733	Not regulated	NC-NC-NC	246339_at	A13g44890	FAD-dependent oxidoreductase family protein contains Pfam profile PF01266 FAD dependent oxidoreductase (68418.m06321)
4734	Not regulated	NC-NC-NC	246348_at	A13g56840	ABA-responsive element-binding protein 3 (AREB3) identical to ABA-responsive element binding protein 3 (AREB3) [Arabidopsis thaliana] GI:9967421 (68418.m06322)
4735	Not regulated	NC-NC-NC	246314_at	A13g56850	

4736	Not regulated	NC-NC-NC	246319_at	A13g56680	expressed protein (68416.m06305) calmodulin-2/3/5 (CAM3) identical to calmodulin Gi:474183 from [Arabidopsis thaliana], almost identical to calmodulin-2/3/5 SP:P25089 [Arabidopsis thaliana] (68416.m06317)
4737	Not regulated	NC-NC-NC	246290_at	A13g56680	expressed protein (68416.m06319)
4738	Not regulated	NC-NC-NC	246291_at	A13g56620	expressed protein (68416.m06330)
4739	Not regulated	NC-NC-NC	246292_at	A13g56910	phosphoinositide phosphatase family protein contains similarity to phosphoinositide phosphatase SAC1 [Rattus norvegicus] gi11095248[gb AAG29810; contains Pfam domain, PF02383; Sac1 homology domain; Contains nonconsensus A/TAA splice site at intron 7 (68416.m05684)]
4740	Not regulated	NC-NC-NC	246300_at	A13g51830	calcium-dependent protein kinase, putative / CDPK, putative similar to calcium-dependent protein kinase [Arabidopsis thaliana] gi1836942[gb AAAG7655; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00038; INTERPRO:IPR002048 (68416.m05686)]
4741	Not regulated	NC-NC-NC	246301_at	A13g51850	mitochondrial substrate carrier family protein peroxisomal Ca-dependent solute carrier - Oryctolagus cuniculus, EMBL:AF004161 (68416.m05688)
4742	Not regulated	NC-NC-NC	246303_at	A13g51870	expressed protein (68416.m05691)
4743	Not regulated	NC-NC-NC	246305_at	A13g51890	BAG domain-containing protein low similarity to SP Q89933 BAG-family molecular chaperone regulator-1 (Homo sapiens); contains Pfam profile PF02179; BAG (Apoptosis regulator Bc2 protein) domain (68416.m05676)
4744	Not regulated	NC-NC-NC	246306_at	A13g51780	chlorophyll synthetase, putative identical to gi:972938 putative chlorophyll synthetase from Arabidopsis thaliana (68416.m05693)
4745	Not regulated	NC-NC-NC	246308_at	A13g51820	high mobility group protein alpha (HMGAlpha) / HMG protein alpha nearly identical to HMG protein (HMGAlpha) [Arabidopsis thaliana] Gi:2832357; contains Pfam profile PF00505; HMG (high mobility group) box (68416.m05689)
4746	Not regulated	NC-NC-NC	246311_at	A13g51880	amino acid permease family protein weak similarity to y-LAT1a (amino acid transporter) [Mus musculus] Gi:3970791; contains Pfam profile PF00324; Amino acid permease (68414.m03909)
4747	Not regulated	NC-NC-NC	246259_at	A11g31830	conserved oligomeric Golgi complex component-related / COG complex component-related similar to Conserved oligomeric Golgi complex component 6 (Swiss-Prot Q9Y2V7) [Homo sapiens]; (68414.m03901)
4748	Not regulated	NC-NC-NC	246263_at	A11g31780	histidine biosynthesis bifunctional protein (HISIE) identical to histidine biosynthesis bifunctional protein hisE, chloroplast [precursor] SP: O82768 from [Arabidopsis thaliana]; identical to cDNA phosphoribosyl-ATP pyrophosphohydrolase Gi:3481883 (68414.m03916)
4749	Not regulated	NC-NC-NC	246265_at	A11g31880	Cytochrome P450 family protein similar to Cytochrome P450 97B2 (SP:O48921) [Glycine max]; contains Pfam profile: PF00087; Cytochrome P450 (68414.m03903)
4750	Not regulated	NC-NC-NC	246266_at	A11g31800	expressed protein (68417.m05202)
4751	Not regulated	NC-NC-NC	246280_at	A14g36680	LIM domain-containing protein low similarity to LIM-domain protein [Branchiostoma floridae] Gi:3360516, DRAL/Slim3/FHL2 [Homo sapiens] Gi:7209525; contains Pfam profile PF00412; LIM domain (68417.m05226)
4752	Not regulated	NC-NC-NC	246283_at	A14g36860	brassinosteroid signalling positive regulator-related contains similarity to BZR1 protein [Arabidopsis thaliana] gi20270971[gb AAM18490 (68417.m05218)]
4753	Not regulated	NC-NC-NC	246284_at	A14g36780	thioredoxin family protein contains Pfam profile: PF00085 Thioredoxin; identical to cDNA thioredoxin-like protein (hcf184 gene) Gi:12049652 (68417.m05266)
4754	Not regulated	NC-NC-NC	246226_at	A14g37200	expressed protein (68417.m05198)
4755	Not regulated	NC-NC-NC	246232_at	A14g36630	U-box domain-containing protein low similarity to immediate-early fungal elicitor protein CMPG1 [Petroselinum crispum] Gi:14582200; contains Pfam profile PF04564; U-box domain (68417.m05190)
4756	Not regulated	NC-NC-NC	246233_at	A14g36550	MRG family protein contains Pfam domain PF05712; MRG (68417.m05276)
4757	Not regulated	NC-NC-NC	246234_at	A14g37280	hydroxyproline-rich glycoprotein family protein (68417.m05258)
4758	Not regulated	NC-NC-NC	246240_at	A14g37130	leucine-rich repeat family protein / protein kinase family protein contains protein kinase domain, Pfam:PF00069; contains leucine-rich repeats, Pfam:PF00560 (68417.m05273)
4759	Not regulated	NC-NC-NC	246244_at	A14g37250	expressed protein (68417.m05176)
4760	Not regulated	NC-NC-NC	246245_at	A14g36440	CBS domain-containing protein contains Pfam profile PF00571; CBS domain (68417.m05232)
4761	Not regulated	NC-NC-NC	246225_at	A14g36910	accelerated cell death 2 (ACD2) identical to accelerated cell death 2 (ACD2) Gi:12484129 from [Arabidopsis thaliana] (68417.m05242)
4762	Not regulated	NC-NC-NC	246194_at	A14g37000	geranylgeranyl pyrophosphate synthase (GGPS1) / GGPP synthetase / farnesyltransferase identical to Gi:413730 to farnesyltransferase (68417.m05221)
4763	Not regulated	NC-NC-NC	246198_at	A14g36810	hydrolase, alpha/beta fold family protein low similarity to hydrolase [Sphingomonas sp.] Gi:3426124; contains Pfam profile PF00561; hydrolase, alpha/beta fold family (68417.m05186)
4764	Not regulated	NC-NC-NC	246199_at	A14g36530	quinone reductase family protein similar to 1,4-benzoquinone reductase [Phanerochaete chrysosporium] Gi:4454983; similar to Trp repressor binding protein [Escherichia coli] SP:P30848; contains flavodoxin domain PF00258 (68417.m05214)
4765	Not regulated	NC-NC-NC	246201_at	A14g36750	metallopeptidase M24 family protein similar to SPO33343 Methionine aminopeptidase (EC 3.4.11.18) [Peptidase M] (Mycobacterium tuberculosis); contains Pfam profile PF00557; metallopeptidase family M24 (68417.m05248)
4766	Not regulated	NC-NC-NC	246202_at	A14g37040	hydrolase, alpha/beta fold family protein low similarity to 2-hydroxy-6-oxo-7-methyl-2,4-dienoate hydrolase [Pseudomonas fluorescens] Gi:1871461; contains Pfam profile PF00561; hydrolase, alpha/beta fold family (68417.m05198)
4767	Not regulated	NC-NC-NC	246203_at	A14g36610	expressed protein (68417.m05244)
4768	Not regulated	NC-NC-NC	246204_at	A14g37020	remorin family protein contains Pfam domain, PF03763; Remorin, C-terminal region (68417.m05239)
4769	Not regulated	NC-NC-NC	246205_at	A14g36870	RNA recognition motif (RRM)-containing protein similar to SLIP48809 Heterogeneous nuclear ribonucleoprotein 27C (hnRNP 48) [Drosophila melanogaster]; contains InterPro entry IPR000504; RNA-binding region RNP-1 (RNA recognition motif) (RRM); non-consensus TA donor splice site at exon 6 (68417.m05238)
4770	Not regulated	NC-NC-NC	246207_at	A14g36560	consensus TA donor splice site at exon 6 (68417.m05238)
4771	Not regulated	NC-NC-NC	246211_at	A14g36730	G-box binding factor 1 (GBF1) identical to G-box binding factor 1 SP:P42774 from [Arabidopsis thaliana]; contains Pfam profile: PF00170 bZIP transcription factor (68417.m05211)

4772	Not regulated	NC-NC-NC	246214_at	Al6g36990	heat shock factor protein 4 (HSF4) / heat shock transcription factor 4 (HSF4) SP-Q56320 from [Arabidopsis thaliana] (68417.m05241)
4773	Not regulated	NC-NC-NC	246219_at	Al6g36760	aminopeptidase P similar to Xaa-Pro aminopeptidase 2 [Lycopodium obscurum] Gi:15384991; contains Pfam profile PF00557: metallopeptidase family M24 (68417.m05215)
4774	Not regulated	NC-NC-NC	246220_at	Al6g37210	tetratricopeptide repeat (TPR)-containing protein low similarity to SP Q02508 Protein HGV2 Halocynthia roretzi; contains Pfam profile PF00515 TPR Domain (68417.m05267)
4775	Not regulated	NC-NC-NC	246221_at	Al6g37120	expressed protein (68417.m05257)
4776	Not regulated	NC-NC-NC	246169_at	Al5g32470	expressed protein (68418.m03828)
4777	Not regulated	NC-NC-NC	246171_at	Al5g32440	expressed protein (68418.m03825)
4778	Not regulated	NC-NC-NC	246189_at	Al5g20910	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (68418.m02483)
4779	Not regulated	NC-NC-NC	246192_at	Al5g20920	eukaryotic translation initiation factor 2 subunit 2, putative / eIF-2-beta, putative similar to SP P41035 Eukaryotic translation initiation factor 2 subunit (eIF-2-beta) [Oryctolagus cuniculus]; contains Pfam profile PF01873: Domain found in IF2B/IF5 (68418.m02484)
4780	Not regulated	NC-NC-NC	246159_at	Al5g20935	expressed protein (68418.m02487)
4781	Not regulated	NC-NC-NC	246160_at	Al5g21040	F-box family protein / WD-40 repeat family protein contains G-protein beta WD-40 repeats (68418.m02503)
4782	Not regulated	NC-NC-NC	246131_at	Al5g20990	Molybdopter biosynthesis CNX1 protein / molybdenum cofactor biosynthesis enzyme CNX1 (CNX1) identical to SP Q39054 Molybdopter biosynthesis CNX1 protein (Molybdenum cofactor biosynthesis enzyme CNX1) [Arabidopsis thaliana] (68418.m02495)
4783	Not regulated	NC-NC-NC	246135_at	Al5g20885	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (68418.m02480)
4784	Not regulated	NC-NC-NC	246146_at	Al5g20050	protein kinase family protein contains protein kinase domain, Pfam: PF00089 (68418.m02387)
4785	Not regulated	NC-NC-NC	246147_s_at	Al5g20000	26S proteasome AAA-ATPase subunit, putative almost identical to 26S proteasome AAA-ATPase subunit RPT6a Gi:9652888 from [Arabidopsis thaliana]; almost identical to a member of conserved Sug1 CAD family AISUG1 Gi:13537115 from [Arabidopsis thaliana] (68418.m02380)
4786	Not regulated	NC-NC-NC	246154_at	Al5g19940	plastid-lipid associated protein PAP-related / fibrillin-related weak hit to Pfam profile PF04755: PAP_fibrillin (68418.m02372)
4787	Not regulated	NC-NC-NC	246156_at	Al5g20090	expressed protein contains Pfam domain, PF03650: Uncharacterized protein family (UPF0041) (68418.m02392)
4788	Not regulated	NC-NC-NC	246157_at	Al5g20080	NADH-cytochrome b5 reductase, putative similar to SP P36060 NADH-cytochrome b5 reductase precursor (EC 1.6.2.2) (Saccharomyces cerevisiae); contains Pfam profiles PF00175: Oxidoreductase NAD-binding domain, PF00870: oxidoreductase, FAD-binding (68418.m02391)
4789	Not regulated	NC-NC-NC	246150_at	Al5g19855	expressed protein (68418.m02359)
4790	Not regulated	NC-NC-NC	246124_at	Al5g20060	phospholipase/carboxylesterase family protein similar to lysophospholipase II [Mus musculus] Gi:4569453; contains Pfam profile PF02230: Phospholipase/Carboxylesterase family (68418.m02398)
4791	Not regulated	NC-NC-NC	246109_at	Al5g20120	expressed protein (68418.m02395)
4792	Not regulated	NC-NC-NC	246112_at	Al5g20200	nucleoporin-related contains weak similarity to Nucleoporin NUP1 (Nuclear pore protein NUP1) (Swiss-Prot:P20876) [Saccharomyces cerevisiae] (68418.m02406)
4793	Not regulated	NC-NC-NC	246119_at	Al5g20350	zinc finger (DHC type) family protein / ankyrin repeat family protein similar to patsas protein [Drosophila melanogaster] Gi:9002770; contains Pfam profiles PF00023: Ankyrin repeat, PF01529: DHC zinc finger domain (68418.m02421)
4794	Not regulated	NC-NC-NC	246098_at	Al5g20400	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to naringenin 3-oxoglutarate 3-dioxygenase (flavonone-3-hydroxylase) (SP Q06942) [Malus domestica]; contains PF031712OG-Fe(II) oxygenase superfamily domain (68418.m02428)
4795	Not regulated	NC-NC-NC	246069_at	Al5g20290	40S ribosomal protein S6 (RPS6A) ribosomal protein S6 - Zea mays, PIR: T04088 (68418.m02415)
4796	Not regulated	NC-NC-NC	246069_at	Al5g20130	zinc knuckle (CCHC-type) family protein contains Pfam domain, PF00098: Zinc knuckle (68418.m02407)
4797	Not regulated	NC-NC-NC	246074_at	Al5g20570	expressed protein (68418.m02396)
4798	Not regulated	NC-NC-NC	246089_at	Al5g20570	ring-box protein-related similar to ring-box protein 1 Gi:4768004 from [Homo sapiens] (68418.m02442)
4799	Not regulated	NC-NC-NC	246090_at	Al5g20520	expressed protein (68418.m02438)
4800	Not regulated	NC-NC-NC	246092_at	Al5g20500	glutaredoxin, putative similar to glutaredoxin [Populus tremula x Populus tremuloides] gi 19548658 gb AA180750 (68418.m02436)
4801	Not regulated	NC-NC-NC	246062_at	Al5g19330	armadillo/beta-catenin repeat family protein / BTB/POZ domain-containing protein contains armadillo/beta-catenin-like repeats, Pfam: PF00514 and a BTB/POZ domain, Pfam: PF00651 (68418.m02303)
4802	Not regulated	NC-NC-NC	246064_at	Al5g19350	RNA-binding protein 45 (RBP45), putative (68418.m02306)
4803	Not regulated	NC-NC-NC	246040_at	Al5g19370	rhodanese-like domain-containing protein / PPIC-type PPIase domain-containing protein low similarity to MPT-synthase sulfurylase [Synecococcus sp. PCC 7942] Gi:2950364; contains Pfam profiles PF00581: Rhodanese-like domain, PF00638: PPIC-type PPIase domain; identical to cDNA pepioly-proti cis-trans isomerase Gi:2246379 (68418.m02338)
4804	Not regulated	NC-NC-NC	246041_at	Al5g19290	esterase/lipase/thioesterase family protein low similarity to monoglyceride lipase [Homo sapiens] Gi: 4594904; contains Interpro entry IPR000378 (68418.m02296)
4805	Not regulated	NC-NC-NC	246044_at	Al5g19450	calcium-dependent protein kinase 18 (CDPK18) identical to calcium-dependent protein kinase [Arabidopsis thaliana] gi 836942 gb AA487655 (68418.m02317)
4806	Not regulated	NC-NC-NC	246051_at	Al5g28840	NAD-dependent epimerase/dehydratase family protein similar to sugar epimerase BinG from Streptomyces verticillus Gi:9937230; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family (68418.m03547)
4807	Not regulated	NC-NC-NC	246055_at	Al5g08380	alpha-galactosidase, putative / melibiase, putative / alpha-D-galactoside galactohydrolase, putative similar to alpha-galactosidase SP_Q42658 from [Coffea arabica]; contains Pfam profile PF02065: Melibiase (68418.m00987)
4808	Not regulated	NC-NC-NC	246057_at	Al5g08400	expressed protein predicted proteins, Arabidopsis thaliana and Synecocystis sp. (68418.m00989)
4809	Not regulated	NC-NC-NC	246058_at	Al5g08430	SWIB complex BAF60b domain-containing protein / plus-3 domain-containing protein / GYF domain-containing protein similar to CPRF interacting protein [Petroselinum crispum] Gi:9588690; contains Pfam profiles PF02201: BAF60b domain of the SWIB complex, PF03126: Plus-3 domain, PF02213: GYF domain; contains non-consensus AT-AC splice sites at intron 5 (68418.m00693)

4810	Not regulated	NC-NC-NC	A15g08450	expressed protein KED, Nicotiana tabacum, EMBL:AB009883 (68418.m00985)
4811	Not regulated	NC-NC-NC	A15g08420	expressed protein (68418.m00982)
4812	Not regulated	NC-NC-NC	A15g08280	hydroxymethylglutamate synthase / porphobilinogen deaminase, chloroplast / pre-urophorphinogen synthase identical to SPJQ43318 (68418.m00975)
4813	Not regulated	NC-NC-NC	A15g08370	alpha-galactosidase, putative / melibiose, putative / alpha-D-galactoside galactohydrolase, putative similar to alpha-galactosidase SP_Q42656 from [Coffea arabica] (68418.m00986)
4814	Not regulated	NC-NC-NC	A15g08415	lipidic acid synthase family protein similar to lipidic acid synthase from Arabidopsis thaliana [gi:3928758], from Mus musculus [gi:1469828] Pfam profile PF04055; radical SAM domain protein (68418.m00991)
4815	Not regulated	NC-NC-NC	A15g08290	yellow-tear-specific protein 6 (YLS6) / mitosis protein DIM1, putative contains Pfam domain PF02866; Mitosis protein DIM1; identical to cDNA YLS8 mRNA for Dim1 homolog Gi:13122293 (68418.m00976)
4816	Not regulated	NC-NC-NC	A15g08410	thioredoxin reductase subunit A, FTR-A [Zea mays] SWISS-PROT:P80680 (68418.m00990)
4817	Not regulated	NC-NC-NC	A15g08320	thioredoxin reductase, putative similar to ferredoxin-thioredoxin reductase, variable chain (FTR-V, Ferredoxin-thioredoxin reductase subunit A, FTR-A) [Zea mays] SWISS-PROT:P80680 (68418.m00990)
4818	Not regulated	NC-NC-NC	A15g10700	expressed protein predicted proteins, Homo sapiens and Caenorhabditis elegans (68418.m00978)
4819	Not regulated	NC-NC-NC	A15g10730	expressed protein (68418.m01239)
4820	Not regulated	NC-NC-NC	A15g10710	expressed protein (68418.m01243)
4821	Not regulated	NC-NC-NC	A15g21090	leucine-rich repeat protein, putative similar to leucine rich repeat protein (LRP) Gi:1619300 from [Lycopodium esculentum]; contains leucine rich-repeat (LRR) domains Pfam:PF00590, INTERPRO:IPR001611 (68418.m02511)
4822	Not regulated	NC-NC-NC	A15g21160	La domain-containing protein / proline-rich family protein contains proline-rich extensin domains, INTERPRO:IPR002965, PF05383; La domain (68418.m02528)
4823	Not regulated	NC-NC-NC	A15g13070	MSF1-like family protein similar to px19 [Gallus gallus] Gi:969170; contains Pfam profile PF04707; MSF1-like conserved region (68418.m01488)
4824	Not regulated	NC-NC-NC	A15g13140	expressed protein (68418.m01505)
4825	Not regulated	NC-NC-NC	A15g13100	expressed protein (68418.m01501)
4826	Not regulated	NC-NC-NC	A15g13050	5-formyltetrahydrofolate cyclo-ligase (5-FCL) nearly identical to gi:22087553 (68418.m01486)
4827	Not regulated	NC-NC-NC	A15g13090	expressed protein predicted proteins - Arabidopsis thaliana (68418.m01500)
4828	Not regulated	NC-NC-NC	A15g13120	peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein contains Pfam domain, PF00160; peptidyl-prolyl cis-trans isomerase, cyclophilin-type (68418.m01503)
4829	Not regulated	NC-NC-NC	A15g20810	expressed protein (68418.m02448)
4830	Not regulated	NC-NC-NC	A15g20820	polyubiquitin (UBQ4) identical to Gi:17677 (68418.m02449)
4831	Not regulated	NC-NC-NC	A15g20700	senescence-associated protein-related similar to senescence-associated protein SAG102 (Gi:22331931) [Arabidopsis thaliana]; (68418.m02458)
4832	Not regulated	NC-NC-NC	A15g20650	copper transporter family protein similar to SPIQ39065 Copper transporter 1 (COPT1) (Arabidopsis thaliana); contains Pfam profile PF04145; Cu copper transporter family (68418.m02453)
4833	Not regulated	NC-NC-NC	A15g20830	germin-like protein (GER3) identical to germin-like protein subfamily 3 member 3 [SPIP84072] (68418.m02450)
4834	Not regulated	NC-NC-NC	A15g20680	expressed protein predicted proteins, Arabidopsis thaliana (68418.m02456)
4835	Not regulated	NC-NC-NC	A15g19500	tryptophan/tyrosine permease family protein contains Pfam profile PF03222; Tryptophan/tyrosine permease family (68418.m02323)
4836	Not regulated	NC-NC-NC	A15g19530	spermine/spermidine synthase family protein similar to SPIP09158 Spermidine synthase (EC 2.5.1.16) (Putrescine aminopropyltransferase) [Escherichia coli]; contains Pfam profile PF01564; Spermine/spermidine synthase (68418.m02326)
4837	Not regulated	NC-NC-NC	A15g19540	expressed protein (68418.m02327)
4838	Not regulated	NC-NC-NC	A15g19510	elongation factor 1B alpha-subunit 2 (eEF1Balpha2) identical to elongation factor 1B alpha-subunit [Arabidopsis thaliana] Gi:6666821 (68418.m02324)
4839	Not regulated	NC-NC-NC	A15g28500	expressed protein predicted proteins, Arabidopsis thaliana and Synechocystis sp. (68418.m03469)
4840	Not regulated	NC-NC-NC	A15g18590	expressed protein contains Pfam profile PF04398; Protein of unknown function, DUF538 (68418.m02332)
4841	Not regulated	NC-NC-NC	A15g19850	hydrolase, alpha/beta fold family protein low similarity to hydrolase [Tetrahymena sp. D9F63] Gi:14186240; contains Pfam profile PF00561; hydrolase, alpha/beta fold family (68418.m02358)
4842	Not regulated	NC-NC-NC	A15g19750	peroxisomal membrane 22 kDa family protein similar to SPIP42925 22 kDa peroxisomal membrane protein [Mus musculus]; contains Pfam profile PF04117; Mpv17 / PMP22 family (68418.m02348)
4843	Not regulated	NC-NC-NC	A15g19680	leucine-rich repeat family protein contains leucine rich repeat (LRR) domains, Pfam:PF00560 (68418.m02341)
4844	Not regulated	NC-NC-NC	A15g19760	dicarboxylate/tricarboxylate carrier (DTC) identical to dicarboxylate/tricarboxylate carrier [Arabidopsis thaliana] Gi:18913113 (68418.m02348)
4845	Not regulated	NC-NC-NC	A15g19830	expressed protein (68418.m02336)
4846	Not regulated	NC-NC-NC	A15g19820	PBS lyase HEAT-like repeat-containing protein contains Pfam profile: PF03130 PBS lyase HEAT-like repeat (68418.m02355)
4847	Not regulated	NC-NC-NC	A15g19600	sulfate transporter, putative similar to sulfate transporter [Arabidopsis thaliana] Gi:2285685; contains Pfam profiles PF00916; Sulfate transporter family, PF01740; STAS domain; supporting cDNA gi14141683/dbjAB061738.1 (68418.m02333)
4848	Not regulated	NC-NC-NC	A15g19860	expressed protein contains Pfam profile PF04398; Protein of unknown function, DUF538 (68418.m02381)
4849	Not regulated	NC-NC-NC	A15g09330	no apical meristem (NAM) family protein similar to NAC1 (Gi:7718952) (Medicago truncatula); contains Pfam PF02365; No apical meristem (NAM) protein (68418.m01081)
4850	Not regulated	NC-NC-NC	A15g09410	calmodulin-binding protein similar to anther ethylene-upregulated calmodulin-binding protein ER1 Gi:11612392 from [Nicotiana tabacum] (68418.m01090)
4851	Not regulated	NC-NC-NC	A15g09510	40S ribosomal protein S15 (RPS15D) ribosomal protein S15 - Arabidopsis thaliana, EMBL:Z23161 (68418.m01100)
4852	Not regulated	NC-NC-NC	A15g09390	CD2-binding protein-related similar to CD2 cytoplasmic domain binding protein [Homo sapiens] Gi:3983427 (68418.m01068)

4853	Not regulated	NC-NC-NC	245891_at	A15g09220	amino acid permease 2 (AAP2), identical to amine acid permease AAP2 [Arabidopsis thaliana] GI:510236 (68418.m01045)
4854	Not regulated	NC-NC-NC	245892_at	A15g09270	expressed protein (68418.m01071)
4855	Not regulated	NC-NC-NC	245894_at	A15g09310	expressed protein (68418.m01078)
4856	Not regulated	NC-NC-NC	245900_at	A15g11040	serine-rich protein weak similarity to hypercellular protein [Aspergillus nidulans] GI:309269 (68418.m01290)
4857	Not regulated	NC-NC-NC	245905_at	A15g11090	WD-40 repeat family protein similar to WD-repeat protein WDC148 (SP:Q9CUJ8) [Homo sapiens]; contains 3 weak Pfam PF00400; WD domain, G-beta repeats; (68418.m01554)
4858	Not regulated	NC-NC-NC	245948_at	A15g13480	ribosomal protein L10 family protein ribosomal protein L10; Nicotiana glauca; (68418.m01560)
4859	Not regulated	NC-NC-NC	245952_at	A15g13510	expressed protein predicted protein A2p25260 - Arabidopsis thaliana, EMBL:AC007070 (68418.m01557)
4860	Not regulated	NC-NC-NC	245953_at	A15g13500	sulfate transporter family, PF01740 STAS domain (68418.m01565)
4861	Not regulated	NC-NC-NC	245855_at	A15g13550	expressed protein (68418.m00001)
4862	Not regulated	NC-NC-NC	245882_at	A15g10110	purine permease-related low similarity to purine permease [Arabidopsis thaliana] GI:7620007; contains Pfam profile PF03151; Domain of unknown function, DUF250 (68414.m06572)
4863	Not regulated	NC-NC-NC	245866_s_at	A11g57990	chaperonin, putative similar to SWISS-PROT: P08927 - Rubisco subunit binding-protein beta subunit, chloroplast precursor (80 kDa chaperonin beta subunit, CPN-80 beta) [Plum sativum]; contains Pfam: PF00118 domain, TCP-1/cpn60 chaperonin family (68414.m03200)
4864	Not regulated	NC-NC-NC	245868_at	A11g58032	
4865	Not regulated	NC-NC-NC	245876_at	A11g28230	GCN5-related N-acetyltransferase (GNAT) family protein low similarity to SPIP09453 Ribosomal-protein-adenine acetyltransferase (EC 2.3.1.128) [Escherichia coli]; contains Pfam profile PF00583; acetyltransferase, GNAT family (68414.m03198)
4866	Not regulated	NC-NC-NC	245877_at	A11g28220	cytochrome B561 family protein contains Pfam domain, PF03188; Cytochrome b561 (68414.m03184)
4867	Not regulated	NC-NC-NC	245818_at	A11g26100	phosphatidylinositol 3- and 4-kinase family protein similar to phosphatidylinositol 4-kinase type-II beta [Homo sapiens]
4868	Not regulated	NC-NC-NC	245821_at	A11g28270	GI:20159787; contains Pfam profile PF00454; Phosphatidylinositol 3- and 4-kinase (68414.m03205)
4869	Not regulated	NC-NC-NC	245822_at	A11g28110	expressed protein (68414.m03186)
4870	Not regulated	NC-NC-NC	245825_at	A11g57870	shaggy-related protein kinase kappa, putative / ASK-kappa, putative similar to shaggy-related protein kinase kappa SP:Q39019 (68414.m03186)
4871	Not regulated	NC-NC-NC	245841_s_at	A11g58380	GI:717180 from [Arabidopsis thaliana] (68414.m06566)
4872	Not regulated	NC-NC-NC	245809_at	A11g58440	40S ribosomal protein S2 (RPS2A) similar to ribosomal protein S2 (Urethra caupo) (68414.m06842)
4873	Not regulated	NC-NC-NC	245786_at	A11g32150	squalene monooxygenase, putative / squalene epoxidase, putative similar to SP:Q65404 (SE 1.1); SPIQ65404 (SE 1.2) 8586341
4874	Not regulated	NC-NC-NC	245790_at	A11g32200	GI:AB008021.1 AB008021 (68414.m06848)
4875	Not regulated	NC-NC-NC	245783_at	A11g32220	bZIP transcription factor family protein contains Pfam profile, PF00170 bZIP transcription factor (68414.m03955)
4876	Not regulated	NC-NC-NC	245756_at	A11g35190	glycerol-3-phosphate acyltransferase, chloroplast precursor (EC 2.3.1.15) (GPAT) (AT1S1) (Arabidopsis thaliana); contains Pfam profile PF01553; acyltransferase (68414.m03960)
4877	Not regulated	NC-NC-NC	245760_s_at	A11g66920	oxidoreductase, 2OG-Fe(II) oxygenase family protein low similarity to hyoscyamine 6-dioxygenase hydroxylase from Hyoscyamus niger [GB:PF24397][SPIP24397]; Aropea belladonna [gi:4986123]; contains Pfam domain PF03171; 2OG-Fe(II) oxygenase superfamily (68414.m04365)
4878	Not regulated	NC-NC-NC	245760_at	A11g66890	serine/threonine protein kinase, putative similar to receptor serine/threonine kinase PR55K gik1235880[gb]AAC48208; contains protein kinase domain, Pfam:PF00089; contains serine/threonine protein kinase domain, INTERPRO:IPR002290 (68414.m07805)
4879	Not regulated	NC-NC-NC	245777_at	A11g73540	expressed protein (68414.m07802)
4880	Not regulated	NC-NC-NC	245724_at	A11g73390	MutT/nudix family protein low similarity to SPIQ09780 Diadenosine 5',5''-P1, P6-hexaphosphate hydrolase (EC 3.6.1.-) (Ap6A hydrolase) (Schizosaccharomyces pombe); contains Pfam profile PF00293; NUDIX domain (68414.m08512)
4881	Not regulated	NC-NC-NC	245729_at	A11g73490	RNA recognition motif (RRM)-containing protein contains INTERPRO:IPR000504 RNA-binding region RNP-1 (RNA recognition motif) domain (68414.m08508)
4882	Not regulated	NC-NC-NC	245730_at	A11g73470	expressed protein (68414.m08505)
4883	Not regulated	NC-NC-NC	245731_at	A11g73500	mitogen-activated protein kinase kinase (MAPKK), putative (MKK9) mitogen-activated protein kinase kinase (MAPKK) family, PMID:12119167 (68414.m08509)
4884	Not regulated	NC-NC-NC	245732_at	A11g73440	calmodulin-related low similarity to calmodulin 8 [Arabidopsis thaliana] GI:5825600; contains Pfam profile PF02809; Ubiquitin interaction motif, PF00036; EF hand (68414.m08501)
4885	Not regulated	NC-NC-NC	245733_at	A11g73380	expressed protein (68414.m08495)
4886	Not regulated	NC-NC-NC	245740_at	A11g44100	amino acid permease 5, putative (AAP5) nearly identical to amino acid permease (AAP5) GI:608873 from [Arabidopsis thaliana] (68414.m05094)
4887	Not regulated	NC-NC-NC	245742_at	A11g44170	aldehyde dehydrogenase, putative (ALDH) similar to aldehyde dehydrogenase ALDH [Craterostigma plantagineum]
4888	Not regulated	NC-NC-NC	245748_at	A11g51070	basic helix-loop-helix (bHLH) family protein similar to bHLH transcription factor GI:3757520 from [Arabidopsis thaliana] (68414.m05741)
4889	Not regulated	NC-NC-NC	245747_at	A11g51100	expressed protein (68414.m05745)
4890	Not regulated	NC-NC-NC	245894_at	A15g04170	calcium-binding EF hand family protein low similarity to peflin [Homo sapiens] GI:6015440; contains INTERPRO:IPR002048 calcium-binding EF-hand domain (68418.m00405)
4891	Not regulated	NC-NC-NC	245715_s_at	A15g08890	ATP synthase beta chain 2, mitochondrial precursor (EC 3.6.3.14) (Arabidopsis thaliana); strong similarity to SPIP17814 ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14) (Nicotiana glauca); contains Pfam profile PF00006; ATP synthase alpha/beta family nucleotide-binding domain, PF00306; ATP synthase ab C terminal, PF02874; ATP synthase alpha/beta family beta-barrel domain, supporting cDNA gi26452187[dbj]AK118582.1 (68418.m01034)

4892	Not regulated	4892	NC-NC-NC	245682_at	A15g08750	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (88418.m01039)
4893	Not regulated	245687_at	NC-NC-NC	245687_at	A11g28320	protease-degrader similar to Protease degS [Procurator] (SP_P44947) [Haemophilus influenzae]; similar to DegP protease precursor (Gi:2565436) [Arabidopsis thaliana] (88414.m03475)
4894	Not regulated	245685_at	NC-NC-NC	245685_at	A11g28250	expressed protein (88414.m03467)
4895	Not regulated	245686_at	NC-NC-NC	245686_at	A11g28280	VQ motif-containing protein contains PF05678: VQ motif (88414.m03471)
4896	Not regulated	245687_at	NC-NC-NC	245687_at	A11g28200	GRAM domain-containing protein / ABA-responsive protein-related similar to ABA-responsive protein [Hordeum vulgare] (Gi:4103635; contains Pfam profile PF02893: GRAM domain (88414.m03461))
4897	Not regulated	245679_at	NC-NC-NC	245679_at	A11g56590	catenin adaptor complex medium subunit family protein contains Pfam profile: PF00928 adaptor complex medium subunit family (88414.m06508)
4898	Not regulated	245681_at	NC-NC-NC	245681_at	A11g56560	beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative similar to neutral invertase [Daucus carota] (Gi:4200185; contains Pfam profile PF04853: Plant neutral invertase (88414.m06505))
4899	Not regulated	245628_at	NC-NC-NC	245628_at	A11g56700	pyridoxine-carboxylate peptidase family protein similar to Pyridoxine-carboxylate peptidase (5-oxopropyl-peptidase) (Pyroglytamyl-peptidase) (Pyrase) (Swiss-Prot:O73944) [Pyrococcus furiosus]; similar to Pyridoxine-carboxylate peptidase (5-oxopropyl-peptidase) (Pyroglytamyl-peptidase) (PGP-I), (Swiss-Prot:O07883) [Thermococcus litoralis]; contains Pfam PF01470: pyridoxine-carboxylate peptidase (88414.m06521)
4900	Not regulated	245633_at	NC-NC-NC	245633_at	A11g25280	F-box family protein / tubby family protein similar to Tubby protein homolog (SP_O88808) [Rattus norvegicus]; contains Pfam PF00848: F-box domain and Pfam PF01167: Tub family; (88414.m03137)
4901	Not regulated	245637_at	NC-NC-NC	245637_at	A11g25230	purple acid phosphatase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase; similar to purple acid phosphatase (Gi:20257479) [Arabidopsis thaliana] (88414.m03131)
4902	Not regulated	245638_s_at	NC-NC-NC	245638_s_at	A11g24996	expressed protein nearly identical to A11g25170, A11g25097, A11g24822; similar to ESTs dbj AV530941.1, dbjAV530975.1, gbIEC037999.1, gbIEC037993.1, gbIAI095009.1, gbIAI095031.1, gbIN37908.1, gbI176894.1 (88414.m03115)
4903	Not regulated	245639_at	NC-NC-NC	245639_at	A11g25280	acidic ribosomal protein PO-related contains similarity to 60S acidic ribosomal protein Gi:5815233 from [Homo sapiens] (88414.m03134)
4904	Not regulated	245651_s_at	NC-NC-NC	245651_s_at	A11g24793	UDP-3-O-acetyl N-acetylglucosamine decarboxylase family protein / F-box protein-related contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain and weak hit to Pfam PF00846: F-box domain; similar to ESTs dbj AV424895.1, gbIE522756.1, gbIT42945.1, gbIE525288.1, gbIE523201.1, gbIE526298.1, gbI142945.1, gbAA651584.1, dbjAV552851.1, dbjAV547151.1, dbjAV563142.1 (88414.m03107)
4905	Not regulated	245600_at	NC-NC-NC	245600_at	A14g14230	CBS domain-containing protein-related contains Pfam profile PF01595: Domain of unknown function (88417.m02196)
4906	Not regulated	245601_at	NC-NC-NC	245601_at	A14g14240	expressed protein contains Pfam profile PF01595: Domain of unknown function (88417.m02197)
4907	Not regulated	245605_at	NC-NC-NC	245605_at	A14g14300	heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative (88417.m02203)
4908	Not regulated	245532_at	NC-NC-NC	245532_at	A14g15110	cytochrome P450 97B3, putative (CYP97B3) identical to Cytochrome P450 97B3 (SP_O23365) [Arabidopsis thaliana] (88417.m02322)
4909	Not regulated	245557_at	NC-NC-NC	245557_at	A14g15410	UBX domain-containing protein low similarity to XY40 protein [Rattus norvegicus] (Gi:2547025; contains Pfam profile PF00789: UBX domain (88417.m02355))
4910	Not regulated	245562_at	NC-NC-NC	245562_at	A14g15520	RNA/RNA methyltransferase (Spou) family protein similar to SP19396 RNA (Guanosine-2'-O)-methyltransferase (EC 2.1.1.34) [Escherichia coli O157:H7]; contains Pfam profile PF00588: Spou RNA Methylase (RNA methyltransferase, TrmH) family; contains non-consensus donor splice site TA at exon 4 (88417.m02371)
4911	Not regulated	245529_at	NC-NC-NC	245529_at	A14g15570	RNA-splicing endonuclease positive effector-related contains similarity to SEN1, a positive effector of RNA-splicing endonuclease [Saccharomyces cerevisiae] gi1172574/gbAA863976 (88417.m02379)
4912	Not regulated	245513_at	NC-NC-NC	245513_at	A14g15780	synaptobrevin-related family protein similar to Vesicle-associated membrane protein 722 (AIVAMP722) Synaptobrevin-related protein 1 (SP_P47192) [Arabidopsis thaliana] (88417.m02402)
4913	Not regulated	245525_at	NC-NC-NC	245525_at	A14g15930	dynein light chain, putative similar to dynein light chain 2 [Mus musculus] Gi:15545995; contains Pfam profile PF01221: Dynein light chain type 1 (88417.m02419)
4914	Not regulated	245479_at	NC-NC-NC	245479_at	A14g16140	proline-rich family protein contains proline-rich extensin domains, INTERPRO:IPR002985 (88417.m02445)
4915	Not regulated	245481_at	NC-NC-NC	245481_at	A14g16170	expressed protein (88417.m02455)
4916	Not regulated	245484_at	NC-NC-NC	245484_at	A14g16210	enoyl-CoA hydratase/isomerase family protein similar to 3-hydroxybutyryl-CoA dehydratase (Crotonase) from Clostridium acetobutylicum (SP:P52046), FadB1x (enoyl-CoA hydratase) from Pseudomonas putida (Gi:13310130); contains Pfam profile PF00378 enoyl-CoA hydratase/isomerase family protein (88417.m02460)
4917	Not regulated	245493_at	NC-NC-NC	245493_at	A14g16380	expressed protein (88417.m02480)
4918	Not regulated	245494_at	NC-NC-NC	245494_at	A14g16390	chloroplastic RNA-binding protein P87, putative nearly identical to 67kD chloroplastic RNA-binding protein, P87 [Arabidopsis thaliana] Gi:9755842 (88417.m02481)
4919	Not regulated	245446_at	NC-NC-NC	245446_at	A14g16800	enoyl-CoA hydratase, putative similar to AU-binding protein/Enoyl-CoA hydratase [Homo sapiens] Gi:780241, [Mus musculus] Gi:8840920, contains Pfam profile PF00378 enoyl-CoA hydratase/isomerase family protein (88417.m02537)
4920	Not regulated	245456_at	NC-NC-NC	245456_at	A14g16950	disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.; closest homolog in Col-0 to RPP5 of clutier Landsberg erecta. (88417.m02556)
4921	Not regulated	245460_at	NC-NC-NC	245460_at	A14g16990	disease resistance protein (TIR-NBS class), putative domain signature TIR-NBS exists, suggestive of a disease resistance protein. (88417.m02561)
4922	Not regulated	245463_at	NC-NC-NC	245463_at	A14g17030	expansin-related identical to SWISS-PROT:Q23547 expansin-related protein 1 precursor (At-EXPR1)[Arabidopsis thaliana], related to expansins, http://www.bio.psu.edu/expansins/ (88417.m02569)
4923	Not regulated	245432_at	NC-NC-NC	245432_at	A14g17100	expressed protein; expression supported by MPSS (88417.m02577)
4924	Not regulated	245433_at	NC-NC-NC	245433_at	A14g17110	asparaginyl-IRNA synthetase, chloroplast, mitochondrial / asparagine-IRNA ligase / AsnRS (SYNO) nearly identical to SP Q48593 (88417.m02598)
4925	Not regulated	245413_at	NC-NC-NC	245413_at	A14g17300	oxidoreductase family protein weak similarity to SP P26935 Myo-inositol 2-dehydrogenase (EC 1.1.1.18), (Bacillus subtilis); contains Pfam profiles PF01408: Oxidoreductase family NAD-binding Rosamann fold, PF02684: Oxidoreductase family C-terminal alpha/beta domain (88417.m02604)
4926	Not regulated	245418_at	NC-NC-NC	245418_at	A14g17370	

4927	Not regulated	NC-NC-NC	A14g17510	ubiquitin carboxyl-terminal hydrolase, putative / ubiquitin thioesterase, putative similar to SPIQ3JB1 Ubiquitin carboxyl-terminal hydrolase isoform L3 (EC 3.4.19.12) (UCH-L3) (Ubiquitin thioesterase L3) [Mus musculus]; contains Pfam profile PF01088; family 1 (88417.m02620)
4928	Not regulated	NC-NC-NC	A14g17540	Ubiquitin carboxyl-terminal hydrolase, family 1 (88417.m02620)
4929	Not regulated	NC-NC-NC	A14g17620	expressed protein (88417.m02623)
4930	Not regulated	NC-NC-NC	A14g17800	glycine-rich protein (88417.m02636)
4931	Not regulated	NC-NC-NC	A14g17810	DNA-binding protein-related contains Pfam domain PF03478: Domain of unknown function (DUF298), found in AT-hook motifs
4932	Not regulated	NC-NC-NC	A14g17810	Pfam:PF02178 (88417.m02656)
4933	Not regulated	NC-NC-NC	A14g17810	zinc finger (C2H2 type) family protein contains Pfam domain PF00086: Zinc finger, C2H2 type (88417.m02657)
4934	Not regulated	NC-NC-NC	A14g17850	rapid alkalization factor (RALF) family protein (88417.m02187)
4935	Not regulated	NC-NC-NC	A14g17850	aromatic-rich family protein contains Pfam PF03654: Aromatic-Rich Protein Family (88417.m02638)
4936	Not regulated	NC-NC-NC	A14g17420	expressed protein (88417.m02492)
4937	Not regulated	NC-NC-NC	A14g17420	expressed protein contains Pfam domain, PF01887: Protein of unknown function (88417.m02608)
4938	Not regulated	NC-NC-NC	A14g17420	ATP-dependent Clp protease proteolytic subunit, putative similar to ATP-dependent Clp protease proteolytic subunit Gi:7264063 from <i>Synechococcus</i> sp. PCC 7942 (88417.m02570)
4939	Not regulated	NC-NC-NC	A14g17040	60S ribosomal protein L15 (RPL15A) (88417.m02528)
4940	Not regulated	NC-NC-NC	A14g16720	F-box family protein (FBL4) 99.7% identical to F-box protein family, AFB4 (GP:21536497) [Arabidopsis thaliana]; similar to grr1 Gi:2407790 from [Glycine max] (88417.m02365)
4941	Not regulated	NC-NC-NC	A14g15475	glycosyl transferase family 20 protein / trehalose-phosphatase family protein contains Pfam profile: PF02358 trehalose-phosphatase (88417.m02652)
4942	Not regulated	NC-NC-NC	A14g17770	esterase/lipase/thioesterase family protein similar to ethylene-induced esterase [Citrus sinensis] Gi:14278437, polyneuridine aldehyde esterase [Rauvolfia serpentina] Gi:6651393, SPIQ40708 PIR7A protein (Oryza sativa); contains InterPro entry IPR000379 (88417.m02520)
4943	Not regulated	NC-NC-NC	A14g16690	casein kinase II beta chain, putative similar to casein kinase II beta chain (CK II) [Arabidopsis thaliana] SWISS-PROT:P40229 (88417.m02637)
4944	Not regulated	NC-NC-NC	A14g17640	UDP-glucuronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase; similar to UDP-glucose sinapate glucosyltransferase Gi:9794913 from [Brassica napus] (88417.m02387)
4945	Not regulated	NC-NC-NC	A14g15490	III3 protein identical to L13 protein [Arabidopsis thaliana] gi4741966[gb AA028780 (88417.m02632)
4946	Not regulated	NC-NC-NC	A14g17390	60S ribosomal protein L15 (RPL15B) (88417.m02606)
4947	Not regulated	NC-NC-NC	A14g17560	ribosomal protein L19 family protein similar to plastid ribosomal protein L19 precursor [Spinacia oleracea] gi17582403[gb AA084312 (88417.m02625)
4948	Not regulated	NC-NC-NC	A14g15800	PP1/PP2A phosphatases pleiotropic regulator 1 (PRL1) identical to PP1/PP2A phosphatases pleiotropic regulator PRL1 (SP:Q42384) [Arabidopsis thaliana]; PRL1 [Arabidopsis thaliana] Gi:577733; contains Pfam PF00400: WD domain, G-beta repeat (7 copies) (88417.m02416)
4949	Not regulated	NC-NC-NC	A14g14430	enoyl-CoA hydratase/isomerase family protein low similarity to 2-cyclohexenylcarboxyl CoA isomerase [Streptomyces collinus] Gi:813318; enoyl-CoA isomerase [Escherichia coli] Gi:2764829; contains Pfam profile PF00378 enoyl-CoA hydratase/isomerase family protein (88417.m02475)
4950	Not regulated	NC-NC-NC	A14g16330	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to flavonone-3-hydroxylase [naringenin,2-oxoglutarate 3-dioxygenase] from <i>Malus domestica</i> [SPIQ06942]; Pyrus communis [Gi:20269881]; contains Pfam domain PF03171, 2OG-Fe(II) oxygenase superfamily (88417.m02475)
4951	Not regulated	NC-NC-NC	A14g17780	expressed protein (88417.m02655)
4952	Not regulated	NC-NC-NC	A14g17460	homeobox-leucine zipper protein 1 (HAT1) / HD-ZIP protein 1 identical to Homeobox-leucine zipper protein HAT1 (SP:P46600) [Arabidopsis thaliana] (88417.m02612)
4953	Not regulated	NC-NC-NC	A14g17720	RNA recognition motif (RRM)-containing protein (88417.m02646)
4954	Not regulated	NC-NC-NC	A14g14965	cytochrome b5 domain-containing protein similar to SPIQ15173 Membrane associated progesterone receptor component 2 (Steroid receptor protein DC6) (Homo sapiens); contains Pfam profile PF00173: Helix/Steroid binding domain (88417.m02300)
4955	Not regulated	NC-NC-NC	A14g15510	phosphatase II reaction center PsaP family protein contains Pfam domain PF01789; identical to SP:Q23403 (Arabidopsis thaliana) (88417.m02389)
4956	Not regulated	NC-NC-NC	A14g16840	expressed protein (88417.m02542)
4957	Not regulated	NC-NC-NC	A14g14716	iron-deficiency-responsive protein, putative strong similarity to iron-deficiency induced gene [Hordeum vulgare] Gi:14522834; contains Pfam profile PF03078: ARD/ARD' family (88417.m02283)
4958	Not regulated	NC-NC-NC	A14g14420	lesion inducing protein-related similar to ORF, able to induce HR-like lesions [Nicotiana tabacum] gi1762945[gb AAC49875 (88417.m02225)
4959	Not regulated	NC-NC-NC	A14g14000	expressed protein (88417.m02165)
4960	Not regulated	NC-NC-NC	A14g16444	expressed protein (88417.m02490)
4961	Not regulated	NC-NC-NC	A14g15545	expressed protein (88417.m02375)
4962	Not regulated	NC-NC-NC	A14g17260	L-lactate dehydrogenase, putative strong similarity to L-lactate dehydrogenase from <i>Lycopodium obscurum</i> (Gi:1820870, Gi:1820872), <i>Hordeum vulgare</i> (SPIP22888, SPIP22989); contains InterPro entry IPR001236: Lactate/malate dehydrogenase (88417.m02595)
4963	Not regulated	NC-NC-NC	A14g14130	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative (XTR7) almost identical to xyloglucan endotransglycosylase-related protein XTR7 Gi:1244780 from [Arabidopsis thaliana], one amino acid difference (88417.m02180)
4964	Not regulated	NC-NC-NC	A14g14465	DNA-binding protein-related contains Pfam domain PF03479: Domain of unknown function (DUF298), found in AT-hook motifs Pfam:PF02178 (88417.m02231)

4964	Not regulated	NC-NC-NC	245330_at	A14g14930	acid phosphatase survival protein SurE, putative similar to Swiss-Prot:P36664 acid phosphatase surE (EC 3.1.3.2) (Stationary-phase survival protein surE) [Escherichia coli O157:H7]; contains Pfam domain PF01875; Survival protein SurE (88417.m02283)
4965	Not regulated	NC-NC-NC	245331_at	A14g14410	basic helix-loop-helix (bHLH) family protein (88417.m02223)
4966	Not regulated	NC-NC-NC	245332_at	A14g15940	fumarylacetoacetate hydrolase family protein contains Pfam domain, PF01557; fumarylacetoacetate hydrolase family protein (88417.m02420)
4967	Not regulated	NC-NC-NC	245333_at	A14g14615	expressed protein (88417.m02248)
4968	Not regulated	NC-NC-NC	245334_at	A14g15800	rapid alkalization factor (RALF) family protein similar to RALF precursor [Nicotiana tabacum] Gi:16568316 (88417.m02404)
4969	Not regulated	NC-NC-NC	245336_at	A14g18515	expressed protein (88417.m02499)
4970	Not regulated	NC-NC-NC	245337_at	A14g16566	histidine triad family protein / HIT family protein contains Pfam domain, PF01230; HIT family (histidine triad protein family) (88417.m02507)
4971	Not regulated	NC-NC-NC	245307_at	A14g16770	oxidoreductase, 2OG-Fe(II) oxygenase family protein low similarity to flavonol synthase from Petunia hybrida [SP Q07512], Citrus unshu [Gi:4126403]; contains Pfam domain PF03171, 2OG-Fe(II) oxygenase superfamily, non-consensus GG acceptor splice site at exon 8 (88417.m02534)
4972	Not regulated	NC-NC-NC	245308_at	A14g17486	expressed protein (88417.m02616)
4973	Not regulated	NC-NC-NC	245278_at	A14g17270	Mo25 family protein similar to Mo25 protein (early mouse development protein family) [Mouse] SWISS-PROT:Q06138 (88417.m02596)
4974	Not regulated	NC-NC-NC	245280_at	A14g16845	vermalization 2 protein (VRN2) identical to vermalization 2 protein [Arabidopsis thaliana] gi 16945788 gb AA132135 (88417.m02543)
4975	Not regulated	NC-NC-NC	245284_at	A14g14210	phytoene dehydrogenase, chloroplast / phytoene desaturase (PDS) identical to SP Q07356 Phytoene dehydrogenase, chloroplast precursor (EC 1.14.99.-) (Phytoene desaturase)[Arabidopsis thaliana]; high similarity to phytoene desaturase [Lycopodium esculentum][Gi:19287] (88417.m02192)
4976	Not regulated	NC-NC-NC	245285_s_at	A14g14040	selenium-binding protein, putative contains Pfam profile PF05694: 56kDa selenium binding protein (SBP56); similar to Putative selenium-binding protein [Swiss-Prot:Q23264] [Arabidopsis thaliana]; similar to selenium binding protein (Gi:15485232) [Arabidopsis thaliana] (88417.m02168)
4977	Not regulated	NC-NC-NC	245286_at	A14g14880	cysteine synthase / O-acetylserine (thiol)-lyase / O-acetylserine sulfhydrylase (OAS1) nearly identical to SP P47998 Cysteine synthase (EC 4.2.99.8) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) [Arabidopsis thaliana]; identical to cDNA O-acetylserine lyase (At.OAS.5-8) Gi:6983573 (88417.m02285)
4978	Not regulated	NC-NC-NC	245287_at	A14g14910	imidazoleglycerol-phosphate dehydratase, putative similar to SP P34047 imidazoleglycerol-phosphate dehydratase 1 (EC 4.2.1.19) (IGPD 1) [Arabidopsis thaliana]; contains Pfam profile PF00475: imidazoleglycerol-phosphate dehydratase (88417.m02281)
4979	Not regulated	NC-NC-NC	245291_at	A14g16155	dihydroiponide dehydrogenase 2, plastidic / liponide dehydrogenase 2 (PTLPD2) identical to plastidic liponide dehydrogenase from Arabidopsis thaliana [gi:7159284] (88417.m02451)
4980	Not regulated	NC-NC-NC	245282_at	A14g15063	catalytic LgB subunit of aromatic ring-opening dioxygenase family contains Pfam PF02900: Catalytic LgB subunit of aromatic ring-opening dioxygenase (88417.m02318)
4981	Not regulated	NC-NC-NC	245295_at	A14g16100	expressed protein (88417.m02441)
4982	Not regulated	NC-NC-NC	245296_at	A14g16370	oligopeptide transporter OPT family protein similar to oligopeptide transporter Opt1p [Candida albicans] Gi:2367388; contains Pfam profile PF03169: OPT oligopeptide transporter protein (88417.m02479)
4983	Not regulated	NC-NC-NC	245297_at	A14g16510	YbaK/prolyl-IRNA synthetase-related contains weak hit to Pfam profile PF04073: YbaK/prolyl-IRNA synthetases associated domain (88417.m02498)
4984	Not regulated	NC-NC-NC	245299_at	A14g17530	Ras-related GTP-binding protein, putative very strong similarity to RAB1C [Lotus corniculatus var. japonicus] Gi:1370198; contains Pfam profile PF00071: Ras family (88417.m02622)
4985	Not regulated	NC-NC-NC	245278_at	A14g17730	syntaxin 23 (SYP23) / PEP12-like protein identical to SPO04378 Syntaxin 23 (AISYP23) (AIPLP) (AIP12-like protein) [Arabidopsis thaliana] (88417.m02847)
4986	Not regulated	NC-NC-NC	245249_at	A14g18760	acyl-CoA oxidase (ACX1) identical to acyl-CoA oxidase [Arabidopsis thaliana] Gi:30444214 (88417.m02531)
4987	Not regulated	NC-NC-NC	245280_at	A14g16360	S-AMP-activated protein kinase beta-2 subunit, putative similar to Swiss-Prot:Q8QZM4 S-AMP-activated protein kinase, beta-2 subunit (AMPK beta-2 chain) [Rattus norvegicus] (88417.m02478)
4988	Not regulated	NC-NC-NC	245285_at	A14g14400	ankyrin repeat family protein contains ankyrin repeats, Pfam domain PF00023 (88417.m02220)
4989	Not regulated	NC-NC-NC	245269_at	A14g14500	expressed protein weak similarity to SP Q9UKL6 Phosphatidylcholine transfer protein (PC-TP) (Homo sapiens) (88417.m02235)
4990	Not regulated	NC-NC-NC	245216_at	A14g18143	importin alpha-2, putative (IMPA-2) similar to importin alpha 2 [Capsicum annuum] Gi:13752592; contains Pfam profiles PF01748; importin beta binding domain, PF00514: Armadillo/beta-catenin-like repeat; non-consensus GG donor splice site at exon 1 and 6; CT acceptor splice site at exon 2 (88417.m02447)
4991	Not regulated	NC-NC-NC	245219_at	A11g59124	disease resistance protein (CC-NBS-LRR class), putative / PRM1 homolog, putative domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein; identical to cDNA RXF10 mRNA for PRM1 homolog, partial cds Gi:6520172; contains Pfam profiles PF00931: NB-ARC domain and PF00590: Leucine Rich Repeat (88417.m06872)
4992	Not regulated	NC-NC-NC	245228_at	A13g29810	phytochelatin synthase family protein / COBRA cell expansion protein COBL2 similar to phytochelatin synthetase [Hordeum vulgare subsp. vulgare] Gi:25570314; identified in Roudier, et al. Plant Phys. (2002) 130:538-548 (PMID:12376223); contains Pfam profile PF04633: Phytochelatin synthetase-like conserved region (88416.m03794)
4993	Not regulated	NC-NC-NC	245229_at	A14g25620	hydroxyproline-rich glycoprotein family protein contains proline-rich extensin domains, INTERPRO:IPR002865; Common family member A15g2430 [Arabidopsis thaliana]; (88417.m03688)
4994	Not regulated	NC-NC-NC	245235_at	A14g25550	expressed protein (88417.m03683)
4995	Not regulated	NC-NC-NC	245236_at	A14g25540	DNA mismatch repair protein MSH3 (MSH3) identical to SP Q65607 DNA mismatch repair protein MSH3 (A1Mah3) [Arabidopsis thaliana] (88417.m03682)
4996	Not regulated	NC-NC-NC	245238_at	A14g25570	cytochrome b561 family protein contains Pfam domain, PF03188: Cytochrome b561 (88417.m03685)

4997	Not regulated	NC-NC-NC	245242_at	A11g44446	chlorophyll a oxygenase (CAO) / chlorophyll b synthase identical to chlorophyll a oxygenase GI:5853117 from [Arabidopsis thaliana]; contains Pfam PF00355 Rieske [2Fe-2S] domain (68414.m05113)
4998	Not regulated	NC-NC-NC	245213_at	A11g44457	photosystem II 22kDa protein, chloroplast / photosystem II 22 kDa protein, chloroplast [precursor] SP-Q9XF91 from [Arabidopsis thaliana], contains Pfam profile PF00504; Chlorophyll A-B binding protein (68414.m05118)
4998	Not regulated	NC-NC-NC	245187_s_at	A11g67680	expressed protein (68414.m07723)
5000	Not regulated	NC-NC-NC	245195_at	A11g67740	photosystem II core complex proteins psbY, chloroplast (PSBY) / L-arginine metabolising enzyme identical to SP-Q49347
5001	Not regulated	NC-NC-NC	245198_at	A11g67700	Photosystem II core complex proteins psbY, chloroplast precursor (L-arginine metabolising enzyme) (L-AME) [Contains: Photosystem II protein psbY-1 (psbY-A1); Photosystem II protein psbY-2 (psbY-A2)] [Arabidopsis thaliana] (68414.m07730)
5002	Not regulated	NC-NC-NC	245199_at	A11g67730	expressed protein (68414.m07725)
5002	Not regulated	NC-NC-NC	245199_at	A11g67730	b-keto acyl reductase, putative (GLOSSY8) similar to b-keto acyl reductase GI:2588127 from [Hordeum vulgare] (68414.m07729)
5003	Not regulated	NC-NC-NC	245200_at	A11g67850	expressed protein (68414.m07745)
5004	Not regulated	NC-NC-NC	245207_at	A1g12310	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) (68418.m01447)
5005	Not regulated	NC-NC-NC	245209_at	A1g12340	expressed protein (68418.m01457)
5006	Not regulated	NC-NC-NC	245178_at	A1g12390	THUMP domain-containing protein contains Pfam profile PF02928: THUMP domain (68418.m01459)
5007	Not regulated	NC-NC-NC	245180_at	A1g12410	expressed protein (68418.m01460)
5008	Not regulated	NC-NC-NC	245181_at	A1g12420	expressed protein (68418.m01465)
5009	Not regulated	NC-NC-NC	245155_at	A1g12470	expressed protein (68418.m04065)
5010	Not regulated	NC-NC-NC	245165_at	A1g33180	synaptobrevin-related protein / vesicle-associated membrane protein 22 (VAMP722) (SAR1) identical to r to Vesicle-associated membrane protein 22 (VAMP722) Synaptobrevin-related protein 1 (SP-P47192) [Arabidopsis thaliana]; identical to cDNA synaptobrevin-related protein (SAR1) GI:800709 (68415.m04060)
5011	Not regulated	NC-NC-NC	245167_s_at	A1g33120	expressed protein (68415.m04070)
5012	Not regulated	NC-NC-NC	245169_at	A1g33220	pollen Ole e 1 allergen and extension family protein contains Pfam domain, PF01190: Pollen proteins Ole e 1 family (68415.m05933)
5013	Not regulated	NC-NC-NC	245172_at	A1g47540	mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein (68415.m05928)
5014	Not regulated	NC-NC-NC	245152_at	A1g47490	60S ribosomal protein L7A (RPL7aA) (68415.m05940)
5015	Not regulated	NC-NC-NC	245121_at	A1g47610	dimethyladenosine transferase, putative similar to SP-P41819 Dimethyladenosine transferase (EC 2.1.1.-) (S-adenosylmethionine-8 dimethyladenosine transferase) [Saccharomyces cerevisiae]; contains Pfam profile PF00388: ribosomal RNA adenine N ⁶ , N'-adenosyl(RNA) dimethyltransferase (68415.m05919)
5016	Not regulated	NC-NC-NC	245122_at	A1g47420	dimethylase family protein (68415.m05919)
5017	Not regulated	NC-NC-NC	245124_at	A1g47580	small nuclear ribonucleoprotein U1A / spliceosomal protein U1A / U1snRNP-specific protein identical to GB-Z48981 U1snRNP-specific protein [Arabidopsis thaliana] (68415.m05937)
5018	Not regulated	NC-NC-NC	245127_at	A1g47600	magnesium/proton exchanger (MHX1) identical to magnesium/proton exchanger AMHX [Arabidopsis thaliana] gi1649233 [gbAAAF14229; Ca ²⁺ -Cation Antiporter (CaCA) Family member PMID:11500563 (68415.m05939)
5019	Not regulated	NC-NC-NC	245131_s_at	A1g45330	RNA 2'-phosphotransferase, putative contains similarity to Swiss-Prot:Q12272 (RNA 2'-phosphotransferase) [Saccharomyces cerevisiae]; contains Pfam domain PF01885: RNA 2'-phosphotransferase, Tdt1 / Kpa family (68415.m05641)
5020	Not regulated	NC-NC-NC	245136_at	A1g45210	auxin-responsive protein-related weakly to small auxin up RNA (GI:546392) [Arabidopsis thaliana] (68415.m05629)
5021	Not regulated	NC-NC-NC	245144_at	A1g45240	methionyl aminopeptidase, putative / methionine aminopeptidase, putative / putative similar to SP-Q01862 Methionine aminopeptidase 1 precursor (EC 3.4.11.18) [Saccharomyces cerevisiae]; contains Pfam profile PF00557: metalloprotease family M24 (68415.m05632)
5022	Not regulated	NC-NC-NC	245146_at	A1g45200	Golgi SNARE 12 protein / Golgi SNAP receptor complex member 1 identical to Probable 28 kDa Golgi SNARE protein (Golgi SNAP receptor complex member 1) (SP-Q22151) [Arabidopsis thaliana] (68415.m05628)
5023	Not regulated	NC-NC-NC	245148_at	A1g45220	pectinesterase family protein contains Pfam profile: PF01095 pectinesterase (68415.m05630)
5024	Not regulated	NC-NC-NC	245090_at	A1g40900	nodulin MIN21 family protein similar to MIN21 [Medicago truncatula] (GI:2598575; contains Pfam profile PF00892: Integral membrane protein (68415.m05047)
5025	Not regulated	NC-NC-NC	245097_at	A1g40935	expressed protein low similarity to PGPS/D12 [Petunia x hybrida] (GI:4105794; contains Pfam profile PF04748: Protein of unknown function, DUF614 (68415.m05053)
5026	Not regulated	NC-NC-NC	245088_at	A1g40940	ethylene response sensor / ethylene-responsive sensor (ERS) identical to ethylene response sensor (ERS) [Arabidopsis thaliana] (GI:1048225 (68415.m05055)
5027	Not regulated	NC-NC-NC	245115_at	A1g41530	esterase, putative similar to SP-P10768 Esterase D (EC 3.1.1.1) [Homo sapiens]; contains Pfam profile: PF00756 putative esterase (68415.m05132)
5028	Not regulated	NC-NC-NC	245116_at	A1g41620	nucleoside interacting component family protein contains Pfam profile PF04097: Nucleoside interacting component (68415.m05143)
5029	Not regulated	NC-NC-NC	245118_at	A1g41680	thioredoxin reductase, putative / NADPH-dependent thioredoxin reductase, putative The last 2 exons encode thioredoxin. There is an EST match to exons 5-7, and the distance between exon 7 and exon 8 is only 90bp. It is unlikely this is two separate genes, but more likely a hybrid protein. (68415.m05149)
5030	Not regulated	NC-NC-NC	245059_at	A1g39720	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger) (68415.m04874)
5031	Not regulated	NC-NC-NC	245060_at	A1g39770	GDP-mannose pyrophosphorylase (GMP1) identical to GDP-mannose pyrophosphorylase from Arabidopsis thaliana (GI:3589858); updated per Conklin PL et al. PNAS 1996, 96(7):4198-203 (68415.m04883)
5032	Not regulated	NC-NC-NC	245081_at	A1g39730	ribulose biphosphate carboxylase/oxygenase activase / RuBisCO activase identical to SWISS-PROT:P10896 ribulose biphosphate carboxylase/oxygenase activase, chloroplast precursor (RuBisCO activase, RA) [Arabidopsis thaliana] (68415.m04877)
5033	Not regulated	NC-NC-NC	245062_at	A1g39780	speckle-type POZ protein (SP-Q43781) [Homo sapiens] (68415.m04882)

ribonuclease 2 (RNS2) identical to ribonuclease 2 precursor SP:P42814, Gi:2892;10, contains a ribonuclease T2 family histidine active site signature [PDOC00459] (68415.m04884)	245037_at	NC-NC-NC	5034	Not regulated
RER1C protein identical to SPIQ3ZW7 RER1C protein (ARIRIC1) (Arabidopsis thaliana) (68415.m02782)	245083_at	NC-NC-NC	5035	Not regulated
polyadenylate-binding protein, putative / PABP, putative (68415.m02788)	245085_at	NC-NC-NC	5036	Not regulated
glycosyl hydrolase family 17 protein (68415.m03181)	245039_at	NC-NC-NC	5037	Not regulated
uroporphyrinogen-III synthase family protein contains Pfam PF02602: uroporphyrinogen-III synthase, weak similarity to Porphyrin biosynthesis protein (HEMD), Uroporphyrinogen III methylase (UROM); Uroporphyrinogen-III synthase (EC 4.2.1.75) (Swiss-Prot:Q59284) [Clostridium josui] (68415.m03184)	245042_at	NC-NC-NC	5038	Not regulated
ania-da type cyclin (RCY1) nearly identical to ania-6a type cyclin [Arabidopsis thaliana] Gi:13924511 (68415.m03171)	245043_at	NC-NC-NC	5039	Not regulated
adhesion regulating molecule family similar to oocyte membrane glycoprotein (Gp110) (Swiss-Prot:Q16186) [Homo sapiens], contains regulating molecule - 1 precursor (110 kDa cell membrane glycoprotein) (68415.m03190)				
PSII I protein	A1g26590	NC-NC-NC	5040	Not regulated
ATPase I subunit	psbl	NC-NC-NC	5041	Not regulated
RNA polymerase beta subunit	245023_at	NC-NC-NC	5042	Not regulated
PSII D2 protein	245025_at	NC-NC-NC	5043	Not regulated
ribosomal protein S14	244989_at	NC-NC-NC	5044	Not regulated
ATPase epsilon subunit	245002_at	NC-NC-NC	5045	Not regulated
hypothetical protein	245005_at	NC-NC-NC	5046	Not regulated
ribosomal protein S18	245013_at	NC-NC-NC	5047	Not regulated
ribosomal protein S19	245018_at	NC-NC-NC	5048	Not regulated
NADH dehydrogenase ND1	244989_at	NC-NC-NC	5049	Not regulated
ribosomal protein S15	244936_at	NC-NC-NC	5050	Not regulated
cyclochrome c biogenesis orf452	244838_at	NC-NC-NC	5051	Not regulated
protein phosphatase 2C family protein / PP2C family protein similar to protein phosphatase-2c (Gi:3608412) [Mesembryanthemum crystallinum]; contains Pfam PF00481: Protein phosphatase 2C domain (68415.m03511)	244951_s_at	NC-NC-NC	5052	Not regulated
expressed protein contains Pfam profile: PF04601 protein of unknown function (DUF569) (68414.m033003)	257377_at	NC-NC-NC	5053	Not regulated
monooxygenase family protein similar to polyketide hydroxylases from several bacterial species; contains Pfam:PF01360 [Monooxygenase]] (68414.m03070)	257407_at	NC-NC-NC	5054	Not regulated
kcal repeat-containing protein low similarity to mrgB protein, Dictyostelium discoideum, PIR:S68824; contains Pfam profile PF01344; Kcalc motif (68415.m04482)	257410_at	NC-NC-NC	5055	Not regulated
ubiquitin-associated (UBA)/T-S-N domain-containing protein low similarity to NUBT (MEDO8-interacting protein) [Homo sapiens]	257431_at	NC-NC-NC	5056	Not regulated
GI:13383476; contains Pfam profile PF00627: UBA/T-S-N domain (68415.m01357)	257435_at	NC-NC-NC	5057	Not regulated
SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein contains Pfam PF00650: CRAJ/TRIO domain; similar to phosphatidylinositol/phosphatidylcholine transfer protein SP:P24280 [Saccharomyces cerevisiae (Baker's yeast)] (68414.m01771)	257444_at	NC-NC-NC	5058	Not regulated
expressed protein (68414.m01208)				
protein kinase-related (68414.m07187)	A11g14820	NC-NC-NC	5059	Not regulated
thioredoxin family protein low similarity to protein disulfide isomerase 4 [Giardia intestinalis] Gi:13489047; contains Pfam profile PF00085: Thioredoxin (68414.m00885)	A11g10660	NC-NC-NC	5060	Not regulated
expressed protein contains Pfam profile PF03080: Arabidopsis proteins of unknown function (68414.m06327)	A11g63560	NC-NC-NC	5061	Not regulated
comichron family protein contains Pfam profile: PF03311 comichron protein (68414.m01426)	A11g07960	NC-NC-NC	5062	Not regulated
ACT domain containing protein (ACR4) low similarity to underyfinferase [Glucoseacetobacter diazotrophicus] Gi:17226253; contains Pfam profile PF01842: ACT domain (68414.m07899)	A11g55360	NC-NC-NC	5063	Not regulated
RNA recognition motif (RRM)-containing protein (68416.m00027)	A11g12340	NC-NC-NC	5064	Not regulated
WD-40 repeat family protein contains 10 WD-40 repeats (PF00400) (1 weak) (68416.m02149)				
galactose-4-epimerase family protein contains Pfam profile: PF01762 galactose-4-epimerase (68416.m01892)	A11g68040	NC-NC-NC	5065	Not regulated
zinc finger (GATA type) family protein contains Pfam profile: PF00320 GATA-GATA zinc finger (68416.m02157)	257516_at	NC-NC-NC	5066	Not regulated
expressed protein (68414.m07552)	257518_at	NC-NC-NC	5067	Not regulated
	257553_at	NC-NC-NC	5068	Not regulated
	257560_at	NC-NC-NC	5069	Not regulated
	257571_at	NC-NC-NC	5070	Not regulated
	257593_at	NC-NC-NC	5070	Not regulated

WHAT IS CLAIMED IS:

1. A method for improving nitrogen assimilation and usage in a plant in which more nitrogen is available for biosynthesis, said method comprising overexpressing *GLK1* in the plant.
2. The method according to claim 1, further comprising overexpressing *CCA1* in the plant.
3. A method for improving nitrogen assimilation and usage in a plant in which more nitrogen is available for biosynthesis, said method comprising underexpressing *bZIP1* in the plant.
4. The method according to claim 3, in which the *bZIP1* gene is mutated such that a functional protein is no longer produced.
5. The method according to claim 4, in which the mutation in the *bZIP1* gene is a frame-shift mutation.
6. The method according to claim 4, in which the mutation in the *bZIP1* gene is a mutation resulting in a stop codon in the wild-type coding sequence.
7. The method according to claim 4, in which the mutation is removal of *bZIP1* transcribed sequences from the plant genome.
8. The method according to claim 4, in which the mutation is an insertion into the *bZIP1* transcribed sequence or an insertion upstream or downstream of the transcribed sequence.
9. A method for improving nitrogen assimilation and usage in a plant in which more nitrogen is available for biosynthesis, said method comprising overexpressing *GLK1* and underexpressing *bZIP1* in the plant.
10. The method according to claim 3, further comprising overexpressing *CCA1* in the plant.
11. The method according to claim 9, further comprising overexpressing *CCA1* in the plant.
12. A method for altering nitrogen accumulation and storage in a plant, said method comprising overexpressing *bZIP1* in the plant.
13. A method for altering nitrogen accumulation and storage in a plant, said method comprising underexpressing *CCA1* in the plant.
14. The method according to claim 13, further comprising overexpressing *bZIP1* in the plant.
15. A method for altering nitrogen accumulation and storage in a plant, said method comprising overexpressing *bZIP1* in the plant and underexpressing *GLK1* in the plant.

16. The method according to claim 12, further comprising underexpressing *GLK1*.
17. The method according to claim 13, further comprising underexpressing *GLK1*.
18. The method of any one of claims 1-17, wherein the plant is species of woody, ornamental, decorative, crop, cereal, fruit, or vegetable.
19. The method of any one of claims 1-17, wherein said plant is a species of one of the following genres: *Acorus*, *Aegilops*, *Allium*, *Amborella*, *Antirrhinum*, *Apium*, *Arabidopsis*, *Arachis*, *Beta*, *Betula*, *Brassica*, *Capsicum*, *Ceratopteris*, *Citrus*, *Cryptomeria*, *Cycas*, *Descurainia*, *Eschscholzia*, *Eucalyptus*, *Glycine*, *Gossypium*, *Hedyotis*, *Helianthus*, *Hordeum*, *Ipomoea*, *Lactuca*, *Linum*, *Liriodendron*, *Lotus*, *Lupinus*, *Lycopersicon*, *Medicago*, *Mesembryanthemum*, *Nicotiana*, *Nuphar*, *Pennisetum*, *Persea*, *Phaseolus*, *Physcomitrella*, *Picea*, *Pinus*, *Poncirus*, *Populus*, *Prunus*, *Robinia*, *Rosa*, *Saccharum*, *Schedonorus*, *Secale*, *Sesamum*, *Solanum*, *Sorghum*, *Stevia*, *Thellungiella*, *Theobroma*, *Triphysaria*, *Triticum*, *Vitis*, *Zea*, or *Zinnia*.
20. A transgenic plant produced by a method as claimed in any one of claims 1-19.
21. A transgenic plant comprising a polynucleotide encoding *GLK1* operatively linked to a promoter with activity in plants, wherein the promoter is optionally (a) a constitutive or inducible promoter or (b) associated with a constitutive or inducible regulatory element.
22. A transgenic plant comprising a polynucleotide encoding *GLK1* operatively linked to a promoter with activity in plants and comprising a polynucleotide encoding *CCA1* operatively linked to a second promoter with activity in plants, wherein the first and second promoter are optionally (a) a constitutive or inducible promoter or (b) associated with an constitutive or inducible regulatory element, and wherein the first and second promoter can be the same or different.
23. A transgenic plant comprising a mutation in the coding sequence of *bZIP1* or a mutation in the transcriptional or translational control sequences of *bZIP1*, such that the levels of *bZIP1* produced in the plant are less compared to a non-transgenic control plant.
24. The transgenic plant according to claim 21, further comprising a mutation in the coding sequence of *bZIP1* or a mutation in the transcriptional or translational control sequences of *bZIP1*, such that the levels of *bZIP1* produced in the plant are less compared to a non-transgenic control plant.
25. The transgenic plant according to claim 22, further comprising a mutation in the coding sequence of *bZIP1* or a mutation in the transcriptional or translational control sequences of *bZIP1*, such that the levels of *bZIP1* produced in the plant are less compared to a non-transgenic control plant.

26. The transgenic plant according to claim 23, further comprising a polynucleotide encoding *CCAI* operatively linked to a second promoter with activity in plants, wherein the first and second promoter are optionally (a) a constitutive or inducible promoter or (b) associated with a constitutive or inducible regulatory element, and wherein the first and second promoter can be the same or different.
27. The transgenic plant of any one of claims 21-26, wherein the plant is species of woody, ornamental, decorative, crop, cereal, fruit, or vegetable.
28. The transgenic plant of any one of claims 21-26, wherein said plant is a species of one of the following genres: *Acorus*, *Aegilops*, *Allium*, *Amborella*, *Antirrhinum*, *Apium*, *Arabidopsis*, *Arachis*, *Beta*, *Betula*, *Brassica*, *Capsicum*, *Ceratopteris*, *Citrus*, *Cryptomeria*, *Cycas*, *Descurainia*, *Eschscholzia*, *Eucalyptus*, *Glycine*, *Gossypium*, *Hedyotis*, *Helianthus*, *Hordeum*, *Ipomoea*, *Lactuca*, *Linum*, *Liriodendron*, *Lotus*, *Lupinus*, *Lycopersicon*, *Medicago*, *Mesembryanthemum*, *Nicotiana*, *Nuphar*, *Pennisetum*, *Persea*, *Phaseolus*, *Physcomitrella*, *Picea*, *Pinus*, *Poncirus*, *Populus*, *Prunus*, *Robinia*, *Rosa*, *Saccharum*, *Schedonorus*, *Secale*, *Sesamum*, *Solanum*, *Sorghum*, *Stevia*, *Thellungiella*, *Theobroma*, *Triphysaria*, *Triticum*, *Vitis*, *Zea*, or *Zinnia*.
29. A transgenic plant comprising a polynucleotide encoding *bZIP1* operatively linked to a promoter with activity in plants, wherein the promoter is optionally (a) a constitutive or inducible promoter or (b) associated with a constitutive or inducible regulatory element.
30. A transgenic plant comprising a mutation in the coding sequence of *CCAI* or a mutation in the transcriptional or translational control sequences of *CCAI*, such that the levels of *CCAI* produced in the plant are less compared to a non-transgenic control plant.
31. The transgenic plant according to claim 29 or 30, further comprising a mutation in the coding sequence of *GLK1* or a mutation in the transcriptional or translational control sequences of *GLK1*, such that the levels of *GLK1* produced in the plant are less compared to a non-transgenic control plant.
32. A transgenic plant comprising a polynucleotide encoding *bZIP1* operatively linked to a promoter with activity in plants and comprising a mutation in the coding sequence of *CCAI* or a mutation in the transcriptional or translational control sequences of *CCAI*, such that the levels of *CCAI* produced in the plant are less compared to a non-transgenic control plant, wherein the promoter is optionally (a) a constitutive or inducible promoter or (b) associated with an constitutive or inducible regulatory element.
33. The transgenic plant according to claim 32, further comprising a mutation in the coding sequence of *GLK1* or a mutation in the transcriptional or translational control

sequences of *GLK1*, such that the levels of *GLK1* produced in the plant are less compared to a non-transgenic control plant.

34. The transgenic plant of any one of claims 29-33, wherein the plant is species of woody, ornamental, decorative, crop, cereal, fruit, or vegetable.

35. The transgenic plant of any one of claims 29-33, wherein said plant is a species of one of the following genres: *Acorus*, *Aegilops*, *Allium*, *Amborella*, *Antirrhinum*, *Apium*, *Arabidopsis*, *Arachis*, *Beta*, *Betula*, *Brassica*, *Capsicum*, *Ceratopteris*, *Citrus*, *Cryptomeria*, *Cycas*, *Descurainia*, *Eschscholzia*, *Eucalyptus*, *Glycine*, *Gossypium*, *Hedyotis*, *Helianthus*, *Hordeum*, *Ipomoea*, *Lactuca*, *Linum*, *Liriodendron*, *Lotus*, *Lupinus*, *Lycopersicon*, *Medicago*, *Mesembryanthemum*, *Nicotiana*, *Nuphar*, *Pennisetum*, *Persea*, *Phaseolus*, *Physcomitrella*, *Picea*, *Pinus*, *Poncirus*, *Populus*, *Prunus*, *Robinia*, *Rosa*, *Saccharum*, *Schedonorus*, *Secale*, *Sesamum*, *Solanum*, *Sorghum*, *Stevia*, *Thellungiella*, *Theobroma*, *Triphysaria*, *Triticum*, *Vitis*, *Zea*, or *Zinnia*.

36. A transgenic plant-derived commercial product produced by a method according to any one of claims 1-19.

37. The transgenic plant-derived commercial product of claim 36, wherein said transgenic plant is a tree, and said commercial product is pulp, paper, a paper product, or lumber.

38. The transgenic plant-derived commercial product of claim 36, wherein said transgenic plant is tobacco, and said commercial product is a cigarette, cigar, or chewing tobacco.

39. The transgenic plant-derived commercial product of claim 36, wherein said transgenic plant is a crop, and said commercial product is a fruit or vegetable.

40. The transgenic plant-derived commercial product of claim 36, wherein said transgenic plant is a grain, and said commercial product is bread, flour, cereal, oat meal, or rice.

41. The transgenic plant-derived commercial product of claim 36, wherein said commercial product is a biofuel or plant oil.

42. A transgenic plant-derived commercial product, which is derived from a transgenic plant according to any one of claims 21-35.

43. The transgenic plant-derived commercial product of claim 42, wherein said transgenic plant is a tree, and said commercial product is pulp, paper, a paper product, or lumber.

44. The transgenic plant-derived commercial product of claim 42, wherein said transgenic plant is tobacco, and said commercial product is a cigarette, cigar, or chewing tobacco.

45. The transgenic plant-derived commercial product of claim 42, wherein said transgenic plant is a crop, and said commercial product is a fruit or vegetable.

46. The transgenic plant-derived commercial product of claim 42, wherein said transgenic plant is a grain, and said commercial product is bread, flour, cereal, oat meal, or rice.
47. The transgenic plant-derived commercial product of claim 42, wherein said commercial product is a biofuel or plant oil.

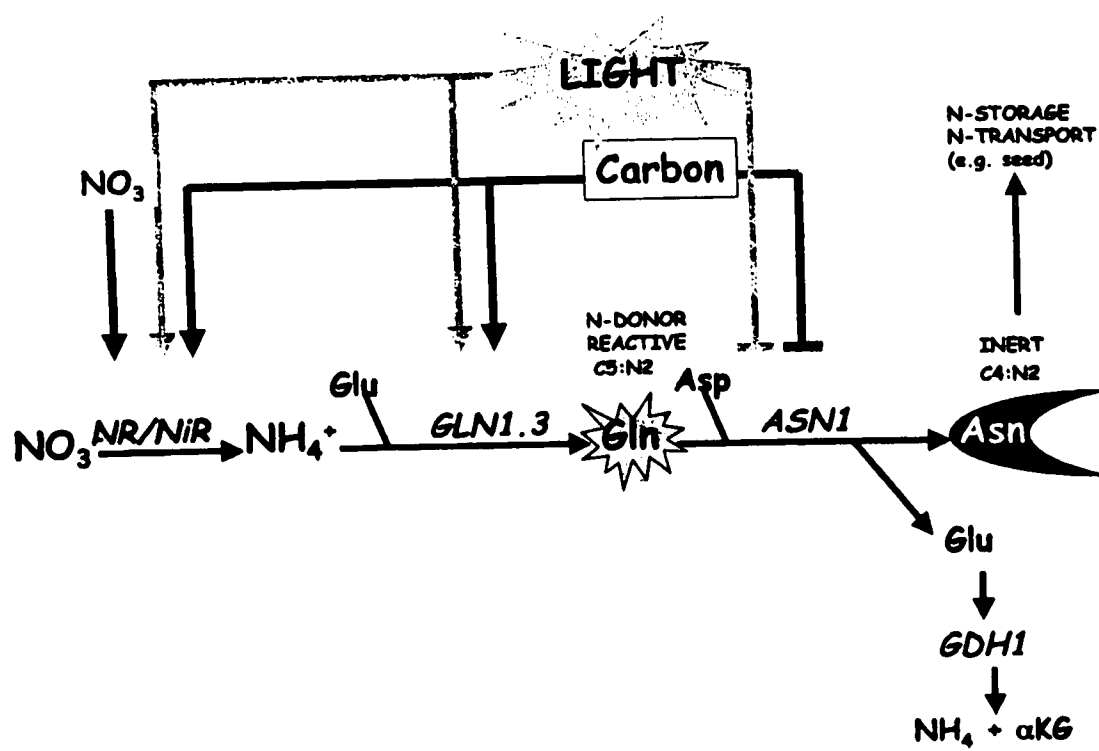


FIGURE 1

TRANSGENE	TARGET 1	TARGET 2	TARGET 3	N-assimilatio GLN1 Gln synthesis	N-storage ASN1 Asn synthesis	Recycle N GDH1 Glu degradation	CROP	Examples
	GLN1.3	BZIP/ASN1	GDH1					
GLN GROUP								
CCA1-UP	UP	DOWN	DOWN	MORE GLN	less Asn	more Glu	VEGETATIVE	trees, tobacco, lettuce, potato,
GLK1-UP	UP	DOWN	DOWN	MORE GLN	less Asn	more Glu	VEGETATIVE	as above
BZIP-DOWN	NC	DOWN	NC		less Asn		VEGETATIVE	as above
ASN GROUP								
CCA1-DOWN	DOWN	UP	UP	less Gln	MORE ASN	less Glu	FRUIT/SEED	Brassica (including canola), corn, soybean,
GLK1-DOWN	DOWN	UP	UP	less Gln	MORE ASN	less Glu	FRUIT/SEED	cotton, rice, wheat, safflower, sunflower,
BZIP-UP	NC	UP	NC		MORE ASN		FRUIT/SEED	tomato
								as above

Genes for 3 sequential REACTIONS in N-assimilation whose genes are reciprocally regulated by CCA1 and GLK1:

GLN1.3 gene (GLUTAMINE SYNTHETASE) functions in assimilating inorganic N (ammonium) into glutamine (primary n-assimilation).
Reaction: $\text{NH}_4 + \text{GLU} = \text{GLN}$ (reactive, N-donor in synthesis of all DNA, amino acids, chlorophyll, etc)

ASN1 gene (ASPARAGINE SYNTHETASE) functions to convert assimilated GLN to ASN (inert, for N-transport to seed & N-storage):
Reaction: $\text{GLN} + \text{ASP} = \text{ASN} + \text{GLU}$

GDH1 gene (GLUTAMATE DEHYDROGENASE) functions to deaminate the GLU by-product of ASN1 reaction
Reaction: $\text{Glu} = \text{NH}_4 + \alpha \text{ Ketoglutarate}$

FIGURE 2



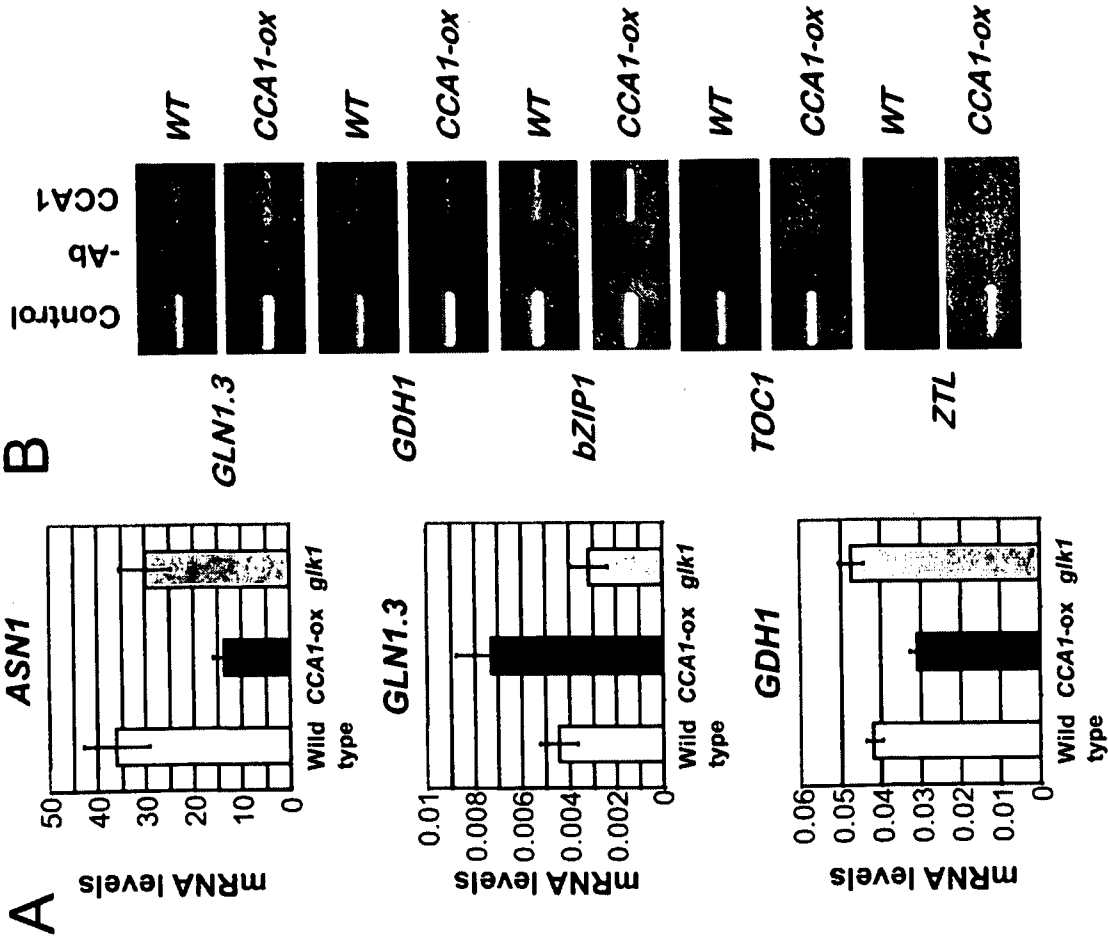
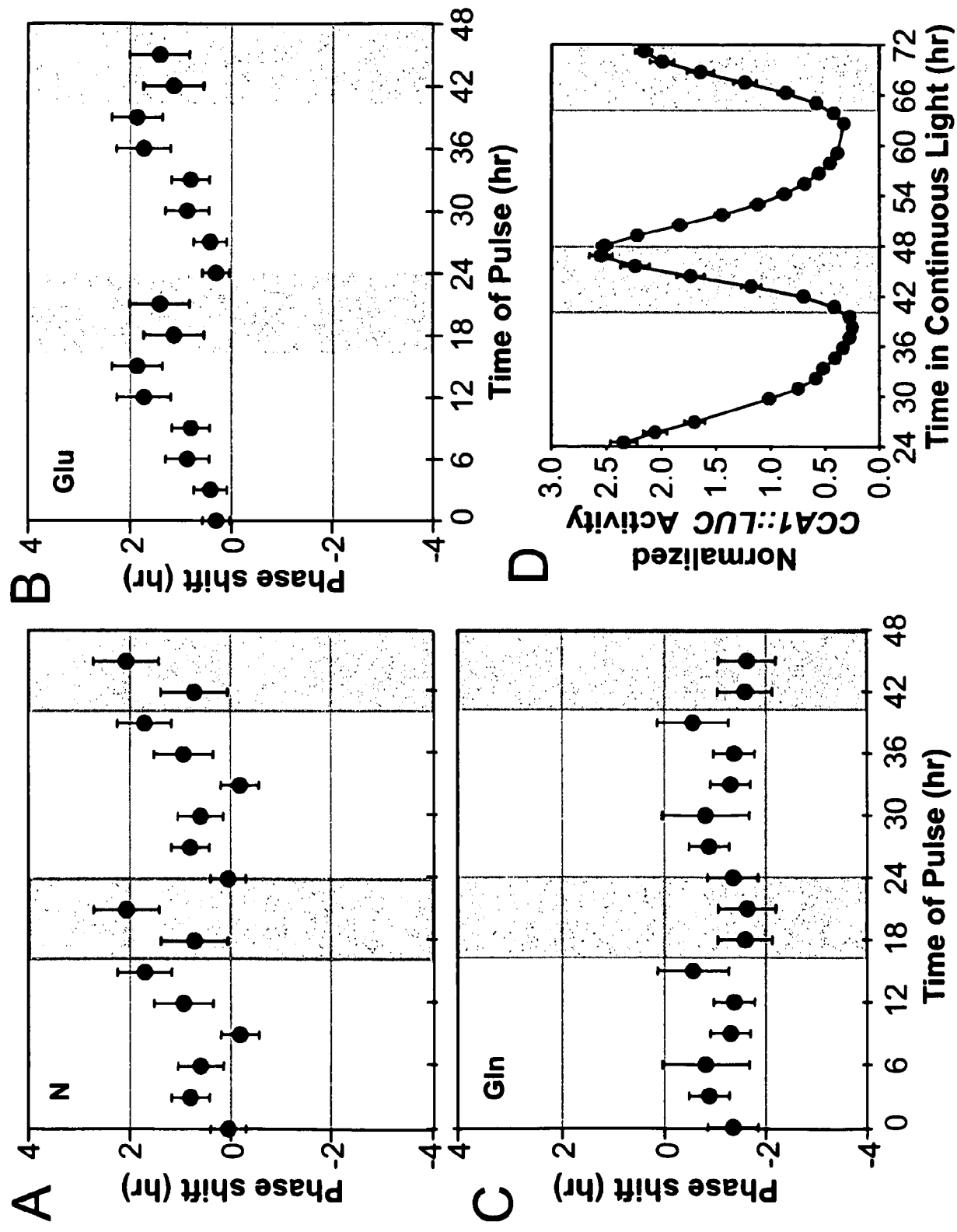


FIGURE 4

FIGURE 5



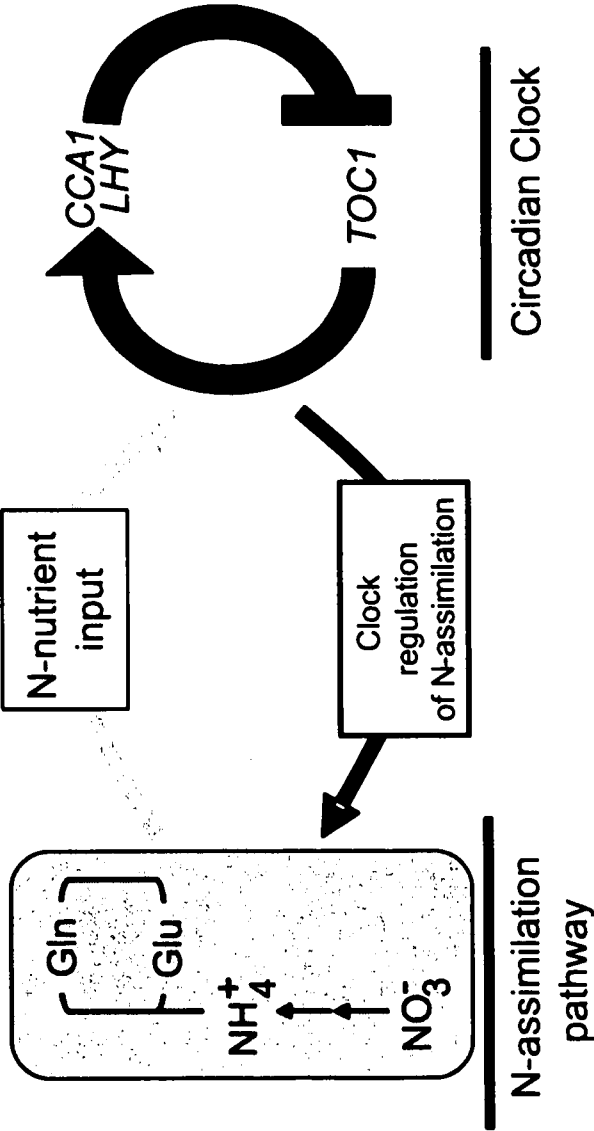


FIGURE 6

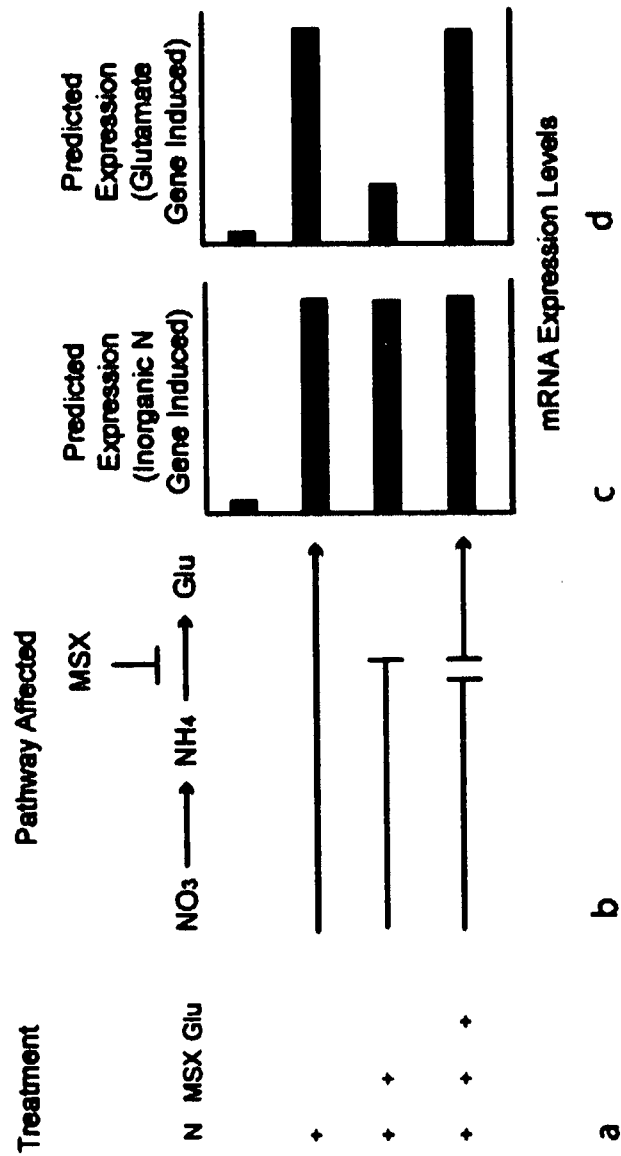
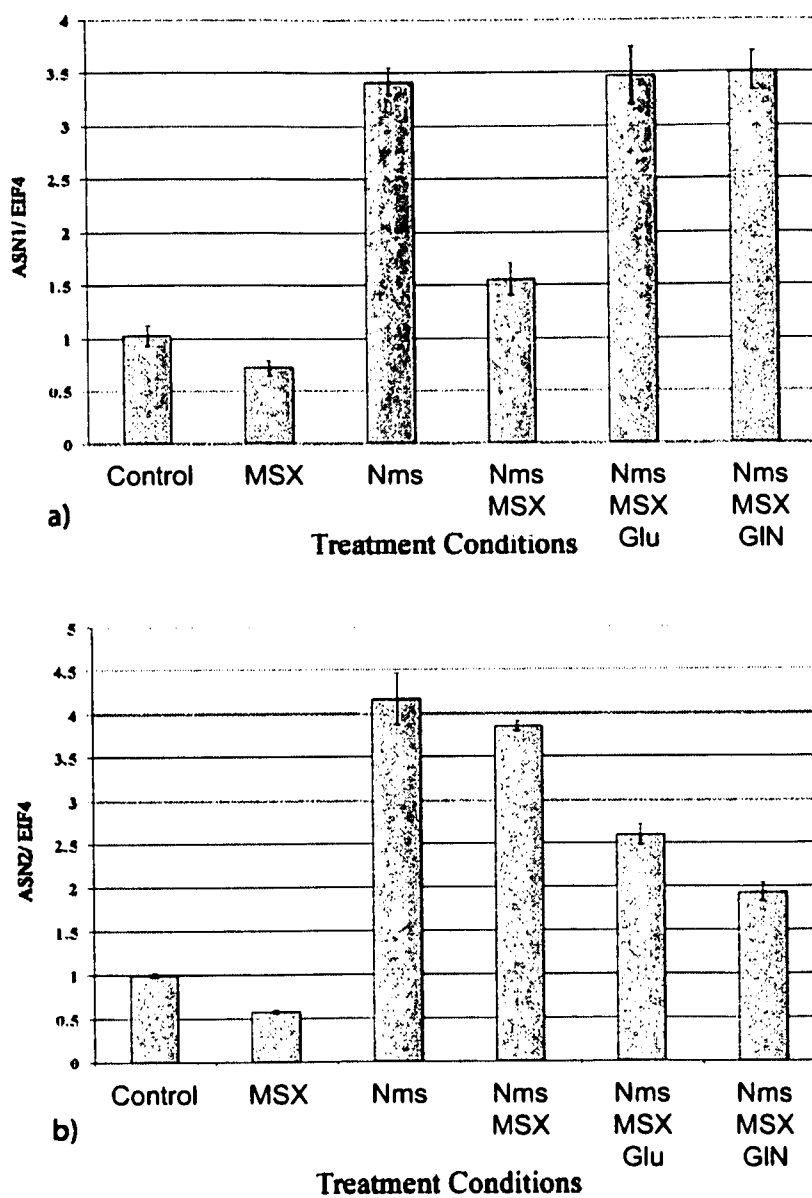
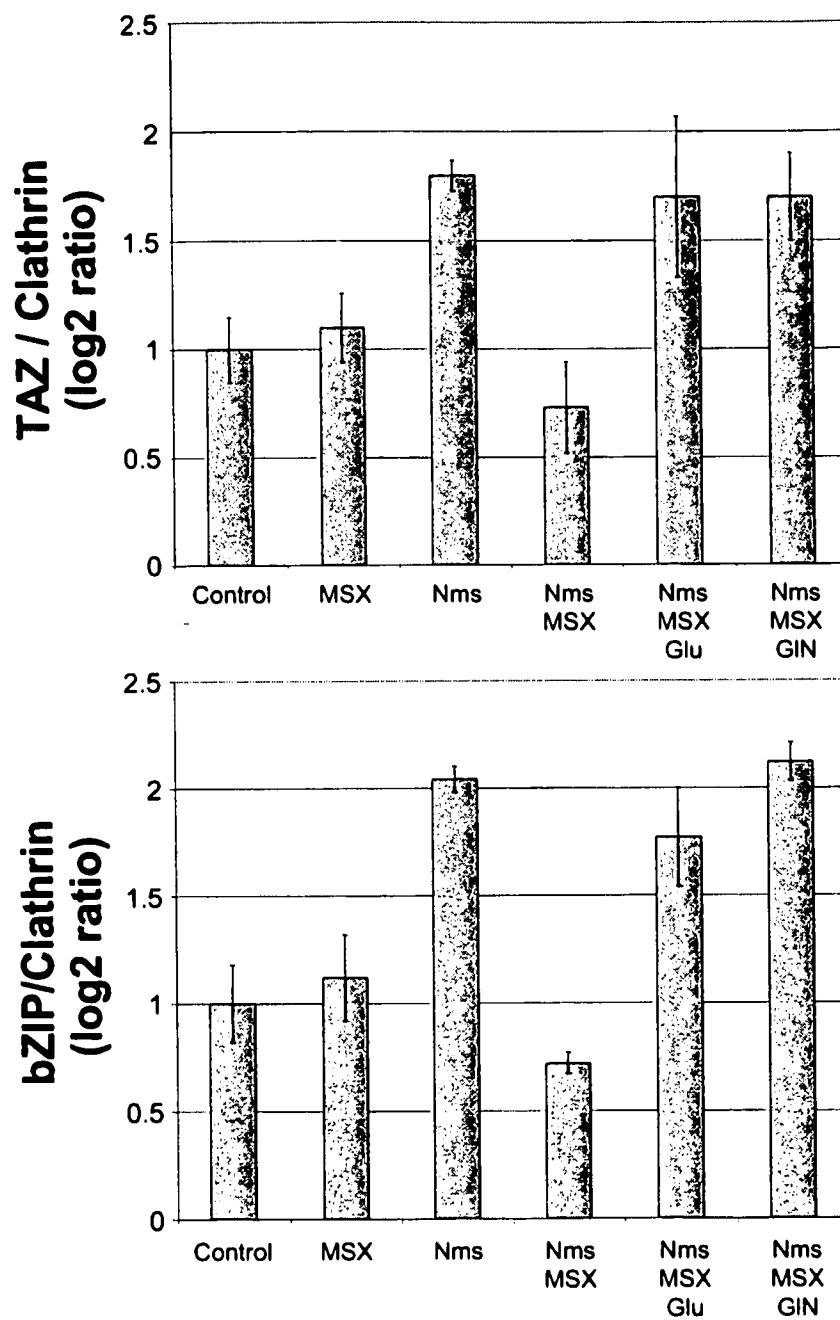
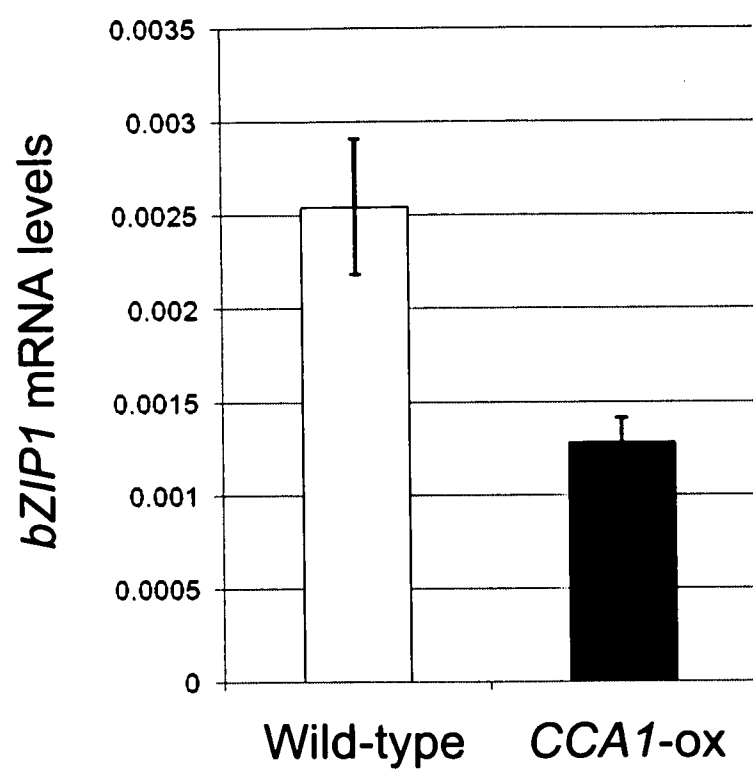
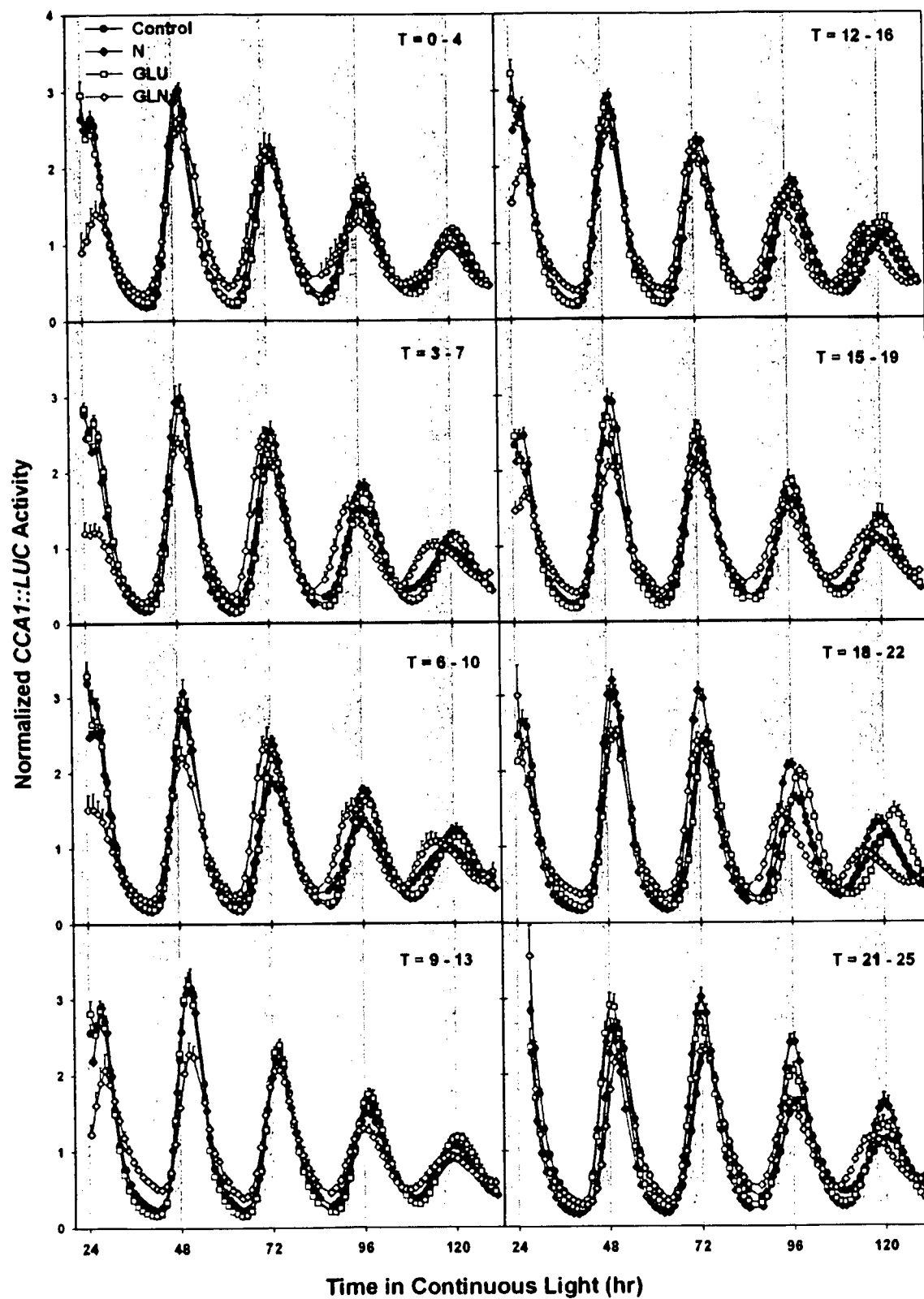


FIGURE 7

**FIGURE 8**

**FIGURE 9**

**FIGURE 10**

**FIGURE 11**

CCA1/GLK1/BZIP transcription factors coordinate the nitrogen regulation of genes in N-assimilation pathway

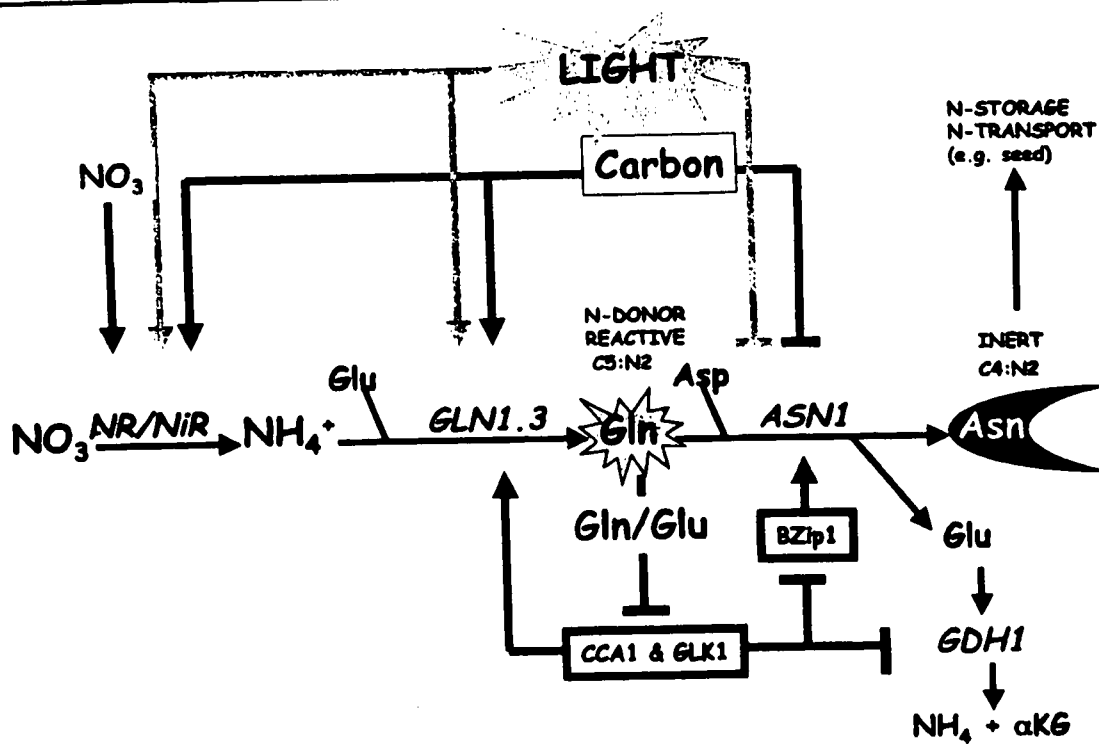


FIGURE 12

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 08/03813

A. CLASSIFICATION OF SUBJECT MATTER

IPC(8) - C12N 15/82; A01H 1/00 (2008.04)

USPC - 800/278, 435/419, 435/320.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

USPC - 800/278, 435/419, 435/320.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

USPC - 800/278, 435/419, 435/320.1

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

WEST, DialogWEB, Google Scholar, PubMed - Search Terms Used: glk, glk1, golden 2-like genes, glucokinase, gene, nitrogen, nitrate, urea, plant, assimilate, mutate, express, promoter, frameshift, functional protein, cca1, bzip1, growth, yield, biosynthesis, improve, EF156463, At2g20570

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 5,955,651 A (Coruzzi et al.) 21 September 1999 (21.09.1999) col 5 ln 26-34, col 15 ln 35-40, abstract, entire document	1-19, 21-33
Y	"GLK gene pairs regulate chloroplast development in diverse plant species" by Fitter et al. (Fitter) The Plant Journal (2002) 31(6), 713-727. 714 col 2 end of first paragraph	1, 2, 9-11, 13-17, 21-26, 30-33
Y	US 6,388,172 B1 (Tobin et al.) 14 May 2002 (14.05.2002), col 12, ln 62-65, col 14, ln 57 - col 15, ln 1	2, 10, 11, 13, 14, 17, 22, 25, 26, 30, 32, 33
Y	"Sucrose-specific signaling represses translation of the Arabidopsis ATB2 bZIP transcription factor gene" by Rook et al. (Rook) The Plant Journal (1998) 15(2) 253-263. page 254 second and third paragraphs	3-12, 14-16, 18, 19, 23-33

☐ Further documents are listed in the continuation of Box C.


* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

19 June 2008 (19.06.2008)

Date of mailing of the international search report

27 JUN 2008

Name and mailing address of the ISA/US

Mail Stop PCT, Attn: ISA/US, Commissioner for Patents

P.O. Box 1450, Alexandria, Virginia 22313-1450

Facsimile No. 571-273-3201

Authorized officer:

Lee W. Young

PCT Helpdesk: 571-272-4300

PCT OSP: 571-272-7774

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 08/03813

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☒ Claims Nos.: 20, 34-47
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.